2012 International Society for Disease Surveillance Conference

Expanding Collaborations to Chart a New Course in Public Health Surveillance

The International Society for Disease Surveillance held its eleventh annual conference in San Diego on December 4th and 5th, 2012, under the theme *Expanding Collaborations to Chart a New Course in Public Health Surveillance*. During these two days, practitioners and researchers across many disciplines gathered to share best practices, lessons learned and cutting edge approaches to timely disease surveillance. A record number of abstracts were received, reviewed and presented – the schedule included 99 orals, 4 panels, 94 posters, 5 roundtables and 12 system demonstrations. Presenters represented 24 different countries from Africa, North and South America, Europe, and Asia . Topics covered included, but were not limited to, statistical methods for outbreak detection, border health, data quality, evaluation of novel data streams, influenza surveillance, best practices and policies for information sharing, social network analysis, data mining techniques, surveillance during weather events and mass gatherings, syndrome development, and novel uses of syndromic surveillance data. There were also discussions on the impact of regulations and standards development on disease surveillance, including Meaningful Use and the International Health Regulations.

The 2012 Conference was also host to several exciting keynote and plenary talks, including those given by James Fowler, Professor of Medical Genetics and Political Science at the University of California, San Diego and Bill Davenhall, Global manager of Esri's Health and Human Service Solutions Group. Plenary speakers Steve Waterman, Centers for Disease Control and Prevention (CDC); Simon Hay, University of Oxford; and Brian McCloskey, Health Protection Agency in London, reflected on the importance of effective collaborations in their respective topics of migrant and border health, malaria disease epidemiology and mass gathering health. National and international representatives from the CDC, the World Health Organization and the Department of Homeland Security also discussed their respective strategic plans for disease surveillance.

In addition, the 2012 Data Visualization Event enabled conference attendees to collaborate and gain knowledge of visualization tools and techniques applied to a rich, de-identified set of ambulatory electronic health record (EHR) data. Participants developed visualizations of chronic disease events using this common data set and presented their work during the evening poster session. The goals for this event were to demonstrate and share visualization tools and techniques that attendees could learn to apply to their own data and also to provide exposure to data elements available in ambulatory EHR systems and highlight their potential for surveillance and research.

My hope is that attendees of the 2012 ISDS Conference strengthened existing collaborations and fostered new ones, and returned to their places of work or study energized with new ideas and approaches to disease surveillance. The challenge for all of us is to sustain this new energy throughout the coming year and to leverage the tools available to us to share best practices and reach out for assistance when needed. We all want to improve the health of our populations, and collaborations will enable us to achieve that goal.

A. Ising
Carolina Center for Health Informatics,
Department of Emergency Medicine, School of Medicine,
University of North Carolina at Chapel Hill, Chapel Hill, NC, USA;
2012 ISDS Scientific Program Committee Chair

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

ISDS
INTERNATIONAL SOCIETY FOR DISEASE SURVEILLANCE

2012 ISDS Annual Conference Abstracts

10 **Case Based Surveillance for Measles in Lagos, South Western Nigeria, September 2011**
Olawunmi O. Adeoye, Abimbola Aman-Oloniyo, Patrick Nguku, Abiola Oduneye and Modupe Dawodu

11 **BioSense Enhanced Surveillance; 2012 U.S. Mid-Atlantic Power Outage and Heat Wave**
Loren K. Akaka, Matthew Miller, Paul McMurray, Soyoun Park and Achintya N. Dey

12 **Detection of a Swine Erysipelas Outbreak Using Enhanced Passive Surveillance**
Judy Akkina, Wolf Weber and Lisa Becton

13 **One World, One Health, One Medicine: An Assessment of Intersectoral Collaboration in Avian Influenza Control in Lagos State**
Abimbola Aman-Oloniyo, Olalekan Allison and Musbau A. Razaq

14 **Using Cultural Modeling to Inform a NEDSS-Compatible System Functionality Evaluation**
Olympia Anderson and Miguel Torres-Urquidy

15 **Syndromic Surveillance for Outbreak Detection and Investigation**
Tom Andersson, Pär Bjelkmar, Anette Hulth, Johan Lindh, Stephan Stenmark and Mikael Widerström

16 **National Collaborative for Bio-Preparedness**
Meredith Arasaratnam, David Potenziani, Marc Hoit, Colleen Jenkins, and Charles Cairns,

17 **Can We Use Syndromic Surveillance Data to Identify Primary Care Visits to NYC EDs?**
Jessica Athens

18 **Enhanced Disease Surveillance during the 2012 Republican National Convention, Tampa, FL**
David Atrubin, Michael Wiese, Rebecca Snider, Kiley Workman and Warren McDougle

19 **Using GI Syndrome Data as an Early Warning Tool for Norovirus Outbreak Activity**
Erin E. Austin, Jun Yang and Tim Powell

20 **MoH+: A Global, Integrated, and Automated View of Official Outbreak Reporting**
Chi Bahk,, David Scales, Sumiko Mekaru,, John S. Brownstein,, and Clark Freifeld

21 **Evaluation of Cholera and Other Diarrheal Disease Surveillance System, Niger State, Nigeria-2012**
Adebobola T. Bashorun, Anthony Ahumibe, Saliman Olugbon, Patrick Nguku and Kabir Sabitu

22 **New Strategy and Innovative Projects at the National Biosurveillance Integration Center**
Steven Bennett and Teresa Quitugua

23 **Evaluation of Heat-related Illness Surveillance Based on Chief Complaint Data from New Jersey Hospital Emergency Rooms**
Michael Berry, Jerald Fagliano, Stella Tsai, Katharine McGreevy, Andrew Walsh and Teresa Hamby

24 **Refactoring INDICATOR into an Advanced Information System for One Health Monitoring**
Ian Brooks, Mario Felarca and Bernie A'cs

25 **Tracking Drug Overdose Trends in Ohio using ED Chief Complaints**
Alise L. Brown, William E. Storm and Brian E. Fowler

26 **Update from CDC's Public Health Surveillance & Informatics Program Office (PHSIPO)**
James Buehler, Laura Conn, Carol Crawford and Kathleen Gallagher

27 **Development of a Vietnamese Language Outbreak Mapping and Surveillance System**
David Bui, Sumiko Mekaru, Clark Freifeld, and John S. Brownstein,

28 **One Health Surveillance with Electronic Integrated Disease Surveillance System**
Alexey V. Burdakov, Andrey O. Ukharov and Thomas G. Wahl

29 **Coverage and Timeliness of Combined Military and Veteran Surveillance Systems**
Howard S. Burkom, Yevgeniy Elbert, Carla Winston, Julie Pavlin, Cynthia Lucero-Obusan and Mark Holodniy

30 **Refinement of a Population-Based Bayesian Network for Fusion of Health Surveillance Data**
Howard Burkom, Yevgeniy Elbert, Liane Ramac-Thomas, Christopher Cuellar and Vivian Hung

31 **Use of Syndromic Data to Determine Oral Health Visit Burden on Emergency Departments**
Howard Burkom, Sherry Burrer, Laurie Barker, Valerie Robison, Peter Hicks and Amy Ising

32 **Localized Cluster Detection Applied to Joint and Separate Military and Veteran Subpopulations**
Howard Burkom, Yevgeniy Elbert, Carla Winston, Julie Pavlin, Cynthia Lucero-Obusan and Mark Holodniy

33 **Nontraumatic Oral Health Classification for Alternative Use of Syndromic Data**
Sherry Burrer, Howard Burkom, Christopher Okunseri, Laurie Barker and Valerie Robison

34 **Increasing Mild Enterovirus Cases Provides An Important Signal of Up-coming Trends in Elevating Severe Enterovirus Cases**
Ta-Chien Chan, Rung-Hung Chen and Chwan-Chuen King

36 **Evaluation of Emergency Department Data Quality following PHIN Syndromic Surveillance Messaging Guide**
Hwa-Gan Chang, Charlene Weng, Charlie DiDonato, Dave DiCesare, Jian-Hua Chen and Debra Blog

37 **BioSense 2.0**
Kelley G. Chester

38 **Evaluation of the Pyrrolizidine Alkaloid Induced Liver Disease (PAILD) Active Surveillance System in Tigray, Ethiopia**
Cindy Chiu, Danielle Buttke, Girmay Welde, Richard Luce, Asfaw Debela, Amsalu Bitew, Tesfaye Bayleyegn, Sara Vagi, Matthew Murphy, Daniel Woldemichael, Teshale Seboxa, Gidey G. Libanos, Zeyeda Beyene, Yohannes G. Hawaria, Daddi Jimma, Isra

39 **Multiagent Simulation of the Hepatitis B Epidemic Process**
Tetyana Chumachenko, Dmytro Chumachenko and Olexandr Sokolov

40 **Flu Near You: An Online Self-reported Influenza Surveillance System in the USA**
Rumi Chunara, Susan Aman, Mark Smolinski and John S. Brownstein,

41 **Use of BioSense for Rapid Assessment of the Safety of Medical Countermeasures**
Ralph J. Coates and Kathleen Gallagher

42 **Tweeting Fever: Are Tweet Extracts a Valid Surrogate Data Source for Dengue Fever?**
Jacqueline S. Coberly, Clayton R. Fink, Eugene Elbert, In-Kyu Yoon, John M. Velasco, Agnes Tomayo, V. Roque, S. Ygano, Durinda Macasoco and Sheri Lewis

43 **User Experience of the U.S. Department of Defense (DoD) Respiratory Disease Dashboard**
Jennifer A. Cockrill, Alice Y. Tsai, Timothy C. Campbell, Jean-Paul Chretien, Julie A. Pavlin and Ronald L. Burke

44 **S&I Public Health Reporting Initiative: Improving Standardization of Surveillance**
Michael Coletta, Nikolay Lipskiy, David Birnbaum and John Abellera

45 **An ISDS-Based Initiative for Conventions for Biosurveillance Data Analysis Methods**
Michael Coletta, Howard Burkom, Jeffrey Johnson and Wendy Chapman

46 **Disease Models for Event Prediction**
Courtney D. Corley and Laura Pullum

47 **CaseFinder: A Flexible Real-time Online Surveillance Registry for Infectious Disease Physicians to Report Cases of Carbapenem-resistant Enterobacteriaceae (CRE)**
Donald Curtis, Scott Weissman, Dimitri Drekonja, Susan Beekmann, Benjamin Buckmaster, John Lynch, April Abbott, Ferric Fang and Philip Polgreen

48 **Public Health Surveillance in Pilot Drinking Water Contamination Warning Systems**
Chrissy Dangel, Steven C. Allgeier, Darcy Gibbons and Adam Haas

49 **Biosurveillance Ecosystem (BSVE) Workflow Analysis**
Timothy Dasey, Hayley Davison Reynolds, Nancy Nurthen, Christopher Kiley and John Silva

50 **Biosurveillance Adaptable Framework for Teaming, Exploration and Reuse (BioAFTER)**
Timothy Dasey and Lars Fiedler

51 **State Foodborne Illness Surveillance and Response Laws: Compilation and Analysis**
Stephanie David, Jenna Burton, Chris Chadwick and Rebecca Katz

52 **A System for Surveillance Directly from the EMR**
Richard F. Davies, Jason Morin, Ramanjot S. Bhatia and Lambertus de Bruijn

53 **A Grid Based Approach to Share Public Health Surveillance Applications - The R Example**
Kailah Davis and Julio Facelli,

54 **Multi-dimensional Problems in Health Settings: A Review of Approaches to Decision Making**
Victor J. Del Rio Vilas, Gilberto Montibeller, L. Alberto Franco and Willy Aspinall

55 **Computerized Text Analysis to Enhance Automated Pneumonia Detection**
Sylvain DeLisle, Tariq Siddiqui, Adi Gundlapalli, Matthew Samore, and Leonard D'Avolio,

56 **A Systematic Evaluation of Data Streams for Global Disease Surveillance**
Alina Deshpande, Mac Brown, Lauren Castro, William B. Daniel, Eric N. Generous, Andrea Hengartner, Kristen Margevicius and Kirsten Taylor-McCabe

57 **Challenges and Opportunities in Routine Time Series Analysis of Surveillance Data**
Isabelle Devaux, Esther Kissling, Gilles Desve, Frantiska Hruba, Francisco Luquero, Chantal Quinten, Joana Gomes-Diaz, Marta Valenciano and Denis Coulombier

58 **Evaluating Usefulness of Maine's Syndromic Surveillance System for Hospitals, 2012**
Stefanie DeVita and Amy Robbins

59 **Mental Illness and Co-morbid Conditions: BioSense 2008 - 2011**
Achintya N. Dey, Anna Grigoryan, Soyoun Park, Stephen Benoit and Taha Kass-Hout

60 **Enhanced Surveillance during the Democratic National Convention, Charlotte, NC**
Lana Deyneka, Amy Ising and Meichun Li

61 **LOINC and SNOMED CT Code Use in Electronic Laboratory Reporting—US, 2011**
Sanjaya Dhakal, Sherry L. Burrer, Carla A. Winston, Mathew Miller and Samuel L. Groseclose

62 **Towards Interoperability for Public Health Surveillance: Experiences from Two States**
Brian E. Dixon, Jason A. Siegel, Tanya V. Oemig and Shaun J. Grannis,

63 **Towards Estimation of Electronic Laboratory Reporting Volumes in a Meaningful Use World**
Brian E. Dixon, Roland E. Gamache, and Shaun J. Grannis,

64 **State and Local Health Agency Engagement in HIE: A Cross-Sectional Survey**
Brian E. Dixon, Roland E. Gamache, and Shaun J. Grannis,

65 **Improving ILI Surveillance using Hospital Staff Influenza-like Absence (ILA)**
Lydia Drumright, Simon D. Frost, Mike Catchpole, John Harrison, Mark Atkins, Penny Parker, Alex J. Elliot, Douglas M. Fleming and Alison H. Holmes,

66 **Multiple Source Spatial Cluster Detection Through Multi-criteria Analysis**
Luiz H. Duczmal, Alexandre C. L. Almeida, Fabio R. da Silva and Martin Kulldorff

67 **Influenza Forecasting with Google Flu Trends**
Andrea F. Dugas, Mehdi Jalalpour, Yulia Gel, Scott Levin, Fred Torcaso, Takeru Igusa and Richard Rothman

68 **Synergies Between Human and Animal Health Syndromic Surveillance: Triple-S Outputs**
Céline Dupuy, Jean-Baptiste Perrin, Anne Bronner, Didier Calavas, Pascal Hendrikx and Anne Fouillet

69 **International Collaboration for Improved Public Health Emergency Preparedness and Response in India**
Obaghe Edeghere, Giri Shankar, Alastair Bartholomew, SriKrishna Ramachandra, Vivek Singh, Pradeep Banandur, Linda Parr, Kenny Yap, Babatunde Olowokure and Sue Ibbotson

70 **Evaluation of Clinical and Administrative Data to Augment Public Health Surveillance**
Joseph R. Egger, Brooks Lowe, Erica Johnson, Randy Durbin, Erica Griffin, Sanjaya Dhakal, Achintya Dey and Sam Groseclose

71 **Utility of System Generated Syndromic Surveillance Alerts to Detect Reportable Disease Outbreaks**
Carrie Eggers, Aaron Kite-Powell and Janet Hamilton

72 **Operational Experience: Integration of ASPR Data into ESSENCE-FL during the RNC**
Carrie Eggers, Dina Passman, Aaron Chern, Dara Spector, Aaron Kite-Powell, Tim Davis, Wayne Loschen, Joe Lombardo, Douglas Char and Janet Hamilton

73 **Category-Specific Comparison of Univariate Alerting Methods for Biosurveillance Decision Support**
Yevgeniy Elbert, Vivian Hung and Howard Burkom

74 **Statistical Models for Biosurveillance of Multiple Organisms**
Doyo G. Enki, Angela Noufaily, C. P. Farrington, Paul H. Garthwaite, Nick Andrews, André Charlett and Chris Lane

76 **Identification and Assessment of Public Health Surveillance Gaps under the IHR (2005)**
Ngozi Erondu, Betiel Hadgu Haile, Lisa Ferland, Meeyoung Park, Affan Shaikh, Heather Meeks and Scott JN McNabb

77 **Incorporation of School Absenteeism Data into the Maryland Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE)**
Zachary Faigen, Anikah Salim and Isaac Ajit

78 **Using the Flow of People in Cluster Detection and Inference**
Sabino J. Ferreira, Francisco S. Oliveira, Ricardo Tavares and Flavio R. Moura

79 **A Biosurveillance-driven Home Score to Guide Strep Pharyngitis Treatment**
Andrew Fine, Victor Nizet and Kenneth Mandl,

80 **SurSaUD® Software: A Tool to Support the Data Management, the Analysis and the Dissemination of Results from the French Syndromic Surveillance System**
Anne Fouillet, Nelly Fournet, Nadege Caillère, Arnaud Musset, Lucas Mercier, Cécile Durand, Céline Caserio-Schönemann and Loic Josseran

81 **Towards Linking Anonymous Authorship in Casual Sexual Encounter Ads**
Jason A. Fries, Alberto M. Segre and Philip M. Polgreen

82 **A Review of Evaluations of Electronic Event-based Biosurveillance Systems**
Kimberly Gajewski, Jean-Paul Chretien, Amy Peterson, Julie Pavlin and Rohit Chitale

83 **U.S. Dept. Veterans Affairs (VA) SMEC-bio Reporting for Leadership Decision Support**
Shantini D. Gamage, Loretta A. Simbartl, Stephen M. Kralovic, Katherine S. Wallace and Gary A. Roselle,

84 **Evaluating Biosurveillance System Components using Multi-Criteria Decision Analysis**
Eric Nicholas Generous, Alina Deshpande, Mac Brown, Lauren Castro, Kristen Margevicius, William Brent Daniel and Kirsten Taylor-McCabe

85 **Parametric Uncertainty in Intra-Herd Foot-and-Mouth Disease Epidemiological Models**
Eric Nicholas Generous

86 **#wheezing: A Content Analysis of Asthma-Related Tweets**
Gwendolyn Gillingham, Michael A. Conway, Wendy W. Chapman, Michael B. Casale and Kathryn B. Pettigrew

87 **Using Google Dengue Trends to Estimate Climate Effects in Mexico**
Rebecca T. Gluskin, Mauricio Santillana and John S. Brownstein,

88 **An Experimental Study Using Opt-in Internet Panel Surveys for Behavioral Health Surveillance**
Carol A. Gotway Crawford, Catherine A. Okoro, Haci M. Akcin and Satvinder Dhingra,

89 **Advancing Surveillance Outside the USA: The Canadian Policy, Practice, and Research Context**
Effie Gournis, and David Buckeridge,

90 **Using Information Entropy to Monitor Chief Complaint Characteristics and Quality**
Shaun Grannis, Brian Dixon, Yuni Xia and Jianmin Wu,

92 **The Epidemiologic Vocabulary of the West and the Former Soviet Union: Different Sides of the Same Science**
Anna Grigoryan, Carmen Clarke, Lyudmila Zueva, Tetyana Chumachenko, Edmond F. Maes and Bonnie Smoak

93 **Co-morbidity Factors Associated with Influenza in Nigeria**
Aishatu B. Gubio, Saka J. Muhammad, Aisha Mamman, Ado Zakari and Oladayo Biya

94 **Extracting Surveillance Data from Templated Sections of an Electronic Medical Note: Challenges and Opportunities**
Adi Gundlapalli, Guy Divita, Marjorie Carter, Shuying Shen, Miland Palmer, Tyler Forbush, Brett South, Andrew Redd, Brian Sauer, and Matthew Samore,

95 **Paralysis Analysis: Investigating Paralysis Visit Anomalies in New Jersey**
Teresa Hamby, Stella Tsai, Carol Genese, Andrew Walsh, Lauren Bradford and Edward Lifshitz

96 **Implications of ICD-9/10 CM Transition for Public Health Surveillance: Challenges, Opportunities, and Lessons Learned from Multiple Sectors of Public Health**
Peter Hicks and Atar Baer

97 **Processing of Novel Electronic Health Data to Support Public Health Surveillance**
Peter Hicks, Henry Rolka, Mark Wooster and Lynette Brammer

98 Disease Surveillance and Achieving Synergy In Public Health Quality Improvement
Peggy A. Honoré and Laura C. Streichert

99 Serum Zinc Concentration and Acute Diarrhea in Children from Different Regions of Uzbekistan
Gulnara A. Ibadova, T. A. Merkushina, E. S. Abdumutalova and Aybek V. Khodiev

100 A Binational Influenza Surveillance Network – California/Baja California
Esmeralda Iniguez-Stevens, Sarah Marikos and Karen Ferran

101 The Activity of Rabies Vaccines against Genetic Clusters of Rabies Virus Circulating at the Territory of Ukraine
Mykola Ivanov, Ivan Polupan and Oleg Deryabin

102 Determinants of Outbreak Detection Performance
Nastaran Jafarpour, Doina Precup and David Buckeridge

103 An Algorithm That Identifies Coronary and Heart Failure Events In The Electronic Health Record
Jawali Jaranilla, Thomas E. Kottke and Courtney J. Baechler

104 Using Syndromic Emergency Department Data to Augment Oral Health Surveillance
John P. Jasek, Nicole Hosseinipour, Talia Rubin and Ramona Lall

105 Recommendations for Syndromic Surveillance Using Inpatient and Ambulatory EHR Data
Geraldine Johnson, Charles Ishikawa, Rebecca Zwickl, Maiko Minami, Taha Kass-Hout and Laura Streichert

106 Use of Syndromic Surveillance Information for Expanded Assessment of Wildfire Disaster
Jeffrey Johnson, Michele Ginsberg, Nancy French, Brian Thelen and Benjamin Koziol

107 Monitoring the Impact of Heat Waves with Emergency Service Utilization Data in Los Angeles County
Emily Kajita, Patricia Araki, Monica Luarca and Bessie Hwang

108 ILI and SARI Surveillance along the California & Arizona Borders with Mexico, 2011-12
Pete Kammerer, Gary Brice, Anthony Hawksworth and Chris Myers

109 EIDSS Application for CCHF Foci Activity Epi-Analysis and Prediction in Kazakhstan
Stanislav V. Kazakov, Alexey V. Burdakov, Kenes S. Ospanov, Aizhan S. Esmagambetova, Andrey O. Ukharov, Veronika P. Sadovskaya and Umirbek B. Usenov

110 Content Analysis of Syndromic Twitter Data
Bethany Keffala, Mike Conway, Son Doan and Nigel Collier

111 Evaluating the Variation on Public Health's Perceived Field Need of Communicable Disease Reports
Uzay Kirbiyik, Roland Gamache, Brian E. Dixon, and Shaun Grannis,

113 TRACnet: A National Phone-based and Web-based Tool for the Timely Integrated Disease Surveillance and Response in Rwanda
Kayumba Kizito, Kabeja Adeline, Koama Jean Baptiste, Asiimwe Anita, Binagwaho Agnes, Pamela Johnson and Nyatanyi Thierry

114 A Health Department's Collaborative Model for Disease Surveillance Capacity Building
Ikechi Konkwo, Robert G. Harmon, William C. Livingood, Thomas BryantIII and Saad Zaheer

115 Evaluating Syndromic Data for Surveillance of Non-infectious Disease
Ramona Lall and Marc Paladini

116 Evaluating Utility of Cold-Injury Syndromic Surveillance Data in New York City
Kathryn Lane, Ramona Lall, Katherine Wheeler, Kazuhiko Ito and Thomas Matte

117 Collaborative Automation Reliably Remediating Erroneous Conclusion Threats (CARRECT)
Jonathan C. Lansey, Paul Picciano, Ian Yohai, Fred Grant and Robert Gern

118 Potential use of multiple surveillance data in the forecast of hospital admissions
Eric H. Lau, T. L. Cheung, Dennis K.M. Ip, Eva Tsui, Edwina Shung, S. V. Lo and Benjamin J. Cowling

119 Poison Center Data for Public Health Surveillance: Poison Center and Public Health Perspectives
Royal K. Law, Josh Schier, Jay Schauben, Katherine Wheeler and Prakash Mulay

120 Surveillance for Radiation-Related Exposures Reported to the National Poison Data System
Royal K. Law, Colleen Martin, Alvin Bronstein, Arthur Chang and Joshua Schier

121 A Piece of the Public Health Surveillance Puzzle: Social Contacts among School-Aged Children
Molly Leecaster, Warren Pettey, Damon Toth, Jeanette Rainey, Amra Uzicanin and Matthew Samore

122 Time of Arrival Analysis in NC DETECT to Find Clusters of Interest from Unclassified Patient Visit Records
Meichun Li, Wayne Loschen, Lana Deyneka, Howard Burkom, Amy Ising and Anna Waller

123 Implementation of a Mobile-Based Surveillance System in Saudi Arabia for the 2009 Hajj
Wei Li

124 COPD-Related ED Visits in North Carolina: Hospitalizations and Return Visits
Steven J. Lippmann, Karin B. Yeatts, Anna Waller, Kristen Hassmiller Lich, Debbie Travers, Morris Weinberger and James F. Donohue

125 Detection of Patients with Influenza Syndrome Using Machine-Learning Models Learned from Emergency Department Reports
Arturo López Pineda, Fu-Chiang Tsui, Shyam Visweswaran and Gregory F. Cooper

126 Development of Automated Data Quality Indicators and Visualizations using Florida's ESSENCE System
Wayne Loschen and Aaron Kite-Powell

127 Sharing Public Health Information with Non-Public Health Partners
Wayne Loschen, Rekha Holtry, Kalman Hazins and Sheryl Happel Lewis

128 Evaluation of ESSENCE in the Cloud Using Meaningful Use Syndromic Surveillance Data
Wayne Loschen, William Stephens, Taha Kass-Hout, Miles Stewart, Dave Heinbaugh and Joseph Lombardo

129 Enhanced Influenza Surveillance using Telephone Triage Data in the VA ESSENCE Biosurveillance System
Cynthia A. Lucero-Obusan, Carla A. Winston, Patricia L. Schirmer, Gina Oda, Anoshiravan Mostaghimi and Mark Holodniy,

130 Sequential Bayesian Inference for Detection and Response to Seasonal Epidemics
Michael Ludkovski and Junjing Lin

131 Characteristics of Veterans Accessing the Veterans Affairs Telephone Triage Who Have Depression or Suicidal Ideation: Opportunities for Intervention
Alison Ludwig, Cynthia Lucero-Obusan, Patricia Schirmer and Mark Holodniy,

132 Enabling Syndromic Surveillance in Pakistan
Ross Maciejewski, Shehzad Afzal, Adam J. Fairfield, Arif Ghafoor, David S. Ebert, Naeem Ayyaz and Maaz Ahmed

133 The Use of the International Classification of Diseases, Ninth Revision (ICD-9) Coding in Identifying Chronic Hepatitis B Virus Infection in Health System Data: Implications for Surveillance
Reena Mahajan, Anne C. Moorman, Stephen J. Liu, Loralee Rupp, Monina Klevens and (CHeCS) for the Chronic Hepatitis Cohort Investigators,

134 Analysis of Heat Illness using Michigan Emergency Department Syndromic Surveillance
Fatema Mamou and Tiffany Henderson

135 SMART Platforms: Building The App Store for Biosurveillance
Kenneth D. Mandl

136 Disease Mapping with Spatially Uncertain Data
Justin Manjourides, Ted Cohen, Caroline Jeffery and Marcello Pagano

137 A Web-based Electronic Health Record System for National Surveillance
Jake R. Marcus

138 The Biosurveillance Resource Directory - A One-Stop Shop for Systems, Sources, and Tools
Kristen Margevicius, Mac Brown, Lauren Castro, William B. Daniel, Eric N. Generous, Kirsten Taylor-McCabe and Alina Deshpande

139 Establishment of a One Health Surveillance Initiative in the CA/Baja CA Border Region
Sarah C. Marikos, Karen L. Ferran, Esmeralda Iniguez-Stevens and Francisco Javier Monge Navarro

140 Raccoons in San Diego County as Sentinels for West Nile Virus Surveillance
Sarah C. Marikos, Karen L. Ferran, Esmeralda Iniguez-Stevens and Nikos Gurfield

141 Risk of Cardiovascular Morbidity and Mortality in Relation to Temperature
Robert Mathes, Kazuhiko Ito and Thomas Matte

142 Surveillance of Heat-related Morbidity: Relation to Heat-related Excess Mortality
Robert Mathes, Kristina B. Metzger, Kazuhiko Ito and Thomas Matte

143 A Syndromic Approach to Emergency Department Surveillance for Skin and Soft Tissue Infections
Larissa May, Marcus Rennick, Leah Gustafson and Julia Gunn

144 The Surveillance Window – Contextualizing Data Streams
Kirsten McCabe, Lauren Castro, Mac Brown, William Daniel, Eric Nick Generous, Kristen Margevicius and Alina Deshpande

145 Enhancing Surveillance for Arboviral Infections in the Arizona Border Region
Orion McCotter, Frank Vanskike, Kacey Ernst, Ken Komatsu, Harold Margolis, Stephen Waterman, Laura Tippit, Kay Tomashek, Anne Wertheimer, Sonia Montiel, Catherine Golenko and Elizabeth Hunsperger

146 New Strategy to Monitor and Assess Laboratory Biosafety Programs
Heather N. Meeks, Betiel H. Haile, Ngozi A. Erondu, Lisa Ferland, Meeyoung Park and Scott J. McNabb,

147 Use of a Real-Time Syndromic Surveillance System to Improve Influenza Like Illness Screening and Documentation in Emergency Departments during the H1N1 Pandemic
David Meurer, and James Talbot,

148 Mining Surveillance Data: Does Radiation Treatment of Prostate Cancer Cause Rectal Cancer?
John W. Morgan, Brice Jabo, Mark E. Ghamsary and Kevork Kazanjian

149 Using Surveillance Data to Identify Risk Factors for Severe H1N1 in First Nations
Kathryn Morrison, Yanyu Xiao, Seyed Moghadas and David Buckeridge

150 A Framework for Detecting and Classifying Outbreaks of Gastrointestinal Disease
Kathryn Morrison, Katia Charland, Anya Okhmatovskaia and David Buckeridge

151 Evaluating a Social Network Analytic Tool to Support Outbreak Management and Contact Tracing in an Outbreak of Pertussis
Esther Munene, S. Mottice and J. Reid

153 Evaluation of Integrated Disease Surveillance and Response (IDSR) using Bacillary Dysentery as a Priority Disease, Tanzania, 2012
Alfred G. Mwanyika, Senga Sembuche and Agricola Joachim

154 Content Analysis of Tobacco-related Twitter Posts
Mark Myslín, Shu-Hong Zhu and Michael Conway

155 Malaria Trends in Six Outpatient Sites in Uganda, 2008—2011
Ruth K. Nassali, Arthur Mpimbaza, Stella Kakeeto, Asadu Sserwanga, Fred Kizito, Denis Rubahika, Melody Miles, Michelle Chang, Grant Dorsey and Moses Kamya

156 Fast Multidimensional Subset Scan for Outbreak Detection and Characterization
Daniel B. Neill and Tarun Kumar

157 Tau-leaped Particle Learning
Jarad Niemi and Michael Ludkovski

158 An Improved Algorithm for Outbreak Detection in Multiple Surveillance Systems
Angela Noufaily, Doyo Enki, Paddy Farrington, Paul Garthwaite, Nick Andrews and Andre Charlett

159 Who's Not Coming to Dinner? Evaluating Trends in Online Restaurant Reservations for Outbreak Surveillance
Elaine O. Nsoesie, David L. Buckeridge and John S. Brownstein,

160 Improvement Control System of Rabies in Ukraine
Serhiy Nychyk, Ostap Zhukorskiy, Ivan Polupan, Mykola Ivanov and Alina Nikitova

161 The Natural Reservoirs of Salmonella Enteritidis in Populations of Wild Birds
Olga Obukhovska

162 Estimation of Influenza Incidence by Age in the 2011/12 Seasons in Japan using SASSy
Yasushi Ohkusa, Yoshinori Yasui, Tamie Sugawara, Nobuhiko Okabe, Kiyosu Taniguchi and Kazunori Oishi

163 Defining Public Health Situation Awareness – Outcomes and Metrics for Evaluation
Don Olson, Rob Mathes, Marc Paladini and Kevin Konty

164 Syndromic Surveillance from a Local Perspective – A Review of the Literature
Don Olson, Kevin Konty, Rob Mathes and Marc Paladini

165 Open Source Health Intelligence (OSHINT) for Foodborne Illness Event Characterization
Catherine Ordun, Jane W. Blake, Nathanael Rosidi, Vahan Grigoryan, Christopher Reffett, Sadia Aslam, Anastasia Gentilcore, Marek Cyran, Matthew Shelton and Juergen Klenk

166 A Binational Model of Collaboration for Enhancing Cross-border ID Surveillance
Kristine Ortwine, Karen Ferran and Esmeralda Iniguez-Stevens

167 FSWs Typology and Condoms Use Among HIV High Risk Groups in Sindh, Pakistan: A Developing Country Perspective
Suleman M. Otho, Shazia Perveen and Qamar Abbas

168 Effectiveness of the 2011-12 Influenza Vaccine: Data from US Military Dependents and US-Mexico Border Civilians
Damaris Padin, Anthony Hawksworth, Peter Kammerer, Erin McDonough and Gary Brice

169 Using Change Point Detection for Monitoring the Quality of Aggregate Data
Ian Painter, Julie Eaton and Bill Lober

170 Differentiating ZIP Codes in Syndromic Data; What Can They Tell Us?
Marc Paladini, Romona Lall and Stephen E. Schachterle

171 Establishing a Federal and State Data Exchange Pilot for Public Health Situational Awareness
Dina B. Passman, Aaron Kite-Powell, Dara Spector, Wayne Loschen, Barry Harp, Aaron Chern, Janet Hamilton, Cary Eggers and Joseph Lombardo

172 Fusion Analytics: A Data Integration System for Public Health and Medical Disaster Response Decision Support
Dina B. Passman

173 Using Cloud Technology to Support Monitoring During High Profile Events
Megan Patel, Enyinnaya Adighibe, Joseph Lombardo, Wayne Loschen, Miles Stewart and Michael O. Vernon

174 Comparing Prescription Sales, Google Trends and CDC Data as Flu Activity Indicators
Avinash Patwardhan and David Lorber

175 HIV Surveillance in India: An Overview & Implications for Future
Divya Persai

176 Comparing Syndromic Surveillance and Poison Center Data for Snake Bites in Missouri
Karen H. Pugh, Amy Kelsey and Rebecca Tominack,

177 Modeling Baseline Shifts in Multivariate Disease Outbreak Detection
Jialan Que and Fu-Chiang Tsui

178 Extraction of Disease Occurrence Patterns Using MiSTIC: Salmonellosis in Florida
Vipul Raheja and K. S. Rajan

179 Traditional and Mobile Public Health Alert Communications with Health Care Providers
Debra Revere, Ian Painter and Janet Baseman

180 Collaboration for Improved Disease Surveillance Literature Review
Tera Reynolds, Katie Suda, Blaine Reeder, William Storm, Al Ozonoff and Howard Burkom

181 Data Quality: A Systematic Review of the Biosurveillance Literature
Tera Reynolds, Ian Painter and Laura Streichert

182 Detecting the Determinants of Health in Social Media
Caitlin Rivers, Bryan Lewis and Sean Young

183 Searching for Complex Patterns Using Disjunctive Anomaly Detection
Maheshkumar Sabhnani, Artur Dubrawski and Jeff Schneider

184 Adapting Syndromic Surveillance Systems to Increase Value to Local Health Departments
Erika Samoff, Mary T. Fangman, Amy Ising, Lana Deyneka and Anna E. Waller

185 Surveillance-Based Program Planning
Rossi Sanusi

186 Age, Triage Score, and Disposition in Emergency Department Visit Records: Potential Utility for Prediction of Influenza-related Hospitalizations in Montreal, Canada
Noémie Savard, Lucie Bédard, Robert Allard, and David L. Buckeridge,

187 Coded Chief Complaints for Influenza-like Illness Surveillance in Montreal, Canada: Challenges in Choosing a Syndrome Definition
Noémie Savard, Lucie Bédard, Robert Allard, and David L. Buckeridge,

188 Long-Term Asthma Trend Monitoring in New York City: A Mixed Model Approach
Stephen E. Schachterle, Robert W. Mathes, Marc Paladini and Don Weiss

189 Does Antimicrobial Prescription Data Improve Influenza Surveillance in VA?
Patricia Schirmer, Carla Winston, Russell Ryono, Cynthia Lucero-Obusan, Gina Oda and Mark Holodniy,

190 Utilization of Various Data Sources to Locate West Nile Clusters in Tulsa County
Nicole Schlaefli, Kiran Duggirala and Scott Meador

191 Detecting Changes in Chief Complaint Word Count: Effects on Syndromic Surveillance
Jessica Sell, Robert Mathes and Marc Paladini

192 A Survey of Data Recording Procedures at New York City Emergency Departments
Jessica Sell and Alyssa Wong

193 Bayesian Contact Tracing for Communicable Respiratory Disease
Ayman Shalaby and Daniel Lizotte

194 SAGES Update: Electronic Disease Surveillance in Resource-Limited Settings
Lewis L. Sheri, Timothy C. Campbell, Jacqueline S. Coberly, Richard A. Wojcik, Shraddha V. Patel and Brian Feighner

195 A Novel Syndrome Definition Validation Approach for Rarely Occurring Diseases
Julio C. Silva, Shital C. Shah, Dino P. Rumoro, Marilyn M. Hallock, Gillian S. Gibbs and Michael J. Waddell

196 Adaptation of GUARDIAN for Syndromic Surveillance During the NATO Summit
Julio C. Silva, Dino P. Rumoro, Shital C. Shah, Gillian S. Gibbs, Marilyn M. Hallock, Michael Waddell and Shon Doseck

197 Using Search Volume for Surveillance of Medication Prescribing
Jacob E. Simmering, Linnea A. Polgreen and Philip M. Polgreen

198 Can Novel Flu Surveillance Be Conducted With Limited Resources?
Alan Siniscalchi and Amanda Schulte

199 Applying Zero-inflated Mixed Model to School Absenteeism Surveillance in Rural China
Xiaoxiao Song, Tao Tao, Qi Zhao, Fuqiang Yang, Palm Lars, Diwan Vinod, Hui Yuan and Biao Xu

200 When it Rains it Pours: Real-time Situational Awareness for Two Weather Emergencies in Connecticut
Kristen Soto, Jaime Krasnitski, Therese Rabatsky-Ehr and Matthew Cartter

201 Spatial Scan Statistics for Models with Excess Zeros and Overdispersion
Max Sousa de Lima, Luiz H. Duczmal and Letícia P. Pinto

202 Tracking Dynamic Water-borne Outbreaks with Temporal Consistency Constraints
Skyler Speakman, Yating Zhang and Daniel B. Neill

203 Geographical Information Systems: A Tool to Map and Analyze Disease Spread
Indumathi Srinath, Barbara Szonyi, Maria Esteve-Gassent, Blanca Lupiani, Raju Gautam, Alfonso Clavijo, Sang-shin Park and Renata Ivanek-Miojevic

204 Enabling ESSENCE to Process and Export Meaningful Use Syndromic Surveillance Data
Miles Stewart, Wayne Loschen and Taha Kass-Hout

205 Evaluation of Electronic Ambulatory Care Data for Use in the Influenza-like Illness Surveillance Network (ILINet)
Kathleen Stigi, Atar Baer and Kathy Lofy

206 Framing the Use of Social Media Tools in Public Health
Jennifer Stoll, Richard Quartarone and Miguel Torres-Urquidy

207 Novel Emergency Department High Utilizer Surveillance In New Hampshire
David J. Swenson, Cole Zanetti, Elizabeth R. Daly and Jose T. Montero

208 Selecting Targeted Symptoms/Syndromes for Syndromic Surveillance in Rural China
Li Tan, Jie Zhang, Liwei Cheng, Weirong Yan, Vinod K. Diwan, Lu Long and Shaofa Nie

209 Use of Control Bar Matrix for Outbreak Detection in Syndromic Surveillance System
Tao Tao, Qi Zhao, Huijian Cheng, Lars Palm, Xin Lu, Hui Yuan, Xiaoxiao Song and Biao Xu

210 Risk and Protective Factors for Arthritis Status and Severity
Masaru Teramoto, Fred Breukelman, Ferdinando A. Gatto and Sheniz Moonie

211 On the implementation of the Biological Threat Reduction Program in the Republic of Uzbekistan
Laziz Tuychiev and Marifjon Madaminov

212 Usefulness of Syndromic Surveillance for Early Outbreak Detection in Small Islands: The Case of Mayotte
Pascal Vilain, Olivier Maillard, Julien Raslan-Loubatie, Mohamed Ahmed Abdou, Tinne Lernout and Laurent Filleul

214 Syndromic Surveillance Based on Emergency Visits: A Reactive Tool for Unusual Events Detection
Pascal Vilain, Arnaud Bourdé, Pierre-Jean Marianne dit Cassou, Yves Jacques-Antoine, Philippe Morbidelli and Laurent Filleul

215 Advancing Surveillance of Chronic and Non-Communicable Disease—A Path Forward
Elissa R. Weitzman, and Nadia Waheed,

216 Syndromic Surveillance at the New York State Veterinary Diagnostic Laboratory
Kylius Wilkins, Bruce Akey, Belinda Thompson, and Daryl Nydam

217 The Black Canyon Forecast Station: Experiences And Lessons Learned
James M. Wilson, Bonnie Koehler, Kathleen Sramek and Treve Henwood

218 Early Detection of Influenza Activity Using Syndromic Surveillance in Missouri
Fei Wu and Amy Kelsey

219 An Integrated Syndromic Surveillance System for Monitoring Scarlet Fever in Taiwan
Wan-Jen Wu, Yu-Lun Liu, Hung-Wei Kuo, Wan-Ting Huang, Shiang-Lin Yang and Jen-Hsiang Chuang

220 The Organizational Structures and Human Resources Allocation of Infectious Disease Surveillance System in Rural China
Biao Xu, Qi Zhao, Huijian Cheng, Tao Tao, Yipin Zhu, Miao Yu and Hui Yuan

221 Using Medications Sales from Retail Pharmacies for Syndromic Surveillance in Rural China
Weirong Yan, Liwei Cheng, Li Tan, Miao Yu, Shaofa Nie, Biao Xu, Lars Palm and Vinod Diwan

222 A Bayesian Approach to Characterize Hong Kong Influenza Surveillance Systems
Ying Zhang, Ali Arab and Michael A. Stoto

223 The Distribution of Infectious Related Symptoms in an Internet-based Syndromic Surveillance System in Rural China
Qi Zhao, Fuqiang Yang, Lars Palm, Hui Yuan, Weirong Yan and Biao Xu

224 Automated Surveillance of Outpatients with Pneumonia: A Performance Evaluation
Hongzhang Zheng, Tariq Siddiqui, and Sylvain DeLisle,

225 Utility of Syndromic Surveillance Using Novel Clinical Data Sources
Rebecca Zwickl, Charles Ishikawa and Laura C. Streichert

Case Based Surveillance for Measles in Lagos, South Western Nigeria, September 2011

Olawunmi O. Adeoye*[1], Abimbola Aman-Oloniyo[2], Patrick Nguku[1], Abiola Oduneye[2] and Modupe Dawodu[2]

[1]Nigeria Field Epidemiology and Laboratory Training Programme, Abuja, Nigeria; [2]Lagos State Ministry of Health, Alausa, Ikeja, Lagos, Nigeria

Objective

The objective of this study was to describe the performance of the measles surveillance in Lagos, characterize the epidemiologic pattern of measles infection and determine the measles vaccine efficacy.

Introduction

Measles is a vaccine preventable disease that has been successfully eliminated in some parts of the world. It causes high morbidity and mortality with the potential of large outbreaks. About a third of reported measles cases involve one or more complications including diarrhea, pneumonia, otitis media, blindness, post infections encephalitis and subacute sclerosing panencephalitis. It is however, one of the leading causes of childhood morbidity and mortality in Nigeria despite availability of safe and effective vaccines

Methods

We obtained the measles surveillance data for all the 20 Local Governments Areas (LGAs) in Lagos and reviewed all the measles case based investigation forms between the period 1st January to 31st December 2010.The WHO Recommended Surveillance Standards for Measles was used. Data was analyzed using EPI INFO version 3.5.3.

Results

Of the 615 suspected measles cases, 63(10.2%) were laboratory confirmed (measles IGM+) and 3(0.5%) clinically confirmed. Cases investigated within 48 hours was 222 (36%) (target ≥ 80%), 510 (83%) had adequate blood sample collected (target ≥ 80%) and 595 (97%) of sample results were received from the lab within 7 days (target ≥ 80%). The surveillance system sensitivity was 6.5/100,000 (target >2/100,000) with a predictive value positive of 10.73%. The overall attack rate was 0.73/100,000 population with 1 mortality (case fatality rate 1.5%). The Under 1 year attack rate (8.33/100,000) was higher than the 1- 4 years attack rate (3.48/100,000) (p= 0.01). Those vaccinated with at least 1 dose of measles vaccine had a 3 times lower risk of measles infection than the unvaccinated. The proportion of unvaccinated cases was 36%. The measles vaccine efficacy was 60%.

Conclusions

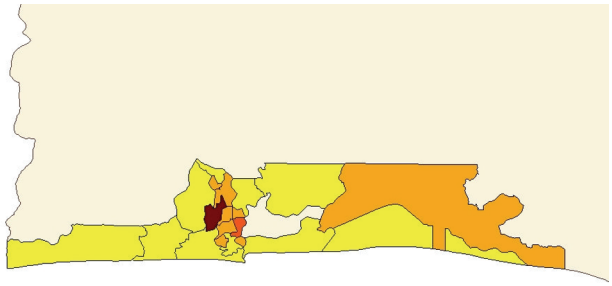
The quality of surveillance need to be strengthened by improving the time lapse between notification and investigation of suspected cases. Measles is still a significant cause of morbidity particularly among the under 1 year age group.The proportion of unvaccinated cases is also high, suggesting a low vaccine coverage among susceptibles.

Prompt investigation of cases, good vaccine coverage and high vaccine efficacy are all vital in eliminating measles from Nigeria.

Morbidity and Mortality rates

AGE GROUP	ATTACK RATES
<1 Year	8.33/100,000
1- 4 Years	3.48/100,000
5 and above	0.11/100,000
overall attack rate	0.73/100,000
CASE FATALITY RATE	1.5%

No of Reported Measles Cases in Lagos, South Western Nigeria by LGA with onset date from 1st January - 31st December 2010



Legend

Keywords

Surveillance; Measles; Case based; Lagos

Acknowledgments

Lagos State Ministry of Health, Alausa, Ikeja, Lagos.
Central Public Health Laboratory, Yaba, Lagos.
World Health Organisation, Lagos Office, Ikoyi, Lagos.

References

Kohlhagen JK et al. 2011. Meeting Measles Elimination Indicators: Surveillance Performance in a Regional Area of Australia. Western Pacific Surveillance and Response Journal,2011,2(3).

WHO.2001. Modules on Best Practisesfor Measles Surveillance. Available at www.who.int/vaccines-document. (Accessed September 2011).

WHO.2003.Recommended Standards for Surveillance of Selected Vaccine Preventable Diseases.Available at www.who.int/vaccines-document. (Accessed September 2011).

*Olawunmi O. Adeoye
E-mail: wunmiolat@yahoo.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

BioSense Enhanced Surveillance; 2012 U.S. Mid-Atlantic Power Outage and Heat Wave

Loren K. Akaka*[1], Matthew Miller[2], Paul McMurray[1], Soyoun Park[2] and Achintya N. Dey[1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA; [2]McKing Consulting Corporation, Atlanta, GA, USA

Objective

To demonstrate the ability of the BioSense system to supply timely situational awareness during large-scale natural disasters.

Introduction

BioSense is a near real-time surveillance system designed to provide national disease detection, monitoring and health situational awareness. The system currently receives data from Non-Federal hospital emergencies departments (ED) providing chief complaint and/or final diagnoses data, U.S. Department of Defense (DoD) outpatient (OP) facilities and Veterans Affairs (VA) OP facilities providing final diagnoses data.

On June 29, 2012, a multi-state thunderstorm resulted in power outages throughout the U.S. Mid-Atlantic region. In addition, a heat wave was engulfing the region with excessively high weather temperatures. The power outages and high temperatures had the potential to increase heat-related illness (HRI) in a large portion of the country.

Methods

Within 24 hours after the initial storm, the BioSense Epidemiology and Surveillance Team (BEST) initiated enhanced surveillance in Delaware, Maryland, Ohio, Pennsylvania, Virginia, Washington DC, and West Virginia. There are 164 non-Federal hospital ED, 71 DoD OP facilities and 166 VA OP facilities in the area supplying data to the BioSense system.

From June 30 to July 13, 2012, BEST monitored the BioSense 2.0 application for Heat, excessive sub-syndrome (Fig. 1) based on the following:

- For chief complaint data, definition is based on the specific keywords; ensolacion, heat, hypertermia, hyperthermia, insolacion, overheated, sobre calentado, and sobre caliente.

- For final diagnosis data, definition is based on ICD-9 codes; 992.0 - 992.9 and E900.

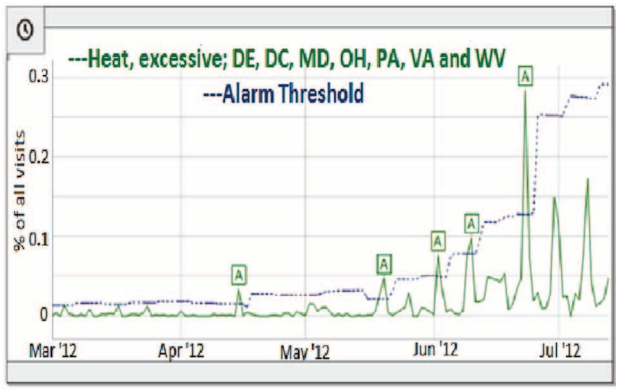
To identify clusters of patient visits of interest, BioSense 2.0 employs a modified version of the early aberration reporting system (EARS) C2 statistic [1] [2].

Results

We found 205 total HRI visits (0.34 per 1000 visits) in the area. Among the 205 visits; 123 were from non-Federal hospital ED, 56 from DoD OP facilities and 26 from VA OP facilities. Age group breakdown included 14% 0-18 years old, 39% 19-40 year old and 47% 40+ years. 133 were males (65%), 63 were female (31%) and 9 were of unknown gender (4%). None of the HRI visits were association with severe illness or death sub-syndrome.

Conclusions

The BioSense system is limited by currently receiving data from non-Federal EDs that are not a representative sample of the overall EDs in the nation. However, the results seem to indicate that BioSense is a critical and timely source of information on HRI that could be used to track morbidity and inform public health interventions during large-scale natural disasters.



Keywords

Surveillance; Situational awareness; Heat-related illness; Natural disasters

References

[1] Tokars JI, Burkom H, Xing J, et al. Enhancing time series detection algorithms for automated biosurveillance. Emerg Infect Dis 2009;15:533-9.

[2] BioSense 2.0 Analytics Aberration Detection Algorithms. (2012). Retrieved August 1, 2012, from https://docs.google.com/viewer?a=v&pid=sites&srcid=ZGVmYXVsdGRvbWFpbnxiaW9zZW5zZXJlZGVzaWdufGd4OjVmYzExMTgyMjUxZDhiYWY

*Loren K. Akaka
E-mail: gng0@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Detection of a Swine Erysipelas Outbreak Using Enhanced Passive Surveillance

Judy Akkina*[1], Wolf Weber[1] and Lisa Becton[2]

[1]USDA, APHIS, Veterinary Services, Fort Collins, CO, USA; [2]National Pork Board, Des Moines, IA, USA

Objective

To describe detection and response for an erysipelas outbreak in market swine in the United States (U.S.) using Food Safety and Inspection Service (FSIS) slaughter condemnation data, and coordination with the swine industry in an Enhanced Passive Surveillance (EPS) pilot project.

Introduction

EPS is a comprehensive effort to complement other types of surveillance and provide early detection and situational awareness of significant endemic, zoonotic, and emerging diseases of livestock. The concept for EPS involves gathering syndromic and observational data from multiple animal health surveillance sources, including private practitioners, livestock markets, livestock harvest facilities, and veterinary diagnostic laboratories. A signal indicating a potential animal health event in one data stream can be corroborated in the other streams. For swine surveillance in the U.S., USDA-APHIS monitors the number of swine condemned for specific reasons. Likewise, industry practitioners share front-line clinical information within their practitioner network to detect anomalies. This case summary demonstrates the successful outcome of implementing an EPS pilot program through Federal and industry partnership.

Methods

FSIS Animal Disposition Reporting System swine condemnation data are monitored by USDA-APHIS Veterinary Services (VS) for several condemn conditions, including erysipelas, a bacterial disease of swine. Typically, slaughter condemnations for erysipelas are rare. The monitored data represent 83 market swine harvest facilities throughout the U.S. A modification of the 'C3'CUSUM aberration detection method from the Early Aberration Reporting System (EARS) is applied to the data at both the slaughter plant level and at a larger multi-plant swine catchment basin level which represents separate swine production areas. The National Pork Board (NPB), a U.S. swine producer association, hosts a quarterly conference call with a sentinel network of swine veterinarians to exchange information about anomalies in swine health observed by practitioners. During mid-February 2012, several practitioners suspected a local increase in erysipelas in finishing swine. Absent baseline data on erysipelas occurrence nationally, the scope of the problem was uncertain. Following the call, the NPB in collaboration with VS attempted to validate the information reported by swine practitioners.

Results

Beginning the week of January 8, 2012, VS analysts noted a slight increase in erysipelas CUSUM signaling activity in the greater Iowa catchment basin slaughter plants. During the seven-week period between January 8 and February 25, eight weekly plant-level CUSUM signals were observed, while the previous 36-week period yielded only fourteen plant-level signals. On average, 0.39 signals per week were noted in the weeks prior to the outbreak period while the corresponding average for the seven-week outbreak period was 1.14 plant signals per week. Seven of the eight plants that signaled during the outbreak period did not report large weekly spikes; however, the weekly accumulation of condemns were sufficient to trigger concern. Since the erysipelas signals were not large compared to the background noise, there was uncertainty whether the increased signaling activity truly represented a disease event. After cross validating the slaughter surveillance data with front line practitioner information, a swine health alert regarding the increase in erysipelas cases was issued by the American Association of Swine Veterinarians. Intervention measures were initiated as deemed appropriate by each private veterinarian.

Conclusions

This example of an Enhanced Passive Surveillance Program demonstrates use of independent streams of information from government and private industry to detect an outbreak of erysipelas in market swine. The communication process was facilitated by the NPB and the American Association of Swine Veterinarians, and coordinated with the industry resulting in an appropriate response to prevent swine losses at very early stages of the outbreak. Corroboration and validation between the two data streams (slaughter and practitioner) provided confidence that an outbreak was beginning and assisted the swine industry in decision making to enhance disease prevention activities. This type of early warning and response can reduce the cost of disease outbreaks to swine producers as well as provide confidence in the national disease status for swine in the United States.

Keywords

animal health surveillance; Federal and industry partnership; enhanced passive surveillance; swine erysipelas

*Judy Akkina
E-mail: judy.e.akkina@aphis.usda.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

One World, One Health, One Medicine: An Assessment of Intersectoral Collaboration in Avian Influenza Control in Lagos State

Abimbola Aman-Oloniyo*[1], Olalekan Allison[2] and Musbau A. Razaq[3]

[1]Lagos State Ministry of Health, Nigeria; [2]Lagos State Ministry of Agriculture and Cooperatives, Nigeria; [3]Lagos State Ministry of Information, Nigeria

Objective

To assess the collaborative efforts in Avian Influenza control that could be harnessed for the control of other Zoonotic diseases.

Introduction

The livestock sector is vital to the socio-economic development of Nigeria; it contributes about 9-10% of agricultural GDP. Livestock represents an important source of high quality animal protein providing about 36.5 % of total protein intake of Nigerians (1). Lagos State, located in the south-western part of Nigeria, has the smallest landmass (3577 sq. km) and the highest human population density (2519.75 per sq. km) in the Country (2). The State has a poultry population of 2.5 million birds and the largest outlet for poultry products with 207 Live bird markets, 375 poultry farms and a large number of poultry products consumers (3). Avian influenza ("bird flu") is an infectious disease of birds caused by type A strains of the influenza virus. The infection is known to cross species barrier to infect humans (4). Between March 2006 and September 2007 Avian influenza (AI) outbreaks occurred in 99 poultry farms in Lagos State (3). The only human case of AI in Nigeria was detected at a health facility in Lagos in January 2007.

Methods

Following the AI outbreaks in Nigeria, a lot of human and material resources were devoted to the control of AI in the Health, Information and Veterinary sectors at all levels of administration. A desk review of the AI response activities and collaborative efforts at the State level was conducted.

Results

The inter-ministerial State Steering Committee and State Technical Committee on Avian Influenza (STCAI) were established comprising of stakeholders in the Health, Information and Veterinary sectors drawn from public and private institutions. A number of interventions were carried out including formation of Public enlightenment, Health and Veterinary sub-committees to deal with sector-specific issues. Also, reconstitution and training of State and local council Epidemic Response Teams (ERT), training/retraining of State and local council Health, Information and Veterinary officers on Epidemic Preparedness and Response to Avian Influenza, establishment and equipping of desk offices in the State departments of Health, Veterinary and Information, and appointment of AI desk officers the local council level. These interventions facilitated the conduct of joint surveillance of poultry and live bird markets by stakeholders, joint outbreak investigation and response, joint sensitization of Human and animal Health workers on AI, joint public enlightenment and community/grassroots mobilization activities (including advocacy visits to local government council administrators, traditional leaders and trade union leaders) on Avian Influenza Control. All of these were instrumental in the quick containment of AI in Lagos State.

Conclusions

The collaboration between Health, Information and Veterinary departments following the AI epidemic helped to curb the disease within the State. A good structure has been put in place for control of AI that can be harnessed for the control of other Zoonotic diseases in the spirit of One World, One Health, One Medicine (OWOHOM).

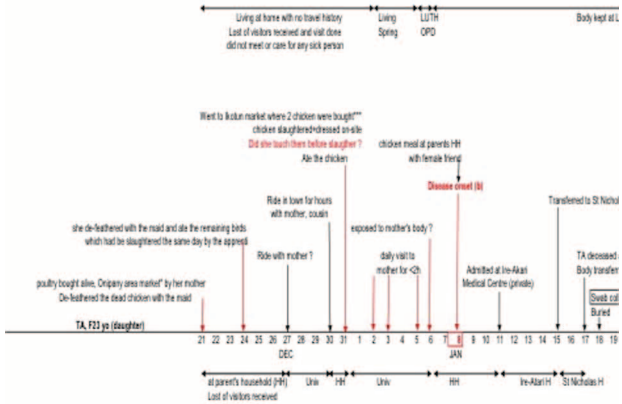


Figure 1. Clinico-Epidemic Curve of the Investigated Human Case of Avian Influenza.

Keywords

Collaborate; Avian Influenza; Zoonotic

References

1. The Integrated National Avian and Pandemic Influenza Response Plan, 2007. 3, 19 - 23
2. Reducing Health Disparities in Lagos State- An investment case, 2012. 7-8
3. Lagos State Ministry of Agriculture and Cooperatives, 2009.
4. World Health Organization. Avian Influenza fact sheet. <www.who.int/mediacentre/factsheets/avian_influenza/en/>. Accessed July 30, 2007.
5. World Health Organization. Cumulative number of confirmed human cases of avian influenza A/(H5N1) reported to WHO. <http://www.who.int/csr/disease/ avian_influenza/country /cases_table2007_07_25/en/index.html>. Accessed July 30, 2007.

*Abimbola Aman-Oloniyo
E-mail: bimskoms@yahoo.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using Cultural Modeling to Inform a NEDSS-Compatible System Functionality Evaluation

Olympia Anderson and Miguel Torres-Urquidy*

Centers for Disease Control and Prevention, Atlanta, GA, USA

Objective

The culture by which public health professionals work defines their organizational objectives, expectations, policies, and values. These aspects of culture are often intangible and difficult to qualify. The introduction of an information system could further complicate the culture of a jurisdiction if the intangibles of a culture are not clearly understood. This report describes how cultural modeling can be used to capture intangible elements or factors that may affect NEDSS-compatible (NC) system functionalities within the culture of public health jurisdictions.

Introduction

The National Notifiable Disease Surveillance System (NNDSS) comprises many activities including collaborations, processes, standards, and systems which support gathering data from US states and territories. As part of NNDSS, the National Electronic Disease Surveillance System (NEDSS) provides the standards, tools, and resources to support reporting public health jurisdictions (jurisdictions). The NEDSS Base System (NBS) is a CDC-developed, software application available to jurisdictions to collect, manage, analyze and report national notifiable disease (NND) data. An evaluation of NEDSS with the objective of identifying the functionalities of NC systems and the impact of these features on the user's culture is underway.

Methods

We used cultural models to capture additional NC system functionality gaps within the culture of the user. Cultural modeling is a process of graphically depicting people and organizations referred to as influencers and the intangible factors that affect the user's operations or work as influences. Influencers are denoted as bubbles while influences are depicted as arrows penetrating the bubbles. In the cultural model, influence can be seen by the size and proximity (or lack of) in the model. We restricted the models to secondary data sources and interviews of CDC programs (data users) and public health jurisdictions (data reporters).

Results

Three cultural models were developed from the secondary information sources; these models include the NBS vendor, public health jurisdiction (jurisdiction) activities, and NEDSS technical consultants. The vendor cultural model identified channels of communication about functionalities flowing from the vendor and the NBS users with CDC as the approval mechanism. The jurisdiction activities model highlighted perceived issues external to the organization that had some impact in their organization. Key disconnecting issues in the jurisdiction model included situational awareness, data competency, and bureaucracy. This model also identified poor coordination as a major influencer of the jurisdiction's activities. The NEDSS technical model identified major issues and disconnects among data access, capture and reporting, processing, and ELR functionalities (Figure 1). The data processing functionality resulted in the largest negative influencer with issues that included: loss of data specificity, lengthy submission strategies, and risk of data use. Collectively, the models depict issues with the system functionality but mostly identify other factors that may influence how jurisdictions use the system, moreover determining the functionalities to be included.

Conclusions

By using the cultural model as a guide, we are able to clarify complex relationships using multiple data sources and improve our understanding of the impacts of the NC system functionalities on user's operations. Modeling the recipients of the data (e.g. CDC programs) will provide insight on additional factors that may inform the NEDSS evaluation.

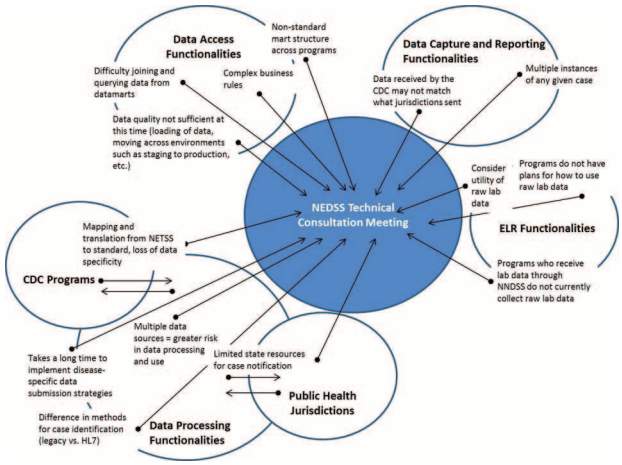


Figure 1. Cultural model from a NEDSS technical consultation meeting.

Keywords

evaluation; cultural modeling; functionality; NEDSS

Acknowledgments

We acknowledge the leadership and staff of CDC's stakeholders and the Division of Notifiable Disease and Healthcare Information.

References

Beyer H, Holtzblatt K. Contextual Design: Defining Customer-Centered Systems. San Diego (CA): Academic Press; 1998.

*Miguel Torres-Urquidy
E-mail: jvu5@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Syndromic Surveillance for Outbreak Detection and Investigation

Tom Andersson*[1, 2, 4], Pär Bjelkmar[3], Anette Hulth[1], Johan Lindh[1], Stephan Stenmark[5] and Mikael Widerström[6]

[1]Swedish Institute for Communicable Disease Control (SMI), Solna, Sweden; [2]National Food Agency, Uppsala, Sweden; [3]Inera AB, Stockholm, Sweden; [4]Stockholm University Section for Mathematical Statistics, Stockholm, Sweden; [5]Västerbotten County Medical Officer, Umeå, Sweden; [6]Jämtland County Medical Officer, Östersund, Sweden

Objective

For the purpose of developing a national system of outbreak surveillance, we compared local outbreak signals in three sources of syndromic data – telephone triage of acute gastroenteritis (Swedish Health Care Direct 1177), web queries about symptoms of gastrointestinal illness (Stockholm County's website for healthcare information), and OTC pharmacy sales of anti-diarrhea medication.

Introduction

A large part of the applied research on syndromic surveillance targets seasonal epidemics, e.g. influenza, winter vomiting disease, rotavirus and RSV, in particular when dealing with preclinical indicators, e.g. web traffic (Hulth et al, 2009). The research on local outbreak surveillance is more limited. Two studies of teletriage data (NHS Direct) have shown positive and negative results respectively (Cooper et al, 2006; Smith et al, 2008). Studies of OTC pharmacy sales have reported similar equivocal performance (Edge et al, 2004; Kirian and Weintraub, 2010). As far as we know, no systematic comparison of data sources with respect to multiple point-source outbreaks has so far been published (cf. Buckeridge, 2007). In the current study, we evaluated the potential of three data sources for syndromic surveillance by analyzing the correspondence between signal properties and point-source outbreak characteristics.

Methods

The extracted data streams were compared with respect to nine waterborne and foodborne outbreaks in Sweden in 2007-2011. The analysis consisted of three parts: (1) the validation of outbreak signals by comparing signal counts during outbreak and baseline periods, (2) the estimation of detection limits by modeling signal rates (signal-to-case ratios), and (3) the evaluation of early warning potential by means of signal detection analysis.

Results

The four largest outbreaks generated strong and clear outbreak signals in the 1177 triage data. The two largest outbreaks produced signals in OTC sales of anti-diarrhea. No signals could be identified in the web query data. The outbreak detection limit based on triage data was about 100-1000 cases. For two outbreaks, triage data on diarrhea provided outbreak signals early on, weeks and months respectively, potentially serving the purpose of early warning.

Conclusions

The sensitivity and specificity were highest for telephone triage data on patient symptoms. It provided the most promising source of syndromic data for surveillance of point-source outbreaks. Currently, a project has been initialized to develop and implement a national system in Sweden for daily syndromic surveillance based on 1177 Health Care Direct, supporting regional and local outbreak detection and investigation.

Keywords

syndromic surveillance; outbreak detection; point-source outbreak; outbreak investigation; data analysis

Acknowledgments

The study is part of an ongoing research and development project on syndromic surveillance (SUMO) funded by the Swedish Agency for Contingency Planning (MSB).

References

Buckeridge DL. Outbreak detection through automated surveillance: a review of the determinants of detection. J Biomed Inform. 2007 Aug;40(4):370-9.

Cooper DL, Verlander NQ, Smith GE, Charlett A, Gerard E, Willocks L, O'Brien S. Can syndromic surveillance data detect local outbreaks of communicable disease? A model using a historical cryptosporidiosis outbreak. Epidemiol Infect. 2006 Feb;134(1):13-20.

Edge VL, Pollari F, Lim G, Aramini J, Sockett P, Martin SW, Wilson J, Ellis A. Syndromic surveillance of gastrointestinal illness using pharmacy over-the-counter sales. A retrospective study of waterborne outbreaks in Saskatchewan and Ontario. Can J Public Health. 2004 Nov-Dec;95(6):446-50.

Hulth A, Rydevik G, Linde A. Web queries as a source for syndromic surveillance. PLoS One. 2009;4(2).

Kirian ML, Weintraub JM. Prediction of gastrointestinal disease with over-the-counter diarrheal remedy sales records in the San Francisco Bay Area. BMC Med Inform Decis Mak. 2010 Jul 20;10:39.

Smith S, Elliot AJ, Mallaghan C, Modha D, Hippisley-Cox J, Large S, Regan M, Smith GE. Value of syndromic surveillance in monitoring a focal waterborne outbreak due to an unusual Cryptosporidium genotype in Northamptonshire, United Kingdom, June - July 2008. Euro Surveill. 2010 Aug 19;15(33):19643.

*Tom Andersson
E-mail: tom.andersson@smi.se

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

National Collaborative for Bio-Preparedness

Meredith Arasaratnam*[1, 2], David Potenziani[1, 2], Marc Hoit[3, 1], Colleen Jenkins[4, 1] and Charles Cairns[2, 1]

[1]National Collaborative for Bio-Preparedness, Chapel Hill, NC, USA; [2]University of North Carolina, Chapel Hill, NC, USA; [3]North Carolina State University, Raleigh, NC, USA; [4]SAS Institute, Cary, NC, USA

Objective

Demonstrate the functionality of the National Collaborative for Bio-Preparedness system.

Introduction

The National Collaborative for Bio-Preparedness (NCB-Prepared) was established in 2010 to create a biosurveillance resource to enhance situational awareness and emergency preparedness. This joint-institutional effort has drawn on expertise from the University of North Carolina- Chapel Hill, North Carolina State University, and SAS Institute, leveraging North Carolina's role as a leader in syndromic surveillance, technology development and health data standards. As an unprecedented public/private alliance, they bring the flexibility of the private sector to support the public sector. The project has developed a functioning prototype system for multiple states that will be scaled and made more robust for national adoption.

Methods

NCB-Prepared recognizes that the capability of any biosurveillance system is a function of the data is analyzes. NCB-Prepared is designed to provide information services that analyze and integrate national data across a variety of domains, such as human clinical, veterinary and physical data. In addition to this one-health approach to surveillance, a primary objective of NCB-Prepared is to gather data that is closer in time to the event of interest. NCB-Prepared has validated the usefulness of North Carolina emergency medical services data for the purposes of biosurveillance of both acute outbreaks and seasonal epidemics (1).

A unique model of user-driven valuing of data-providing value back to the provider in their terms-motivates collaboration from potential data providers, along with timely and complete data. NCB-Prepared approaches potential data providers, partners and users with the proposition that enhanced data quality and analysis is valuable to them individually and that an integrated information system can be valuable to all. With the onboarding of new data sources, NCB-Prepared implements a formal process of data discovery and integration. The goal of this process is three-fold: 1) to develop recommendations to enhance data quality going forward, 2) to integrate information across data sources, and 3) to develop novel analytic techniques for detecting health threats. NCB-Prepared is committed to both utilizing standard methods for event detection and to developing innovative analytics for biosurveillance such as the Text Analytics and Proportional charts method (TAP). The sophisticated analytic functionality of the system, including improved time to detection, query reporting, alert detection, forecasting and predictive modeling, can be attributed to collaboration between analysts from private industry, academia and public health.

NCB-Prepared followed the formal software development process known as agile development to create the user interface of the system. This method is based on iterative cycles wherein requirements evolve from regular sessions between user groups and developers. The result of agile development and collaborative relationships is a system which visualizes signals and diverse data sources across time and place while providing information services across all levels of users and stakeholders.

Conclusions

Lessons Learned:

1. Understand the functionality of new biosurveillance system, NCB-Prepared
2. Identify the benefit of creating collaborative relationships with data providers and users
3. Appreciate the value of a public/private partnership for biosurveillance and bio-preparedness

Keywords

Biosurveillance; Analytics; Preparedness; Emergency

References

Cairns C., Potenziani D., Hoit M., Jenkins C., Edgemon S. Novel approach to statewide biosurveillance using emergency medical services (EMS) information. Emerg Health Threats J 2011; 4, DOI: 4: 10.3402/ehtj.v4i0.11183 (abstract).

*Meredith Arasaratnam
E-mail: arasarat@med.unc.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Can We Use Syndromic Surveillance Data to Identify Primary Care Visits to NYC EDs?

Jessica Athens*

New York City Department of Health and Mental Hygiene, New York City, NY, USA

Objective

To develop a syndrome classification based on patient chief complaint to (1) estimate the proportion of primary care-related emergency department (ED) visits in New York City (NYC) hospitals and (2) explore predictors of such visits.

Introduction

NYC EDs saw nearly 4 million visits in 2011. Studies have demonstrated that non-urgent visits can account for more than 50% of visits to EDs [1,2]. Designed to provide rapid diagnosis and first-line treatment of serious illness, EDs often function as a primary care site due to their accessibility. Unfortunately, use of EDs for primary care may affect their ability to meet the needs of severely ill patients.

Methods

We examined syndromic surveillance data from 45 hospitals in NYC for 2011 and classified visits into a primary care syndrome based on the chief complaint field. Data from 4 hospitals were omitted due to data quality issues, as were records from non-NYC residents. Primary care (PC) syndrome visits included visits recorded as referrals, screenings, suture removal/dressing changes, or medication refills; records with a blank or non-informative (e.g. "X") chief complaint field were omitted from analysis. Using unique patient IDs, we identified patients who visited the same ED multiple times in the previous 12 months. A hierarchical generalized linear mixed effects model with hospital-level random effects was used to explore patient characteristics associated with PC syndrome visits. The model included a random intercept for hospital and the following covariates: duplicate visit, patient gender and age group (ages 0-4, 5-17, 18-64, and 65+), and time of visit (midnight to 8 AM, 8 AM to midnight). Covariates for month and day of week were included to control for temporal trends in ED visits. Model parameters were estimated by maximum likelihood. Estimation was performed in SAS version 9.2 [3] using the GLIMMIX procedure.

Results

Citywide, 7.5% (N=190,431) of visits to EDs during 2011 were classified as PC syndrome visits, but varied by hospital with a median of 4.6% (IQR: 3% to 9%) across hospitals.The average proportion of PC syndrome visits varied by hospital. Of the 45 hospitals included in the analysis, 18 had a lower baseline, 13 were the same, and 14 had a higher baseline than the city mean. Hospitals with a larger census had a larger proportion of PC syndrome visits.

Age had a significant effect on the odds of a PC syndrome visit; ages 0–4 had the greatest odds of a PC syndrome visit relative to the 65+ age group. Visits from patients ages 5–17 and 18–64 were also more likely to be primary care visits. Patients with repeat visits were more likely to have PC syndrome visits. Female gender and early morning visits (12A–8A) were associated with lower odds of a PC syndrome visit.

Conclusions

With limited detail on patient visits, our syndrome likely undercounts primary care visits to EDs. However, the relationships between our explanatory variables—age, time of day, and duplicate visits—and PC syndrome visits are consistent with the literature on ED usage for primary care. Gender is an exception [1], but earlier findings may be confounded by the fact that females seek health care more frequently in general. The variation in PC syndrome visits among NYC EDs is significant and may be explained by hospital or community measures not captured in our model, such as clinic wait times, ED capacity, or insurance coverage. In fact, disparities in such predictors of PC syndrome visits could be targets for interventions. Our ability to replicate previous findings on the use of EDs for primary care visits suggests that syndromic data may be a near real-time data source for following trends in such visits.

Predictors of PC Syndrome Visits

Covariate	OR (95% CI)
Duplicate visit	1.84 (1.82-1.86)
Female	0.84 (0.83-0.85)
Age 0-4	2.15 (2.11-2.19)
Age 5-17	1.55 (1.52-1.58)
Age 18-64	1.26 (1.24-1.28)
Age 65+	Reference group for age
Early AM (12A-8A)	0.85 (0.84-0.86)

All covariates significant at $p < .001$.

Keywords

Misuse of emergency medical services; Primary care; Variation in emergency department use

References

1. Carret M, Gastal Fass A, Rodrigues Domingues A. Inappropriate use of emergency services: a systematic review of prevalence and associated factors. Cad. Saúde Pública. 2009;25(1): 7–28.
2. Tang N, Stein J, Hsia RY, Masselli JH, Gonzales R. Trends and characteristics of US emergency department visits, 1997–2007. JAMA. 2010;304(6):664–70.
3. SAS Institute, Inc., Cary, NC.

*Jessica Athens
E-mail: jathens@health.nyc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Enhanced Disease Surveillance during the 2012 Republican National Convention, Tampa, FL

David Atrubin*, Michael Wiese, Rebecca Snider, Kiley Workman and Warren McDougle

Hillsborough County Health Department, Tampa, FL, USA

Objective

To describe disease and illness surveillance utilized during the 2012 Republican National Convention (RNC) held August 26-30, 2012 in Tampa, FL.

Introduction

While the Tampa Bay Area has previously hosted other high profile events that required heightened disease surveillance (e.g., two Super Bowls), the 2012 RNC marked the first national special security event (NSSE) held in Florida. The Hillsborough County Health Department (HCHD), in conjunction with the Pinellas County Health Department (PinCHD) coordinated disease surveillance activities during this time frame. This presentation will focus of the disease surveillance efforts of the Hillsborough County Health Department during the 2012 RNC.

In addition to the surveillance systems that are used routinely, the HCHD Epidemiology Program implemented additional systems designed to rapidly detect individual cases and outbreaks of public health importance. The short duration of RNC, coupled with the large number of visitors to our area, provided additional surveillance challenges.

Tropical Storm Isaac, which threatened Tampa in the days leading up to RNC, and an overwhelming law enforcement presence likely dissuaded many protestors from coming to Tampa. As a result, a tiny fraction of the number of protestors that were expected actually showed up.

Methods

Our normal daily analysis of the emergency department (ED) data using the Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE) was expanded to look in detail at ED volumes and chief complaints of those patients who live outside of a 5-county Tampa Bay area. This analysis used patient zip code to determine place of residence. Additionally, ESSENCE queries were utilized to look for heat, tear gas, and RNC related exposures. The ESSENCE system also receives Poison Control data every 15 minutes. Expanded analyses of the Poison Control data were conducted as well. Two Disaster Medical Assistance Teams (DMATs) were deployed in Tampa during the RNC. Data was collected electronically and transmitted through ESSENCE as well.

The HCHD also asked infection preventionists, health care providers, hotels, labs, and Mosquito Control to lower their reporting threshold to us during the RNC period. We provided updates to all our partners with respect to diseases and outbreaks of public health importance occurring in our county.

Results

No epidemiologic events linked to the RNC were detected through the HCHD's enhanced surveillance that was conducted. Decreased patient volumes were seen during the RNC at our EDs closest to the convention site. No significant increases in ED visits from outside of our 5-county area were noted during the RNC. Urgent care centers reported seeing patients associated with the RNC for a variety of reasons including respiratory and gastrointestinal illness. DMAT surveillance showed mainly routine visits but four secret service agents did seek care for respiratory illness during the convention.

Conclusions

Substantial time and resources were devoted to disease surveillance in the 6 months leading up to the RNC and during the event. While no epidemiologic events were detected, the public health surveillance infrastructure has clearly been strengthened in our county. We are receiving our ED syndromic data, from many of our hospitals, every two hours as opposed to every day. We have established relationships with our urgent case centers and hope to begin receiving urgent care center data on a daily basis in the near future. Receiving DMAT data through ESSENCE could prove very useful in the future, especially in Florida where hurricanes are always a threat. Lastly the improved relationships with our health care providers should be beneficial as we move forward.

Keywords

mass gathering; national special security event; convention

Acknowledgments

Janet Hamilton, Aaron Kite-Powell, and Aaron Chern, Florida Department of Health, Bureau of Epidemiology

Cynthia Lewis-Younger and Joann Chambers-Emerson, Florida Poison Information Center –Tampa

Dina Passman, Health and Human Services

References

Hick J, Frascone R, Grimm K, Hillman M, Griffith J, Hogan M, Trotsky-Sirr R, Branu. Health and Medical Preparedness and Response to the 2008 Republican National Convention. Disaster Medicine and Public Health Preparedness 3(4);224-232.

Kade K, Brinsfield K, Serino R, Savoia E, Koh H. Emergency Medical Consequence Planning and Management for National Special Security Events After September 11: Boston 2004., Disaster Medicine and Public Health Preparedness 2(3);166-173.

*David Atrubin
E-mail: David_Atrubin@doh.state.fl.us

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using GI Syndrome Data as an Early Warning Tool for Norovirus Outbreak Activity

Erin E. Austin*, Jun Yang and Tim Powell

Division of Surveillance and Investigation, Virginia Department of Health, Richmond, VA, USA

Objective

To assess the relationship between emergency department (ED) and urgent care center (UCC) chief complaint data for gastrointestinal (GI) illness and reported norovirus (NV) outbreaks to develop an early warning tool for NV outbreak activity. The tool will provide an indicator of increasing NV outbreak activity in the community allowing for earlier public health action to mitigate NV outbreaks.

Introduction

Norovirus infection results in considerable morbidity in the United States where an estimated 21 million illnesses, 70,000 hospitalizations, and 800 deaths are caused by NV annually (1). Additionally, NV is responsible for approximately 50% of foodborne outbreaks (1). Between January 2008 and June 2012, 875 NV outbreaks were reported to the Virginia Department of Health (VDH). To assist in detecting possible disease outbreaks such as NV, VDH utilizes the web-based Electronic Surveillance System for Early Notification of Community-based Epidemics (ESSENCE) to monitor and detect public health events across Virginia. ESSENCE performs automated parsing of chief complaint text into 10 syndrome categories, including a non-specific GI syndrome that serves as a proxy for GI illnesses like NV.

Methods

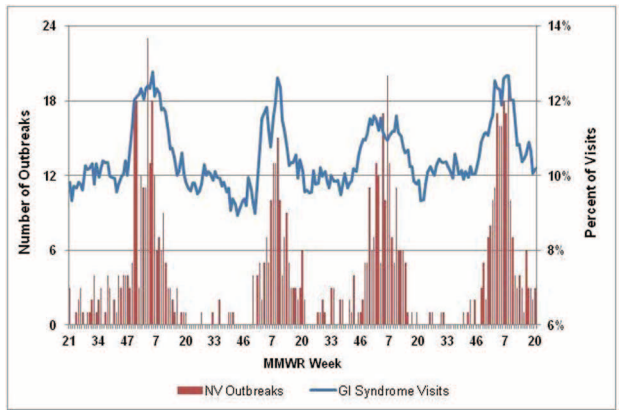
ED and UCC chief complaints parsed into the ESSENCE GI syndrome category were compared to confirmed and suspected NV outbreaks across four years. In this study, the analysis periods were defined as week 21 through week 20 of the subsequent year. GI syndrome visits as a proportion of all ED and UCC visits and NV outbreak counts were aggregated by week. Time-series, correlation, and logistic regression analyses were performed. Low NV outbreak activity weeks were defined as those with 4 or fewer outbreaks, and high NV outbreak activity weeks were those with 5 or more outbreaks. Based on low NV outbreak activity weeks, baseline and threshold values for the weekly percent of GI syndrome visits were calculated for each analysis period. Baseline calculation was the average weekly percent of GI syndrome visits from week 21 to week 31 and threshold value was baseline plus two standard deviations. Weekly percent of GI syndrome visits was compared to the threshold value to serve as an indicator of increasing NV outbreak activity.

Results

The study period was from May 18, 2008 to May 19, 2012 (Fig 1). A total of 1,425,728 GI syndrome visits and 804 confirmed and suspected NV outbreaks were analyzed. Weekly visits to ED and UCC facilities with GI syndrome were highly correlated with outbreaks of NV in the community ($r = 0.809$, $p < .0001$). Median and mean number of NV outbreaks per week were 2 and 4, respectively (range 0-23). NV outbreaks were more prominent during the winter months with peaks occurring between weeks 3-9. Median and mean percent of GI syndrome visits per week were 10.2% and 10.5%, respectively (range 8.9%-12.8%). Weeks with high NV outbreak activity were more likely to occur when the weekly percent of GI syndrome visits had surpassed the threshold value (OR =110.7, 95% CI: 31.9-384.8). On average, weekly percent of GI syndrome visits surpassed the threshold value 1.25 weeks prior to the start of high NV outbreak activity weeks (range 0-3).

Conclusions

These results support the use of syndromic surveillance GI illness data as an early warning indicator of increasing NV outbreak activity in Virginia. This study identified that GI syndrome visits crossed a calculated threshold value on average 1.25 weeks before the initiation of high NV outbreak activity. Although NV outbreaks occur year round, this study attempted to identify an indicator to trigger meaningful risk communication to the community immediately prior to high NV outbreak activity with the goal of reducing the magnitude of NV outbreaks. This early warning tool for NV outbreak activity will be implemented in the following year to validate its effectiveness and timeliness in mitigating NV outbreaks in Virginia.



Percent of Emergency Department and Urgent Care Center Visits with GI Syndrome and Reported Norovirus Outbreaks, Virginia, May 2008-May 2012.

Keywords

Syndromic surveillance; ESSENCE; Norovirus; GI illness

References

Centers for Disease Control and Prevention (2012). Burden of norovirus illness and outbreaks. Retrieved September 5, 2012, from http://www.cdc.gov/norovirus/php/illness-outbreaks.html.

*Erin E. Austin
E-mail: erin.austin@vdh.virginia.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

MoH+: A Global, Integrated, and Automated View of Official Outbreak Reporting

Chi Bahk*[1,2], David Scales[1], Sumiko Mekaru[1,3], John S. Brownstein[1,4,5] and Clark Freifeld[1,6]

[1]Children's Hospital Informatics Program, Division of Emergency Medicine, Children's Hospital Boston, Boston, MA, USA; [2]Dept of Global Health and Population, Harvard School of Public Health, Boston, MA, USA; [3]Dept of Epidemiology, Boston University School of Public Health, Boston, MA, USA; [4]Dept of Pediatrics, Harvard Medical School, Boston, MA, USA; [5]Dept of Epidemiology, Biostatistics and Occupational Health, McGill University, Montreal, QC, Canada; [6]Dept of Biomedical Engineering, Boston University, Boston, MA, USA

Objective

To introduce MoH+, HealthMap's (HM) real-time feed of official government sources, and demonstrate its utility in comparing the timeliness of outbreak reporting between official and unofficial sources.

Introduction

Previous studies have documented significant lags in official reporting of outbreaks compared to unofficial reporting (1,2). MoH+ provides an additional tool to analyze this issue, with the unique advantage of actively gathering a wide range of streamlined official communication, including formal publications, online press releases, and social media updates.

Methods

Outbreaks reported by official sources were identified through MoH+ (healthmap.org/mohplus), which collects surveillance data published globally by ministries of health (MoH), other related ministries, government portals, government-affiliated organizations, and international governing bodies (Fig. 1). Reporting of these outbreaks was also identified in unofficial sources using various HM feeds including Google News, ProMED, and participatory surveillance feeds.

Of the 109 outbreaks identified since May 2012, 65 were excluded as they started before data collection, 7 were excluded as they were not reported by unofficial sources, and 1 was excluded as it was a non-natural outbreak. For the remaining 36 outbreaks, the median difference in first date of report between official and unofficial sources was analyzed using a Wilcoxon sign rank test.

Results

Outbreak reporting in official sources lagged by a statistically significant median of 2 days (p=0.003). Among unofficial sources, online news most often (75%) was the fastest to report an outbreak, followed by ProMED (22%) and participatory surveillance (3%). Among official sources, national government affiliated institutes were most often (41%) the fastest, and repeatedly providing prompt outbreak reports were the US Centers for Disease Control and Prevention (CDC), Public Health Agency of Canada, Finnish Food Safety Authority, Health Protection Scotland, UK Health Protection Agency, and French Institute of Public Health Surveillance (FIPHS). Following such institutes were the European CDC (ECDC) with 22% of first reports of outbreaks; MoH's (17%); and WHO (10%). There were 4 instances in which official sources reported before unofficial sources—3 by the ECDC and 1 by FIPHS.

Conclusions

Compared to the Chan study reporting a 16 day lag between first public communication and WHO Outbreak News (1) and the Mondor study reporting a 10 day lag between non-government and government sources (2), the present study shows a much condensed lag of 2 days between unofficial and official sources. Because the two earlier studies cover a much broader historical time frame, one explanation for the reduced lag time is increased adoption of online communication by official government agencies. However, despite such improvements in communication, the lag persists, pointing to the importance of using informal sources for outbreak surveillance.

The present study was limited by small sample size, as the study is in its early stages. We will continue to gather data and all numbers will be updated in time for the presentation to reflect the larger database. Future directions of this study include characterization of official and unofficial reporting by region, language, disease, and source.

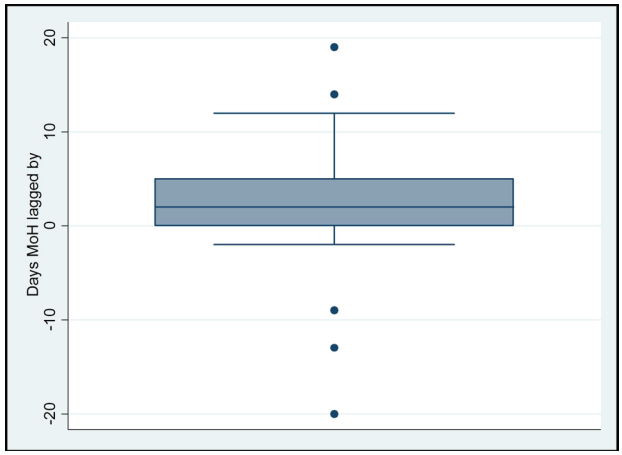


Fig. 1. Interactive visualization of HealthMap MoH+, at healthmap.org/mohplus

Keywords

disease surveillance; outbreak reporting; timeliness; MOH; official sources

References

1. Chan et al. Global capacity for emerging infectious disease detection. PNAS 2010.
2. Mondor et al. Timeliness of Nongovernmental versus Governmental Global Outbreak Communications. EID 2012.

*Chi Bahk
E-mail: cbahk@hsph.harvard.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluation of Cholera and Other Diarrheal Disease Surveillance System, Niger State, Nigeria-2012

Adebobola T. Bashorun*[1], Anthony Ahumibe[1], Saliman Olugbon[1], Patrick Nguku[1] and Kabir Sabitu[2]

[1]Nigeria Field Epidemiology and Laboratory Training Program, FCT, Nigeria; [2]Ahmadu Bello University, Zaria, Nigeria

Objective

To determine how the cholera and other diarrheal disease surveillance system in Niger state is meeting its surveillance objectives, to evaluate its performance and attributes and to describe its operation to make recommendations for improvement.

Introduction

Cholera causes frequent outbreaks in Nigeria, resulting in mortality. In 2010 and 2011, 41,936 cases (case fatality rate [CFR]-4.1%) and 23,366 cases (CFR-3.2%) were reported (1). Reported cases in Nigeria by week 26, 2012 was 309 (CFR-1.29%) involving 20 Local Government Areas in 6 States. In Nigeria, there are currently eleven (11) States including Niger state at high risk for cholera/bloodless diarrhea outbreaks.

In 2011, Niger state had 2472 cholera cases (CFR-2%) and 45,111 other diarrhea diseases cases, recorded in more than half of state Purpose of surveillance system is to ensure early detection of cholera and other diarrheal cases and to monitor trends towards evidence-based decision for management, prevention and control.

Methods

We conducted evaluation in July, 2012. We used CDC guideline on surveillance system evaluation (2001) as guide to assess operation, performance and attributes (2). We conducted key informant/in-depth interviews with stakeholders. We examined cholera action plans for preparedness and response, conducted laboratory assessment, extracted and analyzed cholera surveillance (2005-2012) for frequencies/proportions using Microsoft Excel. Thematic analysis was done for qualitative data. We shared findings with stakeholders at all levels.

Results

Surveillance system was setup for early detection and monitoring towards evidence-based decision. State government funds system. Case definition used is highly sensitive and is any patient aged 5 years or more who develops acute watery diarrhea, with/without vomiting. Though simple case definition, laboratory confirmation makes surveillance complex. A passive system, active during outbreaks; has formal and informal sources of information and part of Integrated Disease Surveillance and Response (IDSR) system and flow(fig.1). It takes 24-48 hours between outbreaks onset, confirmation and response.

Line list showed undefined/poorly labeled outcomes. Of 2472 cases in 2011 1320 (49%) were found in line list. 2011 monthly data completeness was 75%. So far in 2012, 5(0.02%) of all diarrhea cases were cholera. System captures only age as sociodemographics.

Of 11 suspected cholera cases tested during 2011 epidemic, 7 confirmed as cholera (PPV-63%). Of 3 rumours of cholera outbreaks (January 2011-July 2012), one (PPV-33%) was true. Acceptability of system is high among all stakeholders interviewed. Timeliness of monthly reporting was 68.7% (Table 1).

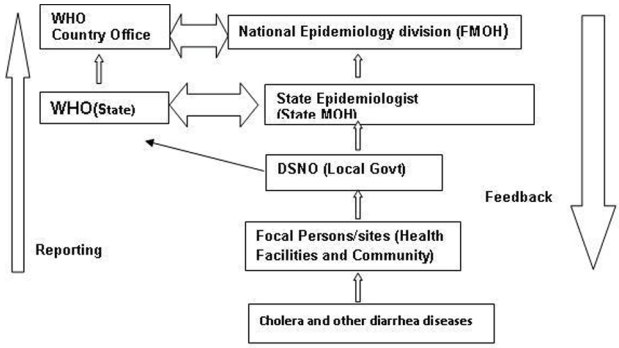
Laboratory can isolate Vibro cholerae isolation but has no Cary Blair transport medium and cholera rapid test kits.

Conclusions

Evaluation revealed that surveillance system is meeting its objectives by early detection and response to cholera outbreaks. System is simple, stable, flexible, sensitive with poor data quality, low PPV, fair laboratory capacity and moderate timeliness. We recommended electronic and internet-based reporting for timeliness and data quality improvement; and provision of laboratory consumables.

Table 1. Summary of performance attributes of cholera surveillance system, Niger state, 2012.

Performance attributes	Excellent (>90%)	Very good (80-89%)	Good (70-79%)	Average (60-69%)	Fair (50-59%)	Poor (<50%)
Simplicity		●				
Flexibility	●					
Data Quality					●	
Acceptability	●					
Sensitivity		●				
Positive Predictive Value				●		
Representativeness				●		
Timeliness			●			
Stability		●				



Keywords

Surveillance; Evaluation; Cholera; Nigeria

Acknowledgments

Niger State Ministry of Health

References

1. Federal Ministry of Health, Nigeria Weekly Epidemiology Reports, NCDC/Federal Ministry of Health – Nigeria Volume 1 No 1-52. 2011
2. Centers for Disease Control and Prevention. Updated guidelines for evaluating public health surveillance systems: recommendations from the guidelines working group. MMWR 2001;50 (No. RR-13)

*Adebobola T. Bashorun
E-mail: bashogee@yahoo.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

New Strategy and Innovative Projects at the National Biosurveillance Integration Center

Steven Bennett and Teresa Quitugua*

Homeland Security, Washington, DC, USA

Objective

Enhance knowledge of the vision, mission, strategic goals, and objectives of the National Biosurveillance Integration Center (NBIC). Learn about innovative biosurveillance projects ongoing in NBIC.

Introduction

For a number of years, the federal government has provided biosurveillance in various domains within different departments and agencies. Congress recognized the need for a means of integrating these separate information sources into a more useable resource by chartering NBIC within the Department of Homeland Security.

Methods

NBIC engaged the biosurveillance community within and beyond the federal government through a series of extensive discussions, workshops, and symposia to define a strategy for future development of integrated biosurveillance activities grounded in legislative and presidential direction. The NBIC Strategic Plan was extensively reviewed by the twelve federal Departments that comprise the National Biosurveillance Integration System (NBIS) as well as the White House Office of Management and Budget. The NBIC Strategic Plan is currently being revised for release of a public version. The NBIC also engaged partners in the development of projects designed to develop and test new approaches to biosurveillance.

Results

The NBIC Strategic Plan was delivered to Congress in August, 2012. The plan explains the Center's approach, why it is needed, and how it seeks to execute the mission of integrating national biosurveillance information to provide relevant and timely information that effectively supports decision making. Projects are underway involving text analyses of emergency medical system data, changes to poison control center data collection and analysis, and the application of machine learning to social media analyses. A sub-working group of the NBIS has been established to guide selection of future pilot project areas to address prioritized requirements for integrated biosurveillance.

Conclusions

NBIC has increased flexibility in its commitment to collaboration and coordination, engaged in bold new approaches, and is defining requirements that will encourage buy-in and support of the users across the levels of government and the private sector. With success in its mission, NBIC will support its partners' missions and provide relevant and timely information that effectively supports decision making.

Keywords

NBIC; NBIS; strategy

References

(1) Public Law 110-53, "Implementing Recommendations of the 9/11 Commission Act of 2007," August 2007. Accessed online at http://intelligence.senate.gov/laws/pl11053.pdf.

(2) The White House, National Strategy for Biosurveillance, July 2012. Accessed online at http://www.whitehouse.gov/sites/default/files/National_Strategy_for_Biosurveillance_July_2012.pdf.

(3) Institute of Medicine, "Information Sharing and Collaboration: Applications to Integrated Biosurveillance - Workshop Summary," November 2011.

(4) Government Accountability Office, Report on Biosurveillance: Developing a Collaboration Strategy is Essential to Fostering Interagency Data and Resource Sharing, GAO 10-171 (Washington, DC: GAO, 2009).

(5) U.S. Department of Health and Human Services. National Biosurveillance Strategy for Human Health. February 2010. Accessed online at http://www.cdc.gov/osels/pdf/NBSHH_V2_FINAL.PDF.

(6) U.S. Department of Health and Human Services. National Health Security Strategy, December 2009. Accessed online at http://www.phe.gov/preparedness/planning/authority/nhss/strategy/documents/nhss-final.pdf.

(7) U.S. Department of Health and Human Services. Implementation Plan for the National Health Security Strategy of the United States of America, May 2012. Accessed online at http://www.phe.gov/Preparedness/planning/authority/nhss/ip/Documents/nhss-ip.pdf.

(8) The White House, "Biodefense for the 21st Century," Homeland Security Presidential Directive 10, April 28, 2004. Accessed online at http://www.fas.org/irp/offdocs/nspd/hspd-10.html.

(9) The White House, "Defense of United States Agriculture and Food," Homeland Security Presidential Directive 9, January 30, 2004. Accessed online at http://www.aphis.usda.gov/animal_health/emergency_management/downloads/hspd-9.pdf.

*Teresa Quitugua
E-mail: teresa.quitugua@hq.dhs.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluation of Heat-related Illness Surveillance Based on Chief Complaint Data from New Jersey Hospital Emergency Rooms

Michael Berry[1], Jerald Fagliano[1], Stella Tsai*[1], Katharine McGreevy[1], Andrew Walsh[2] and Teresa Hamby[1]

[1]NJDOH, Trenton, NJ, USA; [2]Health Monitoring Systems, Inc., Pittsburgh, PA, USA

Objective

The purpose of this evaluation is to characterize the relationship between a patient's initial hospital emergency room chief complaint potentially related to a heat-related illness (HRI) with final primary and secondary ICD-9 diagnoses.

Introduction

The NJ syndromic surveillance system, EpiCenter, developed an algorithm to quantify HRI visits using chief complaint data. While heat advisories are released by the National Weather Service, an effective HRI algorithm could provide real-time health impact information that could be used to provide supplemental warnings to the public during a prolonged heat wave.

Methods

Data on NJ hospital emergency room visits were evaluated using two data sources: 1) the EpiCenter syndromic surveillance system of emergency room visits; and 2) the Uniform Bill-Patient Summaries (UB) system containing diagnosis data on all hospital visits. Three years of data (2009-2011) were selected, for the time window of May 1 to September 30. The UB data used for matching with the EpiCenter data were limited to facilities participating in EpiCenter during the evaluation period. (EpiCenter facilities captured about 1/3 of all heat-related diagnoses in 2009, increasing to about 2/3 in 2011.) The ICD-9 codes of interest included 992.0-992.9 and external cause of injury codes E900.0 and E900.9. We evaluated the sensitivity and positive predictive value (PPV) of the EpiCenter algorithm in relation to the patients' eventual diagnoses coded in the UB data.

Results

During the 15 months of data examined, there were a total of 871 people identified with HRI visits based on the EpiCenter algorithm. Over the same time period in the same emergency room facilities, there were a total of 2,146 people with a primary or secondary HRI diagnosis in UB. The algorithm for the EpiCenter's HRI definition had a sensitivity of 16% (348/2,146) when any primary or secondary ICD or E-code matched; the PPV was 40% (348/871). When data during a major heat event (July 21-23, 2011) was examined separately, both sensitivity (23%) and PPV (59%) improved.

Graph 1 presents the 2011 daily number of HRI visits from EpiCenter data and the subset of UB data from facilities also reporting to EpiCenter. The pattern in the EpiCenter data tracked with the UB data for HRI visits and correctly identified several major episodes in 2011.

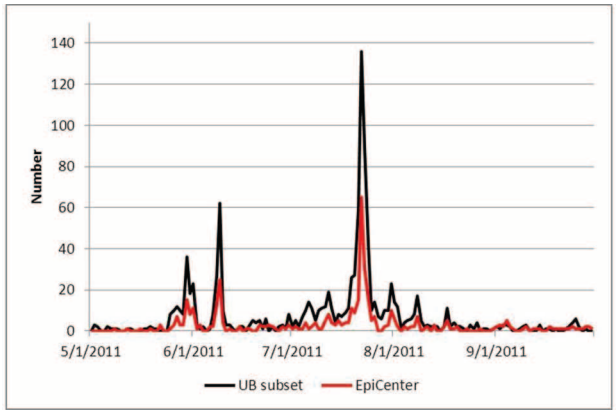
The major heat-related illness episode of July 2011 was selected to evaluate the non-matched EpiCenter and UB data. A total of 210 (95%) of the non-matched UB cases were able to be matched to EpiCenter chief complaint data. The EpiCenter information displayed a diverse range of general complaints, including syncope, dizziness, weakness, and headache. Similarly, non-matched EpiCenter data were compared to UB data to examine diagnoses, and 22 (48%) of the EpiCenter HRI cases were matched to UB diagnostic data. Diagnosis codes for these cases were for a variety of conditions classified under "general symptoms"; fluid balance disorders; asthma; diabetes; and unspecified hypertension.

Conclusions

The evaluation found that using chief complaint data to monitor HRI was relatively insensitive in comparison to the UB diagnosis codes, with a sensitivity of just over 16% for any UB HRI diagnosis. Sensitivity and PPV improved during a peak heat event.

The evaluation of the non-matched data (both EpiCenter and UB) provided little guidance for modifying the algorithm. While expanding the algorithm to include complaints such as syncope, dizziness, or weakness may capture a few more HRI cases, it would also likely result in a greater number of false positive cases (i.e., higher background noise).

Though not especially sensitive, EpiCenter data did identify all major episodes of HRI in 2011. The degree of correspondence indicates that the EpiCenter HRI algorithm provides a useful real-time gauge of the daily HRI trends.



Graph 1. 2011 HRI visits identified by EpiCenter data and UB data subset for the same EpiCenter reporting facilities.

Keywords

Chief complaint; Heat Related Illness; UB data

Acknowledgments

This evaluation was supported in part by the Environmental Public Health Tracking Program, Centers for Disease Control and Prevention, Cooperative Agreement #5U38EH000196.

*Stella Tsai
E-mail: stella.tsai@doh.state.nj.us

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Refactoring INDICATOR into an Advanced Information System for One Health Monitoring

Ian Brooks*[1, 2], Mario Felarca[1] and Bernie A'cs[1]

[1]NCSA, Urbana, IL, USA; [2]University of Saskatchewan, Saskatoon, SK, Canada

Objective

To redesign INDICATOR for One Health, establish a common data format, and provide for long term scalability.

Introduction

INDICATOR is a multi-stream open source platform for biosurveillance and outbreak detection, currently focused on Champaign County in Illinois[1]. It has been in production since 2008 and is currently receiving data from emergency departments, patient advisory nurse call center, outpatient convenient care clinic, school absenteeism, animal control, and weather sources. Long term scalability was however compromised during the 2009 H1N1 influenza pandemic as immediate public health needs took priority over our systematic development plan. With the impending addition of veterinary clinic data and recognizing that the health of a community also depends on animal and environmental factors, we decided to revisit the INDICATOR architecture and redesign it to be a more holistic and scalable system. We also decided to revisit the data submission format, keeping in line with the philosophy of making opportunistic secondary use of as much data about the health of a community that we can obtain.

Methods

Following a formal evaluation of the existing production version of INDICATOR we established the systems architecture shown in Figure 1 to leverage work in other cyberinfrastructure projects at NCSA.

Results

We have now implemented the back end changes, including unifying the multiple physical MySQL database systems and multiple Apache Tomcat application engines into a single system. A web application, using service oriented principles and the GWT library, has been developed that can query and display the newly unified data and provide new options for input of data to the system.

In order to streamline and simplify the data format we decided to define a single format that can be used by different kinds of healthcare providers, both human and veterinary. Although we recognize the limitations in this approach we define a reported event to be a simple what, when, and where containing the following seven fields or the relevant subset based roughly on the ISDS meaningful use recommendations [2]

1. Date of incident
2. ICD-9 code for the primary diagnosis
3. Free text of the diagnosis (not the text definition of the ICD-9 code)
4. Text chief complaint at triage
5. Location
6. Count
7. Species

In this way we can handle, in a single format, data from emergency departments, convenient care clinics, patient advisory nurse call centers, veterinary clinics, veterinary labs, and veterinary poison control centers.

Conclusions

INDICATOR has been significantly redesigned and is now more integrated, scalable, and secure. It is now placed to become a One Health integrated monitoring system.

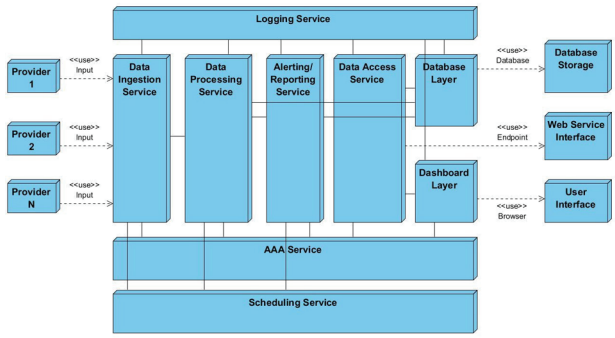


Figure 1. INDICATOR system architecture

Keywords

Open Source; Surveillance; Informatics; One Health

Acknowledgments

We would like to thank Carle Foundation, Christie Clinic, Champaign County animal control, Champaign County Humane Society, the Veterinary Medicine Data Base, and schools in Champaign County for sharing their data. We would also like to thank Julie Pryde and Awais Vaid, from Champaign-Urbana Public Health District for their ongoing support and assistance.

References

[1] Brooks I, Edwards W, INDICATOR: A Cyberenvironment for Biosurveillance and Response. Syndromic 2009.

[2] ISDS Meaningful Use Recommendations.

*Ian Brooks
E-mail: ian@ncsa.illinois.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Tracking Drug Overdose Trends in Ohio using ED Chief Complaints

Alise L. Brown*, William E. Storm and Brian E. Fowler

Ohio Department of Health, Columbus, OH, USA

Objective

Preliminary analysis was completed to define, identify, and track the trends of drug overdoses (OD), both intentional and unintentional, from emergency department (ED) and urgent care (UC) chief complaint data.

Introduction

The State of Ohio, as well as the country, has experienced an increasing incidence of drug ODs over the last three decades [3]. Of the increased number of unintended drug OD deaths in 2008, 9 out of 10 were caused by medications or illicit drugs [1]. In Ohio, drug ODs surpassed MVCs as the leading cause of injury death in 2007. This trend has continued through the most current available data [3]. Using chief complaint data to quickly track changes in the geographical distribution, demographics, and volume of drug ODs may aid public health efforts to decrease the number of associated deaths.

Methods

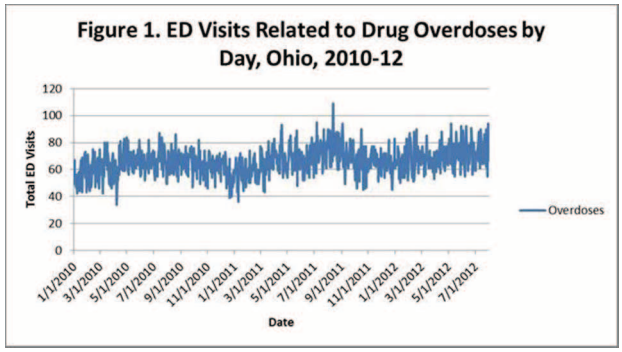
Chief complaint data from ED/UC visits were collected and analyzed from Ohio's syndromic surveillance application for 2010-2012. Ninety-six percent of all Ohio ED visits were captured during this timeframe. Due to the nonspecific nature of chief complaints as well as the lack of detail given upon registration at the ED/UC, attempting to separate visits into intentional vs. unintentional was not feasible. Therefore, a fairly specific classifier was created to define all potential ED/UC visits related to drug ODs. The data were analyzed, using SAS v 9.3, via time series analyses, and stratified by age, gender, and geographic region. Although these data types are pre-diagnostic in nature, they are more readily accessible than discharge data.

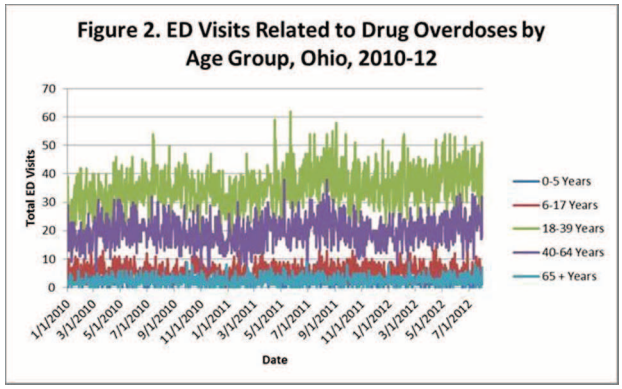
Results

On average, Ohio observed approx 66 ED/UC visits per day related to drug ODs from 2010-2012. The data show an increasing trend from 2010 through 2012 as well as a slight seasonal trend with higher visits observed in the spring/summer months as opposed to the autumn/winter months (Figure 1). The data showed that females attributed to a higher frequency of the drug ODs than males by approximately 4 ED/UC visits per day. Other data sources show a higher incidence in males than females related to unintentional drug ODs [3]. The highest age category attributing to the increase was the 18-39 years of age for both males and females, as shown in Figure 2. Population rates were calculated to identify those counties most affected by drug ODs. The data showed the highest rates of ED/UC visits related to drug ODs to be found in mostly rural areas of Ohio.

Conclusions

The annual death rate from unintentional drug poisonings by Ohio residents has increased from 3.6 in 2000 to 13.4 per 100,000 population in 2010[3]. As a result, the Ohio Governor created a Drug Abuse Task Force in 2009[4]. Ohio legislation (HB 93) implemented a prohibition on the operation of pain management clinics without a license on June 19, 2011[3]. According to this preliminary analysis, ED/UC visits related to drug ODs 1 year post-implementation of HB 93 continue to increase. It is unclear if HB 93 has slowed the rate of increase. Additionally, pre-diagnostic data has significant limitations including the significant possibility of misclassifying non-OD patient encounters as ODs. Further study of post-diagnostic data to confirm these trends is warranted.





Keywords

Drug Overdose; Chief Complaints; prescription drug abuse

References

1. BM Kuehn. Poisonings Top Crashes for Injury-Related Deaths: JAMA. 2012;307(3):242-242. doi:10.1001/jama.2011.1998.
2. Ohio Department of Health. (July, 2012). Ohio's Opioid Epidemic: An Overview of the Problem. http://www.odh.ohio.gov/sitecore/content/HealthyOhio/default/vipp/data/rxdata.aspx
3. Ohio Injury Prevention Partnership, Prescription Drug Abuse Action Group. HB 93 Summary. http://www.ccbh.net/storage/prescription-meds/HB93Summary.pdf
4. Ohio Prescription Drug Abuse Task Force. Final report. http://www.odh.ohio.gov/~/media/ODH/ASSETS/Files/web%20team/features/drug%20overdose/opdatffinalreport.ashx

*Alise L. Brown
E-mail: alise.brown@odh.ohio.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Update from CDC's Public Health Surveillance & Informatics Program Office (PHSIPO)

James Buehler*, Laura Conn, Carol Crawford and Kathleen Gallagher

Centers for Disease Control & Prevention, Atlanta, GA, USA

Objective

To provide updates on current activities and future directions for the National Notifiable Diseases Surveillance System (NNDSS), BioSense 2.0, and the Behavioral Risk Factor Surveillance System (BRFSS) and on the role of PHSIPO as the "home" at CDC for addressing cross-cutting issues in surveillance and informatics practice.

Introduction

The practice of public health surveillance is evolving as electronic health records (EHRs) and automated laboratory information systems are increasing adopted, as new approaches for health information exchange are employed, and as new health information standards affect the entire cascade of surveillance information flow. These trends have been accelerated by the Federal program to promote the Meaningful Use of electronic health records, which includes explicit population health objectives. The growing use of Internet "cloud" technology provides new opportunities for improving information sharing and for reducing surveillance costs. Potential benefits include not only faster and more complete surveillance but also new opportunities for providing population health information back to clinicians.

For public health surveys, new Internet-based sampling and survey methods hold the promise of complementing existing telephone-based surveys, which have been plagued by declining response rates despite the addition of cell-phone sampling. While new technologies hold promise for improving surveillance practice, there are multiple challenges, including constraints on public health budgets and the workforce. This panel will explore how PHSIPO is addressing these opportunities and challenges.

Methods

Panelists will provide updates on 1) PHSIPO's role in engaging health departments, the organizations that represent them, and CDC programs in shaping national policies for implementing the Meaningful Use program, 2) how the BioSense 2.0 program is supporting growth in syndromic surveillance capacity, including its partnership with ISDS in developing standards for syndromic surveillance as part of Meaningful Use, 3) improvements that are underway in strengthening the NNDSS, including efforts to improve CDC's support for health department disease reporting systems and to develop a "shared services" approach that could provide a platform for streamlining the exchange of information between health departments and CDC, 4) pilot development of Internet-based panels of survey volunteers to supplement existing telephone-based sampling in the BRFSS and of approaches to extend BRFSS survey information through consent-based linkage of survey responses to selected measures recorded in respondents' EHRs.

Results

Potential questions or discussion points that might arise include: What can or should be done to assure that the population health objectives of Meaningful Use are fulfilled? What are the lessons learned to date in leveraging investments in the Meaningful Use of EHRs to improve disease reporting and syndromic surveillance systems? What are the next steps in developing BioSense 2.0 to assure that it leads to strengthened surveillance capacity at both state/local and regional/national levels? How can insights from the BioSense redesign be applied to improve case reporting and other surveillance capacities? What is CDC doing to address states' concerns about the growing number of CDC surveillance systems? How will national discussions about the future of public health affect the future surveillance practice? What can be done to assure the ongoing representativeness of population health surveys? Is it feasible to link BRFSS responses to information obtained from EHRs? How can data from surveillance become part of the real-time evidence base for clinical decision making?

Conclusions

The intended outcome of the panel is to foster a conversation between the panelists and the audience, to inform the audience about recent developments in PHSIPO, to obtain insights from the audience about innovations and ideas arising from their experience, and to generate new ideas for approaches to meeting the needs of public health for surveillance information.

Keywords

Surveillance; BioSense 2.0; Notifiable Diseases; BRFSS—Behavioral Risk Factor Surveillance System

Acknowledgments

The authors wish to acknowledge the many individuals from health departments, academia, and other agencies who have contributed to the ongoing operation and improvement of the NNDSS, BioSense 2.0, and the BRFSS.

References

For more information about PHSIPO, see: http://www.cdc.gov/osels/phsipo

*James Buehler
E-mail: jwb2@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Development of a Vietnamese Language Outbreak Mapping and Surveillance System

David Bui*[1, 2], Sumiko Mekaru[1, 3], Clark Freifeld[1, 6] and John S. Brownstein[1, 5, 4]

[1]Children's Hospital Informatics Program, Division of Emergency Medicine, Children's Hospital Boston, Boston, MA, USA; [2]Dept of Epidemiology, Mel Enid Zuckerman College of Public Health, Tucson, AZ, USA; [3]Dept of Epidemiology, Boston University School of Public Health, Boston, MA, USA; [4]Dept of Pediatrics, Harvard Medical School, Boston, MA, USA; [5]Dept of Epidemiology, Biostatistics and Occupational Health, McGill University, Montreal, QC, Canada; [6]Dept of Biomedical Engineering, Boston University, Boston, MA, USA

Objective

To present the development of a surveillance system utilizing online Vietnamese language media sources to detect disease events in Vietnam and the South East Asian Region.

Introduction

In the South East Asia Region (SEAR), infectious disease continues to be a leading cause of death. SEAR countries, like Vietnam, are also at risk for outbreaks of emerging diseases due to high population density, proximity to animals and deforestation.(1) Given Vietnam's location in SEAR and its recurrent outbreaks of zoonotic diseases—timely surveillance in Vietnam is critical to global public health.(1) Online news sources have been recognized as potential sources for early detection of emerging disease outbreaks, as was the case with SARS. (2) HealthMap, an innovative disease surveillance system developed at Boston Children's Hospital, leverages the expediency of online news media by using text-mining technology to monitor and map global disease outbreaks reported by news sources.

Methods

HealthMap currently monitors disease related news in 15 languages. Building on HealthMap's existing infrastructure, we translated the system's existing disease and location name dictionaries to corresponding Vietnamese terms to train the system to detect disease and locations cited in Vietnamese news sources. To ensure comprehensive capture of disease terms, both formal disease names and colloquial synonyms were used. Vietnamese locations were sourced through the official Vietnamese government website. Search queries were developed using a variety of outbreak related terms like "bùng phát" (outbreak) or "bênh" (disease), and specific disease names like "Cúm gia câm" (Avian Influenza). Automated searches are performed in the Vietnamese version of Google News.

Results

As of August 18, 2012, after 2 months in operation, the system has mapped 433 alerts in 27 diseases reported in the Vietnamese media compared to 7 diseases in English in the same time period. The collected alerts were mapped to 699 province level and district level (or lower) locations compared to only 16 in the English feed. To date, the system collected 38 alerts of Avian Influenza from Vietnamese sources compared to only 2 in English sources; 30 alerts of Dengue compared to 7 in English; and 25 alerts of Hand Foot and Mouth compared to 6. The system also collects outbreak case counts in Vietnam. For example, counts of human Dengue cases in 97 locations in Vietnam were collected, providing a rich dataset for monitoring epidemic spread and progression. The surveillance feed also received 2 reports of outbreaks in crops. Zoonotic disease outbreaks in Vietnam were more comprehensively covered in the Vietnamese feed compared to English.

Conclusions

Leveraging the expediency of freely available online news media, the developed surveillance system is able to detect and map outbreaks occurring in Vietnam in near real-time, providing health organizations and researchers with timely and comprehensive coverage of disease events to assess pandemic risk and mobilize aid as necessary.

Screenshot of HealthMap Vietnamese Alerts

Keywords

Surveillance; Infectious Disease; Vietnam; HealthMap; Mapping

Acknowledgments

Sumiko Mekaru, John Brownstein, Clark Freifeld, Susan Aman, and the whole HealthMap gang.

References

1. World Health Organization. Combating Emerging Infectious Diseases. Searo.who.int. Available at: http://www.searo.who.int/LinkFiles/Avian_Flu_combating_emerging_diseases.pdf. Accessed August 28, 2012.
2. J.S. Brownstein. Digital Disease Detection: Harnessing the Web for Public Health Surveillance. N Engl J Med 2009; 360:2153-2157 Available at: http://www.nejm.org/doi/full/10.1056/NEJMp0900702. Accessed April 16, 2012.

*David Bui
E-mail: davidbui@email.arizona.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

One Health Surveillance with Electronic Integrated Disease Surveillance System

Alexey V. Burdakov*, Andrey O. Ukharov and Thomas G. Wahl

Black & Veatch, Overland Park, KS, USA

Objective

The objective of this demonstration is to show conference attendees how one-health surveillance in medical, veterinary and environmental sectors can be improved with Electronic Integrated Disease Surveillance System (EIDSS) using CCHF as an example from Kazakhstan.

Introduction

EIDSS supports collection and analysis of epidemiological, clinical and laboratory information on infectious diseases in medical, veterinary and environmental sectors. At this moment the system is deployed in Kazakhstan at 150 sites (planned 271) in the veterinary surveillance and at 8 sites (planned 23) in human surveillance. The system enforces the one-health concept and provides capacity to improve surveillance and response to infectious disease including especially dangerous like CCHF.

EIDSS has been in development since 2005 and is a free-of-charge tool with plans for open-source development. The system development is based on expertise of a number of US and international experts including CDC, WRAIR, USAMRIID, et al.

Methods

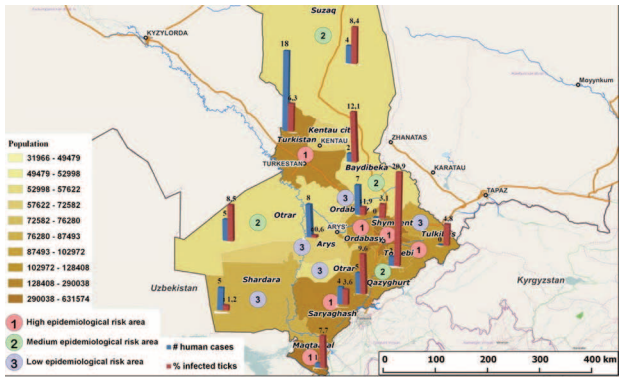
Effective monitoring and control of zoonotic diseases requires integrated approach to surveillance in medical, veterinary and environmental sectors. Capability to rapidly collect and analyze information from these sectors is challenging due to diversity of different systems often used in these areas. EIDSS presented a unique integrated solution which allows collecting, sharing and analyzing data across these sectors. In those countries where this system is implemented both in human and veterinary surveillance (Georgia, Azerbaijan and Kazakhstan), it provides a unique opportunity to improve monitoring and control capability.

In Kazakhstan and other countries experts are working on creating and improving effective analysis methods. In particular a method of real-time control of CCHF situation was developed in Kazakhstan. It allows the assembly of raw data gathered at the lower level in, surveillance system throughout the country on CCHF cases in humans, assemble ticks vector surveillance campaigns and laboratory diagnostic results and analyze these data against population density. This gives a one-step tool to an epidemiologist to understand the situation and plan response at the national and regional level (see sample map). A quick link with the veterinary response teams allow to rapidly act with domestic animals prophylaxis measures.

Demonstration of the tool encouraging the One Health approach to the surveillance which is already in place in a number of countries provides an exclusive opportunity to review different aspects of its utilization in practice as well as discuss challenges and benefits of this method in resource limited environments.

Conclusions

EIDSS provides a capacity to improve one-health disease surveillance in human, veterinary and vector sectors by rapidly collecting, disseminating and analyzing data on infectious diseases. Particular methods which are being developed in Kazakhstan and other participating countries provide an instrument to epidemiologists to make decisions and more effectively plan response measures. Currently particular methods were tested for CCHF infection. It is planned to introduce methods for brucellosis and other infectious diseases of special interest in Central Asia and Caucasus Region.



Keywords

EIDSS; electronic surveillance; one-health

References

1. Burdakov A., Ukharov A. Transforming national human and veterinary disease surveillance systems from paper into integrated electronic form in the FSU countries // 15th International Congress on Infectious Diseases (ICID), Bangkok 2012
2. Burdakov A., Ukharov A. Electronic Integrated Disease Surveillance (EIDSS) // World Congress on Information and Communication Technologies for Development (WCID'09) congress in Beijing, China - 2009
3. Burdakov A. Implementation of Information-Telecommunication part of the Threat Agent Detection and Response (TADR) program in Republic of Kazakhstan // Official Bulletin of State Sanitary-Epidemiological Service of Republic of Kazakhstan, 1/37. 69-70.

*Alexey V. Burdakov
E-mail: BurdakovAV@bv.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Coverage and Timeliness of Combined Military and Veteran Surveillance Systems

Howard S. Burkom[1], Yevgeniy Elbert[1], Carla Winston[2], Julie Pavlin*[3], Cynthia Lucero-Obusan[2] and Mark Holodniy[2]

[1]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA; [2]Veterans Health Administration, Palo Alto, CA, USA; [3]Armed Forces Health Surveillance Center, Silver Spring, MD, USA

Objective

We determined the utility and effective methodology for combining patient record information from the Departments of Veterans Affairs (VA) and Defense (DoD) health surveillance systems.

Introduction

An objective of the Joint VA/DoD BioSurveillance System for Emerging Biological Threats project is to improve situational awareness of the health of combined VA and DoD populations. DoD and VA both use versions of the Electronic Surveillance System for the Early Notification of Community-Based Epidemics (ESSENCE). With a retrospective outpatient data collection available, we analyzed relative coverage and timeliness of the two systems to understand potential benefits of a joint system.

Methods

We used the US Office of Management and Budget's core-based statistical area (CBSA) to group data from the respective systems by megapolitan (>1 million), metropolitan (50,000-1 million) and micropolitan (10,000-50,000) areas. We performed frequency analyses and mapped coverage of the VA and DoD medical systems in these CBSAs. To determine comparability, we compared International Classification of Diseases, 9th Revision (ICD-9) code usage from 2007-2010 by age group in the respective systems and then formulated a working definition of influenza-like illness (ILI). We then compared CBSA-level temporal detection timeliness in the two systems for the H3N2 epidemic of 2007-9 and the H1N1 pandemic in 2009.

Results

We identified a total of 939 CBSAs, with generally diffuse geographic coverage by VA facilities and higher concentration in larger metro and mega areas for DoD facilities. Of the 51 mega CBSAs, all have at least one VA facility and 63% have a DoD facility. Coverage is sparser for the metro CBSAs and lighter still for the micro CBSAs (Table 1). Although the VA coverage is greater, in many CBSAs with dual coverage, the DoD visit volume is comparable or greater. Patient age distribution differs sharply, with >85% of the VA patients over 45 years of age compared to 22% of DoD patients. For all CBSAs, the overall VA/DoD visit ratio is 1.92, but the ratios for 0-17 years is 0.004, 18-44 years 0.33, 45-64 years 5.20 and >65 years 11.63.

Based on an analysis of ICD-9 codes used in the two systems, the DoD uses symptom-based ILI codes far more frequently than the VA, especially codes for diseases often seen in children (e.g., otitis media). Analysis of ILI-related codes assigned in both systems led to a common code set for comparative analysis. From applying alerting algorithms to visit counts based on this code set, detection was better in DoD data for 57% and 77% of CBSAs for seasonal and pandemic influenza, respectively, and better in VA data for 37% and 14% of CBSAs (Table 2). The VA system performed better during the typical H3N2 seasonal flu compared to the H1N1 outbreak. The DoD system performed better during the H1N1 pandemic, although outperformed the VA for both.

Conclusions

The coverage analysis demonstrates two complementary surveillance systems with evident benefits to a fused national health picture. The VA system patient volume roughly doubles the DoD system, and provides better geographic coverage in smaller CBSAs; however, the DoD includes younger populations, better coverage in strategic metro areas, and more pre-diagnostic ILI coding. From analysis of both outbreaks, relative timeliness could be improved in 92% of CBSAs with access to both systems, with more information provided in CBSAs where only one type of facility exists.

Table 1. Counts of CBSAs containing VA and DoD facilities

Coverage Summary	Pop > 1 Million	>50,000-1 million	>10,000-50,000
Both	32	94	6
Neither	0	149	244
DoD Only	0	16	5
VA only	19	292	82
Visit Counts DoD>VA	6	56	5
Visit Counts DoD<VA<5*DoD	10	24	1
Visit Counts VA>5*DoD	16	14	0

Table 2. Relative timeliness by CBSAs with both DoD and VA facilities with a minimum average of 2 ILI visits/week

Alert Timeliness	07-08 H3N2	09 H1N1	Both
Same Week	6 (6%)	5 (5%)	11 (6%)
DoD Earlier	51 (55%)	60 (65%)	111 (60%)
VA Earlier	33 (35%)	10 (11%)	43 (23%)
DoD Only	2 (2%)	12 (13%)	14 (8%)
VA Only	1 (1%)	3 (3%)	4 (2%)
No Alert	0	3 (3%)	3 (2%)

Keywords

Syndromic surveillance; Merged systems; Government

*Julie Pavlin
E-mail: julie.pavlin@us.army.mil

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Refinement of a Population-Based Bayesian Network for Fusion of Health Surveillance Data

Howard Burkom*, Yevgeniy Elbert, Liane Ramac-Thomas, Christopher Cuellar and Vivian Hung

Johns Hopkins Applied Physics Laboratory, Laurel, MD, USA

Objective

The project involves analytic combination of multiple evidence sources to monitor health at hundreds of care facilities. A demonstration module featuring a population-based Bayes Network [1] was refined and expanded for application in the Department of Defense Electronic Surveillance System for Community-Based Epidemics (ESSENCE).

Introduction

The ESSENCE demonstration module was built to help DoD health monitors make routine decisions based on disparate evidence sources such as daily counts of ILI-related chief complaints, ratios of positive lab tests for influenza, patient age distribution, and counts of antiviral prescriptions [1]. The module was a population-based (rather than individual-based) Bayesian network (PBN) in that inputs were algorithmic results from these multiple aggregate data streams, and output was the degree of belief that the combined evidence required investigation. The module reduced total alerts substantially and retained sensitivity to the majority of documented outbreaks while clarifying underlying sources of evidence. The current effort was to advance the prototype to production by refining components of the fusion methodology to improve sensitivity while retaining the reduced alert rate.

Methods

The multi-level approach to sensitivity improvement included expanded syndromic queries, more data-sensitive algorithm selection, improved transformation of algorithm outputs to alert states, and hierarchical training of Bayesian networks. Components were tested individually, and the net result was iteratively refined with performance using documented outbreaks.

We examined time series of classes of prescribed drugs and laboratory tests during known events and discussed outbreak-associated elements with domain experts to liberalize data queries. Algorithms were matched to data streams with injection testing applied to 4.5 years of data from 502 outpatient clinics. A hierarchical approach was applied for improved training and verification of PBNs for events related to categories of Influenza-like Illness, Gastrointestinal, Fever, Neurological, and Rash, chosen both for public health importance and for availability of multiple supporting data types. Hierarchical, modular training was applied to common subnetworks, such as a severity indicator PBN depending on case disposition, acute case indicators, complex evaluation/management codes, and patient bounce-backs, depicted in Figure 1. Conversion of individual algorithm outputs to belief states (e.g. “at least two red alerts/past 7 days”) was broadened using analysis of lags between data sources. With data from the known events, we calculated decision support thresholds for the parent-level PBN decision nodes with a stochastic optimization technique maximizing the ratio of alert rates during outbreak to non-outbreak periods.

Results

The expanded data queries, more stream-specific algorithm selection, generalized state transformation, and hierarchical PBN training detected 22 of an expanded collection of 24 documented outbreaks, with incremental improvement ongoing. The mean alert rate drop achieved by the Bayes Net was 87% (minimum of 85%) compared to the combined alerts of all component algorithms across syndromes and facilities.

Conclusions

Expansion and further technical validation upheld the PBN approach as a user-friendly means of analytic decision support given multiple, variably weighted evidence sources. The PBN affords not only sharply reduced alerting, but also transparent indication of evidence underlying each alert. The older algorithm approach remains available as backup. Beta testing of the resulting production system will drive further modification.

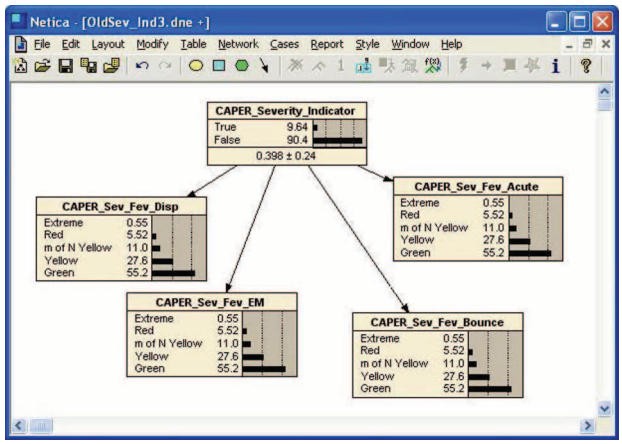


Figure 1: PBN Subnetwork for Event Severity, based on Outpatient Data Fields

Keywords

Fusion; Bayesian Network; Multivariate; Decision Support

Acknowledgments

Drs. Julie Pavlin and Rhonda Lizewski of the Armed Forces Health Surveillance Center for data- and event-related consultation and Joe Lombardo and Wayne Loschen of Johns Hopkins APL for consultation on production enhancement.

References

Burkom H, Elbert Y, Ramac-Thomas L et al., Analytic fusion of ESSENCE clinical evidence sources for routine decision support, Emerging Health Threats Journal Supplements, eISSN 1752-8550, ISSN 2001 1350 (print).

*Howard Burkom
E-mail: howard.burkom@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Use of Syndromic Data to Determine Oral Health Visit Burden on Emergency Departments

Howard Burkom*[1], Sherry Burrer[1], Laurie Barker[3], Valerie Robison[3], Peter Hicks[1] and Amy Ising[2]

[1]CDC, OSELS, Public Health Surveillance Program Office, Atlanta, GA, USA; [2]University of North Carolina Department of Emergency Medicine, Chapel Hill, NC, USA; [3]CDC, NCCDPHP, Div. of Oral Health, Atlanta, GA, USA

Objective

The objective was to use syndromic surveillance data from the North Carolina Disease Event Tracking and Epidemiologic Collection Tool NCDETECT and from BioSense to quantify the burden on North Carolina (NC) emergency departments of oral health-related visits more appropriate for care in a dental office (ED). Calculations were sought in terms of the Medicaid-covered visit rate relative to the Medicaid-eligible population by age group and by county.

Introduction

Concern over oral health-related ED visits stems from the increasing number of unemployed and uninsured, the cost burden of these visits, and the unavailability of indicated dental care in EDs [1]. Of particular interest to NC state public health planners are Medicaid-covered visits. Syndromic data in biosurveillance systems offer a means to quantify these visits overall and by county and age group.

Methods

Using BioSense data received from NCDETECT, 60.8 million records from 12.9 million ED visits were collected, covering all NC visits for state fiscal years (SFY) 2008-2010. Roughly 4% of visits were dropped because of patient residence zip codes missing or outside NC. A careful multi-step procedure involving both dentist consultants and data analysis was used to derive classification criteria for visits whose main reason was a nontraumatic oral health problem [2]. This procedure yielded 243,970 visits by ~174,600 patients based on hospital-specific patient identifiers. Nontraumatic oral health-related visits were collected in a study set with added fields for method of payment, patient residence county, and age group. Based on previous studies, consultant preferences, and NC Medicaid eligibility guidelines, selected age groups were 0-14, 15-19, 20-29, 30-49, 50+ years. Stratified counts of Medicaid-eligibles were obtained from the NC Dental Director by study year. Using these tables and the ED visit study set, rates of nontraumatic oral health-related Medicaid visits per 10,000 eligibles were tabulated by county and age group for each study year. Demographics of multiple-visit patients were also studied.

Results

Rates of ED oral health-related visits were substantially higher for young adults than for other age groups. From statewide rates in Table 1, this age factor was consistent across study years.

County-level rates showed the same age pattern to varying degrees. Detailed analysis showed problem areas, with rates in 21 of 100 counties exceeding 60 per 10,000 eligibles for the 20-29 year age group. Plots and tables complemented understanding of the ED oral health visit burden by age and county. The state total ED burden for oral health problems was ~2% (0.2% - 9.7% by county).

Conclusions

Judicious use of syndromic data with external information, such as the detailed Medicaid denominators and the Method of Payment codes for each visit above, can give quantified estimates for policy-related public health issues. In the current study, the derived oral health visit rates gave numerical detail to concerns about the use of NC EDs for nontraumatic oral health problems by low-income persons affected by the economic recession. Results also show rate variation by county and can be combined with access-to-care data to inform planning of effective local measures to improve access to dental services and thus reduce the ED visit burden.

Table 1. NC Statewide Oral Health Medicaid Visits to Emergency Departments per 10,000 Eligibles

Visits per 10,000 Eligibles	SFY 2008	SFY 2009	SFY 2010
All Age	9.5	9.9	9.2
0-14 yrs	1.9	1.8	1.8
15-19 yrs	8.4	9.0	7.9
20-29 yrs	42.6	43.4	39.6
30-49 yrs	22.9	24.2	22.5
50+ yrs	9.5	2.5	2.4

Keywords

emergency department; chief complaint; BioSense; oral health; NCDETECT

Acknowledgments

Mark Casey, North Carolina Dental Director for Medicaid eligibility and care provider data; Chris Okunseri, Marquette University for case definition advice; Lana Deyneka of the North Carolina Department of Health and Human Services for consultation; Dennis Falls of NCDETECT for Method of Payment information.

References

1. Shortridge, E. and Moore, J. 2010. "Use of Emergency Departments for Conditions related to Poor Oral Health Care." Final Report. Washington, DC: Office of Rural Health Policy. August 2010.
2. Burrer S, Burkom H, Okunseri C, Barker L, Robison V, Nontraumatic Oral Health Classification developed from Syndromic Data, Abstract, International Society of Disease Surveillance Conference 2012.

*Howard Burkom
E-mail: howard.burkom@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Localized Cluster Detection Applied to Joint and Separate Military and Veteran Subpopulations

Howard Burkom*[1], Yevgeniy Elbert[1], Carla Winston[2], Julie Pavlin[3], Cynthia Lucero-Obusan[2] and Mark Holodniy[2]

[1]Johns Hopkins Applied Physics Laboratory, Laurel, MD, USA; [2]Office of Public Health Surveillance Research, Veterans Health Administration, Palo Alto, CA, USA; [3]Armed Forces Health Surveillance Center, Silver Spring, MD, USA

Objective

We examined the utility of combining surveillance data from the Departments of Defense (DoD) and Veterans Affairs (VA) for spatial cluster detection.

Introduction

The Joint VA/DoD BioSurveillance System for Emerging Biological Threats project seeks to improve situational awareness of the health of VA/DoD populations by combining their respective data. Each system uses a version of the Electronic Surveillance System for Early Notification of Community-Based Epidemics (ESSENCE); a combined version is being tested.

The current effort investigated combining the datasets for disease cluster detection. We compared results of retrospective cluster detection studies using both separate and joined data. — Does combining datasets worsen the rate of background cluster determination?

— Does combining mask clusters detected on the separate datasets?

— Does combining find clusters that the separate datasets alone would miss?

Methods

Cluster determination runs were done with a spatial scan statistics implementation previously verified [1] by comparison with SaTScan software [2] using DoD data from the Biosense system.

Input data files were extracted from a repository of outpatient records from both DoD and VA facilities covering 4 years beginning Jan. 1, 2007. This repository includes over 37 million DoD records and over 86 million VA records. Input files were matrices of daily Influenza-like-Illness (ILI) or gastrointestinal (GI) visit counts. Matrix rows were consecutive days, columns were patient residence zip codes, and entry (i, j) was the number of visits on day i from with zip code j. These files were made for DoD data, VA data, and combined data.

For assessing the alerting burden from combining datasets, three sets of runs were executed using data from three regions, Baltimore/Washington D.C. (dominated by DoD data), Los Angeles (mainly VA data), and Tampa (representation of both). For each region, sets of 1672 daily runs were executed for ILI and GI syndrome data. Lastly, focused runs were done to investigate known outbreaks in New York (GI, Jan-Mar 2010), San Diego (ILI, Dec 2007-Apr 2008 and Fall 2009), and New Jersey (GI, Jan-Mar 2010).

Results

Combining the data sources increased the rate of significant cluster alerting by a manageable 1-10% across run sets. Some clusters found only when the data were combined persisted over several days and may have indicated small events not reported in either system; however, we were unable to validate minor events that may have occurred in past years.

Retrospective looks at known outbreaks were successful in that clustering evidence found in separate DoD and VA runs persisted when data sets were combined. For the New York run, a West Point outbreak was seen in repeated clusters of combined data, beginning days before the event report. However, clustering did not consistently produce alerts before outbreak report dates. In the New Jersey DoD runs, repeated clusters indicated a 10-week GI outbreak at Fort Dix; adding VA data that dominated the record counts gave the same clusters with no added cases, so the DoD event was probably self-contained. The San Diego runs were aimed at detecting unusually severe influenza epidemics in February 2008 and in the fall of 2009, and numerous clusters were found but did not enhance regional disease tracking.

Conclusions

From the analysis, combining DoD and VA data enhances cluster detection capability without loss of sensitivity to events isolated in either population and with manageable effect on the customary alert rate. For cluster detection, there may be many geographic regions where a health monitor in one of the systems would benefit from combined data. More detailed outbreak information is needed to quantify the timeliness/sensitivity advantages of combining datasets. In events examined, clustering itself yielded an occasional but not consistent timeliness advantage.

Keywords

ESSENCE; Department of Defense; scan statistics; cluster detection; Veterans Administration

References

[1] Xing J, Burkom H, Moniz L, Edgerton J, Leuze M, and Tokars J. Evaluation of sliding baseline methods for spatial estimation for cluster detection in the biosurveillance system, International Journal of Health Geographics 2009, 8:45

[2] SaTScan: Software for the spatial, temporal, and space-time scan statistics. www.satscan.org (last accessed 20Aug2012)

*Howard Burkom
E-mail: howard.burkom@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Nontraumatic Oral Health Classification for Alternative Use of Syndromic Data

Sherry Burrer*[1], Howard Burkom[1], Christopher Okunseri[2], Laurie Barker[1] and Valerie Robison[1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA; [2]Marquette University, Milwaukee, WI, USA

Objective

To develop a nontraumatic oral health classification that could estimate the burden of oral health-related visits in North Carolina (NC) Emergency Departments (EDs) using syndromic surveillance system data.

Introduction

Lack of access to regular dental care often results in costly, oral health visits to EDs that could otherwise have been prevented or managed by a dentist (1). Most studies on oral health-related visits to EDs have used a wide range of classifications from different databases, but none have used syndromic surveillance data. The volume, frequency, and included details of syndromic data enabled timely burden estimates of nontraumatic oral health visits for NC EDs.

Methods

Literature review, input by subject matter experts (SMEs), and analysis of syndromic data was used to create the nontraumatic oral health classification. BioSense, a near real-time, national-level, electronic health surveillance system was the source of the NC ED syndromic data. Visits with at least one oral health-related ICD-9-CM code were extracted for NC fiscal years 2008–2010. Univariate analyses of chief complaint (CC) and final diagnosis data along with SME consultation were used to determine the CC substrings and 'white list' of ICD-9-CM codes used as inclusion criteria to classify visits as oral health-related. These analyses and consultations also determined the trauma-related codes and substrings used to exclude visits.

Results

Table 1 shows all nontraumatic oral health-related ICD-9-CM codes used for the characterization. Codes likely related to the types of dental emergencies that routine dental care could not have prevented were excluded. Approximately 275,000 patient records were evaluated to determine the CC substrings. The final CC substrings chosen (Table 1) represented over 56% of visits in the candidate record dataset. Over 334,000 BioSense patient records were evaluated, and SMEs reviewed the 32 ICD-9-CM codes that co-occurred most commonly in visits containing oral health-related ICD-9-CM codes to determine which co-occurring ICD-9-CM codes (white list, Table 1) could be present and still maintain the main reason for the visit as an oral health-related problem. Trauma-related visit criteria used for exclusion were derived from a subset of BioSense sub-syndromes (Falls; Fractures and dislocation; Injury, NOS; Sprains and strains; and Motor vehicle traffic accidents) and from selected CC substrings ('assault', 'fight', and 'brawl').

In summary, an ED visit had a nontraumatic oral health classification if it contained 1) an oral health-related CC substring with no trauma-related ICD-9-CM codes or CC substrings or 2) an oral health-related ICD-9 code accompanied by no oral health-related or trauma-related CC substrings and with no other diagnosis codes except for those on the whitelist.

Conclusions

There is increasing demand to determine ways to use syndromic surveillance data in an alternative way for population health surveillance. This use of BioSense data provided a practical classification of patient records for the tracking of nontraumatic oral health-related visits to NC EDs. Visit estimates created using this classification in combination with other pertinent information could prove useful to policymakers when deciding upon resource allocation aimed at reducing this unnecessary burden on the NC ED system. The large volume of records in syndromic surveillance systems offers substantial weight of evidence for alternative use in epidemiological studies; however, accurate classification of records is required to select cases of interest. While data volume precludes validation of every included record, a combination of human expertise and data analysis can provide credible classification criteria.

Table 1. Inclusion Criteria for Nontraumatic Oral Health Classification

Oral Health-Related ICD-9-CM Codes	White List ICD-9-CM Codes		Oral Health-Related CC Substrings
521.x	780.60	388.70	Tooth and ache
522.x	305.1	682.0	Tooth and abscess
523.x	401.9	786.2	Tooth and pain
525.x	784.0	478.19	Tooth and abcess**
528.x*	784.2	780.6	Dental
	526.9		

x = includes all numbers under this ICD-9-CM subheading
*Except 528.3 and 528.5
**Most common misspelling of abscess

Keywords

Syndromic Surveillance; Oral Health; Emergency Departments

Acknowledgments

Amy Ising, NC DETECT; Lana Deyneka, NC DHHS; and Rebecca King, NC DHHS

References

1. Davis EE, Deinard AS, Maïga EW. Doctor, my tooth hurts: the costs of incomplete dental care in the emergency room. J Public Health Dent. 2010 Summer;70(3):205-10.

*Sherry Burrer
E-mail: sburrer@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Increasing Mild Enterovirus Cases Provides An Important Signal of Up-coming Trends in Elevating Severe Enterovirus Cases

Ta-Chien Chan*[1], Rung-Hung Chen[2] and Chwan-Chuen King[3]

[1]Center for GIS, Research Center for Humanities and Social Sciences, Academia Sinica, Taipei City, Taiwan; [2]Department of Medicine, College of Medicine, National Taiwan University, Taipei City, Taiwan; [3]Institute of Epidemiology and Preventive Medicine, College of Public Health, National Taiwan University, Taipei City, Taiwan

Objective

This study was to elucidate the spatio-temporal correlations between the mild and severe enterovirus cases through integrating enterovirus-related three surveillance systems in Taiwan. With these fully understanding epidemiological characteristics, hopefully, we can develop better measures and indicators from mild cases to provide early warning signals and thus minimizing subsequent numbers of severe cases.

Introduction

In July 2012, the 54 children infected with enterovirus-71(EV-71) were died in Cambodia [1]. The media called it as mystery illness and made Asian parents worried. In fact, the severe epidemics of enterovirus occurred frequently in Asia, including Malaysia, Singapore, Taiwan and China [2]. The clinical severity varied from asymptomatic to mild (hand-foot-mouth disease and herpangina) and severe pulmonary edema/hemorrhage and encephalitis [3]. Up to now, the development of vaccine for EV-71 and the more effective antiviral drug was still ongoing [4]. Therefore, surveillance for monitoring the enterovirus activity and understanding the epidemiological characteristics between mild and severe enterovirus cases was crucial.

Methods

Three main databases including national notifiable diseases surveillance, sentinel physician surveillance and laboratory surveillance from July 1, 1999 to December 31, 2008 were analyzed. The Pearson's correlation coefficient was applied for measuring the consistency of the trend. The Poisson space-time scan statistic [5] was used for identifying the most likely clusters. We used GIS (ArcMap, version9.0; ESRI Inc.,Redlands, CA, USA) for visualization of detected clusters.

Results

Temporal analysis found that the Pearson's correlation between mild EV cases and severe EV cases occurring in the same week was 0.553 ($p<0.01$) in Figure 1. Such a correlation became moderate (data) when mild EV cases happened in 1~4 weeks before the current severe EV cases. Among the 1,517 severe EV cases notified to Taiwan CDC during the study period, the mean age was 27 months, 61.4% was male and 12% were fatal. These severe EV cases were significantly associated with the positive isolation rate of EV-71, with much higher correlation than the mild cases [0.498 $p<0.01$ vs. 0.278, $p<0.01$] . Using the space-time cluster method, we identified three possible clusters in June 2008 in six cities/counties (Figure 2).

Conclusions

Taiwan's surveillance data indicate that local public health professionals can monitor the trends in the numbers of mild EV cases in community to provide early warning signals for local residents to prevent the severity of future waves.

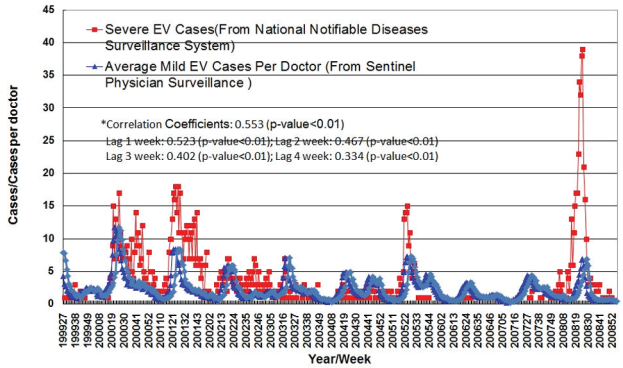


Figure 1. The temporal trend between mild and severe EV cases.

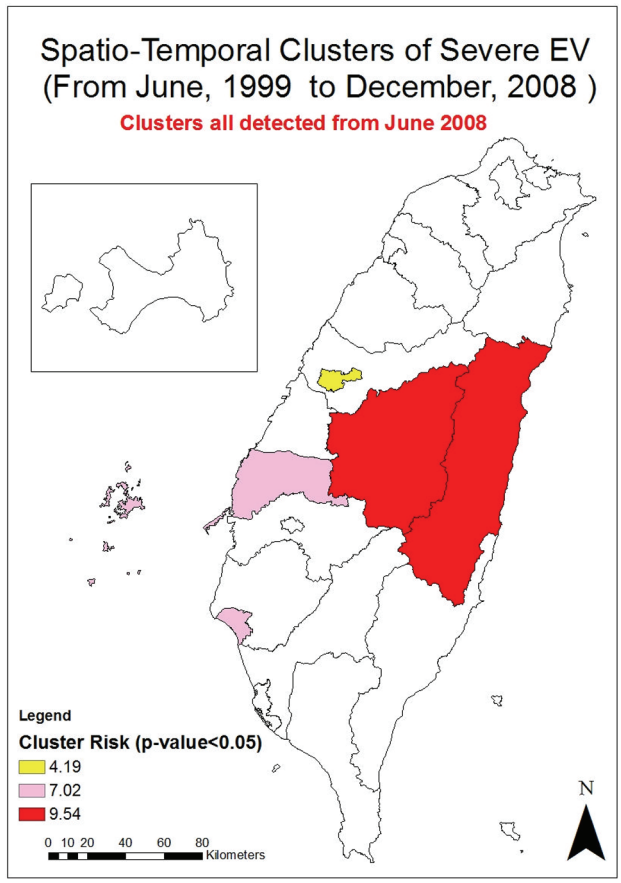


Figure 2. The spatio-temporal clusters of EV severe cases.

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Keywords
Enterovirus; Suveillance; Space Time Clusters

References

1. WHO, Severe complications of hand, foot and mouth disease (HFMD) caused by EV-71 in Cambodia – conclusion of the joint investigation[http://www.who.int/csr/don/2012_07_13/en/index.html]
2. Lee MS, Chiang PS, Luo ST, Huang ML, Liou GY, Tsao KC, Lin TY: Incidence rates of enterovirus 71 infections in young children during a nationwide epidemic in Taiwan, 2008-09. PLoS Negl Trop Dis 2012, 6(2):e1476.
3. Chen SC, Chang HL, Yan TR, Cheng YT, Chen KT: An eight-year study of epidemiologic features of enterovirus 71 infection in Taiwan. Am J Trop Med Hyg 2007, 77(1):188-191.
4. Chang LY: Enterovirus 71 in Taiwan. Pediatr Neonatol 2008, 49(4):103-112.
5. Kulldorff M, Athas WF, Feurer EJ, Miller BA, Key CR: Evaluating cluster alarms: a space-time scan statistic and brain cancer in Los Alamos, New Mexico. Am J Public Health 1998, 88(9):1377-1380.

*Ta-Chien Chan
E-mail: dachianpig@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluation of Emergency Department Data Quality following PHIN Syndromic Surveillance Messaging Guide

Hwa-Gan Chang*[1], Charlene Weng[1], Charlie DiDonato[2], Dave DiCesare[1], Jian-Hua Chen[1] and Debra Blog[1]

[1]NYSDOH, Albany, NY, USA; [2]NTT Data, Albany, NY, USA

Objective

To evaluate the readiness and timeliness of ED data submitted by hospitals following PHIN syndromic surveillance messaging guide and to evaluate the availability of minimum data elements. To validate the accuracy and completeness of data from ADT messages compared with data currently reported to the NY syndromic surveillance system.

Introduction

The final rules released by the Centers for Medicare and Medicaid Services specified the initial criteria for eligible hospitals to qualify for an incentive payment by demonstrating meaningful use of certified Electronic Health Record (EHR) technology. Syndromic surveillance reporting is one of three public health objectives that eligible hospitals can choose for stage 1. The PHIN messaging guide for syndromic surveillance was published for hospitals to construct emergency department data using Admit Discharge Transfer (ADT) messages, with the minimum dataset that is standard among hospitals and public health agencies.

Currently New York hospitals are reporting emergency department (ED) visit data to the NY syndromic surveillance (SS) system. Patient chief complaint data are monitored for trends of illness at the community level in order to detect possible outbreaks and situational awareness.

Methods

12 hospitals using three EHR certified vendors pilot tested syndromic surveillance data for MU. Hospitals started to transmit ED data in HL7 v 2.5.1 to the NY pre-certification server beginning October 2011. The month of data from July 2012 was evaluated for availability by data elements listed in the implementation guide. The ADT message types were analyzed and the timeliness of reporting was calculated from visit date to report date of the first message type. The data from the pre-certification server was matched against data from the production SS system by medical record number and visit date to evaluate the data content.

Results

There were 5 hospitals from vendor A, 3 from vendor B and 4 from vendor C participating in the pilot testing; 5854, 9882, and 13316 ED visits were reported from the three vendors respectively for the month of July. The type of first message by vendor is shown in Table 1. The availability of data elements is listed in Table 2. There were 79%, 82%, and 87% ED visit records received within 24 hours for vendor A, B, and C respectively. One hospital from vendor A, 3 hospitals from vendor B and 4 hospitals from vendor C also reported ED data to the production system, and their comparison with pilot testing data is shown in Table 3.

Conclusions

The types of ADT messages first reported varied by vendor and hospital. Not all data elements specified in the implementation guide were available or complete, and varied by vendor. An average 83% of first messages were received within 24 hours and the chief complaint from ADT messages did not match well with the current ED system in production. It is a very time consuming and resource demanding process to move a hospital from successful attestation stage to production and requires public health, EHR vendor, and hospital IT to work together. The learning experience from these three vendors in implementing syndromic surveillance for MU will help public health and EHR vendors to prepare for stage 2.

Table 1: Type of First ADT Message by Vendor

ADT Message	Vendor A N (%)	Vendor B N (%)	Vendor C N (%)
A01	2543 (43%)	43	198 (2%)
A04	2757 (47%)	0	12396 (93%)
A08	553 (10%)	1635 (17%)	686 (5%)
A03	0	8204 (83%)	8
total	5854	9882	13316

Table 3: Percent Matched Data Content by Vendor

Data Element	Vendor A %	Vendor B %	Vendor C %
Date of birth	99%	74%	100%
Zipcode	93%	99%	99%
Sex	99%	100%	100%
Discharge disposition	52%	65%	75%
Chief complaint	19%	0%	83%

Table 2: Data Element Availability by Vendor

MDS data elements availability	Vendor A	Vendor B	Vendor C
Date of birth	100%	100%	100%
Gender	100%	100%	100%
Zipcode	100%	100%	100%
Race	96%	99%	97%
Ethnicity	100%	0%	87%
Symptoms Onset Date	0%	0%	0%
Chief Complaint: text	80%	95%	91%
Admit Reason	72%	58%	91%
Diagnosis Code	0%	4%	14%
Discharge Disposition	50%	95%	90%
Temperature	0%	3%	24%
Pulse Oximetry	0%	0%	24%

Keywords

Syndromic surveillance; Meaningful Use; PHIN messaging guide

*Hwa-Gan Chang
E-mail: hgc04@health.state.ny.us

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

BioSense 2.0

Kelley G. Chester*

RTI International, Milton, GA, USA

Objective

To familiarize public health practitioners with the BioSense 2.0 application and its use in all hazard surveillance.

Introduction

BioSense 2.0 protects the health of the American people by providing timely insight into the health of communities, regions, and the nation by offering a variety of features to improve data collection, standardization, storage, analysis, and collaboration.

BioSense 2.0 is the result of a partnership between the Centers for Disease Control and Prevention (CDC) and the public health community to track the health and well-being of communities across the country. In 2010, the BioSense Program began a redesign effort to improve features such as centralized data mining and addressing concerns that the system could not meet its original objective to provide early warning or detect local outbreaks.

Methods

Using the latest technology, BioSense 2.0 integrates current health data shared by health departments from a variety of sources to provide insight on the health of communities and the country. By getting more information faster, local, state, and federal public health partners can detect and respond to more outbreaks and health events more quickly. From flu outbreaks to car accidents, BioSense 2.0 provides the critical data, information, and tools that public health officials need to better understand and address health problems at the local, state, regional, and national levels. Also, by knowing what is happening across local borders, public health professionals can anticipate potential health problems and respond effectively to protect the health of all people.

The demonstration will include a basic overview of the BioSense 2.0 application and the functionality available to public health departments and their data providers. The presenter will also show an example of how BioSense 2.0 can be used in a real-world public health example.

Conclusions

Over the past two years much has been accomplished during the redesign effort. BioSense 2.0 was launched in November of 2011 and the collaboration between the BioSense program and the public health community has yielded an application based on a user-centered design approach and built on a platform that allows for flexible data sharing across jurisdictions and with partners. The public health community has played a critical role in designing and improving the BioSense 2.0 application and through continued collaboration the system will continue to improve.

Innovative features of the BioSense 2.0 application include the use of cloud technology, a novel and flexible data sharing feature, a community driven approach, enhanced algorithms, and no cost statistical analysis tools available in the cloud. Each of these features will be discussed during the presentation.

Keywords

Syndromic Surveillance; Informatics; Situation Awareness

*Kelley G. Chester
E-mail: kchester@rti.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluation of the Pyrrolizidine Alkaloid Induced Liver Disease (PAILD) Active Surveillance System in Tigray, Ethiopia

Cindy Chiu*[1], Danielle Buttke[1], Girmay Welde[2], Richard Luce[3], Asfaw Debela[4], Amsalu Bitew[5], Tesfaye Bayleyegn[1], Sara Vagi[1], Matthew Murphy[1], Daniel Woldemichael[2], Teshale Seboxa[6], Gidey G. Libanos[7], Zeyeda Beyene[7], Yohannes G. Hawaria[7], Daddi Jimma[4], Israel Tareke[8], Danielle Rentz[1] and Colleen Martin[1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA; [2]Tigray Agriculture Bureau, Tigray, Ethiopia; [3]Centers for Disease Control and Prevention, Addis Ababa, Ethiopia; [4]Ethiopian Health and Nutrition Research Institute, Addis Ababa, Ethiopia; [5]Suhul Hospital, Tigray, Ethiopia; [6]Addis Ababa University, Addis Ababa, Ethiopia; [7]Tigray Regional Health Bureau, Tigray, Ethiopia; [8]World Health Organization, Addis Ababa, Ethiopia

Objective

To describe the results of the evaluation of the PAILD active surveillance system and lessons learned for similar surveillance efforts in a resource-limited setting.

Introduction

A liver disease of unknown etiology, called unknown liver disease (ULD) by the community, was first identified in 2002 in Tigray; a rugged, semi-arid, mountainous region that is considered one of the most drought-prone and food insecure regions of Ethiopia. ULD is a chronic condition characterized by epigastric pain, abdominal distention, ascites, emaciation, and hepato/splenomegaly. In 2005, the Ethiopian Health and Nutritional Research Institute was assigned by the Ethiopia Ministry of Health to assist the Tigray Regional Health Bureau and oversee the disease investigation. In 2008, Centers for Disease Control and Prevention (CDC) assisted the Ethiopian team and jointly developed the surveillance tools. The surveillance system was implemented in 2009 with the objectives to determine the magnitude and distribution of the disease; identify disease trends; detect cases to provide them with clinical care; and inform health officials and funding bodies for resource allocation. After several investigations, a local plant containing a particular type of pyrrolizidine alkaloid (PA) toxin that contaminated local foodstuffs was identified as the etiologic agent, and ULD was renamed PAILD in 2011.

Methods

From 20 September to 1 October 2011, we conducted site visits, held semi-structured interviews with 20 staff members, reviewed reporting materials, and summarized the information flow including data collection, reporting, analysis, and dissemination.

Results

This surveillance system was implemented in 13 rural, resource-limited districts in the NW, Central and Western Zones. The system identified a total of 1033 cases, including 314 deaths, as of September 2011; guided medication distribution to the health facilities; served as a registry for patient follow up; and provided decision-makers with information needed to allocate resources. A large-scale training was conducted in 2010; however, high staff turnover and a lack of backup surveillance staff at each site suggested that additional training may be needed. Due to the absence of a diagnostic test, the case definition was very simple to enable frontline staff in the communities and at the health posts/centers to identify disease cases. These individuals travelled long distances by foot to deliver paper surveillance forms to the district health offices. A surveillance team placed in the NW Zonal office collected missing reports from the health facilities given limited transportation; however they have left since this evaluation. Information from the surveillance system was shared with partner agencies at the national level every 3 to 6 months; however, this information was not shared with frontline staff.

Conclusions

The PAILD Active Surveillance System met its objectives as originally defined. Evaluation of this unique surveillance system for a chronic disease with unknown cause in a resource-limited setting provides several lessons that can inform similar surveillance efforts. Ongoing logistical challenges (e.g., shortage of paper forms, lack of transportation, and long distances between locations) complicated data collection and reporting. While electronic reporting may have helped overcome some of these difficulties, it was not feasible in this setting. Frontline staff identified cases in the community so that they could receive treatment; these key staff can be further incentivized by receiving regular training and surveillance reports. Ongoing support will be critical to overcome these unique challenges to ensure continual disease monitoring as interventions to disrupt PA exposure are implemented in the community.

Keywords

Evaluation; Pyrrolizidine Alkaloid Induced Liver Disease; Active Surveillance System; Ethiopia

*Cindy Chiu
E-mail: vic2@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Multiagent Simulation of the Hepatitis B Epidemic Process

Tetyana Chumachenko*[1], Dmytro Chumachenko[2] and Olexandr Sokolov[2]

[1]Epidemiology Department, Kharkiv National Medical University, Kharkiv, Ukraine; [2]National Aerospace University "Kharkiv Aviation Institute", Kharkiv, Ukraine

Objective

To develop multiagent model of hepatitis B (HBV) infection spreading.

Introduction

The standard approaches to simulation include solving of differential equation systems. Such approach is good for obtaining general picture of epidemics (1, 2). When the detailed analysis of epidemics reasons is needed such model becomes insufficient. To overcome the limitations of standard approaches a new one has been offered. The multiagent approach has been offered to be used for representation of the society. Methods of event-driven programming give essential benefits of the processing time of the events (3).

Methods

For model development C# computing language has been used. We have used demographical data, the incidence rate of HBV infection of all population and different population groups (age, professional and other groups), coverage of hepatitis B vaccination, the proportion of HBV carriers in population, the prevalence rate of chronic HBV infection, percent of dominated transmission routes and factors and other rates in Kharkiv region. All parameters, expressed in the model were estimated using sero-surveys data and data of epidemiological surveillance of Kharkiv region sanitary-epidemiological station. Also the theoretical knowledge about HBV infection has been used. 26 conditions have been derived from the problem domain. The transition from one condition to another depends on stochastic value and time of the event change. All events are organized in priority queue which results in high rate of computation performance. The dependence on time and random value determines automata theory conceptions.

Results

The prototype of software system, which includes a subsystem of the multiagent simulation and specialized statistical and mathematical sub-system which can process the simulation results and perform a conditional optimization of the selected objective functions (morbidity, the effectiveness of specific preventive and control activities and their price, measure of reducing the socio-economic impact of HBV infection, etc.) have been developed. Screen form is presented in Figure 1.

Conclusions

The multiagent simulation model of the HBV infection epidemic situation development, based on data obtained in Kharkiv (Ukraine) has been created.

The simulation results allow us to:

1. predict the dynamics of the epidemic process in time in a particular area, taking into account specific epidemic situation;
2. test the effectiveness of various preventive measures (sterilization of instruments, coverage of hepatitis B vaccination of certain groups of people, etc.).

Using the present model in public health system suggests improvment of the epidemiological diagnostics of HBV infection and of the quality of management decisions about epidemiological surveillance. The evolution of multiagent simulation in epidemiology will broaden the possibilities of epidemiological surveillance and control.

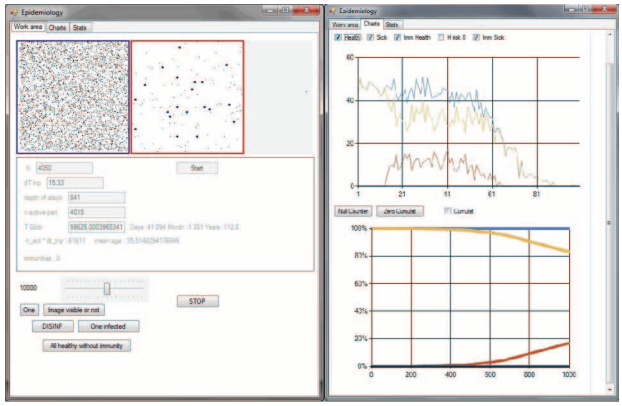


Fig. 1. The main panel of simulation management and graphic visualization.

Keywords

Multiagent modeling; Event-driven programming; Predictive disease modeling; Epidemiological surveillance

References

1. Shoujun Zhao, Zhiyi Xu, Ying Lu.: Mathematical model of hepatitis B virus transmission and its application for vaccination strategy in China. International Journal of Epidemiology. 2000;29:744-52.
2. O'Leary, C., Hong, Z., Zhang, F., Dawood, M., Smart, G., Kaita, K., Wu, J.: A mathematical model to study the effect of hepatitis B virus vaccine and antivirus treatment among the Canadian Inuit population.Eur J Clin Microbiol Infect Dis. 2010 Jan;29(1):63-72.
3. Hethcote, H.W.: The mathematics of infectious diseases. SIAM Rev. 2000; 42(4): 599–653.

*Tetyana Chumachenko
E-mail: tatalchum@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Flu Near You: An Online Self-reported Influenza Surveillance System in the USA

Rumi Chunara*[1, 2], Susan Aman[2], Mark Smolinski[3] and John S. Brownstein[1, 2]

[1]Harvard Medical School, Boston, MA, USA; [2]Boston Children's Hospital, Boston, MA, USA; [3]Skoll Global Threats Fund, San Francisco, CA, USA

Objective

To develop a participatory system for monitoring the activity of influenza-like-illness among the United States general population.

Introduction

The emergence of new influenza strains including H1N1, H5N1, H3N2v as well as other respiratory pathogens such as SARS, along with generally weak information about household and community transmission of influenza, enforce the need for augmented influenza surveillance. At the same time, Internet penetration and access has grown, with 82% of American adults using the Internet [1], enabling transfer and communication of information that can be collected and aggregated in near real-time. Surveillance targeted towards influenza in other countries, and towards malaria in India, has previously been executed with good user engagement [2,3]. In this study, we created an online participatory influenza surveillance tool in the United States, called Flu Near You.

Methods

Volunteer users were primarily solicited via collaboration with the American Public Health Association and their members' networks starting Oct. 24, 2011. Upon registration, each user is sent a weekly email, taking them to the Flu Near You website. On the website they fill in a short survey asking if they had any of 10 symptoms: fever, cough, sore throat, shortness of breath, chills/night sweats, fatigue, nausea or vomiting, diarrhea, body aches and headache, in the last week. Users can also enroll their household members and enter information in for them weekly. A map of influenza activity is made available to users, and anyone accessing the website [Figure 1]. On the map, the number of individuals reporting with no symptoms, some symptoms, or Influenza-like illness are visualized, aggregated to the zip code level. Users can also compare the contributed data with other surveillance systems: the Centers for Disease Control and Prevention, and Google Flu Trends for the same time period [Figure 1]. We also obtained user feedback through a survey in early July 2012.

Results

As of August 21, 2012, there are over 9300 Flu Near You users, from all 50 states. 94.0% of users are between 20 and 70 years, although 37.2% of household members are < 20 years old. Overall 62.0% of members (users and household) were female. We found that 46.4% of users answered 3 or more surveys. Qualitatively from survey responses, we learned that simple feedback and an emphasis on public health education are important in this type of system.

Conclusions

We found that it is possible to engage users in a symptom self-reporting system and augment information about influenza for the nation. Increased uptake would increase the value of the system for the public and public health professionals. Flu Near You is expanding in its second season, working to increase user participation. Other connected projects are also examining the expansion into other diseases with high prevalence and in need of augmented surveillance. With a larger user base and through a longer period of execution, systems like Flu Near You will help to improve our understanding of influenza epidemiology as well as guide implementation of relevant and timely public health interventions, for example in estimating vaccination rates and efficacy among different demographic groups. Information reported by individuals can augment traditional public health surveillance methods for more timely detection of disease outbreaks, monitoring disease activity and increasing the public's engagement in their own and population's health.

Keywords

influenza; surveillance; crowdsourcing

Acknowledgments

All of the Flu Near You users who have contributed information.

References

[1] Pew Internet & Aerican Life Project. Available at: pewinternet.org. Accessed Aug. 22, 2012.

[2] Marquet RL, et al. Internet-based monitoring of influenza-like illness (ILI) in the general population of the Netherlands during the 2003-2004 influenza season. BMC Public Health. 2006; 6: 242.

[3] Chunara R, et al. (2012) Online reporting for malaria surveillance using micro-monetary incentives, in urban India 2010-2011. Malaria J 11: 43.

*Rumi Chunara
E-mail: rumi@alum.mit.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Use of BioSense for Rapid Assessment of the Safety of Medical Countermeasures

Ralph J. Coates* and Kathleen Gallagher

Division of Notifiable Diseases and Healthcare Information, Centers for Disease Control and Prevention, Atlanta, GA, USA

Objective

To conduct an initial examination of the potential use of BioSense data to monitor and rapidly assess the safety of medical countermeasures (MCM) used for prevention or treatment of adverse health effects of biological, chemical, and radiation exposures during a public health emergency.

Introduction

BioSense is a national human health surveillance system for disease detection, monitoring, and situation awareness through near real-time access to existing electronic healthcare encounter information, including information from hospital emergency departments (EDs). MCM include antibiotics, antivirals, antidotes, antitoxins, vaccinations, nuclide-binding agents, and other medications. Although some MCM have been extensively evaluated and have FDA approval, many do not (1). Current FDA and CDC systems that monitor drug and vaccine safety have limited ability to monitor MCM safety, and in particular to conduct rapid assessments during an emergency (1).

Methods

To provide a preliminary assessment of the use of BioSense for this purpose, we reviewed selected publications evaluating the use of electronic health records (EHRs) to monitor safety of drugs and vaccinations (medications), focusing particularly on systematic reviews, reviewed BioSense data elements, and consulted with a number of subject matter experts.

Results

More than 40 studies have examined use of EHR data to monitor adverse effects (AEs) of medications using administrative, laboratory, and pharmacy records from inpatient- and out-patient settings, including EDs (2-4). To identify AEs, investigators have used diagnostic codes; administration of antidotes, laboratory measures of drug levels and of biologic response, text searches of unstructured clinical notes, and combinations of those data elements. BioSense ED data include chief complaint text, triage notes, text diagnosis, as well as diagnostic and medical procedure codes.

Investigations used a variety of study designs in various populations and settings; examined a wide range of medications, vaccinations, and AEs; and developed a diverse set of analytic algorithms to search EHR data to detect and signal AEs (2-4). Most research has been done on FDA-approved medications. Most studies used EHR data to identify individuals using specific medications and then searched for potential AEs identified from previous research. None of the studies investigated use of EHR data to monitor safety when records of an individual's medication use could not be linked to that individual's records of AEs. BioSense data could be used for AE detection, but linking AEs to MCM use would require follow-back investigation. Since there is limited research on AEs of some MCM, there would be limited information to guide identification of potential AEs.

Performance characteristics of the AE monitoring systems have been mixed with reported sensitivities ranging from 40-90%; specificities from 1% to 90%, and positive predictive values from < 1% to 64%, depending on the medication, AE and other characteristics of the study (2, 4). However, the small numbers of studies with common characteristics has limited the ability of reviewers to determine which types of systems have better performance for different medications and AEs.

Some experts suggest that data in BioSense, might contribute to safety surveillance of MCM. They also caution that poor predictive values and high rates of false positives reported in the literature raise concerns about burden to those conducting investigations in response to AE alerts, particularly in the context of a public health emergency.

Conclusions

These findings suggest that BioSense data could potentially contribute to rapid identification of safety issues for MCM and that some methods from published research could be applicable to the use of BioSense for this purpose. However, such use would require careful development and evaluation.

Keywords

BioSense; countermeasures; safety; monitoring; medical

References

1. National Biodefense Science Board. Where are the countermeasures? Protecting America's health from CBRN threats. U. S. Department of Health and Human Services, March, 2010.
2. Forster AJ, et al. A systematic review to evaluate the accuracy of electronic adverse drug event detection. JAMIA 2012;29:31-38.
3. Lucado J, et al. Medication-related adverse outcomes in U.S. hospitals and emergency departments, 2008. HCUP Statistical Brief # 109. AHRQ, 2011.
4. Handler SM, et al. A systematic review of the performance characteristics of clinical event monitor signals used to detect adverse drug events in the hospital setting. JAMIA 2007;14:451-8.

*Ralph J. Coates
E-mail: rjc5@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Tweeting Fever: Are Tweet Extracts a Valid Surrogate Data Source for Dengue Fever?

Jacqueline S. Coberly*[1], Clayton R. Fink[1], Eugene Elbert[1], In-Kyu Yoon[2], John M. Velasco[2], Agnes Tomayo[2], V. Roque[3], S. Ygano[4], Durinda Macasoco[4] and Sheri Lewis[3]

[1]The Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA; [2]Armed Forces Research Institute for Medical Research, Bangkok, Thailand; [3]National Epidemiology Center, Manila, Philippines; [4]Cebu City Health Office, Cebu City, Philippines

Objective

To determine whether Twitter data contains information on dengue-like illness and whether the temporal trend of such data correlates with the incidence dengue or dengue-like illness as identified by city and national health authorities.

Introduction

Dengue fever is a major cause of morbidity and mortality in the Republic of the Philippines (RP) and across the world. Early identification of geographic outbreaks can help target intervention campaigns and mitigate the severity of outbreaks. Electronic disease surveillance can improve early identification but, in most dengue endemic areas data pre-existing digital data are not available for such systems. Data must be collected and digitized specifically for electronic disease surveillance. Twitter, however, is heavily used in these areas; for example, the RP is among the top 20 producers of tweets in the world. If social media could be used as a surrogate data source for electronic disease surveillance, it would provide an inexpensive pre-digitized data source for resource-limited countries. This study investigates whether Twitter extracts can be used effectively as a surrogate data source to monitor changes in the temporal trend of dengue fever in Cebu City and the National Capitol Region surrounding Manila (NCR) in the RP.

Methods

We obtained two sources of ground truth incidence for dengue. The first was daily dengue fever incidence for Cebu City and the NCR taken from the Philippines Integrated Disease Surveillance and Response System (PIDSR). The second ground truth source was fever incidence from Cebu City for 2011. The Cebu City Health Office (CCHO) has monitored fever incidence as a surrogate for dengue fever since the 1980s. Tweets from Cebu City, and the NCR were collected prospectively thru Twitter's public application program interface. The Cebu City fever ground truth data set was smoothed with a seven day moving average to facilitate comparison to the PIDSR and Twitter data. A vocabulary of words and phrases describing fever and dengue fever in the tweets collected were identified and used to mark relevant tweets. A subset of these 'fever' tweets that mentioned fever related to a medical situation were identified. The incidence and the temporal pattern of these medically-relevant tweets were compared with the incidence and pattern of fever and dengue fever in the two ground truth data sets. Pearson correlation coefficient was used to compare the correlation among the different data sets. Noted lag periods were adjusted by moving the data in time and re-computing the correlation coefficient.

Results

26,023,103 tweets were collected from the two geographic regions: 10,303,366 from Cebu City and 15,719,767 tweets from the NCR. 8,814 (0.02%) Tweets contained the word fever and 4099 (0.01% of total) mentioned fever in a medically-relevant context, for example. "…I have a fever…" vs. "…football fever…." The medically-relevant tweets were compared with both ground truth data sets. The correlation between the Tweets and each of the incidence data sets is shown below.

Conclusions

Tweets containing medically-relevant fever references were correlated ($p<0.0001$) with both fever and dengue fever incidence in the ground truth data sets. The signal indicating fever in the medically-related tweets led the incidence data significantly: by 6 days for the Cebu City fever incidence; and by 12 days for the PIDSR dengue fever incidence. Temporal adjustment to account for observed lag periods increased the correlation coefficient by about one-third in both cases. This was a limited pilot study, but it suggests that Twitter extracts may provide a valid and timely surrogate data source to monitor dengue fever in this population. Further study of the correlation of Twitter and dengue in other areas, and of Twitter with other illnesses is warranted.

Table 1: Correlation between Twitter Extracts and Fever & Dengue Fever Incidence Data Sets

	Pearson Correlation Coefficients	
Incidence Data	Raw Data	Temporally Adjusted
Twitter vs. PIDSR Dengue	0.629*	0.829*‡
Twitter vs. CCHO Fever	0.575*	0.769*†

* $p<0.0001$
† Twitter shifted right by 6 days
‡ Twitter shifted right by 12 days

Keywords

Dengue; Social Media; Twitter

*Jacqueline S. Coberly
E-mail: jacqueline.coberly@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

User Experience of the U.S. Department of Defense (DoD) Respiratory Disease Dashboard

Jennifer A. Cockrill*[1], Alice Y. Tsai[1], Timothy C. Campbell[2], Jean-Paul Chretien[3], Julie A. Pavlin[1] and Ronald L. Burke[1]

[1]Division of GEIS Operations, Armed Forces Health Surveillance Center, Silver Spring, MD, USA; [2]Applied Physics Laboratory, Johns Hopkins University, Laurel, MD, USA; [3]Division of Integrated Biosurveillance, Armed Forces Health Surveillance Center, Silver Spring, MD, USA

Objective

Evaluate the user experience of a novel electronic disease reporting and analysis system deployed across the DoD global laboratory surveillance network

Introduction

Lessons learned from the 2009 influenza pandemic have driven many changes in the standards and practices of respiratory disease surveillance worldwide. In response to the needs for timely information sharing of emerging respiratory pathogens (1), the DoD Armed Forces Health Surveillance Center (AFHSC) collaborated with the Johns Hopkins University Applied Physics Laboratory (JHU/APL) to develop an Internet-based data management system known as the Respiratory Disease Dashboard (RDD). The goal of the RDD is to provide the AFHSC global respiratory disease surveillance network a centralized system for the monitoring and tracking of lab-confirmed respiratory pathogens, thereby streamlining the data reporting process and enhancing the timeliness for detection of potential pandemic threats. This system consists of a password-protected internet portal that allows users to directly input respiratory specimen data and visualize data on an interactive, global map. Currently, eight DoD partner laboratories are actively entering respiratory pathogen data into the RDD, encompassing specimens from sentinel sites in eleven countries: Cambodia, Colombia, Kenya, Ecuador, Egypt, Honduras, Nicaragua, Paraguay, Peru, Uganda, and the United States. A user satisfaction survey was conducted to guide further development of the RDD and to support other disease surveillance efforts at the AFHSC.

Methods

User training was provided to partner laboratories during a transition of data submission from Excel spreadsheet to RDD electronic data entry between November 2011 and May 2012. A user experience survey was distributed to the participating laboratories in August 2012 and based on the experience of 139 entries. The survey adopted elements of the SWOT (Strength-Weaknesses-Opportunities-Threats) analysis to determine the system's strengths and weaknesses as well as to solicit users' perspectives on the efficiency of the system in assisting with disease surveillance data entry and visualization. Questionnaires in an open-ended (free-text response) format were distributed to all eight participating laboratories. Common themes were identified based on the solicited responses.

Results

Although only four of eight participating laboratory partners replied to the survey (50% survey response rate), all survey were completed without any omission of questions (100% completion rate). 2/25 (8%) total responses were neutral comments and therefore omitted in the thematic analysis (Table 1). In general, there was a distinct dichotomy in opinion between overseas laboratories and domestic laboratories with regard to the usefulness of the RDD, with overseas laboratories viewing the RDD as more useful than domestic laboratories. A review of the comparison between weekly specimens submitted to the AFHSC via Excel spreadsheet and data entered directly into the RDD revealed misunderstandings about the meaning of the data entry labels in the RDD interface. It was noted by four laboratories that a "Quick Start" user manual would be useful to clarify the definitions of some data labels.

Conclusions

Overall, this user experience evaluation has identified the needs for additional training on RDD data entry procedures and a "Quick Start" user manual to support the standardization of surveillance definitions. In general, users appreciate the visualization of the global DoD laboratory network data. This evaluation demonstrated the importance of active participation from data contributors and the invaluable organizational support in the development of the RDD as an electronic disease reporting and analysis system.

Keywords

Outbreak Detection; Disease Surveillance; User Experience Evaluation; Data Management

Acknowledgments

Sheri Lewis, MPH, JHU/APL Program Manager & Jose L. Sanchez, MD, MPH, AFHSC/Global Emerging Infections Surveillance and Response Systems (GEIS) Operations, STI Pillar Head. This work was supported in part by an appointment to the Postgraduate Research Participation Program at the U.S. Army Public Health Command (USAPHC) administered by the Oak Ridge Institute for Science and Education through an interagency agreement between the U.S. Department of Energy and USAPHC.

References

1. WHO. Pandemic influenza preparedness framework for the sharing of influenza viruses and access to vaccines and other benefits. Geneva:WHO Press, 2011. http://whqlibdoc.who.int/publications/2011/9789241503082_eng.pdf

*Jennifer A. Cockrill
E-mail: Jennifer.Cockrill@us.army.mil

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

S&I Public Health Reporting Initiative: Improving Standardization of Surveillance

Michael Coletta*[1], Nikolay Lipskiy[2], David Birnbaum[3] and John Abellera[2]

[1]NACCHO, Washington, DC, USA; [2]CDC, Atlanta, GA, USA; [3]Washington State Department of Health, Olympia, WA, USA

Objective

The objective of this panel is to inform the ISDS community of the progress made in the Standards & Interoperability (S&I) Framework Public Health Reporting Initiative (PHRI). Also, it will provide some context of how the initiative will likely affect biosurveillance reporting in Meaningful Use Stage 3 and future harmonization of data standards requirements for public health reporting.

Introduction

The S&I Framework is an Office of National Coordinator (ONC) initiative designed to support individual working groups who focus on a specific interoperability challenge. One of these working groups within the S&I Framework is the PHRI, which is using the S&I Framework as a platform for a community-led project focused on simplifying public health reporting and ensuring EHR interoperability with public health information systems. PHRI hopes to create a new public health reporting objective for Meaningful Use Stage 3 that is broader than the current program-specific objectives and will lay the ground work for all public health reporting in the future. To date, the initiative received over 30 descriptions of different types of public health reporting that were then grouped into 5 domain categories. Each domain category was decomposed into component elements and commonalities were identified. The PHRI is now working to reconstruct a single model of public health reporting through a consensus process that will soon lead to a pilot demonstration of the most ready reporting types. This panel will outline progress, challenges, and next steps of the initiative as well as describe how the initiative may affect a standard language for biosurveillance reporting.

Methods

Michael Coletta will provide an introduction and background of the S&I PHRI. He will describe how the PHRI intends to impact reporting in a way that is universal and helpful to both HIT vendors and public health programs.

Nikolay Lipskiy will provide an understanding of the ground breaking nature of collaboration and harmonization that is occurring across public health programs. He will describe the data harmonization process, outcomes, and hopes for the future of this work.

David Birnbaum has been a very active member of PHRI and has consistently advocated for the inclusion of Healthcare Associated Infections (HAI) reporting in Meaningful Use as a model. David has been representing one of the largest user communities among those farthest along toward automated uploading of data to public health agencies. He will describe the opportunities and challenges of this initiative from the perspective of a participant representing an already highly evolved reporting system (CDC's National Healthcare Safety Network system).

John Abellera has been the steward of the communicable disease reporting user story for the PHRI. He will describe the current challenges to reporting and how the PHRI proposed changes could improve communicable disease reporting efforts.

This will be followed by an open discussion with the audience intended to elicit reactions regarding an eventual consolidation from individual report specific specification documents to one core report specification across public health reporting programs which is then supplemented with both program specific specifications and a limited number of implementation specific specifications.

Results

Plan to engage audience: Have a prepared list of questions to pose to the audience for reactions and discussion (to be supplied if participation is low).

Keywords

Standards; Interoperability; Meaningful Use; Reporting; Stage 3

*Michael Coletta
E-mail: mcoletta@naccho.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

An ISDS-Based Initiative for Conventions for Biosurveillance Data Analysis Methods

Michael Coletta[4], Howard Burkom*[1], Jeffrey Johnson[2] and Wendy Chapman[3]

[1]Johns Hopkins Applied Physics Laboratory, Laurel, MD, USA; [2]San Diego County Health and Human Services Agency, San Diego, CA, USA; [3]University of California San Diego, San Diego, CA, USA; [4]National Association of County and City Health Officials, Washington, DC, USA

Objective

The panel will present the problem of standardizing analytic methods for public health disease surveillance, enumerate goals and constraints of various stakeholders, and present a straw-man framework for a conventions group.

Introduction

Twelve years into the 21st century, after publication of hundreds of articles and establishment of numerous biosurveillance systems worldwide, there is no agreement among the disease surveillance community on most effective technical methods for public health data monitoring. Potential utility of such methods includes timely anomaly detection, threat corroboration and characterization, follow-up analysis such as case linkage and contact tracing, and alternative uses such as providing supplementary information to clinicians and policy makers.

Several factors have impeded establishment of analytical conventions. As immediate owners of the surveillance problem, public health practitioners are overwhelmed and understaffed. Goals and resources differ widely among monitoring institutions, and they do not speak with a single voice. Limited funding opportunities have not been sufficient for cross-disciplinary collaboration driven by these practitioners. Most academics with the expertise and luxury of method development cannot access surveillance data. Lack of data access is a formidable obstacle to developers and has caused talented statisticians, data miners, and other analysts to abandon the field. The result is that older research is neglected and repeated, literature is flooded with papers of varying utility, and the decision-maker seeking realistic solutions without detailed technical knowledge faces a difficult task.

Regarding conventions, the disease surveillance community can learn from older, more established disciplines, but it also poses some unique challenges. The general problem is that disease surveillance lies on the fringe of disparate fields (biostatistics, statistical process control, data mining, and others), and poses problems that do not adequately fit conventional approaches in these disciplines.

In its eighth year, the International Society of Disease Surveillance is well positioned to address the standardization problem because its membership represents the involved stakeholders including progressive programs worldwide as well as resource-limited settings, and also because best practices in disease surveillance is fundamental to its mission. The proposed panel is intended to discuss how an effective, sustainable technical conventions group might be maintained and how it could support stakeholder institutions.

Methods

Members of a Technical Conventions Group would have experience and dedication to advancing the science of disease surveillance. Primary functions would include:

1. Specify and communicate technical problems facing professionals involved in routine monitoring of population health. Alternative use applications would also be considered, such as the use of epidemiological findings to inform clinical diagnoses.

2. Independently evaluate the utility of proposed analytical solutions to well-defined problems in public health surveillance and confer approval or certification, perhaps on several levels, such as whether results can be replicated with shareable data. Approved solutions might be restricted to commonly available software such as the R language or Microsoft EXCEL.

3. Facilitate sharing of tools and methodologies to evaluate methods and to visualize their results

The framework to be discussed in the proposed panel would be a means of keeping open lines of collaboration and idea-sharing. Overcoming obstacles toward this goal is worthy of a conference panel discussion whether or not it concludes that a conventions group is a viable approach.

Results

Three 15-minute panelist talks are proposed:

1. Background: in-depth description of the dimensions of the problem above

2. Constraints facing public health practitioners and requirements for practical analytic tools

3. Strawman conventions group: role, logistics, inclusiveness, methods of communicating with stakeholders and related organizations and producing/disseminating output.

For the 45 minutes of discussion, the first 15-20 will invite reactions to the first two talks to sharpen the scope of the effort. The remainder of the session will cover the advisability, feasibility, and logistics of an ISDS-based conventions group, and modify the strawman group concept.

Keywords

Standards; Data Analysis; Statistical Algorithms; Certification

*Howard Burkom
E-mail: howard.burkom@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Disease Models for Event Prediction

Courtney D. Corley*[1] and Laura Pullum[2]

[1]Pacific Northwest National Laboratory, Richland, WA, USA; [2]Oak Ridge National Laboratory, Oak Ridge, TN, USA

Objective

The objective of this manuscript is to present a systematic review of biosurveillance models that operate on select agents and can forecast the occurrence of a disease event.

Introduction

One of the primary goals of this research was to characterize the viability of biosurveillance models to provide operationally relevant information to decision makers, in order to identify areas for future research. Two critical characteristics differentiate this work from other infectious disease modeling reviews [1,2]. First, we reviewed models that attempted to predict the disease event, not merely its transmission dynamics. Second, we considered models involving pathogens of concern as determined by the US National Select Agent Registry.

Background: A rich and diverse field of infectious disease modeling has emerged over the past 60 years and has advanced our understanding of population- and individual-level disease transmission dynamics, including risk factors, virulence and spatio-temporal patterns of disease spread. Recent modeling advances include biostatistical methods, and massive agent-based population, biophysical, ordinary differential equation, and ecological-niche models. Diverse data sources are being integrated into these models as well, such as demographics, remotely-sensed measurements and imaging, environmental measurements, and surrogate data such as news alerts and social media. Yet, there remains a gap in the sensitivity and specificity of these models not only in tracking infectious disease events but also predicting their occurrence.

Methods

We searched dozens of commercial and government databases and harvested Google search results for eligible models utilizing terms and phrases provided by public health analysts relating to biosurveillance, remote sensing, risk assessments, spatial epidemiology, and ecological niche-modeling, This returned 13,767 webpages and 12,152 citations. After de-duplication and removal of extraneous material, a core collection of 6,503 items was established, these publications and their abstracts are presented in a semantic wiki at http://BioCat.pnnl.gov. Next, PNNL's IN-SPIRE visual analytics software was used to cross-correlate these publications with the definition for a biosurveillance model. As a result, we systematically reviewed 44 papers, and the results are presented in this analysis.

Results

The models were classified as one or more of the following types: event forecast (9%), spatial (59%), ecological niche (64%), diagnostic or clinical (14%), spread or response (20%), and reviews (7%). The distribution of transmission modes in the models was: direct contact (55%), vector-borne (34%), water- or soil-borne (16%), and non-specific (7%). The parameters (e.g., etiology, cultural) and data sources (e.g., remote sensing, NGO, epidemiological) for each model were recorded. A highlight of this review is the analysis of verification and validation procedures employed by (and reported for) each model, if any. All models were classified as either a) Verified or Validated (89%), or b) Not Verified or Validated (11%; which for the purposes of this review was considered a standalone category).

Conclusions

The verification and validation (V&V) of these models is discussed in detail. The vast majority of models studied were verified or validated in some form or another, which was a surprising observation made from this portion of the study. We subsequently focused on those models which were not verified or validated in an attempt to identify why this information was missing. One reason may be that the V&V was simply not reported upon within the paper reviewed for those models. A positive observation was the significant use of real epidemiological data to validate the models. Even though 'Validation using Spatially and Temporally Independent Data' was one of the smallest classification groups, validation through the use of actual data versus predicted data represented approximately 33% of these models. We close with initial recommended operational readiness level guidelines, based on established Technology Readiness Level definitions.

Keywords

Disease models; Event prediction; Operational readiness

References

[1] Lloyd-Smith JO, George DB, Pepin KP, Pitzer VE, Pulliam JRC, Dobson A, Hudson PJ, and Grenfell BT. Epidemic Dynamics at the Human-Animal Interface. Science 4 December 2009: 326 (5958), 1362-1367. [DOI:10.1126/science.1177345]

[2] Bravata DM, Sundaram V, McDonald KM, Smith WM, Szeto H, Schleinitz MD, et al. Detection and diagnostic decision support systems for bioterrorism response. Emerg Infect Dis [serial online] 2004 Jan [9-Sept 2012]. http://wwwnc.cdc.gov/eid/article/10/1/03-0243.htm

*Courtney D. Corley
E-mail: court@pnnl.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

CaseFinder: A Flexible Real-time Online Surveillance Registry for Infectious Disease Physicians to Report Cases of Carbapenem-resistant *Enterobacteriaceae* (CRE)

Donald Curtis*[1], Scott Weissman[2], Dimitri Drekonja[3], Susan Beekmann[4], Benjamin Buckmaster[1], John Lynch[5], April Abbott[6], Ferric Fang[6] and Philip Polgreen[4]

[1]Coe College, Cedar Rapids, IA, USA; [2]Seattle Children's Hospital, Seattle, WA, USA; [3]Minneapolis Veterans Affairs Medical Center, Minneapolis, MN, USA; [4]University of Iowa, Iowa City, IA, USA; [5]Harborview Medical Center, Seattle, WA, USA; [6]University of Washington, Seattle, WA, USA

Objective

To create a flexible online surveillance system for infectious disease experts to report cases of emerging infectious diseases.

Introduction

The Infectious Disease Society of America's Emerging Infections Network (EIN) is a sentinel network of over 1,200 practicing infectious disease physicians, supported by the Centers for Disease Control and Prevention (CDC). In January 2012, the EIN listserv fielded a member inquiry about treatment recommendations for a complicated polymicrobial wound infection in a traveler returning to the United States from India. The posting led to a member-to-member communication that resulted in shipment of clinical microbiology isolates from one member's hospital to another's research laboratory. Molecular evaluation of the clinical isolates uncovered previously undetected carriage of the emerging NDM-1 enzyme in 2 of the *Enterobacteriaceae* species. Based on this interaction, we built a flexible online surveillance registry (CaseFinder) for infectious disease physicians to report cases of CRE.

Methods

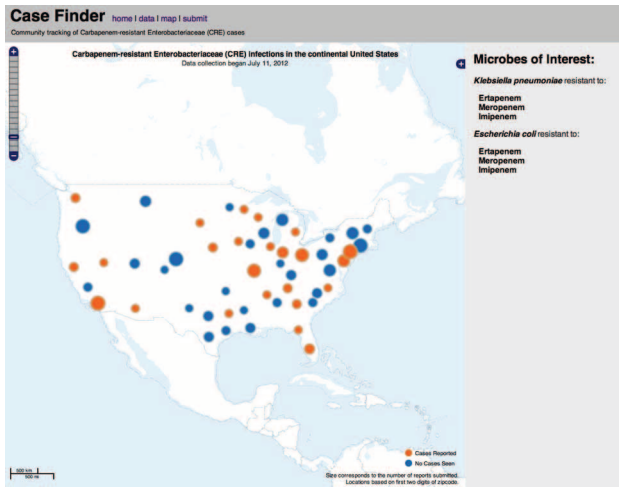
To ascertain the frequency and nature of CRE infections treated by EIN members, a survey was sent to EIN members in July 2012 that elicited risk factors and clinical features associated with CRE. Survey opt-out items also allowed respondents to specify that they had not treated any CRE infections. Concurrently, we developed a formal relational data model for CRE infection survey data, allowing for analysis and visualization. The data model was implemented in Python using the Object-Relational Mapping provided by the Django web framework, which we used to implement the backend server component to the online registry. An interactive front-end web application, written in Javascript using the jQuery library, retrieves data via the AJAX web protocol. Geolocated data is visualized using the OpenLayers library to render map tiles and provide interactive controls such as panning and zooming.

Results

The crowd-sourced online registry for infectious disease experts to report CRE infections, called CaseFinder (http://casefinder.org/), was developed, released, and seeded with data from the EIN survey. To date, a total of 69 cases have been submitted, describing 53 infections with *Klebsiella pneumoniae*, 7 with *Escherichia coli* and 9 with other *Enterobacteriaceae*, representing 7 of 9 US Census divisions. Another 214 members have indicated that they have not seen any cases to date. CaseFinder includes: an online data entry component (to supplant the original EIN listserv survey); real-time filtering of data; and interactive maps that geolocate survey responses using the first 2 digits of the treating facility's zip code. Users can filter data based on species, clinical features (age, gender), resistance profile, or 2-digit zip code. CaseFinder can also display clinical case data in an exportable line-item format.

Conclusions

We have created a web-based data registry for CRE infections in the US. Populated by EIN survey responses, the registry already has a collection 283 data points—69 cases of CRE and 214 reports indicating the absence of cases—and is open for ongoing submission of data represented in real time. This system can serve as a de facto national surveillance system for CRE infections - an important but not yet universally reportable condition. Our platform can be expanded to map and track other emerging infections seen by infectious diseases physicians. We are currently working to incorporate molecular fingerprinting and typing information into the data model. The site will also provide incentives for infectious disease experts to submit cases in underrepresented geographic areas. In future efforts we will incorporate "machine learning" techniques to leverage knowledge from infectious disease experts on existing cases and provide features such as an intelligent automated alert system.



Keywords

Surveillance; Carbapenemases; Antibiotic resistance; *Enterobacteriaceae*; *Klebsiella pneumoniae*

***Donald Curtis**
E-mail: dcurtis@coe.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Public Health Surveillance in Pilot Drinking Water Contamination Warning Systems

Chrissy Dangel*[1], Steven C. Allgeier[1], Darcy Gibbons[2] and Adam Haas[2]

[1]US EPA, Cincinnati, OH, USA; [2]CSC Science & Engineering, Alexandria, VA, USA

Objective

This paper describes the lessons learned from operation and maintenance of the public health surveillance (PHS) component of five pilot city drinking water contamination warning systems (CWS) including: Cincinnati, New York, San Francisco, Philadelphia, and Dallas.

Introduction

The U.S. Environmental Protection Agency (EPA) designed a program to pilot multi-component contamination warning systems (CWSs), known as the "Water Security initiative (WSi)." The Cincinnati pilot has been fully operational since January 2008, and an additional four pilot utilities will have their own, custom CWSs by the end of 2012. A workshop amongst the pilot cities was conducted in May 2012 to discuss lessons learned from the design, implementation, operation, maintenance, and evaluation of each city's PHS component.

Methods

When evaluating potential surveillance tools to integrate into a drinking water contamination warning system, it is important to consider design decisions, dual use applications/considerations, and the unique capabilities of each tool. The pilot cities integrated unique surveillance tools, which included a combination of automated event detection tools and communication and coordination procedures into their respective PHS components. The five pilots performed a thorough, technical evaluation of each component of their CWS, including PHS.

Results

Four key lessons learned were identified from implementation of the PHS component in the five pilot cities. First, improved communication and coordination between public health and water utilities was emphasized as an essential goal even if it were not feasible to implement automated surveillance systems. The WSi pilot project has helped to strengthen this communication pathway through the process of collaborating to develop the component, and through the need to investigate PHS alerts.

Second, the approximate location of specific cases associated with PHS alerts was found to be an essential feature that allowed a cross-comparison to water pressure zones when attempting to locate the source of possible contamination. More specific location data (e.g., latitude and longitude) leads to a more efficient investigation, however, just narrowing the case location down to a specific hydraulic region within the water distribution system is extremely useful.

Third, the ability to quickly visualize spatial distribution of cases via a visual interface was reported to be valuable to investigators during alert investigations. Most pilots implemented a CWS dashboard, in the form of a central graphical display, which presents the alerts and was used by the water utility and public health to obtain an understanding of geospatial relationships between cases, alerts and water pressure zones.

Finally, public health and water utility representatives from several of the WSi pilots acknowledged that their automated surveillance tools currently have limited capabilities for detection of chemical contaminants (which may result in a sudden onset of symptoms), with the main deficiency being the timeliness of the alerts relative to the window of opportunity to respond in a meaningful and effective manner. While they currently focus on detection of traditional waterborne diseases, these tools could potentially be adapted to also detect chemical contaminants.

Conclusions

The results of the pilots have demonstrated that it is important to construct and formalize standard operating procedures, so that public health personnel and water utilities have a standard communication protocol. As a basic step to a PHS component, it is important to establish a relationship between utilities and public health. In addition to the efforts of the WSi pilots, research is currently being conducted by the U.S. EPA to analyze health seeking behavior of symptomatic individuals, because all PHS tools rely on data generated from behavior pursued by the affected population during a public health incident. Results from analysis of both emergency department data and poison control center follow-up phone data are currently underway.

Keywords

Evaluation; Public Health Surveillance; Lessons Learned; Contamination Warning System; Drinking Water

References

[1] US EPA. 2008. Water Security Initiative: Cincinnati Pilot Post-Implementation System Status Report. EPA 817-R-08-004.

*Chrissy Dangel
E-mail: dangel.chrissy@epa.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Biosurveillance Ecosystem (BSVE) Workflow Analysis

Timothy Dasey*[1], Hayley Davison Reynolds[1], Nancy Nurthen[2], Christopher Kiley[2] and John Silva[3]

[1]Chemical and Biological Defense Systems, MIT Lincoln Laboratory, Lexington, MA, USA; [2]DTRA Chemical & Biological Technologies Directorate, Ft. Belvoir, VA, USA; [3]Silva Consulting Services, LLC, Sykesville, MD, USA

Introduction

The Defense Threat Reduction Agency Chemical and Biological Technologies Directorate (DTRA CB) has initiated the Biosurveillance Ecosystem (BSVE) research and development program. Operational biosurveillance capability gaps were analyzed and the required characteristics of new technology were outlined, the results of which will be described in this contribution.

Methods

Work process flow diagrams, with associated explanations and historical examples, were developed based on in-person, structured interviews with public health and preventative medicine analysts from a variety of Department of Defense (DoD) organizations, and with one organization in the Department of Health and Human Services (DHHS) and with a major U.S. city health department. The particular nuanced job characteristics of each organization were documented and subsequently validated with the individual analysts. Additionally, the commonalities across different organizations were described in meta-workflow diagrams and descriptions.

Results

Two meta-workflows were evident from the analysis. In the first type, epidemiologists identify and characterize health-impacting events, determine their cause, and determine community-level responses to the event. Analysts of this type monitor information (primarily statistical case information) from syndromic or disease reporting system or other sources to determine whether there are any unusual diseases or clusters of disease outbreaks in the jurisdiction. This workflow involved three consecutive processes: triage, analysis and reporting. Investigation and response processes to disease outbreaks are both parallel and overlapping in many circumstances. In the second meta-workflow type, analysts monitor for a potential health event through text-based sources and data reports within their particular area of responsibility. This surveillance activity is often interspersed with other activities required of their job. They may generate a daily/weekly/monthly report or only report when an event is detected that requires notification/response. There are similar triage, analysis and reporting workflow stages to the first meta-workflow type, but in contrast these analysts are focused on informing leadership and response in the form of policy modification. They are also subject to answering leadership-driven biosurveillance queries.

Conclusions

In these interviews, analysts described the shortcomings of various technologies that they use, or technology features that they wish were available. These can be grouped into the following feature categories:

Data: Analysts want rapid access to all relevant data sources, advisories for data that may be relevant to their interests, and availability of information at the appropriate level for their analysis (e.g., output of interpretations from expert analysts instead of raw data).

Enhanced search: Analysts would like customization of information based on relevance, selective filtering of sources, prioritization of search topics, and the ability to view other analysts searches.

Verification: Analysts want indications of information that has been verified or discarded by other analysts, a trail of information history and uses, and automatic verification (e.g., data quality editing) if possible.

Analytics: Analysts want access to forecasting models, services to suggest analysis methods, pointers to other analysts' expertise, methods, and reports, and tools for "big data" exploitation.

Collaboration and communication: Analysts want assistance identifying people who may have needed information, real-time chat, the ability to compare analyses with colleagues, and the ability to shield data, results, or collaborations from selected others.

Archival: Analysts want automation to provide lessons learned, methods and outcomes for related events, the ability to automatically improve baselines with analyzed data, and assistance with reporting on interim analytic decisions.

The current understanding of the biosurveillance analyst's functions and processes, based on the results of these interviews, will continue to evolve as further dialog with analysts are combined with results of evaluations during subsequent phases of the new BSVE program.

Keywords

biosurveillance; workflow; collaboration; operations

Acknowledgments

This work is sponsored by the Defense Threat Reduction Agency under Air Force Contract #FA8721-05-C-0002. Opinions, interpretations, recommendations and conclusions are those of the authors and are not necessarily endorsed by the United States Government.

*Timothy Dasey
E-mail: TimD@LL.mit.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Biosurveillance Adaptable Framework for Teaming, Exploration and Reuse (BioAFTER)

Timothy Dasey* and Lars Fiedler

Chemical and Biological Defense Systems, MIT Lincoln Laboratory, Lexington, MA, USA

Introduction

Next-generation software environments for disease surveillance will need to have several important characteristics, among which are collaboration and search and discovery features, access to various data sets, and a variety of analytic methods. However, perhaps the most important feature is the least often mentioned – the ability to have the system adapt over time without high reengineering cost. The public health community cannot afford software redesigns every few years as data sets expand, analysis needs evolve, and software deficiencies are exposed. In addition to the need to adapt an environment over longer time periods, epidemiologists have high variability in their day-to-day needs that require adaptability over short time periods as well. Each outbreak or health situation has unique aspects, and analysts need to be able to bring in data and methods unique to that situation that may not be easily anticipated a priori.

The most common approach to increasing reusability and decreasing upgrade costs are open architecture software frameworks such as Service-Oriented Architectures (SOAs). If well implemented, SOAs can significantly reduce software upgrade costs by allowing services (a software module) to be easily swapped out for improvements or supplemented with additional services. SOAs can help with long-term adaptability, but are not useful in short-term adaptability, since the software development team must be engaged in each cycle. Another approach is to include an App Store. Unfortunately, App Stores for government use have often been disappointing. Apps can tend to be quite simple, and even slight changes from what is programmed – a predictable situation with the variability seen in disease surveillance realm - will result in an epidemiologist having to get a software developer to make them a new App.

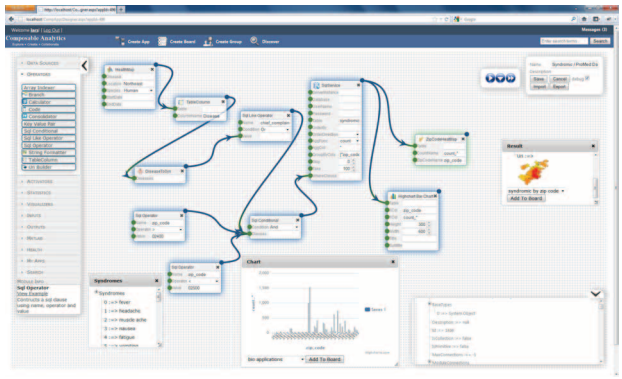
Methods

Instead of the power for adaptability remaining solely in the control of software developers, that power needs to also be in the hands of the users themselves. The BioAFTER project builds upon SOA and App Store concepts by allowing Apps to be strung together in unique combinations, according to the problem of the day. As examples, these Apps can be data access programs, data quality editing, algorithms of various complexity, or reporting and visualization modules. The App Store feature allows software developers, including the public health academic community, to add new methods to the environment, while the composability feature allows ad-hoc combinations of Apps to suit particular situations.

The user composability feature would be of limited value without collaboration features in the environment. We expect that only a subset of users will make the effort to do composition. The rest will want to learn from those "super users". The BioAFTER environment allows data, Apps (including new Apps created by compositions of other Apps), and analysis results to be shared with the entire epidemiological community, or with a set of "friends" or people with common interests. Analysts who use various Apps can rate their value. The environment is intended to allow search and discovery of Apps, expertise, or even people who may have needed expertise or experience with similar situations (these features are in development).

Results

The motivations and features of the BioAFTER environment will be described at the ISDS Conference, and a brief demonstration of the capabilities on an example use case will be given.



Keywords

biosurveillance; collaboration; discovery; composition; adaptability

Acknowledgments

This work is sponsored by the Office of the Assistant Secretary of Defense for Research and Engineering (ASD(R&E)) under Air Force Contract #FA8721-05-C-0002. Opinions, interpretations, recommendations and conclusions are those of the authors and are not necessarily endorsed by the United States Government.

*Timothy Dasey
E-mail: TimD@LL.mit.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

State Foodborne Illness Surveillance and Response Laws: Compilation and Analysis

Stephanie David, Jenna Burton, Chris Chadwick and Rebecca Katz*

George Washington University, Washington, DC, USA

Objective

To document and assess the variation in state legislation relating to foodborne disease surveillance and outbreak response for all 50 states and the District of Columbia by creating a database and appendix of laws and regulations that will be made available to researchers and policymakers.

Introduction

Foodborne illnesses sicken 48 million and kill 3,000 Americans every year, presenting an enduring threat to the public's health. In just the past three years alone, the United States has experienced at least four major multistate outbreaks in food. Despite this growing problem, efforts to prevent foodborne illness pose a particular public health challenge due in part to the widely variable laws governing foodborne illness surveillance and outbreak response. The recent passage of the Food Safety Modernization Act (FSMA) presents an opportunity for researchers, program managers, and policy makers to assess and correct the legal barriers that may hinder states in effectively implementing the FSMA's vision with regard to increased state and local capacity for surveillance and outbreak response.

Methods

We conducted a systematic review and analysis of laws and regulations relating to foodborne illness surveillance and outbreak response in all 50 states and the District of Columbia, using the following methods: (1) we created a database to record state laws and regulations relating to foodborne illness surveillance and outbreak response in all 50 states and the District of Columbia; (2) we conducted a basic gap analysis of state foodborne illness surveillance and outbreak response laws and policies collected in the database; and (3) we conducted case study analyses of previous multistate outbreaks from 2008-2011.

Results

Through compilation of the state foodborne illness surveillance and outbreak response laws and regulations and analysis of previous multistate outbreaks, we are able to present trends, variations, and gaps in the legislation that directly impacts the ability of public health officials to conduct foodborne outbreak investigations. We also present policy recommendations for strengthening state laws and regulations.

Keywords

Surveillance; Foodborne disease; Outbreak response; Public health law; Legal preparedness

Acknowledgments

This research was funded by a grant from the RWJ Foundation.

*Rebecca Katz
E-mail: rlkatz@gwu.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A System for Surveillance Directly from the EMR

Richard F. Davies*[1], Jason Morin[1], Ramanjot S. Bhatia[1] and Lambertus de Bruijn[2]

[1]University of Ottawa Heart Institute, Ottawa, ON, Canada; [2]National Research Council Canada, Ottawa, ON, Canada

Objective

Our objective was to conduct surveillance of nosocomial infections directly from multiple EMR data streams in a large multi-location Canadian health care facility. The system developed automatically triggers bed-day-level-location-aware reports and detects and tracks the incidents of nosocomial infections in hospital by ward.

Introduction

Hospital acquired infections are a major cause of morbidity, mortality and increased resource utilization. CDC estimates that in the US alone, over 2 million patients are affected by nosocomial infections costing approximately $34.7 billion to $45 billion annually (1). The existing process of detection and reporting relies on time consuming manual processing of records and generation of alerts based on disparate definitions that are not comparable across institutions or even physicians.

Methods

A multi-stakeholder team consisting of experts from medicine, infection control, epidemiology, privacy, computing, artificial intelligence, data fusion and public health conducted a proof of concept from four complete years of admission records of all patients at the University of Ottawa Heart Institute . Figure 1 lists the data elements investigated. Our system uses an open source enterprise bus 'Mirth Connect' to receive and store data in HL7 format. The processing of information is handled by individual components and alerts are pushed back to respective locations.The free text components were classified using natural language processing. Negation detection was performed using NegEx (2). Data-fusion algorithms were used to merge information to make it meaningful and allow complex syndrome definitions to be mapped onto the data.

Results

The system monitors: Ventilator Associated Pneumonia (VAP), Central Line Infections (CLI), Methicillin Resistant Staph Aureus (MRSA), Clostridium difficile (C. Diff) and Vancomycin resistant Enterococcus (VRE).

21452 hospital admissions occurred in 17670 unique patients over four years. There were 41720 CXRs performed in total, of which 10546 were classified as having an infiltrate. 4575 admissions were associated with at least one CXR showing an infiltrate, 2266 of which were hospital-acquired. Hospital acquired infiltrates were associated with an increased hospital mortality (6.3% vs 2.6%)* and length of stay (19.5 days vs 6.5 days)*. 253 patients had at least one positive blood culture. This was also associated with an increased hospital mortality (23,3% vs. 2.8%)* and length of stay (10.8 vs 40.9 days)*. (* all p values < 0.00001)

Conclusions

This proof of concept system demonstrates the capability of monitoring and analyzing multiple available data streams to automatically detect and track infections without the need for manual data capture and entry. It acquires directly from the EMR data to identify and classify health care events, which can be used to improve health outcomes and costs. The standardization of definitions used for detection will allow for generalization across institutions.

Data element/source	**Microbiology**
Medical Record Number	bacteriology requests
Patient Record System	bacteriology results
year of birth	virology request
Sex	virology results
partial postal code	**Hematology**
Ward	CBC results
Transfers	**Biochemistry**
date of admission	Creatinine
date of discharge	**Pharmacy**
isolation/respiratory, enteric precautions status	orders for antidiarrheals, antibiotics, antivirals
MRSA/VRE screening status	medication list
Radiology	**Surgical Information Management System**
Chest x-ray requests	Operative report or surgical list
Chest x –ray results	**Other information**
Emergency Room	Clinical Stores:
Chief complaint	Requests and utilization of ventilators, masks, gloves, hand sanitizer and linens
Final diagnosis	Payroll:
CTAS code	Staffing levels, absenteeism
Date of ER visit	

Keywords

electronic health records; surveillance; pneumonia; hospital acquired infections

Acknowledgments

This work was supported by Defence Research and Development Canada Centre for Security Science and the Chemical, Biological, Radiological/Nuclear, and Explosives Research and Technology Initiative (CRTI) under project CRTI 06-0234TA and the following participatory and advisory partners.

References

1. Report on CDC Website (http://www.cdc.gov/hai/pdfs/hai/scott_cost-paper.pdf) Accessed: 10th September, 2012.
2. Chapman, W. et. al. 2001. Evaluation of negation phrases in narrative clinical reports. Proc AMIA Symposium, 105-114.

*Richard F. Davies
E-mail: rfdavies@ottawaheart.ca

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Grid Based Approach to Share Public Health Surveillance Applications - The R Example

Kailah Davis*[1] and Julio Facelli[1, 2]

[1]Department of Biomedical Informatics, University of Utah, Salt Lake City, UT, USA; [2]Center of High Performance Computing, University of Utah, Salt Lake City, UT, USA

Objective

This poster describes an approach which leverages grid technology for the epidemiological analysis of public health data. Through a virtual environment, users, particularly epidemiologists, and others unfamiliar with the application, can perform on-demand powerful statistical analyses.

Introduction

Currently, there's little effective communication and collaboration among public health departments. The lack of collaboration has resulted in more than 300 separate biosurveillance systems (1), which are disease specific, not integrated or interoperable, and may be duplicative (1). Grid architecture is a promising methodology to aid in building a decentralized health surveillance infrastructure because it encourages an ecosystem development culture (2), which has the potential to increase collaboration and decrease duplications.

Methods

This project had two major steps: creation and validation of the grid service. For the first step [creation of the service], we first determined the parameter set required to execute R from the command line. We then used the caGrid Introduce toolkit (3) and Grid Rapid Application Virtualization Interface (gRAVI) (4) to wrap the R command line interface into a grid service. The service was then deployed to the caGrid training grid. After deployment, the service was invoked using the R grid service client which was automatically created by Introduce and gRAVI.

Our second step was aimed at validating the service by using using the grid service client to illustrate the working principles of R in a grid environment. For this illustration, we selected the article by Hohle et al (5). In this article, the 'surveillance' package was developed to provide different algorithms for the detection of aberrations in routinely collected surveillance data. For validation purposes, only a subset of the analyses presented in the article, namely the Farrington and CUSUM algorithms, were reproduced. Using the grid web client, we uploaded the necessary data files for processing, as well as the Rscript which was used to replicate the results of (5). The application then ran the R script on the execution machine; this machine had all the necessary R packages needed for the specific scenario.

Results

The implementation of was validated by showing that the results of the original paper can be reproduced using gird based version of R. Figure 1 shows the plots related to the steps described above; the plots illustrating the Farrington and CUSUM algorithms are seen to be identical to that in (5).

Conclusions

We demonstrated that it is possible to easily deploy applications for public health surveillance uses. We conclude that the techniques we used could be generalized to any application that has a command line interface. Future work will be aimed creating a workflow to access data services and grid-enabled text processing and analytic tools. We believe that by providing a set of examples to demonstrate the benefit of this technology to public health surveillance infrastructure may provide insight that may lead to a better, more collaborative system of tools that will become the future of public health surveillance.

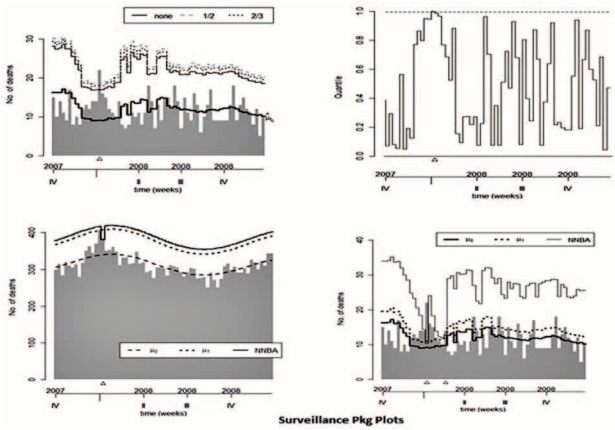


Fig 1. Recreated Plots

Keywords

Grid computing; Public health grid; analytical service

Acknowledgments

This work was supported by NLM training grant #T15LM007124 and CDC Center of Excellence for Public Health Informatics # 1P01HK000069-10.

References

1. Subcommittee NBA. Improving the Nation's Ability to Detect and Respond to 21st Century Urgent Health Threats: First Report of the National Biosurveillance Advisory Subcommittee. 2009.
2. Facelli JC. An agenda for ultra-large-scale system research for global health informatics. ACM SIGHIT Record. 2012;2(1):12-.
3. Hastings S, Oster S, Langella S, Ervin D, Kurc T, Saltz J. Introduce: an open source toolkit for rapid development of strongly typed grid services. Journal of Grid Computing. 2007;5(4):407-27.
4. Chard K, Tan W, Boverhof J, Madduri R, Foster I, editors. Wrap scientific applications as WSRF grid services using gRAVI. 2009: IEEE.
5.Höhle M, Mazick A. Aberration detection in R illustrated by Danish mortality monitoring. Biosurveillance: Methods and Case Studies. 2010:215-37.

*Kailah Davis
E-mail: kailah.davis@utah.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Multi-dimensional Problems in Health Settings: A Review of Approaches to Decision Making

Victor J. Del Rio Vilas*[1], Gilberto Montibeller[2], L. Alberto Franco[3] and Willy Aspinall[4]

[1]PAHO, Rio de Janeiro, Brazil; [2]London School of Economics, London, United Kingdom; [3]University of Hull, Hull, United Kingdom; [4]University of Bristol, Bristol, United Kingdom

Introduction

There appears to be a growing number of prioritization exercises, for example of diseases, in health related settings (1). The decision process around these exercises involves comparing competing alternatives, i.e. diseases, and irreducible objectives. In addition to the multi-dimensional nature of the problem, the lack of reliable data, group dynamics associated to the involvement of experts, and the multiplicity of stakeholders, among other contextual factors, add complexity to the decision process. Here we review trends in such prioritization exercises and applications in different settings and for different events of interest, for example the management of emerging risks. Based on our findings, we discuss a conceptual framework based on multi-attribute utility theory presented to the World Organization for Animal Health (OIE) for the modification of its qualitative assessment of veterinary services performance into a quantifiable decision support system.

Methods

We searched PubMed for articles containing the key words 'multi-criteria', 'multi-attribute', 'multi-objective', 'prioritization', 'decision making' and their variations (e.g. without hyphenation) for the period 1990 to 2011 for human and veterinary medicine. We focused on prioritization methodologies and their sound application.

Results

A large number of prioritization efforts in health settings aim to produce a rank order of diseases to help allocation of scarce surveillance and disease control budgets. A number of applications target the prioritization of competing health interventions against specific diseases. Fewer target different events, for example emerging threats. Common mistakes found in multi-attribute prioritization approaches reported in the social sciences (2) appear also in public and animal health settings. In particular, the application of linear additive models to non-preferentially independent evaluation criteria, the poor design of attributes to assess the decision alternatives, the failure to define suitable criteria scales, and mistakes in defining trade-off weights were prevalent. In addition, most decision support tools tend to be overly complex. This not only compromises their acceptability and long-term sustainability but also increases the likelihood of methodological mistakes in their design and regular application. For example, the failure to properly identify and separate 'ends' objectives, such as the improvement of a country's health, from 'means' objectives, i.e. required resources, in the definition of the fundamental drivers in any decision process.

Conclusions

Our findings, and experience in the practical application of formal prioritization methodologies (3), informed our advice to the OIE for the quantification of its tools for the assessment of veterinary services performance. The current framework used by the OIE produces a purely qualitative output with ordinal scales. The suggested quantitative extension allows additional outputs not available in their current form, for example, the aggregation of assessment scores at any level within the framework to produce a country's overall score. It also permits the assessment of marginal performance improvements for every criterion and the consideration of trade-offs among the different criteria. The final output of our extension is the identification of the best portfolio of actions that will maximize the overall capability of national veterinary services given available resources. Quantification of the existing tool will deliver obvious benefits such as enhanced accountability and transparency in the decision making process, and will allow the historical analysis of a country's veterinary services performance. The approach suggested to the OIE is adaptable to similar decision problems, such as monitoring the implementation of the International Health Regulations in a given country.

Keywords

Prioritisation; Multi-attribute utility theory; Decision support

References

1. Krause G., 2008. Prioritisation of infectious diseases in public health – call for comments. Euro Surveillance 13, 40.
2. Keeney R.L. (2002). Common Mistakes in Making Value Trade-Offs. Operations Research, 50, 6, 935–945.
3. Del Rio Vilas V.J., Voller F., Montibeller G., Franco A., Sribhashyam S., Watson E., Hartley M., Gibbens J. An integrated process and management tools for ranking multiple emerging threats to animal health. Preventive Veterinary Medicine (in press).

*Victor J. Del Rio Vilas
E-mail: vdelriovilas@yahoo.co.uk

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Computerized Text Analysis to Enhance Automated Pneumonia Detection

Sylvain DeLisle*[1, 2], Tariq Siddiqui[1, 2], Adi Gundlapalli[3, 4], Matthew Samore[3, 4] and Leonard D'Avolio[5, 6]

[1]VA Maryland Health Care System, Baltimore, MD, USA; [2]Medicine, University of Maryland, Baltimore, MD, USA; [3]VA Salt Lake City Health Care System, Salt Lake City, UT, USA; [4]University of Utah, Salt Lake City, UT, USA; [5]VA Boston Health Care System, Boston, MA, USA; [6]Harvard Medical School, Boston, MA, USA

Objective

To improve the surveillance for pneumonia using the free-text of electronic medical records (EMR).

Introduction

Information about disease severity could help with both detection and situational awareness during outbreaks of acute respiratory infections (ARI). In this work, we use data from the EMR to identify patients with pneumonia, a key landmark of ARI severity. We asked if computerized analysis of the free-text of clinical notes or imaging reports could complement structured EMR data to uncover pneumonia cases.

Methods

A previously validated ARI case-detection algorithm (CDA) (sensitivity, 99%; PPV, 14%) [1] flagged VAMHCS outpatient visits with associated chest imaging (n = 2737). Manually categorized imaging reports (Non-Negative if they could support the diagnosis of pneumonia, Negative otherwise; kappa = 0.88), served as a reference for the development of an automated report classifier through machine-learning [2]. EMR entries related to visits with Non-Negative chest imaging were manually reviewed to identify cases with Possible Pneumonia (new symptom(s) of cough, sputum, fever/chills/night sweats, dyspnea, pleuritic chest pain) or with Pneumonia-in-Plan (pneumonia listed as one of two most likely diagnoses in a physician's note). These cases were used as reference for the development of the EMR-based CDAs. CDA components included ICD-9 codes for the full spectrum of ARI [1] or for the pneumonia subset, text analysis aimed at non-negated ARI symptoms in the clinical note [1] and the above-mentioned imaging report text classifier.

Results

The manual review identified 370 reference cases with Possible Pneumonia and 250 with Pneumonia-in-Plan. Statistical performance for illustrative CDAs that combined structured EMR parameters with or without text analyses are shown in the Table. Addition of the "Text of Imaging Report" analyses increased PPV by 38-70% in absolute terms. Despite attendant losses in sensitivity, this classifier increased the F-Measure of all CDAs based on a broad ARI ICD-9 codeset. With the possible exception is CDA 6, whose F-measure was the highest achieved in this study, the text analysis seeking ARI symptoms in the clinical note did not add further value to those CDAs that also included analyses of the chest imaging reports.

Conclusions

Automated text analysis of chest imaging reports can improve our ability to separate outpatients with pneumonia from those with a milder form of ARI.

CDA Number	1	2	3	4	5	6	7	8	9	10	11	12
	Possible Pneumonia						Pneumonia-in-Plan					
CDA Components												
(Pneumonia ICD-9 Codes	●	●					●	●				
(ARI ICD-9 Codes			●	●	●	●			●	●	●	●
OR Text of Clinical Notes)					●	●					●	●
AND Chest Imaging Obtained	●	●	●	●	●	●	●	●	●	●	●	●
AND Text of Imaging Reports		●		●		●		●		●		●
Sensitivity (%)	36.8	28.4	85.9	58.4	99.7	66.2	52	40.8	93.6	68.8	100	74.8
Specificity (%)	95.4	99.7	29.8	98.5	2.2	98	95.4	99.6	29.8	96.8	2.3	95.7
PPV (%)	55.3	93.8	16	86.1	13.7	83.3	52.8	91.1	12	68.5	9.3	63.6
NPV (%)	91	90	93.2	93.8	98.1	95	95.2	94.4	98	97	100	97.4
F-Measure	44.2	43.6	27	69.6	24.1	73.8	52.4	56.4	21	68.6	17	68.7

Keywords

situational awareness; influenza; surveillance; electronic medical record; pneumonia

References

[1] DeLisle S, South B, Anthony JA, Kalp E, Gundlapalli A, et al. Combining Free Text and Structured Electronic Medical Record Entries to Detect Acute Respiratory Infections. PLoS ONE (2010) 5(10): e13377.

[2] D'Avolio L, Nguyen T, Goryachev S, Fiore L. Automated Concept-Level Information Extraction to Reduce the Need for Custom Software and Rules Development. Journal of the American Medical Informatics Association 2011 18(5): 607.

*Sylvain DeLisle
E-mail: sdelisle@umaryland.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Systematic Evaluation of Data Streams for Global Disease Surveillance

Alina Deshpande*, Mac Brown, Lauren Castro, William B. Daniel, Eric N. Generous, Andrea Hengartner, Kristen Margevicius and Kirsten Taylor-McCabe

Defense Systems Analysis Division, Los Alamos National Laboratory, Los Alamos, NM, USA

Objective

The overall objective of this project is to provide a robust evaluation of data streams that can be leveraged from existing and developing national and international disease surveillance systems, to create a global disease monitoring system and provide decision makers with timely information to prepare for and mitigate the spread of disease.

Introduction

Living in a closely connected and highly mobile world presents many new mechanisms for rapid disease spread and in recent years, global disease surveillance has become a high priority. In addition, much like the contribution of non-traditional medicine to curing diseases, non-traditional data streams are being considered of value in disease surveillance. Los Alamos National Laboratory (LANL) has been funded by the Defense Threat Reduction Agency to determine the relevance of data streams for an integrated global biosurveillance system through the use of defined metrics and methodologies. Specifically, this project entails the evaluation of data streams either currently in use in surveillance systems or new data streams having the potential to enable early disease detection. An overview of this project will be presented, together with results of data stream evaluation. This project will help gain an understanding of data streams relevant to early warning/monitoring of disease outbreaks.

Methods

Three specific aims were identified to address the overall goal of determining the relevance of data streams for global disease surveillance. First, identify data streams as well as define metrics for the evaluation. Second, evaluate data streams using two different methodologies, decision analysis modeling using a support tool called Logical Decisions® that assigns utility scores to data streams based on weighted metrics and assigned values specific to data stream categories; and a Surveillance Window concept developed at LANL that assigns a window or windows of time specific to a disease within which information coming from various data streams can be determined to have utility. This would obtain a ranked list of useful data streams. Additionally, evaluate data integration algorithms useful for a global disease surveillance system through a review of scientific literature. Finally, validate the top-ranked data streams by application of specific historical outbreaks to determine whether the data streams are capable of providing early warning or detection of the particular disease before it became a large outbreak.

Results

Seventeen categories of data streams were identified that ranged from traditional ones such as clinic/healthcare provider and laboratory records to newly emerging sources of information such as social media and internet search queries. The Logical Decisions® based evaluation of data streams identified 5 data streams that consistently showed utility regardless of the goal of biosurveillance. However, different data streams varied in rank, given different biosurveillance goals, and there is no one top ranked data stream. Surveillance window based evaluation of data streams during disease outbreaks identified data streams that had high utility for early detection and early warning regardless of disease, while others were more disease and operations specific. Additionally, we have built a searchable biosurveillance resource directory that houses information on global disease surveillance systems.

Conclusions

LANL has developed a robust evaluation framework to determine the relevance of various traditional and non-traditional data streams in integrated global disease surveillance. Through the use of defined surveillance goals, metrics and data stream categories, not only have we identified data streams currently in use that have high utility, but also new data streams that could be exploited for the early warning/monitoring of disease outbreaks. Our robust evaluation framework facilitates the identification of a defensible set of options for decision makers to use to prepare for and mitigate the spread of disease.

Keywords

evaluation; disease surveillance; data streams

Acknowledgments

We would like to acknowledge the Defense Threat Reduction Agency (DTRA)-Joint Science and Technology Office (JSTO) for their support and guidance on this project.

References

Dr. Alina Deshpande, Dr. Mac Brown, Ms. Lauren Castro, Dr. William Brent Daniel, Mr. Eric Nicholas Generous, Ms Andrea Hengartner, Dr. Kristen Margevicius, Dr. Kirsten Taylor-McCabe, Los Alamos National Laboratory, Los Alamos, NM 87545.

*Alina Deshpande
E-mail: deshpande_a@lanl.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Challenges and Opportunities in Routine Time Series Analysis of Surveillance Data

Isabelle Devaux*[1], Esther Kissling[2], Gilles Desve[2], Frantiska Hruba[1], Francisco Luquero[2], Chantal Quinten[1], Joana Gomes-Diaz[1], Marta Valenciano[2] and Denis Coulombier[1]

[1]ECDC, Solna, Sweden; [2]Epiconcept, Paris, France

Objective

To discuss challenges and opportunities in the introduction of an automated approach for time series analysis (TSA) regarding epidemiological methodology for generation of hypotheses, steps to be performed and interpretation of outputs.

Introduction

ECDC long term strategies for surveillance include analysis of trends of communicable disease of public health importance for European Union countries to guide public health actions. The European Surveillance System (TESSy) holds data on 49 communicable diseases reported by 30 countries for at least the past five years. To simplify time related analysis using surveillance data, ECDC launched a project to enable descriptive and routine TSA without the need for complex programming.

Methods

Protocols for TESSy data were developed specifying hypotheses to be tested, types and format of variables needed for TSA for several diseases, including VTEC, and legionellosis. Stata scripts were developed to comply with the basic steps of TSA, including data aggregation, data checking, data description, analysis of trends and seasonality, residual analysis, simple modelling and long-term forecasting. TSA steps were presented as successive tabs in a TSA dialogue box in Stata. Before using the Stata TSA dialogue box, experts were offered a two-day training, and provided with an in-depth manual supporting use and interpretation of TSA outputs using the Stata TSA dialogue box.

Results

For VTEC, it was possible to identify a small increase in the trend and a seasonal pattern in surveillance data with an estimate of the start of the increased risk for infection in the beginning of the summer season [1]. For legionellosis, an increasing trend in the number of reported cases was observed in 2010 [2]. Feedback from the training showed that using the Stata TSA dialogue box enables a quick exploratory analysis even by non-Stata users who could focus on interpretation of results, rather than the programme writing. However, we emphasise that statistical knowledge of TSA as well as rigorous preparation of the datasets (including data quality checks) and generation of hypotheses, are essential to ensure appropriate analysis and meaningful interpretation of the results.

Conclusions

Using the Stata TSA dialogue box saves time when performing rapid exploratory TSA of epidemiological data, avoiding the need for complex programming which is still needed for sophisticated TSA. Results of exploratory TSA analysis can trigger new hypothesis, for more advanced and sophisticated TSA. The introduction of a new technology (Stata TSA dialogue box) does not replace multi-disciplinary approach, knowledge and application of a methodological approach to TSA to produce meaningful results that can inform public health decision making. Further testing and training will be performed to enhance simplicity before appropriate dissemination of the Stata TSA dialogue box for a wider use.

Keywords

surveillance; epidemiology; statistical model; data analysis; software tool

Acknowledgments

ECDC experts in food and water-borne diseases (Angela Lahuerta-Marin, Taina Niskanen, Johanna Takkinen, Therese Westrell), and Legionnaires' disease (Julien Beaute).

References

[1] Joana Gomes Dias, Františka Hrubá, Chantal Quinten, Bruno Ciancio, Isabelle Devaux, Taina Niskanen, Therese Westrell, Angela Lahuerta-Marin, Johanna Takkinen. Time-series analysis of VTEC/STEC surveillance data, 2008–2010. Poster to be presented in ESCAIDE (www.escaide.org) 24-26 October 2012.

[2] Julien Beaute, Birgita De Jong. Time series analysis of community-acquired Legionnaires' disease in Europe. Poster to be presented in ESCAIDE (www.escaide.org) 24-26 October 2012.

*Isabelle Devaux
E-mail: isabelle.devaux@ecdc.europa.eu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluating Usefulness of Maine's Syndromic Surveillance System for Hospitals, 2012

Stefanie DeVita* and Amy Robbins

Infectious Disease Epidemiology, Maine CDC, Augusta, ME, USA

Objective

To assess the usefulness and acceptability of Maine's syndromic surveillance system among hospitals who currently participate.

Introduction

Maine has been conducting syndromic surveillance since 2007 using the Early Aberration Reporting System (EARS). An evaluation of the syndromic surveillance system was conducted to determine if system objectives are being met, assess the system's usefulness, and identify areas for improvement. According to CDC's Guidelines for Evaluating Public Health Surveillance Systems, a surveillance system is useful if it contributes to the timely prevention and control of adverse health events. Acceptability includes the willingness of participants to report surveillance data; participation or reporting rate; and completeness of data.

Methods

A survey was created in 2012 to measure usefulness and acceptability among hospital partners who submit emergency department data to Maine CDC for syndromic surveillance. Currently, 24 of Maine's 36 acute care hospitals collect syndromic surveillance data and 22 of those receive a weekly syndromic surveillance report from Maine CDC. The survey was included with the report on August 14, 2012, and hospitals were given two weeks for completion. The survey included questions about how useful hospitals find syndromic surveillance and how data is shared back with the hospitals; which syndromes are most and least useful; and chief complaint data collection at individual hospitals.

Results

The survey was completed by 13 out of 22 hospitals (59% participation rate), and six out of 13 respondents (46%) completed the entire survey. The factors reported as having an influence on a hospital's decision to submit data for syndromic surveillance were: public health importance of events (6 respondents) and assurance of privacy/confidentiality (5 respondents). The majority of respondents (5 respondents) reported that there are no factors that limit their ability to send emergency department data. Among hospitals that did report factors that limit their ability to send data, lack of information technology support in the hospital (2 respondents) and manually entering data/lack of electronic health records (1 respondent) were the most frequently reported. Six out of seven hospitals who answered (86%) report the current method of sharing syndromic surveillance data on a weekly basis, including a statewide data summary, as useful. Respondents also recommended that data be shared back with participants using 30-day line graphs for each syndrome (4 respondents). The three syndromes respondents found most useful were influenza-like illness (7 respondents), gastrointestinal (5 respondents), and respiratory (5 respondents). The three syndromes respondents found least useful were the broad heat syndrome (4 respondents), the narrow heat syndrome (4 respondents), and the other syndrome that captures all visits not classified into any syndrome (4 respondents). Chief complaint data, which is used to classify emergency department visits into syndromes, is most often recorded by a drop-menu (4 respondents).

Conclusions

With a low survey completion rate, it is difficult to generalize responses to all hospitals who participate in syndromic surveillance. Hospitals that did not respond to or complete the survey will be followed up with to determine their reasons for not doing so, as this may be useful information. In general, those who responded have more factors that influence them to contribute to syndromic surveillance than factors that hinder them. Most hospitals find the current method of sharing data back with the hospitals useful. Also, it is advantageous to know which syndromes the hospitals find most useful, as they are the entities that collect and report the data. Opinions differ among system users, which is why it is important to evaluate a system throughout all points of interaction.

Keywords

Syndromic surveillance; Evaluation; Acceptability

Acknowledgments

The authors would like to acknowledge those hospital partners who completed the survey.

References

Updated guidelines for evaluating public health surveillance systems. (2001) Morbidity and Mortality Weekly Report, 50(RR13);1-35. Retrieved from http://www.cdc.gov/mmwr/preview/mmwrhtml/rr5013a1.htm

*Stefanie DeVita
E-mail: stefanie.devita@maine.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Mental Illness and Co-morbid Conditions: BioSense 2008 - 2011

Achintya N. Dey*, Anna Grigoryan, Soyoun Park, Stephen Benoit and Taha Kass-Hout

DNDHI, CDC, Atlanta, GA, USA

Objective

The purpose of this paper was to analyze the associated burden of mental illness and medical comorbidity using BioSense data 2008-2011.

Introduction

Understanding the relationship between mental illness and medical comorbidity is an important aspect of public health surveillance. In 2004, an estimated one fourth of the US adults reported having a mental illness in the previous year (1). Studies showed that mental illness exacerbates multiple chronic diseases like cardiovascular diseases, diabetes and asthma (2). BioSense is a national electronic public health surveillance system developed by the Centers for Disease Control and Prevention (CDC) that receives, analyzes and visualizes electronic health data from civilian hospital emergency departments (EDs), outpatient and inpatient facilities, Veteran Administration (VA) and Department of Defense (DoD) healthcare facilities. Although the system is designed for early detection and rapid assessment of all-hazards health events, BioSense can also be used to examine patterns of healthcare utilization.

Methods

We used 4 years (2008 – 2011) of BioSense civilian hospitals' EDs visit data to perform the analysis. We searched final diagnoses for ICD-9 CM codes related to mental illness (290 – 312), schizophrenia (295), major depressive disorder (296.2 – 296.3), mood disorder (296, 300.4 and 311) and anxiety, stress & adjustment disorders (300.0, 300.2, 300.3, 308, and 309). We used BioSense syndromes/sub-syndromes based on chief complaints and final diagnoses for comorbidity. For the purpose of this study, comorbidity was defined broadly as the co-occurrence of mental and physical illness in the same person regardless of the chronological order. The proportion was calculated as the number of mental health visits associated with comorbidity divided by the total number of mental illness relevant visits. We ranked the top 10 proportions of comorbidity for adult mental illness by year.

Results

From 2008-2011, there were 4.6 million visits where mental illness was reported in the EDs visits. Average age of those reported mental illness was 44 years, 55% were women and 45% were men. More women were reported with anxiety (67%), mood (66%), and major depressive disorders (59%) than men; while men were reported more with schizophrenia (56%) than women (44%). The most common comorbid condition was hypertension, followed by chest pain, abdominal pain, diabetes, nausea & vomiting and dyspnea (Table 1). Ranks of injury, falls, headache and asthma were slightly variant by year.

Conclusions

This study supports prior findings that adult mental illness is associated with substantial medical burden. We identified 10 most common comorbid condition associated with mental illness. The major limitation of this work was that electronic data does not allow determination of the causal pathway between mental illness and some medical comorbidity. In addition, data represents only those who have access to healthcare or those with health seeking behaviors. Familiarity with comorbid conditions affecting persons with adult mental illness may assist programs aimed at providing medical care for the mentally ill.

Table1. Rankings of comorbidity conditions reported in adults wiht episodes of mental illness in EDs

Rank	2008	2009	2010	2011
1	Hypertension	Hypertension	Hypertension	Hypertension
2	Chest Pain	Chest Pain	Chest Pain	Chest Pain
3	Abdominal pain	Abdominal pain	Abdominal pain	Abdominal pain
4	Diabetes mellitus	Diabetes mellitus	Diabetes mellitus	Diabetes mellitus
5	Nausea & vomiting	Nausea & vomiting	Nausea & vomiting	Nausea & vomiting
6	Dyspnea	Dyspnea	Dyspnea	Dyspnea
7	Injury, NOS	Falls	Falls	Falls
8	Falls	Asthma	Headache	Headache
9	Headache	Headache	Asthma	Injury, NOS
10	Asthma	Injury, NOS	Injury, NOS	Asthma

Keywords

ED visits; Adult mental illness; Medical comorbidity

References

[1] Kessler RC, Heeringa S, Lacoma MD et al Individual and societal effects of mental disorders on earnings in the united States: results from the National Comorbidity Survey replication. Am.J.Psychiatry 2008; 165:703-11

[2] Chapman DP, Perry GS, Strine TW. The vital link between chronic disease and depressive disorders. Prev.Chronic Dis 2005;2;A14

*Achintya N. Dey
E-mail: adey@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Enhanced Surveillance during the Democratic National Convention, Charlotte, NC

Lana Deyneka*[1], Amy Ising[2] and Meichun Li[2]

[1]North Carolina Division of Public Health, Raleigh, NC, USA; [2]University of North Carolina, Chapel Hill, NC, USA

Objective

To describe how the existing state syndromic surveillance system (NC DETECT) was enhanced to facilitate surveillance conducted at the Democratic National Convention in Charlotte, North Carolina from August 31, 2012 to September 10, 2012.

Introduction

North Carolina hosted the 2012 Democratic National Convention, September 3-6, 2012. The NC Epidemiology and Surveillance Team was created to facilitate enhanced surveillance for injuries and illnesses, early detection of outbreaks during the DNC, assist local public health with epidemiologic investigations and response, and produce daily surveillance reports for internal and external stakeholders. Surveillane data were collected from several data sources, including North Carolina Electronic Disease Surveillance System (NC EDSS), triage stations, and the North Carolina Disease Event Tracking and Epidemiologic Collection Tool (NC DETECT).

NC DETECT was created by the North Carolina Division of Public Health (NC DPH) in 2004 in collaboration with the Carolina Center for Health Informatics (CCHI) in the UNC Department of Emergency Medicine to address the need for early event detection and timely public health surveillance in North Carolina using a variety of secondary data sources. The data from emergency departments, the Carolinas Poison Center, the Pre-hospital Medical Information System (PreMIS) and selected Urgent Care Centers were available for monitoring by authorized users during the DNC.

Methods

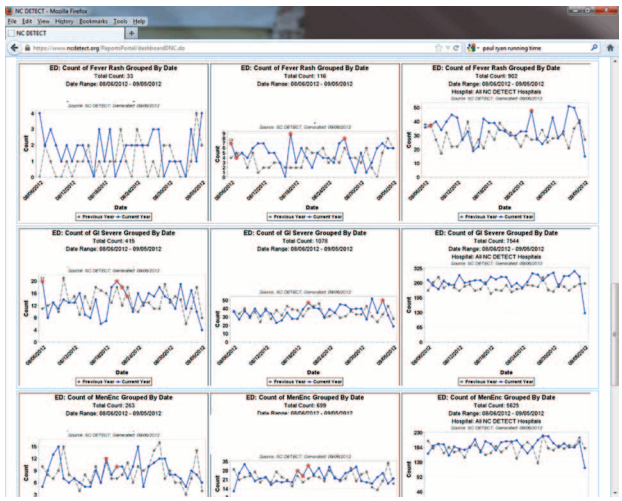
Within NC DETECT, new dashboards were created that allowed epidemiologists to monitor ED visits and calls to the poison center in the Charlotte area, the greater Cities Readiness Initiative region and the entire state for infectious disease signs and symptoms, injuries and any mention of bioterrorism agents. The dashboards also included a section to view user comments on the information presented in NC DETECT. Data processing changes were also made to improve the timeliness of the EMS data received from PreMIS.

Results

The DNC dashboards added to NC DETECT streamlined the workflow by placing all syndromes and annotations of interest in one place, with the date ranges and locations already pre-selected. Graphs in the dashboards could be easily copied and pasted into situation reports. The prompt development of these user-friendly tools provided effective surveillance for this mass gathering and ensured timely control measures, if necessary.

Conclusions

Syndromic surveillance systems can be enhanced to provide detailed, specific surveillance during mass gathering events. Elements that facilitate this enhancement include strong communication between skilled users and the informatics team, in order to minimize the burden placed on the surveillance team system users, data sources and system developers during the event. The visualizations developed as part of these new dashboards will be leveraged to provide additional tools to other NC DETECT user groups, including hospital-based public health epidemiologists and local health department users.



Keywords

dashboards; enhanced surveillance; Democratic National Convention

Acknowledgments

1.Stephanie Griese, MD, MPH Lieutenant Commander, US Public Health Service EIS Officer, CDC, Communicable Disease Branch NC DPH
2. Aaron Fleischauer, PhD, MSPH,Commander, US Public Health Service,Career Epidemiology Field Officer (CEFO),Centers for Disease Control and Prevention (CDC),Communicable Disease Branch NC DPH
3. Jennifer MacFarquhar, RN, MPH, CIC,Career Epidemiology Field Officer,Centers for Disease Control and Prevention,Communicable Disease Branch NC DPH
4. Grace Oguntebi, MPH CDC/CSTE Applied Public Health Informatics Fellow, Communicable Disease Branch NC DPH

References

1.Joseph S. Lombardo, Carol A. Sniegoski, Wayne A. Loschen, Matthew Westercamp, Michael Wade, Shandy Dearth, and Guoyan Zhang Public Health Surveillance for Mass Gatherings Johns Hopkins APL Technical Digest, Volume 27, Number 4 (2008)
2.Kaiser R, Coulombier D. Epidemic intelligence during mass gatherings. Euro Surveill. 2006;11
3.Ising A, Li M, Deyneka L, Vaughan-Batten H, Waller A. Improving syndromic surveillance for nonpower users: NC DETECT dashboards. Emerging Health Threats Journal 2011, 4: 11702 - DOI: 10.3402/ehtj.v4i0.11702

*Lana Deyneka
E-mail: lana.deyneka@dhhs.nc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

LOINC and SNOMED CT Code Use in Electronic Laboratory Reporting—US, 2011

Sanjaya Dhakal*[1], Sherry L. Burrer[1], Carla A. Winston[2], Mathew Miller[3] and Samuel L. Groseclose[4]

[1]CDC/OSELS/PHSIPO, Atlanta, GA, USA; [2]Department of Veterans Affairs, Washington, DC, USA; [3]McKing Consulting, Atlanta, GA, USA; [4]CDC/OPHPR/SPHP, Atlanta, GA, USA

Objective

To examine the use of LOINC and SNOMED CT codes for coding laboratory orders and results in laboratory reports sent from 63 non-federal hospitals to the BioSense Program in calendar year 2011.

Introduction

Monitoring laboratory test reports could aid disease surveillance by adding diagnostic specificity to early warning signals and thus improving the efficiency of public health investigation of detected signals. Laboratory data could also be employed to direct and evaluate interventions and countermeasures, while monitoring outbreak trends and progress; this would ultimately result in better outbreak response and management, and enhanced situation awareness. Since Electronic Laboratory Reporting (ELR) has the potential to be more accurate, timely, and cost-effective than reporting by other means of communication (e.g., mail, fax, etc.), ELR adoption has been systematically promoted as a public health priority. However, the continuing use of non-standard, local codes or text to represent laboratory test type and results complicates the use of ELR data in public health practice. Use of structured, unique, and widely available coding system(s) to support the concepts represented by locally assigned laboratory test order and result information improves the computational characteristics of ELR data. Out of several coding strategies available, the Office of the U.S. National Coordinator for Health Information Technology has recently suggested incorporating Logical Observation Identifiers Names and Codes (LOINC) for laboratory orders and Systemized Nomenclature of Medicine- Clinical Terms (SNOMED CT) codes for laboratory results to standardize ELR.

Methods

We assessed the use of LOINC and SNOMED CT codes in laboratory data reported to BioSense, a near real-time national-level, electronic syndromic surveillance system, managed by the Centers for Disease Control and Prevention. ELR data reported by 63 non-federal hospitals to BioSense in 2011 were analyzed to examine LOINC and SNOMED CT use in coding laboratory orders and results. We used Relma software, developed and distributed by Regenstrief Institute Inc for identifying LOINC codes.

Results

In 2011, a total of 14,028,774 laboratory test order or result reports from 821,108 individual patients were reported from the 63 hospitals in 14 states. Since, by design the BioSense Program monitors a select set of syndromes mainly representing infectious conditions, 94% of the total reports were microbiology test orders or results. Seventy-seven percent of all test orders (n = 10,776,494) used LOINC codes. Of all test results with at least one value either in observation identifier (OBX3) or observation value (OBX5) segments of their Health Level 7 (HL7) ELR message (n = 12,313,952), 81% had only LOINC codes, 0.1% had only SNOMED codes, 7% had both LOINC and SNOMED codes, and 12% used no codes. In total, 1,428 unique LOINC and 608 unique SNOMED codes were used to describe the results, and 805 unique LOINC codes were used to describe the orders. Of the 608 unique SNOMED codes, 111 (18.3%) did not have corresponding LOINC codes. Fifty-one (46%) of these 111 SNOMED codes could have been matched to corresponding LOINC codes based on the concept. However, our search for matching LOINC codes in Relma for certain SNOMED concepts indicated that LOINC does not have codes for select types of laboratory test results, particularly qualifier (such as reactive, negative, and resistant) or structural (labia, urethra, and vagina) concepts.

Conclusions

Our analysis showed that the use of SNOMED CT codes for laboratory test results by non-federal hospitals reporting laboratory data to BioSense was extremely limited. These hospitals more frequently used LOINC codes than SNOMED CT in reporting test results. We found that a large percentage of test results with SNOMED CT codes could be represented by LOINC codes that exactly or closely match SNOMED CT codes. Using LOINC codes to report both test order and results in these databases could increase the availability and use of laboratory data in public health and surveillance activities. However, to increase the sensitivity of the coding further, a small number of tests could benefit by using LOINC along with SNOMED CT codes. Evaluation of use of syndromic surveillance case definitions that incorporate laboratory result information is required to determine if it improves syndromic surveillance performance for enhanced outbreak detection or improved situation awareness.

Keywords

LOINC; SNOMED; Laboratory reporting; ELR

*Sanjaya Dhakal
E-mail: hgj2@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Towards Interoperability for Public Health Surveillance: Experiences from Two States

Brian E. Dixon*[1, 2, 3], Jason A. Siegel[5], Tanya V. Oemig[5] and Shaun J. Grannis[4, 2]

[1]Indiana University, Indianapolis, IN, USA; [2]Regenstrief Institute, Indianapolis, IN, USA; [3]Center of Excellence on Implementing Evidence-Based Practice, Department of Veterans Affairs, Veterans Health Administration, Health Services Research and Development Service, Indianapolis, IN, USA; [4]Indiana University School of Medicine, Indianapolis, IN, USA; [5]Atlas Development Corporation, Calabasas, CA, USA

Objective

To characterize the use of standardized vocabularies in real-world electronic laboratory reporting (ELR) messages sent to public health agencies for surveillance.

Introduction

The use of health information systems to electronically deliver clinical data necessary for notifiable disease surveillance is growing. For health information systems to be effective at improving population surveillance functions, semantic interoperability is necessary.

Semantic interoperability is "the ability to import utterances from another computer without prior negotiation" (1). Semantic interoperability is achieved through the use of standardized vocabularies which define orthogonal concepts to represent the utterances emitted by information systems. There are standard, mature, and internationally recognized vocabularies for describing tests and results for notifiable disease reporting through ELR (2). Logical Observation Identifiers Names and Codes (LOINC) identify the specific lab test performed. Systematized Nomenclature of Medicine-Clinical Terms (SNOMED CT) identify the diseases and organisms tested for in a lab test.

Many commercial laboratory and hospital information systems claim to support LOINC and SNOMED CT on their company websites and in marketing materials, and systems certified for Meaningful Use are required to support LOINC and SNOMED CT. There is little empirical evidence on the use of semantic interoperability standards in practice.

Methods

To characterize the use of standardized vocabularies in electronic laboratory reporting (ELR) messages sent to public health agencies for notifiable disease surveillance, we analyzed ELR messages from two states: Indiana and Wisconsin. We examined the data in the ELR messages where tests and results are reported (3). For each field, the proportion of field values that used either LOINC or SNOMED CT codes were calculated by dividing the number of fields with coded values by the total number of non-null values in fields.

Results

Results are summarized in Table-1. In Indiana, less than 17% of incoming ELR messages contained a standardized code for identifying the test performed by the laboratory, and none of the test result fields contained a standardized vocabulary concept. For Wisconsin, none of the incoming ELR messages contained a standardized code for identifying the test performed, and less than 13% of the test result fields contained a SNOMED CT concept.

Conclusions

Although Wisconsin and Indiana both have high adoption of advanced health information systems with many hospitals and laboratories using commercial systems which claim to support interoperability, very few ELR messages emanate from real-world systems with interoperable codes to identify tests and clinical results. To effectively use the arriving ELR messages, Indiana and Wisconsin health departments employ software and people workarounds to translate the incoming data into standardized concepts that can be utilized by the states' surveillance systems. These workarounds present challenges for budget constrained public health departments seeking to leverage Meaningful Use Certified technologies to improve notifiable disease surveillance.

Table 1 – Proportion of "Raw" ELR Data Samples with LOINC or SNOMED CT Concepts

Sample	% OBX-3 Fields with LOINC	% OBX-5 Fields with SNOMED CT
INPC Messages	16.5%	0.0%
WDHS Messages	0.0%	12.3%

Keywords

Standards; Interoperability; Electronic Laboratory Reporting; Public Health Surveillance; Computerized Medical Records Systems

Acknowledgments

The authors further thank Shahid Khokhar of the Regenstrief Institute and Keith Michaelson of Atlas Public Health for their help with the extraction of the ELR message data.

This work was supported, in part, by the Indiana Center of Excellence in Public Health Informatics through a grant award (501HK000077) from the U.S. Centers for Disease Control and Prevention.

References

1. Dolin RH, Alschuler L. Approaching semantic interoperability in Health Level Seven. J Am Med Inform Assoc. 2011;18(1):99-103.
2. Wurtz R, Cameron BJ. Electronic laboratory reporting for the infectious diseases physician and clinical microbiologist. Clin Infect Dis. 2005;40(11):1638-43.
3. Dixon BE, McGowan JJ, Grannis SJ. Electronic laboratory data quality and the value of a health information exchange to support public health reporting processes. AMIA Annu Symp Proc. 2011;2011:322-30.

*Brian E. Dixon
E-mail: bdixon@regenstrief.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Towards Estimation of Electronic Laboratory Reporting Volumes in a Meaningful Use World

Brian E. Dixon*[1, 2, 4], Roland E. Gamache[1, 2] and Shaun J. Grannis[3, 2]

[1]School of Informatics, Indiana University, Indianapolis, IN, USA; [2]Regenstrief Institute, Indianapolis, IN, USA; [3]Indiana University School of Medicine, Indianapolis, IN, USA; [4]Center of Excellence on Implementing Evidence-Based Practice, Department of Veterans Affairs, Veterans Health Administration, Health Services Research and Development Service, Indianapolis, IN, USA

Objective

To support health department estimation of future electronic laboratory report volumes from hospitals that achieve Stage 2 meaningful use.

Introduction

The American Recovery and Reinvestment Act of 2009 authorized the Centers for Medicare and Medicaid Services (CMS) to incentivize hospitals and physicians to become meaningful users of electronic health record (EHR) systems. In a final rule issued August 2012, CMS outlined the requirements for Stage 2 meaningful use to be effective in 2014 (1). The Stage 2 criteria require eligible hospitals to submit electronic laboratory reports to health departments.

While many state health departments receive some portion of notifiable disease reports electronically, the final Stage 2 rule is likely to increase the volume of incoming electronic reports. The Centers for Disease Control and Prevention are urging health departments to prepare for the sharp increase in electronic laboratory reporting (ELR). Crucial to preparedness is estimation of how many ELR reports can be expected. However, few health departments have experience with high volume ELR, making estimation difficult.

The Indiana Network for Patient Care (INPC), a regional health information exchange, has been processing high volumes of ELR for over a decade (2). To support health departments estimate potential ELR increases, the INPC examined its current volumes from hospitals with advanced EHR capabilities.

Methods

The INPC uses an automated case-detection system called the Notifiable Condition Detector (NCD) developed by investigators at the Regenstrief Institute (3). The NCD uses a standards-based messaging and vocabulary infrastructure to process more than 350,000 clinical transactions daily, including laboratory studies, diagnoses, and transcriptions from more than 40 hospitals, national labs and local ancillary service organizations.

Data processed between January 1, 2010 and December 15, 2011 were extracted from the NCD. Validated cases of notifiable conditions of interest to the Indiana State Department of Health were filtered out for use in this analysis. We further eliminated duplicate cases of the same reportable record for the same individual. Unique notifiable disease cases were divided by the population of the Indianapolis Metropolitan Statistical Area (MSA) to obtain a ratio for estimation of future volume.

Results

We identified a total of 77,199 unique notifiable disease cases. According to 2010 census data, the population of the Indianapolis MSA is 1,834,672. This produces a ratio of 2,104 ELR cases per 100,000 population per year.

Conclusions

Roughly 2% of the population had an unique notifiable disease case reported, more than double current rates (4). Actual rates could be higher given this analysis eliminated duplicate reports for chronic diseases, such as tuberculosis, hepatitis B and C, and sickle cell disease. The impact on local and state health departments is likely to be significant given scarce resources.

Although the calculated ratio may stimulate conversations within health departments, it represents an approximate estimator. Future work will seek to refine estimation techniques by accounting for acute versus chronic notifiable disease as well as additional factors, such as the notifiable condition and/or the relative size of the hospital sending lab data to the health department. These refined estimators will enable improved planning efforts within state and local health departments.

Keywords

Electronic Laboratory Reporting; Public Health Surveillance; Public Health Informatics; Electronic Health Records

Acknowledgments

This work was funded in part by a grant (5R01HS020209) from the Agency for Healthcare Research and Quality.

References

1. Centers for Medicare & Medicaid Services. Medicare and Medicaid Programs; Electronic Health Record Incentive Program—Stage 2. Federal Register [Internet]. 2012 [cited 2012 August 24]. Available from: http://www.ofr.gov/OFRUpload/OFRData/2012-21050_PI.pdf.
2. Dixon BE, McGowan JJ, Grannis SJ. Electronic laboratory data quality and the value of a health information exchange to support public health reporting processes. AMIA Annu Symp Proc. 2011;2011:322-30.
3. Fidahussein M, Friedlin J, Grannis S. Practical Challenges in the Secondary Use of Real-World Data: The Notifiable Condition Detector. AMIA Annu Symp Proc. 2011:402-8.
4. Centers for Disease Control and Prevention. Summary of notifiable diseases: United States, 2009. MMWR Morb Mortal Wkly Rep. 2011 May 13;58(53):1-100.

*Brian E. Dixon
E-mail: bdixon@regenstrief.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

State and Local Health Agency Engagement in HIE: A Cross-Sectional Survey

Brian E. Dixon*[1, 2, 3], Roland E. Gamache[1, 2] and Shaun J. Grannis[4, 2]

[1]School of Informatics, Indiana University, Indianapolis, IN, USA; [2]Regenstrief Institute, Indianapolis, IN, USA; [3]Center of Excellence on Implementing Evidence-Based Practice, Department of Veterans Affairs, Veterans Health Administration, Health Services Research and Development Service, Indianapolis, IN, USA; [4]Indiana University School of Medicine, Indianapolis, IN, USA

Objective

To characterize state and local health agency relationships with health information exchange organizations.

Introduction

There is growing interest in leveraging available health information exchange (HIE) infrastructures to improve public health surveillance (1). The Health Information Technology for Clinical and Economic Health Act and Meaningful Use criteria for electronic health record (EHR) systems are among the factors driving the development, adoption and use of HIEs. HIEs deliver or make accessible clinical and administrative data as patients are admitted, discharged, and transferred across hospitals, clinics, medical centers, counties, states and regions (2). While several HIE infrastructures exist (3), there is little evidence on the engagement in HIE initiatives by state and local health agencies.

Methods

An online survey of state and local health officials was conducted in six states where HIEs were known to be present. Half of the states were funded by the Centers for Disease Control and Prevention (CDC) to engage public health agencies in HIE activities; the other half received no such funding. A total of 143 officials were invited to participate; 73 (51%) responded. The survey asked respondents about their agencies awareness, engagement, and data exchange with HIEs. The survey further asked agencies about their perceptions of barriers and challenges to public health engagement with HIE organizations.

Results

Just 25% of agencies had a formal relationship, typically created through a memorandum of understanding or data usage agreement, with at least one nearby HIE. The majority (54%) of agencies either had no relationship (20%) or only an informal relationship (34%) with an HIE. The remaining agencies (18%) reported that no HIE existed in their jurisdiction. Agencies in states that had received CDC funding for HIE engagement were more likely (14 versus 2) to be formally partnered with an HIE.

Conclusions

Few public health agencies are formally engaged in HIE. Financial costs, human resources, and concerns regarding privacy/security were the top cited barriers to broader engagement in HIE. For public health to be an active participant in and reap the benefits of HIE, greater investment in state and local public health informatics capacity, including human resources, and education regarding HIE privacy and security practices are needed.

Keywords

Health Information Exchange; Electronic Laboratory Reporting; Public Health Surveillance; Public Health Informatics

Acknowledgments

This work was supported, in part, by the Indiana Center of Excellence in Public Health Informatics through a grant from the CDC (501HK000077).

References

1. Savel TG, Foldy S. The role of public health informatics in enhancing public health surveillance. MMWR Surveill Summ. 2012;61:20-4.
2. Dixon BE, Zafar A, Overhage JM. A Framework for evaluating the costs, effort, and value of nationwide health information exchange. J Am Med Inform Assoc. 2010;17(3):295-301.
3. eHealth Initiative. The State of Health Information Exchange in 2010: Connecting the Nation to Achieve Meaningful Use. Washington, DC2010 [cited 2010 September 29]; Available from: http://ehealthinitiative.org/uploads/file/Final%20Report.pdf.

*Brian E. Dixon
E-mail: bdixon@regenstrief.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Improving ILI Surveillance using Hospital Staff Influenza-like Absence (ILA)

Lydia Drumright*[1], Simon D. Frost[2], Mike Catchpole[3], John Harrison[5], Mark Atkins[5], Penny Parker[5], Alex J. Elliot[4], Douglas M. Fleming[6] and Alison H. Holmes[1, 5]

[1]Medicine, Imperial College London, London, United Kingdom; [2]University of Cambridge, Cambridge, United Kingdom; [3]Centre for Infections, Health Protection Agency, London, United Kingdom; [4]Health Protection Agency Syndromic Surveillance Team, Birmingham, United Kingdom; [5]Imperial College Healthcare NHS Trust, London, United Kingdom; [6]Royal College of General Practitioners Research and Surveillance Centre, Birmingham, United Kingdom

Objective

To address the feasibility and efficiency of a novel syndromic surveillance method, monitoring influenza-like absence (ILA) among hospital staff, to improve national ILI surveillance and inform local hospital preparedness.

Introduction

Surveillance of influenza in the US, UK and other countries is based primarily on measures of influenza-like illness (ILI), through a combination of syndromic surveillance systems, however, this method may not capture the full spectrum of illness or the total burden of disease. Care seeking behaviour may change due to public beliefs, for example more people in the UK sought care for pH1N1 in the summer of 2009 than the winters of 2009/2010 and 2010/2011, resulting in potential inaccurate estimates from ILI (1). There may also be underreporting of or delays in reporting ILI in the community, for example in the UK those with mild illness are less likely to see a GP (2), and visits generally occur two or more days after onset of symptoms (3). Work absences, if the reason is known, could fill these gaps in detection.

Methods

Weekly counts and rates of hospital staff ILA (attributed to colds or influenza) were compared to GP ILI consultation rates (Royal College of General Practitioners Weekly Returns Service)(4) for 15-64 year olds, and positive influenza A test results (PITR) for all inpatients hospitalised in the three London hospitals for which staff data were collected using both retrospective time series and prospective outbreak detection methods implemented in the surveillance package in R (5)

Results

Rates of ILA were about six times higher than rates of ILI. Data on hospital staff ILA demonstrated seasonal trends as defined by ILI. Compared to the ILI rates, ILA demonstrated a more realistic estimate of the relative burden of pandemic H1N1 during July 2009 (1) (Figure). ILA provides potentially earlier warnings than GP ILI as indicated by its ability to predict ILI data for the local region ($p < 0.001$), as well as its potential for daily 'real time' updates. Using outbreak detection methods and examining peak weeks, alarms and thresholds, ILA alarmed, reached threshold rates and peaked consistently earlier or in the same week as ILI and PITR, with the exception of the July 2009, suggesting that it may be predictive of both community and patient cases of influenza (Table).

Conclusions

This study has demonstrated the potential to further explore the usefulness of using ILA data to complement existing national influenza surveillance systems. This work could improve our accuracy in monitoring of influenza and has the potential to improve emergency response to influenza for individual hospitals.

Table: Week of the year that alarms commenced and peaks were reached for each of the four official influenza events from March 2008 to April 2011.

	Winter 2008/2009			Winter 2009/2010			Winter 2010/2011			Summer 2009		
	Commence	Threshold	Peak	Commence	Threshold	Peak	Commence	Threshold	Peak	Commence	Threshold	Peak
ILA	33	37	51	38	36	44	47	47	51	27	24	29
ILI	36	49	51	39	40	49	49	49	51	26	26	29
PITR	49	NA	51	39	NA	44	47	NA	52	25	NA	31

ILA = influenza like absences among hospital staff; ILI = influenza like illness from RCGP data in London, ages 15-64; PITR = positive influenza A test results among patients from the same hospital as staff contributing ILA data; Threshold for ILI data was set at 30/100,000 as defined by the Health Protection Agency. The ILA threshold set at 60/100,000, such that all ILI above a threshold of 30/100000 were also above a threshold for ILA.

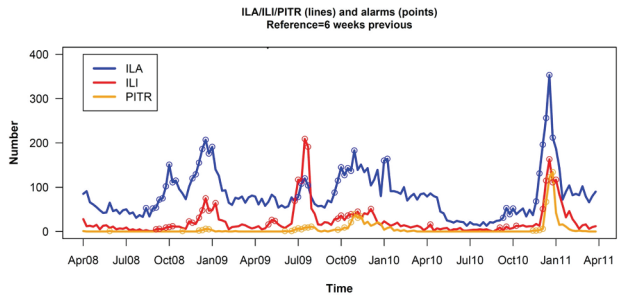


Figure: Weekly counts of ILA among hospital staff (blue), PITR among hospital patients (orange), and ILI in the community (red) from April 2008 to March 2011 and prospective alarms for elevated counts (circles) using a Bayesian subsystem algorithm, using the previous six weeks as the reference for prediction. Data plotted by counts rather than rates for clarity.

Keywords

influenza; syndromic surveillance; hospital staff; emergency preparedness

References

1) Birrell PJ, et al. Bayesian modeling to unmask and predict influenza A/H1N1pdm dynamics in London. Proceedings of the National Academy of Sciences 2011;108(45):18238-18243.
2) Evans B, et al. Has estimation of numbers of cases of pandemic influenza H1N1 in England in 2009 provided a useful measure of the occurrence of disease? Influenza and other respiratory viruses 2011.
3) Ross AM, et al. Presentation with influenza-like illness in general practice: implications for use of neuraminidase inhibitors. Communicable Disease and Public Health 2000;3:256-260.
4) Fleming DM. Weekly Returns Service of the Royal College of General Practitioners. Communicable Disease and Public Health 1999;2(2):96-100.
5) Hoehle M. An R package for the monitoring of infectious diseases. Computational Statistics 2007;22(4):571-582.

*Lydia Drumright
E-mail: l.drumright@imperial.ac.uk

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Multiple Source Spatial Cluster Detection Through Multi-criteria Analysis

Luiz H. Duczmal*[1], Alexandre C. L. Almeida[2], Fabio R. da Silva[1] and Martin Kulldorff[3]

[1]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil; [2]Universidade Federal de São João del-Rei, Ouro Branco, Brazil; [3]Harvard Medical School, Boston, MA, USA

Objective

To incorporate information from multiple data streams of disease surveillance to achieve more coherent spatial cluster detection using statistical tools from multi-criteria analysis.

Introduction

Multiple data sources are essential to provide reliable information regarding the emergence of potential health threats, compared to single source methods [1,2]. Spatial Scan Statistics have been adapted to analyze multivariate data sources [1]. In this context, only ad hoc procedures have been devised to address the problem of selecting the most likely cluster and computing its significance. A multi-objective scan was proposed to detect clusters for a single data source [3].

Methods

For simplicity, consider only two data streams. The j-th objective function evaluates the strength of candidate clusters using only information from the j-th data stream. The best cluster solutions are found by maximizing two objective functions simultaneously, based on the concept of dominance: a point is called dominated if it is worse than another point in at least one objective, while not being better than that point in any other objective [4]. The nondominated set consists of all solutions which are not dominated by any other solution. To evaluate the statistical significance of solutions, a statistical approach based on the concept of attainment function is used [4].

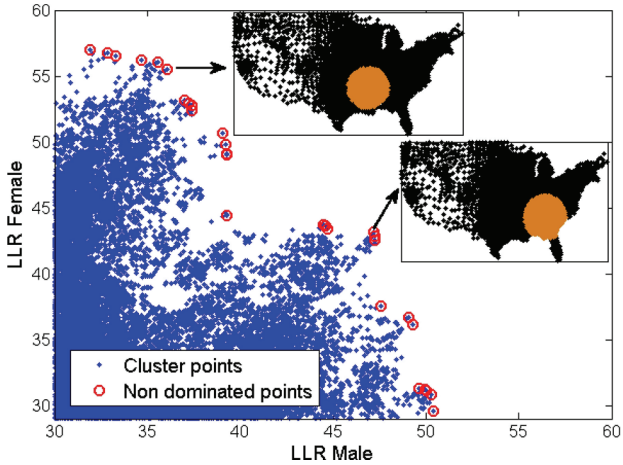
Results

The two datasets are standardized brain cancer mortality rates for male and female adults for each of the 3111 counties in the 48 contiguous states of the US, from 1986 to 1995 [5].

We run the circular scan and plot the (m(Zi),w(Zi)) points in the Cartesian plane, where m(Zi) and w(Zi) are the LLR for the zone Zi in the men's and women's brain cancer map, respectively, and i, i=1,...,N(r) is the set of all circular zones up to a radius r>0. The non-dominated set is inspected to observe possible correlations between the two maps regarding brain cancer clustering (Figure 1); e.g., the upper inset map has high LLR value on women's map, but not on men's; the inverse happens to the lower inset map. Other nondominated clusters in the middle have lower LLR values on both datasets. The first two examples have comparatively lower p-value (they belong to the two "knees" in the nondominated set), as computed using the attainment surfaces (not shown in the figure).

Conclusions

The multi-criteria multivariate approach has several advantages: (i) the representation of the evaluation function for each datastream is very clear, and does not suffer from an artificial, and possibly confusing mixture with the other datastream evaluations; (jj) it is possible to attribute, in a rigorous way, the statistical significance of each candidate cluster; (iii) it is possible to analyze and pick-up the best cluster solutions, as given naturally by the non-dominated set.



Part of the solution set in the LLR(male) X LLR(female) space of the male/female brain cancer datasets for the US counties map. Clusters are indicated by blue points, with the non-dominated solutions represented by small red circles. The inset maps depict the geographic location of the clusters found in the US counties map (yellow circles) for two sample non-dominated solutions.

Keywords

spatial scan statistic; Multi-criteria; attainment surface; Multiple data stream

Acknowledgments

The authors acknowledge the grants from CNPq and Capes.

References

[1] Kulldorff M, Mostashari F, Duczmal L, Yih K, Kleinman K, Platt R.(2007) Multivariate Scan Statistics for Disease Surveillance. Stat Med,26,1824-1833.

[2] Jonsson et al. Analysis of simultaneous space-time clusters of Campylobacter spp. in humans and in broiler flocks using a multiple dataset approach (2010). IJ Health Geogr,9:48

[3] Duczmal L, Cançado ALF, Takahashi RHC (2008) Geographic Delineation of Disease Clusters through multi-objective Optimization. J Comp Graph Stat,17:243-262.

[4] Cançado ALF, Duarte AR, Duczmal L, Ferreira SJ, Fonseca CM, Gontijo ECDM (2010). Penalized likelihood and multiobjective spatial scans for the detection and inference of irregular clusters. IJ Health Geogr,9:55.

[5] Fang Z, Kulldorff M, Gregorio DI (2004). Brain cancer mortality in the United States, 1986 to 1995: A geographic analysis. Neuro-Oncology 03-045, May 6.

*Luiz H. Duczmal
E-mail: duczmal@ufmg.br

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Influenza Forecasting with Google Flu Trends

Andrea F. Dugas*[1], Mehdi Jalalpour[1], Yulia Gel[1, 2], Scott Levin[1], Fred Torcaso[1], Takeru Igusa[1] and Richard Rothman[1]

[1]Johns Hopkins University, Baltimore, MD, USA; [2]University of Waterloo, Waterloo, ON, Canada

Objective

We sought to develop a practical influenza forecast model, based on real-time, geographically focused, and easy to access data, to provide individual medical centers with advanced warning of the number of influenza cases, thus allowing sufficient time to implement an intervention. Secondly, we evaluated how the addition of a real-time influenza surveillance system, Google Flu Trends, would impact the forecasting capabilities of this model.

Introduction

Each year, influenza results in increased Emergency Department crowding which can be mitigated through early detection linked to an appropriate response. Although current surveillance systems, such as Google Flu Trends, yield near real-time influenza surveillance, few demonstrate ability to forecast impending influenza cases.

Methods

Forecasting models designed to predict one week in advance were developed from weekly counts of confirmed influenza cases over seven seasons (2004 – 2011) divided into training and out-of-sample verification sets. Forecasting procedures using classical Box-Jenkins, generalized linear, and autoregressive methods were employed to develop the final model and assess the relative contribution of external variables such as, Google Flu Trends, meteorological data, and temporal information. Models were developed and evaluated through statistical measures of global deviance and log-likelihood ratio tests. An additional measure of forecast confidence, defined as the percentage of forecast values, during an influenza peak, that are within 7 influenza cases of the actual data, was examined to demonstrate practical utility of the model.

Results

A generalized autoregressive Poisson (GARMA) forecast model integrating previous influenza cases with Google Flu Trends information provided the most accurate influenza case predictions. Google Flu Trend data was the only source of external information providing significant forecast improvements ($p = 0.00002$). The final model, a GARMA intercept model with the addition of Google Flu Trends, predicted weekly influenza cases during 4 out-of-sample outbreaks within 7 cases for 80% of estimates (Figure 1).

Conclusions

Integer-valued autoregression of influenza cases provides a strong base forecast model, which is enhanced by the addition of Google Flu Trends confirming the predictive capabilities of search query based syndromic surveillance. This accessible and flexible forecast model can be used by individual medical centers to provide advanced warning of future influenza cases.

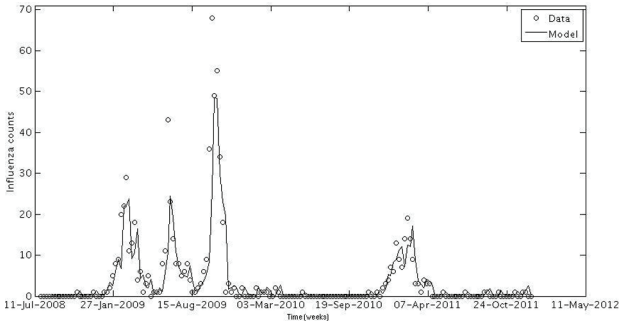


Figure 1: Number of weekly confirmed influenza cases during the verification period (2008-2011) comparing actual data (circles) and values forecasted by the final model [3rd order Generalized Autoregressive Poisson intercept model with Google Flu Trends] (solid line).

Keywords

Google Flu Trends; Crowding; Surveillance; Influenza; Forecasting

Acknowledgments

This work was supported by the Department of Homeland Security (PACER: National Center for Study of Preparedness and Response [grant number: 2010-ST-061-PA0001]); the National Science Foundation Systems Engineering and Design Program [grant number: NSF CMMI 0927207]; and the Natural Sciences and Engineering Research Council of Canada.

*Andrea F. Dugas
E-mail: adugas1@jhmi.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Synergies Between Human and Animal Health Syndromic Surveillance: Triple-S Outputs

Céline Dupuy*[1], Jean-Baptiste Perrin[1], Anne Bronner[1], Didier Calavas[1], Pascal Hendrikx[2] and Anne Fouillet[3]

[1]French Agency for food, environmental and occupational health safety (Anses), Lyon, France; [2]French Agency for food, environmental and occupational health safety (Anses), Maisons-Alfort, France; [3]French institute for public health surveillance (InVS), Saint-Maurice, France

Objective

The objective of this study, based on the Triple-S project outputs, was to present the existing synergies between human and animal health syndromic surveillance (SyS) systems in Europe and a proposal to enhance this kind of collaboration.

Introduction

The Triple-S project (Syndromic Surveillance Systems in Europe, www.syndromicsurveillance.eu), co-financed by the European Commission and involving twenty four organizations from fourteen countries was launched in September 2010 with the following objectives 1) performing an inventory of existing or planned SyS systems in Europe both in animal and public health, 2) building a network of experts involved in SyS 3) producing guidelines to implement SyS systems, 4) developing synergies between human and animal health SyS systems. The project is based on a cooperation between human and animal health experts, as supported by the One Health initiative [1].

Methods

A network of European experts involved in SyS was identified through the Triple-S inventory of SyS systems. A meeting of human health experts was organized back to back with a similar meeting with animal health experts in Paris, September 12-14, 2011. A joint session human/animal health allowed experts to discuss the interest of synergies between both sides. The objectives were to 1) encourage experience and knowledge transfer, 2) discuss what and how information should be shared between both sides to improve respective performances.

Results

The results of the inventory of veterinary SyS systems showed that 40% of identified systems already shared or had planned to share information with human health sector. For these systems the collaboration between human and animal health sectors consisted in meetings on a regular basis to discuss the surveillance results.

Discussions during the Triple-S meeting highlighted two reasons for enhancing synergies between both sides. First human health and animal health epidemiologists face common statistical and epidemiological issues when dealing with SyS, i.e. use of data collected for other purpose than surveillance; standardization of clinical observations; syndrome definition; anomaly detection; interpretation of unspecific signals; response to alerts. Both sides have thus interest in sharing their experiences and knowledge to improve their respective systems.

Second, systems on both sides have similar objectives and target health events potentially threatening both animal and human populations: zoonoses, extreme weather events, environmental / food contamination, bioterrorist attack... For those events, animal population can play the role of sentinel for human population. Regular information flow between human and animal SyS could thus enhance the timeliness and sensitivity of SyS systems for detecting unexpected health events. Moreover, sharing information could help animal and human health experts to interpret and confirm unspecific signals, and confirm the impact of common health threats.

All participants of the meeting agreed on the idea to routinely share outputs of the systems but were sceptical about sharing raw data to perform global analysis.

Conclusions

Each aspect of the Triple-S project includes both human and animal health and will thus contribute to build natural collaboration between both sides. Such a project has demonstrated that scientific community is more and more willing to collaborate beyond the boundaries of these two health fields.

Synergies between human and animal health seem as necessary for syndromic surveillance as it is for traditional surveillance, if not more. They seem especially important for the detection of emerging zoonotic threats but not only. Sharing surveillance outputs from both sides would be the first step of collaboration but deeper synergy, e.g. sharing data and analyse them globally, could also be considered. Triple-S guidelines for implementation of SyS systems in Europe will take into account and promote synergies between human and animal health.

Keywords

syndromic surveillance; synergy; early warning

Acknowledgments

The authors thank all participants to the Triple-S project activities.

References

1.Zinsstag, J., et al., Potential of cooperation between human and animal health to strengthen health systems. The Lancet, 2005. 366(9503): p. 2142-2145.

*Céline Dupuy
E-mail: celine.dupuy@anses.fr

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

International Collaboration for Improved Public Health Emergency Preparedness and Response in India

Obaghe Edeghere*[1], Giri Shankar[1], Alastair Bartholomew[1], SriKrishna Ramachandra[2], Vivek Singh[2], Pradeep Banandur[3], Linda Parr[1], Kenny Yap[1], Babatunde Olowokure[1] and Sue Ibbotson[1]

[1]The Health Protection Agency, Birmingham, United Kingdom; [2]Indian Institute of Public Health, Hyderabad, India; [3]Rajarajeswari Medical College and Hospital, Bangalore, India

Objective

This project aimed to contribute to ongoing efforts to improve the capability and capacity to undertake disease surveillance and Emergency Preparedness and Response (EPR) activities in India. The main outcome measure was to empower a cadre of trainers through the inter-related streams of training & education to enhance knowledge and skills and the development of collaborative networks in the regions.

Introduction

The International Health Regulations (IHR) 2005, provides a framework that supports efforts to improve global health security and requires that, member states develop and strengthen systems and capacity for disease surveillance and detection and response to public health threats. To contribute to this global agenda, an international collaborative comprising of personnel from the Health Protection Agency, West Midlands, United Kingdom (HPA); the Indian Institute of Public Health (IIPH), Hyderabad, Andhra Pradesh (AP) state, India and the Department of Community Medicine, Rajarajeswari Medical College and Hospital (RRMCH), Bangalore, Karnataka state, India was established with funding from the HPA Global Health Fund to deliver the objectives stated above.

Methods

In 2010, the project partners jointly developed training materials on applied Epidemiology & Disease Surveillance and EPR using existing HPA material as the foundation. Over a 2 year period, a total of two training courses per year were planned for each of the two locations in India. Courses were designed to be delivered through didactic lectures, simulation exercises, workshops and group discussions at the two locations, namely Bangalore and Hyderabad. The target audience included senior state level programme officers, District Medical and Health Officers, postgraduate students, academic and research staff from Community Medicine departments and staff from the collaborating institutions.

Course modules were formally evaluated by participants using structured questionnaires and an external evaluator. Debrief sessions were also arranged after each course to review the key lessons and identify areas for improvement.

In addition, staff exchanges of up to six weeks duration were planned during which public health specialists from both countries would spend time observing health protection systems/processes in their host country.

Results

During January 2010 to December 2011, a total of seven (n=7) training courses were delivered in Bangalore and Hyderabad with approximately 231 public health personnel in attendance over the period. Participants comprised of 128 personnel representing 74 organisations in 41 districts (22 districts from AP) at the Hyderabad location and 103 personnel from 14 organisations (30 districts) at the Bangalore location.

Course participants evaluated the content of the courses favourably with the majority (92%) rating the course modules as excellent or good. External evaluation of the courses was also favourable with several aspects of the course rated as good or excellent. IIPH and RRMC continue to deliver the courses and in the state of Karnataka, some participants at the EPR course were chosen by the health ministry to be part of Rapid Response Teams at District levels.

Two public health specialists from each of the Indian organisations spent six (6) weeks in the United Kingdom as part of the planned staff exchanges. The exchanges were assessed to have been successful with important areas for future collaboration identified including proposals to jointly develop an Emergency Preparedness and Response Manual for the Indian Public Health audience.

Conclusions

The implementation and maintenance of effective and sustainable systems to ensure global health security relies on a well-trained public health workforce in member states. This innovative collaborative project has gone some way towards meeting its objective of establishing and supporting a cadre of trainers to ensure sustainable improvement in public health capacity and capability in India. After the initial (training) phase of the project that was completely funded by the HPA, the partner organisations in India have worked to sustain and further develop the core objectives of this project. As a further step, course materials developed as part of this project will be used to provide a framework upon which e-learning material and postgraduate modules will be developed in each of these institutions in India.

Keywords

Surveillance; Training; EPR; IHR

Acknowledgments

Leanne Baker – HPA, UK
Krishna Gayathri - IIPH, Hyderabad

*Obaghe Edeghere
E-mail: obaghe.edeghere@hpa.org.uk

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluation of Clinical and Administrative Data to Augment Public Health Surveillance

Joseph R. Egger*[1], Brooks Lowe[1], Erica Johnson[1], Randy Durbin[2], Erica Griffin[2], Sanjaya Dhakal[3], Achintya Dey[3] and Sam Groseclose[3]

[1]SciMetrika, LLC, Research Triangle Park, NC, USA; [2]The Altarum Institute, Atlanta, GA, USA; [3]Centers for Disease Control and Prevention, Atlanta, GA, USA

Objective

To assess the utility of inpatient and ambulatory clinical data compiled by public and commercial sources to enhance the Centers for Disease Control and Prevention's surveillance activities.

Introduction

Medical claims and EHR data sources offer the potential to ascertain disease and health risk behavior prevalence and incidence, evaluate the use of clinical services, and monitor changes related to public health interventions. Passage of the HITECH Act of 2009 supports the availability of standardized EHR data for use by public health officials to obtain actionable information. While full adoption of EHRs is still years away, there are presently publicly- and commercially-available EHR and medical claims data sets that could enhance public health surveillance at a national, regional and state level. The purposes of this evaluation were to i.) demonstrate the feasibility of gaining access to such data, ii.) evaluate their ability to augment current surveillance activities by developing measures for twenty separate healthcare indicators (e.g., HIV screening), iii.) evaluate each data source across a set of criteria needed for an effective surveillance system, and iv.) assess the ability of the data sources to evaluate changes in healthcare utilization and preventive services that may be a result of the 2009 Health Reform legislation.

Methods

Ten separate data sources were selected for inclusion in the study based on a number of criteria, including availability, representativeness, population, data structure and content, cost, and longitudinality. In collaboration with staff from seven Divisions across the CDC, detailed specifications were developed for twenty separate indicators of healthcare utilization or preventive services using best practices in healthcare quality measurement. Specifications were developed separately for EHR and medical claims data due to their differing structure, content and use of medical code sets and terminologies. Specifications for EHR data sources relied on the National Quality Forum (NQF) Meaningful Use (MUse) clinical quality measure specifications. The use of NQF MUse specification guidelines allowed us to gauge the current ability of each data source to measure healthcare utilization and preventive services as recommended by NQF, the national leader in healthcare measurement. Each of the data sources was also evaluated across established public health surveillance criteria, including data quality, representativeness, and flexibility, among others. Data analysis was performed using SAS 9.3 (SAS Institute, Cary, NC).

Results

All twenty of the healthcare indicators were developed for at least one data source; however, many of the indicator specifications had to be modified due to the low frequency of certain code sets (e.g., CPT-4 II, LOINC). The observed strengths of medical claims data were the relatively low cost, ability to track patients longitudinally, and the standardized representation of procedures and diagnoses through use of medical codes, such as ICD-9-CM, CPT-4 and HCPCS. The observed strengths of EHR data sources were the availability of information related to health behavior (e.g., current smoker), health assessment (e.g., BMI), prognostic indicators (e.g., vital signs, laboratory result), diagnostic testing, and functional status. While EHR data also capture diagnoses using ICD-9-CM, procedures such as medical and laboratory procedures remain documented through use of free text or semi-structured text fields, making it difficult to process.

Conclusions

Currently available healthcare data can improve the timeliness of health outcome monitoring and add complementary information on healthcare utilization to improve our interpretation of traditional public health surveillance data. Medical claims data support measurement of health outcomes and healthcare services provided to patient populations; however, without clinical encounter information, they cannot develop measures estimating the impact of services received on quality of care. EHR data have richer clinical information; however, the continued use of non-standards-based medical codes and free and semi-structured text fields make it difficult to analyze data at scale. Meaningful Use and other HITECH initiatives are changing this by incentivizing the standardization and aggregation of electronic healthcare data. In time, these data may yield timely, accurate and actionable information for public health surveillance.

Keywords

Surveillance; Evaluation; Healthcare; Electronic Health Record

*Joseph R. Egger
E-mail: joseph.egger@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Utility of System Generated Syndromic Surveillance Alerts to Detect Reportable Disease Outbreaks

Carrie Eggers*, Aaron Kite-Powell and Janet Hamilton

Bureau of Epidemiology, Florida Department of Health, Tallahassee, FL, USA

Objective

In light of recent outbreaks of pertussis, the ability of Florida Department of Health's (FDOH) Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE-FL) to detect emergent disease outbreaks was examined. Through a partnership with the Johns Hopkins University Applied Physics Laboratory (JHU/APL), FDOH developed a syndromic surveillance system, ESSENCE-FL, with the capacity to monitor reportable disease case data from Merlin, the FDOH Bureau of Epidemiology's secure web-based reporting and epidemiologic analysis system for reportable diseases. The purpose of this evaluation is to determine the utility and application of ESSENCE-FL system generated disease warnings and alerts originally designed for use with emergency department chief complaint data to reportable disease data to assist in timely detection of outbreaks in promotion of appropriate response and control measures.

Introduction

Reportable disease case data are entered into Merlin by all 67 county health departments in Florida and assigned confirmed, probable, or suspect case status. De-identified reportable disease data from Merlin are sent to ESSENCE-FL once an hour for further analysis and visualization using tools in the surveillance system. These data are available for ad hoc queries, allowing users to monitor disease trends, observe unusual changes in disease activity, and to provide timely situational awareness of emerging events. Based on system algorithms, reportable disease case weekly tallies are assigned an awareness status of increasing intensity from normal to an alert category. These statuses are constantly scrutinized by county and state level epidemiologists to guide disease control efforts in a timely manner, but may not signify definitive actionable information.

Methods

Within the ESSENCE-FL query portal, the Merlin Reportable Diseases Data Source was selected with a weekly time resolution by event date. Case Classification included all confirmed, probable and suspect cases, reported and not yet reported, during the time period of week 35, 2011, to week 35, 2012. The ESSENCE Weighted Moving Average (EWMA 1.2) detector was used to classify weekly counts as either of normal, warning or alert status based on previous weeks' counts, indicating the possibility of an emerging outbreak. These weekly statuses were then compared with outbreaks reported in Merlin's fully integrated outbreak reporting system and with outbreak reports submitted to EpiCom, Florida's EpiX or health alert network. An ESSENCE-FL generated warning or alert was considered valid if a corresponding outbreak of 2 or more epi-linked pertussis cases were reported in either Merlin's outbreak module or in EpiCom. For the sake of brevity in this abstract, the analysis of pertussis is presented, while other reportable disease conditions of immediate interest will be presented at the conference.

Results

Examination of 494 pertussis cases reported from September 2011 to September 2012 showed that of 53 weeks, 38 weeks contained normal case counts, 11 weeks generated warnings, and 4 weeks produced alerts. The number of warnings that corresponded to actual outbreaks was 6 of 11, whereas 2 of the 4 alerts matched reported outbreaks. Of the remaining 38 weeks, 12 had outbreaks reported with no warning or alert generated by ESSENCE-FL. When comparing confirmed outbreak status with ESSENCE-FL weekly data count status, warning/alert versus normal, it was found that the sensitivity of ESSENCE-FL to detect a true outbreak was 40.0% while the specificity was 78.8%. This comparison generated a positive-predictive value of 53.3% and a negative predictive value of 68.4%.

Conclusions

The ability of ESSENCE-FL to act as a first alert system for emerging disease events using Merlin reportable disease data should be considered with constraint. While warnings or alerts about potential pertussis outbreaks were generated correctly about half the time, the nearly one-third of reported outbreaks with no warning or alert makes the utility of the alerts questionable as far as initiating immediate action without prior verification of the alert. Florida does not currently have a requirement for centrally documenting all outbreaks, so it is likely that outbreaks occurred but were not recorded, precluding verification of all outbreaks.

Keywords

Syndromic; Surveillance; Outbreaks

Acknowledgments

Applied Public Health Informatics Fellowship CDC in collaboration with CSTE, ASTHO and PHII.

*Carrie Eggers
E-mail: Carrie_Eggers@doh.state.fl.us

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Operational Experience: Integration of ASPR Data into ESSENCE-FL during the RNC

Carrie Eggers*[1], Dina Passman[2], Aaron Chern[1], Dara Spector[2], Aaron Kite-Powell[1], Tim Davis[2], Wayne Loschen[3], Joe Lombardo[3], Douglas Char[2] and Janet Hamilton[1]

[1]Florida Department of Health, Bureau of Epidemiology, Tallahassee, FL, USA; [2]Health and Human Services, Office of the Assistant Secretary for Preparedness and Response, Washington, D.C., DC, USA; [3]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Objective

The Florida Department of Health (FDOH), Bureau of Epidemiology, partnered with the U.S. Department of Health and Human Services (HHS) Office of the Assistant Secretary for Preparedness and Response (ASPR) to improve surveillance methods in post disaster or response events. A new process was implemented for conducting surveillance to monitor injury and illness for those presenting for care to ASPR assets such as Disaster Medical Assistance Team (DMAT) sites when they are operational in the state. The purpose of the current work was to field test and document the operational experience of the newly implemented ASPR data module in ESSENCE-FL (syndromic surveillance system) to receive near real-time automated data feeds when ASPR federal assets were deployed in Florida during the 2012 Republican National Convention (RNC).

Introduction

Florida has implemented various surveillance methods to augment existing sources of surveillance data and enhance decision making with timely evidence based assessments to guide response efforts post-hurricanes. Historically, data collected from deployed federal assets have been an integral part of this effort. However, a number of factors have made this type of surveillance challenging: logistical issues of field work in a post-disaster environment, the resource intensive manual data collection process from DMAT sites, and delayed analysis and interpretation of these data to inform decision makers. The ESSENCE-FL system is an automated and secure web-based application accessed by FDOH epidemiologists and staff at participating hospitals.

Methods

ESSENCE-FL was configured by the Johns Hopkins University Applied Physics Laboratory (JHU/APL) to receive ASPR electronic medical record (EMR) data. A scheduled program to generate data files for FDOH was created using SAS Enterprise Business Intelligence (EBI) software and a script was set up on the ASPR server to send an updated file via secure file transfer protocol (sftp) every 15 minutes. A case definition was created by ASPR field teams to identify which encounter visits would be entered into the electronic medical record (EMR) and received in ESSENCE-FL. To assess completeness of data elements and total patient encounters received in ESSENCE-FL, DMAT field teams maintained Excel line lists of patient encounters and emailed them to FDOH three times daily during the RNC. ASPR data were reviewed and analyzed by FDOH staff multiple times a day in near real time utilizing the existing ESSENCE-FL robust analysis tools.

Results

Three separate ASPR missions were deployed to Florida to support the RNC. ASPR EMR data files were received at 15-minute intervals by ESSENCE-FL from the ASPR central server during each day of the 2012 RNC (August 26-31). Reduced patient counts within ESSENCE-FL as compared with DMAT-maintained Excel line lists indicated an incomplete input, upload, or transfer of patient data from one of two ASPR sites to the central ASPR servers. Although only 11 of 34 total patient encounters were received by ESSENCE-FL during the event, the system design enabled users to run specific queries and display the results of their queries in time series graphs, pie and bar charts, GIS maps, dashboards, and statistical tables.

Conclusions

There is a great need to have timely access to data sources to enhance disease surveillance efforts and help guide decision makers' situational awareness and disease control efforts during a response. The FDOH, Bureau of Epidemiology's collaboration with JHU/APL and ASPR takes advantage of ASPR's EMR-S to make data sharing and analysis efficient as evidenced during the RNC. Automated data feeds to ESSENCE-FL removed resource intensive manual data collection by public health, improved standardization of syndrome and demographic categorizations, increased access to these data by local, state, and federal epidemiologists in a timely manner, and expedited analysis and interpretation for situational awareness. Future recommendations include pre-event testing of the entire data flow process, establishing an on-site specialist to immediately assist with any issues, greater understanding of the field team use of the EMR-S, and ensuring field staff is aware of data quality needs for effective public health surveillance.

Keywords

surveillance; response; disaster

*Carrie Eggers
E-mail: Carrie_Eggers@doh.state.fl.us

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Category-Specific Comparison of Univariate Alerting Methods for Biosurveillance Decision Support

Yevgeniy Elbert*, Vivian Hung and Howard Burkom

JHUAPL, Laurel, MD, USA

Objective

For a multi-source decision support application, we sought to match univariate alerting algorithms to surveillance data types to optimize detection performance.

Introduction

Temporal alerting algorithms commonly used in syndromic surveillance systems are often adjusted for data features such as cyclic behavior but are subject to overfitting or misspecification errors when applied indiscriminately.

In a project for the Armed Forces Health Surveillance Center to enable multivariate decision support, we obtained 4.5 years of outpatient, prescription and laboratory test records from all US military treatment facilities. A proof-of-concept project phase produced 16 events with multiple evidence corroboration for comparison of alerting algorithms for detection performance.

We used the representative streams from each data source to compare sensitivity of 6 algorithms to injected spikes, and we used all data streams from 16 known events to compare them for detection timeliness.

Methods

The six methods compared were:

1) Holt-Winters generalized exponential smoothing method (1)
2) automated choice between daily methods, regression and an exponential weighted moving average (2)
3) adaptive daily Shewhart-type chart
4) adaptive one-sided daily CUSUM
5) EWMA applied to 7-day means with a trend correction; and
6) 7-day temporal scan statistic

Sensitivity testing: We conducted comparative sensitivity testing for categories of time series with similar scales and seasonal behavior. We added multiples of the standard deviation of each time series as single-day injects in separate algorithm runs. For each candidate method, we then used as a sensitivity measure the proportion of these runs for which the output of each algorithm was below alerting thresholds estimated empirically for each algorithm using simulated data streams. We identified the algorithm(s) whose sensitivity was most consistently high for each data category.

For each syndromic query applied to each data source (outpatient, lab test orders, and prescriptions), 502 authentic time series were derived, one for each reporting treatment facility. Data categories were selected in order to group time series with similar expected algorithm performance:

1) Median > 10
2) 0 < Median ≤ 10
3) Median = 0
4) Lag 7 Autocorrelation Coefficient ≥ 0.2
5) Lag 7 Autocorrelation Coefficient < 0.2

Timeliness testing: For the timeliness testing, we avoided artificiality of simulated signals by measuring alerting detection delays in the 16 corroborated outbreaks. The multiple time series from these events gave a total of 141 time series with outbreak intervals for timeliness testing.

The following measures were computed to quantify timeliness of detection:

1. Median Detection Delay – median number of days to detect the outbreak.
2. Penalized Mean Detection Delay –mean number of days to detect the outbreak with outbreak misses penalized as 1 day plus the maximum detection time.

Results

Based on the injection results, the Holt-Winters algorithm was most sensitive among time series with positive medians. The adaptive CUSUM and the Shewhart methods were most sensitive for data streams with median zero. Table 1 provides timeliness results using the 141 outbreak-associated streams on sparse (Median=0) and non-sparse data categories.

[Insert table #1 here]

The gray shading in the table 1 indicates methods with shortest detection delays for sparse and non-sparse data streams. The Holt-Winters method was again superior for non-sparse data. For data with median=0, the adaptive CUSUM was superior for a daily false alarm probability of 0.01, but the Shewhart method was timelier for more liberal thresholds.

Conclusions

Both kinds of detection performance analysis showed the method based on Holt-Winters exponential smoothing superior on non-sparse time series with day-of-week effects. The adaptive CUSUM and Shewhart methods proved optimal on sparse data and data without weekly patterns.

Data median	Detection Delay, days	Holt-Winters	Regression EWMA	Adaptive Shewhart	Adaptive CUSUM	7-day Trend-adj. EWMA	7-day Temporal Scan
Median 0	Median	3	2	4	2	4.5	2
	Penalized Mean	7.2	7	6.6	6.2	7.3	7.6
Median > 0	Median	2	2	2.5	2	6	4
	Penalized Mean	6.1	7	7.2	7.1	7.7	6.8

Keywords

biosurveillance; timeliness; detection; alerting methods; sensitivity

References

1. Elbert Y, Burkom H, Shmueli G, Development and evaluation of a data-adaptive alerting algorithm for univariate temporal biosurveillance data Stat. Med. 2009; 28:3226-3248
2. Burkom H, Elbert Y, Thompson M, et al, Development, adaptation, and assessment of alerting algorithms for biosurveillance JHUAPL Technical Digest, Volume 24, Number 4 (2003)

*Yevgeniy Elbert
E-mail: yevgeniy.elbert@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Statistical Models for Biosurveillance of Multiple Organisms

Doyo G. Enki*[1], Angela Noufaily[1], C. P. Farrington[1], Paul H. Garthwaite[1], Nick Andrews[2], André Charlett[2] and Chris Lane[2]

[1]Mathematics and Statistics, The Open University, Milton Keynes, United Kingdom; [2]Health Protection Agency, London, United Kingdom

Objective

To look at the diversity of the patterns displayed by a range of organisms, and to seek a simple family of models that adequately describes all organisms, rather than a well-fitting model for any particular organism.

Introduction

There has been much research on statistical methods of prospective outbreak detection that are aimed at identifying unusual clusters of one syndrome or disease, and some work on multivariate surveillance methods (1). In England and Wales, automated laboratory surveillance of infectious diseases has been undertaken since the early 1990's. The statistical methodology of this automated system is described in (2). However, there has been little research on outbreak detection methods that are suited to large, multiple surveillance systems involving thousands of different organisms.

Methods

We obtained twenty years' data on weekly counts of all infectious disease organisms reported to the UK's Health Protection Agency. We summarized the mean frequencies, trends and seasonality of each organism using log-linear models. To identify a simple family of models which adequately represents all organisms, the Poisson model, the quasi-Poisson model and the negative binomial model were investigated (3,4). Formal goodness-of-fit tests were not used as they can be unreliable with sparse data. Adequacy of the models was empirically studied using the relationships between the mean, variance and skewness. For this purpose, each data series was first subdivided into 41 half-years and de-seasonalized.

Results

Trends and seasonality were summarized by plotting the distribution of estimated linear trend parameters for 2250 organisms, and modal seasonal period for 2254 organisms, including those organisms for which the seasonal effect is statistically significant.

Relationships between mean and variance were summarized as given in Figure 1.

Similar plots were used to summarize the relationships between mean and skewness.

Conclusions

Statistical outbreak detection models must be able to cope with seasonality and trends. The data analyses suggest that the great majority of organisms can adequately – though far from perfectly – be represented by a statistical model in which the variance is proportional to the mean, such as the quasi-Poisson or negative binomial models.

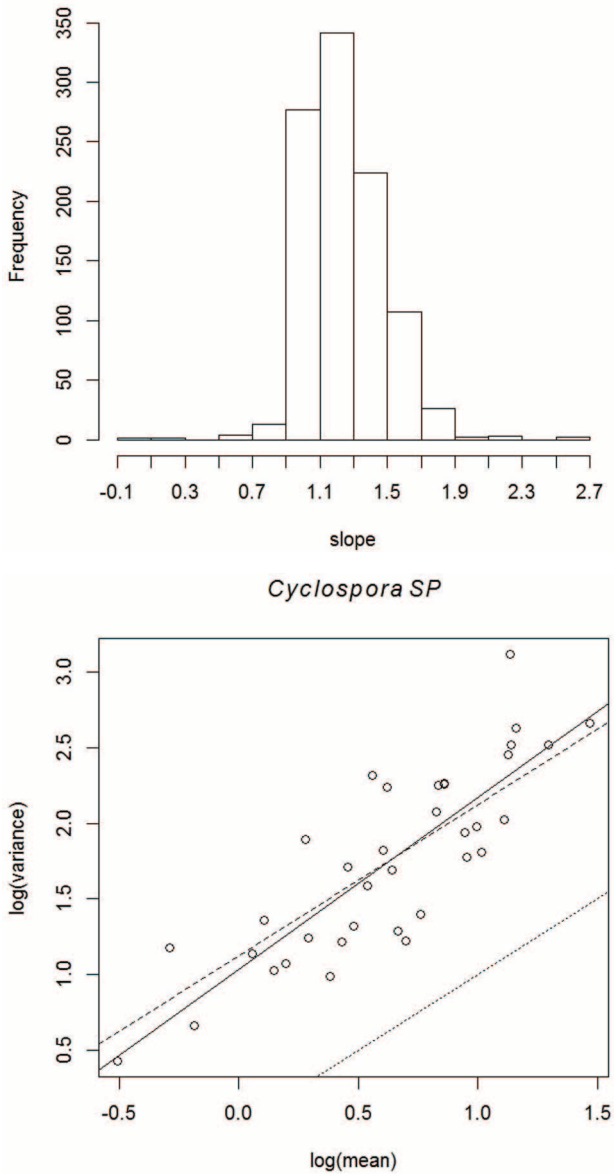


Figure 1. Relationships between mean and variance. (top) Histogram of the slopes of the best fit lines for 1001 organisms; the value 1 corresponds to the quasi-Poisson model; (bottom) log of variance plotted against log of mean for one organism. The full line is the best fit to the points; the dashed line corresponds to the quasi-Poisson model; the dotted line corresponds to the Poisson model.

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Keywords

Biosurveillance; Public Health Surveillance; Data Analysis; Infectious Disease Outbreaks; Statistical Model

Acknowledgments

This research was supported by a project grant from the UK Medical Research Council, and by a Royal Society Wolfson Research Merit Award.

References

1. Unkel S, Farrington CP, Garthwaite PH, Robertson C, Andrews N. Statistical methods for the prospective detection of infectious disease outbreaks: a review. J. R. Statist. Soc. A 2012; 175:49-82.
2. Farrington CP, Andrews NJ, Beale AD, Catchpole MA. A statistical algorithm for the early detection of outbreaks of infectious disease. J. R. Statist. Soc. A 1996; 159: 547-563.
3. McCullagh P, Nelder JA. Generalized Linear Models. 2nd ed. London: Chapman & Hall; 1989.
4. Hastie TJ, Tibshirani RJ. Generalized Additive Models. London: Chapman & Hall; 1990.

*Doyo G. Enki
E-mail: d.gragn@open.ac.uk

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Identification and Assessment of Public Health Surveillance Gaps under the IHR (2005)

Ngozi Erondu*[1], Betiel Hadgu Haile[1], Lisa Ferland[1], Meeyoung Park[1], Affan Shaikh[1], Heather Meeks[2] and Scott JN McNabb[1]

[1]Public Health Practice, Atlanta, GA, USA; [2]Defense Threat Reduction Agency, Washington, DC, USA

Objective

To conceive and develop a model to identify gaps in public health surveillance performance and provide a toolset to assess interventions, cost, and return on investment (ROI).

Introduction

Under the revised International Health Regulations (IHR [2005]) one of the eight core capacities is public health surveillance. In May 2012, despite a concerted effort by the global community, the World Health Organization (WHO) reported out that a significant number of member states would not achieve targeted capacity in the IHR (2005) surveillance core capacity.

Currently, there is no model to identify and measure these gaps in surveillance performance. Likewise, there is no toolset to assess interventions by cost and estimate the ROI.

We developed a new conceptual framework that: (1) described the work practices to achieve effective and efficient public health surveillance; (2) could identify impediments or gaps in performance; and (3) will assist program managers in decision making.

Methods

Published articles and grey-literature reports, manuals and logic model examples were gathered through a literature review of PubMed, Web of Science, Google Scholar, and other databases. Logic models were conceived by categorizing discrete surveillance inputs, activities, outputs, and outcomes. Indicators were selected from authoritative sources or developed and then mapped to the logic model elements. These indicators will be weighted using the principle component analysis (PCA), a method for enhanced precision of statistical analysis. Finally, on the front end of the tool, indicators will graphically measure the surveillance gap expressed through the tool's architecture and provide information using an integrated cost-impact analysis.

Results

We developed five public health surveillance logic models: for IHR (2005) compliance; event-based; indicator-based; syndromic; and predictive surveillance domains. The IHR (2005) domain focused on national-level functionality, and the others described the complexities of their specific surveillance work practices. Indicators were then mapped and linked to all logic model elements.

Conclusions

This new framework, intended for self-administration at the national and subnational levels, measured public health surveillance gaps in performance and provided cost and ROI information by intervention. The logic model framework and PCA methodology are tools that both describe work processes and define appropriate variables used for evaluation. However, both require real-world data. We recommend pilot testing and validation of this new framework. Once piloted, the framework could be adapted for the other IHR (2005) core capacities.

Keywords

Public health surveillance; Evaluation; IHR (2005); Gaps assessment; Cost-impact analysis

Acknowledgments

Defense Threat Reduction Agency and the World Health Organization

References

1. Implementation of the International Health Regulations., Stat. Resolution WHA65.23 (26 May 2012).
2. May L, Chretien JP, Pavlin JA. Beyond traditional surveillance: applying syndromic surveillance to developing settings—opportunities and challenges. BMC Public Health. 2009;9:242. Epub 2009/07/18.
3. Wilson K, McDougall C, Fidler DP, Lazar H. Strategies for implementing the new International Health Regulations in federal countries. Bulletin of the World Health Organization. 2008;86(3):215-20. Epub 2008/03/28.
4. Organization WH. International Health Regulations (2005) Second Edition. 2008.
5. Sturtevant JL, Anema A, Brownstein JS. The new International Health Regulations: considerations for global public health surveillance. Disaster Med Public Health Prep. 2007;1(2):117-21. Epub 2008/04/05.
6. Lyons S, Zidouh A, Ali Bejaoui M, Ben Abdallah M, Amine S, Garbouj M, et al. Implications of the International Health Regulations (2005) for communicable disease surveillance systems: Tunisia's experience. Public Health. 2007;121(9):690-5. Epub 2007/06/05.
7. Calain P. Exploring the international arena of global public health surveillance. Health Policy Plan. 2007;22(1):2-12. Epub 2007/01/24.
8. Baker MG, Forsyth AM. The new International Health Regulations: a revolutionary change in global health security. N Z Med J. 2007;120(1267):U2872. Epub 2007/12/25.
9. Cash RA, Narasimhan V. Impediments to global surveillance of infectious diseases: consequences of open reporting in a global economy. Bulletin of the World Health Organization. 2000;78(11): 1358-67. Epub 2001/01/06.
10. Fidler DP. Globalization, international law, and emerging infectious diseases. Emerg Infect Dis. 1996;2(2):77-84. Epub 1996/04/01.
11. Organization WH. World Health Organization: Disease Surveillance. Weekly Epidemiological Record [Internet].1998.

*Ngozi Erondu
E-mail: ngozierondu@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Incorporation of School Absenteeism Data into the Maryland Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE)

Zachary Faigen*, Anikah Salim and Isaac Ajit

Office of Preparedness & Response, Maryland Department of Health and Mental Hygiene, Baltimore, MD, USA

Objective

The state of Maryland has incorporated 100% of its public school systems into a statewide disease surveillance system. This session will discuss the process, challenges, and best practices for expanding the ESSENCE system to include school absenteeism data as part of disease surveillance. It will also discuss the plans that Maryland has for using this new data source, as well as the potential for further expansion.

Introduction

Syndromic surveillance offers the potential for earlier detection of bioterrorism, outbreaks, and other public health emergencies than traditional disease surveillance. The Maryland Department of Health and Mental Hygiene (DHMH) Office of Preparedness and Response (OP&R) conducts syndromic surveillance using the Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE). Since its inception, ESSENCE has been a vital tool for DHMH, providing continuous situational awareness for public health policy decision makers. It has been established in the public health community that syndromic surveillance data, including school absenteeism data, has efficacy in monitoring disease, and specifically, influenza activity. Schools have the potential to play a major role in the spread of disease during an epidemic. Therefore, having school absenteeism data in ESSENCE would provide the opportunity to monitor schools throughout the school year and take appropriate actions to mitigate infections and the spread of disease.

Methods

DHMH partnered with the Maryland State Department of Education (MSDE), local health departments, and local school systems to incorporate school absenteeism data into the syndromic surveillance program. There are 24 local public school systems and 24 local health departments in the state of Maryland. OP&R contacted each local school superintendent and each local health officer to arrange a joint meeting to discuss the expansion of the ESSENCE program to include school absenteeism data. Once the meetings were arranged, OP&R epidemiologists traveled to each local jurisdiction and presented their plan for the ESSENCE expansion. At each meeting were representatives from the local health department, as well as school health, school attendance, and school IT staff. This allowed all questions and concerns to be addressed from both sides. In addition to the targeted meetings and presentations, the Secretary of Health issued an executive order which required all local school systems to sign a memorandum of understanding (MOU) with DHMH. This MOU detailed the data elements to be shared with the ESSENCE program and the process by which this would be shared. While this order made data contribution mandatory, the site visits by the OP&R staff created a working relationship and partnership with the local jurisdictions. Data was collected from all public schools in the state including elementary, middle, and high schools.

Results

As of June 30, 2012, Maryland became the first state in the United States to incorporate 100% of its public school systems (1,424 schools) into ESSENCE. Each school system reports absenteeism data daily via an automated secure FTP (sFTP) transfer to DHMH. Due to its unique properties, Johns Hopkins Applied Physics Laboratory (JHUAPL) designed a new detection algorithm in ESSENCE specifically for this data source. OP&R epidemiologist review and analyze this data for disease surveillance purposes in conjunction with other data sources in ESSENCE (emergency department chief complaints, poison control center data, thermometer sales data, and over-the-counter medication sales data). Integrating school absenteeism data will provide a more complete analysis of potential public health threats. The process by which Maryland incorporated their public school systems' data could potentially be used as a best practice for other jurisdictions. Not only was DHMH able to obtain data from all public schools in the state, but the process also enhanced collaboration between local health departments and public school systems.

Keywords

ESSENCE; Surveillance; Absenteeism

Acknowledgments

The Office of Preparedness & Response at the Maryland Department of Health and Mental Hygiene would like to acknowledge and thank the Maryland State Department of Education and the 24 local health departments and public school systems for their support and collaboration to successfully implement this project.

*Zachary Faigen
E-mail: zfaigen@dhmh.state.md.us

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using the Flow of People in Cluster Detection and Inference

Sabino J. Ferreira*[1], Francisco S. Oliveira[1], Ricardo Tavares[2] and Flavio R. Moura[2]

[1]Federal University of Minas Gerais, Belo Horizonte, Brazil; [2]Federal University of Ouro Preto, Ouro Preto, Brazil

Objective

We present a new approach to the circular scan method [1] that uses the flow of people to detect and infer clusters of regions with high incidence of some event randomly distributed in a map. We use a real database of homicides cases in Minas Gerais state, in southeast Brazil to compare our proposed method with the original circular scan method in a study of simulated clusters and the real situation.

Introduction

The traditional SaTScan algorithm[1],[2] uses the euclidean distance between centroids of the regions in a map to assemble a connected (in the sense that two connected regions share a physical border) sets of regions. According to the value of the respective logarithm of the likelihood ratio (LLR) a connected set of regions can be classified as a statistically significant detected cluster. Considering the study of events like contagious diseases or homicides we consider using the flow of people between two regions in order to build up a set of regions (zone) with high incidence of cases of the event. In this sense the regions will be closer as the greater the flow of people between them. In a cluster of regions formed according to the criterion of proximity due to the flow of people, the regions will be not necessarily connected to each other.

Methods

We consider a study map with a number of observed cases and risk population for each region. The original circular scan algorithm randomly chooses one region as the first zone and calculates its respective LLR. In the next step a new zone is created including the first region and the region closest to it according the euclidean distance between their centroids and the respective LLR is calculated. This process is repeated until the zone population exceeds a certain percentage of the total population of the map. In our spatial flow scan algorithm everything works in the same manner except that the degree of proximity of two regions is given by the flow of people between them, the higher the flow between the regions closest one is the other. Instead of considering an order of increasing distances to add a region and create a new zone our algorithm uses a decreasing flow of people. In this way we can obtain a zone/cluster candidate composed of a number of non necessarily connected regions.

Results

Minas Gerais state is located in Brazil south-eastern region composed of 853 municipalities or regions with an estimated population of 19,150,344 in 2005. All data were obtained from the Brazilian Ministry of Health (WWW.DATASUS.GOV.BR) and Brazilian Institute of Geography and Statistics (WWW.IBGE.GOV.BR). In the period of 2003 to 2008 were recorded 20,912 homicides at a rate of 22 cases per 100,000. To measure the flow of people between the cities we obtain the data of bus round trips between all the 853 Minas Gerais municipalities from state department of highways (www.der.mg.gov.br). As a large number of pairs of cities have zero bus trips between them we use a gravity model [3] to estimate the flow of people. We use 30% as upper percentage for a zone population. With the real data of homicides cases the original circular scan found a significant cluster containing the city of Belo Horizonte which is the Minas Gerais state capital and large urban area that include Belo Horizonte and 22 more cities totalizing a population of about 3.5 milion people. Our adapted spatial scan algorithm also found a similar cluster including the capital Belo Horizonte but with two small cities less.

Conclusions

In simulation studies where the real cluster is known we observe that our spatial flow scan algorithm has a performance similar to the circular scan concerning detection power and slightly worse in relation to the positive predicted value (PPV) and the sensitivity when the real cluster is regular. However, the performance of our algorithm is clearly better with regard to the sensitivity and the PPV when the real cluster is irregular and or non-connected.

Keywords

Spatial scan statistics; flow of people; spatial flow scan algorithm; gravity models

Acknowledgments

SJF acknowledges the support by Fapemig, MG, Brazil.

References

[1] Kulldorff M. A Spatial Scan Statistic, Comm. Statist. Theory Meth., 1997, 26(6), 1481-1496.

[2] Kulldorff M. SaTScan: Software for the spatial, tem-poral and space-time scan statistics. [www.satscan.org].

[3] Signorino G.; Pasetto R.; Gatto E.; Mucciardi M.; Rocca M. La; Muso P. Gravity models to classify commuting vs. resident workers. An application to the analysis of residential risk in a contaminated area. . Int. J. of Health Geographics, 2011. 10:11, pp. 1-10.

*Sabino J. Ferreira
E-mail: sabjfn@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Biosurveillance-driven Home Score to Guide Strep Pharyngitis Treatment

Andrew Fine*[1, 2], Victor Nizet[3] and Kenneth Mandl[1, 2]

[1]Boston Children's Hospital, Boston, MA, USA; [2]Harvard Medical School, Boston, MA, USA; [3]UCSD, La Jolla, CA, USA

Objective

1. To derive and validate an accurate clinical prediction model ("home score") to estimate a patient's risk of group A streptococcal (GAS) pharyngitis before a health care visit based only on history and real-time local biosurveillance, and to compare its accuracy to traditional clinical prediction models composed of history and physical exam features. 2. To examine the impact of a home score on patient and public health outcomes.

Introduction

GAS pharyngitis affects hundreds of millions of individuals globally each year, and over 12 million seek care in the United States annually for sore throat. Clinicians cannot differentiate GAS from other causes of acute pharyngitis based on the oropharynx exam, so consensus guidelines recommend use of clinical scores to classify GAS risk and guide management of adults with acute pharyngitis. When the clinical score is low, consensus guidelines agree patients should neither be tested nor treated for GAS. A prediction model that could identify very-low risk patients prior to an ambulatory visit could reduce low-yield, unnecessary visits for a most common outpatient condition. We recently showed that real-time biosurveillance can further identify patients at low-risk of GAS. With increasing emphasis on patient-centric health care and the well-documented barriers impeding clinicians' incorporation of prediction models into medical practice, this presents an opportunity to create a patient-centric model for GAS pharyngitis based on history and recent local epidemiology. We refer to this model as the "home score," because it is designed for use prior to a physical exam.

Methods

Analysis of data collected from 110,208 patients 3 years and older who presented with pharyngitis to a national retail health chain, from 2006-08. Practitioners collected standardized historical and physical exam information based on algorithm-driven care, and all patients with pharyngitis were tested for GAS. We used a previously validated biosurveillance variable reflecting disease incidence called recent local proportion positive (RLPP), which represents the proportion of patients who tested GAS positive in a local market in the previous 14 days. To derive the "home score," candidate variables were restricted to demographic factors, historical items and the RLPP, while physical exam variables (such as exudate), were excluded. Multivariate analytic techniques were used to identify predictors of GAS. For each home score (0-100), we calculated the percent of patients who tested positive, and we examined the relationship between the home score and GAS positivity. Standard metrics (sensitivity, specificity, positive and negative predictive value, and AUC) were used to compare the performance of the home score to standard scores. We computed the number of patients aged >= 15 years who, according to the home score, were at low risk for GAS, and therefore might avoid or delay a trip to a medical provider. Outcomes included the numbers of reduced visits and the number of additional missed GAS cases compared to the standard Centor score approach (Do not test/Do not treat if Centor score is 0-1). To facilitate comparison across different risk thresholds, we calculated outcomes for hypothetical cohorts of 1000 patients, and extrapolated these findings to provide the impact on 12 million annual national pharyngitis visits.

Results

The 3 best predictors were fever (OR 2.43, 95%CI 2.33-2.54), absence of cough (1.71,1.63-1.80) and RLPP (1.04,1.04-1.04 per unit change in RLPP). Using a home score cutoff of 0.10 to identify adults at low risk would save 230,000 ambulatory visits annually while missing only 8500 additional GAS cases. At a 0.20 cutoff, 2.9 million visits would be saved, and 320,000 more cases missed each year. There was a strong correlation between the percent testing positive and the home score (r-square=0.98). As the home score increases, there is a linear increase in the risk of GAS (slope=1.02). The home score AUC was 0.66, approaching the Centor score (0.69) even without any physical exam information.

Conclusions

A biosurveillance-driven home score to guide treatment of strep pharyngitis could save millions of visits annually by identifying patients in the pre-visit setting who would be unlikely to be tested or treated.

Keywords

biosurveillance; pharyngitis; retail health

*Andrew Fine
E-mail: andrew.fine@childrens.harvard.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

SurSaUD® Software: A Tool to Support the Data Management, the Analysis and the Dissemination of Results from the French Syndromic Surveillance System

Anne Fouillet*[1], Nelly Fournet[1], Nadege Caillère[1], Arnaud Musset[1], Lucas Mercier[1], Cécile Durand[1], Céline Caserio-Schönemann[1] and Loic Josseran[2]

[1]French Institute for Public Health Surveillance (InVS), Saint Maurice, France; [2]Université de Versailles St-Quentin-en-Yvelines (UVSQ), Montigny-Le-Bretonneux, France

Objective

The presentation describes the design and the main functionalities of the software developed to support the data management and data analysis of the French syndromic surveillance system.

Introduction

The French syndromic surveillance system SurSaUD® was set up by the French institute for public health surveillance (InVS) in 2004. The system is based on three main data sources: 1/the attendances in the Emergency departments (ED), 2/the consultations to emergency General Practitioners' associations SOS Médecins 3/the mortality data from civil status offices and e-certificates.

In 2012, 400 of the 710 ED and 59 of the 62 GP's associations are involved in the system. 80% of the national mortality is also collected. Given this large database and the need to analyze data in a short delay to reach the early warning objective of the system, a specific software has been developed.

Methods

The application has been designed in order to support the users with automatised process of the three main following steps:

1. Data integration in a database, data management and the control of data quality transmitted by the providers

2. The statistical analysis of the data, according to different demographic, geographic and syndromic criteria. Individual and aggregated data are consultated using reporting tools (graphs and tables).

3. The output and reporting for decision makers and feedback for data providers through epidemiological bulletins and dashboards.

Each night, XML files containing data recorded during the previous day are sent from the ED and GP's association SOS Médecins to InVS. All files are automatically integrated in the national database. A data quality process is done to check the completeness and the validity of the transmitted data. The data are managed by aggregating by age groups, syndromes, by day and ED or association.

After the data management, bulletins and dashboards are automatically generated. Those Word® documents contain graphs, tables or maps with the most recent data. This functionality allows producing already formatted documents, including an updated overview of the health situation of the previous days. Through those documents available at 10:30 AM every day, the epidemiologists can analyse, add comments of the results and publish their bulletins in a short delay.

The users can also consult aggregated data through a BI tool to have a more in-depth analysis of the public health. Such tool can also support the investigation of abnormal signals.

Results

Sursaud software is a login and password-protected and secured internet web site. Since its deployment in 2010, about 300 users have had an access to the software and 25% are data providers.

In August 2012, almost 35,000 new patients are daily caught by the system and nearly 50 millions of patients are recorded in the database since 2004.

To analyse data, the diagnosis coded either in ICD10 for ED visits or with specific thesaurus for GP's calls are pre-aggregated in about 200 syndromes covering a large part of the medical diagnosis and call reasons collected in the system. 22 age groups are also available with a focus on the most frailty population, like the youngest and the elderly. Finally, various geographic levels can be chosen, from the local ED or association to the national level.

An average of 25 bulletins or dashboards is daily produced by the software and about 10,000 documents have been produced since the deployment. They support the analysis of general overviews of population health or are focused on the surveillance of specific health situations, such as epidemics, emergent pathologies or exceptional events (disasters, mass gatherings,…)

Conclusions

The software is a fundamental support for the French syndromic surveillance system. A new version is being developed in order to add improvements and integrate the mortality data. The deployment of this second version is expected in 2013.

Keywords

software; France; Emergency department, General practitioners

References

1. Broome C, Loonsk J. Public health information network – Improving early detection by using a standards-based approach to connecting public health and clinical medicine. MMWR (2004) Vol53. Supplement:199-202.

2. Josseran L, Nicolau J, Caillère N, Astagneau P, Brücker G. Syndromic surveillance based on emergency department activity and crude mortality: 2 examples. Euro Surveill 2006,11(12):225-29

*Anne Fouillet
E-mail: a.fouillet@invs.sante.fr

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Towards Linking Anonymous Authorship in Casual Sexual Encounter Ads

Jason A. Fries*[1], Alberto M. Segre[1] and Philip M. Polgreen[2]

[1]Computer Science, The University of Iowa, Iowa City, IA, USA; [2]The University of Iowa - Department of Internal Medicine, Iowa CIty, IA, USA

Objective

This paper constructs an authorship-linked collection or corpus of anonymous, sex-seeking ads found on the classifieds website Craigslist. This corpus is then used to validate an authorship attribution approach based on identifying near duplicate text in ad clusters, providing insight into how often anonymous individuals post sex-seeking ads and where they meet for encounters.

Introduction

The increasing use of the Internet to arrange sexual encounters presents challenges to public health agencies formulating STD interventions, particularly in the context of anonymous encounters. These encounters complicate or break traditional interventions. In previous work [1], we examined a corpus of anonymous personal ads seeking sexual encounters from the classifieds website Craigslist and presented a way of linking multiple ads posted across time to a single author. The key observation of our approach is that some ads are simply reposts of older ads, often updated with only minor textual changes. Under the presumption that these ads, when not spam, originate from the same author, we can use efficient near-duplicate detection techniques to cluster ads within some threshold similarity. Linking ads in this way allows us to preserve the anonymity of authors while still extracting useful information on the frequency with which authors post ads, as well as the geographic regions in which they seek encounters.

While this process detects many clusters, the lack of a true corpus of authorship-linked ads makes it difficult to validate and tune the parameters of our system. Fortunately, many ad authors provide an obfuscated telephone number in ad text (e.g., 867-5309 becomes 8sixseven5three oh nine) to bypass Craigslist filters, which prohibit including phone numbers in personal ads. By matching phone numbers of this type across all ads, we can create a corpus of ad clusters known to be written by a single author. This authorship corpus can then be used to evaluate and tune our existing near-duplicate detection system, and in the future identify features for more robust authorship attribution techniques.

Methods

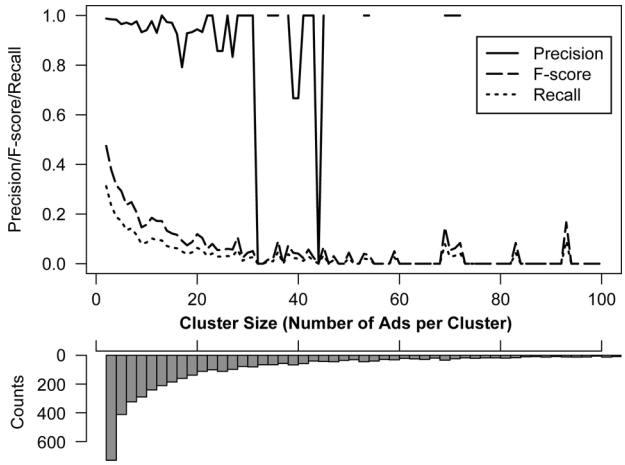
From 7-1-2009 until 7-1-2011, RSS feeds were collected daily for 8 personal ad categories from 414 sites across the United States, for a total of 67 million ads. To create an anonymous, author-linked corpus, we used a regular expression to identify obfuscated phone numbers in ad text. We measure the ability of near-duplicate detection to link clusters in two ways: 1) detecting all ads in a cluster; and 2) correctly detecting a subset of ads within a single cluster. Ads incorrectly assigned to more than 1 cluster are considered false positives. All results are reported in terms of precision, recall, and F-scores (common information retrieval metrics) across cluster size, expressed as number of ads.

Results

652,014 ads contained phone numbers, producing a total of 46,079 authorship-linked ad clusters. For detecting all ads within a cluster, precision ranged from 0.05 to 0.0 and recall from 0.02 to 0.0 for all cluster sizes. For detecting partial clusters, see Figure 1.

Conclusions

We find that near-duplicate detection alone is insufficient to detect all ads within a cluster. However, we do find that the process can, with high precision and low recall, detect a subset of ads associated with a single author. This follows the intuition that an author's total set of ads is itself comprised of multiple self-similar subsets. While a near-duplicate detection approach can correctly identify subsets of ads linked to a single author, this process alone cannot attribute multiple clusters to a single author. Future work will explore leveraging additional linguistic features to improve author attribution.



(Top) Evaluations for partial cluster detection using the near-duplicate identification approach to linking anonymous authorship in Craigslist ads and (bottom) the distribution of ad cluster sizes.

Keywords

Surveillance; Public Health; STDs; Authorship Attribution; Computer Science

References

[1] JA Fries, AM Segre, PM Polgreen .Using Online Classified Ads to Identify the Geographic Footprints of Anonymous, Casual Sex-seeking Individuals. ASE/IEEE International Conference on Social Computing 2012.

*Jason A. Fries
E-mail: jason-fries@uiowa.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Review of Evaluations of Electronic Event-based Biosurveillance Systems

Kimberly Gajewski*[1], Jean-Paul Chretien[2], Amy Peterson[2], Julie Pavlin[3] and Rohit Chitale[2]

[1]Emory University, Atlanta, GA, USA; [2]Division of Integrated Biosurveillance, Silver Spring, MD, USA; [3]Headquarters, Armed Forces Health Surveillance Center, Silver Spring, MD, USA

Objective

To assess evaluations of electronic event-based biosurveillance systems (EEBS's) and define priorities for EEBS evaluations.

Introduction

EEBS's that use near real-time information from the Internet are an increasingly important source of intelligence for public health organizations (1, 2). However, there has not been a systematic assessment of EEBS evaluations, which could identify uncertainties about current systems and guide EEBS development to effectively exploit digital information for surveillance.

Methods

We searched PubMed and consulted EEBS experts to identify EEBS's that met the following criteria: uses publicly-available Internet info sources, includes events that impact humans, and has global scope. We constructed a list of 17 key evaluation variables using guidelines for evaluating health surveillance systems, and identified the key variables included in evaluations per EEBS, as well as the number of EEBS's evaluated for each key variable (3,4).

Results

We identified 10 EEBS's and 17 evaluations (Table 1). The number of evaluations per EEBS ranged from 1 (Gen-Db, GODsN) to 7 (GPHIN, HealthMap). The median number of variables assessed per EEBS was 6 (range, 3-12), with 5 (25%) evaluations assessing 7+ variables. Nine (53%) published evaluations contained quantitative assessments of at least 1 variable. The least-frequently studied variable was cost. No papers examined usefulness as specific public health decisions or outcomes resulting from early event detection, though 8 evaluations assessed usefulness by citing instances where the EEBS detected an outbreak earlier, or by eliciting user feedback.

Conclusions

While EEBS's have demonstrated their usefulness and accuracy for early outbreak detection, no evaluations have cited specific examples of public health decisions or outcomes resulting from the EEBS. Future evaluations should discuss these critical indicators of public health utility. They also should assess the novel aspects of EEBS and include variables such as policy readiness, system redundancy, input/output geography (5); and test the effects of combining EEBS's into a "super system".

Table 1. Number of published evaluations and variables on identified EEBS's

EEBS	Year started	No. evaluations	No. key variables assessed
Argus	2005	5	7
BioCaster	2006	5	9
EpiSpider	2006	2	4
Geni-Db	2012	1	4
GODSn	2006	1	3
GPHIN	1997	7	10
Health Map	2006	7	12
MedISys	2006	2	4
ProMed	1994	5	12
PULS	2006	2	5

Table 2. Key variables used in evaluations of EEBS

Key eval var	Ref.	No. evals using the var	No. of EEBS's evaluated on this var
Acceptability	3,4	6	4
Accessibility	4	5	4
Cost	4	3	2
Data quality	3,4	5	3
Flexibility	3,4	2	3
Population coverage	4	9	5
Predict. value pos.	3	5	4
Purpose	4	15	10
Portability	4	2	2
Representativeness	3,4	5	5
Resources	3,4	7	3
Sensitivity	3	9	5
Simplicity	3	5	4
Stability	3,4	0	0
Timeliness	3,4	14	9
Usefulness	3,4	8	7
Validity	4	5	4

Keywords

evaluation; biosurveillance; event-based surveillance

References

Heymann DL, et al. Hot spots in a wired world: WHO surveillance of emerging and re-emerging infectious diseases. Lancet Infect Dis. 2001;1:345–53.

Keller M, et al. Use of unstructured event-based reports for global infectious disease surveillance. Emerg Infect Dis. 2009;15:689–95.

German RR, et al. Guidelines working group centers for disease control and prevention (CDC).Updated guidelines for evaluating public health surveillance systems: Recommendations from the Guidelines Working Group. MMWR Recomm Rep. 2001;50(RR-13):1–35.

Buehler JW, et al. Framework for evaluating public health surveillance systems for early detection of outbreaks: Recommendations from the CDC working group. MMWR Recomm Rep. 2004;53(RR-5):1–11.

Corley CD, et al. Assessing the continuum of event-based biosurveillance through an operational lens. Biosecur Bioterror 2012;10:131-141.

*Kimberly Gajewski
E-mail: kimberly.gajewski@emory.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

U.S. Dept. Veterans Affairs (VA) SMEC-bio Reporting for Leadership Decision Support

Shantini D. Gamage*[1, 2], Loretta A. Simbartl[1], Stephen M. Kralovic[1, 2, 3], Katherine S. Wallace[4] and Gary A. Roselle[1, 2, 3]

[1]National Infectious Diseases Service, Veterans Health Administration (VHA), Washington, DC, USA; [2]University of Cincinnati College of Medicine, Cincinnati, OH, USA; [3]Cincinnati VA Medical Center, Cincinnati, OH, USA; [4]Office of Operations, Security and Preparedness (OSP), VA Central Office, Washington, DC, USA

Objective

To assess Reports sent from the United States VA Subject Matter Expertise Center for Biological Events (SMEC-bio) – a proof-of-concept decision support initiative – to the VA Integrated Operations Center (VA IOC).

Introduction

VA is the U.S. federal agency responsible for providing services to America's Veterans. Within VA, VHA is the organization responsible for administration of health care services. VHA, with 152 Medical Centers and over 900 outpatient clinics located throughout the U.S. and territories, provided care to over 5 million patients in 2011.

After the 2009 H1N1 influenza pandemic, OSP, which oversees VA senior level briefing of preparedness issues, conceptualized and initiated SMEC-bio as a protocol-based mechanism to incorporate timely VHA subject matter expertise into leadership decision making via the VA IOC. Previous work has examined collection and integration of data from VA and interagency sources for trend and predictive analyses (1). This current work is an initial assessment of SMEC-bio reporting, which has been in development for the past year and functions on an ad hoc basis for decision support; needs and gaps can be assessed toward a formalized communication plan with the VA IOC.

Methods

In May, 2011, SMEC-bio designed a Report template. All SMEC-bio Reports submitted to the VA IOC using the template were assessed based on reason for the Report, timing, data sources used, and outcome. A gap analysis was conducted to identify areas for further improvement.

Results

Eight SMEC-bio Reports were produced since the template was initiated in May, 2011. The reasons for reporting fell into the following categories: 1) briefings of interagency protocol activations [e.g. National Biosurveillance Integration System (NBIS) protocol]; 2) Requests for Information (RFIs) from the VA IOC regarding specific biological events (e.g. 2012 H3N2v influenza associated with swine at fairs); 3) RFIs from the VA IOC on general infectious diseases issues (e.g. 2011 dust storm in Arizona); and 4) SMEC-bio-initiated Reports to provide situational awareness to the VA IOC on a biological event (e.g. the measles outbreak at the time of the 2012 Super Bowl in Indiana).

Reports in response to RFIs were all submitted within the day, often within hours including those that required data collection and interpretation, indicating that SMEC-bio can be a viable source for timely decision support to senior leadership. Some Reports, such as the one on possible infectious diseases issues after hurricane Irene in August, 2011, were subsequently shared by VA IOC with VHA Operations and with field facilities, thus highlighting the potential for facilitating provision of timely subject matter expertise for local response.

The primary information source for Reports was the Centers for Disease Control and Prevention website, press releases, and interagency briefings. Data sources used were the VHA centrally-administered electronic health records system and syndromic surveillance via VA-adapted ESSENCE.

Gap analysis results included common themes for biopreparedness: uncertainty in data quality and interpretation, communication of results and confidence levels to leadership, and coordination among stakeholders. Furthermore, the development of a decision tool to guide selection of events for reporting will be a critical initial requirement of a formal communications plan.

Conclusions

As SMEC-bio progresses from proof-of-concept phase to development status, knowledge gained from ad hoc reporting, as described in this work, will be critical for developing a routine and effective communications plan. Other ongoing work that will support communications include staffing assessments, development of analysis tools, and incorporating automated report capabilities.

Keywords

Reporting; Decision Support; Communications

Acknowledgments

The authors thank JC Cantrell, VA IOC Director, and VA IOC staff for helpful interactions regarding reporting.

References

1. Wallace, KS, et al. U.S. Department of Veterans Affairs Integrated Operations Center (VA IOC): Collaborations for Surveillance, Analysis, and Prediction for Infectious Disease Threat Preparedness — Pilot Review of Dengue Occurrence. Emerg. Health Threats J. 4:s155, 2011

*Shantini D. Gamage
E-mail: shantini.gamage@va.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluating Biosurveillance System Components using Multi-Criteria Decision Analysis

Eric Nicholas Generous*[1], Alina Deshpande[1], Mac Brown[1], Lauren Castro[1], Kristen Margevicius[1], William Brent Daniel[1] and Kirsten Taylor-McCabe[2]

[1]Defense Systems Analysis Division, Los Alamos National Laboratory, Los Alamos, NM, USA; [2]Bioscience Division, Los Alamos National Laboratory, Los Alamos, NM, USA

Objective

The use of Multi-Criteria Decision Analysis (MCDA) has traditionally been limited to the field of operations research, however many of the tools and methods developed for MCDA can also be applied to biosurveillance. Our project demonstrates the utility of MCDA for this purpose by applying it to the evaluation of data streams for use in an integrated, global biosurveillance system.

Introduction

The evaluation of biosurveillance system components is a complex, multi-objective decision that requires consideration of a variety of factors. Multi-Criteria Decision Analysis provides a methodology to assist in the objective analysis of these types of evaluation by creating a mathematical model that can simulate decisions. This model can utilize many types of data, both quantitative and qualitative, that can accurately describe components. The decision-maker can use this model to determine which of the system components best accomplish the goals being evaluated. Before MCDA can be utilized effectively, an evaluation framework needs to be developed. We built a robust framework that identified unique metrics, surveillance goals, and priorities for metrics. Using this framework, we were able to use MCDA to assist in the evaluation of data streams and to determine which types would be of most use within a global biosurveillance system.

Methods

MCDA was implemented using the Logical Decisions® software. The construction of the evaluation framework was carried out in several steps: identification and definition of data streams, metrics and surveillance goals, and the determination of the relative importance of each metric to the respective surveillance goal being evaluated. Sixteen data streams types were defined and identified for evaluation from a survey we conducted that collected over 200 surveillance products. A subject matter expert (SME) panel was assembled to help identify the biosurveillance goals and metrics in which to evaluate the data streams. To assign values for the metrics, we referenced properties of data streams used in currently operational systems.

Results

Our survey identified sixteen different classes of data streams: Ambulance Records, Clinic/ Health Care Provider Records, ED/ Hospital Records, Employment/School Records, Established Databases, Financial Records, Help Lines, Internet Search Queries, Laboraotry Records, News Aggregators, Official Reports, Police/Fire Department Records, Personal Communication, Prediction Markets, Sales, and Social Media.

Four biosurveillance goals were identified: Early Warning of Health Threats, Early Detection of Health Events, Situational Awareness, and Consequence Management.

Eleven metrics were identified: Accessibility, Cost, Credibility, Flexibility, Integrability, Geographic/Population Coverage, Granularity, Specificity of Detection, Sustainability, Time to Indication, and Timeliness.

Using the framework, it was possible to use MCDA to rank the utility of each data stream for each goal.

Conclusions

The results suggest that a "one size fits all" approach does not work and that there is no ideal data stream that is most useful for each goal. Data streams that scored more highly for speed tended to rank more highly when the biosurveillance goal is early warning or early detection, whereas data streams that scored more highly for data credibility and geographic/population coverage ranked highly when the goal was situational awareness or consequence management. However, there are several data streams that rank consistently within the top 5 for each goal: Internet Search Queries, News Aggregators, Clinic/ Health Care Provider records, ED/ Hospital Records, and Laboratory Records and may be considered useful for integrated, global biosurveillance for infectious disease.

Early Warning of Health Threats	Early Detection of Health Events	Situational Awareness	Consequence Management
1. Internet Search Queries	1. News Aggregators	1. Laboratory Records	1. ED/ Hospital Records
2. News Aggregators	2. Internet Search Queries	2. ED/ Hospital Records	1. Clinic/ Healthcare Provider Records
3. Social Media	3. Social Media	2. Clinic/ Healthcare Provider Records	2. Laboratory Records
4. Laboratory Records	4. ED/ Hospital Records	3. News Aggregators	3. Internet Search Queries
5. ED/Hospital Records	4. Clinic/ Healthcare Provider Records	4. Internet Search Queries	4. News Aggregators
5. Clinic/ Healthcare Provider Records	5. Laboratory Records	5. Official Reports	5. Official Reports
6. Help Lines	6. Help Lines	6. Employment/ School Records	6. Ambulance Records
7. Ambulance Records	7. Amublance Records	7. Social Media	7. Employment/ School Records
8. Employment/ School Records	8. Employment / School records	8. Ambulance Records	8. Social Media
9. Sales	9. Official Reports	9. Personal Communication	9. Established Databases
10. Crowd Sourcing	9. Sales	10. Established Databases	10. Personal Communication
11. Official Reports	10. Crowd Sourcing	11. Help Lines	11.Sales
12. Personal Communication	11. Personal Communication	12. Prediction Markets	12.Help Lines
13. Financial Records	12. Financial Records	13. Financial Records	13. Financial Records
14. Established Databases	13. Prediction Markets	14. Sales	14. Police/ Fire Department records
15. Police/ Fire Department Records	14. Police / Fire Department Records	15. Police / Fire Department Records	15. Prediction Markets
16. Prediction Markets	15. Established Databases	16. Crowd Sourcing	16. Crowd Sourcing

Keywords

evaluation; biosurveillance; multi-criteria decision analysis; data stream; evaluation framework

Acknowledgments

This project is supported by the Chemical and Biological Technologies Directorate Joint Science and Technology Office (JSTO), Defense Threat Reduction Agency (DTRA)

*Eric Nicholas Generous
E-mail: generous@lanl.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Parametric Uncertainty in Intra-Herd Foot-and-Mouth Disease Epidemiological Models

Eric Nicholas Generous*

Defense Systems Analysis Division, Los Alamos National Laboratory, Los Alamos, NM, USA

Objective

The objective of this project is to understand how parametric uncertainty within intra-herd Foot-and-Mouth disease epidemiological models affects the outbreak simulations and what implications this has on surveillance and control strategy and policy.

Introduction

The rapid transmission and poor control policy response during recent Foot-and-Mouth disease (FMD) outbreaks have underscored the need for better decision support tools. At the foundation of these decision support tools are the epidemiological models that are parameterized with the data generated from pathogenesis studies of the FMD virus that contain contact transmission data. These values being used to parameterize the model, contrary to assumption, contain a significant amount of uncertainty, which propagates throughout the model affecting output. To understand how parametric uncertainty might affect output, a variety of disease transmission parameters were generated from contact transmission data and parameterized to an intra-herd model.

Methods

Data was initially collected and analyzed for papers that could meet several criteria: they must be contact transmission studies, they must measure viremia (the level of virus in the blood), and they must observe clinical signs.

For the studies that met the criteria, tables were constructed and the following information from each paper was collected: serotype, strain, animal species, unique animal identifier, unit of measurement utilized by virus quantification, duration and quantity of viremia, and the time to first report of clinical signs.

Three different durations of disease states for the latent, sub-clinically infectious, and clinically infectious periods were generated from the viremia data for each individual animal and grouped in three ways: by strain of virus, by similar experimental design, and all together. Gamma, weibull, and normal distributions were fitted to the data in each group.

The distributions for each group were then used to parameterize a stochastic, state transition intra-herd model. Output from the model was analyzed by examining the uncertainty and variance in time to 50% herd infected, time to 2% herd clinically infected, and percentage of herd infected at 2% herd clinically infected for each distribution and group.

Results

There is a lack of a standardized definition for disease state durations of the Foot-and-Mouth Disease virus in the literature. As a result, many different models utilize slightly differing values generated from the same data. This project discovered that depending on the definitions used to determine the disease state durations, the model output varied significantly. Additionally, durations of the disease state periods do not follow a normal distribution as may be assumed by many modelers, and are more accurately described by distributions that allow for non-zero skewness.

Conclusions

The data being used to parameterize intra-herd Foot-and-Mouth disease models contains a significant amount of uncertainty that can cause the model output to vary significantly. This uncertainty needs to be clearly communicated to decision makers who use results generated from FMD intra-herd models and illustrates the need for more resources to be put into addressing the issue of basic parameters such as contact rate and disease state duration. Currently no studies have been conducted on the contact rate of animals on farms and the current values used for disease state durations vary drastically depending on the data and methods used. Without a better understanding of the basic parameters, even the most advanced models will not be accurate.

Keywords

Control; Foot and Mouth Disease; Epidemiological Model; Uncertainty; Parameters

*Eric Nicholas Generous
E-mail: generous@lanl.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

#wheezing: A Content Analysis of Asthma-Related Tweets

Gwendolyn Gillingham*[1], Michael A. Conway[2], Wendy W. Chapman[2], Michael B. Casale[3] and Kathryn B. Pettigrew[3]

[1]Linguistics, UCSD, La Jolla, CA, USA; [2]UCSD - Division of Biomedical Informatics, La Jolla, CA, USA; [3]West Health Institute, La Jolla, CA, USA

Objective

We present a Content Analysis project using Natural Language Processing to aid in Twitter-based syndromic surveillance of Asthma.

Introduction

Recently, a growing number of studies have made use of Twitter to track the spread of infectious disease. These investigations show that there are reliable spikes in traffic related to keywords associated with the spread of infectious diseases like Influenza [1], as well as other Syndromes [2]. However, little research has been done using Social Media to monitor chronic conditions like Asthma, which do not spread from sufferer to sufferer. We therefore test the feasibility of using Twitter for Asthma surveillance, using techniques from NLP and machine learning to achieve a deeper understanding of what users Tweet about Asthma, rather than relying only on keyword search.

Methods

We retrieved a large volume of Tweets from the Twitter API. Search terms included "asthma," and several misspellings of that word; terms for common medical devices associated with Asthma such as "inhaler" and "nebulizer"; and names of prescription drugs used to treat the condition, including "albuterol" and "Singulair." A randomly sampled subset of these Tweets (N=3511) was annotated for content, based on an annotation scheme that coded for the following elements: the Experiencer of Asthma symptoms (Self, Family, Friend, Named Other, Unidentified, and All-Non-Self, which was the union of these last four categories); aspects of the type of information being conveyed by each Tweet (Medication, Triggers, Physical Activity, Contacting of a Medical Practitioner, Allergies, Questions, Suggestions, Information, News, Spam); as well as Negative Sentiment, Future temporality, and Non-English content. Further details on the annotation scheme used can be found at http://idiom.ucsd.edu/~ggilling/annotation.pdf. Inter-annotator agreement on a subset of the Tweets (N=403) fell in an acceptable range for all categories (Cohen's Kappa >0.6). Once annotation was complete, the Tweets' texts were stemmed and converted into vectors of unigram and bigram counts. These were then stripped of sparse terms (all those words appearing in fewer than 1 in 200 Tweets), which left multi-dimensional vectors consisting of the counts of the remaining words in all Tweets. Statistical machine-learning classifiers including K-nearest neighbors, Naive Bayes and Support Vector Machines were then trained on the unigram and bigram models.

Results

SVM with 10-fold cross-validation achieved greatest prediction accuracy with the unigram model, as shown in Table 1. Categories that showed the greatest reduction in classification error using the unigram model were Non-English, Self, All-Non-Self, Medication, Symptoms and Spam. The majority of these categories showed very high Precision, as well as fairly high Recall for the unigram model. Unexpectedly, the bigram model faired far worse than the Unigram model, which suggests that individual words in these Tweets were more reliably predictive of content than pairs of words, which occurred less frequently.

Conclusions

Text-classification increases the utility of Twitter as a data-source for studying chronic conditions such as Asthma. Using these methods, we can automatically reject Tweets that are non-English or Spam. We can also determine who is experiencing symptoms: the Twitter user or another individual. Fairly simple models are able to predict with good certainty whether a user is talking about their Symptoms, their Medication, or Triggers for their Asthma, as well as whether they are expressing Negative sentiment about their condition. We demonstrate that Social Media such as Twitter is a promising means by which to conduct surveillance for chronic conditions such as Asthma.

Table 1: Performance of Classifiers on Unigram and Bigram Models

Dimension	Baseline Error (= 1-Majority Classification/N)	Unigram Model Error	Bigram Model Error	Unigram Precision	Unigram Recall
Non-English	0.19	0.07	0.17	0.9	0.82
Self	0.22	0.16	0.18	0.94	0.76
All-Non-Self	0.19	0.14	0.17	0.94	0.59
Medication	0.15	0.098	0.16	0.89	0.77
Symptoms	0.21	0.16	0.17	0.9	0.76
Spam	0.07	0.055	0.17	0.93	0.43

Keywords

social media; natural language processing; asthma; content analysis

Acknowledgments

This work was financially supported by the West Wireless Health Institute and iDASH Summer Internship program (NIH U54HL108460).

References

1. Chew, C. & Eysenbach, G. 2010. Pandemics in the Age of Twitter: Content Analysis of Tweets in the H1N1 Outbreak. PLoS ONE 5(11): e14118.
2. Collier, N. & Doan, S. 2011. Syndromic Classification of Twitter Messages. Proc. eHealth 2011, Malaga, Spain. November 21-23.

*Gwendolyn Gillingham
E-mail: gwen.gillingham@ling.ucsd.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using Google Dengue Trends to Estimate Climate Effects in Mexico

Rebecca T. Gluskin*[1], Mauricio Santillana[2] and John S. Brownstein[1, 3]

[1]Boston Children's Hospital, Boston, MA, USA; [2]Harvard School of Engineering and Applied Sciences, Cambridge, MA, USA; [3]Department of Pediatrics, Harvard Medical School, Boston, MA, USA

Objective

To evaluate the association between Dengue Fever (DF) and climate in Mexico with real-time data from Google Dengue Trends (GDT) and climate data from NASA Earth observing systems.

Introduction

The incidence of dengue fever (DF) has increased 30 fold between 1960 and 2010 [1]. The literature suggests that temperature plays a major role in the life cycle of the mosquito vector and in turn, the timing of DF outbreaks [2]. We use real-time data from GDT and real-time temperature estimates from NASA Earth observing systems to examine the relationship between dengue and climate in 17 Mexican states from 2003-2011. For the majority of states, we predict that a warming climate will increase the number of days the minimum temperature is within the risk range for dengue.

Methods

The GDT estimates are derived from internet search queries and use similar methods as those developed for Google Flu Trends [3]. To validate GDT data, we ran a correlation between GDT and dengue data from the Mexican Secretariat of Health (2003-2010). To analyze the relationship between GDT and varying lags of temperature, we constructed a time series meta-analysis. The mean, max and min of temperature were tested at lags 0 -12 weeks using data from the Modern Era Retrospective-Analysis for Research and Applications. Finally, we built a binomial model to identify the minimum 5° C temperature range associated with a 50% or higher Dengue activity threshold as predicted by GDT.

Results

The time series plot of GDT data and the Mexican Secretariat of Health data (2003- 2010) (Figure 1) produced a correlation coefficient of 0.87. The time series meta-analysis results for 17 states showed an increase in minimum temperature at lag week 8 had the greatest odds of dengue incidence, 1.12 Odds Ratio (1.09-1.16, 95% Confidence Interval). The comparison of dengue activity above 50% in each state to the minimum temperature at lag week 8 showed 14/17 states had an association with warmest 5 degrees of the minimum temperature range. The state of Sonora was the only state to show an association between dengue and the coldest 5 degrees of the minimum temperature range.

Conclusions

Overall, the incidence data from the Mexican Secretariat of Health showed a close correlation with the GDT data. The meta-analysis indicates that an increase in the minimum temperature at lag week 8 is associated with an increased dengue risk. This is consistent with the Colon-Gonzales et al. Mexico study which also found a strong association with the 8 week lag of increasing minimum temperature [4]. The results from this binomial regression show, for the majority of states, the warmest 5 degree range for the minimum temperature had the greatest association with dengue activity 8 weeks later. Inevitably, several other factors contribute to dengue risk which we are unable to include in this model [5]. IPCC climate change predictions suggest a 4° C increase in Mexico. Under such scenario, we predict an increase in the number of days the minimum temperature falls within the range associated with DF risk.

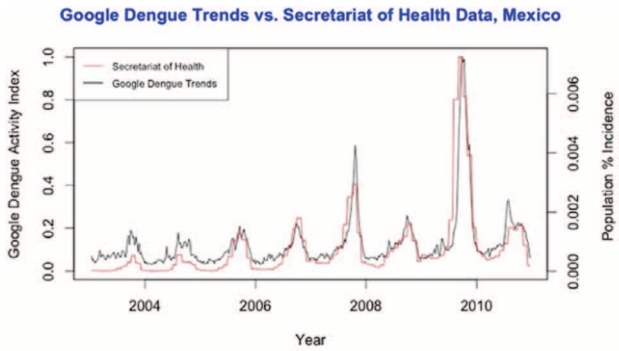


Figure 1. Time Series Correlation: Google Dengue Trends vs. Secretariat of Health, Mexico 2003-2010

Keywords

Time Series; Mexico; Google Dengue Trends; Climate Change; Meta-analysis

Acknowledgments

Funded by the NIH Grant # 1R01LM010812-01 and the Applied Public Health Informatics Fellowship Program administered by CSTE and funded by the Centers for Disease Control and Prevention (CDC) Cooperative Agreement 3U38HM000414-04W1.

References

1.(WHO), W.H.O., Dengue. 2010.
2.Yang, H.M., et al., Assessing the effects of temperature on the population of Aedes aegypti, the vector of dengue. Epidemiol Infect, 2009. 137(8): p. 1188-202.
3.Chan, E.H., et al., Using web search query data to monitor dengue epidemics: a new model for neglected tropical disease surveillance. PLoS Negl Trop Dis, 2011. 5(5): p. e1206.
4.Colon-Gonzalez, F.J., I.R. Lake, and G. Bentham, Climate variability and dengue fever in warm and humid Mexico. Am J Trop Med Hyg, 2011. 84(5): p. 757-63.
5.Thai, K.T. and K.L. Anders, The role of climate variability and change in the transmission dynamics and geographic distribution of dengue. Exp Biol Med (Maywood), 2011. 236(8): p. 944-54.

*Rebecca T. Gluskin
E-mail: rgluskin@health.nyc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

An Experimental Study Using Opt-in Internet Panel Surveys for Behavioral Health Surveillance

Carol A. Gotway Crawford*[1], Catherine A. Okoro[1], Haci M. Akcin[1] and Satvinder Dhingra[2, 1]

[1]Centers for Disease Control, Atlanta, GA, USA; [2]Northrop Grumman, Atlanta, GA, USA

Objective

To present the design and preliminary results of a pilot study to investigate the use of opt-in Internet panel surveys for behavioral health surveillance.

Introduction

Today, surveyors in both the private and public sectors are facing considerable challenges with random digit dialed (RDD) landline telephone samples. The population coverage rates for landline telephone surveys are being eroded by wireless-only households, portable telephone numbers, telecommunication barriers (e.g., call forwarding, call blocking and pager connections), technological barriers (call-blocking, busy circuits) and increased refusal rates and privacy concerns. Addressing these issues increasingly drives up the costs associated with dual-frame telephone surveys designed to be representative of the target population as well as hinders their ability to be fully representative of the adult population of each state and territory in the United States.

In an effort to continue to meet these challenges head on and assist state and territorial public health professionals in the continued collection of data that are representative of their respective populations, novel approaches to behavioral health surveillance need continued examination. Both private and public sector researchers are evaluating the use of Internet opt-in panels to augment dual-frame RDD survey methods. Compared to dual-frame RDD, opt-in Internet panels offer lower costs, quick data collection and dissemination, and the ability to gather additional data on panelists over time. However, as with dual-frame RDD, this mode has similar challenges with coverage error and non-response. Nevertheless, survey methodologists are moving forward and exploring ways to reduce or eliminate biases between the sample and the target population.

Methods

A collaborative pilot project was designed to assess the feasibility and accuracy of opt-in Internet panel surveys for behavioral health surveillance. This pilot project is a collaboration between the CDC, four state departments of health, opt-in Internet panel providers and the leads of several large surveys and systems such as the Patient-Reported Outcome Measures Information System (PROMIS) and the Cooperative Congressional Election Study (CCES). Pilot projects were conducted in four states (GA, IL, NY, and TX) and four Metropolitan Statistical Areas (Atlanta, Chicago, New York City, and Houston). Data were collected using three different opt-in Internet panels and sampling methods that differ with respect to recruitment strategy, sample selection and sample matching to the adult population of each geography. A question bank consisting of 80 questions was developed to benchmark with other existing surveys used to assess various public health surveillance measures (e.g., the Behavioral Risk Factor Surveillance System, the PROMIS, National Survey on Drug Use and Health, and the CCES).

Results

We present comparative analyses that assess the advantages and disadvantages of different opt-in Internet panels sampling methodologies across a range of parameters including cost, geography, timeliness, usability, and ease of use for technology transfer to states and local communities. Recommendations for future efforts in behavioral health surveillance are given based on these results.

Keywords

Random Digit Dialing; BRFSS; Survey Methods; Sample Matching; Representativeness

References

Ansolabehere S, Schaffner BF. 2010. Re-examining the validity of different survey modes for measuring public opinion in the U.S.: Findings from a 2010 multi-mode comparison. http://projects.iq.harvard.edu/cces/files/ansolabehere_schaffner_mode.pdf.

Curtin R, Presser S, Singer E. 2005. Changes in telephone survey nonresponse over the past quarter century. Public Opinion Quarterly;69(1):87-98.

Liu H, Cella D, Gershon R, Shen J, Morales LS, Riley W, Hays RD. 2010. Representativeness of the Patient-Reported Outcomes Measurement Information System Internet panel. J Clin Epidemiol 63(11):1169-78.

Rivers, D., 2007. Sampling for Web Surveys, Paper presented at the Joint Statistical Meetings. http://www.laits.utexas.edu/txp_media/html/poll/files/Rivers_matching.pdf

*Carol A. Gotway Crawford
E-mail: cdg7@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Advancing Surveillance Outside the USA: The Canadian Policy, Practice, and Research Context

Effie Gournis*[1, 2] and David Buckeridge[3, 4]

[1]Toronto Public Health, Toronto, ON, Canada; [2]Dalla Lana School of Public Health - University of Toronto, Toronto, ON, Canada; [3]McGill University, Montreal, QC, Canada; [4]Direction de Sante Publique de Montreal, Montreal, QC, Canada

Objective

1) To explore how ISDS can better support researchers and public health practitioners working in the field of disease surveillance outside the United States; and

2) To identify current surveillance issues in the Canadian public health system where ISDS can support dialogue and action.

Introduction

The international Society for Disease Surveillance has successfully brought together practitioners and researchers to share tools, ideas, and strategies to strengthen health surveillance systems. The Society has evolved from an initial focus on syndromic surveillance to a broader consideration of innovation in health surveillance. More recently, ISDS has also worked to support surveillance research and practice in International resource-constrained settings. Individuals who work in surveillance in developed countries outside the USA, however, have received little direct attention from ISDS. The policy and practice contexts in these countries are often quite different than the USA, so there is a need to support surveillance innovation in these countries in a manner that fits the context. Canadian surveillance practitioners and researchers comprise the largest International group of ISDS members, and these members have expressed an interest in working with ISDS to translate surveillance innovations into practice in Canada, where a national surveillance network and forum is lacking. This Round Table will consider how ISDS can help to support members in countries like Canada and will identify next steps for promoting the science and practice of disease surveillance in the Canadian context.

Methods

Individuals attending the ISDS 2012 Conference with an interest in public health surveillance in Canada or other similar countries outside the USA will be invited to discuss how ISDS can better support their activities. The discussion will be structured around questions and results received for a survey circulated to Canadian ISDS members. The goal will be to discuss whether there is a specific formal role ISDS can play in helping members in Canada and other similar countries working in public health surveillance.

Results

Discussion will be prompted through sharing results of a recent survey distributed to all Canadian ISDS members and affiliates aimed at gauging their interest in developing a Canadian focused group within ISDS, whether they believe there is a need, and how we might accomplish this. The survey questions, range of answers, and implications to future actions suggested in survey responses would drive the discussion.

Keywords

International surveillance; Canada; Surveillance network

*Effie Gournis
E-mail: egourni@toronto.ca

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using Information Entropy to Monitor Chief Complaint Characteristics and Quality

Shaun Grannis*[1, 2], Brian Dixon[4, 2], Yuni Xia[3] and Jianmin Wu[4, 2]

[1]Indiana University School of Medicine, Indianapolis, IN, USA; [2]Regenstrief Institute, Indianapolis, IN, USA; [3]Indiana University Purdue University Indianapolis, Indianapolis, IN, USA; [4]Indiana University School of Informatics, Indianapolis, IN, USA

Objective

We describe how entropy, a key information measure, can be used to monitor the characteristics of chief complaints in an operational surveillance system.

Introduction

Health care processes consume increasing volumes of digital data. However, creating and leveraging high quality integrated health data is challenging because large-scale health data derives from systems where data is captured from varying workflows, yielding varying data quality, potentially limiting its utility for various uses, including population health. To ensure accurate results, it's important to assess the data quality for the particular use. Examples of sub-optimal health data quality abound: accuracy varies for medication and diagnostic data in hospital discharge and claims data; electronic laboratory data used to identify notifiable public-health cases shows varying levels of completeness across data sources; data timeliness has been found to vary across different data sources. Given that there is clear increasing focus on large health data sources; there are known data quality issues that hinder the utility of such data; and there is a paucity of medical literature describing approaches for evaluating these issues across integrated health data sources, we hypothesize that novel methods for ongoing monitoring of data quality in rapidly growing large health data sets, including surveillance data, will improve the accuracy and overall utility of these data.

Methods

Our analysis used chief complaint data derived from the original real-time HL7 registration transactions for ED encounters over a 3-year study period between January 1, 2008 and December 30, 2010 from over 100 institutions participating in the Indiana Public Health Emergency Surveillance System (PHESS) [1]. We used the following syndrome categories based on various definitions: respiratory, influenza like illness, gastrointestinal, neurological, undifferentiated infection, skin, and lymphatic. We calculated entropy for chief complaint data [2]. Entropy measures uncertainty and characterizes the density of the information contained in a message, commonly measured in bits. We analyzed entropy stratified a) by syndrome category, b) by syndrome category and time, and c) by syndrome category, time, and source institution.

Results

Analysis of more than 7.4 million records revealed the following: First, overall information content varied by syndrome, with "neurological" showing greatest entropy (Figure 1). Second, entropy measures followed consistent intraorganizational trends: information content varied less within an organization than across organizations (Figure 2). Third, information entropy enables detection of otherwise unannounced changes in system behavior. Figure 3 illustrates the monthly entropy measures for the respiratory syndrome from 5 sources over 36 months. One source changed registration software. Their visit volume didn't change, but the information content of the chief complaint changed, as indicated by a substantial shift in entropy.

Conclusions

As we face greater data volumes, methods assessing the data quality for particular uses, including syndrome surveillance, are needed. This analysis shows the value of entropy as a metric to support monitoring of surveillance systems. Future work will refine these measures and further assess the inter-organizational variations of entropy.

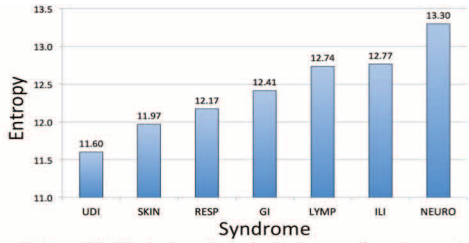


Figure 1: Entropy (bits) for chief complaints classified into specific syndrome categories.

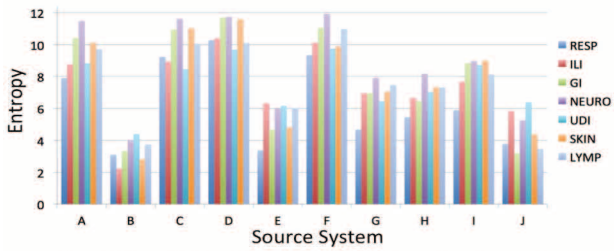


Figure 2: Entropy (bits) for chief complaints classified into specific syndrome categories stratified by source system for 10 high-volume emergency departments.

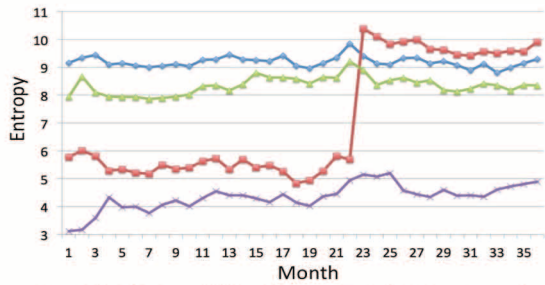


Figure 3: Monthly entropy (bits) for chief complaints classified into specific syndrome categories, stratified by source system for 5 high-volume emergency departments. Note the shift in values for one source that changed registration software.

Keywords

analytics; data quality; surveillance; system monitoring; information theory

Acknowledgments

This work was performed at the Regenstrief Institute in Indianapolis, Indiana. This study is supported in part by the CDC through the Indiana Center of Excellence in Public Health Informatics (1P01HK000077-01).

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

References

1. Finnell JT, Overhage JM, Grannis S. All health care is not local: an evaluation of the distribution of Emergency Department care delivered in Indiana. AMIA Annu Symp Proc. 2011; 409-16.
2. Shannon, Claude E. (July/October 1948). "A Mathematical Theory of Communication". Bell System Technical Journal 27 (3): 379–423.

*Shaun Grannis
E-mail: sgrannis@regenstrief.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

The Epidemiologic Vocabulary of the West and the Former Soviet Union: Different Sides of the Same Science

Anna Grigoryan*[1], Carmen Clarke[2], Lyudmila Zueva[3], Tetyana Chumachenko[4], Edmond F. Maes[1] and Bonnie Smoak[2]

[1]CDC, Atlanta, GA, USA; [2]WRAIR, Silver Spring, MD, USA; [3]North-Western State Medical University after I.I. Mechnikov, St.Petersburg, Russian Federation; [4]Kharkiv National Medical University, Kharkiv, Ukraine

Objective

The purpose of this project was to develop an English-Russian Epidemiology Dictionary, which is needed for improved international collaboration in public health surveillance.

Introduction

As part of the US Department of Defense strategy to counter biological threats, the Defense Threat Reduction Agency's Cooperative Biological Engagement Program is enhancing the capabilities of countries in the former Soviet Union (FSU) to detect, diagnose, and report endemic and epidemic, man-made or natural cases of especially dangerous pathogens. During these engagements, it was noted that Western-trained and Soviet-trained epidemiologists have difficulty, beyond that of simple translation, in exchanging ideas.

The Soviet public health system and epidemiology developed independently of that of other nations. Whereas epidemiology in the West is thought of in terms of disease determinants in populations and relies on statistics to make inferences, classical Soviet epidemiology is founded on a more ecological view with the main focus on infectious diseases' spread theory. Consequently many fundamental Soviet terms and concepts lack simple correlates in English and other languages outside the Soviet sphere; the same is true when attempting to translate from English to Russian and other languages of the FSU. Systematic review of the differences in FSU and Western epidemiologic concepts and terminology is therefore needed for strengthening understanding and collaboration in disease surveillance, pandemic preparedness, response to biological terrorism, etc.

Methods

Following an extensive search of the Russian and English literature by a working group of Western and FSU epidemiologists, we created a matrix containing English and Russian definitions of key epidemiologic terms found in FSU and Western epidemiology manuals and dictionaries, such as A Dictionary of Epidemiology (1), Epidemiology Manual (2) and many other sources. Particular emphasis was placed on terms relating to infectious disease surveillance, analysis of surveillance data, and outbreak investigation. In order to compare the definitions of each term and to elucidate differences in usage and existing gaps, all definitions were translated into English and Russian so that the definitions could be compared side by side and discussed by the working group.

Results

Six hundred and thirty one terms from 27 English and 51 Russian sources were chosen for inclusion based on their importance in applied epidemiology in either the West or the FSU. Review of the definitions showed that many terms within biosurveillance and infectious disease public health practice are used differently, and some concepts are lacking altogether in the Russian or English literature. Significant gaps in FSU epidemiology are in the areas of biostatistics and epidemiologic study designs. There are distinctive differences in FSU and Western epidemiology in the conceptualization and classification of disease transmission, surveillance practices, and control measures.

Conclusions

Epidemiologic concepts and definitions significantly differed in the FSU and Western literature. To improve biosurveillance and international collaboration, recognition of these differences must occur. Detailed analysis of epidemiology terminology differences will be discussed in the presentation and paper. Major limitations of the work were scarcity of prior research on the subject and lack of bilingual epidemiologists with the good understanding of FSU and Western approaches. A bilingual reference in the form of a dictionary will greatly improve mutual comprehension and collaboration in the areas of biosurveillance and public health practice.

Keywords

Surveillance; Dictionary; Collaboration

References

1. Porta Miquel. A Dictionary of Epidemiology, Fifth Edition, Oxford university press, USA, 2008
2. Zueva L.P.Yafaev P.Kh. Epidemiology: Manual. "Foliant publishers", Russia, 2005.

*Anna Grigoryan
E-mail: Ffg7@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Co-morbidity Factors Associated with Influenza in Nigeria

Aishatu B. Gubio*[1], Saka J. Muhammad[2], Aisha Mamman[3], Ado Zakari[4] and Oladayo Biya[1]

[1]Nigeria Field Epidemiology and Laboratory Training Program (NFELTP), Federal Capital Territory, Nigeria; [2]Department of Epidemiology and community Health University of Ilorin, Faculty of Clinical Science, College of Medicine, Ibadan, Nigeria; [3]Ahmadu Bello University Zaria, Zaria shika, Nigeria; [4]Kaduna State Ministry of Health Kaduna, Kaduna, Nigeria

Objective

To analyze Influenza surveillance data from 2009 to 2010 the Northern, Southern, and Western zones in Nigeria and determined co-morbidity factors associated with influenza in Nigeria.

Introduction

Influenza is viral illness that affects mainly the nose, throat, bronchi and occasionally, the lungs. Influenza viruses have been an under-appreciated contributor to morbidity and mortality in Nigeria. They are a substantial contributor to respiratory disease burden in Nigeria and other developing countries. Nigeria started influenza sentinel surveillance in 2008 to inform disease control and prevention efforts.

Methods

We conducted a cross sectional study on secondary data analysis of Influenza surveillance data from January 2009 to December 2010 obtained from Nigeria's Federal Ministry of Health. Epidemiological data were obtained for suspected ILI and SARI cases defined in accordance with WHO Regional Office for Africa's guidelines. Laboratory confirmation for presence of influenza viruses was done using real time PCR assays.

Standardized case investigation forms used for sample collection were analyzed using Epi-Info software to generate frequency and proportions.

Results

Of the 5,860 suspected influenza cases reported between 2007 and 2011 from all the influenza sites in Nigeria, 1104 (18.8%) and 2,510 (42.8%) of the total cases were recorded in 2009 and 2010 respectively. A total of 296 (7.3%) were positive for Flu A, while 147 (2.9%) for Flu B. The Northern zone recorded a total of 1908(AR: 2.6/100,000) suspected cases while the Southern zone recorded 554(AR: 1.48/100,000) and the Western zone reported 549(2/100,000) suspected cases. Of the 443 that were positive 43 (1.5%) were health workers, 446 (8.0%) had co infection of chronic respiratory tract disease, 50(3.7%) had co infection with heart disease. Exposure to poultry was 2797(98.2%).

Conclusions

Co-morbidity factors associated with influenza viruses are an important contribution to the burden of respiratory illnesses in Nigeria predominantly affecting children less than 5years and adults 25years and above. Additional years of data are needed to better understand the co-morbidity factors associated epidemiology of influenza viruses in Nigeria.

INFLUENZA AND CHRONIC OBSTRUCTIVE PULMONARY DISEASE (COPD)

INFLUENZA AND CHRONIC OBSTRUCTIVE PULMONARY DISEASE (COPD)	Influenza with COPD N (%)	Influenza only N(%)	Total
A/H1	0 (0.0)	12 (100.0)	12 (100.0)
A/H3	10(11.2)	79 (88.8)	89 (100.0)
All Negative	551 (11.1)	4392 (88.9)	4943 (100.0)
pdmA/H1N1	14 (9.3)	137 (90.7)	151 (100.0)
pdmA/H1N1	10(5.6)	170 (99.4)	180 (100.0)
Total	585(10.9)	4790(89.1)	5375(100.0)

Only 585 (10.9%) had chest indrawing, with majority of the influenza subtype pdm A/H1N1 cases 14 (9.3%) had chest indrawing.

INFLUENZA AND CHRONIC CHEST DISEASE

Influenza Sub-type	Influenza with Chronic Shortness of Breath N (%)	Influenza cases without Chronic Shortness of Breath N(%)	Total
A/H1	0 (0.0)	16 (100.0)	16 (100.0)
A/H3	1(0.9)	115 (99.1)	116 (100.0)
All Negative	56 (1.1)	5204 (98.9)	5204 (100.0)
pdm A/H1N1	0 (1.3)	152 (98.7)	152 (100.0)
Un-subtype-able	0 (0.0)	181 (100.0)	181 (100.0)
Total	57(1.0)	5668(99.0)	5725(100.0)

Less than 5% of the respondents with influenza cases had chronic shortness of breath

Keywords

Surveillance; Influenza; Nigeria; Co-morbidity

Acknowledgments

We would like to acknowledge and express our sincere gratitude to the personnel of the National Influenza Reference Laboratory, and the sentinel surveillance sites for assisting us technically during this write up. We would also like to thank the Federal Ministry of Health specifically epidemiology division for all the support to the sentinel surveillance site.

References

Oshin O. Enzyme immunoassay of antibodies to influenza A virus in Nigerian children. Trop Geogr Med. 1979;31:509-17

Njoku-Obi AN OO. Viral respiratory diseases in Nigeria: a serological survey. II Complement fixing antibody levels of influenza A, B and C and para-influenza 1. J Trop Med Hyg 1966;69:147-9

McCoy L et al. A multiple cause-of-death analysis of asthma mortality in the United States, 1990-2001.Journal of Asthma, 2005, 42:757–763.

Olaleye OD, Omilabu SA, Olabode AO and Fagbami AH. Serological evidence for influenza virus activity in Nigeria (1985-1987). Virologie 1989;40:11-7

Adams A et al. The influence of patient and doctor gender on diagnosing coronary heart disease.Sociology of Health and Illness, 2008, 30:1–18.

*Aishatu B. Gubio
E-mail: yabintu@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Extracting Surveillance Data from Templated Sections of an Electronic Medical Note: Challenges and Opportunities

Adi Gundlapalli*[1, 2], Guy Divita[1, 2], Marjorie Carter[1, 2], Shuying Shen[1, 2], Miland Palmer[1], Tyler Forbush[1, 2], Brett South[1, 2], Andrew Redd[1, 2], Brian Sauer[1, 2] and Matthew Samore[1, 2]

[1]VA Salt Lake City Health Care System, Salt Lake City, UT, USA; [2]Internal Medicine, University of Utah School of Medicine, Salt Lake City, UT, USA

Objective

To highlight the importance of templates in extracting surveillance data from the free text of electronic medical records using natural language processing (NLP) techniques.

Introduction

The main stay of recording patient data is the free text of electronic medical records (EMR). While stating the chief complaint and history of presenting illness in the patients 'own words', the rest of the electronic note is written by the provider in their words. Providers often use boiler-plate templates from EMR pull-downs to document information on the patient in the form of checklists, check boxes, yes/no and free text responses to questions. When these templates are used for recording symptoms, demographic information or medical, social or travel history, they represent an important source of surveillance data [1]. There is a dearth of literature on the use of natural language processing in extracting data from templates in the EMR.

Methods

A corpus of 1000 free text medical notes from the VA integrated electronic medical record (CPRS) was reviewed to identify commonly used templates. Of these, 500 were enriched for the surveillance domain of interest for this project (homelessness). The other 500 were randomly sampled from a large corpus of electronic notes. An NLP algorithm was developed to extract concepts related to our target surveillance domain. A manual review of the notes was performed by three human reviewers to generate a document-level reference standard that classified this set of documents as either demonstrating evidence of homelessness (H) or not (NH). A rule-based NLP algorithm was developed that used a combination of key word searches and negation based on an extensive lexicon of terms developed for this purpose. A random sample of 50 documents each of H and NH documents were reviewed after each iteration of the NLP algorithm to determine the false positive rate of the extracted concepts.

Results

The corpus consisted of 48% H and 52% NH documents as determined by human review. The NLP algorithm successfully extracted concepts from these documents. The H set had an average of 8 concepts related to homelessness per document (median 8, range 1 to 34). The NH set had an average 2 concepts (median 1, range 1 to 13)". Thirteen template patterns were identified in this set of documents. The three most common were check boxes with square brackets, Yes/No and free text answer after a question. Several positively and negatively asserted concepts were noted to be in the responses to templated questions such as "Are you currently homeless: Yes or No"; "How many times have you been homeless in the past 3 years: (free text response)"; "Have you ever been in jail? [Y] or [N]"; Are you in need of substance abuse services? Yes or No". Human review of a random sample of documents at the concept level indicated that the NLP algorithm generated 28% false positives in extracting concepts related to homelessness when templates were ignored among the H documents. When the algorithm was refined to include templates, the false positive rate declined to 22%. For the NH documents, the corresponding false positive rates were 56% and 21%.

Conclusions

To our knowledge, this is one of the first attempts to address the problem of information extraction from templates or templated sections of the EMR. A key challenge of templates is that they will most likely lead to poor performance of NLP algorithms and cause bottlenecks in processing if they are not considered. Acknowledging the presence of templates and refining NLP algorithms to handle them improves information extraction from free text medical notes, thus creating an opportunity for improved surveillance using the EMR. Algorithms will likely need to be customized to the electronic medical record and the surveillance domain of interest. A more detailed analysis of the templated sections is underway.

Keywords

natural language processing; surveillance; templates; VA

Acknowledgments

Funding from the US Department of Veterans Affairs (HSR&D); resources from Veterans Informatics Computing Infrastructure and VA Salt Lake City Health Care System and all our research team members who have worked on this project.

References

1. DeLisle, S., et al., Combining free text and structured electronic medical record entries to detect acute respiratory infections. PloS one, 2010. 5(10): p. e13377.

*Adi Gundlapalli
E-mail: adi.gundlapalli@hsc.utah.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Paralysis Analysis: Investigating Paralysis Visit Anomalies in New Jersey

Teresa Hamby*[1], Stella Tsai[1], Carol Genese[1], Andrew Walsh[2], Lauren Bradford[2] and Edward Lifshitz[1]

[1]NJ Department of Health, Trenton, NJ, USA; [2]Health Monitoring Systems, Inc, Pittsburgh, PA, USA

Objective

To describe the investigation of a statewide anomaly detected by a newly established state syndromic surveillance system and usage of that system.

Introduction

On July 11, 2012, New Jersey Department of Health (DOH) Communicable Disease Service (CDS) surveillance staff received email notification of a statewide anomaly in EpiCenter for Paralysis. Two additional anomalies followed within three hours. Since Paralysis Anomalies are uncommon, staff initiated an investigation to determine if there was an outbreak or other event of concern taking place. Also at question was whether receipt of multiple anomalies in such a short time span was statistically or epidemiologically significant.

Methods

In New Jersey, 68 of 81 total acute care and satellite Emergency Departments (EDs) are connected to EpiCenter, an online syndromic surveillance system developed by Health Monitoring Systems, Inc (HMS) that incorporates statistical management and analytical techniques to process health-related data in real time. Chief complaint text is classified, using text recognition methods, into various public health-related and other categories. Anomalies occur when any of several statistical methods detect increases in incoming data that are outside of established thresholds.

After receiving three anomaly notifications related to Paralysis in a 4-hour time period, NJDOH surveillance data staff enlisted CDS and local epidemiologist colleagues to review the data and determine if there was an infectious cause.

Results

The first EpiCenter anomaly notification was received on July 11, 2012 at 1:22 pm as a result of increased ED visits classified as Paralysis based on facility location for the period beginning at noon on July 10, 2012. Using Cusum EMA analysis, 76 reported interactions exceeded the predicted value of 50.49 and the threshold of 70.72. The second anomaly, also based on facility location, was received at 3:20 pm and the third anomaly notification, based on home location, was received at 4:32 pm. Cusum EMA and Exponential Moving Average analysis methods detected these anomalies. Table 1 describes the anomalies in more detail.

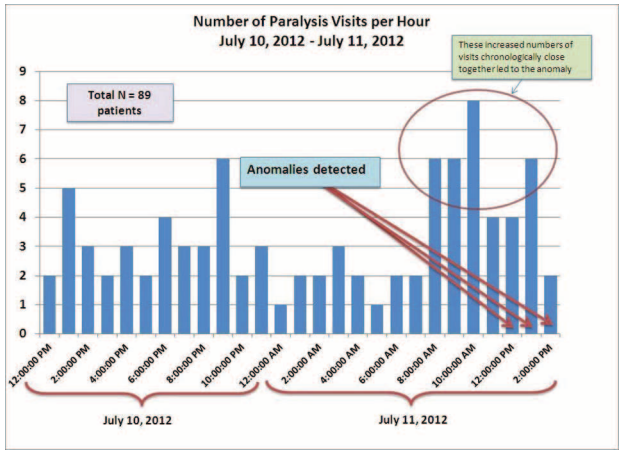
Compiled data from all anomalies were reviewed by CDS epidemiology and surveillance staff to determine whether there was a public health event taking place. A total of 89 patients were seen in 39 (57%) of the 68 NJ facilities reporting to EpiCenter with no geographic centralization. Age and gender of patients were reviewed with no clear pattern discerned. Figure 1 shows the time distribution of these visits. Upon further investigation, it was determined that a moderate increase in Paralysis visits over a relatively short time span was sufficient to create an anomaly under the default threshold for those visits. Multiple analysis methods created multiple anomalies which gave an impression the event was of greater significance compared to a single anomaly. To follow up, NJDOH requested that local epidemiologists investigate within their jurisdictions by contacting hospitals directly where EpiCenter data proved inconclusive. Their reports confirmed NJDOH's findings that the anomalies did not signal an event of public health concern.

Conclusions

This investigation of three Paralysis anomalies is an important introduction to the newly implemented system's capabilities in anomaly detection, and also to anomaly investigation procedures developed by NJDOH for local surveillance staff. As a result of this experience, these anomaly investigation procedures are being fine-tuned. The fact that these sequential anomalies resulted in an investigation being undertaken highlights the importance in setting investigation- generating alert thresholds within EpiCenter at a level that will minimize "false" positives without risking the missing of "true" positives.

TABLE 1: Anomaly Details

Anomaly Date/Time	24 hour end time	Location	Analysis Method	# Interactions	Expected Value/Threshold of Alert
7/11/2012, 1:22 PM	12:00 PM	By Facility	Cusum EMA	76	50.49 / 70.72
7/11/2012, 3:20 PM	2:00 PM	By Facility	Exponential Moving Average	80	50.47 / 79.64
7/11/2012, 4:32 PM	3:00 PM	By Home	Cusum EMA	70	44.94 / 66.32



Keywords

Syndromic; Surveillance; Investigation

Acknowledgments

NJ LINCS Epidemiologists, NJ DOH Epideimologists, NJ DOH Surveillance Staff

*Teresa Hamby
E-mail: Teresa.Hamby@doh.state.nj.us

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Implications of ICD-9/10 CM Transition for Public Health Surveillance: Challenges, Opportunities, and Lessons Learned from Multiple Sectors of Public Health

Peter Hicks*[1] and Atar Baer[2]

[1]CDC, Atlanta, GA, USA; [2]Public Health Seattle And King County, Seattle, WA, USA

Objective

To provide a forum for local, state, federal, and international public health/ health care sectors to share promising practices and lessons learned in transitioning their organizations in the use of ICD-9 to ICD-10 codes for their respective surveillance activities.

Introduction

This roundtable will provide forum for a diverse set of representatives from the local, state, federal and international public health care sectors to share tools, resources, experiences, and promising practices regarding the potential impact of the transition on their surveillance activities. This forum will promote the sharing of lessons learned, foster collaborations, and facilitate the reuse of existing resources without having to "reinvent the wheel". It is hope that this roundtable will lay the ground-work for a more formal, collaborative, and sustainable venue within ISDS to aid in preparing the public health surveillance community for the coming ICD-9/10 CM transition.

Methods

The moderators will engage the participants in the discussion through dialogue in how their programs are currently using ICD-9 CM codes for surveillance and how the transition will impact their respective programs.

Keywords

ICD-9; ICD-10; Transition

*Peter Hicks
E-mail: phicks@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Processing of Novel Electronic Health Data to Support Public Health Surveillance

Peter Hicks*, Henry Rolka, Mark Wooster and Lynette Brammer

CDC, Atlanta, GA, USA

Objective

To describe data management and analytic processes undertaken to rapidly acquire and use previously unavailable data during a public health emergency response.

Introduction

Accurately gauging the health status of a population during an event of public health significance (e.g. hurricanes, H1N1 2009 pandemic) in support of emergency response and situation awareness efforts can be a challenge for established public health surveillance systems in terms of geographic and population coverage as well as the appropriateness of health indicators. The demand for timely, accurate, and event-specific data can require the rapid development of new data assets to "fill-in" existing information gaps to better characterize the scope, scale, magnitude, and population health impact of a given event within a very narrow time-window. Such new data assets may be concurrently under development and evaluation while being used to support response efforts. Recent examples include the "drop-in" surveillance processes deployed at evacuation centers following Hurricane Katrina1 and the illness and injury surveillance systems established for response workers during the Deepwater Horizon Oil spill response. During the 2009 H1N1 pandemic response, CDC acquired access to data from several national-level health information systems that previously had been un-vetted as public health information sources. These sources provided data extracts from massive administrative or electronic medical records (EMR) based in hospital and primary care settings. It was hoped that such data could supplement existing influenza surveillance systems and aid in the characterization of the pandemic. Few of these new data sources had formal documentation or concise information on the underlying populations and geographies represented.

Methods

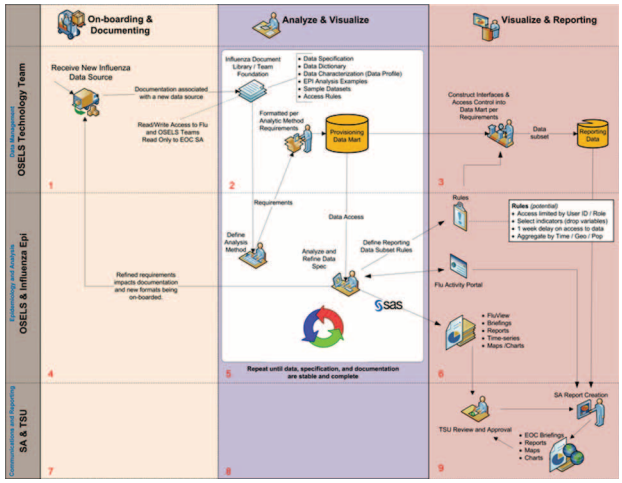
Throughout CDC's H1N1 response; epidemiologists, data managers, and IT specialists collaborated to develop standardized methods to rapidly characterize, process, store, and provision these new data for analysis and reporting by subject matter experts.These new data were not part of a formally designed sample so each data source needed to undergo extensive empirical review to understand, representativeness, unique nuances, and facilitate the interpretation of analytic results and accurate reporting to public health decision makers.

Results

Such work requires a multi-disciplinary approach that cyclically reviews incoming data iteratively while concurrently documenting findings, modifying initial business rules (e.g. extraction, binning, or coding logic), and analytic techniques to produce the most interpretable and informative results. To elucidate the underlying complexity for these sequential and contingent activities occurring across information technology, informatics, and epidemiology domains, we retrospectively described the intersection of the discrete tangible tasks and workforce roles via a TaskFlow diagram (Figure 1). Vertical "swim lanes" represent discrete tasks: On-boarding/Documentation, Analysis/Visualization, and Visualization/Reporting. Workforce roles such as Data management, Epidemiological Analysis, and Communications are broken into three horizontal "swim lanes" as each requires dramatically different skillsets and are accomplished by different individuals. Each of the steps (1-9) in the diagram were leveraged to produce supplemental artifacts (e.g. code books, extraction guides, defined analytic methods, etc.) to support ongoing analysis, interpretation, reporting, and over process improvement. The totality of all of these interrelated activities have an a priori purpose of characterizing population health during an event of public health significance to support disease prevention and control efforts in a timely fashion.

Conclusions

This presentation describes the underlying business processes, activities, and roles used in transforming novel data sources, during the H1N1 response, into informative assets to support public health surveillance. By formally articulating and describing each of these steps, in a structured manner, we hope to contribute to the dialogue of developing useful practices for leveraging electronic health data to meet public health surveillance challenges.



Keywords

informatics; surveillance; emergency response; h1n1; data management

*Peter Hicks
E-mail: phicks@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Disease Surveillance and Achieving Synergy In Public Health Quality Improvement

Peggy A. Honoré*[1] and Laura C. Streichert[2]

[1]U.S. Department of Health and Human Services, Washington, DC, USA; [2]International Society for Disease Surveillance, Brighton, MA, USA

Objective

To examine disease surveillance in the context of a new national framework for public health quality and to solicit input from practitioners, researchers, and other stakeholders to identify potential metrics, pivotal research questions, and actions for achieving synergy between surveillance practice and public health quality.

Introduction

National efforts to improve quality in public health are closely tied to advancing capabilities in disease surveillance. Measures of public health quality provide data to demonstrate how public health programs, services, policies, and research achieve desired health outcomes and impact population health. They also reveal opportunities for innovations and improvements. Similar quality improvement efforts in the health care system are beginning to bear fruit. There has been a need, however, for a framework for assessing public health quality that provides a standard, yet is flexible and relevant to agencies at all levels.

The U.S. Health and Human Services (HHS) Office of the Assistant Secretary for Health, working with stakeholders, recently developed and released a Consensus Statement on Quality in the Public Health System that introduces a novel evaluation framework. They identified nine aims that are fundamental to public health quality improvement efforts and six cross-cutting priority areas for improvement, including population health metrics and information technology; workforce development; and evidence-based practices (1).

Applying the HHS framework to surveillance expands measures for surveillance quality beyond typical variables (e.g., data quality and analytic capabilities) to desired characteristics of a quality public health system. The question becomes: How can disease surveillance help public health services to be more population centered, equitable, proactive, health-promoting, risk-reducing, vigilant, transparent, effective, and efficient—the desired features of a quality public health system?

Any agency with a public health mission, or even a partial public health mission (e.g., tax-exempt hospitals), can use these measures to develop strategies that improve both the quality of the surveillance enterprise and public health systems, overall. At this time, input from stakeholders is needed to identify valid and feasible ways to measure how surveillance systems and practices advance public health quality. What exists now and where are the gaps?

Methods

Improving public health by applying quality measures to disease surveillance will require innovation and collaboration among stakeholders. This roundtable will begin a community dialogue to spark this process. The first goal will be to achieve a common focus by defining the nine quality aims identified in the HHS Consensus Statement. Attendees will draw from their experience to discuss how surveillance practice advances the public health aims and improves public health. We will also identify key research questions needed to provide evidence to inform decision-making.

Results

The roundtable will discuss how the current state of surveillance practice addresses each of the aims described in the Consensus Statement to create a snapshot of how surveillance contributes to public health quality and begin to articulate practical measures for assessing quality improvements. Sample questions to catalyze discussion include:

—How is surveillance used to identify and address health disparities and, thereby, make public health more equitable? What are the data sources? Are there targets? How can research and evaluation help to enhance this surveillance capability and direct action?

—How do we identify and address factors that inhibit quality improvement in surveillance? What are the gaps in knowledge, skills, systems, and resources?

—Where can standardization play a positive role in the evaluation of quality in public health surveillance?

—How can we leverage resources by aligning national, state, and local goals?

—What are the key research questions and the quality improvement projects that can be implemented using recognized models for improvement?

—How can syndromic surveillance, specifically, advance the priority aims?

The roundtable will conclude with a list of next steps to develop metrics that resonate with the business practices of public health at all levels.

Keywords

public health quality; metrics; framework

References

1. Honoré PA, Wright D, Berwick DM, Clancy CM, Lee P, Nowinski J, Koh HK. Creating a framework for getting quality into the public health system. Health Aff (Millwood). 2011 Apr;30(4):737-45.

*Peggy A. Honoré
E-mail: Peggy.Honore@hhs.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Serum Zinc Concentration and Acute Diarrhea in Children from Different Regions of Uzbekistan

Gulnara A. Ibadova*, T. A. Merkushina, E. S. Abdumutalova and Aybek V. Khodiev

Infectious and Parasitic Diseases of Children, Tashkent Institute of Postgraduate Medical Education, Tashkent City, Uzbekistan

Objective

To study the blood serum zinc concentration in children with acute diarrhea (AD) in in-patient facilities before and after therapy.

Introduction

There are several reports of zinc deficiency in pathogenesis of acute and chronic diarrhea. The literature review showed children with diarrhea and chronic gastroduodenitis performed zinc deficiency in majority of cases (1). The normal values of zinc in blood serum are 12.8-27.8 μmol/l (2). There is a threshold of 13μmol/l zinc concentration for zinc deficiency diagnosis. The zinc level 8.2 μmol/l and below is poor prognostic criteria (3).

Methods

Totally 102 children (1-14 years old) with AD in in-patient facility from different regions were studied for serum zinc concentration before and after treatment. Termez and Saraosie cities are located in south of Uzbekistan, in the region with high negative impact from the nearly Tajikistan located aluminum producing plant. The serum zinc level measured by neutron-activation method in the Institute of Nuclear Research (INR).

Results

The zinc concentration in serum significantly varied by the region (Table 1).

The level of zinc in children from Tashkent estimated at lower normal limit with reduction below normal values after treatment. Children from Termez during admission to the in-patient facilities were zinc deficient with further reduction to the poor prognostic level. Children in Saraosie admitted to the in-patient with significant zinc deficiency that remained on poor prognostic level after treatment.

Conclusions

The study results may indicate the treatment of AD in children do not replenish the zinc to the appropriate level. Though some confounding factors may contribute the observed zinc disorders the results may indicate environmental factors, such as pollution by aluminum producing plant emission to contribute the difference in zinc concentration and should be considered for the correction and treatment of AD in children.

Table 1.The serum zinc concentration in children with acute diarrhea from different regions of Uzbekistan before and after treatment.

City	n	Zinc concentration, μmol/l (mean ± SD)	
		Before treatment	After treatment
Tashkent city (capital)	36	13.8±1.5	12.5±1.3
Termez city	40	9.1±0.08	7.47±0.01
Saraosie city	26	7.9±0.3	7.5±0.8

Keywords

Acute diarrhea; zinc; zinc deficiency

Acknowledgments

Authors express their gratitude to the staff of Institute of Nuclear Research.

References

1. Brooks WA, Santosham M, Roy SK, Faruque ASG, Wahed MA, Nahar K, Khan AI, Khan a F, Fuchs GJ, Black RE. Efficacy of zinc in young infants with acute watery diarrhea. [Internet]. The American journal of clinical nutrition 2005 Sep;82(3):605–10.Available from: http://www.ncbi.nlm.nih.gov/pubmed/16155274
2. Ackland ML, Michalczyk A. Zinc deficiency and its inherited disorders -a review. [Internet]. Genes & nutrition 2006 Mar;1(1):41–9.Available from: http://www.ncbi.nlm.nih.gov/pubmed/18850219
3. Karlinskiy VM. Zinc deficiency syndrome. Nutrition issues 1980;1:10–18.

*Gulnara A. Ibadova
E-mail: prof.Ibadova@mail.ru

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Binational Influenza Surveillance Network – California/Baja California

Esmeralda Iniguez-Stevens*, Sarah Marikos and Karen Ferran

EWIDS, California Department of Public Health, San Diego, CA, USA

Objective

To enhance cross-border surveillance for Influenza-Like-Illness (ILI) in the California/Baja California (CA/BC) border region through the formation of a border binational surveillance network.

Introduction

In response to the 2009 H1N1 pandemic, the Early Warning Infectious Disease Surveillance Program (EWIDS) Office of Binational Border Health in the California Department of Public Health sought to strengthen outpatient ILI surveillance along the CA/BC border by creating the first binational influenza surveillance network in the region. The establishment of this network was crucial for enhancing cross-border situational awareness of influenza activity, especially in a region characterized by high levels of population mobility.

Methods

During summer of 2009, an assessment of current ILI surveillance activities in the CA/BC border region was conducted. Findings were utilized to guide recruitment efforts and build a cross-border surveillance network. In CA the assessment revealed that sentinel sites in the border region participating in CDC's ILINet surveillance program were primarily pediatric or school-based clinics and that family practice patients were not equally represented. In BC the need to enhance surveillance among the private sector was identified, particularly among patients belonging to binational healthcare service plans. These plans offer care to US workforce individuals who seek medical care in BC. Other needs identified included the need to enhance surveillance among underserved populations such as farm workers and tribal communities which were not currently being represented. Working together with partners from both sides of the border EWIDS initiated efforts to address identified gaps. Over a three-year period EWIDS recruited private and public sector clinics to participate in the network.

Results

As a result of the assessment recruitment efforts were focused on inviting family practice clinics, private clinics, tribal health centers and clinics that provide care to underserved populations to participate in the network. These efforts led to the establishment of the California/Baja California Border Outpatient Provider ILI Surveillance Network, which monitors syndromic and virologic influenza activity. In total EWIDS recruited 22 (13 in CA, 9 in BC) sentinel sites to participate; of these, 17 are family practice sites and 5 are pediatric sites. Additionally, prior to the EWIDS enhancement local tribal health clinics were not represented in the surveillance system. EWIDS efforts resulted in the inclusion of 8 tribal sites in CA and 1 in BC. Figure 1 shows the geographical location of network sites, which includes sites recruited by EWIDS post-assessment as well as pre-existing sites. Over the past three influenza seasons (2009-2012) EWIDS recruited sites have constituted 47% of all network sites. Since the 2009-2010 influenza season 483,772 individuals have been screened for ILI by participating sites; of these, 65.8% (n=318,295) were screened by EWIDS recruited sites. Since the establishment of the network EWIDS has focused on sentinel site retention, logistical support, data collection, and dissemination of surveillance results. A weekly report summarizing syndromic and virologic activity is distributed to public health officials throughout the influenza season.

Conclusions

The network serves as an example of a successful binational coordinated effort to establish an early warning system for enhancing situational awareness of influenza activity in a cross-border setting. Next steps include conducting a formal evaluation of the existing surveillance system, enhancing specimen collection for virologic testing, and continuing to foster and build public/private partnerships.

Figure 1. Surveillance Network

Keywords

influenza; surveillance; syndromic; virologic; binational

Acknowledgments

We gratefully acknowledge all our border partners for their contributions and support including: Border Infectious Disease Surveillance Program, Imperial County Public Health Department, County of San Diego Public Health Services Epidemiology & Immunization Services Branch, Naval Health Research Center Laboratory, California Department of Public Health Center for Infectious Diseases, Laboratorio Estatal de Salud Publica de Baja California, Departamento de Epidemiologia Estatal Baja California, and our medical partners.

*Esmeralda Iniguez-Stevens
E-mail: einiguez@cdph.ca.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

The Activity of Rabies Vaccines against Genetic Clusters of Rabies Virus Circulating at the Territory of Ukraine

Mykola Ivanov*, Ivan Polupan and Oleg Deryabin

Institute of Veterinary Medcine, Kyiv, Ukraine

Objective

To identify the presence of genetic clusters of rabies virus at the territory of Ukraine and to determine the degree of activity of rabies vaccines against these genetic clusters.

Introduction

To develop and implement an effective program of rabies eradication in Ukraine in 2008 was founded the unique collection of samples of pathological materials confirmed as positive in rabies at the regional veterinary laboratories of Ukraine. The collection is constantly updated and to present moment it includes 1389 samples from all regions of Ukraine, selected from 17 animal species and humans.

Methods

Identification of the rabies virus in samples of pathological material for their further selection was carried out using the test developed by us which based on RT-PCR with primers complementary to the conservative fragments of the 5'-end of nucleoprotein gene of rabies virus.

For the study of the street rabies virus isolates from the collection we use RT-PCR with the primers pair (509, 304) flanking the variable 3'-end part of nucleoprotein gene of the reference strain of rabies virus CVS (fragment in 377 bp).

Studies of rabies vaccines activity were carried out with modified method of U.S. National Institutes of Health using rabies virus street isolates of both genetic clusters instead of the Challenge Virus Standard (CVS). All isolates of street rabies virus were inoculated in a dose of 5–50 LD_{50}. The criteria for evaluation of protective activity of rabies vaccine was effective dose (- lg ED_{50}).

Results

In molecular genetic studies with variant-specific primers we established the presence in Ukraine of two clusters of rabies virus. Clusters I circulates on the right bank of the Dnipro river (the largest water barrier that divides the country into eastern and western side), and cluster II – on the left bank of the Dnieper.

The relationship of these variants with the epizootic situation was researched. For this purpose epizootological zoning of Ukraine according to the intensity of the epizootic situation in 2005-2009 was carried out. As a result of this analysis all the regions of Ukraine belong to three categories: high, medium and low epizootic situation intensity of rabies.

The projection of differentiated genetic clusters on the epizootic situation showed that cluster II circulating at Left Bank of the Dnieper in areas with high and medium intensity of the epizootic situation, and the cluster I – at the Right Bank of the Dnieper, mainly in the areas with low intensity of the epizootic situation.

That's why our interest was in the degree of protection of rabies vaccines against street rabies virus isolates belonging to these two genetic clusters.

The commercial vaccines made with rabies virus vaccine strains SAD (Street-Alabama-Dufferin) and Wistar PM/WI were chosen to evaluate this parameter.

After the mathematical calculations of effective dose and the analysis of the data the less effective protection of rabies vaccines (at 29–30 %) against street rabies virus isolates belonging to cluster II in comparison with isolates belonging to cluster I irrespective to the strain vaccine is made was shown.

Conclusions

The data will be used for the effective planning of specific prophylaxis of rabies in Ukraine based on differentiated approach to distribution of rabies vaccines in according to region and their activity.

Keywords

rabies vaccine; vaccine activity; street rabies virus isolates; genetic variants of rabies virus

*Mykola Ivanov
E-mail: IvanovNY@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Determinants of Outbreak Detection Performance

Nastaran Jafarpour*[1], Doina Precup[2] and David Buckeridge[2]

[1]Department of Computer Engineering, Ecole Polytechnique de Montreal, Montreal, QC, Canada; [2]McGill University, Montreal, QC, Canada

Objective

To predict the performance of outbreak detection algorithms under different circumstances which will guide the method selection and algorithm configuration in surveillance systems, to characterize the dependence of the performance of detection algorithms on the type and severity of outbreak, to develop quantitative evidence about determinants of detection performance.

Introduction

The choice of outbreak detection algorithm and its configuration can result in important variations in the performance of public health surveillance systems. Our work aims to characterize the performance of detectors based on outbreak types. We are using Bayesian networks (BN) to model the relationships between determinants of outbreak detection and the detection performance based on a significant study on simulated data.

Methods

The simulated surveillance data that we used was generated by Surveillance Lab of McGill University using Simulation Analysis Platform [1] considering surveillance in an urban area to detect waterborne outbreaks due to the failure of a water treatment plant. We focus on predicting the performance of the C-family of algorithms, because they are widely used, state-of-art outbreak detection algorithms [2]. We investigate the influence of algorithm characteristics and outbreak characteristics in determining outbreak detection performance. The C1, C2, and C3 are distinguished by the configuration of 2 parameters,the guardband and memory. Generally, gradually increasing outbreaks can bias the test statistic upward, so the detection algorithm will fail to flag the outbreak. To avoid this situation, the C2 and C3 use a 2-day gap, guardband, between the baseline interval and the test interval. The C3 includes 2 recent observations, called memory, in the computation of the test statistic. The W2 algorithm is a modified version of the C2 which takes weekly patterns of surveillance time series into account [3]. In the W2, the baseline data is stratified to 2 distinct baselines: one for weekdays, the other for weekends. The W3 includes 2 recent observations of each baseline while calculating the test statistic in the corresponding baseline.

We ran the C1, C2, C3, W2, and W3 on 18k simulated time series and measured the sensitivity and specificity of detection. Then we created the training data set of 5400000 instances. Each instance was the result of performance evaluation of an outbreak detection algorithm with a specific setting of parameters. In order to investigate the determinants of detection performance and reveal their effects quantitatively, we used BN to predict the performance based on algorithm characteristics and outbreak characteristics.

Results

We developed 2 BN models in the Weka machine learning software [4] using 5-fold cross-validation. The first BN determines the effect of the guardband, memory, alerting threshold, and the weekly pattern indicator (0 for C-algorithms, 1 for W-algorithms) and outbreak characteristics (contamination level and duration) on the sensitivity of detection. The value of sensitivity was mapped to 4 classes: (0, 0.3], (0.3, 0.6], (0.6, 0.9], (0.9, 1]. The developed BN correctly classified 67.74% of instances. The misclassification error was 0.9407. The second BN for predicting the specificity of detection correctly classified 95.895% of instances in 10 classes and the misclassification error was 0.2975.

Conclusions

The contamination level and duration of outbreaks, alerting threshold, memory, guardband, and whether the weekly pattern was considered or not influence the sensitivity and specificity of outbreak detection and given the C-algorithm parameter settings, we can predict outbreak detection performance quantitatively. In future work, we plan to investigate other predictors of performance and study how these predictions can be used in algorithm and policy choices.

Keywords

outbreak detection; public health surveillance; machine learning; bayesian networks; detection performance

References

1.Buckeridge, D.L., et al. Simulation Analysis Platform (SnAP): a Tool for Evaluation of Public Health Surveillance and Disease Control Strategies. 2011. American Medical Informatics Association.

2.Hutwagner, L., et al., The bioterrorism preparedness and response early aberration reporting system (EARS). Journal of Urban Health: Bulletin of the New York Academy of Medicine, 2003. 80(Supplement 1): p. i89-i96.

3.Tokars, J.I., et al., Enhancing time-series detection algorithms for automated biosurveillance. Emerging Infectious Diseases, 2009. 15(4): p. 533.

4.Hall, M., et al., The WEKA data mining software: an update. ACM SIGKDD Explorations Newsletter, 2009. 11(1): p. 10-18.

*Nastaran Jafarpour
E-mail: nastaran.jafarpour@polymtl.ca

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

An Algorithm That Identifies Coronary and Heart Failure Events In The Electronic Health Record

Jawali Jaranilla*[1], Thomas E. Kottke[1] and Courtney J. Baechler[2]

[1]Health Partners Institute for Education and Research, Minneapolis, MN, USA; [2]University of Minnesota, Minneapolis, MN, USA

Objective

The objective of this project was to identify criteria that accurately categorize acute coronary and heart failure events exclusively with electronic health record data so that the medical record can be used for surveillance without manual record review.

Introduction

Surveillance to track the incidence, prevalence and treatment of disease is a fundamental task of public health. The advent of universal health care coverage in the United States and electronic health records could make the medical record a valuable disease surveillance tool. This can only happen, however, if the necessary data can be extracted from the medical record without manual review.

Methods

We serially compared 3 different computer algorithms to manual record review. The first two algorithms relied on ICD9CM codes, troponin levels, ECG data and echocardiographic data. The 3rd algorithm relied on a very detailed coding system, IMO statements, troponin levels and echocardiographic data.

Results

Cohen's Kappa for the initial algorithm was 0.47 (95%CI 0.41-0.54). Cohen's Kappa was 0.61 (95%CI 0.55-0.68) for the second algorithm. Cohen's Kappa for the third algorithm was 0.99 (95%CI 0.98-1.00).

Conclusions

We conclude that electronic medical record data are sufficient to categorize coronary heart disease and heart failure events without manual record review. However, only moderate agreement with medical record review can be achieved when the classification is based on 4-digit ICD9CM codes because ICD9CM 410.9 includes myocardial infarction with ST elevation (STEMI) and myocardial infarction without ST elevation (nSTEMI). Nearly perfect agreement can be achieved using IMO statements, a more detailed coding system that tracks to ICD9, ICD10 and SnoMED-CT. IMO statements are available in many electronic medical record systems.

Keywords

validity; surveillance; coronary artery disease; heart failure; electronic medical record

Acknowledgments

Funding provided by the following: The HealthPartners Research Foundation (a partnership grant to TEK); The Heart Disease and Stroke Prevention Unit at the Minnesota Department of Health from a Capacity Building - Cooperative Agreement grant from the Centers for Disease Control and Prevention CDC) 5U50DP000721-04; and, NIH training grant T32 HL69764 (supporting CJB).

*Jawali Jaranilla
E-mail: jjaranil@jhsph.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using Syndromic Emergency Department Data to Augment Oral Health Surveillance

John P. Jasek*[1], Nicole Hosseinipour[1], Talia Rubin[1] and Ramona Lall[2]

[1]NYC Department of Health and Mental Hygiene, Bureau of Health Care Access and Planning, Long Island City, NY, USA; [2]NYC Department of Health and Mental Hygiene, Bureau of Communicable Diseases, Long Island City, NY, USA

Objective

To utilize an established syndromic reporting system for surveillance of potentially preventable emergency department (ED) oral health visits (OHV) in New York City (NYC).

Introduction

NYC Department of Health and Mental Hygiene recently reoriented its oral health care strategy to focus on health promotion and expanded surveillance. One surveillance challenge is the lack of timely OHV data; few dental providers are in our electronic health record project, and statewide utilization data are subject to delays. Prior research has examined OHV using ICD-9-CM from ED records, and has suggested that diagnostic specificity may be limited by ED providers' lack of training in dental diagnoses (1-3). We considered our existing ED syndromic system as a complement to periodic population-based surveys. This system captures approximately 95% of all ED visits citywide; 98% of records have a completed chief complaint text field whereas only 52% contain an ICD-9-CM diagnosis.

Methods

We used chief complaint text to define OHV in two ways: (1) a basic definition comprised of 'TOOTH' or 'GUM' in combination with a pain term (e.g., 'ACHE'); (2) a more inclusive definition of either specific oral health diagnoses (e.g., 'PULPITIS') or definition (1). For both definitions, we excluded visits likely to have stemmed from trauma (e.g., 'ACCIDENT'). Data from 2009-2011 were analyzed by facility, patient age and residential zip code, and day/time using SAS v9.2 (SAS Institute; Cary, NC).

Results

OHV in 2009-2011 totaled 72,410 (def. 1) and 103,594 (def. 2), or 0.6% and 0.9% of all ED visits, respectively. OHV (def. 2) spiked at age 18 and were highest among 18 to 29 year olds (Fig. 1). Neighborhood OHV rates (def. 2) ranged from 74 to 965 per 100,000 persons. 59% of OHV occurred between 8am and 6pm (Fig. 2). Highly specific dental conditions were rare; terms such as "tooth ache" were most common.

Conclusions

Findings suggest that OHV are a particular problem among ages 18 to 29. This pattern may reflect lower insurance coverage among young adults. The proportion of daytime visits suggests that EDs are substituting for regular dental treatment and there may be opportunities to promote daytime linkages to office-based dental providers.

A well-established syndromic reporting system holds promise as a method of OHV surveillance. Strengths include near complete chief complaint reporting, rapid availability, and the potential to identify populations and facilities that could benefit from expanded access and preventive education. Limitations include the need to gather site-specific facility information (e.g., presence of dental residents, coding practices) to better understand patterns. Also, the absence of some important fields in the syndromic system (e.g., insurance coverage, income) limit assessment of the degree to which cost barriers may be driving OHV.

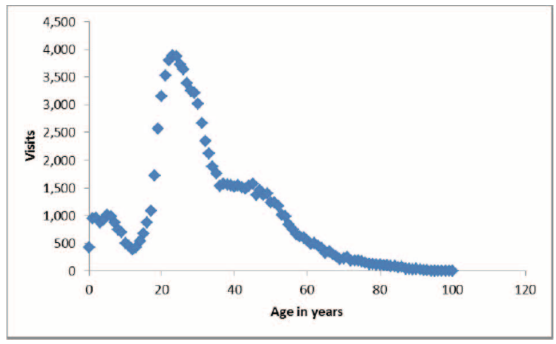


Fig 1. OHV (def.2) by age, 2009-2011

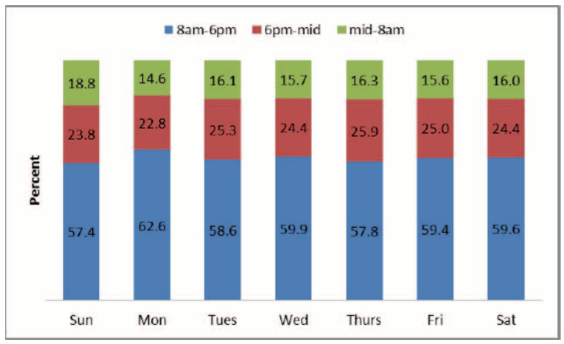


Fig 2. OHV (def.2) by day/time, 2009-2011

Keywords

chief complaint; surveillance; syndrome definition; oral health

Acknowledgments

The authors would like to thank the Bureau of Communicable Diseases' Data Analysis and Syndromic Surveillance Unit for data collection and analytic guidance.

References

1. PEW Center on the States, "A Costly Dental Destination," accessed August 22, 2012, http://www.pewstates.org/research/reports/a-costly-dental-destination-85899379755
2. Hong L, Ahmed A, McCunniff M, et al. Secular Trends in Hospital Emergency Department Visits for Dental Care in Kansas City, Missouri, 2001-2006. Public Health Reports; (March-April 2011) Vol 126, No. 2, 210-219.
3. California Health Care Foundation, "Emergency Department Visits for Preventable Dental Conditions in California," accessed August 22, 2012, http://www.chcf.org/~/media/MEDIA%20LIBRARY%20Files/PDF/E/PDF%20EDUseDentalConditions.pdf

*John P. Jasek
E-mail: jjasek@health.nyc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Recommendations for Syndromic Surveillance Using Inpatient and Ambulatory EHR Data

Geraldine Johnson[1], Charles Ishikawa[2], Rebecca Zwickl[2], Maiko Minami[4], Taha Kass-Hout[3] and Laura Streichert*[2]

[1]NY State Health Dept., Albany, NY, USA; [2]ISDS, Brighton, MA, USA; [3]Division of Informatics Solutions and Operations, CDC, Atlanta, GA, USA; [4]HLN Consulting, San Diego, CA, USA

Objective

To develop national Stage 2 Meaningful Use (MUse) recommendations for syndromic surveillance using hospital inpatient and ambulatory clinical care electronic health record (EHR) data.

Introduction

MUse will make EHR data increasingly available for public health surveillance. For Stage 2, the Centers for Medicare & Medicaid Services (CMS) regulations will require hospitals and offer an option for eligible professionals to provide electronic syndromic surveillance data to public health. Together, these data can strengthen public health surveillance capabilities and population health outcomes (Figure 1).

To facilitate the adoption and effective use of these data to advance population health, public health priorities and system capabilities must shape standards for data exchange. Input from all stakeholders is critical to ensure the feasibility, practicality, and, hence, adoption of any recommendations and data use guidelines.

Methods

ISDS, in collaboration with the Division of Informatics Solutions and Operations at the Centers for Disease Control and Prevention (CDC), and HLN Consulting, convened a multi-stakeholder Workgroup of clinicians, technologists, epidemiologists, and public health officials with expertise in syndromic surveillance. Recommended MUse guidelines were developed by performing an environmental scan of current practice and by using an iterative, expert and community input-driven process. The Workgroup developed initial guidelines and then solicited and received feedback from the stakeholder community via interview, e-mail, and structured surveys. Stakeholder feedback was analyzed using quantitative and qualitative methods and used to revise the recommendations.

Results

The MUse Workgroup defined electronic syndromic surveillance (ESS) characteristics. Specifically, data are characterized by their timeliness, sensitivity rather than specificity, population focus, limited personally identifiable information, and inclusion of all patient encounters within a specific healthcare setting (e.g., emergency department, inpatient, outpatient). Based on stakeholder input (n=125) and Workgroup expertise, the guidelines identify priority syndromic surveillance uses that can assist with:

1. Monitoring population health;
2. Informing public health services; and
3. Informing interventions, health education, and policy by characterizing the burden of chronic disease and health disparities.

Similarly, the Workgroup identified data elements to support these uses in the hospital inpatient setting and possibly in the ambulatory care setting. They were aligned to previously identified emergency department and urgent care center data elements and Stage 1-2 clinical MUse objectives. Core data elements (required for certification) cover treating facility; patient demographics; subjective and objective clinical findings, including chief complaint, body mass index, smoking history, diagnoses; and outcomes. Other data elements were designated as extended (not required for certification) or future (for future consideration). The data elements and their specifications are subject to change based on applicable state and local laws and practices.

Based on their findings and recommended guidelines detailed in the report, the Workgroup also identified community activities and additional investments that would best support public health agencies in using EHR technology with syndromic surveillance methodologies.

Conclusions

The widespread adoption of EHRs, catalyzed by MUse, has the potential to improve population health. By identifying and describing potential ESS uses of new sources of EHR data and associated data elements with the greatest utility for public health, the recommendations set forth by the ISDS MUse Workgroup will serve to facilitate the adoption of MUse policy by both healthcare and public health agencies.

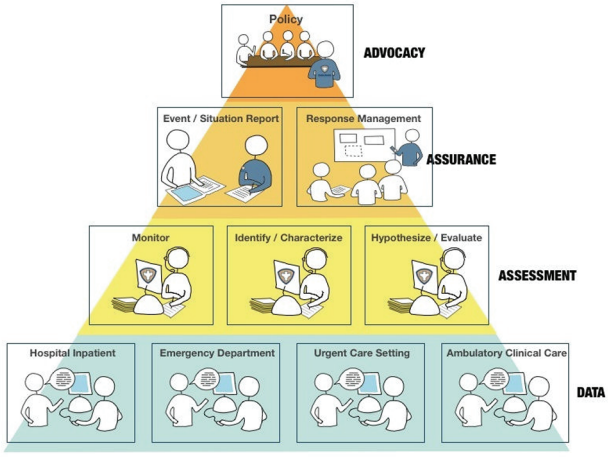


Figure 1: Syndromic surveillance data can inform public health functions.

Keywords

EHR; syndromic surveillance; Meaningful Use; inpatient; ambulatory

Acknowledgments

We thank the ISDS MUse Workgroup. This work supported by CDC contract #200-2011-41831.

*Laura Streichert
E-mail: lstreichert@syndromic.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

ISDS 2012 Conference Abstracts

Use of Syndromic Surveillance Information for Expanded Assessment of Wildfire Disaster

Jeffrey Johnson*[1], Michele Ginsberg[1], Nancy French[2], Brian Thelen[2] and Benjamin Koziol[2]

[1]San Diego County Public Health Services, San Diego, CA, USA; [2]Michigan Tech Research Institute, Ann Arbor, MI, USA

Objective

This presentation describes how syndromic surveillance information was combined with fire emission information and spatio-temporal fire occurrence data to evaluate, model and forecast climate change impacts on future fire scenarios.

Introduction

Syndromic surveillance information can be a useful for the early recognition of outbreaks, acute public health events and in response to natural disasters. Inhalation of particulate matter from wildland fire smoke has been linked to various acute respiratory and cardiovascular health effects. Historically, wildfire disasters occur across Southern California on a recurring basis. During 2003 and 2007, wildfires ravaged San Diego County and resulted in historic levels of population evacuation, significant impact on air quality and loss of lives and infrastructure. In 2011, the National Institutes of Health-National Institute of Environmental Health Sciences awarded Michigan Tech Research Institute a grant to address the impact of fire emissions on human health, within the context of a changing climate. San Diego County Public Health Services assisted on this project through assessment of population health impacts and provisioning of syndromic surveillance data for advanced modeling.

Methods

Various historical data sets were used during this study. These included: emergency department syndromic surveillance from 17 hospitals, as well as air quality and particulate matter, meteorological, wildland burn fuel, and atmospheric dispersion data. The study area was San Diego County. These data were linked temporally and spatially to create statistical models based on selected modeling approaches including generalized additive modeling. Future fire frequency was modeled for the entire region to determine the impacts of climate change on future fire and health outcomes. Modeling based upon previous fire occurrence was used to develop models for future fire indexes, risk of ignition, potential burning, and fire weather.

Results

Several models were developed to produce expected respiratory health impacts under future climate conditions for the San Diego County region. Model results showed that at peak fire par-ticulate concentrations, the odds of a person seeking emergency care increased by approxi-mately 50% compared to non-fire conditions. Also developed was a model to forecast future fire occurrence based on regional climate model predictions. This forecast covering the next the next three decades reveals that San Diego County will experience approximately two extreme fire seasons each decade by 2040.

Conclusions

Syndromic surveillance data are useful during disasters for situational awareness. These data may also provide value for post-disaster analytic work and predictive modeling for future disas-ters. This study demonstrates utility of syndromic data for collaborative work resulting in better understanding of environmental interactions on human health. We do know that wildfire oc-curs with some degree of historic regularity and these results may be useful for preparedness planning. We also know the conditions which must be present for medium to high wildland fire impact upon the population. This study further supports the notion that agencies should be able to strategically deploy resources and messaging immediately preceding the fire period with the goal of reducing human health risk factors and encouraging changes in community behaviors before, during and after a fire. Future fire model shows San Diego County will experience approximately two extreme fire seasons each decade by 2040. This project also promoted collaboration between public health and environmental health entities to better understand de-terminants of health during a disaster. In addition to developing a better understanding of the consequences of climate change on fire-induced respiratory illness, the project funding has provided support for San Diego County to improve their syndromic surveillance capacity and infrastructure.

Keywords

Syndromic; Disaster; Forecasting; Wildfire; San Diego

Acknowledgments

This work has been supported by the NIH-NIEHS Climate Change Grant #1RC1ES018612-01. We would also like to acknowledge the research teams at Michigan Tech Research Institute, Michigan Technology University, and the University of Maryland Department of Geography.

*Jeffrey Johnson
E-mail: jeffrey.johnson@sdcounty.ca.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Monitoring the Impact of Heat Waves with Emergency Service Utilization Data in Los Angeles County

Emily Kajita*, Patricia Araki, Monica Luarca and Bessie Hwang

Los Angeles County Dept. of Public Health, Los Angeles, CA, USA

Objective

To assess current indicators for situational awareness during heat waves derived from electronic emergency department (ED) and 911 emergency dispatch call (EDC) center data.

Introduction

Los Angeles County's (LAC) early event detection system captures over 60% of total ED visits, as well as 800 to 1,000 emergency dispatch calls from Los Angeles City Fire (LACF) daily. Both ED visits and EDC calls are classified into syndrome categories, and then analyzed for aberrations in count and spatial distribution. During periods of high temperatures, a heat report is generated and sent to stakeholders upon request. We describe how syndromic surveillance serves as an important near real-time, population-based instrument for measuring the impact of heat waves on emergency service utilization in LAC.

Methods

Daily electronic ED registration data, EDC calls, and high temperatures from Palmdale, California were queried from January 1, 2010 to August 26, 2012 and aggregated into Centers for Disease Control (CDC) weeks. A custom "heat exposure" category was created by searching ED chief complaints for key terms such as "Heat stroke," "hyperthermia," "overheat," and relevant ICD9 diagnosis codes. Similarly, EDC calls were classified if related to "heat exposure." Pearson correlation tests were used to determine correlation between total ED visits, heat-related ED visits, heat-related EDC calls, and daily maximum temperatures.

Results

Thus far 2012 has exceeded counts cumulative to August 26th for the past two years in the number of heat-related ED visits, heat-related EDC calls, and hot days (Table 1). In particular, the number of 105 degree-and-up days this year has already doubled what was observed all year during 2010 and 2011.

Age groups were similarly distributed in total ED visits, heat-related ED visits and EDC calls, with a 18 to 44 year old majority (37%, 37%, and 42% respectively), followed by 45 to 64 year olds (23%, 21%, 23%). Total ED visits did not increase during summer months, and were therefore not found to be correlated to temperature (ρ=-0.06, p=0.46) or heat-related EDC calls (ρ=0.07, p=0.4). Heat-related ED visits however, were positively correlated with both EDC calls (ρ=0.85, p< 0.001) and temperatures (ρ=0.59, p<0.001). Heat-related EDC calls were also correlated with temperature (ρ=0.56, p<0.001).

Conclusions

Due to small numbers of heat-related visits relative to total ED visits, any effects that increased temperatures may have on total ED visits are undetectable. Total ED volume should therefore not be used as an indicator for measuring the impact of heat on LAC's population. Filtering chief complaints to obtain heat-specific ED visits, however, enables patterns of increase to emerge which correlate with higher temperatures and heat-related emergency dispatch calls. About 35% of the week to week variation in heat-related ED visits, and 32% of the week to week variation in heat-related EDC calls can be explained by week to week variations in temperature. That heat-related visits were similarly distributed in age as all visitors suggests that heat does not disproportionately affect children and the elderly any more than the other acute health conditions that bring visitors to the ED. Syndromic analysis of ED data and EDC can provide baselines for health conditions such as hyperthermia that are otherwise difficult to obtain.

	2010 to 8/26 (year end total)	2011 to 8/26 (year end total)	2012 to 8/26
Heat-related ED visits	214(319)	195(304)	246
Heat-related 911 calls	102(169)	73(128)	163
Number of days > 80F	102(148)	99(152)	123
Number of days > 90F	72(100)	67(96)	87
Number of days > 100F	18(23)	14(17)	27
Number of days > 105F	3(3)	4(4)	7

Table 1. Number of heat-related ED visits, EDC calls, and days exceeding temperatures to 8/26 and to the year's end.

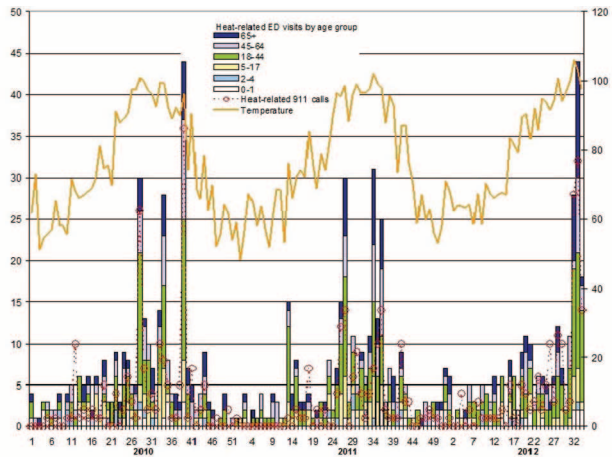


Figure 1. Weekly heat-related ED visits and heat-related EDC calls (left axis); and 7-day averaged maximum daily temperatures in Palmdale, California (right axis). Heat-related ED visits are stratified by age group.

Keywords

Emergency department; Dispatch; Heat; Situational awareness

References

Weather underground. 2012. 27 Aug. 2012. The Weather Channel Companies. <http://www.wunderground.com/>

*Emily Kajita
E-mail: ekajita@ph.lacounty.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

ILI and SARI Surveillance along the California & Arizona Borders with Mexico, 2011-12

Pete Kammerer*, Gary Brice, Anthony Hawksworth and Chris Myers

Operational Infectious Diseases, NHRC, San Diego, CA, USA

Objective

To identify the pathogens responsible for influenza-like illness (ILI) and severe acute respiratory illness (SARI) along the U.S.-Mexico border region in San Diego and Imperial Counties, CA and Pima County, AZ.

Introduction

National borders do not prevent the transmission of pathogens and associated vectors among border populations. The Naval Health Research Center (NHRC) has collaborated with the Mexican Secretariat of Health, the U. S. Department of State's Biosecurity Engagement Program (BEP) and the U. S. Centers for Disease Control and Prevention (CDC) in concert with local health officials to conduct ILI surveillance (since 2004) and SARI surveillance (since 2009) in the border region.

Methods

Respiratory swabs were collected from patients with ILI (fever ≥ 100F, and sore throat or cough) or SARI (≥ 5 y.o.: ILI with hospital admission; < 5 y.o.: clinical suspicion of pneumonia with hospital admission) and stored at -70C. Specimens were tested with molecular techniques, viral and bacterial culture.

Results

NHRC received and tested 295 ILI specimens collected from four surveillance sites in 2011-12. Demographics: 53% female, 47% male; 36% 0-4 yrs old, 50% 5-24 yrs old, 8% 25-49 yrs old, 4% 50-64 yrs old, 2% >64 yrs old. Pathogens identified included influenza A (15%); rhinovirus (8%); respiratory syncytial virus (RSV) (7%); adenovirus (6%); influenza B (4%) and parainfluenza virus (PIV) 1; (4%). 335 SARI specimens were collected from 6 sites. Demographics: 52% female, 48% male; 41% 0-4 yrs old; 9% 5-24 yrs old, 12% 25-49 yrs old, 11% 50-64 yrs old, 28% >64 yrs old. Pathogens identified included RSV (17%); rhinovirus (10%); influenza A (9%); adenovirus (6%); influenza B (2%) and PIV 1 (1%).

Conclusions

In 2011-12, our surveillance identified a difference in the proportion of respiratory pathogens affecting outpatients and inpatients. Influenza A was isolated more frequently in outpatients, whereas RSV was more frequent in hospitalized patients. We also noted an increased proportion of specimens from the 50-64 yr old and the >64 yr old age groups in the SARI surveillance, whereas 86% of the ILI specimens are from patients 24 yrs old or less. Additional benefits of this collaborative surveillance have been the cooperation, joint training and communication between the participating entities. These pre-established lines of communication are invaluable during a public health emergency, which was demonstrated during the recent influenza pandemic.

Keywords

influenza; ILI; respiratory syncytial virus; US-Mexico border; SARI

*Pete Kammerer
E-mail: peter.kammerer@med.navy.mil

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

EIDSS Application for CCHF Foci Activity Epi-Analysis and Prediction in Kazakhstan

Stanislav V. Kazakov[1], Alexey V. Burdakov*[2], Kenes S. Ospanov[3], Aizhan S. Esmagambetova[4], Andrey O. Ukharov[2], Veronika P. Sadovskaya[1] and Umirbek B. Usenov[3]

[1]Kazakh Scientific Center of Quarantine and Zoonotic Diseases, Almaty, Kazakhstan; [2]Black & Veatch, Overland Park, KS, USA; [3]Scientific Center of Sanitary and Epidemiological Expertise and Monitoring, Almaty, Kazakhstan; [4]Committee of State Sanitary and Epidemiological Surveillance of the Ministry of Health of Kazakhstan, Astana, Kazakhstan

Objective

Test of the Electronic Integrated Disease Surveillance System (EIDSS) for epi-analysis and prediction of situation in CCHF foci in Kazakhstan.

Introduction

CCHF foci are reported in 3 southern regions of Kazakhstan with population of 1 million. The ixodic ticks in the area are CCHF carriers. Human infections (3 to 12 cases per year) occur through tick bites and contact with CCHF patient blood. CCHF epidemiological process in Kazakhstan has prominent seasonality (spring-summer period) and the rhythm of epidemic appearances (5-6-years). The rhythmical population incidence rate is associated with natural and climate factors, which govern the increase in the number of ixodic ticks, their infection rate (virus carrier state), and directly correlates with the population density and the livestock number that are the principal tick feeders in nature.

Methods

EIDSS version 4 provides capability to collect, share and process epidemiological, clinical and laboratory data on infectious diseases in medicine, veterinary and environment sectors. It is currently deployed in Kazakhstan at 150 sites of the Ministry of Agriculture (planned up to 271), and at 8 sites of the Ministry of Health (planned up to 23).

Three available indicators (for 2007-2011) were used for analysis: population; tick infection rate (relative density of CCHF seropositive tick samples per total number of tested laboratory samples); CCHF human case rate by districts per 10'000.

The following procedure was conducted:

1) Demographic information, diagnosis and location data entry into EIDSS
2) Tick collection location data, total number of tested samples (pools), and number of seropositive data entry into EIDSS
3) Correlation joint analysis of data on vectors and epidemiological surveillance in Analysis, Visualization and Reporting (AVR) module

Results

EIDSS generated 12 different maps filtered according to the selected regions, ticks, demographics and CCHF human incidence, aggregated by region, correlated by 3 indicators entered into the database. This allowed visualizing information to support epi-analysis. As a result, for each of the 3 regions specific districts with the highest risk of the CCHF epidemic outbreaks were identified. The resulting information was grouped into 3 clusters of risk with the following criteria: population density, tick infection rate and human cases for each of 25 CCHF-disadvantaged districts (see map). These results predict the epidemic situation in a particular area and support management decisions for planning and correction of preventive anti-tick and anti-epidemic measures and funding requirements.

Conclusions

EIDSS with Natural Vectors and the AVR modules has capabilities for analysis and prediction of epizootic and epidemic processes in vector-borne virus infections foci. It is an easy to use and free-of-charge tool that can become the basic instrument for especially dangerous diseases field epidemiologists as well as for the ministries and local governments for CCHF prophylaxis decision support.

Keywords

CCHF; one health; electronic disease surveillance; EIDSS; multi-factor analysis

References

1. Kazakov S.V., et.al. CCHF Causation model in the Roitman's ring graphs // Hygiene, Epidemiology and Immunobiology, 2000, Nos.3-4, pp.88-90
2. Durumbetov E.E., et.al. Practical Application of Epidemiological Triad Model for Managerial Decision-Making within the System of Epi-Surveillance in Moyinkum Foci of CCHF // Proceedings of New Technologies in Medicine and Pharmacy, Astana 2001, pp.34-35
3. Kazakov S.V., et.al. Methodological Approaches to Study Epidemic Process of CCHF in Moyinkum Foci of Zhambyl Region. // Hygiene, Epidemiology and Immunobiology, 2001. Nos.1-2, pp.75-84
4. Onishchenko G.G., et.al. Using IFA and RT-PCR in Study of Ixodic Tick Infection Rate Collected in CCHF Foci in Kazakhstan and Tajikistan in 2001-02. // Virology Matters. - M., 2005. No.1 - pp.23-27
5. Ospanov K.S., Kazakov S.V., et.al. On Prospects of Further Study of CCHF Foci in Kazakhstan // Science and Disease Surveillance Review, BTRP, Atlanta, 2009, p.126
6. Burdakov A., Ukharov A. Transforming national human and veterinary disease surveillance systems from paper into integrated electronic form in the FSU countries // 15th International Congress on Infectious Diseases (ICID), Bangkok 2012

*Alexey V. Burdakov
E-mail: BurdakovAV@bv.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Content Analysis of Syndromic Twitter Data

Bethany Keffala*[1], Mike Conway[2], Son Doan[2] and Nigel Collier[3]

[1]Linguistics, University of California, San Diego, La Jolla, CA, USA; [2]University of California, San Diego - Division of Biomedical Informatics, La Jolla, CA, USA; [3]National Institute of Informatics, Tokyo, Japan

Objective

We present an annotation scheme developed to analyze syndromic Twitter data, and the results of its application to a set of respiratory syndrome-related tweets [1]. The scheme was designed to differentiate true positive tweets (where an individual is experiencing respiratory symptoms) from false positive tweets (where an individual is not experiencing respiratory symptoms), and to quantify more fine-grained information within the data.

Introduction

The popularity of Twitter, a social-networking service, creates the opportunity for researchers to collect large amounts of free, localizable data in real-time. Data takes the form of short, user-written messages, and has been employed for general syndromic surveillance [2] and surveillance of public attitudes toward the H1N1 flu outbreak [3]. Accessibility of tweets in real-time makes them particularly appropriate for use in early warning systems. Data collected through keyword search contains a significant amount of noise, however, annotation can help boost the signal for true positive tweets.

Methods

The annotation scheme was developed based on information relevant for early warning systems (e.g. who is experiencing symptoms, and when) as well as other information present in the tweets (e.g. aspirations regarding symptoms, or abuse of substances such as cough syrup). Categories included Experiencer: Self/Other, Temporality: Current/Non-Current, Sentiment: Positive/Negative, Information: Providing/Seeking, Language: Non-English, Aspiration, Hyperbole, and Substance Abuse. All categories with the exception of Language and Substance Abuse were defined in reference to diseases or symptoms. The scheme was applied to 1,100 respiratory syndrome-related tweets (544 false positive, 556 true positive) from a previously collected corpus of syndromic twitter data [2]. Inter-annotator agreement was calculated for 9% of the data (100 tweets).

Results

Inter-annotator agreement was generally good, however certain categories had lower scores. Categories for Experiencer, Temporality, Sentiment: Negative, Information: Providing, and Language all had Kappa values above .9, Sentiment: Positive, Aspiration, and Substance abuse had Kappa values above .7, and Information: Seeking and Hyperbole had Kappas above .6. There was good separation between true positive tweets and false positive tweets, especially for the Experiencer: Self, Temporality: Current, Sentiment: Negative, Aspiration, Hyperbole, and Substance Abuse categories (see Table). True positive data were more likely to belong to any category except Information: Providing, and Substance Abuse, in which cases false positive tweets had greater likelihood of category inclusion. Within the true positive data, we found that users were more likely to reference symptoms that they themselves were currently experiencing than they were to reference another person's symptoms or non-current symptoms. Sentiment was largely negative, and there was significant use of aspiration and hyperbole.

Conclusions

Future work will apply the scheme to other syndromes, including constitutional, gastrointestinal, neurological, rash, and hemorrhagic.

	% True Positive Tweets	% False Positive Tweets
Experiencer: Self	98.2	0.4
Temporality: Current	98.7	0.2
Sentiment: Negative	79.7	1.7
Information: Providing	0.7	2.8
Language: Non-English	2.7	1.3
Aspiration	11.0	0.2
Hyperbole	18.3	0.2
Substance Abuse	1.3	8.1

Table 1. Percentages of tweets included in each category.

Keywords

social media; surveillance; respiratory syndrome

References

1. N. Collier, R. Matsuda Goodwin, J. McCrae, S. Doan, A. Kawazoe, M. Conway, A. Kawtrakul, K. Takeuchi, D. Dien. (2010). "An ontology-driven system for detecting global health events", Proc. 23rd International Conference on Computational Linguistics (COLING), Beijing, China, August 23-27, pp. 215-222, available from http://aclweb.org/anthology/C/C10/C10-1025.pdf.
2. Collier, N. & Doan, S. (2011). "Syndromic Classification of Twitter Messages", Proc. eHealth 2011, Malaga, Spain. November 21-23.
3. Chew, C. & Eysenbach, G. (2010). Pandemics in the Age of Twitter: Content Analysis of Tweets during the 2009 H1N1 Outbreak. PLoS ONE 5(11): e14118.

*Bethany Keffala
E-mail: bkeffala@ucsd.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluating the Variation on Public Health's Perceived Field Need of Communicable Disease Reports

Uzay Kirbiyik*[1, 3], Roland Gamache[2, 3], Brian E. Dixon[2, 3] and Shaun Grannis[1, 3]

[1]Indiana University, School of Medicine, Indianapolis, IN, USA; [2]Indiana University, School of Informatics, Indianapolis, IN, USA; [3]Health Informatics, Regenstrief Institute, Inc., Indianapolis, IN, USA

Objective

To assess communicable disease report fields required by public health practitioners and evaluate the variation in the perceived utility of these fields.

Introduction

Communicable disease surveillance is a core Public Health function. Many diseases must be reported to state and federal agencies (1). To manage and adjudicate such cases, public health stakeholders gather various data elements. Since cases are identified in various healthcare settings, not all information sought by public health is available (2) resulting in varied field completeness, which affects the measured and perceived data quality. To better understand this variation, we evaluated public health practitioners' perceived value of these fields to initiate or complete communicable disease reports.

Methods

We chose four diseases: Histoplasmosis, acute hepatitis B, hepatitis C and salmonella. We asked public health practitioners from Marion County Health Department (MCHD) of Indianapolis to list the fields they felt were necessary when submitting a communicable disease report. We then asked them to evaluate those fields using the following criteria:

Required – A critical case attribute, when missing or unknown, would make the task of initiating and/or closing a case impossible or exceedingly difficult.

Desired – A case attribute allowing more complete epidemiologic profiles to be developed but, if missing, would not prohibit initiating and/or closing a case.

Not applicable – A case attribute that is not usually collected to initiate and/or close a case for the particular condition.

To quantify the need for the fields, we assigned a number to each response as follows:

0 - Not applicable 1 - Desired 2- Required

We summed the numbers for each field for each disease and created a table for the perceived need of that field (table 1).

Results

The perceived needs table showed a difference between the fields needed to initiate or close a case. Moreover the perceived need for fields varied by disease as well. To assess the difference in perceived needs, we calculated the standard deviation of the fields (table 2).

Conclusions

Data quality is essential, not only for research but to support routine public health practice as well. Many factors affect data quality; one of them is perceived need of the information by Public Health Practitioners. Despite working with public health stakeholders from the same organization we observed variation in their perceived needs for these fields to initiate or close a communicable case. These results highlight another source of the problem regarding health information quality and its goodness of fit issues.

The perceived need for the field	FUNGAL		HEPATITIS				ENTERIC		
	Histoplasmosis		Hepatitis B-acute		Hepatitis C		Salmonella		
Field Name	Initiate	Close	Initiate	Close	Initiate	Close	Initiate	Close	Sum
Disease	8	8	8	8	8	8	8	8	64
First Name	8	8	8	8	8	8	8	8	64
Middle Initial	4	5	4	5	4	5	4	5	36
Last Name	8	8	8	8	8	8	8	8	64
Parent - First Name	3	4	3	4	3	4	3	4	28
Parent - Middle Initial	1	1	1	1	1	1	1	1	8
Parent - Last Name	3	4	3	4	3	4	3	4	28
Phone Number	7	7	7	8	7	8	7	8	59
Street Number	7	8	7	8	7	8	7	8	60
Street Name	7	8	7	8	7	8	7	8	60
City	7	8	7	8	7	8	7	8	60
Zip Code	5	7	5	7	5	7	5	7	48
County	7	8	7	8	7	8	7	8	60
Date of Birth	8	8	8	8	8	8	8	8	64
Age	3	4	3	4	3	4	3	4	28
Sex	6	8	6	8	6	8	6	8	56
Pregnant	3	4	7	8	4	5	3	4	38
Race	4	8	4	8	4	8	4	8	48
Ethnicity	4	7	4	7	4	7	4	7	44
Health Care Worker Food Service Worker School (student/staff) Day Care (attendee/staff)	4	5	3	3	3	3	5	7	33
Name of School/Day Care	4	5	1	1	1	1	4	7	24
Part of an Outbreak	4	5	4	4	3	4	4	6	34
Etiologic Agent	7	8	7	8	7	8	7	8	60
Site of Infection	6	8	0	0	0	0	6	8	28
Date of Diagnosis (m, d, y)	5	7	6	7	6	7	6	7	51
Symptoms associated with infection	5	8	6	8	5	7	5	8	52
If yes to Symptoms: Onset Date (m, d, y)	5	7	6	8	5	7	5	7	50
If yes to Symptoms: Pertinent Symp/Signs	5	8	5	8	5	7	5	7	50
If yes to Symptoms: Died? (y/n)	6	8	6	8	6	7	7	8	56
Lab test(s) and result(s)	8	8	8	8	8	8	8	8	64
Lab test(s)/result(s) Date	7	8	7	8	7	8	7	8	60
Treatment (name of antibiotic)	4	8	1	1	1	1	5	7	28
Dosage	4	5	1	1	1	1	4	4	21
Date initiated	4	5	1	1	1	1	4	6	23
Antibiotic Resistance (y, n, nd)	1	1	0	0	0	0	4	5	11
If yes, what antibiotic?	0	0	0	0	0	0	3	4	7
Reporting Facility Code	2	3	2	3	2	3	2	3	20
If Hospital, Name Hospital	7	8	7	8	7	8	7	8	60
Name of Physician and Address	7	8	7	8	7	8	7	8	60
Record Number	5	6	5	6	5	6	5	6	44
Person Reporting (other than physician)	5	6	5	6	5	6	5	6	44
Telephone Number	7	7	7	7	7	7	7	7	56
Telephone Number (2)	2	2	2	2	2	2	2	2	16
Date of Report	6	6	6	6	6	6	6	6	48
TOTAL (max possible 360)	*223*	*273*	*210*	*248*	*204*	*241*	*233*	*285*	

Table 1. Perceived need for the selected communicable disease reports fields. Higher numbers (darker color) reflect greater perceived need.

The Disagreement for the field	FUNGAL		HEPATITIS				ENTERIC		
	Histoplasmosis		Hepatitis B-acute		Hepatitis C		Salmonella		
Field Name	Initiate	Close	Initiate	Close	Initiate	Close	Initiate	Close	Sum
Disease	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
First Name	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Middle Initial	0.00	0.43	0.00	0.43	0.00	0.43	0.00	0.43	1.73
Last Name	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Parent - First Name	0.50	0.00	0.50	0.00	0.50	0.00	0.50	0.00	2.00
Parent - Middle Initial	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	4.00
Parent - Last Name	0.50	0.00	0.50	0.00	0.50	0.00	0.50	0.00	2.00
Phone Number	0.43	0.43	0.43	0.00	0.43	0.00	0.43	0.00	2.17
Street Number	0.43	0.00	0.43	0.00	0.43	0.00	0.43	0.00	1.73
Street Name	0.43	0.00	0.43	0.00	0.43	0.00	0.43	0.00	1.73
City	0.43	0.00	0.43	0.00	0.43	0.00	0.43	0.00	1.73
Zip Code	0.43	0.43	0.43	0.43	0.43	0.43	0.43	0.43	3.46
County	0.43	0.00	0.43	0.00	0.43	0.00	0.43	0.00	1.73
Date of Birth	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Age	0.43	0.71	0.43	0.71	0.43	0.71	0.43	0.71	4.56
Sex	0.50	0.00	0.50	0.00	0.50	0.00	0.50	0.00	2.00
Pregnant	0.43	0.71	0.43	0.00	0.00	0.43	0.43	0.71	3.15
Race	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Ethnicity	0.00	0.43	0.00	0.43	0.00	0.43	0.00	0.43	1.73
Health Care Worker Food Service Worker School (student/staff) Day Care (attendee/staff)	0.00	0.43	0.43	0.43	0.43	0.43	0.43	0.43	3.03
Name of School/Day Care	0.00	0.43	0.43	0.43	0.43	0.43	0.00	0.43	2.60
Part of an Outbreak	0.00	0.43	0.00	0.00	0.43	0.71	0.00	0.50	2.07
Etiologic Agent	0.43	0.00	0.43	0.00	0.43	0.00	0.43	0.00	1.73
Site of Infection	0.50	0.00	0.00	0.00	0.00	0.00	0.50	0.00	1.00
Date of Diagnosis (m, d, y)	0.43	0.43	0.50	0.43	0.50	0.43	0.50	0.43	3.67
Symptoms associated with infection	0.43	0.00	0.50	0.00	0.43	0.43	0.43	0.00	2.23
If yes to Symptoms: Onset Date (m, d, y)	0.43	0.43	0.50	0.00	0.43	0.43	0.43	0.43	3.10
If yes to Symptoms: Pertinent Symp/Signs	0.43	0.00	0.43	0.00	0.43	0.43	0.43	0.43	2.60
If yes to Symptoms: Died? (y/n)	0.50	0.00	0.50	0.00	0.50	0.43	0.43	0.00	2.37
Lab test(s) and result(s)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Lab test(s)/result(s) Date	0.43	0.00	0.43	0.00	0.43	0.00	0.43	0.00	1.73
Treatment (name of antibiotic)	0.00	0.00	0.43	0.43	0.43	0.43	0.43	0.43	2.60
Dosage	0.00	0.43	0.43	0.43	0.43	0.43	0.00	0.00	2.17
Date initiated	0.00	0.43	0.43	0.43	0.43	0.43	0.00	0.50	2.67
Antibiotic Resistance (y, n, nd)	0.43	0.43	0.00	0.00	0.00	0.00	0.00	0.43	1.30
If yes, what antibiotic?	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.47	0.47
Reporting Facility Code	0.47	0.47	0.47	0.47	0.47	0.47	0.47	0.47	5.15
If Hospital, Name Hospital	0.43	0.00	0.43	0.00	0.43	0.00	0.43	0.00	1.73
Name of Physician and Address	0.43	0.00	0.43	0.00	0.43	0.00	0.43	0.00	1.73
Record Number	0.43	0.50	0.43	0.50	0.43	0.50	0.43	0.50	3.73
Person Reporting (other than physician)	0.43	0.50	0.43	0.50	0.43	0.50	0.43	0.50	3.73
Telephone Number	0.43	0.43	0.43	0.43	0.43	0.43	0.43	0.43	3.46
Telephone Number (2)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Date of Report	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	4.00

Table 2. Standard deviation of perceived need values for each field. Higher numbers reflect more disagreement among responses.

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Keywords
completeness; Data quality; Communicable disease reports

Acknowledgments

We thank the MCHD of Indianapolis for their help with this research.

References

1. Morbidity and Mortality Weekly Report (MMWR) June 1, 2012 / 59(53);1-111 http://www.cdc.gov/mmwr/preview/mmwrhtml/mm5953a1.htm
2. Indiana Confidential Report of Communicable Diseases - State Form 43823 (R2/11-96) https://forms.in.gov/Download.aspx?id=5082
3. Wang R Y, Strong D M, Guarascio L M. Beyond accuracy: what data quality means to data consumers. Journal of Management Information Systems 1996; 12 (4); 5–33.

*Uzay Kirbiyik
E-mail: ukirbiyi@iupui.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

TRACnet: A National Phone-based and Web-based Tool for the Timely Integrated Disease Surveillance and Response in Rwanda

Kayumba Kizito*[1], Kabeja Adeline[2], Koama Jean Baptiste[3], Asiimwe Anita[2], Binagwaho Agnes[4], Pamela Johnson[5] and Nyatanyi Thierry[2]

[1]Voxiva SARL, Kigali, Rwanda; [2]Rwanda Biomedical Center, Kigali, Rwanda; [3]CDC Rwanda, Kigali, Rwanda; [4]Ministry of Health, Kigali, Rwanda; [5]Voxiva Inc, Washington, WA, USA

Objective

(1) To describe the implementation of the electronic system for integrated disease surveillance in Rwanda. (2) To present the sensitivity and specificity of the electronic reporting system to detect potential outbreaks

Introduction

In Rwanda, communicable diseases are the mostly predominant representing 90% of all reported medical consultations in health centers. The country has often faced epidemics including emerging and re-emerging infectious diseases. To enhance its preparedness to identify and respond to outbreaks and prevent epidemics, the Government of Rwanda has developed and deployed an electronic Integrated Disease Surveillance and Response (eIDSR) working with Voxiva with funding from the U.S. Centers for Disease Control and Prevention(CDC).

Methods

The eIDSR is built on Rwanda's existing national phone and web-based HIV-reporting system, "TRACnet" that has been operating nationwide since 2004. Data is collected for 23 communicable diseases under surveillance in Rwanda categorized into immediately and weekly reportable. If a lab test is required, the sample is taken and sent to laboratory for testing. Immediate, Weekly, Lab request and lab results forms are completed before submitting data in the system. Data is entered using phone or web based application and is stored in the central database.

Results

The design of eIDSR module was completed in November 2011. As of September 2012, 252 out of 457 health facilities in Rwanda have been trained and are using the electronic system (over 50% of coverage); the national roll out is still going on with complete coverage planned for December 2012. The system sends SMS reminders for due and overdue reports. The timeliness and completeness of reporting are 98% and 100% respectively. Notifications are sent to the concerned personnel when the threshold for outbreak detection is reached. When lab results are available and entered in the system, the results are automatically communicated to the health centers originating samples. Data is automatically summarized in predefined tables, graphs, dashboards and maps.

As of September 3rd, 2012, a total of 5813 reports including 1325 immediate reports and 4488 weekly reports were submitted electronically. Out of 1325 immediate reports submitted, 406 potential outbreaks were detected and immediately notified and 7 of them were confirmed for cholera, rubella, Influenza-like illness (H1N1), measles and food poisoning. From these data, the eIDSR system shows a sensitivity of 100% and a specificity of 70% for outbreak detection. The early notification of probable outbreaks stimulated the early investigations and the quick response to outbreaks within the country and across the borders.

Conclusions

The electronic disease surveillance system has improved timeliness and completeness of reporting and extremely supports early detection and notification of outbreaks for timely response. This system should be a model for the East African region as it has demonstrated advantages in the cross-border disease surveillance.

Keywords

Disease Surveillance; Informatics; m-Health

Acknowledgments

The government of Rwanda for having adopted ICT as pivotal for Development.

MoH/ Rwanda Biomedical Center for promoting innovations in Health sector including m Health technology. The US Centers for Disease Control and Prevention (CDC) for funding TRACnet under the Cooperative Agreement. Voxiva &other stakeholders who worked to implement TRACnet: NRL, HIV Division, EID Division, SPH, ICAP, KIST, MTN. All partners in ICT: Rapid SMS, JEMBI, PIH.

References

A. KABEJA: eIDSR in Rwanda. East Africa Public Health Laboratory Network Project workshop, Kigali, Rwanda (April 2012).

BOX, G. E. P.; JENKINS, G. M.; and REINSEL, G. C. (1994). Time Series Analysis, Forecasting and Control. Prentice-Hall, Englewood Cliffs, NJ.

Harris, T.J. and Ross, W.H.: Statistical process control procedures for correlated observations. The Canadian Journal of Chemical Engineering, 69, 48-57. (1991)

*Kayumba Kizito
E-mail: kkayumba@voxiva.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Health Department's Collaborative Model for Disease Surveillance Capacity Building

Ikechi Konkwo*[1, 2], Robert G. Harmon[1], William C. Livingood[2, 1], Thomas BryantIII[1] and Saad Zaheer[1]

[1]Institute for Public Health Informatics and Research, Duval County Health Dept, Jacksonville, FL, USA; [2]Center for Health Equity and Research - University of Florida/Shands Medical Center, Jacksonville, FL, USA

Objective

Highlight one academic health department's unique approach to optimizing collaborative opportunities for capacity development and document the implications for chronic disease surveillance and population health.

Introduction

Public Health departments are increasingly called upon to be innovative in quality service delivery under a dwindling resource climate as highlighted in several publications of the Institute of Medicine. Collaboration with other entities in the delivery of core public health services has emerged as a recurring theme. One model of this collaboration is an academic health department: a formal affiliation between a health professions school and a local health department. Initially targeted at workforce development, this model of collaboration has since yielded dividends in other core public health service areas including community assessment, program evaluation, community-based participatory research and data analysis.

The Duval County Health Department (DCHD), Florida, presents a unique community-centered model of the academic health department. Prominence in local informatics infrastructure capacity building and hosting a CDC-CSTE applied public health informatics fellowship (APHIF) in the Institute for Public Health Informatics and Research (IPHIR) in partnership with the Center for Health Equity Research, University of Florida & Shands medical center are direct dividends of this collaborative model.

Methods

We examined the collaborative efforts of the DCHD and present the unique advantages these have brought in the areas of entrenched data-driven public health service culture, community assessments, program evaluation, community-based participatory research and health informatics projects.

Results

Advantages of the model include a data-driven culture with the balanced scorecard model in leadership and sub-departmental emphases on quality assurance in public health services. Activities in IPHIR include data-driven approaches to program planning and grant developments, program evaluations, data analyses and impact assessments for the DCHD and other community health stakeholders.

Reports developed by IPHIR have impacted policy formulation by highlighting the need for sub county level data differentiation to address health disparities. Unique community-based mapping of Duval County into health zones based on health risk factors correlating with health outcome measures have been published. Other reports highlight chronic disease surveillance data and health scorecards in special populations.

Partnerships with regional higher institutions (University of Florida, University of North Florida and Florida A&M University) increased public health service delivery and yielded rich community-based participatory research opportunities.

Cutting edge participation in health IT policy implementation led to the hosting of the fledgling community HIE, the Jacksonville Health Information Network, as well as leadership in shaping the landscape of the state HIE. This has immense implications for public health surveillance activities as chronic disease surveillance and public health service research take center stage under new healthcare payment models amidst increasing calls for quality assurance in public health services.

DCHD is currently hosting a CDC-funded fellowship in applied public health informatics. Some of the projects materializing from the fellowship are the mapping of the current public health informatics profile of the DCHD, a community based diabetes disease registry to aid population-based management and surveillance of diabetes, development of a proposal for a combined primary care/general preventive medicine residency in UF-Shands Medical Center, Jacksonville and mobilization of DCHD healthcare providers for the roll-out of the state-built electronic medical records system (Florida HMS-EHR).

Conclusions

Academic health centers provide a model of collaboration that directly impacts on their success in delivering core public health services. Disease surveillance is positively affected by the diverse community affiliations of an academic health department. The academic health department, as epitomized by DCHD, is also better positioned to seize up-coming opportunities for local public health capacity building.

Keywords

Academic Health Departments; collaborative model; health informatics projects

Acknowledgments

This study was supported in part by an appointment to the APHIF Program administered by CSTE and funded by the CDC Cooperative Agreement 3U38HM000414-04W1.

*Ikechi Konkwo
E-mail: Ikechi_Konkwo@doh.state.fl.us

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluating Syndromic Data for Surveillance of Non-infectious Disease

Ramona Lall* and Marc Paladini

New York City Department of Health and Mental Hygiene, Queens, NY, USA

Objective

To evaluate several non-infectious disease related syndromes that are based on chief complaint (cc) emergency department (ED) syndromic surveillance (SS) data by comparing these with the New York Statewide Planning and Research Cooperative System (SPARCS) clinical diagnosis data. In particular, this work compares SS and SPARCS data for total ED visits and visits associated with three non-infectious disease syndromes, namely asthma, oral health and hypothermia.

Introduction

Syndromic surveillance data has predominantly been used for surveillance of infectious disease and for broad symptom types that could be associated with bioterrorism. There has been a growing interest to expand the uses of syndromic data beyond infectious disease. Because many of these conditions are specific and can be swiftly diagnosed (as opposed to infectious agents that require a lab test for confirmation) there could be added value in using the ICD9 ED discharge diagnosis field collected by SS. However, SS discharge diagnosis data is not complete or as timely as chief complaint data. Therefore, for the time being SS chief complaint data is relied on for non-infectious disease surveillance.

SPARCS data are based on clinical diagnoses and include information on final diagnosis, providing a means for comparing the chief complaint (from SS) to a diagnosis code (from SPARCS), for evaluating how well the syndrome is captured by SS and for assessing if it would be advantageous to get SS ED diagnosis codes in a more timely and complete manner.

Methods

Syndromes previously developed by the DOHMH were used for this work. Syndrome definitions are based on querying the cc field in SS data for terms associated with asthma, oral health and hypothermia. The asthma syndrome consists of search terms for 'ASTHMA', 'WHEEZING' and 'COPD'. The oral health syndrome uses ('TOOTH' or 'GUM') and ('ACHE', 'HURT') and excludes visits resulting from trauma (e.g., 'INJURY', 'ACCIDENT'). The hypothermia syndrome is limited to search for the word 'HYPOTHERMIA'. For the purpose of comparison of the SS data with SPARCS data for the three syndromes, the following ICD9 diagnosis codes were considered in SPARCS: 493 for asthma, 521-523, 525, 528-529 for oral health and 991 for hypothermia.

SS and SPARCS data for 2007 were used for this work as this was the most recent and complete SPARCS ED dataset that was available. Overall city-wide daily counts and hospital-level annual counts for total ED, asthma-, oral health- and hypothermia-related visits were computed for SS ED data and SPARCS ED data. A comparison of daily and hospital trends for SS and SPARCS for total and syndrome-related counts were conducted using correlation coefficients.

Results

There is a high correlation between total ED SS and SPARCS daily counts ($r=0.98$, p-value<0.001). On average, SPARCS daily counts are higher by approximately 75 visits (range: -674, 591) per day. Correlations between SS and SPARCS daily counts for asthma, oral health and hypothermia were 0.96 (p-value<0.001), 0.66 (p-value<0.001) and 0.45 (p-value<0.001), respectively. Correlations between SS and SPARCS hospital-level annual counts for asthma, oral health and hypothermia were 0.89 ($p<0.001$), 0.87 ($p<0.001$) and 0.07 ($p=0.61$). In 2007, less than 8% of individual SS records had a discharge diagnosis, and this was found to vary between hospitals (0-69%); therefore, a comparison between SS discharge diagnosis and SPARCS diagnosis data was not possible.

Conclusions

Overall, syndromic surveillance data was found to be a useful data source for public health surveillance of non-infectious disease. Total ED visits were found to be comparable between SS and SPARCS. While direct comparison of counts for syndromes is not possible, the daily syndrome counts between SS and SPARCS correlated well. However, the strength of correlation varied depending on the syndrome, with a better correlation for syndromes with larger volume of visits to the ED (e.g., asthma) and with more commonly used terms in the cc search (e.g., 'tooth ache') compared to syndromes with very specific search terms (e.g., 'hypothermia').

In certain instances, it is hypothesized that SS discharge diagnosis would provide more reliable and representative estimates than cc for tracking non-infectious disease. Future work will consider a period with more complete SS ED discharge diagnosis data for further comparisons and to test the hypothesis that more complete and timely SS ED discharge diagnosis data could improve surveillance efforts.

Keywords

chief complaint; syndromic surveillance; New York City; non-infectious disease; discharge diagnosis

Acknowledgments

Data Analysis and Syndromic Surveillance Unit, Bureau of Communicable Diseases

*Ramona Lall
E-mail: rlall@health.nyc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluating Utility of Cold-Injury Syndromic Surveillance Data in New York City

Kathryn Lane*[1], Ramona Lall[2], Katherine Wheeler[1], Kazuhiko Ito[1] and Thomas Matte[1]

[1]Bureau of Environmental Surveillance & Policy, NYC Department of Health & Mental Hygiene, New York, NY, USA; [2]NYC Department of Health & Mental Hygiene - Bureau of Communicable Diseases, New York, NY, USA

Objective

1) Develop cold exposure-related injury syndromic case definitions 2) use historical data to compare trends among cases identified in syndromic surveillance and cases identified in NY Statewide Planning and Research Cooperative System (SPARCS) hospital discharge data to evaluate representativeness and 3) develop regression models to examine relationships with cold weather conditions, and compare relationships across case definitions and data sources.

Introduction

Cold weather exposure-related injuries range from hypothermia to less severe conditions such as frost bite, trench foot, and chilblains, which are all preventable causes of mortality and morbidity. In recent years, NYC has successfully used syndromic surveillance of heat-related ED visits to inform emergency response during heat waves. Similar timely surveillance of cold-exposure related injuries could also inform public health protection measures during severe winter weather or cold season power outages. We conducted a retrospective analysis to compare hypothermia and cold-injury patient case characteristics, as well as temporal and meteorological correlates, between syndromic surveillance data and hospital discharge data.

Methods

Using chief complaint key words, we developed syndromic case definitions for 1) hypothermia only and 2) all injury caused by environmental cold exposure. Case definitions were applied to an archive of 2008-2010 cold season (October to April) syndromic surveillance data reported from a subset of NYC emergency departments (ED SS), representing 95% of all ED visits in NYC. Relevant ICD-9 codes (991, E901.0, E901.8, E901.9, E988.3) were applied to ED discharge data (ED Dx) to detect hypothermia and cold injury cases. Age, gender, and alcohol involvement were compared using tests of proportion to determine whether characteristics of cases identified through ED SS were representative of cases identified in ED Dx data. Poisson regression models were fit to estimate the relation of daily ED SS and Dx counts with daily temperature, snow depth, and other weather conditions. Models were adjusted for month, holiday, day of week, and year to account for potential temporal confounding.

Results

Fewer hypothermia and cold injury cases were detected with ED SS than with ED Dx but the two populations did not differ significantly with respect to age and sex. From 2008-2010, there were 292 hypothermia cases with an average annual rate of 1.2 per 100,000 people, and 445 cold injury cases (1.8 per 100,000) identified in ED SS data. Over the same time period, there were 566 hypothermia cases (2.3 per 100,000) and 933 cold injury cases (3.7 per 100,000) identified in ED Dx data. Daily counts of hypothermia and cold injury were correlated across data sources. In preliminary analyses using both case definitions, minimum daily temperature was associated with increases in daily ED SS and ED Dx counts. Mean daily snow depth was associated with ED SS and ED Dx cold injury cases, although not with hypothermia counts. Risk increased at lower temperatures for both case definitions.

Conclusions

There were no meaningful differences between ED SS and ED Dx weather models. Minimum temperature is associated with both case definitions. Snow depth is associated with cold injury. Daily minimum temperature and mean snow depth are potentially useful in determining timing of surveillance. Syndromic surveillance data are a timely means for monitoring hypothermia and other cold-related injuries, and could provide health departments with useful information during severe winter weather to guide prevention.

Keywords

syndromic; cold-injury; environmental surveillance

Acknowledgments

Data Analysis and Syndromic Surveillance Unit, Bureau of Communicable Diseases, NYC DOHMH

*Kathryn Lane
E-mail: klane1@health.nyc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Collaborative Automation Reliably Remediating Erroneous Conclusion Threats (CARRECT)

Jonathan C. Lansey*[1], Paul Picciano[1], Ian Yohai[1], Fred Grant[2] and Robert Gern[2]

[1]Aptima inc., Woburn, MA, USA; [2]Northrop Grumman Corporation, Falls Church, VA, USA

Objective

The objective of the CARRECT software is to make cutting edge statistical methods for reducing bias in epidemiological studies easy to use and useful for both novice and expert users.

Introduction

Analyses produced by epidemiologists and public health practitioners are susceptible to bias from a number of sources including missing data, confounding variables, and statistical model selection. It often requires a great deal of expertise to understand and apply the multitude of tests, corrections, and selection rules, and these tasks can be time-consuming and burdensome. To address this challenge, Aptima began development of CARRECT, the Collaborative Automation Reliably Remediating Erroneous Conclusion Threats system. When complete, CARRECT will provide an expert system that can be embedded in an analyst's workflow. CARRECT will support statistical bias reduction and improved analyses and decision making by engaging the user in a collaborative process in which the technology is transparent to the analyst.

Methods

Older approaches to imputing missing data, including mean imputation and single imputation regression methods, have steadily given way to a class of methods known as "multiple imputation" (hereafter "MI"; Rubin 1987). Rather than making the restrictive assumption that the data are missing completely at random (MCAR), MI typically assumes the data are missing at random (MAR).

There are two key innovations behind MI. First, the observed values can be useful in predicting the missing cells, and thus specifying a joint distribution of the data is the first step in implementing the models. Second, single imputation methods will likely fail not only because of the inherent uncertainty in the missing values but also because of the estimation uncertainty associated with generating the parameters in the imputation procedure itself. By contrast, drawing the missing values multiple times, thereby generating m complete datasets along with the estimated parameters of the model properly accounts for both types of uncertainty (Rubin 1987; King et al. 2001). As a result, MI will lead to valid standard errors and confidence intervals along with unbiased point estimates.

In order to compute the joint distribution, CARRECT uses a bootstrapping-based algorithm that gives essentially the same answers as the standard Bayesian Markov Chain Monte Carlo (MCMC) or Expectation Maximization (EM) approaches, is usually considerably faster than existing approaches and can handle many more variables.

Results

Tests were conducted on one of the proposed methods with an epidemiological dataset from the Integrated Health Interview Series (IHIS) producing verifiably unbiased results despite high missingness rates. In addition, mockups (Figure 1) were created of an intuitive data wizard that guides the user through the analysis processes by analyzing key features of a given dataset. The mockups also show prompts for the user to provide additional substantive knowledge to improve the handling of imperfect datasets, as well as the selection of the most appropriate algorithms and models.

Conclusions

Our approach and program were designed to make bias mitigation much more accessible to much more than only the statistical elite. We hope that it will have a wide impact on reducing bias in epidemiological studies and provide more accurate information to policymakers.

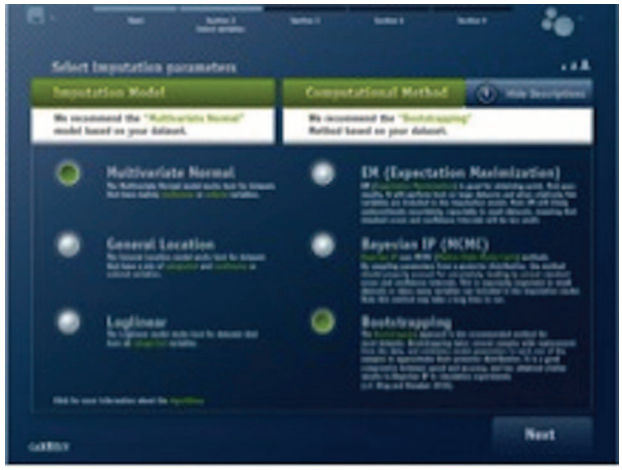


Figure 1 - Screenshot of user selecting imputation parameters.

Keywords

Bias reduction; Missing data; Statistical model selection

Acknowledgments

This material is based upon work supported by the Walter Reed Army Institute of Research (WRAIR) under Contract No. W81XWH-11-C-0505. Any opinions, findings and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the WRAIR.

References

James Honaker and Gary King, "What to do About Missing Values in Time Series Cross-Section Data" American Journal of Political Science Vol. 54, No. 2 (April, 2010): Pp. 561-581.

Gary King, James Honaker, Anne Joseph, and Kenneth Scheve. "Analyzing Incomplete Political Science Data: An Alternative Algorithm for Multiple Imputation", American Political Science Review, Vol. 95, No. 1 (March, 2001): Pp. 49-69.

*Jonathan C. Lansey
E-mail: jlansey@aptima.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Potential use of multiple surveillance data in the forecast of hospital admissions

Eric H. Lau*[1], T. L. Cheung[2], Dennis K.M. Ip[1], Eva Tsui[2], Edwina Shung[2], S. V. Lo[2] and Benjamin J. Cowling[1]

[1]The University of Hong Kong, Hong Kong; [2]Hospital Authority, Hong Kong

Objective

This paper describes the potential use of multiple influenza surveillance data to forecast hospital admissions for respiratory diseases.

Introduction

A sudden surge in hospital admissions in public hospital during influenza peak season has been a challenge to healthcare and manpower planning. In Hong Kong, the timing of influenza peak seasons are variable and early short-term indication of possible surge may facilitate preparedness which could be translated into strategies such as early discharge or reallocation of extra hospital beds. In this study we explore the potential use of multiple routinely collected syndromic data in the forecast of hospital admissions.

Methods

A multivariate dynamic linear time series model was fitted to multiple syndromic data including influenza-like illness (ILI) rates among networks of public and private general practitioners (GP), and school absenteeism rates, plus drop-in fever count data from designated flu clinics (DFC) that were created during the pandemic. The latent process derived from the model has been used as a measure of the influenza activity [1]. We compare the cross-correlations between estimated influenza level based on multiple surveillance data and GP ILI data, versus accident and emergency hospital admissions with principal diagnoses of respiratory diseases and pneumonia & influenza (P&I).

Results

The estimated influenza activity has higher cross-correlation with respiratory and P&I admissions (ρ=0.66 and 0.73 respectively) compared to that of GP ILI rates (Table 1). Cross correlations drop distinctly after lag 2 for both estimated influenza activity and GP ILI rates.

Conclusions

The use of a multivariate method to integrate information from multiple sources of influenza surveillance data may have the potential to improve forecasting of admission surge of respiratory diseases.

Table 1. Cross correlations between the estimated influenza activity based on the multivariate dynamic linear model, GP ILI rate versus A&E respiratory diseases and P&I admissions

Surveillance data			Cross correlations / lags*		
	-2	-1	0	1	2
Respiratory disease admissions					
GP ILI	0.48	0.53	0.55	0.50	0.45
Estimated influenza activity	0.59	0.66	0.66	0.58	0.46
P&I admissions					
GP ILI	0.57	0.62	0.65	0.59	0.49
Estimated influenza activity	0.66	0.73	0.73	0.65	0.53

*negative lags refer to correlations between lagged surveillance data and hospital admissions

Keywords

influenza; surveillance; admission; respiratory

References

Lau EH, Cheng CK, Ip DK, Cowling BJ. Situational awareness of influenza activity based on multiple streams of surveillance data using multivariate dynamic linear model. PLoS ONE 7(5): e38346. doi:10.1371/journal.pone.0038346

*Eric H. Lau
E-mail: ehylau@hku.hk

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Poison Center Data for Public Health Surveillance: Poison Center and Public Health Perspectives

Royal K. Law*[1], Josh Schier[1], Jay Schauben[2], Katherine Wheeler[3] and Prakash Mulay[4]

[1]Centers for Disease Control and Prevention, Chamblee, GA, USA; [2]Florida Poison Information Center - Jacksonville, Jacksonville, FL, USA; [3]New York City Department of Health and Mental Hygiene, New York City, NY, USA; [4]Florida Department of Health, Tallahassee, FL, USA

Objective

To describe the use of poison center data for public health surveillance from the poison center, local, state, and federal public health perspectives and to generate meaningful discussion on how to address the challenges to collaboration.

Introduction

Since 2008, poisoning has become the leading cause of injury-related death in the United States (US); since 1980, the poisoning-related fatality rate in the US has almost tripled.[1] Many poison-related injuries and deaths are reported to regional poison centers (PCs) which receive about 2.4 million reports of human chemical and poison exposures annually.[2] Federal, state, and local public health (PH) agencies often collaborate with poison centers and use PC data for public health surveillance of poisoning-related health issues. Many state and local PH agencies have partnerships with regional PCs for direct access to local PC data which help them perform this function. At the national level, CDC conducts public health surveillance for exposures and illnesses of public health significance using the National Poison Data System (NPDS), the national PC reporting database.

Though most PC and PH officials agree that PC data play an important role in PH practice and surveillance, collaboration between PH agencies and PCs has been hindered by numerous challenges. To address these challenges and bolster collaboration, the Poison Center and Public Health Collaborations Community of Practice (CoP) was created in 2010 by CDC as a means to share experiences, identify best practices, and facilitate relationships among federal, state and local public health agencies and PCs. To date, the Poison Center and Public Health Collaborations CoP includes over 200 members from state and local public health, regional PCs, CDC, the American Association of Poison Control Centers (AAPCC), and the Environmental Protection Agency (EPA). A leadership team was created with representatives of the many stakeholders of the community to drive its direction and oversee activities.

Methods

The panel will consist of 4 presenters and 1 moderator, who are members of the Poison Center and Public Health Collaborations CoP leadership team. Each presenter will bring a unique perspective of the use of PC data for PH practice and surveillance: CDC, state department of health, a local department of health, and a PC. Royal Law from the CDC National Center for Environmental Health will present on using PC data for identification of exposures and illnesses of public health significance identified from NPDS data collected from all 57 PCs. Dr. Jay Schauben from the Florida/USVI Poison Information Center - Jacksonville will discuss PC participation in surveillance and use of PC data for tracking and mitigation of PH events in Florida. Dr. Prakash Mulay from the Florida Department of Health will discuss utilization of PC data to enhance ESSENCE-based chemical-associated exposure and illness surveillance in Florida. Katherine Wheeler from the New York City (NYC) Department of Health and Mental Hygiene will discuss NYC's use of PC data in surveillance of potential emerging issues, from energy drinks to synthetic marijuana. Each presenter will discuss the use of PC data for PH practice and surveillance in his or her organization and jurisdiction, the successes of using PC data, and their challenges.

Results

The moderator will engage the audience by facilitating discussion of the successes and challenges to using PC data for PH practice and surveillance with the audience.

Sample questions:

What are your current capacities and collaborative activities between your state/local health department and your poison center?

What non-funding related barriers hinder the collaboration between your state/local health department and poison center?

If more funding were available, how would you use this funding to increase the level of interactivity with the poison center and state/local health department?

Keywords

Surveillance; Poison Center; Community of practice

References

1. Warner M, Chen LH, Makuc DM, Anderson RN, and Minino AM. Drug Poisoning Deaths in the United States, 1980–2008. National Center for Health Statistics Data Brief, December 2011. Accessed 8/29/2012.
2. Bronstein AC, Spyker DA, Cantilena LR, Green JL, Rumak BH, Dart RC. 2010 Annual Report of the American Association of Poison Control Centers' National Poison Data System (NPDS): 28th Annual Report. Clin Toxicol 2011; 49: 910-941.

*Royal K. Law
E-mail: hua1@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Surveillance for Radiation-Related Exposures Reported to the National Poison Data System

Royal K. Law*[1], Colleen Martin[1], Alvin Bronstein[2], Arthur Chang[1] and Joshua Schier[1]

[1]Centers for Disease Control and Prevention, Chamblee, GA, USA; [2]American Association of Poison Control Centers, Alexandria, VA, USA

Objective

To describe radiation-related exposures of potential public health significance reported to the National Poison Data System (NPDS).

Introduction

For radiological incidents, collecting surveillance data can identify radiation-related public health significant incidents quickly and enable public health officials to describe the characteristics of the affected population and the magnitude of the health impact which in turn can inform public health decision-making. A survey administered by the Council of State and Territorial Epidemiologists (CSTE) to state health departments in 2010 assessed the extent of state-level planning for surveillance of radiation-related exposures and incidents: 70%–84% of states reported minimal or no planning completed. One data source for surveillance of radiological exposures and illnesses is regional poison centers (PCs), who receive information requests and reported exposures from healthcare providers and the public. Since 2010, the Centers for Disease Control and Prevention (CDC) and the American Association of Poison Control Centers (AAPCC) have conducted ongoing surveillance for exposures to radiation and radioactive materials reported from all 57 United States (US) PCs to NPDS, a web-based, national PC reporting database and surveillance system.

Methods

We collaborated with the American Association of Poison Control Centers (AAPCC), Poisindex® and Thomson Reuters Healthcare to develop an improved coding system for tracking radiation-related exposures reported to US PCs during 2011 and trained PC staff on its usage. We reviewed NPDS data from 1 September 2010 – 30 June 2012 for reported exposures to pharmaceutical or nonpharmaceutical radionuclides; ionizing radiation; radiological or nuclear weapons; or X-ray, alpha, beta, gamma, or neutron radiation. CDC medical toxicology and epidemiology staff reviewed each reported exposure to determine whether it was of potential public health concern (e.g. exposures associated with an ongoing public health emergency, several reported exposures clustered in space and time). When further information was needed to classify the potential public health importance of a call, CDC and AAPCC staff contacted the regional PC where each call originated. When exposures were spatially and temporally clustered, we reviewed news stories in the public media for evidence of an associated radiation incident.

Results

Of 419 exposures reported during the study period, 25 were associated with a radiation-related incident. Of these, 4 were related to an exposure to x-ray radiation from an industrial radiography incident, 11 were related to a transportation accident involving potential contamination with radioactive material, and 10 were related to the Fukushima Daiichi Japan nuclear reactor disaster. Public health, hazardous materials, or hospital radiation safety staff were involved in responding to each of these events. We also identified 26 reported exposures associated with a regional radiation anti-terrorism exercise. The reported exposures were followed-up and removed from analysis once we determined they were part of the exercise. The remaining (n=368; 88%) were either requests for information, confirmed non-exposures, or exposures deemed unrelated or non-significant.

Conclusions

The capability to monitor self- or clinician-reported exposures to radiation and radioactive materials is available in NPDS for state and local public health use in collaboration with their regional PC and may improve public health capacity to identify and respond to radiological emergencies. Next steps include testing the system's capability to accurately classify and rapidly respond to a cluster of calls to PCs reporting radiation exposures associated with a "dirty bomb" exercise during July, 2012.

Keywords

Surveillance; Poison center; radiation

References

Council of State and Territorial Epidemiologists. The Status of State-level Radiation Emergency Preparedness and Response Capabilities, 2010. Available at: http://www.cste.org/webpdfs/2010raditionreport.pdf. Accessed July 19, 2012.

*Royal K. Law
E-mail: hua1@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Piece of the Public Health Surveillance Puzzle: Social Contacts among School-Aged Children

Molly Leecaster*[1], Warren Pettey[1], Damon Toth[1], Jeanette Rainey[2], Amra Uzicanin[2] and Matthew Samore[1]

[1]Internal Medicine, University of Utah, Salt Lake City, UT, USA; [2]Centers for Disease Control and Prevention, Atlanta, GA, USA

Objective

To enhance public health surveillance and response for acute respiratory infectious diseases by understanding social contacts among school-aged children

Introduction

Timely and effective public health decision-making for control and prevention of acute respiratory infectious diseases relies on early disease detection, pathogen properties, and information on contact behavior affecting transmission. However, data on contact behavior are currently limited, and when available are commonly obtained from traditional self-reported contact surveys [1, 2]. Information for contacts among school-aged children is especially limited, even though children frequently have higher attack rates than adults, and school-related transmission is commonly predictive of subsequent community-wide outbreaks, especially for pandemic influenza.

Within this context, high-quality data are needed about social contacts. Precise contact estimates can be used in mathematical models to understand infectious disease transmission [3] and better target surveillance efforts. Here we report preliminary data from an ongoing 2-year study to collect social contact data on school-aged children and examine the transmission dynamics of an influenza pandemic.

Methods

Our aim is to capture mixing patterns and contact rates of school-aged children in 24 schools and other non-school-related venues. We used a stratified design to ensure coverage of urban, suburban, and rural school districts, as well as climatically different areas (mountains and desert) in Utah. Elementary, middle, and high schools were chosen in each stratum. We defined a self-reported contact as anyone with whom the participant talked to face-to-face, played with, or touched. Contact logs collected subjective information (age, location, and duration) on self-reported contacts during a 2-day period. Objective contact data were collected by using proximity sensors [4] that recorded signals from other sensors within approximately 3-4 feet.

Mixing patterns during school and non-school-related activities were summarized for participating school-aged children. We developed contact networks using proximity sensor data, providing visualizations of contact patterns as well as numeric contact measures. Contact networks were characterized with respect to degree distribution, and density. The degree for each person was calculated as the number of unique contacts. The density for a network was calculated as the number of observed contacts divided by the number of possible contacts.

Results

Two elementary schools, four summer camps, and one club participated in the study between May and August, 2012. Data were processed for the two schools and one camp. The mean degrees for the two schools were 28 and 29, with network sizes 109 and 129, respectively. The mean degree from camp was 43, whose network size was 141. The density of contacts was 0.26 and 0.22 for the schools and 0.31 for the camp. The density within classrooms at the two schools ranged from 0.78 to 0.98. School-aged children typically underreported contacts using the contact log compared with objective proximity sensor data; this difference was statistically significant.

Conclusions

The variability in these and other contact network characteristics represent factors that could impact influenza transmission. Quantifying these factors improves our understanding of influenza transmission dynamics, which in turn can be used to adapt surveillance methods and control and prevention strategies. Almost all contact among students in our two elementary schools occurs within the classroom and the contact patterns differ by classroom, due to desk arrangement or other characteristics. Thus, during an elementary school outbreak it may be beneficial to focus on classroom-specific surveillance and control strategies.

The study is ongoing and we expect the variability in contact rates and mixing patterns will be even greater for middle and high schools where students switch classrooms and classmates each period. These schools could benefit from alternative surveillance and control strategies that account for the heightened overall mixing of the student body.

Keywords

children; respiratory infectious disease; social network; transmission model; proximity sensor

Acknowledgments

This study is funded by the Centers for Disease Control and Prevention 5U01CK000177.

References

1. Mossong, J, et al 2008 PLOS Medicine 5(3): 381–391.
2. Glass L and R Glass 2008 BMC Public Health 8(61).
3. Keeling M and K Eames 2005 J.R.Soc.Interface 2:295-307.
4. Salathé M, et al 2010 PNAS 1009094108.

*Molly Leecaster
E-mail: molly.leecaster@hsc.utah.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Time of Arrival Analysis in NC DETECT to Find Clusters of Interest from Unclassified Patient Visit Records

Meichun Li*[1], Wayne Loschen[2], Lana Deyneka[3], Howard Burkom[2], Amy Ising[1] and Anna Waller[1]

[1]Emergency Medicine, UNC Chapel Hill, Chapel Hill, NC, USA; [2]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA; [3]North Carolina Division of Public Health, Raleigh, NC, USA

Objective

To describe a collaboration with the Johns Hopkins Applied Physics Laboratory (JHU APL), the North Carolina Division of Public Health (NC DPH), and the UNC Department of Emergency Medicine Carolina Center for Health Informatics (CCHI) to implement time-of-arrival analysis (TOA) for hospital emergency department (ED) data in NC DETECT to identify clusters of ED visits for which there is no pre-defined syndrome or sub-syndrome.

Introduction

TOA identifies clusters of patients arriving to a hospital ED within a short temporal interval. Past implementations have been restricted to records of patients with a specific type of complaint. The Florida Department of Health uses TOA at the county level for multiple subsyndromes (1). In 2011, NC DPH, CCHI and CDC collaborated to enhance and evaluate this capability for NC DETECT, using NC DETECT data in BioSense 1.0 (2). After this successful evaluation based on exposure complaints, discussions were held to determine the best approach to implement this new algorithm into the production environment for NC DETECT. NC DPH was particularly interested in determining if TOA could be used for identifying clusters of ED visits not filtered by any syndrome or sub-syndrome. In other words, can TOA detect a cluster of ED visits relating to a public health event, even if symptoms from that event are not characterized by a predefined syndrome grouping? Syndromes are continuously added to NC DETECT but a syndrome cannot be created for every potential event of public health concern. This TOA approach is the first attempt to address this issue in NC DETECT. The initial goal is to identify clusters of related ED visits whose keywords, signs and/or symptoms are NOT all expressed by a traditional syndrome, e.g. rash, gastrointestinal, and flu-like illnesses. The goal instead is to identify clusters resulting from specific events or exposures regardless of how patients present – event concepts that are too numerous to pre-classify.

Methods

In late 2011, NC DPH and JHU APL signed a Software License Agreement and soon thereafter CCHI received the TOA software package. In May 2012, the TOA controller was adapted and set up to run against ED visit data for all NC DETECT hospitals. The TOA looks for clusters in all ED visits by hospital based solely on arrival time in both 30-minute and 60-minute intervals. There is no pre-classification of the chief complaints or triage notes into syndromes. TOA alerts are viewable on the NC DETECT Web application and, as of August 2012, users are able to document any actions taken on these alerts.

Results

From April 15, 2012 to July 31, 2012, TOA generated 173 alerts across all 115 hospitals reporting to NC DETECT. The TOA identified a group of scabies-related ED visits that was not captured in another syndrome. The TOA also identified clusters identified by hospitals as disaster-related which included misspellings that had not been previously identified, e.g. “diaster” and “disater,” as well as events involving out-of-town groups that will not be identified spatially (Table 1). This preliminary review of TOA alerts did not evaluate TOA for false negatives.

Conclusions

Our preliminary review of TOA shows that this algorithm approach can be helpful for identifying clusters of ED visits that are not captured by existing syndromes and can be used to identify hospital coding schemes for disaster events. The TOA will continue to be monitored in our production environment and evaluated for additional effectiveness. We will also explore tools that will display counts of terms within a TOA alert to assist in signal investigation.

Table 1: Sample clusters detected with TOA analysis

Cluster Event Type	Number of ED Visits in TOA alert / Number of visits related to the specific event cluster	Sample chief complaints in cluster
Disaster-related	13 / 9	Disaster abd pain, diaster flu, disaster phyc, diaster anxity, diaster black
Scabies	16 / 8	Scabies 7FER, Scaobes 7FER, 5M FOLLOW UP
Same out of town location	17 / 7	Cough, laceration(s)

Keywords

Cluster detection; Time-of-arrival analysis; Syndrome classification

References

1. Burkom H, Loschen W, Kite-Powell A et al. A Collaboration to Enhance Detection of Disease Outbreaks Clustered by Time of Patient Arrival, presented at the International Society for Disease Surveillance, 2010 Annual Conference, Park City, Utah, Dec 2, 2010
2. Deyneka L, Xu Z, Burkom H, Hicks P, Benoit S, Vaughan-Batten H, Ising A. Finding time-of-arrival clusters of exposure-related visits to emergency departments in contiguous hospital groups. Emerging Health Threats Journal 2011, 4: 11702 - DOI: 10.3402/ehtj.v4i0.11702

*Meichun Li
E-mail: mcli@email.unc.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Implementation of a Mobile-Based Surveillance System in Saudi Arabia for the 2009 Hajj

Wei Li*

Centers for Disease Control and Prevention, Atlanta, GA, USA

Objective

To develop and implement a mobile-based disease surveillance system in the Kingdom of Saudi Arabia (KSA) for the 2009 Hajj; to strengthen public health preparedness for the H1N1 Influenza A pandemic.

Introduction

The Hajj is considered to be the largest mass gathering to date, attracting an estimated 2.5 million Muslims from more than 160 countries annually (1). The H1N1 Influenza A pandemic of 2009 generated a global wave of concern among public health departments that resulted in the institution of preventive measures to limit transmission of the disease. Meanwhile, the pandemic amplified an urgent need for more innovative disease surveillance tools to combat disease outbreaks.

A collaborative effort between the KSA Ministry of Health (MOH) and the U.S. Centers for Disease Control and Prevention (CDC) was initiated to implement and deploy an informatics-based mobile solution to provide early detection and reporting of disease outbreaks during the 2009 Hajj. The mobile-based tool aimed to improve the efficiency of disease case reporting, recognize potential outbreaks, and enhance the MOH's operational effectiveness in deploying resources (2).

Methods

We designed a case-based system consisting of a mobile-based data collection toolkit and interactive map-based user interface to perform geospatial analysis and visualization. A train-the-trainer approach was adapted to provide training to the KSA MOH.

Results

More than 200 public health and information and communication technology (ICT) professionals were trained, and 100 mobile devices were deployed during the 2009 Hajj. Nine diseases and conditions that were considered as highest priority during the Hajj were under surveillance, including H1N1 Influenza A and Influenza-like Illness.

Pilot testing of the system was conducted during the first week of Ramadan and a modified system was fully operational during the Hajj. Data collected on smartphones were sent to the system via a secured network. The data were processed immediately and visualized on highly interactive maps with local and global views.

Conclusions

Effective public health decision-making requires timely and accurate information from a variety of sources. Mobile-based systems (e.g., personal digital assistants and smartphones) for data collection, transmission, reporting, and analyses provide a faster, easier, and cheaper means to communicate standardized and shareable public health data for decision-making (3). Mobile-based systems have been recognized as a quick and effective response solution to mass gatherings and recommended as data gathering and communication systems with geographical information system (GIS) capability (2). This paper explored the development and implementation of the Global Positioning System/ Geographic Information System (GPS/GIS) enabled mobile-based disease surveillance system as a feasible and effective way to support and strengthen preparedness for H1N1 Influenza A during the 2009 Hajj.

Mobile computing technology can be utilized to provide rapid and accurate data collection for public health decision-making during mass gatherings. The GIS-based interactive mapping tool provided a pioneering example of the power of a geographically based internet-accessible surveillance system with real-time data visualization. The technical challenges in the process of implementation and in the field were also identified.

A need now exists for a comprehensive and comparative review of parameters such as handheld device cost, training required, and system evaluations because selecting the appropriate software/hardware and system remains a challenge not only to public health professionals, but to the development and application of informatics technology as well.

Keywords

Mobile Technology; GIS/GPS; Mass Gatherings; Surveillance System; Public Health Preparedness

Acknowledgments

Many people contributed to the mobile-based surveillance system's development and implementation for the 2009 Hajj. The author would like to acknowledge Dr. Z. Memish and his colleagues at KSA MOH, Mr. C. Gillespie and his colleagues at the U.S. Embassy in KSA, the CDC Foundation, and colleagues across CDC.

References

1. Memish ZA, Ahmed GA. Mecca bound: the challenges ahead. J. Travel Med 2002; 9:202-10
2. Memish ZA, McNabb S, Mahoney F, et al. Establishment of public health security in Saudi Arabia for the 2009 Hajj in response to pandemic influenza A H1N1. The Lancet, Published online November 14, 2009; DOI:10.1016/S0140-6736(09)61927-9
3. Yu, P. et al. The development and evaluation of a PDA-based method for public health surveillance data collection in developing countries, Int. J. Med. Inform. (2009; 78(8):532-42

*Wei Li
E-mail: for5@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

COPD-Related ED Visits in North Carolina: Hospitalizations and Return Visits

Steven J. Lippmann*, Karin B. Yeatts, Anna Waller, Kristen Hassmiller Lich, Debbie Travers, Morris Weinberger and James F. Donohue

University of North Carolina, Chapel Hill, NC, USA

Objective

To investigate hospital admissions and short-term return visits resulting from chronic obstructive pulmonary disease (COPD)-related emergency department (ED) visits.

Introduction

COPD is a prevalent chronic disease among older adults; exacerbations often result in ED visits and subsequent hospital admissions.[1,2] A portion of such patients return to the ED within a few days or weeks.[3] In this study, we investigated patterns of hospital admissions and short-term return visits resulting from COPD-related ED visits.

Methods

We performed a population-based study of ED visits for COPD using state-wide surveillance data from NC DETECT[4], including all ED visits made by NC residents aged ≥45 years in 2008-2009. Visits were considered COPD-related if the first- or second-listed discharge diagnoses contained one of the following ICD-9-CM codes: 491.*, 492.*, 493.2*, 494.*, or 496.*. Hospital admissions were captured by ED disposition codes. If a patient had made another COPD-related ED visit within the prior 3 or 30 days, we defined the current visit as a 3-day or 30-day return visit. We compared the prevalence of hospitalization and 3- and 30-day return visits by age, sex, and payment method. We also described the disposition patterns for return visit pairs.

Results

There were 97,511 COPD-related ED visits made by adults age 45 and older in NC in 2008-2009, made by 64,568 individuals. HOSPITAL ADMISSIONS: Nearly half (46.3%) of all COPD-related ED visits resulted in hospital admission. Hospitalization prevalence increased with age, but there were no differences by gender. ED visits that were non-insured (self-pay) or paid by Medicare or Medicaid were less likely to lead to hospitalization than those with private insurance. RETURN VISITS: 1.6% (1607) of the COPD-related ED visits were categorized as 3-day return visits and 11.2% (10922) were considered 30-day return visits. There were no statistical differences by gender for 3-day returns, while 30-day returns were more likely to be made by men. Prevalence of return visits for both intervals initially increased with age compared to the 45-49 years age group, then decreased steadily after age 65. Visits that were non-insured or paid by Medicare or Medicaid were statistically more likely to be 3-day or 30-day returns than those paid by private insurance. DISPOSITION PATTERNS: We also examined the permutations of 1st and 2nd ED visit dispositions that make up these return visit pairs. While many return visits were discharged at both visits in the return visit pair, a substantial proportion were admitted at one or both visits. Surprisingly, in 8% of the 3-day return visit pairs, the patient was hospitalized at the 1st ED visit but yet still returned to the ED within 3 days; for the 30-day visit pairs, 37% returned despite the patient being admitted at the 1st visit.

Conclusions

This population-based study describes the short-term outcomes of a large number of COPD-related ED visits using a unique state-wide surveillance system. We found a high prevalence of hospital admissions and return ED visits, including many repeat hospitalizations. This study also demonstrates how surveillance data can be used for research on “acute on chronic” disease epidemiology.

Keywords

Chronic obstructive pulmonary disease; Chronic disease surveillance; Emergency department data; Hospitalizations; Return visits

Acknowledgments

The statistical analysis for this research was supported by a University of North Carolina, Gillings School of Public Health Gillings Innovation Laboratory Grant. Data were obtained from the NC DHHS/DPH NC DETECT system under a data use agreement. The NC DETECT Data Oversight Committee does not take responsibility for the scientific validity or accuracy of methodology, results, statistical analyses, or conclusions presented.

References

1. Rowe BH, Voaklander DC, Marrie TJ, Senthilselvan A, Klassen TP, Rosychuk RJ. Outcomes following chronic obstructive pulmonary disease presentations to emergency departments in Alberta: A population-based study. Can Resp J 2010;17(6):295.
2. Tsai C-L, Clark S, Cydulka RK, Rowe BH, Camargo CA. Factors Associated with Hospital Admission among Emergency Department Patients with Chronic Obstructive Pulmonary Disease Exacerbation. Acad Emerg Med 2007;14(1):6–14.
3. Kim S. Prospective Multicenter Study of Relapse Following Emergency Department Treatment of COPD Exacerbation. Chest 2004;125(2):473–81.
4. Carolina Center for Health Informatics, University of North Carolina at Chapel Hill. The UNC Department of Emergency Medicine Carolina Center for Health Informatics Report, NC DETECT Emergency Department Data: 2008 [Internet]. 2010 [cited 2012 Sep 2]. Available from: http://www.ncdetect.org/pubs.html.

*Steven J. Lippmann
E-mail: slippmann@unc.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Detection of Patients with Influenza Syndrome Using Machine-Learning Models Learned from Emergency Department Reports

Arturo López Pineda*, Fu-Chiang Tsui, Shyam Visweswaran and Gregory F. Cooper

University of Pittsburgh. Department of Biomedical Informatics, Pittsburgh, PA, USA

Objective

Compare 7 machine learning algorithms with an expert constructed Bayesian network on detection of patients with influenza syndrome.

Introduction

Early detection of influenza outbreaks is critical to public health officials. Case detection is the foundation for outbreak detection. Previous study by Elkin el al. demonstrated that using individual emergency department (ED) reports can better detect influenza cases than using chief complaints [1]. Our recent study using ED reports processed by Bayesian networks (using expert constructed network structure) showed high detection accuracy on detection of influenza cases [2].

Methods

The dataset used in this study includes 182 ED reports with confirmed PCR influenza tests (Jan 1, 2007-Dec 31, 2009) and 40853 ED reports as control cases from 8 EDs in UPMC (Jul 1, 2010-Aug 31, 2010). All ED reports were deidentified by De-ID software with IRB approval.

An NLP system, Topaz, was used to extract relevant findings and symptoms from the reports and encoded them with the UMLS concept unique identifier codes [2]. Two subsets were created: DS1-train (67% of cases) and DS1-test (remaining 33%).

The algorithms used for training the models are: Naïve Bayes Classifier, Efficient Bayesian Multivariate Classification (EBMC) [3], Bayesian Network with K2 algorithm, Logistic Regression (LR), Support Vector Machine (SVM), Artificial Neural Networks (ANN) and Random Forest (RF).

The predictive performance of each method was evaluated using the area under the receiver operator characteristic (AUROC) and the Hosmer-Lemeshow (HL) statistical significance testing, that describes the lack-of-fit of the model to the dataset.

Results

The evaluation results of all the models using DS1-test, including the AUROC, its confidence interval, p-value (between each algorithm and the expert) and the calibration with HL are shown in Table 1.

Conclusions

All models achieved high AUROC values. The pairwise comparison of p-values in Table 1 demonstrates that the AUROCs of all the machine-learning models and the expert model were not significantly different. Nevertheless, EBMC is the best fitted. The model created by EBMC is shown in Figure 1.

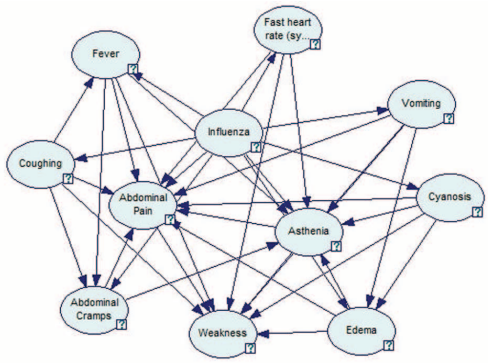
One limitation of the study is that the test dataset has low influenza prevalence, which may bias the detection algorithm performance. We are in the process of testing the algorithms using higher prevalence rate.

The same process could also be applied to other diseases to further research the generalizability of our method.

Predictive performance and Calibration

Algorithm	AUROC	95% CI	p-value	Calibration: HL
NaïveBayes	0.9988	(0.9983, 0.9994)	0.2342	4880.63
EBMC	0.9993	(0.9989, 0.9998)	0.2255	4.53
BN-K2	0.9994	(0.9990, 0.9998)	0.2228	1315.71
LR	0.9829	(0.9512, 1.0000)	0.8935	177.01
SVM	0.9996	(0.9993, 0.9999)	0.2189	12.30
RandForest	0.9995	(0.9993, 0.9998)	0.2201	16.30
A-NN	0.9991	(0.9986, 0.9997)	0.2300	275.81
Expert	0.9798	(0.9483, 1.0000)	1.0000	14374.67

Area under the ROC curve (AUROC) with 95% Confidence Interval; p-value relative to the Expert model; and Hosmer-Lemeshow calibration statistic



Influenza Syndrome model created using the EBMC algorithm

Keywords

influenza; machine-learning; ED reports

Acknowledgments

This research was funded by grant P01-HK000086 from the CDC in support of the University of Pittsburgh Center for Advanced Study of Public Health in Informatics. The International Fulbright S&T Award and CONACyT-Mexico support ALP.

References

[1] Elkin, P. L., Froehling, D. A., Wahner-Roedler, D. L., Brown, S. H., & Bailey, K. R. (2012). Comparison of natural language processing biosurveillance methods for identifying influenza from encounter notes. Annals of Internal Medicine, 156(1 Pt 1), 11–18.

[2] Tsui, F.-C., Wagner, M., Cooper, G. F., Que, J., Harkema, H., Dowling, J., Sriburadej, T., et al. (2011). Probabilistic Case Detection for Disease Surveillance Using Data in Electronic MedicalRecords. Online Journal of Public Health Informatics, 1–17.

[3] Cooper, G. F., Hennings-Yeomans, P. P., & Barmada, M. M. (2010). An efficient bayesian method for predicting clinical outcomes from genome-wide data. AMIA 2010 Symposium Proceedings, 2010, 127–131.

*Arturo López Pineda
E-mail: arl68@pitt.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Development of Automated Data Quality Indicators and Visualizations using Florida's ESSENCE System

Wayne Loschen*[1] and Aaron Kite-Powell[2]

[1]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA; [2]Florida Department of Health, Jacksonville, FL, USA

Objective

The objective of this project was to develop visualizations and tools for public health users to determine the quality of their surveillance data. Users should be able to determine or be warned when significant changes have occurred to their data streams, such as a hospital converting from a free-text chief complaint to a pick list. Other data quality factors, such as individual variable completeness and consistency in how values are mapped to standard system selections should be available to users. Once built, these new visualizations should also be evaluated to determine their usefulness in a production disease surveillance system.

Introduction

Understanding your data is a fundamental pillar of disease surveillance success. With the increase in automated, electronic surveillance tools many public health users have begun to rely on those tools to produce reports that contain processed results to perform their daily jobs. These tools can focus on the algorithm or visualizations needed to produce the report, and can easily overlook the quality of the incoming data. The phrase "garbage in, garbage out" is often used to describe the value of reports when the incoming data is not of high quality. There is a need then, for systems and tools that help users determine the quality of incoming data.

Methods

A series of data quality visualizations were developed and implemented in the Florida Department of Health's version of ESSENCE. Users were given numerous pages that showed different aspects of data quality, such as variable-level percent completeness measurements shown by hospital or county. Other items included the percent of time a value that should have been a part of a specific reference list was actually present and matched to known values, the number of input files received by a hospital, and the time each data source was processed. Finally, an algorithm and visualization was developed to alert users when data quality factors had changed significantly. With access to all these new screens, users of the system were given the opportunity to use the system and their usage and opinions were collected.

Results

The data quality portal has been active the Florida ESSENCE system since March 31st, 2012. Between that time and August the portal has been accessed over 1300 times. The presentation will include additional statistics about which specific features were most used and those features that users have found the most useful. In addition, data quality issues that have been discovered using the new tool will be discussed.

Conclusions

With the ever increasing amount of data that public health must analyze due to meaningful use, it is imperative that tools and visualizations that can decipher data quality issues be made available in an easily accessible format and without the need for tools external to the system. If systems continue to ignore changes in the data they receive automatically, it can easily produce degraded or incorrect analyses and interpretation of events, leading to wasted resources. These results can negatively impact the decisions and responses that public health users make, especially in light of the increasing reliance on these types of systems for up to the minute information. This project has developed tools and visualizations that can help determine the data quality issues as they are occurring. This presentation will outline the lessons learned for using and creating these tools so they can be shared for everyone to benefit.

Keywords

Visualization; Data Quality; Meaningful Use

*Wayne Loschen
E-mail: wayne.loschen@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Sharing Public Health Information with Non-Public Health Partners

Wayne Loschen*, Rekha Holtry, Kalman Hazins and Sheryl Happel Lewis

Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Objective

The objective of this project is to provide a technical mechanism for information to be easily and securely shared between public health ESSENCE users and non-public health partners; specifically, emergency management, law enforcement, and the first responder community. This capability allows public health officials to analyze incoming data and create interpreted information to be shared with others. These interpretations are stored securely and can be viewed by approved users and captured by authorized software systems. This project provides tools that can enhance emergency management situational awareness of public health events. It also allows external partners a mechanism for providing feedback to support public health investigations.

Introduction

Automated Electronic Disease Surveillance has become a common tool for most public health practitioners. Users of these systems can analyze and visualize data coming from hospitals, schools, and a variety of sources to determine the health of their communities. The insights that users gain from these systems would be valuable information for emergency managers, law enforcement, and other non-public health officials. Disseminating this information, however, can be difficult due to lack of secure tools and guidance policies. This abstract describes the development of tools necessary to support information sharing between public health and partner organizations.

Methods

The project initially brought together public health and emergency management officials to determine current gaps in technology and policy that prevent sharing of information on a consistent basis. Officials from across the National Capital Region (NCR) in Maryland, Virginia, and the District of Columbia determined that a web portal in which public health information could be securely posted on and captured by non-public health users (humans and computer systems) would be best. The development team then found open source tools, such as the Pebble blogging system, that would allow information to be posted, tagged, and searched in an easily navigable site. The system also provided RSS feeds both on the site as whole and specific tags to support notification. The team made modifications to the system to incorporate spring security features to allow the site to be securely hosted requiring usernames and passwords for access. Once the Pebble system was completed and deployed, the NCR's aggregated ESSENCE system was adapted to allow users to submit daily reports and post time series images to the new site. An additional feature was created to post visualizations every evening to the site summarizing the day's reports.

Results

The system has been in testing since March of 2012 and users of the system have provided valuable feedback. Based on the success of the tests, public health users in the NCR have begun working on the policy component of the project to determine when and how it should be used. Modifications to the system since deployment have included a single sign on capability for ESSENCE users and the desire to allow other features of ESSENCE to be posted beyond time series graphs, such as GIS maps and statistical reports.

Conclusions

Having tools that can promote exchange of information between public health and non-public health partners such as emergency management, law enforcement, and first responders can greatly enhance the situational awareness and impact overall preparedness and response. By having tools embedded in ESSENCE, users are able to integrate the information sharing aspects into their daily routines with a small amount of effort. With the use of open source tools, the same type of capability can be easily replicated in other jurisdictions. This presentation will describe the lessons learned and potential improvements the project will incorporate in the future.

Keywords

Open Source; Emergency Management; Information Sharing

*Wayne Loschen
E-mail: wayne.loschen@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluation of ESSENCE in the Cloud Using Meaningful Use Syndromic Surveillance Data

Wayne Loschen*[1], William Stephens[2], Taha Kass-Hout[3], Miles Stewart[1], Dave Heinbaugh[2] and Joseph Lombardo[1]

[1]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA; [2]Tarrant County Public Health, Fort Worth, TX, USA; [3]Public Health Surveillance and Informatics Program Office, Office of Surveillance, Epidemiology, & Laboratory Services, Centers for Disease Control and Prevention, Atlanta, GA, USA

Objective

This project represents collaboration among CDC's BioSense Program, Tarrant County Public Health and the ESSENCE Team at the Johns Hopkins University APL. For over six months the Tarrant County Public Health Department has been sending data through the BioSense 2.0 application to a pilot version of ESSENCE on the Amazon GovCloud. This project has demonstrated the ability for local hospitals to send meaningful use syndromic surveillance data to the Internet cloud and provide public health officials tools to analyze the data both using BioSense 2.0 and ESSENCE. The presentation will describe the tools and techniques used to accomplish this, an evaluation of how the system has performed, and lessons learned for future health departments attempting similar projects.

Introduction

In November of 2011 BioSense 2.0 went live to provide tools for public health departments to process, store, and analyze meaningful use syndromic surveillance data. In February of 2012 ESSENCE was adapted to support meaningful use syndromic surveillance data and was installed on the Amazon GovCloud. Tarrant County Public Health Department agreed to pilot the ESSENCE system and evaluate its performance compared to a local version ESSENCE they currently used. The project determined the technical feasibility of utilizing the Internet cloud to perform detailed public health analysis, necessary changes needed to support meaningful use syndromic surveillance data, and any public health benefits that could be gained from the technology or data.

Methods

This project investigated database and visualization changes necessary to support meaningful use syndromic surveillance data in ESSENCE. It evaluated the Internet cloud environment and determined the benefits and disadvantages to using this technology as a platform for ESSENCE. This included scalability, performance, and cost analysis of the Internet cloud platform. After using the system for a period of time, the Tarrant County users evaluated the Internet cloud version of the system.

Results

Many technical adaptations to the ESSENCE system were made to support the new meaningful use syndromic surveillance elements. Several optimizations, including a new database schema and cube table structures, were developed to improve performance of ESSENCE in the Internet cloud and incorporating the meaningful use requirements. The Internet cloud platform offered many levels of performance that could alter the ESSENCE user experience. Smaller configurations allowed for 100 concurrent users to experience 16 second response times, whereas larger configurations supported experiences of 2 second response times.

Conclusions

Public health departments are dealing with new meaningful use syndromic surveillance data elements and the cost of maintaining local systems. This collaborative team have researched and evaluated tools, technologies, and solutions that can be used throughout the country.

Keywords

Electronic Medical Records for Public Health; Interoperability; Meaningful Use; Syndromic Surveillance; Internet Cloud

Acknowledgments

The ESSENCE in the Cloud initiative is supported by the CDC's Division of Notifiable Diseases and Healthcare Information (DNDHI) BioSense Program.

*Wayne Loschen
E-mail: wayne.loschen@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Enhanced Influenza Surveillance using Telephone Triage Data in the VA ESSENCE Biosurveillance System

Cynthia A. Lucero-Obusan*[1], Carla A. Winston[1], Patricia L. Schirmer[1], Gina Oda[1], Anoshiravan Mostaghimi[1] and Mark Holodniy[1, 2]

[1]Department of Veterans Affairs, Office of Public Health, Washington, DC, USA; [2]Division of Infectious Diseases & Geographic Medicine, Stanford University, Stanford, CA, USA

Objective

To evaluate the utility and timeliness of telephone triage (TT) for influenza surveillance in the Department of Veterans Affairs (VA).

Introduction

Telephone triage is a relatively new data source available to biosurveillance systems.[1-2] Because early detection and warning is a high priority, many biosurveillance systems have begun to collect and analyze data from non-traditional sources [absenteeism records, over-the-counter drug sales, electronic laboratory reporting, internet searches (e.g. Google Flu Trends) and TT]. These sources may provide disease activity alerts earlier than conventional sources. Little is known about whether VA telephone program influenza data correlates with established influenza biosurveillance.

Methods

Veterans phoning VA's TT system, and those admitted or seen at a VA facility with influenza or influenza-like-illness (ILI) diagnosis were included in this analysis. Influenza-specific ICD-9-CM coded emergency department (ED) and urgent care (UC) visits, hospitalizations, TT calls, and ILI outpatient visits were analyzed covering 2010-2011 and 2011-2012 influenza seasons (July 11, 2010-April 14, 2012). Data came from 80 VA Medical Centers and over 500 outpatient clinics with complete reporting data for the time period of interest. We calculated Spearman rank-order coefficients, 95% confidence intervals and p-values using Fisher's z transformation to describe correlation between TT data and other influenza healthcare measures. For comparison of time trends, we plotted data for hospitalizations, ED/UC visits and outpatient ILI syndrome visits against TT encounters. We applied ESSENCE detection algorithms to identify high-level alerts for influenza activity. ESSENCE aberration detection was restricted to the 2011-2012 season because limited historical TT and outpatient data from 2009-2010 was available to accurately predict aberrancy in the 2010-2011 season. We then calculated the peak measure of healthcare utilization during both influenza seasons (2010-2011 and 2011-2012) for each data source and compared timing of peaks and alerts between TT and other healthcare encounters to assess maximum healthcare system usage and timeliness of surveillance.

Results

There were 7,044 influenza-coded calls, 564 hospitalizations, 1,849 emergency/urgent visits, and 416,613 ILI-coded outpatient visits. Spearman rank correlation coefficients were calculated for influenza-coded calls with hospitalizations (0.77); ED/UC visits (0.85); and ILI-outpatient visits (0.88), respectively ($P < 0.0001$ for all correlations). Peak influenza activity occurred on the same week or within 1 week across all settings for both seasons. For the 2011-2012 season, TT alerted with increased influenza activity before all other settings.

Conclusions

Data from VA telephone care correlates well with other VA data sources for influenza activity. TT may serve to augment these existing clinical data sources and provide earlier alerts of influenza activity. As a national health care system with a large patient population, VA could provide a robust early-warning system for influenza if ongoing biosurveillance activities are combined with TT data. Additional analyses are needed to understand and correlate TT with healthcare utilization and severity of illness.

Keywords

Surveillance; Influenza; Telephone triage; Veterans

References

1. Yih WK, Teates KS, Abrams A, Kleinman K, Kulldorff M, Pinner R, Harmon R, Wang S, Platt R: Telephone triage service data for detection of influenza-like illness. PLoS One 2009, 4(4):e5260.
2. van Dijk A, McGuinness D, Rolland E, Moore KM: Can Telehealth Ontario respiratory call volume be used as a proxy for emergency department respiratory visit surveillance by public health? CJEM 2008, 10(1):18-24.

*Cynthia A. Lucero-Obusan
E-mail: cynthia.lucero@va.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Sequential Bayesian Inference for Detection and Response to Seasonal Epidemics

Michael Ludkovski* and Junjing Lin

Statistics and Applied Probability, UC Santa Barbara, Santa Barbara, CA, USA

Objective

Development of a sequential Bayesian methodology for inference and detection of seasonal infectious disease epidemics.

Introduction

Detection and response to seasonal outbreaks of endemic diseases provides an excellent testbed for quantitative bio-surveillance. As a case study we focus on annual influenza outbreaks. To incorporate observed year-over-year variation in flu incidence cases and timing of outbreaks, we analyze a stochastic compartmental SIS model that includes seasonal forcing by a latent Markovian factor. Epidemic detection then consists in identifying the presence of the environmental factor ("high" flu season), as well as estimation of the epidemic parameters, such as contact and recovery rates.

Methods

Anticipating policy-making applications, we consider sequential Bayesian inference. To focus on intrinsic model uncertainty, we assume full observation of all individual status changes, but unobserved seasonal factor M underscore "t" and unknown reaction rates. Using theory of nonlinear filtering of point processes, we derive analytic expressions for conditional likelihoods of latent factor trajectories. We then utilize a Sequential Monte Carlo approach based on Particle Learning (PL) [1] to infer the epidemic parameters in conjunction with online filtering of M underscore "t." These tools extend the PL method to continuous-time jump-Markov models and are widely applicable in generic stochastic chemical kinetic models.

Using the developed inference methods, we then investigate cost-efficient sequential policy making. We analyze and compare several heuristic counter-measure strategies that work by modifying the duration/frequency of the high epidemic season.

Results

The proposed algorithm was implemented in R and extensively tested on simulated data [2]. We find that the PL method is able to efficiently carry out joint inference. We also find that counter-measures incorporating sequential learning are generally more efficient that other inference-free policies.

Conclusions

We developed a new Bayesian approach to joint inference of parameters and latent factors in continuous-time stochastic compartmental models. There is ongoing work [3] to adjust our methods for more realistic observation schemes.

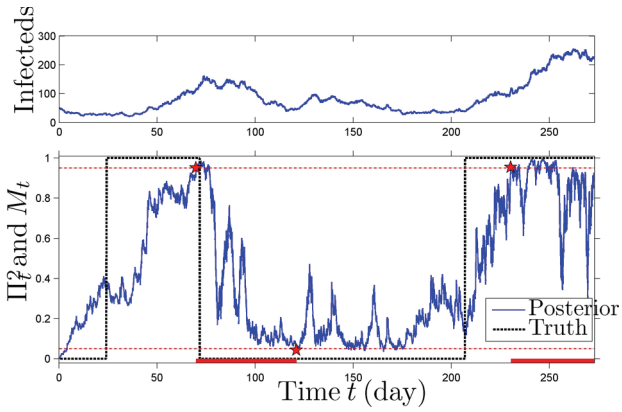


Fig: Response strategy based on the Bayesian posterior probability Π^2_t (use math notation) of high flu season $\{ M_t = 1\}$. Counter-measures begin when prob > 95% and end when prob <5%.

Keywords

Bayesian inference; stochastic compartmental models; seasonal epidemics; hidden Markov models

Acknowledgments

We thank Jarad Niemi for useful discussions.

References

[1] Carvalho, C. M.; Johannes, M.; Lopes, H. F. and Polson, N. Particle learning for sequential Bayesian computation. Bayesian Statistics, 2011, 9, 317-360.

[2] Lin J, and Ludkovski M., Sequential Bayesian Inference in Hidden Markov Stochastic Kinetic Models with Application to Detection and Response to Seasonal Epidemics, Submitted, 2012.

[3] Ludkovski M, Niemi J. Optimal disease outbreak decisions using stochastic simulation. In: Proceedings of the 2011 Winter Simulation Conference. Jain S, et al eds.

*Michael Ludkovski
E-mail: ludkovski@pstat.ucsb.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Characteristics of Veterans Accessing the Veterans Affairs Telephone Triage Who Have Depression or Suicidal Ideation: Opportunities for Intervention

Alison Ludwig*[1, 2], Cynthia Lucero-Obusan[1], Patricia Schirmer[1] and Mark Holodniy[1, 3]

[1]VA Office of Public Health Surveillance and Research, Palo Alto, CA, USA; [2]Epidemic Intelligence Service, Centers for Disease Control and Prevention, Atlanta, GA, USA; [3]Stanford University School of Medicine, Palo Alto, CA, USA

Objective

To characterize Veterans who call telephone triage because of suicidal ideation (SI) or depression and to identify opportunities for suicide prevention efforts among these telephone triage users using a biosurveillance application.

Introduction

Veterans accessing Veterans Affairs (VA) health care have higher suicide rates and more characteristics associated with suicide risk, including being male, having multiple medical and psychiatric comorbidities, and being an older age, compared with the general U.S. population. The Veterans Crisis Line is a telephone hotline available to Veterans with urgent mental health concerns; however, not all Veterans are aware of this resource. By contrast, telephone triage is a national telephone-based triage system used by the VA to assess and triage all Veterans with acute medical or mental health complaints.

Methods

The VA Electronic Surveillance System for Early Notification of Community-based Epidemics (ESSENCE) was queried for telephone triage calls during January 1–June 30, 2012. Calls were classified as SI or depression when the triage nurse selected SI or depression as the Veteran's chief complaint from a set of fixed options. Demographic and recommended follow-up time and location information was reviewed. A random sample of 20 SI calls and 50 depression calls were selected for chart review to determine whether Veterans were examined in a clinic or followed up by a clinician by telephone within 2 weeks of the veteran's call.

Results

During January 1–June 30, 2012, 253,573 total calls were placed to telephone triage. Among these calls, 2,460 unique Veterans placed 417 calls for SI and 2,290 calls for depression. This represents 1% (2,707/253,573) of all calls placed during the period. All encounter information is available in the surveillance application within 24 hours of the call being placed. Median age of callers was 55 years (range: 19–94); 86% were male; and 6% placed repeat calls. The median number of repeat calls was 2 (range: 2–10). Among the 2,707 calls for SI or depression, 1,286 (48%) were made after routine business hours (5:00 p.m.–8:00 a.m.), and 646 (24%) were made on weekends. The greatest proportion of calls were from Wisconsin and Northern Illinois (17%) and the Southeastern United States (14%). Among the 2,290 calls for depression, 1,401 callers (61%) were recommended for urgent follow up or within 24 hours. 771 (34%) were assigned a follow up location of an emergency department; 117 (5%) an urgent care; 1,332 (58%) a physician's office or clinic; 52 (2%) self-care at home; and 18 (1%) were unspecified. Among the 417 calls for SI, callers 410 (98%) were recommended for urgent follow-up or within 24 hours. 330 (79%) were assigned a follow-up location of an emergency department; 38 (9%) an urgent care; 43 (10%) a physician's office or clinic; 3 (1%) self-care at home; and 3 (1%) unspecified. Among the 20 SI and 50 depression calls for which the charts were reviewed, 1 (5%) SI call and 6 (12%) depression calls had no documented follow-up by telephone or in person with a clinician within 2 weeks of initial call.

Conclusions

Telephone triage represents an additional data source available to surveillance applications. Although telephone triage is not the traditional method provided by the VA for triage of urgent mental health concerns, >2,000 Veterans called it with acute symptoms of SI or depression during January–June 2012. Training for suicide prevention should be prioritized for operators working during the high-volume periods of off-hours and weekends when approximately half and one-quarter of calls were received, respectively. We recommend standard notification of suicide prevention coordinators regarding calls to telephone triage for SI or depression to prevent loss to follow-up among Veterans at risk for suicide. Further investigation into reasons for increased call burden in identified geographic areas also is recommended.

Keywords

Surveillance; Veterans; Suicide Risk

*Alison Ludwig
E-mail: Alison.Ludwig@va.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Enabling Syndromic Surveillance in Pakistan

Ross Maciejewski*[1], Shehzad Afzal[2], Adam J. Fairfield[1], Arif Ghafoor[2], David S. Ebert[2], Naeem Ayyaz[4] and Maaz Ahmed[3]

[1]Computer Science, Arizona State University, Tempe, AZ, USA; [2]Purdue University, West Lafayette, IN, USA; [3]King Edward Medical University, Lahore, Pakistan; [4]University of Engineering and Technology, Lahore, Pakistan

Objective

This work presents our first steps in developing a Global Real-time Infectious Disease Surveillance System (GRIDDS) employing robust and novel in-fectious disease epidemiology models with real-time inference and pre/exercise planning capabilities for Lahore, Pakistan. The objective of this work is to address the infectious disease surveillance challenges (specific to developing countries such as Pakistan) and develop a collaborative capability for monitoring and managing outbreaks of natural or manmade infectious diseases in Pakistan.

Methods

Utilizing our partner hospitals in the Lahore, Punjab area, we have begun developing a theoretical model of patient hospital visits with respect to diseases and syndromes within Pakistan. Our first thrust has focused on the collection, categorization and cleansing of data based on expert knowledge from our partnering institutions in Pakistan. Data consists of a patient's home address and chief complaint which is then categorized into syndromes. Home addresses are geocoded utilizing the Google API with a resultant 72% accuracy. Unknown geolocations are aggregated only at the hospital level. Using this cleaned data, we employ methods similar to our previous work [1] on syndromic surveillance for early disease detection. Currently, we have collected over 600,000 patient records over 1.5 years.

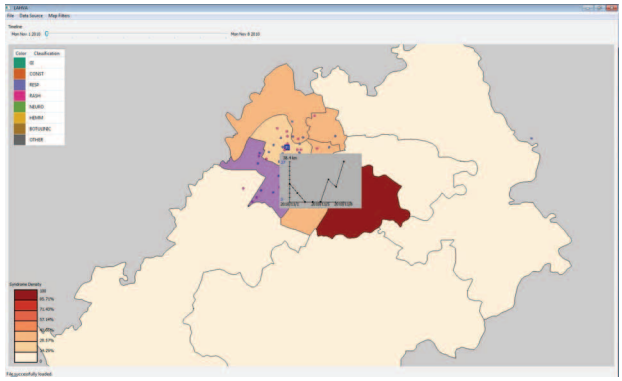
We employ the use of choropleth maps, isopleth maps utilizing kernel density estimation of patient addresses, traditional control chart methods such as exponentially weighted moving averages (EWMA), and a non-parametric time series analysis approach (seasonal trend decomposition using loess smoothing (STL) [2]) which requires only 90 days of historical data to be put into operation. The time series models are deployed as part of a real-time surveillance system in which temporal anomalies over regions can be analyzed and disease outbreaks reported.

Results

Figure 1 illustrates our visual analytics toolkit in operation. Here we see the location of our partner hospital in the Lahore region. The hospital coverage is in the most populous location of the city, providing data as a sentinel site for the overall health of the city. Currently, our system employs the use of interactive filters and linked isopleth or choropleth maps with time series analysis on mouse over.

Conclusions

Currently our research has focused on one partner location within the city of Lahore. Our ongoing work is focusing on the adoption of such a system to other regions of the country and the development of disease spread simulations (particularly Dengue Fever) utilizing baseline data collected by our partners. We plan to integrate these models into our visual analytics system for real-time planning and simulation.



Keywords

syndromic surveillance; visual analytics; pakistan

Acknowledgments

This work is supported by the Defense Threat Reduction Agency Award Number HDTRA1-10-1-0083.

References

[1] Maciejewski, R., et al.., "Forecasting Hotspot – A Predictive Analytics Approach," IEEE Transactions on Visualization and Computer Graphics, 17(4): 440-453, 2011.

[2] Hafen, R. P., et al., "Syndromic surveillance: STL modeling, visualizing and monitoring disease counts," BMC Medical Informatics and Decision Making, 2009.

*Ross Maciejewski
E-mail: rmacieje@asu.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

The Use of the International Classification of Diseases, Ninth Revision (ICD-9) Coding in Identifying Chronic Hepatitis B Virus Infection in Health System Data: Implications for Surveillance

Reena Mahajan*[1], Anne C. Moorman[1], Stephen J. Liu[1], Loralee Rupp[2], Monina Klevens[1] and (CHeCS) for the Chronic Hepatitis Cohort Investigators[3, 2, 1]

[1]Centers for Disease Control and Prevention, Atlanta, GA, USA; [2]Henry Ford Health System, Detroit, MI, USA; [3]Kaiser Permanente-Hawaii; Geisinger Health System, Pennsylvania; Kaiser Permanente-Northwest, Oregon, Atlanta, GA, USA

Objective

To evaluate the sensitivity, specificity, positive and negative predictive values of the ICD-9 coding system for surveillance of chronic hepatitis B virus infection (HBV) using data from an observational cohort study in which ICD-9-coded HBV cases were validated by chart review.

Introduction

In the United States, 800,000- 1.4 million people are chronically infected with hepatitis B virus (HBV); these persons are at increased risk for chronic liver disease and its sequelae (CDC, 2010; Wasley, 2010). Current national viral hepatitis surveillance is a passive laboratory-initiated reporting system to state or local health departments with only 39 health departments reporting chronic HBV infection in the National Notifiable Disease Surveillance System (NNDSS). Since active HBV surveillance can be expensive and labor-intensive, the ICD-9 coding system has been proposed for surveillance of chronic hepatitis B.

Methods

We examined the electronic health records (EHRs) available as part of an existing cohort study of persons with chronic viral hepatitis. Records from 1.6 million adult patients who had one or more services from 2006-2008 in four integrated health care systems were reviewed. Complex algorithms using laboratory data and/or use of qualifying hepatitis B ICD-9 codes were applied to EHR patient data to create the chronic HBV cohort. Disease status was manually validated by abstractor review of the medical record. Sensitivity, specificity, positive and negative predictive values were calculated based upon presence of either one hepatitis B-specific ICD-9 code or two such ICD-9 codes separated by at least six months.

Results

Of 1,652,055 adult patients, 2,202 (0.1%) met criteria for inclusion into the chronic HBV cohort. Of the 2,202 confirmed cases, the sensitivity of use of one ICD-9 code was 83.9%, positive predictive value was 61.0%, specificity was 99.9% and the negative predictive value was over 99.9% (Table 1). In comparison, use of two hepatitis B-specific ICD 9 codes separated by six months, resulted in a sensitivity of 58.4%, a positive predictive value of 89.9%, and specificity and negative predictive value similar to use of one ICD 9 code.

Conclusions

Our findings suggest that use of one or two hepatitis B specific ICD 9 codes can identify cases with chronic HBV infection. For health departments with access to electronic medical records, collection of ICD-9 data may be useful for surveillance and potentially improve reporting of chronic HBV infection.

Measurement of sensitivity, specificity, and predictive values of using one hepatitis B-specific ICD-9 code among persons receiving services from four health care systems from 2006-2008

	Confirmed HBV case	Not a HBV case	Total
One ICD-9 code	1,847	1,182	3,029
No ICD-9 code	355	1,648,671	1,649,026
Total	2,202	1,649,853	1,652,055

Sensitivity= 1,847/2,202= 83.9%
Specificity= 1,648,671/1,649,853= 99.9%
Positive predictive value= 1,847/3,029= 61.0%
Negative predictive value= 1,648,671/1,649,026= >99.9%

Keywords

surveillance; hepatitis B virus; ICD-9

Acknowledgments

The authors thank Dr. Fujie Xu, Division of Viral Hepatitis, Centers for Disease Control and Prevention for her helpful suggestions with this study.

References

1. CDC, 2010. Viral hepatitis statistics and surveillance. http://www.cdc.gov/hepatitis/Statistics/index.htm. Accessed July 20, 2012
2. Wasley A, Kruszon-Moran D, Kuhnert W, Simard EP, Finelli L, McQuillan G, et al. The prevalence of hepatitis B virus infection in the United States in the era of vaccination. J Infect Dis 2010;202:192-201.

*Reena Mahajan
E-mail: rmahajan1120@yahoo.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Analysis of Heat Illness using Michigan Emergency Department Syndromic Surveillance

Fatema Mamou* and Tiffany Henderson

Michigan Department of Community Health, Lansing, MI, USA

Objective

The purpose of this work was to conduct an enhanced analysis of heat illness during a heat wave using Michigan's Emergency Department Syndromic Surveillance System (MSSS) that could be provided to Public Health and Preparedness Stakeholders for situational awareness.

Introduction

The MSSS, described elsewhere (1), has been in use since 2003 and records Emergency Department (ED) chief complaint data along with the patient's age, gender and zip code in real time. There were 85/139 hospital EDs enrolled in MSSS as of June 2012, capturing 77% of the annual hospital ED visits in Michigan. The MSSS is used routinely during the influenza season for situational awareness and is monitored throughout the year for aberrations that may indicate an outbreak, emerging disease or act of bioterrorism. The system has also been used to identify heat-related illnesses during periods of extreme heat. Very young children, the elderly, and people with mental illness and chronic diseases are at the highest risk of preventable heat-related illnesses including sunburn, heat exhaustion, heat stroke and/or death (2). During a heat wave in the summer of 2012, data was reviewed on an ad hoc basis to monitor potential increases in heat-related ED visits.

Methods

MSSS ED visits were queried to identify those with the primary complaints of: "heat", "sun", or "dehydration" including word derivatives and misspellings. The query excluded terms and misspellings such as "Sunday", "heater", and "heatlh". Daily maximum temperatures for four major cities in Michigan were tracked using measures from the National Oceanic and Atmospheric Administration's National Weather Service (3). Multiple analyses were performed. For this abstract, ED data from a 10-day period of sustained above normal temperatures are presented with data from the prior 10-day period used as reference.

Visits were categorized into 1 of 3 syndromes based on the chief complaint: sun-associated, heat-associated, and dehydration. Gender, age group, and syndrome for the period of interest were compared to the reference period. Heat-related visits during the period of extreme heat were also analyzed by Michigan Public Health Preparedness Region.

Results

During the period of June 28–July 7, 2012 the South and Central regions of Michigan sustained maximum daily temperatures surpassing 90°F with maximum temperatures at or above 100°F on at least 2 days. Among the cities reviewed, a total of 9 high temperature records were set or tied during that period. The number of heat-related ED visits reported into MSSS increased compared to the previous period of June 18–June 27, 2012. Heat-associated ED visits such as heat exhaustion and heat stroke were more frequent than the reference period, 30.0% vs. 13.7% ($p<0.0001$). Sun-associated ED visits such as sunburn were lower compared to the reference period, 17.3% vs. 23.8% ($p=0.01$). Dehydration complaints were elevated among those 20-29 years of age, 17.7% vs. 10.0% ($p=0.01$). While the proportion of ED visits due to heat-related complaints was highest in the Central and Northwestern areas of the state, increases were observed in all regions of Michigan.

On July 6, 2012 an initial analysis summary was issued via the Michigan Health Alert Network (MIHAN) to provide situational awareness related to a concurrent heat advisory for much of the state. By July 23, 2012 MDCH issued a media release reporting this increase in heat-related ED visits.

Conclusions

Although cases used in the analysis may not represent all potential cases of heat-related illness and also may represent non-heat-related illnesses, ED data are useful in describing trends in illness presentations over time. As the MSSS covers a large proportion of Michigan's population, the data from the MSSS can be stratified by type of heat-related injury, age group, and region, providing detailed situational awareness to public health stakeholders. This type of in-depth analysis further contributes to our knowledge of heat events and allows public health to relay important information regarding the severity of the situation and information about groups at risk for illness.

Keywords

syndromic surveillance; heat illness; extreme heat

References

1. Sheline KD. Evaluation of the Michigan Emergency Department Syndromic Surveillance System. Advances in Disease Surveillance. 2007; 4: 265
2. CDC. Extreme Heat Prevention Guide. 2012. Available from: http://emergency.cdc.gov/disasters/extremeheat/heat_guide.asp
3. National Oceanic and Atmospheric Administration's National Weather Service. Available from: http://www.nws.noaa.gov/climate/

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

SMART Platforms: Building The App Store for Biosurveillance

Kenneth D. Mandl*

[1]Boston Children's Hospital, Boston, MA, USA; [2]Harvard Medical School, Boston, MA, USA

Objective

To enable public health departments to develop "apps" to run on electronic health records (EHRs) for (1) biosurveillance and case reporting and (2) delivering alerts to the point of care. We describe a novel health information technology platform with substitutable apps constructed around core services enabling EHRs to function as iPhone-like platforms.

Introduction

Health care information is a fundamental source of data for biosurveillance, yet configuring EHRs to report relevant data to health departments is technically challenging, labor intensive, and often requires custom solutions for each installation. Public health agencies wishing to deliver alerts to clinicians also must engage in an endless array of one-off systems integrations.

Despite a $48B investment in HIT, and meaningful use criteria requiring reporting to biosurveillance systems, most vendor electronic health records are architected monolithically, making modification difficult for hospitals and physician practices. An alternative approach is to reimagine EHRs as iPhone-like platforms supporting substitutable apps-based functionality. Substitutability is the capability inherent in a system of replacing one application with another of similar functionality.

Methods

Substitutability requires that the purchaser of an app can replace one application with another without being technically expert, without requiring re-engineering other applications that they are using, and without having to consult or require assistance of any of the vendors of previously installed or currently installed applications. Apps necessarily compete with each other promoting progress and adaptability.

The Substitutable Medical Applications, Reusable Technologies (SMART) Platforms project is funded by a $15M grant from Office of the National Coordinator of Health Information Technology's Strategic Health IT Advanced Research Projects (SHARP) Program. All SMART standards are open and the core software is open source.

The SMART project promotes substitutability through an application programming interface (API) that can be adopted as part of a "container" built around by a wide variety of HIT, providing read-only access to the underlying data model and a software development toolkit to readily create apps. SMART containers are HIT systems, that have implemented the SMART API or a portion of it. Containers marshal data sources and present them consistently across the SMART API. SMART applications consume the API and are substitutable.

Results

SMART provides a common platform supporting an "app store for biosurveillance" as an approach to enabling one stop shopping for public health departments—to create an app once, and distribute it everywhere.

Further, such apps can be readily updated or created—for example, in the case of an emerging infection, an app may be designed to collect additional data at emergency department triage. Or a public health department may widely distribute an app, interoperable with any SMART-enabled EMR, that delivers contextualized alerts when patient electronic records are opened, or through background processes.

SMART has sparked an ecosystem of apps developers and attracted existing health information technology platforms to adopt the SMART API—including, traditional, open source, and next generation EHRs, patient-facing platforms and health information exchanges. SMART-enabled platforms to date include the Cerner EMR, the WorldVista EHR, the OpenMRS EHR, the i2b2 analytic platform, and the Indivo X personal health record. The SMART team is working with the Mirth Corporation, to SMART-enable the HealthBridge and Redwood MedNet Health Information Exchanges. We have demonstrated that a single SMART app can run, unmodified, in all of these environments, as long as the underlying platform collects the required data types. Major EHR vendors are currently adapting the SMART API for their products.

Conclusions

The SMART system enables nimble customization of any electronic health record system to create either a reporting function (outgoing communication) or an alerting function (incoming communication) establishing a technology for a robust linkage between public health and clinical environments.

Keywords

Electronic health records; Biosurveillance; Informatics; Application Programming Interfaces

Acknowledgments

This work was funded by the Strategic Health IT Advanced Research Projects Award 90TR000101 from the Office of the National Coordinator of Health Information Technology.

*Kenneth D. Mandl
E-mail: kenneth_mandl@harvard.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Disease Mapping with Spatially Uncertain Data

Justin Manjourides*[1], Ted Cohen[2, 3], Caroline Jeffery[4] and Marcello Pagano[5]

[1]Dept of Health Sciences, Northeastern University, Boston, MA, USA; [2]Div of Global Health Equity, Brigham & Women's Hospital, Boston, MA, USA; [3]Dept of Epidemiology, Harvard School of Public Health, Boston, MA, USA; [4]Intl Health Group, Liverpool School of Tropical Medicine, Liverpool, United Kingdom; [5]Dept of Biostatistics, Harvard School of Public Health, Boston, MA, USA

Objective

Uncertainty regarding the location of disease acquisition, as well as selective identification of cases, may bias maps of risk. We propose an extension to a distance-based mapping method (DBM) that incorporates weighted locations to adjust for these biases. We demonstrate this method by mapping potential drug-resistant tuberculosis (DRTB) transmission hotspots using programmatic data collected in Lima, Peru.

Introduction

Uncertainty introduced by the selective identification of cases must be recognized and corrected for in order to accurately map the distribution of risk. Consider the problem of identifying geographic areas with increased risk of DRTB. Most countries with a high TB burden only offer drug sensitivity testing (DST) to those cases at highest risk for drug-resistance. As a result, the spatial distribution of confirmed DRTB cases under-represents the actual number of drug-resistant cases[1]. Also, using the locations of confirmed DRTB cases to identify regions of increased risk of drug-resistance may bias results towards areas of increased testing. Since testing is neither done on all incident cases nor on a representative sample of cases, current mapping methods do not allow standard inference from programmatic data about potential locations of DRTB transmission.

Methods

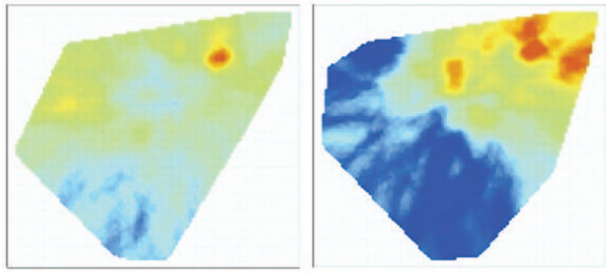
We extend a DBM method [2] to adjust for this uncertainty. To map the spatial variation of the risk of a disease, such as DRTB, in a setting where the available data consist of a non-random sample of cases and controls, we weight each address in our study by the probability that the individual at that address is a case (or would test positive for DRTB in this setting). Once all locations are assigned weights, a prespecified number of these locations (from previously published country-wide surveillance estimates) will be sampled, based on these weights, defining our cases. We assign these sampled cases to DRTB status, calculate our DBM, repeat this random selection and create a consensus map[3].

Results

Following [2], we select reassignment weights by the inverse probability of each untested case receiving DST at their given location. These weights preferentially reassign untested cases located in regions of reduced testing, reflecting an assumption that in areas where testing is common, individuals most at risk are tested. Fig. 1 shows two risk maps created by this weighted DBM, one on the unadjusted data (Fig.1, L) and one using the informative weights (Fig. 1, R). This figure shows the difference, and potentially the improvement, made when information related to the missingness mechanism, which introduces spatial uncertainty, is incorporated into the analysis.

Conclusions

The weighted DBM has the potential to analyze spatial data more accurately, when there is uncertainty regarding the locations of cases. Using a weighted DBM in combination with programmatic data from a high TB incidence community, we are able to make use of routine data in which a non-random sample of drug resistant cases are detected to estimate the true underlying burden of disease.



(L) Unweighted DBM of risk of a new TB case that received DST being positive for DRTB, compared to all new TB cases that received DST. (R) Weighted DBM of the risk of a new TB case that received DST being positive for DRTB, based on lab-confirmed DRTB cases and IPW selected non-DST TB cases, compared to all new TB cases.

Keywords

surveillance; multiple addresses; distance based

References

[1] H Lin, et al. Assessing spatiotemporal patterns of multidrug-resistant and drug-sensitive tuberculosis in a south american setting. Epi Infect, 2010.

[2] C Jeffery. Disease mapping and statistical issues in public health surveillance. PhD thesis, Harvard University, 2010.

[3] J Manjourides, et al. Identifying multidrug resistant tuberculosis transmission hotspots using routinely collected data. Tuberculosis, 92(3), 2012.

*Justin Manjourides
E-mail: Justin.manjourides@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Web-based Electronic Health Record System for National Surveillance

Jake R. Marcus*

Practice Fusion, San Francisco, CA, USA

Objective

This showcase aims to demonstrate the viability of Practice Fusion's web-based electronic health record system for national surveillance. Practice Fusion also wishes to provide aggregate data to public health departments for surveillance for free. This showcase also hopes to engage those potential partners around uses of the company's research database.

Introduction

Practice Fusion is a web-based electronic health record system with over 150,000 medical professional users treating over 50 million patients. The company focuses on small, ambulatory practices and is predominately comprised of practices in the field of primary care. The user base makes it an ideal system for public health surveillance. The Research Division has undertaken pilot projects to demonstrate the viability of using the data for surveillance for acute diseases, like influenza-like illness, chronic diseases, like diabetes, and risk factors, like hypertension.

Methods

Surveillance systems based on electronic health records have clear advantages over case based reporting, but the majority of those systems are limited to the small geographical area affiliated with the hospital or health plan associated with the project. Practice Fusion has coverage in all 50 states and runs on a single, multi-tenant database making comparisons across those states and the localities within them immediately feasible. The company wishes to engage the organizations represented at ISDS in order to advance public health surveillance using the research database. It is very difficult to obtain electronic health record data currently, but with the appropriate data use agreement Practice Fusion believes that it is a moral imperative to use its aggregate data for surveillance. The Research Division has developed methods for the surveillance of influenza-like illness with its system and comparisons to the CDC have proven its viability.

Conclusions

By comparing trends and levels of influenza-like illness generated from Practice Fusion's research database to Google Flu Trends and the gold standard estimates produced by the CDC, web-based electronic health record systems have proved to be a viable foundation for syndromic surveillance. The implementation of the system also shows that case definitions for surveillance need not be overly simplistic if they do not require cases to be submitted from physicians, but rather can be programmed to be identified through automated algorithms.

Keywords

public health surveillance; electronic health record; Practice Fusion

Acknowledgments

The data team at Practice Fusion

References

www.practicefusion.com
research.practicefusion.com

*Jake R. Marcus
E-mail: jmarcus@practicefusion.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

The Biosurveillance Resource Directory - A One-Stop Shop for Systems, Sources, and Tools

Kristen Margevicius*, Mac Brown, Lauren Castro, William B. Daniel, Eric N. Generous, Kirsten Taylor-McCabe and Alina Deshpande

Los Alamos National Laboratory, Los Alamos, NM, USA

Objective

The goal of this project is to identify systems and data streams relevant for infectious disease biosurveillance. This effort is part of a larger project evaluating existing and potential data streams for use in local, national, and international infectious disease surveillance systems with the intent of developing tools to provide decision-makers with timely information to predict, prepare for, and mitigate the spread of disease.

Introduction

Local, national, and global infectious disease surveillance systems have been implemented to meet the demands of monitoring, detecting, and reporting disease outbreaks and prevalence. Varying surveillance goals and geographic reach have led to multiple and disparate systems, each using unique combinations of data streams to meet surveillance criteria. In order to assess the utility and effectiveness of different data streams for global disease surveillance, a comprehensive survey of current human, animal, plant, and marine surveillance systems and data streams was undertaken. Information regarding surveillance systems and data streams has been (and continues to be) systematically culled from websites, peer-reviewed literature, government documents, and subject-matter expert consultations.

Methods

A relational database has been developed and refined to allow for detailed analyses of data streams and surveillance systems. To maximize the utility of the database and facilitate one-stop-shopping for biosurveillance system information, we have expanded our scope to include not only biosurveillance systems, but also data sources, tools, and biosurveillance collectives. Captured in the information collected about the resource (if available) is the name and acronym of the resource, the date the resource became available, the accessibility of the resource (is it open to all, or are there limitations to access), the primary sponsors, if the resource is associated with GIS functionality, and if the focus is health. Also collected is contact information, information regarding the scope and domain of the resource, the pertinent diseases or disease categories, and the geographic and population coverage of the resource. Websites associated with the resource are directly accessible from the database. Data stream information is also captured based on our developed data stream framework. If the resource uses other specified systems/sources/tools for data gathering or analysis, then that is also captured and directly linked within the database.

Results

The Biosurveillance Resource Directory (BRD) is in the process of being tested by multiple potential end users in the public health, biosecurity, and biosurveillance communities. Feedback from these testers is being used to refine the database to maximize functionality and utility. Additionally, methods for dynamically updating and maintaining the database are being evaluated. Automated and semi-automated queriable reports have been developed and are integral to demonstrating specific use-case scenarios in which the BRD would be beneficial for end-users.

Conclusions

A need for a biosurveillance one-stop shop has been increasingly called for to help in evaluating what data streams and systems are available and relevant for many different biosurveillance needs and goals. The prototype Biosurveillance Resource Directory is a searchable, dynamic database for biosurveillance systems, sources, and tools information.

Keywords

infectious disease; biosurveillance; database

Acknowledgments

This project is supported by the Chemical and Biological Technologies Directorate Joint Science and Technology Office (JSTO), Defense Threat Reduction Agency (DTRA).

*Kristen Margevicius
E-mail: kmargevicius@lanl.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Establishment of a One Health Surveillance Initiative in the CA/Baja CA Border Region

Sarah C. Marikos*[1], Karen L. Ferran[1], Esmeralda Iniguez-Stevens[1] and Francisco Javier Monge Navarro[2]

[1]Early Warning Infectious Disease Surveillance (EWIDS), California Department of Public Health, San Diego, CA, USA; [2]Universidad Autónoma de Baja California, Veterinary School, Mexicali, Mexico

Objective

To showcase One Border One Health, a binational, multidisciplinary initiative in the California/Baja California (CA/BC) border region whose aim is to reconfigure traditional species-specific approaches to surveillance for emerging and re-emerging pathogens.

Introduction

The CA/BC border region encompasses a wide range of ecosystems, topography, dense urban areas, and agricultural developments that coexist in a limited geographic area and create numerous human-animal-environmental interfaces. The region is recognized for its high biodiversity, the presence of over 85 endangered plant and animal species, its importance on the Pacific migratory pathway, high levels of population mobility, and hosts the busiest international border in the world. These interfaces pose a significant risk to animal, human, and environmental health, as evidenced by frequent wildlife die offs, antibiotic resistant bacteria in streams, beach closures due to fecal contamination, pesticide toxicities, zoonotic infectious disease outbreaks, and vector borne diseases. In the marked absence of any organization comprehensively addressing the health risks posed by these complex interfaces and recognizing that these issues necessitate a binational, cross-sectoral One Health approach, the Early Warning Infectious Disease Surveillance Program (EWIDS) founded One Border One Health (OBOH) in 2011.

OBOH recognizes that early warning systems should systematically monitor animal, human, and environmental health and that early detection is key to control. Hence OBOH's primary aim is to create and integrate early warning surveillance systems that gather data from disparate sources in order to protect and improve animal, human, and environmental health. This information can be used to inform decision makers about important public health events in the CA/BC border region.

Methods

OBOH is a unique multi-disciplinary initiative comprised of over 30 institutions from Mexico and 60 institutions from the United States, with representation from government, academia, non-profit, private and military sectors. Professionals with expertise in public health, veterinary medicine, ecology, biology, urban planning, epidemiology, wildlife health, and environmental health are working in concert rather than in the traditionally isolated human, environmental health, domestic animal and wildlife sectors. OBOH is actively seeking to translate One Health theory into practice through its diverse, binational network. This demonstration presents OBOH's surveillance, informatics, and education activities, focusing on its strengths, challenges, and future directions.

Conclusions

To the authors' knowledge this is the first trans-border regional network established to enhance cross border epidemiologic information exchange and surveillance using One Health concepts in North America. Despite the large disparities between health systems, cultures, languages, socioeconomics, politics, animal management strategies, industries and ecosystems in the CA/BC border region, professionals from diverse disciplines are dedicated to OBOH and to the creation of a sustainable integrated surveillance system. OBOH is building the infrastructure for an early warning system in the border region, while improving regional infectious disease surveillance capacity and educating a new cadre of students and professionals about the importance of a One Health approach. Challenges include identifying cross-sectoral/multi-disciplinary funding opportunities to support activities, systematically operationalizing One Health without such funding, identifying and involving partners from different sectors, promoting data exchange, and maintaining an equal understanding of One Health surveillance within the initiative as membership increases. This demonstration provides recommendations on how to initiate and sustain cross-border, multidisciplinary, cross-sectoral surveillance engagements in resource-constrained environments.

Keywords

cross-border surveillance; emerging and re-emerging pathogens; One Health; collaboratives; early warning systems

Acknowledgments

The authors acknowledge Dr. Helen Engelke (Western University of Health Sciences) and Dr. Nikos Gurfield (San Diego County, Department of Environmental Health) for their rich contributions to One Border One Health. The authors are also extremely grateful for all the contributions by One Border One Health partners to this initiative.

*Sarah C. Marikos
E-mail: smarikos@cdph.ca.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Raccoons in San Diego County as Sentinels for West Nile Virus Surveillance

Sarah C. Marikos*[1], Karen L. Ferran[1], Esmeralda Iniguez-Stevens[1] and Nikos Gurfield[2]

[1]Early Warning Infectious Disease Surveillance Program (EWIDS), California Department of Public Health, San Diego, CA, USA;
[2]County of San Diego, Department of Environmental Health, San Diego, CA, USA

Objective

To investigate the potential of utilizing raccoons as sentinels for West Nile Virus (WNV) in an effort to guide public health surveillance, prevention, and control efforts.

Introduction

Since its detection in 1999 in New York, WNV spread westward across the continent, and was first detected in California in 2003 in Imperial County (1). In California and in many states, birds, especially corvids, are used as sentinel animals to detect WNV activity. Recent seroprevalence studies have shown WNV activity in different wild mammalian species (1-3); in the United States, WNV seroprevalence in some studies in raccoons has ranged from 34-46% (3,4). In addition, it has been shown that after experimental infection, raccoons can attain high viral titers and shed WNV in their saliva and feces (5). Given their peridomestic nature, we investigated the feasibility of their use as sentinels for early warning of WNV and as indicators of WNV activity as a strategy to better localize WNV transmission foci in guiding vector control efforts.

Methods

Sick, injured or orphaned raccoons undergoing rehabilitation at Project Wildlife, one of the largest, non-profit wildlife rehabilitation organizations in the United States, located in San Diego County, were tested for WNV shedding. Project Wildlife team members who regularly care for sick, injured, or orphaned raccoons were trained to collect oral and fecal samples for viral testing during 2011 and 2012 upon raccoons' arrival to Project Wildlife. Oral and fecal samples were tested using real-time PCR for the envelope gene of WNV.

Results

To date 71 raccoons have been tested for WNV and all PCR test results have been negative. Of the 71 raccoons tested from May 2011 to October 2011 and June 2012 to September 2012, 85.9% (n=61) had age classification data. The majority of these raccoons were young; 52.5% (n=32) were days or weeks old and 39.3% (n=24) were classified as juveniles. All raccoons were found primarily in urban settings at least 20 miles from the northern edge of the County.

Conclusions

While none of the raccoon samples tested in this study were found to be WNV positive, surveillance data from San Diego County suggests that WNV activity during this time period was extremely low. From January-October 2011, San Diego County Vector Control reported all negative results for WNV in dead birds, sentinel chickens, horses, and humans for WNV; only 1 mosquito pool from the northern border region of the County tested positive for WNV (6). Thus, despite WNV activity throughout the state of California, the virus did not appear to be circulating widely in San Diego County in 2011 (7). To date during the 2012 season, San Diego County reported all negatives for WNV in dead birds, sentinel chickens, mosquito pools, and horses; only one human case of WNV was identified in an asymptomatic male during a routine blood donation (6).

Further evaluation is needed to determine if raccoons are useful sentinel species for WNV surveillance. Testing should continue to evaluate if raccoons may serve as a more effective early warning sentinel for WNV than birds which can travel long distances from the exposure site, and to determine if raccoons may allow better localization of WNV activity.

Keywords

West Nile Virus; Early warning surveillance; Raccoons; Sentinels

Acknowledgments

The authors acknowledge Project Wildlife staff and volunteers who generously donated their time to this study, and who provide the utmost quality care for sick, injured, or orphaned raccoons.

References

1 Reisen, W, Lothrop H, Chiles R, Madon M, Cossen C, Woods, L, et al. West Nile in California. Emerg Infect Dis. 2004;10:1369.
2 Docherty, DE, Samuel, MD, Nolden, CA, Egstad, KF,Griffin, KM. West Nile Virus Antibody Prevalence in Wild Mammals, Southern Wisconsin. Emerg Infect Dis. 2006;12:1982.
3 Bentler, KT, Hall, JS, Root, JJ, Klenk, K, Schmit, B, Blackwell, BF. Serologic Evidence of West Nile Virus Exposure in North American Mesopredators. 2007;76:173.
4 Blitvich, BJ, Juarez, LI, Tucker, BJ, Rowley, WA, Platt, KB. Antibodies to West Nile Virus in Raccoons and Other Wild Peridomestic Mammals in Iowa. 2009;45:1163.
5 Root, JJ, Bentler, KT, Nemeth, NM, Gidlewski, T, Spraker, TR, Franklin, AB. Experimental Infection of Raccoons (Procyon lotor) with West Nile Virus. Am J Trop Med Hyg. 2010;83:803.
6 County of San Diego, Department of Environmental Health, "West Nile Cases in San Diego County", accessed September 5, 2012.
7 California Department of Public Health, "West Nile Page", accessed September 5, 2012.

*Sarah C. Marikos
E-mail: smarikos@cdph.ca.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Risk of Cardiovascular Morbidity and Mortality in Relation to Temperature

Robert Mathes*, Kazuhiko Ito and Thomas Matte

New York City Department of Health and Mental Hygiene, Queens, NY, USA

Objective

To examine the effects of temperature on cardiovascular-related (CVD) morbidity and mortality among New York City (NYC) residents.

Introduction

Extreme temperatures are consistently shown to have an effect on CVD-related mortality [1, 2]. A large multi-city study of mortality demonstrated a cold-day and hot-day weather effect on CVD-related deaths, with the larger impact occurring on the coldest days [3]. In contrast, the association between weather and CVD-related morbidity is less clear [4, 5]. The purpose of this study is to characterize the effect of temperature on CVD-related emergency department (ED) visits, hospitalizations, and mortality on a large, heterogeneous population. Additionally, we conducted a sensitivity analysis to determine the impact of air pollutants, specifically fine particulates (PM2.5) and ozone (O3), along with temperature, on CVD outcomes.

Methods

We analyzed daily weather conditions, ED visits classified as CVD-related based on chief complaint text, hospitalizations, and natural cause deaths that occurred in NYC between 2002 and 2006. ED visits were obtained from data reported daily to the city health department for syndromic surveillance. Inpatient admissions were obtained from the Statewide Planning and Research Cooperative System, a data reporting system developed by New York State. Mortality data were obtained from the NYC Office of Vital Statistics. Data for PM2.5 and O3 were obtained from all available air quality monitors within the five boroughs of NYC. To estimate risk of CVD morbidity and mortality, we used generalized linear models using a Poisson distribution to calculate relative risks (RR) and 95% confidence intervals (CI). A non-linear distributed lag was used to model mean temperature in order to allow for its effect on the same day and on subsequent days. Models were fit separately for cold season (October through March) and warm season (April through September) given season may modify the effect on CVD outcomes. For our sensitivity analysis, we included PM2.5 and O3 in our model.

Results

During the cold season, CVD-related ED visits and hospitalizations increased, while mortality decreased, with increasing mean temperature on the same day and lagged days. Extremely cold temperature was associated with a small increase of same day in-hospital mortality though generally cold temperatures did not appear to be associated with higher mortality. The opposite was observed in the warm season as ED visits and hospitalizations decreased, and mortality increased, with increasing mean temperature on the same day and on lagged days. Our sensitivity analysis, in which we controlled for PM2.5 and O3, demonstrated little effect of these air pollutants on the relationship between temperature and CVD outcomes.

Conclusions

Our results suggest a decline in risk of a CVD-related ED visit and hospitalization during extreme temperatures on the same day and on recent day lags for both cold and warm seasons. In contrast, our findings for mortality indicate an increase in risk of CVD-related deaths during hot temperatures. No mortality effect was observed during cold temperatures. The effects of extreme temperatures on CVD-related morbidity may be explained by behavioral patterns, as people are more likely to stay indoors on the coldest and hottest days.

Keywords

Morbidity; Mortality; Cardiovascular; Temperature

Acknowledgments

This research was funded by the Environmental Protection Agency, STAR Grant R833623010, and in conjunction with the Alfred P. Sloan Foundation, grant 2010-12-14. We thank the members of the New York City Department of Health and Mental Hygiene Syndromic Surveillance Unit.

References

1. Basu, R. and B.D. Ostro, A multicounty analysis identifying the populations vulnerable to mortality associated with high ambient temperature in California. Am J Epidemiol, 2008. 168(6): p. 632-7.
2. Braga, A.L., A. Zanobetti, and J. Schwartz, The effect of weather on respiratory and cardiovascular deaths in 12 U.S. cities. Environ Health Perspect, 2002. 110(9): p. 859-63.
3. Medina-Ramon, M. and J. Schwartz, Temperature, temperature extremes, and mortality: a study of acclimatisation and effect modification in 50 US cities. Occup Environ Med, 2007. 64(12): p. 827-33.
4. Josseran, L., et al., Syndromic surveillance and heat wave morbidity: a pilot study based on emergency departments in France. BMC Med Inform Decis Mak, 2009. 9: p. 14.
5. Knowlton, K., et al., The 2006 California heat wave: impacts on hospitalizations and emergency department visits. Environ Health Perspect, 2009. 117(1): p. 61-7.

*Robert Mathes
E-mail: rmathes@health.nyc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Surveillance of Heat-related Morbidity: Relation to Heat-related Excess Mortality

Robert Mathes*[1], Kristina B. Metzger[2], Kazuhiko Ito[1] and Thomas Matte[1]

[1]New York City Department of Health and Mental Hygiene, Queens, NY, USA; [2]City of Austin/Travis County Health and Human Services Department, Austin, TX, USA

Objective

To describe the extent to which heat-illness indicators increase with extreme heat and to evaluate the association among daily weather, heat-related illness and natural cause mortality.

Introduction

The impact of heat on mortality is well documented [1-3] but deaths tend to lag extreme heat and mortality data is generally not available for timely surveillance during heat waves. Recently, systems for near-real time surveillance of heat illness have been reported [4] but have not been validated as predictors of heat related mortality. In this study, we examined the associations among weather, indicators of heat-related ambulance calls and emergency department visits and excess natural cause mortality in New York City (NYC).

Methods

We analyzed daily weather conditions, emergency medical system (EMS) calls flagged as heat-related by EMS dispatchers, emergency department (ED) visits classified as heat-related based on chief complaint text, and natural cause deaths. EMS and ED data were obtained from data reported daily to the city health department for syndromic surveillance. We fit generalized linear models to assess the relationships of daily counts of heat related EMS and ED visits to natural cause deaths after adjustment for weather conditions during the months of May-September between 1999 and 2008.

Results

We observed an increase in mean total calls to EMS and a decrease in mean total visits to EDs during 10 observed heat waves (maximum heat index ≥ 90° F (Fahrenheit) for four or more consecutive days with the first three days ≥ 95° F and at least one day ≥100°F) in NYC between 1999 and 2008. Both EMS and EDs experienced an increase in heat-related incidents during heat waves though the increase in heat-related EMS calls was much greater. A modest increase in mean natural cause deaths was also observed. Controlling for temporal trends, an 11% (95% confidence interval (CI): 5-18) and 7% (95% CI: 4-9) increase in natural cause mortality was associated with an increase from the 50th percentile to 99th percentile of same-day and one-day lagged heat-related EMS calls and ED visits, respectively. After controlling for both temporal trends and weather, we observed a 10% (95% CI: 4-16) increase in natural cause mortality associated with one-day lagged heat-related EMS calls and a 5% mortality increase with one-day lagged ED visits (95% CI: 2-8).

Conclusions

Heat-related EMS calls and ED visits lagged one day predicted natural cause mortality in our temporal and weather-adjusted model. In particular, risk of mortality rapidly increased as the number of heat-related EMS calls approached high levels (>100 heat-related calls/day). Heat-related illness can be tracked during heat waves using EMS and ED data which are indicators of heat associated excess natural cause mortality during the warm weather season.

Keywords

Surveillance; Heat; Morbidity; Mortality

Acknowledgments

This research was funded by the Environmental Protection Agency, STAR Grant R833623010, and in conjunction with the Alfred P. Sloan Foundation, grant 2010-12-14. We thank the members of the New York City Department of Health and Mental Hygiene Syndromic Surveillance Unit.

References

1. Curriero, F.C., et al., Temperature and mortality in 11 cities of the eastern United States. Am J Epidemiol, 2002. 155(1): p. 80-7.
2. Dolney, T.J. and S.C. Sheridan, The relationship between extreme heat and ambulance response calls for the city of Toronto, Ontario, Canada. Environ Res, 2006. 101(1): p. 94-103.
3. Knowlton, K., et al., The 2006 California heat wave: impacts on hospitalizations and emergency department visits. Environ Health Perspect, 2009. 117(1): p. 61-7.
4. Chau, P.H., K.C. Chan, and J. Woo, Hot weather warning might help to reduce elderly mortality in Hong Kong. Int J Biometeorol, 2009. 53(5): p. 461-8.

*Robert Mathes
E-mail: rmathes@health.nyc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Syndromic Approach to Emergency Department Surveillance for Skin and Soft Tissue Infections

Larissa May*[1], Marcus Rennick[2], Leah Gustafson[1] and Julia Gunn[2]

[1]Emergency Medicine, The George Washington University, Washington, DC, USA; [2]Boston Public Health Commission, Boston, MA, USA

Objective

We sought to describe the epidemiology of emergency department (ED) visits for skin and soft tissue infections (SSTI) in an urban area with diverse neighborhood populations using syndromic surveillance system data for the time period from 2007-2011. Our aims were threefold: to demonstrate a proof of concept using syndromic surveillance for SSTI surveillance in the absence of laboratory data, to estimate the burden of ED visits associated with SSTI, and to determine potential geographic "hotspots" for these infections.

Introduction

The incidence of and hospitalizations for SSTI have steadily increased over the last decade in the United States, primarily due to the emergence and spread of community acquired Methicillin resistant Staphylococcus aureus (CA-MRSA). The ED is a common site for SSTI treatment and serves populations not captured by traditional surveillance, including the homeless and uninsured. The use of near real-time syndromic surveillance within the ED to detect unusual activity for further public health investigation has been used to augment traditional infectious disease surveillance. However, the use of this approach for monitoring local epidemiologic trends in SSTI presentation where laboratory data are not available, has not previously been described.

Methods

We sought to describe the epidemiology of ED visits for SSTI in an urban area with diverse neighborhood populations using the Boston Public Health Commission's (BPHC) Syndromic Surveillance System (BSynSS) data for a five year time period (2007 through 2011). SSTI related visits were defined by either chief complaints with SSTI associated words (abscess, cellulitis) or final diagnosis International Classification of Diseases (ICD-9 CM) codes for SSTIs. SSTI related visits were de-duplicated using demographics and visit identifiers and then stratified by age group, gender, race, and neighborhood of residence defined by ZIP code. Each of Boston's 15 neighborhoods has a unique demographic profile with distinct differences in race, socioeconomic status, and age. Finally, we examined trends in characteristics of potential "hotspots" of neighborhood clustering for SSTIs in EDs.

Results

Using our SSTI syndrome definition, we estimated unique SSTI visits represented 3.29 % (n= 45,252) of all visits within Boston's ten EDs during the study period with a seasonal pattern peaking during the summer months (July through September). The majority of SSTI visits (54%) were among patients 18 to 44 years old, which is consistent with the age distribution of the Boston population. However, a disproportionate number of SSTI visits (43%) were among Black patients when compared to both the overall Boston population (22% Black) and to the racial distribution of all ED visits (39% Black). The five-year average rate of SSTI visits for Black patients (281.2 per 10,000 population) was significantly greater at 2.8 times [CI 2.7, 3.0] than the rate for White patients (99.0 per 10,000 population). Geographic neighborhood distribution of SSTI visits ranged from a low of 2.69% to a high of 4.11% of all neighborhood-specific ED visits. Disposition data are available for 2010 and 2011 only and show that 24% and 23% of patients in 2010 and 2011, respectively, were admitted for their SSTI.

Conclusions

Our study results suggest that syndromic surveillance data can be used to track the burden and patterns of SSTI in an urban population, including disease severity through the use of disposition data. Furthermore, syndromic surveillance can provide information on the local epidemiology of SSTI, including data related to health inequalities. The burden of SSTIs should be compared to overall ED use for a specific population to control for biases in health care seeking behaviors and choice of provider type. A local syndromic surveillance system has the potential to provide public health authorities and ED clinicians near real-time monitoring of trends in severity and demographic risk factors, and may provide an alternative to tracking the severity of illness where no laboratory data are readily available.

Keywords

syndromic surveillance; epidemiology; skin and soft tissue infections; racial disparities

*Larissa May
E-mail: larissa.may@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

The Surveillance Window – Contextualizing Data Streams

Kirsten McCabe*, Lauren Castro, Mac Brown, William Daniel, Eric Nick Generous, Kristen Margevicius and Alina Deshpande

Los Alamos National Laboratory, Los Alamos, NM, USA

Objective

The goal of this project is the evaluation of data stream utility in integrated, global disease surveillance. This effort is part of a larger project with the goal of developing tools to provide decision-makers with timely information to predict, prepare for, and mitigate the spread of disease.

Introduction

Los Alamos National Laboratory has been funded by the Defense Threat Reduction Agency to determine the relevance of data streams for an integrated global biosurveillance system. We used a novel method of evaluating the effectiveness of data streams called the "surveillance window". The concept of the surveillance window is defined as the brief period of time when information gathered can be used to assist decision makers in effectively responding to an impending outbreak. We used a stepwise approach to defining disease specific surveillance windows;

1. Timeline generation through historical perspectives and epidemiological simulations.
2. Identifying the surveillance windows between changes in "epidemiological state" of an outbreak.
3. Data streams that are used or could have been used due to their availability during the generated timeline are identified. If these data streams fall within a surveillance window, and provide both actionable and non-actionable information, they are deemed to have utility.

Methods

Figure 1 shows the overall approach to using this method for evaluating data stream types. Our first step was identifying a list of priority diseases to build surveillance windows for and our primary sources were our SME panel, CDC priorities, as well as DOD priorities. We also conducted a literature review to support our selection of diseases. We ensured that there was representation of human, animal and plant diseases and there was enough data available for selected outbreaks to facilitate evaluation of all data stream types identified. We then selected representative outbreaks for diseases to generate a timeline for defining surveillance windows. Surveillance windows were then defined (based on four specific biosurveillance goals developed by LANL) and information for applicable data streams was collected for the duration of the outbreak. A data stream was deemed useful if it was determined to be available within the defined surveillance window. In addition, evaluation of the ideal use case of the data streams was performed. In essence, if used more effectively could this data stream provide greater support to understanding, detection, warning or management of disease outbreaks or event situations?

Results

Results presented in this abstract are from retrospective analyses of historical outbreaks selected as being representative of FMD, Ebola, Influenza and E.coli. Graphs indicating case counts and geographical spread were combined and a timeline was created to determine the length of time between changes in "epidemiological state" that defined various surveillance windows. This timeline was then populated with durations when data streams were used during the outbreak. Results showed varying surveillance windows times are dependent on disease characteristics. In turn, epidemiology of the disease affected the occurrence of data streams on the timeline.

Conclusions

Surveillance window based evaluation of data streams during disease outbreaks helped identify data streams that are of significance for developing an effective biosurveillance system. Some data streams were identified to have high utility for early detection and early warning regardless of disease, while others were more disease and operations specific. This work also identified data streams currently not in use that could be exploited for faster outbreak detection. Key useful data streams that are underlying to all disease categories and thus important for integration into global biosurveillance programs will be presented here.

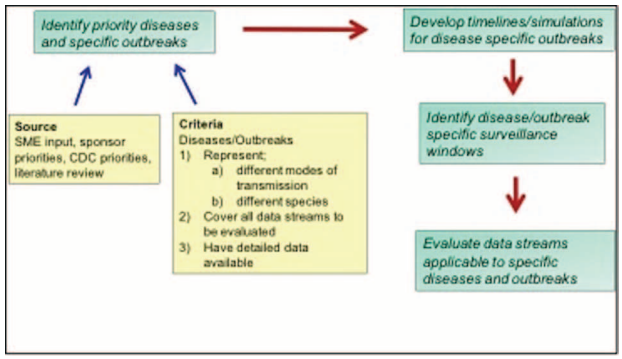


Figure 1: Overall approach to surveillance window based evaluation

Keywords

Surveilliance Windows; Data streams; Biosurveilliance

Acknowledgments

This project is supported by the Chemical and Biological Technologies Directorate Joint Science and Technology Office (JSTO), Defense Threat Reduction Agency (DTRA).

*Kirsten McCabe
E-mail: kjmccab@lanl.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Enhancing Surveillance for Arboviral Infections in the Arizona Border Region

Orion McCotter*[1], Frank Vanskike[1, 2], Kacey Ernst[2], Ken Komatsu[3], Harold Margolis[4], Stephen Waterman[5], Laura Tippit[1], Kay Tomashek[4], Anne Wertheimer[2], Sonia Montiel[5], Catherine Golenko[1] and Elizabeth Hunsperger[4]

[1]Arizona Department of Health Services, Office of Border Health, Tucson, AZ, USA; [2]University of Arizona, Mel and Enid Zuckerman College of Public Health, Tucson, AZ, USA; [3]Arizona Department of Health Services, Phoenix, AZ, USA; [4]Centers for Disease Control and Prevention, Division of Vector-Borne Diseases, Dengue Branch, San Juan, Puerto Rico; [5]Centers for Disease Control and Prevention, Division of Global Migration and Quarantine, U.S. - Mexico Unit, San Diego, CA, USA

Objective

To enhance arboviral surveillance and laboratory capacity to establish a surveillance baseline for the emerging threat of Dengue fever in the Arizona-Mexico border region.

Introduction

West Nile Virus (WNV) and dengue virus (DENV) are both arboviruses which are transmitted to humans by an infected mosquito bite during blood-meal feeding. The clinical presentations of non-neuroinvasive WNV and dengue fever are similar, and symptoms may include acute onset of high fever, headache, myalgia, arthralgia, nausea, vomiting, and often a maculopapular rash. More serious manifestations of these viruses include fatal encephalitis and meningitis in WNV patients and fatal hemorrhagic disease in dengue patients. Over the last decade, WNV has spread rapidly across North America, reaching Arizona in 2004, and has become a significant cause of human illness since that time. Even though dengue has been described as primarily a disease of the tropics and sub-tropical areas, there is a small but significant risk for dengue outbreaks in the continental United States as evidenced by surveillance efforts in Texas that identified local dengue transmission in 2005. In recent years, outbreaks of dengue have occurred in Mexico border states, most notably Sonora in 2010. That same year, Arizona had the highest incidence of WNV cases in the U.S. including number of neuroinvasive disease cases, total cases, and number of deaths per state. The emergence of DENV and WNV as important public health problems maybe have been due to non-effective mosquito control, global demographic changes (urbanization and population growth), increased air travel, and inadequate surveillance.

Methods

Vector mapping: Mapping techniques will be utilized to visually depict *Aedes aegypti* populations captured from previous seasonal public health environmental vector trapping programs.

Laboratory capacity: Multi-state laboratory training by CDC Dengue Branch was held in October 2012.

Surveillance: The WNV cases that present to medical services for WNV testing and reported to public health officials are the most severe nueroinvasive cases. Much less is understood about the non-neuroinvasive cases with often present with non-descript symptoms.

Results

Vector mapping: Comparative densities of *Ae. aegypti* with academic partners of the Entomology and Public Health conducting a study capturing *Ae. aegypti* may help to enhance environmental programs.

Laboratory Capacity: The laboratory training will cover conventional serological methods as well as recently FDA cleared molecular RT-PCR. Participants will include public health laboratory personnel working in molecular and serology diagnostics and other binational partners.

Surveillance: A convenient seroprevalence study at sentinel-hospital site of symptomatic patients presenting in Arizona border hospital sites will be performed to better understand circulating levels of arboviral infections.

Conclusions

Appropriate and timely response to surveillance data is the key to identification human and animal disease associated with WNV, DENV, and other arboviruses. The mosquito vector *Ae. aegypti* is well established widespread and thriving in Arizona yet there is no autochthonous transmission of DENV identified to date. The results from this study will identify gaps and potential prevention and control measures for emerging infectious diseases including WNV and DENV in Arizona.

Keywords

Dengue; Surveillance; Emerging infections; Dengue fever; Arboviral

Acknowledgments

US-Mexico Border States, Local Health Departments, Sonora Secretariat de Salud, Arizona State Public Health Laboratory.

References

Hayden, M.H., et al., Microclimate and human factors in the divergent ecology of Aedes aegypti along the Arizona, U.S./Sonora, MX border. Ecohealth, 2010. 7(1): p. 64-77.

Walker, K.R., et al., Human and environmental factors affecting Aedes aegypti distribution in an arid urban environment. J Am Mosq Control Assoc, 2011. 27(2): p. 135-41.

Hoeck, P.A., et al., Population and parity levels of Aedes aegypti collected in Tucson. J Vector Ecol, 2003. 28(1): p. 65-73.

Botz, J.T., Survey of Aedes aegypti eggs in and around homes in Tucson, Arizona. J Am Mosq Control Assoc, 2002. 18(1): p. 63-4.

Fink, T.M., et al., Aedes aegypti in Tucson, Arizona. Emerg Infect Dis, 1998. 4(4): p. 703-4.

Engelthaler, D.M., et al., The reemergence of Aedes aegypti in Arizona. Emerg Infect Dis, 1997. 3(2): p. 241-2.

*Orion McCotter
E-mail: Orion.McCotter@azdhs.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

New Strategy to Monitor and Assess Laboratory Biosafety Programs

Heather N. Meeks[1], Betiel H. Haile[2], Ngozi A. Erondu[2], Lisa Ferland[2], Meeyoung Park[2] and Scott J. McNabb*[2, 3]

[1]Defense Threat Reduction Agency, Basic & Applied Sciences, Fort Belvoir, VA, USA; [2]Public Health Practice, LLC, Atlanta, GA, USA; [3]Hubert Department of Global Health, Emory University, Rollins School of Public Health, Atlanta, GA, USA

Objective

To develop a toolset to monitor and assess laboratory biosafety program performance and cost

Introduction

Laboratory biosafety – a component of biosecurity – has specific elements that together, comprise a facility's capability to both protect employees and the surrounding public and environment. Measuring these elements permits assessment and the costing of program-specific safety interventions. In the absence of a strategy and toolset, we developed a conceptual framework and toolset that monitors and assesses laboratory biosafety programs (LBPs) and provides useful information (e.g., return on investment [ROI]) for decision makers.

Methods

We conducted academic and open source literature reviews of LBPs and affiliated organizations laboratory manuals to identify objectives, goals, and indicators. These findings were aligned to laboratory biosafety-specific inputs, activities, outputs, and outcomes to create a strategic, conceptual framework (logic models) used to assess performance and measure the cost and ROI. Indicators were identified in existing literature or developed and mapped to the logic model elements.

Results

Six logic models were created: laboratory biosafety, biosurety, procedural, biocontainment, information security, and training. The laboratory biosafety logic model served as the overall framework for the remaining five sub-logic models. We also established a database containing 161 indicators mapped to each of the logic model elements.

Conclusions

We developed a strategic framework that monitors and evaluates LBPs. While evaluation of cost-impacts in LBPs provides business intelligence for resource planning, this integrated approach also provides information about gaps. We plan to pilot this toolset and refine indicators using principal component analysis.

Keywords

Laboratory biosafety; Evaluate Laboratory; program performance

Acknowledgments

Defense Threat Reduction Agency, Basic & Applied Sciences

References

1. Bakanidze L, Imnadze P, Perkins D. Biosafety and biosecurity as essential pillars of international health security and cross-cutting elements of biological nonproliferation. BMC Public Health. 2010;10 Suppl 1:S12.
2. Organization WH. International Health Regulations (2005) IHR Monitoring Framework: Checklist and Indicators for Monitoring Progress in the Development of IHR Core Capacities in States Parties. Geneva; 2010.
3. Carr K, Henchal EA, Wilhelmsen C, Carr B. Implementation of biosurety systems in a Department of Defense medical research laboratory. Biosecurity and bioterrorism : biodefense strategy, practice, and science. 2004;2(1):7-16. Epub 2004/04/08.
4. Garaigordobil M. Evaluation of a program to prevent political violence in the Basque conflict: effects on the capacity of empathy, anger management and the definition of peace. Gac Sanit. 2012. Epub 2012/01/31.
5. Jahrling P, Rodak C, Bray M, Davey RT. Triage and management of accidental laboratory exposures to biosafety level-3 and -4 agents. Biosecurity and bioterrorism : biodefense strategy, practice, and science. 2009;7(2):135-43. Epub 2009/07/29.
6. Le Duc JW, Anderson K, Bloom ME, Estep JE, Feldmann H, Geisbert JB, et al. Framework for leadership and training of Biosafety Level 4 laboratory workers. Emerging Infectious Diseases. 2008;14(11):1685.
7. Lewis M, Development CfG. Governance and corruption in public health care systems: Center for Global Development; 2006.
8. Losinger WC, Bush EJ, Hill GW, Smith MA, Garber LP, Rodriguez JM, et al. Design and implementation of the United States National Animal Health Monitoring System 1995 National Swine Study. Preventive veterinary medicine. 1998;34(2-3):147-59.
9. Miller SR, Bergmann D. Biocontainment design considerations for biopharmaceutical facilities. Journal of Industrial Microbiology & Biotechnology. 1993;11(4):223-34.
10. Murray CJL, Evans DB. Health systems performance assessment: World Health Organization; 2003.

*Scott J. McNabb
E-mail: scottjnmcnabb@emory.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Use of a Real-Time Syndromic Surveillance System to Improve Influenza Like Illness Screening and Documentation in Emergency Departments during the H1N1 Pandemic

David Meurer*[1, 3] and James Talbot[2, 1]

[1]University of Alberta, Edmonton, AB, Canada; [2]Government of Alberta, Edmonton, AB, Canada; [3]Alberta Health Services, Edmonton, AB, Canada

Objective

Screening for Influenza Like Illness (ILI) is an important infection control activity within emergency departments (ED). When ILI screening is routinely completed in the ED it becomes clinically useful in isolating potentially infectious persons and protecting others from exposure to disease. When routinely collected, ILI screening in an electronic clinical application, with real time reporting, can be useful in Public Health surveillance activities and can support resource allocation decisions e.g. increasing decontamination cleaning. However, the reliability of documentation is unproven. Efforts to support the adoption of ILI screening documentation in a computer application, without mandatory field support, can lead to long term success and increased adherence.

Methods

We evaluated the impact of efforts to improve ILI screening documentation adherence in an electronic ED information system (EDIS) during wave 2 of the September-November 2009 H1N1 pandemic. ILI screening documentation rates were calculated across the 8 sites in Edmonton Zone of Alberta Health Services and subsequently correlated to interventions. Five interventions were evaluated: real-time verbal reminders (one-to-one nurse reminders), delayed email reminders (with the ILI screening documentation rates), meetings (strategize to improve documentation rate), media (visual media broadcasts) and clinic awareness (opening and operation of the influenza assessment clinic). A logistic regression model was used to derive odds ratios (OR) and 95% confidence intervals (CI) for correlation between the interventions and the screening rate change.

Results

The ILI screening not-documented (N/D) rate on September 27, 2009, was 75% (N/D = 781; ED visits = 1039). By November 25, the N/D rate had fallen to 11% and remained below 20% into July 2010. October 18, 2009 marked the first day that the daily positive (POS) ILI screen rate was at or above 10% of patient visits with a rate of 12% (POS = 139; ED visits = 1164). The POS rate sustained values >10% until November 25(peaking at 40% on October 28, 2009) reflecting influenza activity and informing public health and other decision makers. When all site screening rates were aggregated and compared to the intervention variables – e-mail reminders (OR = 2.176; 95% CI: 2.078-2.279), meetings (OR = 2.286; 95% CI: 2.089-2.501), media (OR = 4.894; 95% CI: 4.219-5.677), clinic awareness (OR = 1.145; 95% CI: 0.998-1.313) were positively associated with increased adherence. Where one-to-one reminders to document ILI screening were provided at one site, the ILI documentation increased (OR = 2.663; 95% CI: 2.260-3.138). E-mail reminders (OR = 0.852; 95% CI: 0.732-0.992) and meetings (OR = 0.696; 95% CI: 0.505-0.960) had less influence on ILI documentation when the single site was analyzed.

Conclusions

A variety of interventions successfully improved ILI screening documentation. The greatest impact was associated with e-mail reminders for recording ILI screening results, meetings on how to improve adherence and media broadcasts associated with the circulating pandemic influenza. The strongest reported effect size was seen in one site following one-to-one nurse reminders to record the ILI screening results. These results suggest that ILI documentation adherence can be successfully increased using a variety of interventions. Implementing and monitoring the effect of the interventions was made possible by the syndromic surveillance system, which at the same time, contributed to improved data used for infection prevention and control and public health purposes.

Keywords

decision support; Influenza Like Illness; screening; documentation; adherence

Acknowledgments

Alberta Health and Wellness, Government of Alberta. Alberta Health Services.

*David Meurer
E-mail: david.meurer@ualberta.ca

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Mining Surveillance Data: Does Radiation Treatment of Prostate Cancer Cause Rectal Cancer?

John W. Morgan*[1, 2], Brice Jabo[1], Mark E. Ghamsary[1] and Kevork Kazanjian[3]

[1]Dept Epidemiology, Biostatistics & Population Medicine, Loma Linda University School of Public Health, Loma Linda, CA, USA; [2]Desert Sierra Cancer Surveillance Program, Region 5 of California Cancer Registry, Loma Linda, CA, USA; [3]Dept of Surgery, Division of Surgical Oncology, Loma Linda University School of Medicine, Loma Linda, CA, USA

Objective

We sought to assess whether external beam radiation (RAD) treatment of prostate cancer, that exposes the rectum to ionizing radiation, was followed by increased hazards for rectal cancer, relative to prostatectomy (SURG).

Introduction

Prostate cancer (PC) is the most common invasive cancer diagnosed among US men. The majority of PCs are organ-confined at diagnosis making them candidates for treatment using RAD, SURG, or other protocols. Several studies have provided preliminary evidence that radiation treatment of prostate cancer may increase subsequent rectal cancer risk (1-2). Data specifying type of RAD treatment of PC was not available for the study period.

Methods

We conducted record linkage for all 322,327 organ confined new prostate cancers and 53,204 new rectum and rectosigmoid junction (rectal) cancers among California males from 1988-2009, identifying men diagnosed with rectal cancer more than five years following treatment of organ-confined prostate cancer with RAD or SURG. Among the men treated with RAD vs SURG, the Cox proportional hazards ratio (HR) for subsequent rectal cancer was assessed. Demographic covariates included: race/ethnicity as Asian/Other (A-O), non-Hispanic black (NHB), Hispanic (Hisp), and non-Hispanic white (NHW), and socioeconomic status quintiles (1-5 Highest). Other covariates included age, as a continuous variable, and year of PC diagnosis.

Results

Among the 43,130 men having organ-confined prostate cancer that had been treated with RAD only, 166 were diagnosed with rectal cancer more than five years following PC treatment. Likewise, 69,104 men treated with SURG only, yielded 242 rectal cancer cases more than 5 years later. Following is the demographic factor adjusted hazards ratio (HR) for rectal cancer with 95% confidence intervals (CI) contrasting findings for the two PC treatment cohorts: Rectal cancer $HR_{RAD/SURG}$=1.39; 95% CI=1.12-1.74. HR contrasts for demographic factors included age- (HR_{Age}= 1.02; 95% CI=1.01-1.04), race/ethnicity- ($HR_{A\text{-}O/NHW}$= 1.10; 95% CI=0.72-1.67, $HR_{NHB/NHW}$= 1.19; 95% CI=0.82-1.74 and $HR_{Hisp/NHW}$= 1.01; 95% CI=0.72-1.43), and SES-contrasts ($HR_{SES1/SES5}$= 0.95; 95% CI=0.65-1.39), $HR_{SES2/SES5}$=1.20; 95% CI=0.89-1.62, $HR_{SES3/SES5}$= 1.17; 95% CI=0.88-1.55, and $HR_{SES4/SES5}$= 1.14; 95% CI=0.87-1.49). The HR for PC year of diagnosis (HR_{Year}= 0.91; 95% CI=0.89-0.94) a protective effect for more recent years.

Conclusions

These findings reveal increased hazards for rectal cancer among organ-confined prostate cancer patients treated with RAD, relative to patients treated with SURG, that are substantially independent of demographic covariates. Treatment of rectal cancer among these patients is further complicated because they are ineligible for radiation treatment of rectal cancer due to the high-dose pelvic radiation received during prostate cancer treatment. Further analyses that seek to distinguish roles of different dose and delivery methods for RAD are ongoing.

Keywords

radiation; cancer; rectal; prostate; surveilance

References

1. E Rapiti, G Fioretta, HM Verkooijen, R Zanetti, F Schmidlin, H Shubert, A Merglen, R Miralbell, C Bouchardy. Increased risk of colon cancer after external radiation therapy for prostate cancer. Int. J. Cancer: 123, 1141–1145 (2008).
2. NN Baxter, JE Tepper, SB Durham, DA. Rothenberger,BA Virnig. Increased Risk of Rectal Cancer After Prostate Radiation: A Population-Based Study. Gastroenterology 2005;128:819–824.

*John W. Morgan
E-mail: john.w.morgan@att.net

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using Surveillance Data to Identify Risk Factors for Severe H1N1 in First Nations

Kathryn Morrison*[1], Yanyu Xiao[2], Seyed Moghadas[2] and David Buckeridge[1]

[1]Epidemiology & Biostatistics, McGill University, Montreal, QC, Canada; [2]York University, Toronto, ON, Canada

Objective

We sought to measure from surveillance data the effect of proximity to an urban centre (rurality) and other risk factors, (e.g., age, residency on a FN reservation, and pandemic wave) on hospitalization and intensive care unit admission for severe influenza.

Introduction

Research has shown that Canadian First Nation (FN) populations were disproportionately affected by the 2009 H1N1 influenza pandemic. However, the mechanisms for the disproportionate outcomes are not well understood. Possibilities such as healthcare access, infrastructure and housing issues, and pre-existing comorbidities have been suggested. We estimated the odds of hospitalization and intensive care unit admission for cases of H1N1 influenza among FN living in Manitoba, Canada, to determine the effect of location of residency and other factors on disease outcomes during the 2009 H1N1 pandemic.

Methods

We obtained surveillance data on laboratory confirmed cases of pandemic H1N1 influenza from the province of Manitoba. These data described demographic characteristics, residence location, and dates of hospital and ICU admission. We measured the rurality of each case using a pre-exiting scale (Rambeau & Todd, 2000). We tabulated the number of hospitalizations (and ICU admissions) stratified first by reservation residency and second by rurality and calculated unadjusted odds ratios. We then used logistic regression to calculate the odds of hospitalization given infection (and the odds of ICU admission given hospitalization), adjusting for age, reservation residency, rurality, and pandemic wave. We also investigated the effect of rurality and reserve residency on time to hospitalization from infection.

Results

FN individuals diagnosed with influenza and living on-reserve were more likely to be hospitalized than those living off-reserve, even after controlling for the effects of rurality (OR: 2.16, 95% CI: 1.15, 4.05) . FN living in rural areas were hospitalized more frequently and experienced longer delays between infection and hospitalization than FN residing in more urban areas. Rurality and reserve residency had less effect on ICU admissions once an individual was hospitalized.

Conclusions

While it is established that FN individuals had disproportionately high rates of severe outcomes from H1N1, the causal mechanisms at work are not well understood. Reasonable possibilities include barriers to healthcare access, lack of proper housing and infrastructure, and pre-existing comorbidities. This research using surveillance data suggests that geographic location has an effect on healthcare access, including both on vs. off reserve residency as well as rurality.

Keywords

Influenza; First Nations; Severe outcomes

References

Rambeau, Sheila, & Kathleen Todd. January 2000. Census Metropolitan Area and Census Agglomeration Influenced Zone (MIZ) with Census Data. Ottawa: Statistics Canada, Geography Division.

*Kathryn Morrison
E-mail: kt.morrison@mail.mcgill.ca

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Framework for Detecting and Classifying Outbreaks of Gastrointestinal Disease

Kathryn Morrison*, Katia Charland, Anya Okhmatovskaia and David Buckeridge

Epidemiology & Biostatistics, McGill University, Montreal, QC, Canada

Objective

To develop a methodological framework for detecting and classifying outbreaks of gastrointestinal disease on the island of Montreal, with the goal of improving early outbreak detection using simulated surveillance data.

Introduction

Outbreaks of waterborne gastrointestinal disease occur routinely in North America, resulting in considerable morbidity, mortality, and cost (Hrudey, Payment et al. 2003). Outbreak detection methods generally attempt to identify anomalies in time, but do not identify the type or source of an outbreak. We seek to develop a framework for both detection and classification of outbreaks using information in both space and time. Outbreak detection can be improved by using simulated outbreak data to build, validate, and evaluate models that aim to improve accuracy and timeliness of outbreak detection.

Methods

To generate outbreak data, we used a previously validated microsimulation model depicting waterborne outbreaks of gastrointestinal disease (Okhmatovskaia et al. 2010). The model is parameterized based on outbreak characteristics such as concentration and duration of contamination, and calibrated to produce realistic outbreak data (e.g., emergency department visits from GI-illness, laboratory reporting to public health) in space and time. We are interested in identifying unique space-time signatures in the data that would allow not only detection, but also classification based on outbreak type. For example, to be able to detect and classify an outbreak as due to a water plant failure versus an food-borne illness based on unique space-time patterns, even though symptoms and temporal outbreak patterns may be similar. For the detection step, we use a hidden Markov model (HMM) that accounts for spatial information through a spatially correlated random effect with an exponential decay. HMMs have been used previously in disease mapping (Green 2002) but not widely in space-time disease outbreak detection. For the classification step, we use a supervised clustering algorithm to classify the outbreak by source (e.g., water plant location) and type (e.g., disease).

Results

Preliminary results for the detection step show that the HMM can distinguish accurately between regions in an outbreak state versus those in a normal state at each time period. Ongoing work for the detection step includes further evaluation of the HMM accuracy as a function of outbreak characteristics. For the classification step, we are evaluating the suitability of different supervised clustering algorithms for identifying the type of outbreak from the HMM results.

Conclusions

If outbreaks are detected rapidly, interventions, such as boil-water advisories, are available to quickly and effectively limit the human and economic impacts. Traditional public health surveillance systems, however, frequently fail to detect waterborne disease outbreaks. Every disease outbreak has unique characteristics; simulation is the best method to estimate the capacity of syndromic surveillance to more efficiently detect different types of enteric disease outbreaks based on a variety of parameters. Outbreak detection can be improved with advances in data availability, such as syndromic surveillance data that will increase timeliness of detection, and space-time information to allow for simultaneous detection and classification of outbreaks by important characteristics (type of outbreak, source of outbreak).

Keywords

Syndromic surveillance; Disease outbreak detection; Waterborne disease

Acknowledgments

This research is supported by the Canadian Institutes of Health Research (CIHR).

References

Green PJ. (2002). “Hidden Markov Models and Disease Mapping.” Journal of the American Statistical Association 97(460): 1055-1070.

Hrudey S., P. Payment, et al. (2003). “A fatal waterborne disease epidemic in Walkerton, Ontario: comparison with other waterborne outbreaks in the developed world.” Water science & technology 47(3): 7-14.

Okhmatovskaia A, Verma AD, Barbeau B, Carriere A, Pasquet R, Buckeridge DL. (2010). A Simulation Model of Waterborne Gastro-Intestinal Disease Outbreaks: Description and Initial Evaluation. AMIA Annual Symposium.

*Kathryn Morrison
E-mail: kt.morrison@mail.mcgill.ca

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluating a Social Network Analytic Tool to Support Outbreak Management and Contact Tracing in an Outbreak of Pertussis

Esther Munene*, S. Mottice and J. Reid

Utah Department of Health, Slc, UT, USA

Objective

To determine the feasibility and value of a social network analysis tool to support pertussis outbreak management and contact tracing in the state of Utah.

Introduction

Pertussis (i.e., whooping cough) is on the rise in the US. To implement effective prevention and treatment strategies, it is critical to conduct timely contact tracing and evaluate people who may have come into contact with an infected person. We describe a collaborative effort between epidemiologists and public health informaticists at the Utah Department of Health (UDOH) to determine the feasibility and value of a network-analytic approach to pertussis outbreak management and contact tracing.

Methods

The partnership: In early 2012, epidemiologists from UDOH's Vaccine Preventable Disease Program and UDOH's public health informaticists formed a partnership to determine the feasibility and value of the Organizational Risk Analyzer (ORA) in pertussis outbreak management and contact tracing (1). Both entities have a long-standing partnership. A characteristic that has made the collaboration particularly strong and mutually beneficial is that both partners have expertise in disease surveillance and outbreak management. In addition, the informaticists have expertise in devising systems that help frontline healthcare providers.

The Organizational Risk Analyzer (ORA): ORA is a computational tool that extends network analysis by using a meta-matrix model. A meta-matrix is defined as a network of connecting entities. The tool uses one or more matrices in an organization's meta-matrix as input. From this input the tool calculates measures that describe the relationships and ties among the entities. ORA contains over 50 network and node level measures which are categorized by the type of risk they detect (1).

Procedures: Following approval from UDOH's Institutional Review Board, we analyzed records from 629 deidentified pertussis patients from the UT-NEDSS database from January 2011 to December 2011. The test data included demographics and epidemiological information. We used Excel to create .csv data files, uploaded the data into ORA, and displayed the data in meta-matrices consisting of nodes (cases/contacts) and edges (relationships). We used ORA's visualizer to check for data-entry errors before performing the network analysis.

Data Analysis: ORA's centrality measures (degree, closeness, betweenness, hub, and eigenvector) were used to identify geographic locations with high infection rates and the patients who were central to sustaining the outbreak. Next, we applied a concor algorithm to find groups in the meta-network that might be hard to spot visually. Visualizations were used to supplement the metrics.

Results

The ORA analysis identified 5 individuals who were central to perpetuating the outbreak in that their centrality measures were higher than other patients in the network. The index patient (Fig 1) was traced back to Utah County and was linked to 6 direct contacts in the same county and several indirect ties in adjacent counties. The individual was highly connected to others within the network (hub centrality = 1.41 and eigenvector centrality = 1.00). Salt Lake County had the highest number of cases, followed by Utah County and Weber County. The concor analysis revealed hidden networks, including a cluster of patients grouped by age group and case status (Fig 2).

Conclusions

The ORA was found to be a valuable tool for supporting pertussis outbreak management and contact tracing. Although network analysis is relatively new to public health, it can increase public health's understanding of how patterns of social relationships can aid or inhibit the spread of communicable diseases and provide the information needed to target intervention efforts effectively.

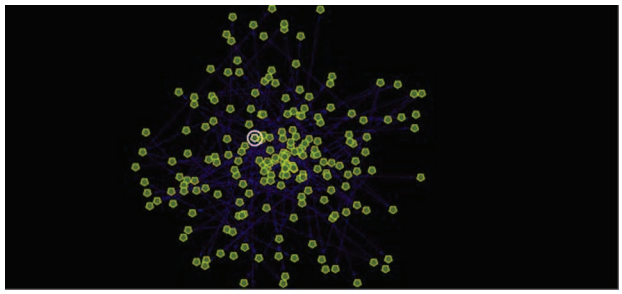


Fig. 1. The index case.

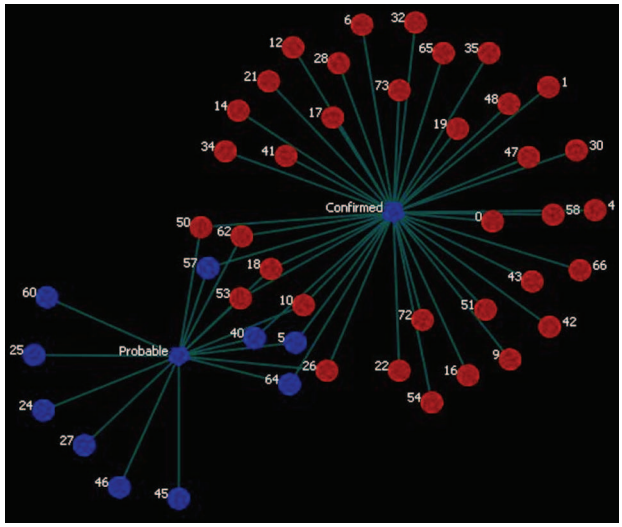


Fig. 2. Concor cluster of patients, by age group and case status.

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Keywords
Surveillance; Informatics; Social Network Analysis

Acknowledgments

This study was supported in part by the CSTE Applied Public Health Informatics Fellowship program and funded by the CDC.

References

1. Organizational Risk Analyzer: Center for Analysis of Social and Organizational Systems 2008.

*Esther Munene
E-mail: EMUNENE@utah.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluation of Integrated Disease Surveillance and Response (IDSR) using Bacillary Dysentery as a Priority Disease, Tanzania, 2012

Alfred G. Mwanyika*[1], Senga Sembuche[1] and Agricola Joachim[2]

[1]Tanzania Field Epidemiology and Laboratory Training Program (TFELTP), Dar es Salaam, United Republic of Tanzania; [2]Muhimbili University of Health and Allied Sciences (MUHAS), Dar es Salaam, United Republic of Tanzania

Objective

To determine whether the IDSR system meets its purpose and objectives, to evaluate the system attributes, and provide recommendations to improve the IDSR system, using the example of bacillary dysentery, a priority disease in Tanzania.

Introduction

Each year Ministry of Health and Social welfare of Tanzania under Epidemiology Section has been reporting many suspected cases of Shigella throughout the country. However only fewer laboratories have been reporting the confirmed cases.

Methods

The study was conducted between November 2011and February 2012.Hospital staff including nurses, physicians and laboratory personnel and other stakeholders from the Ministry of Health and Social Welfare (MOHSW) were enrolled in the study. Data was collected from a review of documents, questionnaires and interview of stakeholders. Surveillance system attributes were evaluated using updated guidelines for evaluating public health surveillance system (2007) from Morbidity and Mortality Weekly Report (MMWR).

Results

Questionnaires were administered to fifteen health personnel from four regional hospitals. Four health staff from epidemiology and laboratory section of MOHSW were interviewed. Only one regional hospital laboratory was conducting laboratory diagnosis for bacillary dysentery and sending reports to MOHSW. Data from this laboratory was reviewed. Out of 641 records from bacillary dysentery testing, 271 (42.3%) did not include age data, 5 (0.78%) missed sex, 624 (97.3%) missed the district where the patient came from, 26 (4.4%) did not include information on specimen quality, 1(0.2%) had no report of pathogens found and 636 (99.2%) did not include antimicrobial sensitivity testing (AST). The Predictive Value Positive (PVP) of the system was 0.62%. One (6.7%) of the health workers was trained in IDSR.

Conclusions

IDSR in Tanzania generally is not performing well as only one (25%) of the four visited hospitals conducts and reports laboratory diagnosis of bacillary dysentery. However the system is representative as it covers all regions of the United Republic of Tanzania and all ages of people. The system is flexible since National IDSR guideline (2001) was revised in 2011. More emphasis should be placed on strengthening laboratory capacity in disease diagnosis and reporting at all levels.

Keywords

Surveillance; Evaluation; IDSR; Bacillary dysentery

Acknowledgments

We acknowledge TFELTP and regional hospitals for their corporations to achieve this study.

References

Monthly diseases reports. Ministry of health and social welfare of Tanzania. www.moh.go.tz

*Alfred G. Mwanyika
E-mail: geofalfred@yahoo.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Content Analysis of Tobacco-related Twitter Posts

Mark Myslín*, Shu-Hong Zhu and Michael Conway

UC San Diego, San Diego, CA, USA

Objective

We present results of a content analysis of tobacco-related Twitter posts (tweets), focusing on tweets referencing e-cigarettes and hookah.

Introduction

Vast amounts of free, real-time, localizable Twitter data offer new possibilities for public health workers to identify trends and attitudes that more traditional surveillance methods may not capture, particularly in emerging areas of public health concern where reliable statistical evidence is not readily accessible. Existing applications include tracking public informedness during disease outbreaks [1].

Twitter-based surveillance is particularly suited to new challenges in tobacco control. Hookah and e-cigarettes have surged in popularity, yet regulation and public information remain sparse, despite controversial health effects [2,3]. Ubiquitous online marketing of these products and their popularity among new and younger users make Twitter a key resource for tobacco surveillance.

Methods

We collected 7,300 tobacco-related Twitter posts at 15-day intervals from December 2011 to July 2012, using ten general keywords such as cig* and hookah. Each tweet was manually classified using a tri-axial scheme, capturing genre (firsthand experience, joke, news, …), theme (underage usage, health, social image, …), and sentiment (positive, negative, neutral). Machine-learning classifiers were trained to detect tobacco-related vs. irrelevant tweets as well as each of the above categories, using Naïve Bayes, k-Nearest Neighbors, and Support Vector Machine algorithms. Finally, phi correlation coefficients were computed between each of the categories to discover emergent patterns.

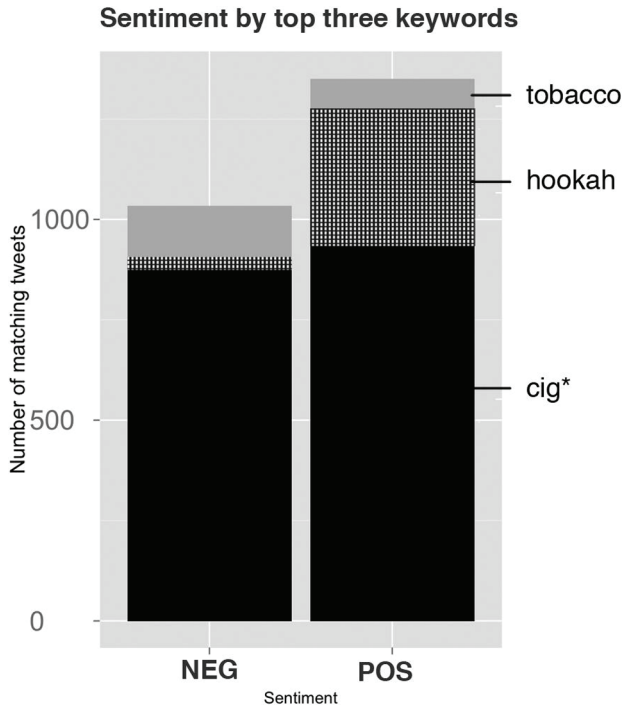
Results

The most prevalent genre of tweets was personal experience, followed by categories such as opinion, marketing, and news. The most common themes were hookah, cessation, and social image, and sentiment toward tobacco was more positive (26%) than negative (20%). The most highly correlated categories were social image–underage, marketing–e-cigs, and personal experience–positive sentiment. E-cigarettes were also correlated with positive sentiment and new users (even excluding marketing posts), while hookah was highly correlated with positive sentiment, pleasure, and social relationships. Further, tweets matching the term "hookah" reflected the most positive sentiment, and "tobacco" the most negative (Figure 1). Finally, negative sentiment correlated most highly with social image, disgust, and non-experiential categories such as opinion and information.

The best machine classification performance for tobacco vs. non-tobacco tweets was achieved by an SVM classifier with 82% accuracy (baseline 57%). Individual categories showed similar improvements over baseline.

Conclusions

Several novel findings speak to the unique insights of Twitter surveillance. Sentiment toward tobacco among Twitter users is more positive than negative, affirming Twitter's value in understanding positive sentiment. Negative sentiment is equally useful: for example, observed high correlations between negative sentiment and social image, but not health, may usefully inform outreach strategies. Twitter surveillance further reveals opportunities for education: positive sentiment toward the term "hookah" but negative sentiment toward "tobacco" suggests a disconnect in users' perceptions of hookah's health effects. Finally, machine classification of tobacco-related posts shows a promising edge over strictly keyword-based approaches, allowing for automated tobacco surveillance applications.



Sentiment in "hookah" tweets is disproportionately more positive than in "cig" and especially "tobacco" tweets.

Keywords

social media; surveillance; Twitter; tobacco; NLP

References

[1] Chew, C. & Eysenbach, G. Pandemics in the age of twitter: Content analysis of tweets during the 2009 H1N1 outbreak. PLoS One. 2010; 5(11):e14118.

[2] Ayers, J. W., Ribisl, K. M., & Brownstein, J. S. Tracking the rise in popularity of electronic nicotine delivery systems (Electronic cigarettes) using search query surveillance. Am J Prev Med. 2011; 40(4):448–453.

[3] Grekin, E. R. & Ayna, D. Waterpipe smoking among college students in the United States: A review of the literature. J Am Coll Health. 2012; 60(3):244–249.

*Mark Myslín
E-mail: mmyslin@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Malaria Trends in Six Outpatient Sites in Uganda, 2008—2011

Ruth K. Nassali*[1], Arthur Mpimbaza[1], Stella Kakeeto[1], Asadu Sserwanga[1], Fred Kizito[1], Denis Rubahika[2], Melody Miles[3], Michelle Chang[3], Grant Dorsey[4] and Moses Kamya[1]

[1]Infectious Diseases Research Collaboration, Kampala, Uganda; [2]National Malaria Control Program, Kampala, Uganda; [3]Centers for Disease Control, Atlanta, GA, USA; [4]Univeristy of California, San Francisco, San Francisco, CA, USA

Objective

To estimate trends in malaria morbidity at six sentinel sites in Uganda.

Introduction

Over the past five years, efforts to control malaria have been intensified in Uganda (1). With the intensification of these efforts, accurate and timely data are needed to monitor impact of the interventions and guide malaria control program planning (2, 3). We present data on trends in malaria burden over four years from six outpatient health facilities located in regions of varying malaria endemicity in Uganda.

Methods

The study utilized data from the on-going malaria sentinel surveillance program involving six level IV outpatient health facilities: Aduku, Nagongera, Walukuba, Kasambya, Kihihi and Kamwezi. Major malaria control interventions between 2008 and 2010 in sub-counties where these sites are located included Indoor residual spraying (IRS) conducted in Aduku; insecticide-treated nets (ITNs) distributed in Nagongera and Kamwezi. There has been no major control intervention(s) in sub-counties where Walukuba, Kasambya and Kihihi are located. Treatment with artemisinin-combination therapies have however been deployed nationally. Patient information; demographics, malaria test results and diagnosis are recorded on a standardized patient record. The test positivity rate (TPR) defined as the number of persons testing positive for malaria divided by the total number of persons tested was calculated by year from 2008 to 2011 for two age categories (< 5 years and > 5 years).

Results

A total of 560,586 patients were seen, of which 25% were <5 years. Over 325,500 patients were suspected to have malaria, with the proportion of these having a confirmatory test done increasing from 62% in 2008 to 98% in 2011. Between 2008 and 2011, the proportion of the <5 years testing positive for malaria significantly decreased from 66% to 34% in Aduku, from 61% to 41% in Nagongera, and from 54% to 24% in Kamwezi. However, significant increases were seen in Kasambya and Kihihi from 41% to 51% and from 28% to 44% respectively. The TPR at Walukuba remained stable (41% to 45%). Similar trends were seen in the > 5 years.

Conclusions

Sentinel site surveillance has been a reliable and timely method/tool for monitoring trends in malaria morbidity thereby informing and guiding the Uganda malaria control program.

Keywords

Surveillance; Malaria; Trends

Acknowledgments

Acknowledgements to NMCP Team/MOH, CDC/PMI, UMSP Team, Health Facility Staff.

References

1) Yeka A, Gasasira A, Mpimbaza A, Achan J, et al. Malaria in Uganda: challenges to control on the long road to elimination: I. Epidemiology and current control efforts. Acta Trop. 2012 Mar;121(3):184-95. Epub 2011 Mar 21
2) Breman JG, Holloway CN. Malaria surveillance counts. Am J Trop Med Hyg 2007;77:36-47
3) Bryce J, Roungou JB, Nguyen-Dinh P, Naimoli JF and Breman JG. Evaluation of national malaria control programmes in Africa. Bull World Health Organ 1994;72:371-81

*Ruth K. Nassali
E-mail: ruth.nassali@yahoo.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Fast Multidimensional Subset Scan for Outbreak Detection and Characterization

Daniel B. Neill* and Tarun Kumar

Event and Pattern Detection Laboratory, Carnegie Mellon University, Pittsburgh, PA, USA

Objective

We present Multidimensional Subset Scan (MD-Scan), a new method for early outbreak detection and characterization using multivariate case data from individuals in a population. MD-Scan extends previous work on multivariate event detection by identifying the characteristics of the affected subpopulation, and enables more timely and accurate detection while maintaining computational tractability.

Introduction

The multivariate linear-time subset scan (MLTSS) [1] extends previous spatial and subset scanning methods [2-3] to achieve timely and accurate event detection in massive multivariate datasets, efficiently optimizing a likelihood ratio statistic over proximity-constrained subsets of locations and all subsets of the monitored data streams. However, some disease outbreaks may only affect a subpopulation of the monitored population (age group, gender, individuals engaging in a specific high-risk behavior, etc.), and MLTSS is unable to use this additional information to enhance detection ability.

Methods

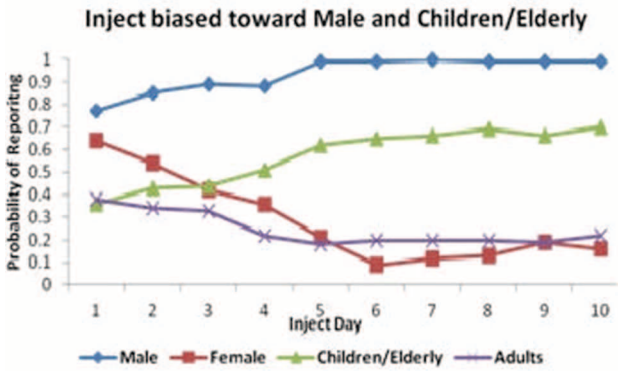
Rather than using the aggregate counts for each monitored location and data stream, we assume a set of multivariate data records representing each affected individual, with attributes such as date, home zip code, prodrome, gender, and age decile. MD-Scan jointly optimizes the likelihood ratio statistic over subsets of the values for each monitored attribute, identifying a space-time region (subset of locations and time steps) and subpopulation (including gender(s) and age groups) where the number of recent cases for a subset of the monitored prodromes is significantly higher than expected. To do so, the linear-time subset scanning property [3] is used to efficiently and exactly optimize over subsets of a given attribute, conditioned on the current subsets of all other attributes. MD-Scan then iterates over all attributes until convergence to a local optimum, and performs multiple random restarts to approach the global optimum. Additional constraints can be incorporated into each conditional optimization step, including spatial proximity, temporal contiguity, and connectedness. More details are provided in [4].

Results

We evaluated MD-Scan using simulated disease outbreaks injected into real-world Emergency Department data from Allegheny County, PA. Each outbreak was assumed to differentially affect a specific subpopulation (e.g. "adult females" or "children and the elderly"). MD-Scan achieved significantly earlier detection than MLTSS when the distribution of injected cases for the monitored attributes was sufficiently different from the background data, particularly when multiple attributes were affected or the inject was biased toward a less common attribute value. For simulated gender-specific and age-biased injects which affected only children and the elderly, MD-Scan detected over one day faster than MLTSS, and achieved 10% higher spatial accuracy. MD-Scan was also able to accurately identify the affected age and gender groups (Figure 1), while MLTSS does not characterize the affected subpopulation. Runtime of MD-Scan, while 9x slower than MLTSS, was still extremely fast, requiring an average of 4.15 seconds per day of data.

Conclusions

Our results demonstrate that MD-Scan is able to accurately identify the subpopulation affected by an outbreak, as represented by a subset of values for each monitored attribute. Additionally, MD-Scan substantially improves timeliness and accuracy of detection for outbreaks which differentially affect a subset of the monitored population. Detection performance was further enhanced by incorporating additional constraints such as spatial proximity and graph connectivity into the iterative MD-Scan procedure.



Keywords

event detection; disease surveillance; scan statistics

Acknowledgments

This work was partially supported by NSF grants IIS-0916345, IIS-0911032, and IIS-0953330, and a UPMC Healthcare Technology Innovation grant.

References

[1] Neill DB, McFowland E, Zheng H, Fast subset scan for multivariate spatial biosurveillance. Emerging Health Threats Journal, 2011, 4: s42.

[2] Kulldorff M, A spatial scan statistic. Communications in Statistics: Theory and Methods, 1997, 26: 1481-1496.

[3] Neill DB, Fast subset scan for spatial pattern detection. J. Royal Statistical Society B, 2012, 74: 337-360.

[4] Kumar T, Neill DB, Fast tensor scan for event detection and characterization. Submitted.

*Daniel B. Neill
E-mail: neill@cs.cmu.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Tau-leaped Particle Learning

Jarad Niemi*[1] and Michael Ludkovski[2]

[1]Iowa State University, Ames, IA, USA; [2]University of California, Santa Barbara, Santa Barbara, CA, USA

Objective

Develop fast sequential Bayesian inference for disease outbreak counts.

Introduction

Development of effective policy interventions to stem disease outbreaks requires knowledge of the current state of affairs, e.g. how many individuals are currently infected, a strain's virulence, etc, as well as our uncertainty of these values. A Bayesian inferential approach provides this information, but at a computational expense. We develop a sequential Bayesian approach based on an epidemiological compartment model and noisy count observations of the transitions between compartments.

Methods

For simplicity, consider an SIR epidemiological compartment model where compartments exist for susceptible, infected, and recovered individuals. Transitions between compartments occur in discrete time with transitions numbers given by Poisson random variables, the tau-leaping approximation, whose means depend on the current compartment occupancy and some unknown fixed parameters, e.g. virulence. Binomial observations, with possible unknown sampling proportion, are made on these transitions.

The standard sequential Bayesian updating methodology is sequential Monte Carlo (SMC), a.k.a. particle filtering. The original bootstrap filter is effective when the system has no fixed parameters, but exhibits marked degeneracy otherwise [1]. An approach based on resampling the fixed parameters from a kernel density estimate provides a generic approach with less degeneracy [2].

We build methodology based on a particle learning framework [3]. In this framework, each particle carries a set of parameter-specific sufficient statistics and samples parameter values whenever necessary. In addition, the methodology promotes a resample-move approach based on the predictive likelihood that reduces degeneracy in the first place.

An improvement on the particle learning framework in this model is that some fixed parameters can be integrated out of the predictive likelihood. This Rao-Blackwellization provides an SMC methodology with reduced Monte Carlo variance.

Results

For a fixed number of particles or computational expense, we show improvements in accuracy relative to the kernel density approach and an alternative approach based on sufficient statistics [4] where compared with a gold-standard Markov chain Monte Carlo analysis.

Conclusions

Many surveillance systems collect counts of adverse events related to some disease. These counts are expected to be a fraction of the true underlying disease extent. The methodology developed here allows a fully Bayesian analysis that uncovers the true number of infected individuals as well as disease virulence based on these count data. This statistical approach can be combined with an optimal policy map to help public health officials react effectively to initial disease reports.

Keywords

surveillance; Bayesian; sequential Monte Carlo; particle learning

References

[1] Gordon, Salmond, and Smith. Novel approach to nonlinear/non-Gaussian Bayesian state estimation. IEE Proceedings Part F: Communications, Radar and Signal Processing. 140(2): 107-113 (1993).

[2] Liu and West. Combined parameter and state estimation in simulation-based filtering. Doucet, De Freitas, and Gordon, ed. Sequential Monte Carlo Methods in Practice. Springer-Verlag, New York. 197—217 (2001).

[3] Carvalho, Johannes, Lopes, and Polson. Particle learning and smoothing. Statistical Science. 25(1): 88—106 (2010).

[4] Storvik. Particle filters in state space models with the presence of unknown static parameters. IEEE Transactions on Signal Processing. 50(2): 281—289 (2002).

*Jarad Niemi
E-mail: niemi@iastate.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

An Improved Algorithm for Outbreak Detection in Multiple Surveillance Systems

Angela Noufaily*[1], Doyo Enki[1], Paddy Farrington[1], Paul Garthwaite[1], Nick Andrews[2] and Andre Charlett[2]

[1]The Open University, Milton Keynes, United Kingdom; [2]Health Protection Agency, London, United Kingdom

Objective

To improve the performance of the England and Wales large scale multiple statistical surveillance system for infectious disease outbreaks with a view to reducing the number of false reports, while retaining good power to detect genuine outbreaks.

Introduction

There has been much interest in the use of statistical surveillance systems over the last decade, prompted by concerns over bio-terrorism, the emergence of new pathogens such as SARS and swine flu, and the persistent public health problems of infectious disease outbreaks. In the United Kingdom (UK), statistical surveillance methods have been in routine use at the Health Protection Agency (HPA) since the early 1990s and at Health Protection Scotland (HPS) since the early 2000s (1,2). These are based on a simple yet robust quasi-Poisson regression method (1). We revisit the algorithm with a view to improving its performance.

Methods

We fit a quasi-Poisson regression model to baseline data.

One of the limitations of the current algorithm is the small number of baseline weeks used. We propose a simple seasonal adjustment using factors. We extend the model to include a 10-level factor.

We fit the trend component always irrespective of its statistical significance.

We are concerned that the existing weighting procedure is too drastic. The baseline at a certain week is down-weighted if the standardized Anscombe residual for that week is greater than 1. This condition was chosen empirically to avoid reducing the sensitivity of the system in the presence of large outbreaks in the baselines, but may be increasing the FPR unduly when there are no or only small outbreaks in the baselines. We investigate several other options, including reducing the down-weighting to cases where the Anscombe residuals are greater than 2 or 3.

We evaluate a new re-weighting scheme informed by past decisions. Using this adaptive scheme, baseline data where an alarm was flagged are down-weighted to reduce their effect on current predictions. The criterion we use for re-weighting, here, is the value of the exceedance score.

Finally, we investigate the validity of the upper threshold values based on the quasi-Poisson model when the data are generated using known negative binomial distributions.

Results

Our evaluation of the existing algorithm showed that the false positive rate (FPR) is too high.

A novel feature of our new models is that they make use of much more baseline data. This resulted in a better estimation of the trend and variance and decreased the FPR. In addition, we found that the trend should always be fitted even when non-significant (or extreme). This decreases the discrepancies in the results when moving from one week to another.

The adaptive reweighting scheme was found to give broadly equivalent results to the reweighting method based on scaled Anscombe residuals. Using the latter as in the original HPA method, but with much higher threshold for reweighting decreased the FPR further.

Our investigations also suggest that the negative binomial model is a reasonable one, though not ideal in all circumstances. Thus, there is a good case for replacing the quasi-Poisson model with the negative binomial.

One of the unusual features of the HPA system is that it is run every week on a database of more than 3300 distinct organisms, which is likely to produce a large number of aberrances. We found that retaining the exceedance score approach based on the 0.995 quantile is perfectly reasonable. This involves ranking aberrant organisms in order of exceedance.

Conclusions

We have undertaken a thorough evaluation of the HPA's outbreak detection system based on simulated and real data. The main conclusion from this evaluation is that the FPR is too high, owing to a combination of factors notably excessive down-weighting of high baselines and reliance on too few baseline weeks.

Keywords

outbreak; negative binomial regression; quasi-Poisson

Acknowledgments

This research was supported by a project grant from the Medical Research Council, and by a Royal Society Wolfson Research Merit Award.

References

1. Farrington CP, Andrews NJ, Beale AJ, Catchpole MA. A Statistical Algorithm for the Early Detection of Outbreaks of Infectious Disease. Journal of the Royal Statistical Society Series A. 1996; 159: 547-563.
2. McCabe GJ, Greenhalgh D, Gettingby G, Holmes E, Cowden J. Prediction of infectious diseases: an exception reporting system. Journal of Medical Informatics and Technologies. 2003;5: 67-74.

*Angela Noufaily
E-mail: a.noufaily@open.ac.uk

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Who's Not Coming to Dinner? Evaluating Trends in Online Restaurant Reservations for Outbreak Surveillance

Elaine O. Nsoesie*[1, 2, 4], David L. Buckeridge[3] and John S. Brownstein[1, 2, 3]

[1]Children's Hospital Informatics Program, Boston Children's Hospital, Boston, MA, USA; [2]Department of Pediatrics, Harvard Medical School, Boston, MA, USA; [3]Department of Epidemiology, Biostatistics and Occupational Health, McGill University, Montreal, QC, Canada; [4]Network Dynamics and Simulation Science Laboratory, Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA, USA

Objective

The objective of this study is to evaluate whether trends in online restaurant table reservations can be used as an early indicator for a disease outbreak.

Introduction

Epidemiologists, public health agencies and scientists increasingly augment traditional surveillance systems with alternative data sources such as, digital surveillance systems utilizing news reports and social media, over-the-counter medication sales, and school absenteeism. Similar to school absenteeism, an increase in reservation cancellations could serve as an early indicator of social disruption including a major public health event. In this study, we evaluated whether a rise in restaurant table availabilities could be associated with an increase in disease incidence.

Methods

We monitored table availability using OpenTable; an online restaurant table reservation site for cities in the USA and Mexico. Our analysis can be summarized as follows. First, using the OpenTable site, we searched for the number of restaurants with available tables for two persons at lunch and dinner. Since different regions and individuals have different eating habits, we defined the lunch period between 12-3:30pm and dinner between 6-10:30pm. We searched for available tables every hour and half past the hour for every day of the week. Next, we investigated any occurrences of social unrest and natural disasters, which might have affected the trend in the time series. Lastly, using moving averages, cross-correlations and regression models, we elucidated and compared the time-trend in the data of table availabilities to data collected for various disease outbreaks. In the USA, we examined table availability for restaurants in Boston, Atlanta, Baltimore and Miami. For Mexico, we studied table availabilities in Cancun, Mexico City, Puebla, Monterrey, and Guadalajara.

Results

Preliminary results indicated differences in mean table availabilities observed during weekdays and weekends. However, these differences were statistically significant only for Boston and Miami ($p < 0.01$). Statistical significant differences were also observed for mean table availabilities at lunch and dinner for all the cities ($p < 0.001$).

Conclusions

The unavailability of reasons for cancellations introduces limitations to this data source. However, monitoring increases in cancellation of restaurant table reservations may be moderately useful for detecting epidemics especially in developing countries with limited public health infrastructures and resources. We therefore present a framework for future surveillance efforts.

Keywords

developing countries; infectious diseases; alternative data sources; reservation sites

*Elaine O. Nsoesie
E-mail: elaine.nsoesie@childrens.harvard.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Improvement Control System of Rabies in Ukraine

Serhiy Nychyk*[1], Ostap Zhukorskiy[2], Ivan Polupan[1], Mykola Ivanov[1] and Alina Nikitova[1]

[1]Institute of Veterinary Medicine, Kyiv, Ukraine; [2]National Academy of Agrarian Sciences of Ukraine, Kyiv, Ukraine

Objective

The purpose of the research was to find out the reasons of rabies antropurgisation in Ukraine.

Introduction

In Ukraine in spite of considerable financial expenses on oral immunization of foxes and parenteral immunization of dogs and cats, it is not succeeded to reach considerable results in the fight with rabies. Unfortunately there was a negative tendency to increasing a part of dogs and cats in the structure of rabies disease which are the main source of rabies in people.

Methods

Analysis of 228 anamnesis data of rabies infected dogs during 2008-2012. Research of 234 samples of the blood serum from dogs on existence of antibodies to the rabies virus by the ELISA method.

Results

Analysis of animal morbidity on rabies in Ukraine in period of 2006-2011 found out the changes of structure of morbidity in animal species that means decreasing a part of wild animals (from 49,0 % in 2006 to 38,7 % in 2011) and increasing a part of dogs (from 18,3 % in 2006 to 23,2 % in 2011) and cats (from 19,8 % in 2006 to 25,0 % in 2011) in the general amount of animals which perished from rabies (Fig. 1).

A lot of Ukrainian scientists and doctors of veterinary medicine consider that the main reason of spreading the rabies is a great number of homeless animals which factually are the reservoirs of infection in towns and villages.

However, in our opinion spreading of rabies shows the insufficient level of measures of control of rabies among home animals. It was confirmed with conducted analysis that only 26 (12,9 %) dogs were stray, others 202 (87,1 %) had owners, but didn't get necessary protective rabies vaccination.

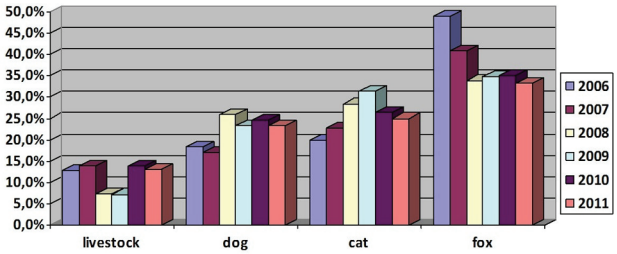
According to Ukrainian instruction "Preventive measures against rabies of animals", all the dogs must be vaccinated against rabies, but it actually appears it is quite not so.

At research of 234 samples of the blood serum of dogs on existence of antibodies to the rabies virus it was determined that the level of population immunity in dogs is 36,6 % in Ukrainian towns, but the protective level of antibodies was found in 9,1 % of village dogs. We consider that the main reason of this is imperfection of the Ukrainian legislation in the questions of responsibility of proprietors of animals.

For breaking of epizootic chain it is necessary the percent of vaccinated animals (in this case dogs) to be on a high level – more than 50%. Nowadays for reaching epidemic welfare in rabies it is important within the framework of the registered epidemic incidents dogs to be brought over to the ecocycles of infection sporadically without taking part in circulation of exciter, stay their biological deadlock and have low epidemic potential.

Conclusions

The conducted analysis expressly demonstrates that at present problems the eradication of rabies in Ukraine is impossible considering the low level of dogs' protection from rabies. Obtained results were sent to the State committee of veterinary medicine of Ukraine and will be the argument for enhancement of control after conducting rabies vaccination of dogs.



Rabies cases in the years 2006-2011.

Keywords

population rabies immunity; rabies vaccination; stray dogs

*Serhiy Nychyk
E-mail: vetmedic@ukr.net

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

The Natural Reservoirs of Salmonella Enteritidis in Populations of Wild Birds

Olga Obukhovska*

IECVM, Kharkiv, Ukraine

Objective

The aim of our study was to identify possible natural reservoirs of Salmonella Enteritidis among wild birds.

Introduction

Salmonella Enteritidis is dangerous for human due the reason of toxicoinfaction. These pathogen demonstrate high virulence for small children and people with chronic pathologies and can causes people die. The main source of infection to humans is birds (poultry and wild).

Wild birds represent the natural reservoir of same bacterial pathogens. It is known that Salmonella can occupy an intestinal tract of birds. This colonization in general is constant, sometimes proceeds with an alternating fever, and usually, without clinical signs. Infected birds can transmit pathogens to other isolates in close contact. This usually occurs on the nesting during seasonal migrations. In the southern region of Ukraine are several points of intersection of migration routes of wild birds on the way from Europe to Africa and Asia (National Park "Askania Nova"and others).

Methods

The study was conducted in populations of wild birds in National Park "Askania Nova" and peninsula "Arabat arrow" (the Azov Sea coast). From bird selected samples of blood serum and egg yolks for research in serum plate agglutination test (SPA) and litter samples for bacteriological research.

Results

The serological monitoring in populations of wild waterfowl in National Park "Askania Nova" (Ichthyaetus relictus, Sterna nilotica, Sterna herundo, Casarca ferruginea) has shown the presence of seropozitive individuals in adult birds (average 18%) and egg yolks (avarrage 12%). The bacteriological investigations confirmed circulation of Salmonella in this group of birds. 32.3% of all bacterial pathogens was Salmonella and more then half of them was the reprezentatives of serovar Salmonella Enteritidis.

Similar studies were conducted on territory of peninsula "Arabat arrow" (the Azov Sea coast). The serological monitoring among of wild waterfowl (Ardea cinerea, Sterna caspia, Phalacrocorax carbo, Podiceps cristatus, Anas platyrhynchos, Cygnus olar) revealed the presence of antibodies in blood serum (avarrage 17%) and egg yolks (avarrage 10%). From litter samples was isolated a great deal of Enterobacteria (Escherichia coli. Salmonella, Citrobacter, Enterobacter), havever 34.8% of them were Salmonella and near half of Salmonella (53.2%) was reprezentatives of serovar Salmonella Enteritidis.

Conclusions

It is proved that M. gallisepticum can persist among decorative waterfowl for her welfare with Galliformes, while waterfowl is a reservoir of the pathogen. Also natural reservoirs of Mycoplasma can be wild waterfowl (Casarca ferruginea). Such groups (populations) of birds may serve as a source of infection for commercial herds.

This shows that wild waterfowl are the natural reservoir for these dangerous pathogens like Salmonella Enteritidis. The carriers may account for 17-18% of all individuals in the population. In nesting different species of wild birds may be infected by Salmonella Enteritidis. In the process of migrating wild birds can carry Salmonella Enteritidis over long distances and is a threat to commercial poultry flocks and humans.

Keywords

Salmonella Enteritidis; natural reservoir; wild birds

Acknowledgments

B. Stegniy, D. Muzika, K. Glebova;
Dept. of Bacterial infection, National Science Center "Institute of experimental and clinical veterinary Medicine", Kharkiv, Ukraine

References

1. Suzuki S. Pathogenicity of Salmonella enteritidis in poultry Int J Foot Microbiol 1994.-21(1-2);89-105.
2. Boonmar S, Bangtrakulnonth A, Pornrunangwong S, Terajima J, Watanabe H, Kaneko K, Ogawa M. Epidemiological analysis of Salmonella enteritidis isolates from humans and broiler chickens in Thailand by phage typing and pulsed-field gel electrophoresis. J Clin Microbiol.-1998 36(4):971-4.
3. Henzler DJ, Ebel E, Sanders J, Kradel D, Mason J.Salmonella enteritidis in eggs from commercial chicken layer flocks implicated in human outbreaks. Avian Dis 1994.-38(1):37-43
4. Characterization of Salmonella Enteritidis isolated from human samples De Oliveira F.A., Pasqualotto A.P., Da Silva W.P., Tondo E.C. Food Research International Vol45, Iss2 2012 P1000-1003

*Olga Obukhovska
E-mail: olgaobuhovskaya@rambler.ru

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Estimation of Influenza Incidence by Age in the 2011/12 Seasons in Japan using SASSy

Yasushi Ohkusa*[1], Yoshinori Yasui[1], Tamie Sugawara[1], Nobuhiko Okabe[2, 1], Kiyosu Taniguchi[1] and Kazunori Oishi[1]

[1]IDSC,NIID, Shinjuku, Japan; [2]Kawasaki City Institute for Public Health, Kawasaki, Japan

Objective

So far, it is difficult to show the incidence rate of influenza in the official sentinel surveillance in Japan. Hence we construct the system which record infectious diseases at schools, kindergartens, and nursery schools, and then can show the accurate incidence rate of influenza in children by age/grade.

Introduction

So as to develop more effective countermeasures against influenza, timely and precise information about influenza activity at schools, kindergartens, and nursery schools may be helpful. At the Infectious Diseases Surveillance Center of the National Institute of Infectious Diseases, a School Absenteeism Surveillance System (SASSy) has been in operation since 2009. SASSy monitors the activity of varicella, mumps, mycoplasma pneumonia, pharyngoconjunctival fever, hand-foot-mouth disease, influenza, and many other infectious diseases in schools. In 2010, SASSy was extended to the Nursery School Absenteeism Surveillance System (NSASSy). These systems record the number of absentees due to infectious diseases in each class of all grades of schools every day. As a powerful countermeasure to the pandemic flu of 2009, SASSy was activated in 9 prefectures, in which included more than 6000 schools, and it is gradually being adopted in other prefectures. As of February 2012, 18 prefectures and 4 big cities, which together comprised 15,700 schools (about 35% of all schools in Japan), utilized SASSy. NSASSy is used in more than 4100 nursery schools, which is about 18% of all nursery schools in Japan. Some studies of similar systems were performed in the UK (1), Hong Kong (2), and the USA (3,4), examined surveillance systems for monitoring infectious disease incidence, but the systems to construct in those studies do not operate nationwide like SASSy or NSASSy, and they cannot provide influenza incidence rates in children.

Methods

All schools, kindergartens, and nursery schools in the community, enter data of the absentees due to infectious diseases into the system every day, thereby providing real-time data regarding infectious diseases prevalent in schools, to the schools around, school boards, public health centers, local governments, and medical professionals. It analyzed data for the 2011/2012 season (from September 1, 2011 to March 31, 2012) mainly, but also two seasons (2010/2011 and 2011/2012) were compared in some prefectures. In total, 12 prefectures, which comprised 2,352,839 children, were participated in 2011/2012 season. In the 2010/2011 season, 1,795,766 children of 9 prefectures were analyzed.

Results

The incidence rate in the first grade of elementary schools is the highest both in the two seasons. The highest incidence rate in this grade distributes from 17.8% to 40.3% in 2011/2012 season, and from 11.0% to 30.7% in 2010/2011 season.

Conclusions

This study proved SASSy and NSASSy are quite useful for monitoring of influenza outbreak in schools and it will be gold standard of surveillance for school children in Japan. The present study also showed incidence rate of influenza in children at schools, kindergartens, and nursery schools, and proved the highest incidence was in the first grade of the elementary school. This is the first finding using such the huge number of subjects, which is more than 2 million. The intervention targeting to the weak age/grade is necessary for effective countermeasure and control of influenza and other infectious diseases.

Keywords

Surveillance; Influenza; School Absenteeism

Acknowledgments

This paper is financial supported by Ministry Health, Labour and Welfare, Japan.

References

1) Schmidt WP, Pebody R, Mangtani P: School absence data for influenza surveillance: a pilot study in the United Kingdom, Eurosurveillance, Volume 15, Issue 3, 21 January 2010

2) Calvin K.Y. Cheng, Benjamin J. Cowling, Eric H.Y. Lau, Lai Ming Ho, Gabriel M. Leung, and Dennis K.M. Ip, Electronic School Absenteeism Monitoring and Influenza Surveillance, Hong Kong, Emerg Infect Dis. 2012 May

3) Buehler JW, Berkelman RL, Hartley DM, Peters CJ: Syndromic surveillance and bioterrorism-related epidemics. Emerg Infect Dis. 2003; 9:1197-204.

4) Besculides M, Heffernan R, Mostashari F, Weiss D.:Evaluation of school absenteeism data for early outbreak detection, New York City. BMC Public Health. 2005 Oct 7;5:105

*Yasushi Ohkusa
E-mail: ohkusa@nih.go.jp

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Defining Public Health Situation Awareness – Outcomes and Metrics for Evaluation

Don Olson*, Rob Mathes, Marc Paladini and Kevin Konty

NYC DOHMH, Long Island City, NY, USA

Objective

Review concept of situation awareness (SA) as it relates to public health surveillance, epidemiology and preparedness [1]. Outline hierarchical levels and organizational criteria for SA [2]. Initiate consensus building process aimed at developing a working definition and measurable outcomes and metrics for SA as they relate to syndromic surveillance practice and evaluation.

Introduction

A decade ago, the primary objective of syndromic surveillance was bioterrorism and outbreak early event detection (EED) [3]. Syndromic systems for EED focused on rapid, automated data collection, processing and statistical anomaly detection of indicators of potential bioterrorism or outbreak events. The paradigm presented a clear and testable surveillance objective: the early detection of outbreaks or events of public health concern. Limited success in practice and limited rigorous evaluation, however, led to the conclusion that syndromic surveillance could not reliably or accurately achieve EED objectives. At the federal level, the primary rationale for syndromic surveillance shifted away from bioterrorism EED, and towards all-hazards biosurveillance and SA [4-6]. The shift from EED to SA occurred without a clear evaluation of EED objectives, and without a clear definition of the scope or meaning of SA in practice. Since public health SA has not been clearly defined in terms of operational surveillance objectives, statistical or epidemiological methods, or measurable outcomes and metrics, the use of syndromic surveillance to achieve SA cannot be evaluated.

Methods

This session is intended to provide a forum to discuss SA in the context of public health disease surveillance practice. The roundtable will focus on defining SA in the context of public health syndromic and epidemiologic surveillance. While SA is often noted in federal level documents as a primary rationale for biosurveillance [1, 4-6], it is rarely defined or described in operational detail. One working definition presents SA as "real-time analysis and display of health data to monitor the location, magnitude, and spread of an outbreak", yet it does not elaborate on the methods, systems or evaluation requirements for SA in public health or biosurveillance [3]. In terms of translating SA into public health surveillance practice [1], we will discuss and define the requirements of public health SA based on its development and practice in other areas [2]. The proposed theoretical framework and evaluation criteria adapted and applied to public health SA [2] follow:

- Level 1: Perceive relevant surveillance data and epidemiological information.
- Level 2: Integrate surveillance and non-surveillance data in conjunction with operator goals to provide understanding of the meaning of the information.
- Level 3: Through perceiving (Level 1) and integrating and understanding (Level 2) provide prediction of future events and system states to allow for timely and effective public health decision making.

Results

Sample questions for discussion: What is the relevance of syndromic surveillance and biosurveillance in the SA framework? Where does it fit within the current public health surveillance environment? To achieve the roundtable discussion objectives, the participants will work towards a consensus definition of SA for public health, and will outline measureable outcomes and metrics for evaluation of syndromic surveillance for public health SA.

Keywords

evaluation; biosurveillance; situational awareness; syndromic surveillance; local public health

Acknowledgments

This work was carried out in conjunction with a grant from the Alfred P. Sloan Foundation (#2010-12-14). We thank the members of the New York City Department of Health and Mental Hygiene Syndromic Surveillance Unit.

References

1. Thacker SB, Qualters JR, Lee LM. Public Health Surveillance in the United States: Evolution and Challenges. MMWR 2012;61:3-9.
2. Endsley MR. Towards a Theory of Situation Awareness. Human Factors 1995;37:32-64.
3. Fricker RD. Some Methodological Issues in Biosurveillance. Stat Med 2011;30:403-15.
4. 109th Congress of the United States, Amendment to the Public Service Act. Pandemic and All-Hazards Preparedness Act (2006). Pub L No. 109-417, 101 et seq.
5. Homeland Security Presidential Directive 21 (HSPD-21), "Public Health and Medical Preparedness," 18 Oct 2007.
6. White House, National Strategy for Biosurveillance, July 2012.

*Don Olson
E-mail: drolson@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Syndromic Surveillance from a Local Perspective – A Review of the Literature

Don Olson*, Kevin Konty, Rob Mathes and Marc Paladini

New York City Department of Health and Mental Hygiene, Long Island City, NY, USA

Objective

Review of the origins and evolution of the field of syndromic surveillance. Compare the goals and objectives of public health surveillance and syndromic surveillance in particular. Assess the science and practice of syndromic surveillance in the context of public health and national security priorities. Evaluate syndromic surveillance in practice, using case studies from the perspective of a local public health department.

Introduction

Public health disease surveillance is defined as the ongoing systematic collection, analysis and interpretation of health data for use in the planning, implementation and evaluation of public health, with the overarching goal of providing information to government and the public to improve public health actions and guidance [1,2]. Since the 1950s, the goals and objectives of disease surveillance have remained consistent [1]. However, the systems and processes have changed dramatically due to advances in information and communication technology, and the availability of electronic health data [2,3]. At the intersection of public health, national security and health information technology emerged the practice of syndromic surveillance [3].

Methods

To better understand the current state of the field, a review of the literature on syndromic surveillance was conducted: topics and keywords searched through PubMed and Google Scholar included biosurveillance, bioterrorism detection, computerized surveillance, electronic disease surveillance, situational awareness and syndromic surveillance, covering the areas of practice, research, preparedness and policy. This literature was compared with literature on traditional epidemiologic and public health surveillance. Definitions, objectives, methods and evaluation findings presented in the literature were assessed with a focus on their relevance from a local perspective, particularly as related to syndromic surveillance systems and methods used by the New York City Department of Health and Mental Hygiene in the areas of development, implementation, evaluation, public health practice and epidemiological research.

Results

A decade ago, the objective of syndromic surveillance was focused on outbreak and bioterrorism early-event detection (EED). While there have been clear recommendations for evaluation of syndromic surveillance systems and methods, the original detection paradigm for syndromic surveillance has not been adequately evaluated in practice, nor tested by real world events (ie, the systems have largely not 'detected' events of public health concern). In the absence of rigorous evaluation, the rationale and objectives for syndromic surveillance have broadened from outbreak and bioterrorism EED, to include all causes and hazards, and to encompass all data and analyses needed to achieve "situational awareness", not simply detection. To evaluate current practices and provide meaningful guidance for local syndromic surveillance efforts, it is important to understand the emergence of the field in the broader context of public health disease surveillance. And it is important to recognize how the original stated objectives of EED have shifted in relation to actual evaluation, recommendation, standardization and implementation of syndromic systems at the local level.

Conclusions

Since 2001, the field of syndromic surveillance has rapidly expanded, following the dual requirements of national security and public health practice. The original objective of early outbreak or bioterrorism event detection remains a core objective of syndromic surveillance, and systems need to be rigorously evaluated through comparison of consistent methods and metrics, and public health outcomes. The broadened mandate for all-cause situation awareness needs to be focused into measureable public health surveillance outcomes and objectives that are consistent with established public health surveillance objectives and relevant to the local practice of public health [2].

Keywords

evaluation; biosurveillance; situational awareness; syndromic surveillance; local public health

Acknowledgments

This work was carried out in conjunction with a grant from the Alfred P. Sloan Foundation (#2010-12-14). We thank the members of the New York City Department of Health and Mental Hygiene Syndromic Surveillance Unit.

References

1. Langmuir AD. Evolution of the Concept of Surveillance in the United States. Proc Roy Soc Med. 1971;64:681-4.
2. Smith PF, Hadler JL, Stanbury M, Rolfs RT, Hopkins RS; CSTE Surveillance Strategy Group. "Blueprint Version 2.0": Updating Public Health Surveillance for the 21st Century. J Public Health Manag Pract. 2012; July 2 [Epub ahead of print].
3. Mostashari F, Hartman J. Syndromic surveillance: a local perspective. J Urban Health 2003;80(2 Suppl 1):i1-7.

*Don Olson
E-mail: drolson@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Open Source Health Intelligence (OSHINT) for Foodborne Illness Event Characterization

Catherine Ordun, Jane W. Blake*, Nathanael Rosidi, Vahan Grigoryan, Christopher Reffett, Sadia Aslam, Anastasia Gentilcore, Marek Cyran, Matthew Shelton and Juergen Klenk

Booz Allen Hamilton, McLean, VA, USA

Objective

We propose a cloud-based Open Source Health Intelligence (OSHINT) system that uses open source media outlets, such as Twitter and RSS feeds, to automatically characterize foodborne illness events in real-time. OSHINT also forecasts response requirements, through predictive models, to allow more efficient use of resources, personnel, and countermeasures in biological event response.

Introduction

An increasing amount of global discourse reporting has migrated to the online space, in the form of publicly accessible social media outlets, blogs, wikis, and news feeds. Social media also presents publicly available and highly accessible information about individual, real-time activity that can be leveraged to detect, monitor, and more efficiently respond to biological events.

Methods

Salmonella and Escherichia Coli (E. coli) events were selected based on the magnitude and number of reported outbreaks to the Centers for Disease Control (CDC) in the last ten years (1). These events affect multiple states and were large enough to ensure appropriate confidence levels when developing response metrics obtained from our prediction models. We collected social media data between 2006 – 2012 due to the emergence of Twitter, Facebook, and other social media utilization during this time period.

Characterization is defined as the process of identifying specific event features that inform overall situational awareness. The number hospitalized, dead, or injured, in addition to patient demographics and symptoms were determined to be useful for our characterization and forecast event metrics. Analytical methods, such as term-frequency-inverse document frequency (TF-IDF), natural language processing (NLP), and information extraction, were used to characterize events according to our metrics. Lexicon development, during NLP implementation, was generated from online news articles used to describe the events. Lastly, forecasting algorithms were developed to predict the potential response based on similar historical events that were initially characterized by our information extraction algorithms.

Results

The OSHINT system was developed in Amazon Web Services and includes real-time social media collection for event characterization (see Figure 1). OSHINT currently characterizes number of victims ill, hospitalized, and dead due to foodborne illness events.

OSHINT was used to characterize the recent national 2012 Salmonella event related to cantaloupes, during which OSHINT characterized social media posts related to the event, as news articles and Twitter tweets streamed into the system (Figure 2). On August 17, 2012 the OSHINT system identified a large increase in Twitter tweets mentioning salmonella. Social media data found absent (victims missing work or school day), death, hospital, and sick events to involve 2, 4, 17, 283 media mentions, respectively. Our TF-IDF algorithm characterized the salmonella event impact as two dead and 150 sickened by salmonella-tainted cantaloupe. Retrospective analysis of CDC reported data on August 30, 2012 indicated the salmonella event involved two deaths in 204 cases (2).

Conclusions

The OSHINT team is continually developing and refining characterization and forecasting algorithms used in the system. Upon completion, OSHINT will characterize symptoms, geography, and demographics for E. coli and Salmonella events. The system will also forecast number sick, dead, and hospitalized for an effective and quick response. We will refine our algorithms and evaluate the system against past and future events to provide confidence in our results.

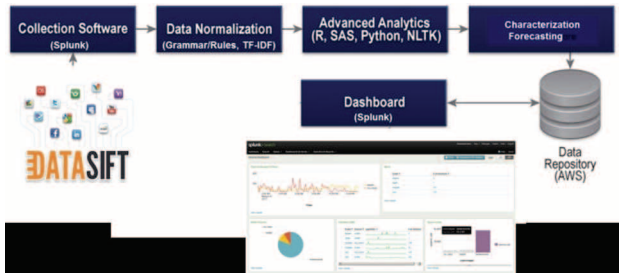


Figure 1. OSHINT System in Amazon Web Services.

Figure 2: 2012 Salmonella Outbreak in Cantaloupe

Keywords

Open Source; Forecasting; Social Media; Response; Food Safety

Acknowledgments

Frederika Conrey, Kenneth Decker, Willam Lei, Dania Shor, Misha Zhurkin

References

(1) CDC. Retrieved September 7, 2012 from http/www.cdc.gov/outbreaknet/investigations.

(2) CDC. Retrieved August 30, 2012, from http://www.cdc.gov/salmonella/typhimurium-cantaloupe-08-12/index.html.

*Jane W. Blake
E-mail: blake_jane@bah.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Binational Model of Collaboration for Enhancing Cross-border ID Surveillance

Kristine Ortwine*[2, 1], Karen Ferran[1] and Esmeralda Iniguez-Stevens[1]

[1]Early Warning Infectious Disease Surveillance, California Department of Public Health, San Diego, CA, USA; [2]San Diego State Graduate School of Public Health, San Diego, CA, USA

Objective

The purpose of this demonstration is to describe the cross-border collaborative processes used for the development of a transparent methodology to identify and prioritize zoonotic infectious disease agents in the California-Baja California border region.

Introduction

International borders present unique challenges for the surveillance of infectious disease. Border communities represent locations with vast differences in cultures and languages, governing institutions, healthcare access, and priorities for the collection and surveillance of disease data. Pathogens and the health and security risks they create do not respect geographical and political boundaries. However, the organizations responsible for the surveillance and control of these agents must function within the borders of their respective governments. One Border One Health (OBOH) is a binational, multidisciplinary initiative aimed at engaging partners in the US and Mexico to identify and implement methods for successful communication and collaboration to enhance health capacity and disease surveillance within the border region. The advancements of international initiatives such as OBOH will help to develop the types of multi-country networks necessary for the effective monitoring of disease patterns and risks.

Methods

One Border One Health Surveillance Committee participants represent multi-disciplinary professionals working together for the advancement of One Health principles in the California/Baja California border region. This showcase documents the identification and prioritization of zoonotic infectious disease agents along the US-Mexico border, by use of a transparent methodology which engaged public and private partners from both countries. Preliminary research and input from collaborators in government, academic, and private sectors in the US and Mexico allowed for review and discussion of current methodologies available for prioritizing infectious agents. The DISCONTOOLS Work Package 2 Prioritization Scoring Model was selected as the basis for scoring and weighting various zoonotic diseases of concern within border region. Subject matter experts were then asked to review and score an initial list of diseases, in order to produce a final ranked list of pathogens. The intent is that these prioritized pathogens will be used by government agencies to make informed decisions, integrating priorities from both nations with regards to infectious disease surveillance. This collaboration provides insight into the binational cooperation needed for the selection of diseases to be considered in a regional, integrated disease surveillance system. To the authors' knowledge this is the first transparent scientific-based approach to pathogen prioritization in the US-Mexico border region.

Conclusions

OBOH is the first binational regional network of its kind along the US-Mexico border recognizing the interconnectivity between human, animal, and environmental health. Given the limited resources in the current economic climate, the use of regional integrated surveillance systems provide an opportunity to protect and improve border health and security by moving away from species-specific surveillance programs. The process showcased here for the transparent review and prioritization of pathogens along the California-Baja California border can be used as a model along the entire US-Mexico Border. The ultimate aim is to protect border communities through the creation of a binational, early warning surveillance system which would allow for actionable and timely interventions to limit emergence, mitigate spread, provide gap analysis, and enhance prevention and control for several emergent and re-emergent diseases. Ultimately, this will decrease negative health and environmental impacts while improving agricultural and economic outcomes in both nations. However, obstacles such as continued sustainability, identification of new multidisciplinary collaborators, cooperation between government agencies, and identifying funding for advancement of integrated regional surveillance systems remain challenges.

Keywords

One Health; disease surveillance; cross-border collaborative

*Kristine Ortwine
E-mail: kristine.ortwine@cdph.ca.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

FSWs Typology and Condoms Use Among HIV High Risk Groups in Sindh, Pakistan: A Developing Country Perspective

Suleman M. Otho*[1], Shazia Perveen[2] and Qamar Abbas[1]

[1]Aga Khan University Hospital, Karachi, Pakistan; [2]Global Funds for AIDS, TB and Malaria, Round 9, Sindh AIDS Control Program, Karachi, Pakistan

Objective

We aimed to determine the association of FSWs typology with condom use among HIV high risk groups in Sindh, Pakistan

Introduction

HIV is growing rapidly worldwide resulting in estimated 34 million population [1]. Recently, its epidemic has spread in Africa, Latin America, and the Caribbean, and most parts of Asia [2]. According to Antenatal sero surveillance study conducted in 2011 by Agriteam canada, it's prevalence in Pakistan is <0.1 [3].Focusing narrowly, its prevalence in Sindh, (one of the provinces of Pakistan) is similar in general population, but it is in the phase of concentrated epidemic (having more than 5% of prevalence in high risk groups)in vulnerable groups like IDUs and Male sex workers and transgender [4].

Sexual intercourse has been identified as major route especially in HIV high risk groups including male sex workers, female sex workers (FSWs), transgender (hijras) and IV drug users. Among them, FSWs are at high risk because of unprotected sex and illicit drug use. Their prevalence is found to be 30.7% in low and middle income countries [5]. South Asia contributed with 12.63 lakh FSW in India only [6]. On the basis of their station of work, they are categorized into facility based (kothikhana, brothel or home) and mobile (street, mobile or beggars). They use different preventive measures including condom for their protection from HIV [7]. It varies with availability and access [8] . FSWs typology have different cliental and mode of action, therefore, it important to explore the preventive methods.

Methods

Data was extracted from Second Generation Surveillance, Integrated behavioral and biological survey, Round IV for HIV infection conducted by Agriteam Canada in partnership with National AIDS Control Program, Pakistan in 2011. It was a cross sectional survey for high risk groups including FSWs from Pakistan. It was ethically approved by Review Board of the Public Health Agency of Canada and HOPE International's Ethical Review Board, Pakistan. From Sindh province, FSWs based in Karachi, Sukkur and Larkana were recruited. Considering typology, they were categorized as mobile or facility based. After informed consent, socio-demographic and risk behavior were inquired. HIV was tested by ELISA/EIA and confirmed by Western Blot. Data was analyzed on SPSS 19. Continuous variables were expressed as mean±SD while categorical as frequency(%). Logistic regression assessed the association of FSWs typology with condoms use among HIV high risk groups.

Results

Out of 4567 high risk population, 1127 were identified as FSWs. Mean age was 26.9 years. Most of them were facility based (72.8%) and 81.3% used condoms. Typology, age, education, duration of involvement, number of client per day, number of paid oral sex per month, knowledge about STI and knowledge about drop in center were significantly associated with condom use among HIV high risk groups.

Conclusions

Majority of facility based FSWs use condoms to prevent HIV infection. Awareness and access to home based FSWs should be increased. It may help in targeting and designing preventive strategies for them at government and mass level.

Keywords

FSW; typology; condoms; HIV high risk groups; Pakistan

References

World Health Organization. Global summary of HIV/AIDS epidemic December 2010. Accessed on June 19, 2012. URL: http://www.who.int/hiv/data/en/.

2. UNAIDS. 2010. UNAIDS report on the global HIV epidemic: 2010. Accessed on June 19, 2012. URL: http://www.unaids.org/globalreport/global_report.htm.
3. USAID/ Pakistan: HIV/ AIDS Health Profile. Accessed on June 19, 2012. URL: http://www.usaid.gov/our_work/global_health/aids/Countries/asia/pakistan_profile.pdf.
4. Enhanced HIV/AIDS Control Program Sindh. Data. Accessed on June 19 2012. URL: http://www.sacp.org.pk/data.php.
5. Baral S, Beyrer C, Muessig K, Poteat T, Wirtz AL, Decker MR, et al. Burden of HIV among female sex workers in low-income and middle-income countries: a systematic review and meta-analysis. Lancet Infect Dis. 2012:DOI:10.1016/S473-3099(12)70066-X.
6. Annual Report 2010-11. National AIDS Control Organization: Department of AIDS Control. Accessed on June 19, 2012. URL: http://www.nacoonline.org/upload/REPORTS/NACO%20Annual%20Report%202010-11.pdf.
7. Joseph TFL, Amy SYT, Tsui HS. The relationship between condom use, sexually transmitted diseases, and location of commercial sex transaction among male Hong Kong clients. AIDS: Epidemiology & Social. 2003;17(1):105-12.
8. Morris CN, Morris SR, Ferguson AG. Sexual behavior of female sex workers and access to condoms in Kenya and Uganda on the Trans-Africa highway. AIDS Behav. 2009 Oct;13(5):860-5.

*Suleman M. Otho
E-mail: drotho@hotmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Effectiveness of the 2011-12 Influenza Vaccine: Data from US Military Dependents and US-Mexico Border Civilians

Damaris Padin*, Anthony Hawksworth, Peter Kammerer, Erin McDonough and Gary Brice

Operational Infectious Diseases, Naval Health Research Center, San Diego, CA, USA

Objective

To assess effectiveness of the influenza vaccine among US military dependents and US-Mexico Border populations during the 2011-12 influenza season.

Introduction

As a result of antigenic drift of the influenza viruses, the composition of the influenza vaccine is updated yearly to match circulating strains. Consequently, there is need to assess the effectiveness of the influenza vaccine (VE) on a yearly basis. Ongoing febrile respiratory illness (FRI) surveillance captures data and specimens that are leveraged to estimate influenza VE on an annual basis.

Methods

Data from ongoing FRI surveillance at US Military and US-Mexico border clinics were used to estimate VE. We conducted a case–control study between weeks 3 and 17 of the 2011-12 influenza season. Specimens were collected from individuals meeting FRI case definition (fever ≥ 100.0 F with either cough or sore throat). Cases were laboratory confirmed influenza infection and controls were negative for influenza. Interviewer-administered questionnaires collected information on patient demographics and clinical factors and vaccination status. Logistic regression was used to calculate the crude and adjusted odds ratios (OR) and VE was computed as (1-OR) x 100%. Vaccine protection was assumed to begin 14 days post-vaccination.

Results

A total of 155 influenza positive cases and 429 influenza negative controls were included in the analysis - 72 cases were influenza A(H3N2), 38 cases were influenza A(H1N1), and 45 cases were influenza B. Overall adjusted VE against laboratory-confirmed influenza was 46% (95% CI, 19–64%); unadjusted was 39% (95% CI, 11–58%). Influenza subtype analyses revealed moderate protection against A/H3 and A/H1 and lower protection against B. Lowest estimated VE was seen in older individuals, age 65 and older.

Conclusions

Influenza vaccination was moderately protective against laboratory confirmed influenza in this population. Continued surveillance is important in monitoring the effectiveness of the influenza vaccine.

Keywords

Influenza; vaccine efficacy; Influenza-like illness surveillance

Acknowledgments

The authors gratefully acknowledge the work of on-site research assistants and NHRC laboratory staff who produced the data used in this analysis. We also thank Global Emerging Infections System (GEIS) division of the Armed Forces Health Surveillance Center (AFHSC) for their support of FRI surveillance.

*Damaris Padin
E-mail: damaris.padin@med.navy.mil

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using Change Point Detection for Monitoring the Quality of Aggregate Data

Ian Painter*, Julie Eaton and Bill Lober

University of Washington, Seattle, WA, USA

Introduction

Data consisting of counts or indicators aggregated from multiple sources pose particular problems for data quality monitoring when the users of the aggregate data are blind to the individual sources. This arises when agencies wish to share data but for privacy or contractual reasons are only able to share data at an aggregate level. If the aggregators of the data are unable to guarantee the quality of either the sources of the data or the aggregation process then the quality of the aggregate data may be compromised.

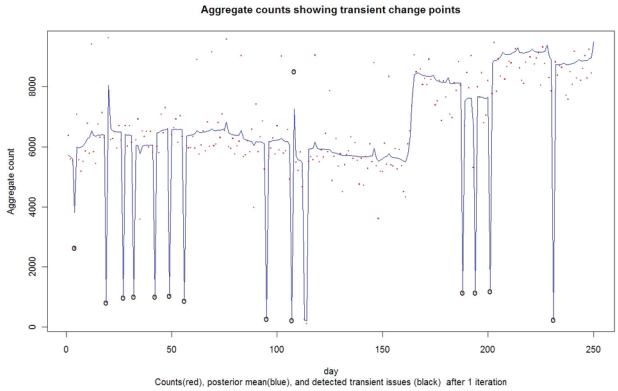
This situation arose in the Distribute surveillance system (1). Distribute was a national emergency department syndromic surveillance project developed by the International Society for Disease Surveillance for influenza-like-illness (ILI) that integrated data from existing state and local public health department surveillance systems, and operated from 2006 until mid 2012. Distribute was designed to work solely with aggregated data, with sites providing data aggregated from sources within their jurisdiction, and for which detailed information on the un-aggregated 'raw' data was unavailable. Previous work (2) on Distribute data quality identified several issues caused in part by the nature of the system: transient problems due to inconsistent uploads, problems associated with transient or long-term changes in the source make up of the reporting sites and lack of data timeliness due to individual site data accruing over time rather than in batch. Data timeliness was addressed using prediction intervals to assess the reliability of the partially accrued data (3). The types of data quality issues present in the Distribute data are likely to appear to some extent in any aggregate data surveillance system where direct control over the quality of the source data is not possible. In this work we present methods for detecting both transient and long-term changes in the source data makeup.

Methods

We examined methods to detect transient changes in data sources, which manifest as classical outliers. We found that traditional statistical process control methods did not work well for detecting transient issues due to the presence of discontinuities cause by long term changes in the source makeup. As both transient and long-term changes in source makeup manifest as step changes, we examined the performance of change point detection methods for monitoring this data. These methods have been previously used for detecting changes in disease trends in data aggregated from Distribute (4). Following Kass-Hout (4), we used the Bayesian change point estimation procedure of Barry (5) as implemented in the R package BCP (6). We examined both offline and online detection using time series held at a constant lag.

Results

We found that transient problems could be detected offline as neighboring change points with high posterior probability. When multiple outliers exist close together, detection can be improved by iteratively removing flagged data points and re-running the change point detection on the reduced data. Following the removal of outliers, remaining change points indicated long-term changes. To enable real-time monitoring for data quality problems we modified this offline detection process to in addition flag individual change points (rather than pairs of change points) detected in the most recent 5 days.



Keywords

Data Quality; Surveillance; Changepoint methods; Distribute

Acknowledgments

We would like to thank the Markle Foundation and the Centers for Disease Control for providing funding for the Distribute project.

References

1. Olson DR, et al. Applying a New Model for Sharing Population Health Data to National Syndromic Influenza Surveillance: DiSTRIBuTE Project Proof of Concept, 2006 to 2009. PLOS Currents Influenza. 2011 Sep 12.
2. Painter I, et al. How good is your data? 2011 ISDS Conference Abstract. Emerging Health Threats Journal 2011, 4
3. Painter I, et al. Generation of Prediction Intervals to Assess Data Quality in the Distribute System Using Quantile Regression. JSM proceedings, Section on Statistics in Defense and National Security. 2011 Dec.
4. Kass-Hout TA, et al. Application of change point analysis to daily influenza-like illness emergency department visits. JAMIA. 2012 Jul 3.
5. Barry D, Hartigan JA. A Bayesian analysis for change point problems. J Am Stat Assoc 1993;35:309–19.
6. Erdman C, et al. bcp: An R package for performing a Bayesian analysis of change point problems. Journal of Statistical Software 23(3). 2007.

*Ian Painter
E-mail: ipainter@uw.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Differentiating ZIP Codes in Syndromic Data; What Can They Tell Us?

Marc Paladini, Romona Lall and Stephen E. Schachterle*

New York City Department of Health and Mental Hygiene, Queens, NY, USA

Objective

To classify visits to NYC emergency departments (ED) into NYC residential, NYC PO Box or commercial building, commuters to NYC, and out-of-town visitors. To describe patterns in each group, to evaluate how they differ, and to consider how the differences can affect syndromic surveillance analyses and results.

Introduction

The NYC Department of Health and Mental Hygiene (DOHMH) ED syndromic surveillance system receives data from 95% of all ED visits in NYC totaling 4 million visits each year. The data include residential ZIP code as reported by the patient. ZIP code information has been used by the DOHMH to separate visits into NYC and non-NYC for analysis; and, a closer examination of non-NYC visits may further inform disease surveillance.

Methods

Visits were initially differentiated into six home ZIP code types. NYC residential ZIP codes, PO Boxes and commercial buildings were identified with 2010 US Census and data from the SAS institute (SAS Institute Inc., Cary, NC, USA). Commuter visits to the EDs were classified as any ZIP codes from the NYC Core Based Statistical Area (CBSA; United States Office of Management and Budget). Out of town visits were identified using with the 2010 US Census. Unknown ZIP codes included all of those ZIP codes that were not identified by any of the previous methods, and missing ZIP codes were those that were blank. ZIP codes were verified with the United States Postal Service website (www.usps.com).

Once ZIP codes were categorized, spatial and temporal trends in total ED visits by home ZIP code type were analyzed.

Results

Of the approximately 4 million ED visits in NYC during 2011, the number of visits by commuters and out-of-town visitors were 125,236 (3.1%) and 45,158 (1.1%) respectively (Figure 1). There were 4,676 (0.1%) visits with a NYC PO Box or building ZIP codes and 48,077 (1.2%) visits with a missing or non-interpretable ZIP codes. The majority of commuter and out-of-town ED visits occur at a smaller set of hospitals. Out-of town visitors mostly visited hospitals in Manhattan rather than hospitals in the outer boroughs. While the seasonal trends and day-of-week patterns for the NYC residents and the commuters appear to be fairly similar, this is not the case for out-of-town visitors. For example, total ED visit trends correlated well for NYC residents and commuters (r=0.77), but there was no correlation between NYC residents and out-of-town visitors (r=-0.18) over time. The number of ED visits among out-of-town visitors was higher during summer months and the winter holiday season, and this trend may have reflected the larger number of visitors during these periods. Day-of-week patterns were similar for NYC residents and commuters with weekdays associated with larger numbers of visits compared to weekends. However, the opposite was found true for out-of-town visitors with larger number of visits occurring over the weekends compared to weekdays.

Conclusions

Considerable differences in temporal trends were found among out-of-town visitors, NYC residents, and commuters to NYC. Out-of-town visitors also tend to visit EDs located in Manhattan rather than in the outer boroughs. These results suggest that out-of-town visitors represent a unique population ED visitors. Analyzing NYC residents, commuters, and out-of-town visitors separately may provide additional information that could prove useful to daily syndromic surveillance activities.

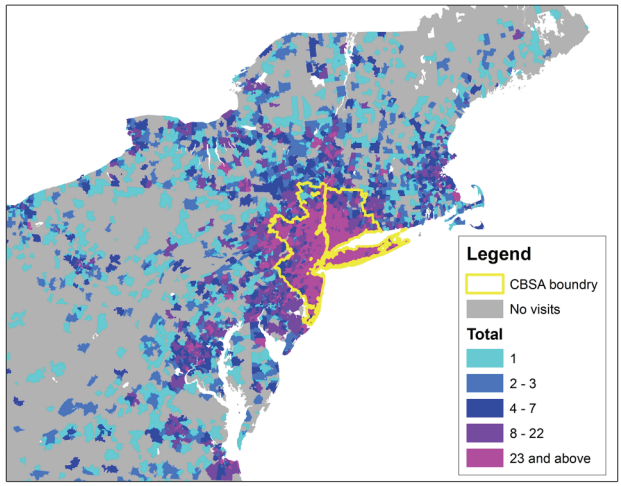


Figure 1: Total ED visits from the NYC Core Based Statistical Area (CBSA) and the surrounding region.

Keywords

GIS; New York; Spatial Analysis

Acknowledgments

This work was carried out in conjunction with a grant from the Alfred P. Sloan Foundation (#2010-12-14). We thank the members of the New York City Department of Health and Mental Hygiene Syndromic Surveillance Unit.

*Stephen E. Schachterle
E-mail: steve.schachterle@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Establishing a Federal and State Data Exchange Pilot for Public Health Situational Awareness

Dina B. Passman*[1], Aaron Kite-Powell[2], Dara Spector[1], Wayne Loschen[3], Barry Harp[1], Aaron Chern[2], Janet Hamilton[2], Cary Eggers[2] and Joseph Lombardo[3]

[1]U.S. Department of Health and Human Services, Office of the Assistant Secretary for Preparedness and Response, Washington, DC, USA; [2]Florida Department of Health, Bureau of Epidemiology, Jacksonville, FL, USA; [3]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Objective

U.S. Department of Health and Human Services (HHS) Office of the Assistant Secretary for Preparedness and Response (ASPR) partnered with the Florida Department of Health (FDOH), Bureau of Epidemiology, to implement a new process for the unidirectional exchange of electronic medical record (EMR) data when ASPR clinical assets are operational in the state following a disaster or other response event. The purpose of the current work was to automate the exchange of data from the ASPR electronic medical record system EMR-S into the FDOH Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE-FL) system during the 2012 Republican National Convention (RNC).

Introduction

ASPR deploys clinical assets, including an EMR system, to the ground per state requests during planned and no-notice events. The analysis of patient data collected by deployed federal personnel is an integral part of ASPR and FDOH's surveillance efforts. However, this surveillance can be hampered by the logistical issues of field work in a post-disaster environment leading to delayed analysis and interpretation of these data to inform decision makers at the federal, state, and local levels. FDOH operates ESSENCE-FL, a multi-tiered, automated, and secure web-based application for analysis and visualization of clinical data. The system is accessible statewide by FDOH staff as well as by hospitals that participate in the system. To improve surveillance ASPR and FDOH engaged in a pilot project whereby EMR data from ASPR would be sent to FDOH in near real-time during the 2012 hurricane season and the 2012 RNC. This project is in direct support of Healthcare Preparedness Capability 6, Information Sharing, and Public Health Preparedness Capability 13, Public Health Surveillance and Epidemiological Investigation.

Methods

In 2011, FDOH approached ASPR about securely transmitting raw EMR data that could be ingested by ESSENCE-FL during ASPR deployments in the state. Upon conclusion of an agreement for a date exchange pilot, data elements of interest from the ASPR EMR were identified. Due to the modular design ESSENCE-FL Microsoft SQL databases were easily adapted by the Johns Hopkins University Applied Physics Laboratory (JHU/APL) to add a new module to handle receipt of ASPR EMR data including code to process the files, remove duplicates and create associations with existing reference information, such as system-defined geographic regions and age groups. Scripts were developed to run on the ASPR server to create and send updated files via secure file transfer protocol (SFTP) every 15 minutes to ESSENCE-FL. Prior ASPR event deployment data was scrubbed and sent to ESSENCE-FL as a test dataset to ensure appropriate receipt and ingestion of the new data source.

Results

EMR data was transmitted through a central server at ASPR to ESSENCE-FL every 15 minutes during each day of the 2012 RNC (August 26-31). In ESSENCE-FL, configuration allowed the data to be queried, analyzed, and visualized similar to existing ESSENCE-FL data sources. In all, data from 11 patient encounters were successfully exchanged between the partners. The data were used by ASPR and FDOH to simultaneously monitor in near real-time onsite medical response activities during the convention.

Conclusions

Timely access to patient data can enhance situational awareness and disease surveillance efforts and provide decision makers with key information in an expedient manner during disaster response and mass gatherings such as the RNC. However, data are siloed within organizations. The collaboration between FDOH, ASPR and JHU/APL made EMR data sharing and analysis more expeditious and efficient and increased timely access to these data by local, state, and federal epidemiologists. The integration of these data into the ESSENCE-FL system created one location where users could go to access data and create epidemiologic reports for a given region in Florida, including the RNC. To achieve these successes with partners in the future, it will be necessary to develop partnerships well in advance of intended data exchange. Future recommendations include robust pre-event testing of the data exchange process and planning for a greater amount of lead-time between enacting the official agreement and beginning data exchange.

Keywords

Syndromic surveillance; Public health informatics; Data exchange; Federal and state collaboration

*Dina B. Passman
E-mail: dina.passman@hhs.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

ISDS 2012 Conference Abstracts

Fusion Analytics: A Data Integration System for Public Health and Medical Disaster Response Decision Support

Dina B. Passman*

ASPR/OPEO, HHS, Washington, DC, USA

Objective

The objective of this demonstration is to show conference attendees how they can integrate, analyze, and visualize diverse data type data from across a variety of systems by leveraging an off-the-shelf enterprise business intelligence (EBI) solution to support decision-making in disasters.

Introduction

Fusion Analytics is the data integration system developed by the Fusion Cell at the U.S. Department of Health and Human Services (HHS), Office of the Assistant Secretary for Preparedness and Response (ASPR). Fusion Analytics meaningfully augments traditional public and population health surveillance reporting by providing web-based data analysis and visualization tools.

Methods

Fusion Analytics serves as a one-stop-shop for the web-based data visualizations of multiple real-time data sources within ASPR. The 24-7 web availability makes it an ideal analytic tool for situational awareness and response allowing stakeholders to access the portal from any internet-enabled device without installing any software. The Fusion Analytics data integration system was built using off-the-shelf EBI software. Fusion Analytics leverages the full power of statistical analysis software and delivers reports to users in a secure web-based environment. Fusion Analytics provides an example of how public health staff can develop and deploy a robust public health informatics solution using an off-the shelf product and with limited development funding. It also provides the unique example of a public health information system that combines patient data for traditional disease surveillance with manpower and resource data to provide overall decision support for federal public health and medical disaster response operations.

Conclusions

We are currently in a unique position within public health. One the one hand, we have been gaining greater and greater access to electronic data of all kinds over the last few years. On the other, we are working in a time of reduced government spending to support leveraging this data for decision support with robust analytics and visualizations. Fusion Analytics provides an opportunity for attendees to see how various types of data are integrated into a single application for population health decision support. It also can provide them with ideas of how they can use their own staff to create analyses and reports that support their public health activities.

Keywords

Situational awareness; Public health informatics; Disaster response

*Dina B. Passman
E-mail: dina.passman@hhs.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using Cloud Technology to Support Monitoring During High Profile Events

Megan Patel*[1], Enyinnaya Adighibe[1], Joseph Lombardo[2], Wayne Loschen[2], Miles Stewart[2] and Michael O. Vernon[1]

[1]Cook County Department of Public Health, Oak Forest, IL, USA; [2]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Objective

In May 2012, thousands of protesters, descended on Chicago during the NATO Summit to voice their concern about social and economic inequality. Given the increased numbers of international and domestic visitors to the Windy City and the tension surrounding protesting during the summit, increased monitoring for health events within the city and Chicago metropolitan region was advised. This project represents the first use of cloud technology to support monitoring for a high profile event.

Introduction

Hospital emergency departments in Cook and surrounding counties currently send data to the Cook County Department of Public Health (CCDPH) instance of ESSENCE on CCDPH servers. The cloud instance of ESSENCE has been enhanced to receive and export all meaningful use data elements in the meaningful use format. The NATO summit provided the opportunity for a demonstration project to assess the ability of an Amazon GovCloud instance of ESSENCE to ingest and process meaningful use data, and to export meaningful use surveillance data to the Cook County Locker in BioSense 2.0.

Methods

In the three weeks leading up to the NATO Summit, HL7 data extracts were sent to BioSense 2.0 and a data feed was established to the Amazon GovCloud instance of ESSENCE. Queries specific to anticipated health events associated with the summit such as injuries, tear gas exposure, and general exposure, were developed. Several features of the cloud instance of ESSENCE enhanced the ability of CCDPH staff epidemiologists to conduct analyses, including the sharing capabilities of queries and the myESSENCE dashboard feature. The sharing capabilities within the cloud instance of ESSENCE allowed queries to be easily shared with multiple staff epidemiologists and across health jurisdictions. The myESSENCE dashboard feature was used to create dashboards of surveillance results, including time series graphs, maps, and records of interest for relevant queries, that were shared with public health staff monitoring population health during the summit. This information was used to provide situational awareness on a daily basis in the Chicago Metropolitan region.

Results

Data feeds to BioSense 2.0 and the Amazon GovCloud instance of ESSENCE were successful. The NATO Summit did not produce any remarkable public health concerns in suburban Cook County. The use of the cloud instance of ESSENCE enhanced the timeliness of generating situational awareness reports for distribution to public health partners in the Chicago Metropolitan region.

Conclusions

While further evaluation of cloud resources to conduct syndromic surveillance is warranted, use of the cloud instance of ESSENCE during the NATO Summit demonstrated the ability of the cloud to support surveillance for both routine and high profile events.

Keywords

Cloud; Meaningful Use; Surveillance; Public Health

Acknowledgments

This project was supported by the Wide Area Recovery and Resiliency Program of the Department of Homeland Security under contract N00024-03-6606. Cloud services were provided by the CDC's BioSense 2.0 Program under contract 200-2011-40934.

*Megan Patel
E-mail: mctoth@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Comparing Prescription Sales, Google Trends and CDC Data as Flu Activity Indicators

Avinash Patwardhan* and David Lorber

Clinical Affairs, Walgreen Co., Deerfield, IL, USA

Objective

To examine if the prescription sales data from a large retail pharmacy chain in the US were comparable to Google Flu trends and CDC's US ILI Network data as flu activity indicator.

Introduction

In a 2007 survey of public health officials in the United States, International Society for Disease Surveillance found that only 7% used pharmacy prescription sales data for surveillance (1). There have been many reports suggesting effective use of prescription sales data in syndromic surveillance (2, 3, 4, 5). Community pharmacies can provide a valuable supplementary tool for syndromic surveillance of infectious diseases.

Methods

We extracted five years of de-identified prescription sales data from the proprietary pharmacy computer system of a large retail pharmacy chain in the United States. The prescriptions were written for the common drugs for the treatment of influenza: Amantadine, Oseltamivir, Rimantadine, and Zanamivir. We acquired Google Flu trends national aggregate counts data that represented the estimates of the ILI cases per 100,000 physician visits. We acquired CDC ILINET data for 2007. We calculated Pearson 'r' between our data and Google and CDC data. We also created comparable trends graphs after converting the counts of the influenza scripts and the counts of the Google estimated ILI cases to logarithmic scale.

Results

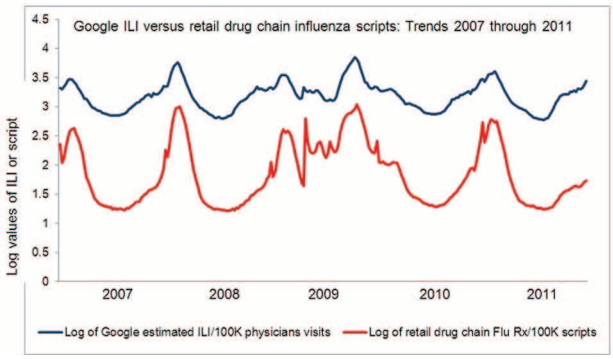
The Pearson 'r' between the aggregate counts of scripts for all the four drugs and the Google estimates of the ILI cases for years 2007, 2008, 2009, 2010, and 2011 were 0.85 (95% CI, 0.75-0.91), 0.92 (95% CI, 0.86-0.95), 0.91(95% CI, 0.85-0.95), 0.88 (95% CI, 0.80-0.93), and 0.87 (95% CI, 0.78-0.92) and 0.92 (95% CI, 0.90-0.94) for years 2007 through 2011 together. The Pearson 'r' between the aggregate counts of scripts and the CDC % unweighted ILI (2007) was 0.97 (95% CI, 0.95-0.98).

Conclusions

A strong to very strong correlation between prescription sales data and Google Flu trends and CDC's ILI activities data for influenza suggests that the former can serve as a good and valid influenza activity indicator. Community pharmacies with large footprints might want to proactively build automated syndromic surveillance systems with near real time reporting capabilities and explore the possibility of building predictive models (3) and of forming partnerships with public health agencies for syndromic surveillance.

Pearson 'r' between prescription sales data and Google Flu trends and CDC ILI data

Prescription sales data and	Year	Pearson 'r'	95% CI (p = 0.05)
Google Trends ILI data	2007	0.85	0.75-0.91
	2008	0.92	0.86-0.95
	2009	0.91	0.85-0.95
	2010	0.88	0.80-0.93
	2011	0.87	0.78-0.92
	Aggregate (2007-2011)	0.92	0.90-0.94
CDC % unweighted ILI data	2007	0.97	0.95-0.98



Keywords

public health; syndromic surveillance; Flu; prescription sales; activity or early warning indicator

Acknowledgments

We wish to acknowledge Criselda Valencia (Lead Analyst Support & Deployment Data Warehouse at Walgreen Co.), Erma Villarreal (IT Manager - Support & Deployment Data Warehouse at Walgreen Co.), and Zhongwen Huang (Senior Analyst Outcomes & Analytics at Walgreen Co.) for pulling data for us.

References

1. The International Society for Disease Surveillance (ISDS) Available: http://www.syndromic.org/ Accessed May 2, 2012. 2. Chadwick D (2009) The Rhode Island Department of Health. The First Statewide System for Tracking Disease Using Prescription Data. Press Release Archives. State of Rhode Island. Department of Health. Available: http://www.health.ri.gov/news/archives/2009/ Published October 27, 2009. Accessed May 2, 2012. 3. Sugawara T, Ohkusa Y, Ibuka Y, Kawanohara H, Taniguchi K, Okabe N (2012) Real-time Prescription Surveillance and its Application to Monitoring Seasonal Influenza Activity in Japan J Med Internet Res. 14(1):e14. 4. Vergu E, Grais RF, Sarter H, et al. (2006) Medication sales and syndromic surveillance, France. Emerging infectious diseases. 12(3):416. 5. van den Wijngaard C, van Pelt W, Nagelkerke N, Kretzschmar M, Koopmans M (2011) Evaluation of syndromic surveillance in the Netherlands: its added value and recommendations for implementation. Euro Surveill. 16(9):19806.

*Avinash Patwardhan
E-mail: avinash.patwardhan@walgreens.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

HIV Surveillance in India: An Overview & Implications for Future

Divya Persai*

public health fiooundation of india, Delhi, India

Objective

To study and analyze the surveillance activities in HIV prevention and control in India.

Introduction

Surveillance of risky behaviors of HIV infection and its manifest diseases has provided a better understanding of the complex nature of the HIV epidemic in India. However, little attempt is made to analyze progress of these surveillance activities.

Methods

A review & analysis of surveillance activities undertaken in India were done. Pub-med, cohrane library and peer-reviewed journals were referred for relevant literature.

Results

Initially, medical officers from multiple types of government hospitals in India were expected to report AIDS cases, including deaths. However, this reporting mechanism was inadequate, complicated by many disparate types of reporting units with incomplete and delayed reports. Therefore AIDS case reporting has been replaced by HIV case reporting from the 4532 Integrated Counseling and Testing Centers. Newer surveillance strategies like Behavior sentinel surveillance measure behaviors that affect risk for acquiring HIV. However, behavioral and biological data are resource-intensive and time-consuming. Facility-based sero-surveillance (also called HIV Sentinel Surveillance or HSS) has emerged as the key surveillance strategy for HIV/AIDS in India. Starting with 55 urban sentinel sites HIV Sentinel Surveillance expanded to 1215 in 1994. Most of these pre-selected sites were antenatal clinics but also included sexually transmitted infection clinics and special facilities. Subsequent expansion of high-risk group sites has improved the representation of all sub-populations in HSS. While stigma against most high-risk populations and HIV-positive people continues, it has lessened as shown by the behavioral surveys. Also, accessibility to testing sites has increased with increased availability of care and treatment options for infected individuals.

Conclusions

While acknowledging the vastness and diversity of India, the key limitations remain suboptimal coverage and lack of representativeness surveillance data. Moreover, due to selection bias, the populations selected for HSS at targeted intervention sites may not represent everyone in that community. There is lack of national information system to collect HIV testing information from the private sector. Further efforts are needed to improve HIV surveillance data and usage of this data to predict the epidemic.

Keywords

Surveillance; HIV; India

References

1. Department of AIDS Control, Ministry of Health and Family Welfare, National AIDS Control Organization (NACO) Annual Report, 2009-2010. www.nacoonline.org/
2. National Family Health Survey, India: http://www.nfhsindia.org/
3. WHO case definitions of HIV for surveillance and revised clinical staging and immunological classification of HIV-related disease in adults and children; ISBN: 978 92 4 159562 9. August 2006.
4. Family Health International (FHI) website: FHI-conducted BSS and IBBSS Reports 1989-2009. www.fhi.org/en/HIVAIDS/pub/survreports/index.htm
5. Bachani D, Sogarwal R, Rao KS. A population bases survey on HIV prevalence in Nagaland, India. SAARC J Tuber Lung Dis HIV/AIDS 2009 (1)1-11.
6. The World Health Organization's global strategy for prevention and assessment of HIV drug resistance; Diane E Bennett, S Bertagnolio, D Sutherland, C F Gilks: Antiviral Therapy 13 Suppl 2:1-13; 2008 International Medical Press:1359-6535.
7. Technical Consultation to Review HIV Surveillance in India, 23-25 April 2008, New Delhi, India. WHO/SEAR and NACO. SEA/AIDS/182. Available at www.searo.int/hiv-aids publications.
8. HIV/AIDS epidemic in India: risk factors, risk behavior & strategies for prevention & control; Godbole S, Mehendale S: Indian J Med Res 121, April 2005(356-368).
9. Stigma in the HIV/AIDS epidemic: A review of the literature and recommendations for the way forward; Mahajan A P, Sayles JN, Patel VA, Remien RH, Ortiz D, Szekeres G, Coates TJ. AIDS 2008 August; 22(Suppl 2): S67-S79.
10. Epidemiological analysis of the quality of HIV sero-surveillance in the world: how well do we track the epidemic?: Walker n, Garcia-Calleja JM, Asamoah-Odei E, Poumerol G, Lazzari S, Ghys PD, Scwartlander B, Stanecki KA. AIDS 2001 Aug 17; 15(12):1545-54.
11. Advances and future directions in HIV surveillance in low- and middle-income countries. Diaz T, Garcia-Calleja JM, Ghys PD, Sabin K. Curr Opin HIV AIDS. 2009 Jul;4 (4):253-9.

*Divya Persai
E-mail: dpersai@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Comparing Syndromic Surveillance and Poison Center Data for Snake Bites in Missouri

Karen H. Pugh*[1], Amy Kelsey[2] and Rebecca Tominack[3, 1]

[1]St. Louis University School of Medicine and School of Public Health, Saint Louis, MO, USA; [2]Missouri Department of Health and Senior Services, Jefferson City, MO, USA; [3]Missouri Poison Center, Saint Louis, MO, USA

Objective

This study intends to use two different surveillance systems available in Missouri to explore snake bite frequency and geographic distribution.

Introduction

In 2010, there were 4,796 snake bite exposures reported to Poison Centers nationwide (1). Health care providers frequently request help from poison centers regarding snake envenomations due to the unpredictability and complexity of prognosis and treatment. The Missouri Poison Center (MoPC) maintains a surveillance database keeping track of every phone call received. ESSENCE, a syndromic surveillance system used in Missouri, enables surveillance by chief complaint of 84 different emergency departments (ED) in Missouri (accounting for approximately 90% of all ED visits statewide). Since calling a poison center is voluntary for health care providers, poison center data is most likely an underestimation of the true frequency of snake envenomations. Comparing MoPC and ESSENCE data for snake envenomations would enable the MoPC to have a more accurate depiction of snake bite frequency in Missouri and to see where future outreach of poison center awareness should be focused.

Methods

Archived data from Toxicall®, the MoPC surveillance system, was used to query the total number of snake bite cases from 01/01/2007 until 12/31/2011 called into the MoPC center by hospitals that also participate ESSENCE. Next, ESSENCE data was used to estimate the total number of snake envenomations presenting to EDs in Missouri. This was accomplished using the same date range as well as searching for key terms in the chief complaints that would signify a snake bite. The results of each datasearch were compared and contrasted by Missouri region.

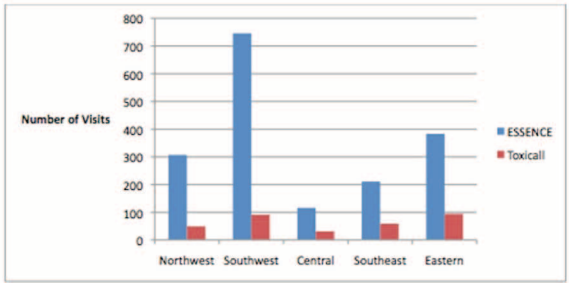
Results

The Toxicall® search showed a total of 324 snake bite cases. The initial ESSENCE data query showed a total of 1983 snake bite cases. After certain data exclusions, there was a total of 1763 ESSENCE snake bite visits. This suggests that approximately 18% of all snake bite visits reported in Missouri ESSENCE were called into the MoPC. The results are demonstrated by Missouri region in Figure 1. This figure also shows that the greatest number of ESSENCE visits for snake bites were reported by Southwest region hospitals whereas the Eastern region hospitals placed the greatest number of calls to MoPC regarding snake bites.

Conclusions

The total number of snake bite cases from Missouri ESSENCE ED visits is much greater than the number of snake bites cases called into the MoPC by ESSENCE participating hospitals. This underutilization of the poison center demonstrates the increased need for awareness of the MoPC's free services. In Missouri, the MoPC should target hospitals in the Southwest region for outreach in particular based on these findings. Poison centers are staffed by individuals trained in all types of poisonings and maintain a list of consulting physicians throughout the United States experienced in management and treatment of venomous snake bites (2). Any heathcare facility would benefit from MoPC assistance. Finally, syndromic surveillance allows for quick and easy data compilation, however there are some difficulties when attempting to search for a particular condition. Communication and partnership between two different public health organizations will be beneficial toward future public health studies.

Figure 1: ESSENCE Snake Bites Cases Compared to Toxicall® Snake Bite Cases in Missouri by Region



Keywords

ESSENCE; surveillance; Missouri; Poison Center; snake

References

1. Bronstein AC, Spyker DA, Cantilena LR, Green JL, Rumack BH, Dart RC. 2010 Annual report of the American Association of Poison Control Centers' national poison data system (NPDS): 28th annual report. Clinical Toxicology. 2011;49:910-41.
2. Gold BS, Barish RA, Dart RC. North American snake envenomation: diagnosis, treatment, and management. Emerg Med Clin N Am. 2004;22:423-43.

*Karen H. Pugh
E-mail: khill9@slu.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Modeling Baseline Shifts in Multivariate Disease Outbreak Detection

Jialan Que* and Fu-Chiang Tsui

University of Pittsburgh, Pittsburgh, PA, USA

Objective

Outbreak detection algorithms monitoring only disease-relevant data streams may be prone to false alarms due to baseline shifts. In this paper, we propose a Multinomial-Generalized-Dirichlet (MGD) model to adjust for baseline shifts.

Introduction

Population surges or large events may cause shift of data collected by biosurveillance systems [1]. For example, the Cherry Blossom Festival brings hundreds of thousands of people to DC every year, which results in simultaneous elevations in multiple data streams (Fig. 1). In this paper, we propose an MGD model to accommodate the needs of dealing with baseline shifts.

Methods

Existing multivariate algorithms only model disease-relevant data streams (e.g., anti-fever medication sales or patient visits with constitutional syndrome for detection of flu outbreak). On the contrary, we also incorporate a non-disease-relevant data stream as a control factor.

We assume that the counts from all data streams follow a Multinomial distribution. Given this distribution, the expected value of the distribution parameter is not subject to change during a baseline shift; however, it has to change in order to model an outbreak. Therefore, this distribution inherently adjusts for the baseline shifts. In addition, we use the generalized Dirichlet (GD) distribution to model the parameter, since GD distribution is one of the conjugate prior of Multinomial [2]. We call this model the Multinomial-Generalized-Dirichlet (MGD) model.

Results

We applied MGD model in our previous proposed Rank-Based Spatial Clustering (MRSC) algorithm [3]. We simulated both outbreak cases and baseline shift phenomena. The experiment includes two groups of data sets. The first includes the data sets only injected with outbreak cases, and the second includes the ones with both outbreak cases and baseline shifts. We apply MRSC algorithm and a reference method, the Multivariate Bayesian Scan Statistic (MBSS) algorithm (which only analyzes the disease-relevant data streams) [4], to both data sets. Fig. 2 shows the performance of outbreak detection: the ROC curves and AMOC curves of analyzing the data sets with baseline shifts (solid lines) and without (dashed lines). We can see from Fig. 2 that the performance of MBSS dropped much more significantly than MRSC when analyzing the data sets with baseline shifts.

Conclusions

The MGD model can be a good supplement model used to detect disease outbreaks in order to achieve both better sensitivity and better specificity especially when baseline shifts are present in the data.

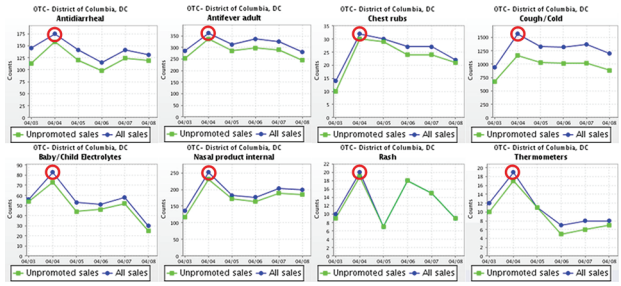


Fig. 1 Eight data streams of NRDM categories collected by RODS system (Anti-Diarrhea, Anti-Fever Adult, Chest Rubs, Cough/Cold, Baby/Child Electrolytes, Nasal Products, Rash and Thermometers) between Apr. 3, 2011 and Apr. 8, 2011 in Washington DC.

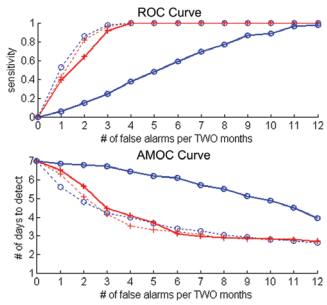


Fig. 2 ROC and AMOC curves of MRSC (red) and MBSS (blue). The solid lines represent the two algorithms applied on the data sets injected with both outbreak cases and baseline shift phenomena. The dashed lines represent the two algorithms applied on the data sets injected with outbreak cases only.

Keywords

Biosurveillance; Disease outbreak detection; Algorithm

Acknowledgments

This research was funded by PA Department of Health syndromic surveillance grant and CDC Center of Excellence grant P01-HK000086.

References

[1] Reis, BY, Kohane, IS and Mandl, KD, An epidemiological network model for disease outbreak detection, PLoS Medicine, vol. 4, p. 210, 2007.

[2] Wong, TT, Generalized Dirichlet distribution in Bayesian analysis, Applied Mathematics and Computation 97, pp. 165-181, 1998.

[3] Que, J and Tsui, FC, Rank-based spatial clustering: an algorithm for rapid outbreak detection, J Am Med Inform Assoc, vol. 18, pp. 218-224, 2011.

[4] Neill, DB and Cooper, GF, A multivariate Bayesian scan statistic for early event detection and characterization, Machine Learning, vol. 29, pp. 261-282, 2010.

*Jialan Que
E-mail: jialan.que@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Extraction of Disease Occurrence Patterns Using MiSTIC: Salmonellosis in Florida

Vipul Raheja* and K. S. Rajan

International Institute of Information Technology Hyderabad (IIIT-H), Hyderabad, India

Objective

This work leverages spatio-temporal data mining (ST-DM), the MiSTIC (Mining Spatio-Temporally Invariant Cores)[1,6] method for infectious disease surveillance, by identifying

a) Extent of spatial spread of disease core regions across populations-scale of disease prevalence

b) Possible causes of the observed patterns-for better prediction, detection & management of infectious disease & its outbreaks

Introduction

Infectious diseases, though initially tend to be limited geographically to a reservoir; a subsequent spatial variation in disease prevalence (including spread & intensity) arises from the underlying differences in physical-biological conditions that support pathogen, its vectors & reservoirs. Different factors like spatial proximity, physical & social connectivity, & local environmental conditions which add to its susceptibility influence the occurrence[2].

In Disease management, analysis of historical data over various aspects of geography, epidemiology, social structures & network dynamics need to be accounted for. Large amounts of data raise issues of data processing, storage, pattern identification, etc. In addition, identifying the source of disease occurrence & its pattern can be of immense value.

ST-DM of disease data can be an effective tool for endemic preparedness[3], as it extracts implicit knowledge, spatial & temporal relationships, or other patterns inherent in such databases.

Here, Core Region is defined as a set of spatial entities(eg.counties) aggregated over time, which occur frequently at places having high values in a defined region (considering areas of influence around them)[1].

Methods

Here, MiSTIC algorithm detects spatio-temporally invariant cores with respect to disease occurrence. It involves both a spatial analysis step to detect focal points & a spatio-temporal analysis over the time period of study to identify core regions, which are then classified as – CHD, CLD & CND. They refer to Cores with High, Low and No (mostly random) dominating points respectively based on frequency of occurrences of disease. The predominantly occurring focal points capture the localized behavior of the disease whereas the neighborhood constraints capture the nature (dynamic or non-dynamic) of the event.

Results

County-level annual data of Salmonellosis incidence from Florida Department of Health [3] covering a period of 50 years (1961-2010) is used.

Two types of cores were identified based on type of neighborhood - Contiguous (CC) & within a defined Radius (CR).

Table1 shows the analysis of counties according to valid frequency criteria for both CC & CR (r=2) & their sub-classification.

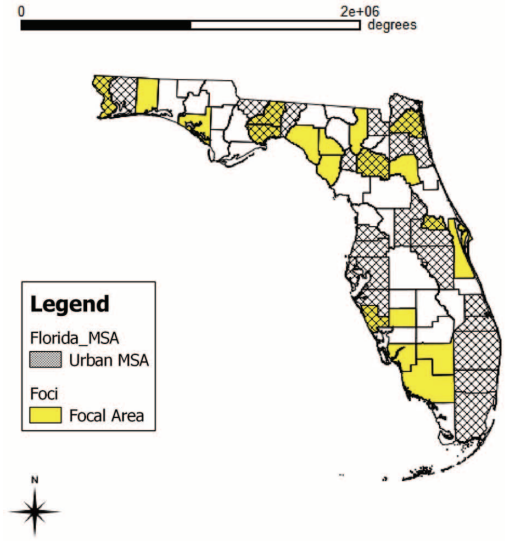
Salmonellosis etiology shows that it is caused by tainted food, hygiene, local environment etc. which are largely sanitation-related [4]. Taking the level of urbanization [5] as a proxy for sanitation, it can be seen from Fig.1, 12 of 19 cores occur in rural counties.

Conclusions

It is observed that CC is better indicator of cores than CR, implying that Salmonellosis manifests itself in a highly localized manner. Thus, use of MiSTIC is promising & provides a way for identifying disease "hot-spots". It also provides valuable insight into the understanding of disease prevalence in different regions based on their history over space and time.

Classification of Core Polygons

	CC	CR
CHD	5	1
CLD	11	13
CND	3	5



Map showing overlay of Metropolitan Areas and Cores

Keywords

Disease Cores; Salmonellosis; Spatio-Temporal Data Mining; Patterns

References

1. K Sravanthi, K S Rajan: Spatio-Temporal Mining of Core Regions - Study of rainfall patterns in Monsoonal India. 11th IEEE International Conference on Data Mining Workshops (ICDMW) 2011, pp.30-37
2. Chris Bailey-Kellogg et al.: Spatial Data Mining to Support Pandemic Preparedness. ACM SIGKDD Explorations Newsletter. 2006; 8(1):80-82
3. http://www.floridacharts.com [20/5/2012]
4. http://www.cdc.gov/healthypets/diseases/salmonellosis.htm [2/7/2012]
5. http://www.census.gov [25/5/2012]
6. K Sravanthi; MiSTIC; MS Thesis. IIIT Hyderabad

*Vipul Raheja
E-mail: vipul.raheja@research.iiit.ac.in

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

ISDS 2012 Conference Abstracts

Traditional and Mobile Public Health Alert Communications with Health Care Providers

Debra Revere*, Ian Painter and Janet Baseman

University of Washington, Seattle, WA, USA

Objective

To systematically compare mobile (SMS) and traditional (email, FAX) communication strategies to identify which modality is most effective for communication of health alerts and advisories between public health agencies and health care providers in order to improve emergency preparedness and response.

Introduction

The effectiveness of emergency preparedness and response systems depends, in part, on the effectiveness of communication between agencies and individuals involved in emergency response, including health care providers who play a significant role in planning, event detection, response and communication with the public. Although much attention has been paid to the importance of communicating clinical data from health care providers to public health agencies for purposes of early event detection and situational awareness (e.g., BioSense) and to the need for alerting health care providers of public health events (e.g., Health Alert Networks), no studies to date have systematically identified the most effective methods of communication between public health agencies and community health care providers for purposes of public health emergency preparedness and response.

The REACH (Rapid Emergency Alert Communication in Health) study is a 4-year randomized controlled trial to evaluate and compare the effectiveness of mobile (SMS) and traditional (email, FAX) communication strategies for sending public health messages to health care providers—physicians, pharmacists, nurse practitioners, physician's assistants and veterinarians.

Methods

Providers were recruited from three sites (King County, WA; Spokane County, WA; and across the state of Montana; N=845) and randomized to receive time-sensitive public health messages via email, Fax, short message service (SMS) or to a control group that did not receive messages. For one year, alerts based on real events of public health interest were sent quarterly with follow-up telephone interviews conducted 5-10 days after the delivery date. Interviews consisted of approximately six questions that elicited information about message receipt, recall of its content and perceived credibility and trustworthiness of the message and source. In addition, provider access to online alert information and delivery success or failure was collected.

Results

Frequency of receipt, timeliness, content awareness, perceived credibility and perceived trustworthiness were measured and compared across communication delivery systems. On average 84.0% of participants were contacted in each follow-up survey following all alerts and across all three sites. Primary data analysis was designed to measure differences between the three communication groups using intent-to-treat methods. A set of secondary analyses examined the outcomes excluding providers who could not have received messages (due to incorrect contact information, known technical failures, or because providers could not receive messages by the assigned delivery message—for example, a provider without a Fax number randomized to the Fax group).

We will discuss preliminary results of intent-to-treat analyses regarding rate of recall of study alert message content between traditional and mobile communications and perceived trustworthiness and credibility of message and message source by providers. In addition, we will report on frequency of accessing online alert information between traditional and mobile delivery groups.

Conclusions

There is currently no evidence-based research to guide or improve the practice of public health communication between public health agencies and health care providers before, during and after a public health emergency. Improving this communication via the use of effective media can enhance disease surveillance, which will aid in early detection and enhance case finding and situational awareness for public health emergencies. By systematically evaluating the relative effectiveness of mobile and traditional message delivery systems for emergency preparedness and response communications, the REACH study contributes to building the evidence base for novel and effective approaches to emergency communications.

Keywords

Emergency Preparedness and Response; Public Health Communication; Surveillance and Alerting

Acknowledgments

This work was made possible by the CDC Office of Public Health Preparedness and Response Extramural Research Program Preparedness and Emergency Response Research Centers award, Grant no. 5P01TP000297, to the University of Washington. The contents are solely the responsibility of the authors and do not necessarily represent the official views of the CDC.

*Debra Revere
E-mail: drevere@uw.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Collaboration for Improved Disease Surveillance Literature Review

Tera Reynolds*[1], Katie Suda[2], Blaine Reeder[3], William Storm[4], Al Ozonoff[5] and Howard Burkom[6]

[1]International Society for Disease Surveillance, Brighton, MA, USA; [2]University of Tennessee, Memphis, TN, USA; [3]University of Washington, Seattle, WA, USA; [4]Ohio Department of Health, Columbus, OH, USA; [5]Boston Children's Hospital, Boston, MA, USA; [6]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Objective

To improve the method of automated retrieval of surveillance-related literature from a wide range of indexed repositories.

Introduction

The ISDS Research Committee (RC) is an interdisciplinary group of researchers interested in various topics related to disease surveillance. The RC hosts a literature review process with a permanent repository of relevant journal articles and bimonthly calls that provide a forum for discussion and author engagement. The calls have led to workgroups and society-wide events, boosted interest in the ISDS Conference, and fostered networking among participants.

Since 2007, the RC has identified and classified published articles using an automated search method with the aim of progressing ISDS's mission of advancing the science and practice of disease surveillance by fostering collaboration and increasing awareness of innovations in the field of surveillance. The RC literature review efforts have provided an opportunity for interprofessional collaboration and have resulted in a repository of over 1,000 articles, but feedback from ISDS members indicated relevant articles were not captured by the existing methodology. The method of automated literature retrieval was thus refined to improve efficiency and inclusiveness of stakeholder interests.

Methods

The earlier literature review method was implemented from March 2007 to March 2012. PubCrawler [1] (articles indexed in Medline) and Google Scholar [2] search results were sent to the RC via automated e-mail. To refine this method, the RC developed search strings in PubMed [3], Embase [4], and Scopus [5], consisting of over 100 terms suggested by members. After evaluating these methods, we found that the Scopus search is the most comprehensive and improved the cross-disciplinary scope. Scopus results allowed filtering of 50-100 titles and abstracts in fewer than 30 minutes each week for the identification of relevant articles (Figure).

Journal titles were categorized to assess the increased range of fields covered; categories include epidemiology, agriculture, economics, and medicine (51 categories total).

Results

Since implementing the new method, potentially relevant articles identified per month increased from an average of 19 (SD: 13; n= 31) to 159 (SD: 63; n= 3). Both methods identified articles in the health sciences, but the new search also captured articles in the life, physical, and social sciences. Between March 2007 and March 2012, articles selected were classified into an average of 10 different categories per literature review (SD: 4; n= 31) versus an average of 33 categories (SD: 5; n= 3) with the updated process.

Conclusions

The new search method improves upon the previous method – it captures relevant articles indexed in health science and other secondary databases beyond Medline. The new method has resulted in a greater number of relevant literature articles, from a broader range of disciplines, and in reduced amount of preparation time as compared to the results of the previous search method. This improvement may increase multi-disciplinary discussions and partnerships, but changes in online publishing pose challenges to continued access of the new range of articles.

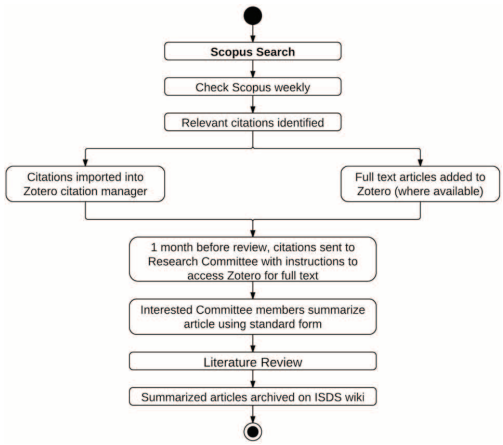


Figure. Overview of 2012 literature review process including, Scopus search [6]; Zotero [7], a freely available web application that streamlines content management; and summarized article archive on ISDS Wiki [8].

Keywords

Disease surveillance literature; ISDS Research Committee; Literature search

Acknowledgments

The ISDS RC would like to thank past contributors and guest authors to the literature review.

References

1. PubCrawler. http://www.webcitation.org/6AZiiSIDH.
2. Google Scholar. http://www.webcitation.org/mainframe.php.
3. Pubmed. http://www.webcitation.org/6AZilS732.
4. Embase. http://www.webcitation.org/6AZj0rxhu.
5. Scopus. http://www.scopus.com/home.url.
6. ISDS Literature Review Search (Scopus). http://www.webcitation.org/6AZiWfC6C.
7. Zotero. http://www.webcitation.org/6AZia0yEd.
8. ISDS Literature Summaries Archive. Wiki. http://www.webcitation.org/6AZkiT9xQ.

*Tera Reynolds
E-mail: treynolds@syndromic.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Data Quality: A Systematic Review of the Biosurveillance Literature

Tera Reynolds*[1], Ian Painter[2] and Laura Streichert[1]

[1]International Society for Disease Surveillance, Brighton, MA, USA; [2]University of Washington, Seattle, WA, USA

Objective

To highlight how data quality has been discussed in the biosurveillance literature in order to identify current gaps in knowledge and areas for future research.

Introduction

Data quality monitoring is necessary for accurate disease surveillance. However it can be challenging, especially when "real-time" data are required. Data quality has been broadly defined as the degree to which data are suitable for use by data consumers [1]. When compromised at any point in a health information system, data of low quality can impair the detection of data anomalies, delay the response to emerging health threats [2], and result in inefficient use of staff and financial resources. While the impacts of poor data quality on biosurveillance are largely unknown, and vary depending on field and business processes, the information management literature includes estimates for increased costs amounting to 8-12% of organizational revenue and, in general, poorer decisions that take longer to make [3].

Methods

To fill an unmet need, a literature review was conducted using a structured matrix based on the following predetermined questions:

-How has data quality been defined and/or discussed?
-What measurements of data quality have been utilized?
-What methods for monitoring data quality have been utilized?
-What methods have been used to mitigate data quality issues?
-What steps have been taken to improve data quality?

The search included PubMed, ISDS and AMIA Conference Proceedings, and reference lists. PubMed was searched using the terms "data quality," "biosurveillance," "information visualization," "quality control," "health data," and "missing data." The titles and abstracts of all search results were assessed for relevance and relevant articles were reviewed using the structured matrix.

Results

The completeness of data capture is the most commonly measured dimension of data quality discussed in the literature (other variables include timeliness and accuracy). The methods for detecting data quality issues fall into two broad categories: (1) methods for regular monitoring to identify data quality issues and (2) methods that are utilized for *ad hoc* assessments of data quality. Methods for regular monitoring of data quality are more likely to be automated and focused on visualization, compared with the methods described as part of special evaluations or studies, which tend to include more manual validation.

Improving data quality involves the identification and correction of data errors that already exist in the system using either manual or automated data cleansing techniques [4]. Several methods of improving data quality were discussed in the public health surveillance literature, including development of an address verification algorithm that identifies an alternative, valid address [5], and manual correction of the contents of databases [6].

Communication with the data entry personnel or data providers, either on a regular basis (e.g., annual report) or when systematic data entry errors are identified, was mentioned in the literature as the most common step to prevent data quality issues.

Conclusions

In reviewing the biosurveillance literature in the context of the data quality field, the largest gap appears to be that the data quality methods discussed in literature are often *ad hoc* and not consistently implemented. Developing a data quality program to identify the causes of lower quality health data, address data quality problems, and prevent issues would allow public health departments to more efficiently and effectively conduct biosurveillance and to apply results to improving public health practice.

Keywords

Biosurveillance; Data quality; Literature review

Acknowledgments

We thank the ISDS Data Quality Workgroup for initiating this project, which was supported by CDC through contract with the Task Force for Global Health.

References

1. Wang RY, Strong DM. Beyond accuracy: What data quality means to data consumers. JMIS. 1996:5–33.
2. Dixon BE, McGowan JJ, Grannis SJ. Electronic Laboratory Data Quality and the Value of a Health Information Exchange to Support Public Health Reporting Processes. Proc AMIA Symp. 2011;2011:322.
3. Redman TC. The impact of poor data quality on the typical enterprise. Commun ACM. 1998;41(2):79–82.
4. Maydanchik A. Data Quality Assessment. Technics Publications, LLC; 2007.
5. Zinszer K, Charland K, Jauvin C, et al. The influence of address errors on detecting outbreaks of campylobacteriosis. Emerg Health Threats J. 2011;4(s59):68–69.
6. Chen L, Dubrawski A, Waidyanatha N, Weerasinghe C. Automated detection of data entry errors in a real time surveillance system. Emerg Health Threats J. 2011;4(s69):9–10.

*Tera Reynolds
E-mail: treynolds@syndromic.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Detecting the Determinants of Health in Social Media

Caitlin Rivers*[1], Bryan Lewis[1] and Sean Young[2]

[1]Network Dynamics and Simulation Science Laboratory, Virginia Bioinformatics Institute, Blacksburg, VA, USA; [2]UCLA David Geffen School of Medicine, Berkley, CA, USA

Objective

Create an analysis pipeline that can detect the behavioral determinants of disease in the population using social media data.

Introduction

The explosive use of social media sites presents a unique opportunity for developing alternative methods for understanding the health of the public. The near ubiquity of smartphones has further increased the volume and resolution of data that is shared through these sites. The emerging field of digital epidemiology[1] has focused on methods to analyze and use this "digital exhaust" to augment traditional epidemiologic methods. When applied to the task of disease detection they often detect outbreaks 1-2 weeks earlier than their traditional counterpart [1]. Many of these approaches successfully employ data mining techniques to detect symptoms associated with influenza-like illness [2]. Others can identify the appearance of novel symptom patterns, allowing the ability to detect the emergence of a new illness in a population [3]. However, behaviors that lead to increased risk for disease have not yet received this treatment.

Methods

We have created a methodology that can detect the behavioral determinants of disease in the population. Initially we have focused on risky behaviors that can contribute to HIV transmission in a population, however, the methodology is generalizable.

We collected 15 million tweets based on 32 broad keywords relating to three types of risky behaviors associated with the transmission of HIV: drug use (e.g. meth), risky sexual behaviors (e.g. bareback), and other STIs (e.g. herpes). We then hand coded a subset of 2,537 unique tweets using a crowd-sourceable "game" that can be distributed online. This hand-coded set was used to train a simple n-gram classifier, which resulted in an algorithm to select relevant tweets from the larger database. We then generated geocodes from text locations provided by the tweet author, supplemented by the ~1% of tweets that are already geolocated. We scaled these geocodes to the state and county levels, which allowed us to compare HIV prevalence in our collected data with public health data.

Results

We present the correlation between behaviors identified in social media and the corresponding impacts on disease incidence across a large population. Hand coding revealed that 34% of tweets with one or more of the 32 initial keywords was relevant to behaviors associated with HIV transmission. Among the three categories of initial search terms, the drug category yielded 21% true positives, compared to 9% for risky behaviors, and 2% for other STIs. The n-gram classifier measured 66% sensitivity and 44% specificity on a test set. In addition, our geolocation algorithm found coordinates for 88% of text locations. Of those, a test sample of 59 text locations showed that 83% of geolocations are correctly identified. These components combine to form an analysis pipeline for detecting risky behaviors across the United States.

Conclusions

We present a surveillance methodology to help sift through the vast volumes of these data to detect behaviors and determinants of health contributing to both disease transmission and chronic illness. This effort allows for identification of at-risk communities and populations, which will facilitate targeted, primary and secondary-prevention efforts to improve public health.

Keywords

social media; hiv/aids; digital epidemiology

Acknowledgments

We thank our external collaborators and members of the Network Dynamics and Simulation Science Laboratory (NDSSL) for their suggestions and comments. This work has been partially supported by: NIH MIDAS Grant 2U01GM070694-09 and DTRA CNIMS Contract HDTRA1-11-D-0016-0001

References

[1] Salathé, M., Bengtsson, L., Bodnar, T. J., Brewer, D. D., Brownstein, J. S., Buckee, C., Campbell, E. M., et al. (2012). Digital Epidemiology. (P. E. Bourne, Ed.)PLoS Computational Biology, 8(7), e1002616. doi:10.1371/journal.pcbi.1002616

[2] Achrekar, H., Lazarus, R., & Park, W. C. (2011). Predicting Flu Trends using Twitter Data. The First International Workshop on Cyber-Physical Networking Systems (pp. 713–718).

[3] Neill DB. Fast Bayesian scan statistics for multivariate event detection and visualization. Stat Med. 2011Feb.28;30(5):455–69.

*Caitlin Rivers
E-mail: cmrivers@vbi.vt.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Searching for Complex Patterns Using Disjunctive Anomaly Detection

Maheshkumar Sabhnani*, Artur Dubrawski and Jeff Schneider

Carnegie Mellon University, Pittsburgh, PA, USA

Objective

Disjunctive anomaly detection (DAD) algorithm [1] can efficiently search across multidimensional biosurveillance data to find multiple simultaneously occurring (in time) and overlapping (across different data dimensions) anomalous clusters. We introduce extensions of DAD to handle rich cluster interactions and diverse data distributions.

Introduction

Modern biosurveillance data contains thousands of unique time series defined across various categorical dimensions (zipcode, age groups, hospitals). Many algorithms are overly specific (tracking each time series independently would often miss early signs of outbreaks), or too general (detections at state level may lack specificity reflective of the actual process at hand). Disease outbreaks often impact multiple values (disjunctive sets of zipcodes, hospitals, multiple age groups) along subsets of multiple dimensions of data. It is not uncommon to see outbreaks of different diseases occurring simultaneously (e.g. food poisoning and flu) making it hard to detect and characterize the individual events.

We proposed Disjunctive Anomaly Detection (DAD) algorithm [1] to efficiently search across millions of potential clusters defined as conjunctions over dimensions and disjunctions over values along each dimension. An example anomalous cluster detectable by DAD may identify zipcode = {z1 or z2 or z3 or z5} and age_group = {child or senior} to show unusual activity in the aggregate. Such conjunctive-disjunctive language of cluster definitions enables finding real-world outbreaks that are often missed by other state-of-art algorithms like What's Strange About Recent Events (WSARE) [3] or Large Average Submatrix (LAS) [2]. DAD is able to identify multiple interesting clusters simultaneously and better explain complex anomalies in data than those alternatives.

Methods

We define the observed counts of patients reporting on a given day as a random variable for each unique combination of values along all dimensions. DAD iteratively identifies K subsets of these variables along with corresponding ranges of their values and time intervals that show increased activity that cannot be explained by random fluctuations (K is generally unknown and could be 0). The resulting set of clusters maximizes data likelihood while controlling for overall complexity. We have successfully derived a versatile set of scoring functions that allow Normal, Poisson, Exponential or Non-parametric assumptions about the underlying data distributions, and accommodate additive-scaled, additive-unscaled or multiplicative-scaled models for the clusters.

Results

We present results of testing DAD on two real-world datasets. One of them contains daily outpatient visit counts from 26 regions in Sri Lanka involving 9 common diseases. The other data contains semi-synthetically generated terrorist activities throughout regions of Afghanistan (Sigacts). Both span multiple years and are representative of data seen in biosurveillance applications.

Figure 1 shows DAD systematically outperforming WSARE and LAS. Each algorithm's parameters were tuned to generate one false positive per month in baseline data. The graphs represent average days-to-detect performance of 100 sets with synthetically injected clusters using additive-scaled (AS), additive-unscaled (AU), and multiplicative-scaled (MS) models of cluster interactions.

Conclusions

We extend applicability of DAD algorithm to handle wide variety of input data distributions and various outbreak models. DAD efficiently scans over millions of potential outbreak patterns and accurately and timely reports complex outbreak interactions with speed that meets requirements of practical applications.

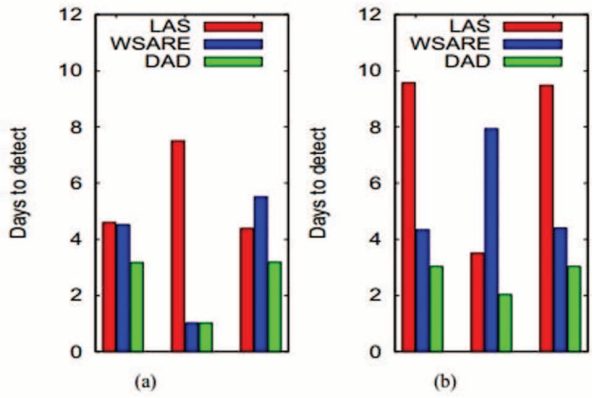


Figure 1: Alg. performance (a) Srilanka, (b) Sigacts

Keywords

outbreak detection; anomalous clusters; disjunctive anomaly detection; prospective surveillance

Acknowledgments

This material is based upon work supported by the National Science Foundation under Grant No. IIS-0911032.

References

1. Sabhnani M., Dubrawski A., Schneider J. Detection of Multiple Overlapping Anomalous Clusters in Categorical Data. Advances in Disease Surveillance, 2010.
2. Shabalin A., Weigman V., Perou C., Nobel A. Finding Large Average Submatrices in high dimensional data. Annals of Statistics 3(3):985-1012, 2009.
3. Wong W., Moore A., Cooper G., Wagner M. What's Strange About Recent Events (WSARE). J. of Machine Learning Research, 6:1961-1998, 2005.

*Robin Sabhnani
E-mail: sabhnani@cs.cmu.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Adapting Syndromic Surveillance Systems to Increase Value to Local Health Departments

Erika Samoff*[1], Mary T. Fangman[1], Amy Ising[2], Lana Deyneka[3] and Anna E. Waller[2]

[1]NCPERRC, University of North Carolina, Chapel Hill, NC, USA; [2]Carolina Center for Health Informatics, University of North Carolina School of Medicine, Chapel Hill, NC, USA; [3]North Carolina Division of Public Health, Chapel Hill, NC, USA

Objective

Our objective was to describe changes in use following syndromic surveillance system modifications and assess the effectiveness of these modifications.

Introduction

Syndromic surveillance systems offer richer understanding of population health. However, because of their complexity, they are less used at small public health agencies, such as many local health departments (LHDs). The evolution of these systems has included modifying user interfaces for more efficient and effective use at the local level. The North Carolina Preparedness and Emergency Response Research Center previously evaluated use of syndromic surveillance information at LHDs in North Carolina. Since this time, both the NC DETECT system and distribution of syndromic surveillance information by the state public health agency have changed. This work describes use following these changes.

Methods

Data from NC DETECT were used to assess the number of users and usage time. Staff from 14 NC LHDs in 2009 and from 39 LHDs in 2012 were surveyed (May-August of 2009 and June of 2012) to gather information on the mode of access to syndromic surveillance information and how this information was used. Data were analyzed to assess the link between the mode of access and use of syndromic surveillance data.

Results

System changes made between 2009 and 2012 included the creation of "dashboards" (Figure 1) which present users with LHD-specific charts and graphs upon login and increases in the distribution of syndromic surveillance information by the state public health agency. The number of LHD-based NC DETECT system users increased from 99 in 2009 to 175 in 2012. Sixty-two of 72 respondents completed the 2012 survey (86%). Syndromic surveillance information was used in 28/40 LHDs (70%) for key public health tasks. Among 20 NC EDSS leads reporting an outbreak in the past year, 25% reported using data from NC DETECT for outbreak response, compared to 23% in 2009 (Figure 2). Among 30 responding NC EDSS leads, 57% reported using data from NC DETECT to respond to seasonal events such as heat-related illness or influenza, compared to 46% in 2009. NC DETECT data were reported to have been used for program management by 30% (compared to 25% in 2009), and to have been used in reports by 33% (compared to 23% in 2009).

Conclusions

Changes in how syndromic surveillance information was distributed supported modest increases in use in LHDs. Because use of syndromic surveillance data at smaller LHDs is rare, these modest increases are important indicators of effective modification of the NC syndromic surveillance system.

Figure 1: NC DETECT dashboards

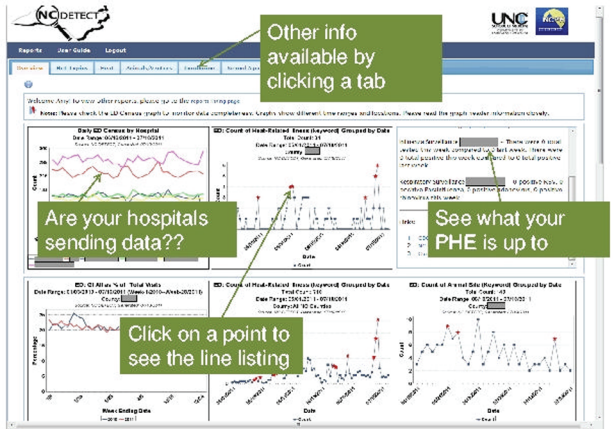
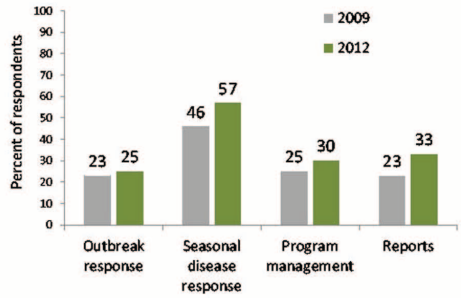


Figure 2: Uses of syndromic surveillance information, communicable disease staff 2009 (13 LHDs) and 2012 (31 LHDs)



Keywords

evaluation; public health practice; syndromic surveillance; surveillance; local health department

Acknowledgments

We thank Aaron Fleischauer, Anne Hakenewerth, and North Carolina local health department staff members for their time and insights. This research was carried out by the North Carolina Preparedness and Emergency Response Research Center (NCPERRC) which is part of the UNC Center for Public Health Preparedness at the University of North Carolina at Chapel Hill's Gillings School of Global Public Health and was supported by the Centers for Disease Control and Prevention (CDC) Grant 1PO1 TP 000296. The contents are solely the responsibility of the authors and do not necessarily represent the official views of CDC. Additional information can be found at http://cphp.sph.unc.edu/ncperrc/.

*Erika Samoff
E-mail: erika.samoff@unc.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Surveillance-Based Program Planning

Rossi Sanusi*

Center for Health Service Management, Gadjah Mada University School of Medicine, Yogyakarta, Indonesia

Objective

to analyze the Integrated Behavioral & Biological Surveillance (IBBS) 2011 data for designing a condom utilization program.

Introduction

The IBBS is part of the Indonesian MoH HIV Surveillance System, which include Serological Surveillance, Behavioral Surveillance, Reproductive Tract Infection Survey, and monthly HIV/AIDS facility-based (hospitals, HCs, VCT Sites) monthly reports. The IBBS 2011 was conducted in 11 provinces (22 districts/municipalities) encompassing eight Most At Risk Populations (MARPs) – injection drug users, transsexuals, men who have sex with men, youths, inmates, mobile men, direct female sex workers (FSWs), and indirect FSWs. Data of 442 direct FSWs of the Jayapura Municipality and Jayawijaya District (Papua Province) showed that 406 (91.85%) have sex with partners who did not use condoms. Of these 406 FSWs 60 (14.78%) were HIV positive and 231 (56.89%) were STD positive.

Methods

Items of the Direct FSW Questionnaire, IBBS 2011, were examined and items that would yield information regarding content and method of HIV prevention interventions by means of condoms were identified. The Stata12 software was used to inspect/codebook the variables related to the selected items, to recode numeric data into categorical data, to generate one-way and two-way tables, and to produce pairwise correlations (and their significance levels).

Results

The Direct FSWs IBBS 2011 data of the Jayapura Municipality and Jayawijaya District showed that there are significant positive correlations between condom use behavior variables of FSWs (i.e., to know, to possess, to buy, and to offer male condoms) and variables of last-sex encounter condom use by customers, and between the latter and HIV and STD lab results. The correlations were low, however, of the condom use behavior variables and variables that are related to comprehensive knowledge of HIV prevention, condom use by more steady sex partners (e.g., husbands, boyfriends, other males) and female condom utilization, and during last-week and last-month sex transactions. The data analyses also indicated details of the distribution of the FSWs, with their condom use behaviors, according to individual characteristics, CIE (communication, information & education) intervention utilization, condom acquirement, and sexual behavior.

Conclusions

The condom utilization campaigns ought to focus on continuous reminders (instead of education programs) about how to persuade customers and other sex partners to use condoms, or to allow FSWs to use female condoms, and about where to go for HIV/STD testing and treatment. The condom promotion drives should use posters, TV ads, and field/health workers, The program should also make certain that good quality condoms be made avaible by local managers (of brothels, hotels, bars, etc.) and local vendors (drugists, stands, mobile carts).

Keywords

IBBS; condom use; HIV; FSWs; Papua

Acknowledgments

The author thanks the Directorate General of Disease Control & Environmental Health, MoH, Republic of Indonesia (for allowing to use the IBBS 2011 data) and Family Health Indonesia (for funding the IBBS 2011 Data Analysis Training Program).

References

Ghimire, L., Smith, W., & van Teijlingen, E.R. (2011). Utilisation of sexual health services by female sex workers in Nepal. BMC Health Services Research 2011, 11:79.

Longfield, K., Panyanouvong, X., Chen, J., & Kays, M.B.. (2011). Increasing safer sexual behavior among Lao kathoy through an integrated social marketing approach. BMC Public Health 2011, 11:872.

MoH, Republic of Indonesia. (2011). Report on the Development of HIV & AIDS in Indonesia until June 2011.

*Rossi Sanusi
E-mail: rossi_sanusi@yahoo.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Age, Triage Score, and Disposition in Emergency Department Visit Records: Potential Utility for Prediction of Influenza-related Hospitalizations in Montreal, Canada

Noémie Savard*[1, 2], Lucie Bédard[1, 2], Robert Allard[2, 3] and David L. Buckeridge[2, 3]

[1]Université de Montréal, Montreal, QC, Canada; [2]Direction de santé publique de Montréal, Montreal, QC, Canada; [3]McGill University, Montreal, QC, Canada

Objective

To evaluate the potential value of age, triage score, and disposition data contained in emergency department (ED) electronic records for surveillance of severe influenza cases and prediction of influenza-related hospitalizations in an urban area.

Introduction

ED triage systems increasingly capture detailed patient and medical visit characteristics, including age and markers of illness severity such as triage score and disposition. Age and disposition are included in the core ED surveillance data set recommendations from ISDS, and triage score is in the extended set (1). While some studies have assessed the time relationship and association of age-specific influenza-like illness (ILI) visits with influenza-related hospitalizations (2,3), none have assessed the value of triage scores and disposition data for influenza surveillance.

Methods

For the period of June 25 2006 to January 29 2011, weekly pneumonia and influenza (P&I) hospitalizations in 5 participating Montreal hospitals were modeled using negative binomial regression. Weekly counts of ED visits with ILI were included as the main predicting variable, testing for different lead times and correcting for secular trends, seasonality, autocorrelation, and total ED visits. Counts of overall ILI visits were then replaced by counts stratified by age, triage score (urgent or not), and disposition (discharge vs admission/transfer/death), and model fit was assessed using Akaike's information criterion (AIC). Separate analyses were done for the H1N1 pandemic year. For non-pandemic years, predictive value was assessed by computing the mean absolute scaled error (MASE) for one step-ahead forecasts on the final year of data.

Results

During the non-pandemic years, ILI visits from the ≥65 year age group and those resulting in admission/transfer/death each provided small improvements in model fit (lower AIC) and prediction (lower MASE) for overall P&I hospitalizations, as compared to overall ILI ED visits (Figure 1). Predictions were improved for hospitalizations occurring the same week and the following week (lead times of 0-1 week). During the H1N1 year, visits from the <18 year age group, visits with urgent triage categories, and visits resulting in admission/transfer/death provided a small improvement in fit compared to overall ILI ED visits, with lead times of 1-3 weeks, 2-3 weeks and 0-1 weeks respectively.

Conclusions

Compared to overall ILI ED visits, visits stratified by age group, triage score, and disposition status provided small improvement in predictive models for overall P&I hospitalizations. It may be valuable to integrate these covariates into an ED-based ILI surveillance system, for improved surveillance of severe influenza cases and prediction of influenza-related hospitalizations. However, our findings should be verified in other settings. Further evaluation should also consider whether adding these covariates into a surveillance system leads to improved public health practices, such as earlier implementation of appropriate infection control measures.

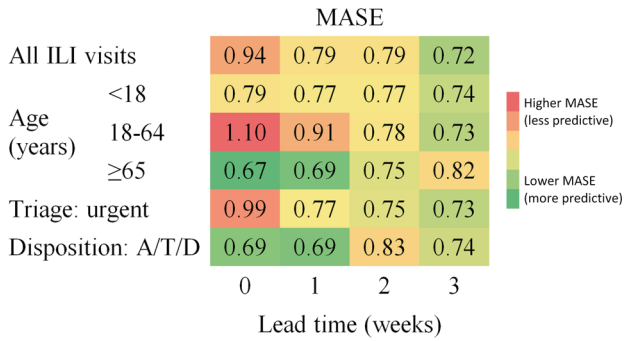


Figure 1: Mean absolute scaled error (MASE) for prediction of P&I hospitalizations, using ED ILI visits stratified by age, triage category, and disposition.
A/T/D: admission/transfer/death.

Keywords

influenza; emergeny department; age; triage; disposition

References

1. International Society for Disease Surveillance. Final Recommendation: Core Processes and EHR Requirements for Public Health Syndromic Surveillance. 2011, January. Available online:www.syndromic.org/projects/meaningful-use.
2. Sebastian R, Skowronski DM, Chong M, Dhaliwal J, Brownstein JS: Age-related trends in the timeliness and prediction of medical visits, hospitalizations and deaths due to pneumonia and influenza, British Columbia, Canada, 1998-2004. Vaccine 2008, 26(10):1397-1403.
3. Chan EH, Tamblyn R, Charland KML, Buckeridge DL: Outpatient physician billing data for age and setting specific syndromic surveillance of influenza-like illnesses. J Biomed Inform 2011, 44(2):221-228.

*Noémie Savard
E-mail: noemie.savard@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Coded Chief Complaints for Influenza-like Illness Surveillance in Montreal, Canada: Challenges in Choosing a Syndrome Definition

Noémie Savard*[1, 2], Lucie Bédard[1, 2], Robert Allard[2, 3] and David L. Buckeridge[2, 3]

[1]Université de Montréal, Montreal, QC, Canada; [2]Direction de santé publique de Montréal, Montreal, QC, Canada; [3]McGill University, Montreal, QC, Canada

Objective

To document challenges and identify solutions regarding the choice of a syndrome definition during the implementation of an automated surveillance system for influenza-like illness (ILI) using emergency department (ED)-based coded chief complaints in Montreal, Canada.

Introduction

The Montreal Public Health Department, as part of its routine surveillance activities, currently receives daily counts of ILI visits manually reported by each ED in the jurisdiction. However, this method of reporting is about to be replaced by automated extraction of coded chief complaints from ED electronic records. In preparation for implementing the automated system, we selected, adapted, and validated two ILI syndrome definitions.

Methods

Eight Montreal EDs (covering approximately 40% of all non-psychiatric ED visits in the jurisdiction) are currently transmitting ED electronic records into a test database. For each ED, we evaluated coding practices (proportion of visits with a recorded chief complaint, number of codes used per visit, and sets of codes preferentially chosen). We chose two ILI definitions from the literature, one meant to be specific (ILI-Sp = (fever and cough) or (fever and sore throat) or influenza keyword) and the other sensitive (ILI-Se = fever or cough or sore throat or influenza keyword). Descriptive statistics and time series were obtained for each definition for each ED. As a preliminary validation step, ILI counts were correlated with daily counts of ILI visits manually reported by EDs.

Results

Chief complaints were recorded for 97% of visits. The main challenge resulted from different coding practices between EDs. The mean number of chief complaint codes per visit ranged from 1.4 to 6.2. The list of codes used by each ED only partially overlapped. The proportion of ILI-Se and ILI-Sp visits varied importantly between EDs (up to 4-fold difference), and so did the extent of the observed seasonal variation (Figure 1). It was not possible to disentangle the effect of coding practices from real differences in ILI visit incidence. The correlation between ILI-Sp, ILI-Se, or their components, and counts of ILI visits reported manually also varied greatly between EDs (Figure 2). For most EDs, ILI-Sp was more strongly correlated with manually reported ILI visits (ρ = 0.41 to 0.94) than was ILI-Se (ρ = 0.28 to 0.70).

Conclusions

Our results suggest that, given the current practices, different syndrome definitions may be appropriate for different EDs. For ILI surveillance in Montreal, we make the following recommendations : 1) to engage partners at the ED level to achieve uniform coding practices, and 2) in the event that standardized practices at the ED level are not feasible, to develop and use ED-specific ILI definitions. Manually reported ILI counts, once validated, may be useful as a gold standard against which to choose ED-specific ILI definitions.

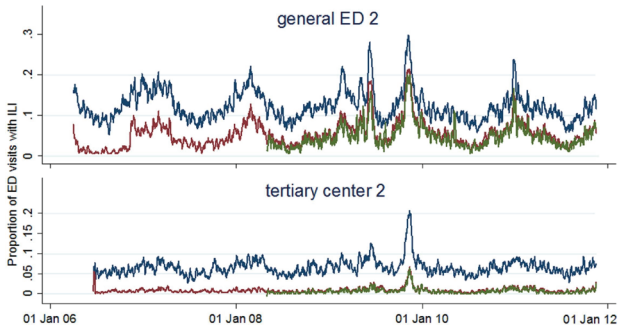


Figure 1: Time series of the proportion of ILI visits, for two EDs, according to syndrome definition. Blue: sensitive definition (ILI-Se); red: specific definition (ILI-Sp); green: ILI counts reported manually.

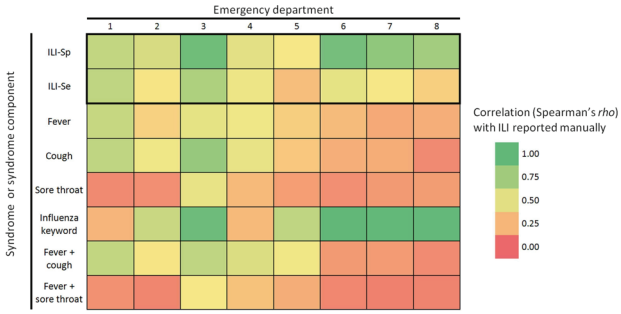


Figure 2: Correlation (Spearman's rho) between counts of ILI reported manually by EDs, and ILI counts obtained with the specific defintion (ILI-Sp), sensitive definition (ILI-Se), or components thereof.

Keywords

chief complaint; influenza; syndrome definition

*Noémie Savard
E-mail: noemie.savard@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Long-Term Asthma Trend Monitoring in New York City: A Mixed Model Approach

Stephen E. Schachterle*, Robert W. Mathes, Marc Paladini and Don Weiss

New York City Department of Health and Mental Hygiene, Queens, NY, USA

Objective

Show the benefits of using a generalized linear mixed model (GLMM) to examine long-term trends in asthma syndrome data.

Introduction

Over the last decade, the application of syndromic surveillance systems has expanded beyond early event detection to include long-term disease trend monitoring. However, statistical methods employed for analyzing syndromic data tend to focus on early event detection. Generalized linear mixed models (GLMMs) may be a useful statistical framework for examining long-term disease trends because, unlike other models, GLMMs account for clustering common in syndromic data, and GLMMs can assess disease rates at multiple spatial and temporal levels (1). We show the benefits of the GLMM by using a GLMM to estimate asthma syndrome rates in New York City from 2007 to 2012, and to compare high and low asthma rates in Harlem and the Upper East Side (UES) of Manhattan.

Methods

Asthma related emergency department (ED) visits, and patient age and ZIP code were obtained from data reported daily to the NYC Department of Health and Mental Hygiene. Demographic data were obtained from 2010 US Census. ZIP codes that represented high and low asthma rates in Harlem and the UES of Manhattan were chosen for closer inspection. The ratio of weekly asthma syndrome visits to total ED visits was modeled with a Poisson GLMM with week and ZIP code random intercepts (2). Age and ethnicity were adjusted for because of their association with asthma rates (3).

Results

The GLMM showed citywide asthma rates remained stable from 2007 to 2012, but seasonal differences and significant inter-ZIP code variation were present. The Harlem ZIP code asthma rate that was estimated with the GLMM was significantly higher (5.83%, 95% CI: 3.65%, 9.49%) than the asthma rate in UES ZIP code (0.78%, 95% CI: 0.50%, 1.21%). A linear time component to the GLMM showed no appreciable change over time despite the seasonal fluctuations in asthma rate. GLMM based asthma rates are shown over time (Figure 1).

Conclusions

GLMMs have several strengths as statistical frameworks for monitoring trends including:

1. Disease rates can be estimated at multiple spatial and temporal levels,
2. Standard error adjustment for clustering in syndromic data allows for accurate, statistical assessment of changes over time and differences between subgroups,
3. "Strength borrowed" (4) from the aggregated data informs small subgroups and smooths trends,
4. Integration of covariate data reduces bias in estimated rates.

GLMMs have previously been suggested for early event detection with syndromic surveillance data (5), but the versatility of GLMM makes them useful for monitoring long-term disease trends as well. In comparison to GLMMs, standard errors from single level GLMs do not account for clustering and can lead to inaccurate statistical hypothesis testing. Bayesian hierarchical models (6), share many of the strengths of GLMMS, but are more complicated to fit. In the future, GLMMs could provide a framework for grouping similar ZIP codes based on their model estimates (e.g. seasonal trends and influence on overall trend), and analyzing long-term disease trends with syndromic data.

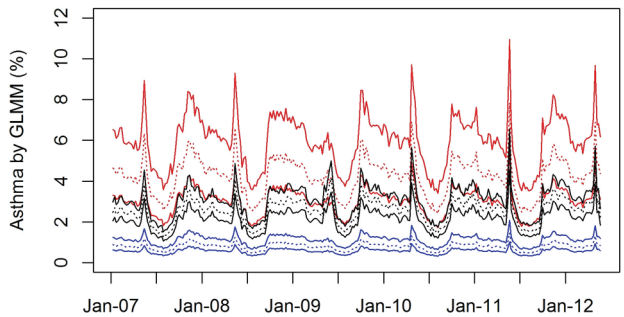


Figure 1: Harlem ZIP code (red), the Upper East Side ZIP code (blue), and citywide (black) estimates are shown as dotted lines surrounded by 30% credibility bands in solid lines.

Keywords

Asthma; Long term trends; Generalized Mixed Models

Acknowledgments

This work was carried out in conjunction with a grant from the Alfred P. Sloan Foundation (#2010-12-14). We thank the members of the New York City Department of Health and Mental Hygiene Syndromic Surveillance Unit.

References

1. Diggle, P.J., Liang K.Y., & Zeger, S. L. (1994). Analysis of Longitudinal Data. Oxford: Oxford University Press.
2. Gelman, A., Hill, J., (2007). Data Analysis Using Regression and Multilevel/Hierarchical Models. New York: Cambridge University Press.
3. Claudio, L. et al. (1999) Socioeconomic Factors and Asthma Hospitalization Rates in New York City. Journal of Asthma. 36(4): pp. 343-350.
4. Jones, K., Johnston R. J., and Pattie C. J. (1992). People, Places and Regions: Exploring the Use of Multi-Level Modelling in the Analysis of Electoral Data. British Journal of Political Science, 22, pp 343-380.
5. Kleinman, K., Lazarus, R., Platt, R., (2004). A Generalized Linear Mixed Models Approach for Detecting Incident Clusters of Disease in Small Areas, with an Application to Biological Terrorism. AJE, 159, pp 217-224.
6. Chan, T.C., et al. Probabilistic Daily ILI Syndromic Surveillance with a Spatio-Temporal Bayesian Hierarchical Model. PLoS ONE. 5(7): e11626.

*Stephen E. Schachterle
E-mail: steve.schachterle@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Does Antimicrobial Prescription Data Improve Influenza Surveillance in VA?

Patricia Schirmer*[1], Carla Winston[1], Russell Ryono[1], Cynthia Lucero-Obusan[1], Gina Oda[1] and Mark Holodniy[1, 2]

[1]Department of Veterans Affairs, Office of Public Health Surveillance and Research, Palo Alto, CA, USA; [2]Stanford University, Division of Infectious Diseases and Geographic Medicine, Palo Alto, CA, USA

Introduction

Antimicrobial prescriptions are a new data source available to the Veterans Health Administration (VHA) biosurveillance program. Little is known about whether antiviral or antibacterial prescription data correlates with influenza ICD-9-CM coded encounters. We therefore evaluated the utility and timeliness of antiviral and antibacterial utilization for influenza surveillance.

Methods

Antiviral (oseltamivir, zanamivir) and antibacterial (azithromycin) outpatient (OP) prescriptions and OP ESSENCE coded respiratory syndrome, influenza-like-illness (ILI) or influenza-specific ICD-9-CM coded visits were analyzed covering the 2010-2011 and 2011-2012 influenza seasons (July 1, 2010-July 31, 2012) for 152 VA medical centers and 971 outpatient clinics using VA Corporate Data Warehouse and ESSENCE biosurveillance tool. Correlation analysis and peak comparisons were performed.

Results

For this time period, there were 2,880,415 respiratory, 1,578,421 ILI, and 5,158 influenza-specific coded visits. For both influenza seasons, respiratory and ILI visits peaked at weeks 1-2 whereas influenza-specific visits had two peaks between weeks 37-40 and weeks 6-11 (See Figure 1 and 2). The total number of prescriptions was 631,272 azithromycin; 8,362 oseltamivir; and 88 zanamivir (See Figure 2). Spearman rank correlation coefficients for daily antiviral prescriptions and influenza-coded visits were (0.70); ILI visits (0.64), and respiratory illness visits (0.62), respectively; and for azithromycin prescriptions 0.77, 0.98, and 0.97 respectively. Oseltamivir and zanamivir prescriptions only increased in 2010-2011 starting with week 51 and peaking week 6 and in 2011-2012 starting with week 8 and peaking week 14. However, azithromycin prescriptions tracked better across the entire influenza season (peaking at weeks 1-2 for both influenza seasons).

Conclusions

VA outpatient prescription data indicated that significantly more ILI and respiratory syndrome visits occurred compared to antiviral prescriptions dispensed with marginal temporal correlation between visits and antiviral prescriptions. Reasons for this finding require further investigation. Although we did not chart review the visit code and antimicrobial prescription in individual records, possible factors may be related to later presentation of cases, perceived lack of efficacy of antivirals, or insufficient coding of influenza. Thus, antiviral prescription data provided minimal additional information for influenza trend monitoring in VA although may still be useful a marker of more severe illness. Interestingly, azithromycin use tracked better with the onset and peaks of the influenza season. Further investigation is also needed to determine whether patients with influenza-specific coded encounters were also prescribed azithromycin and why relatively few encounters were coded with an influenza-specific code.

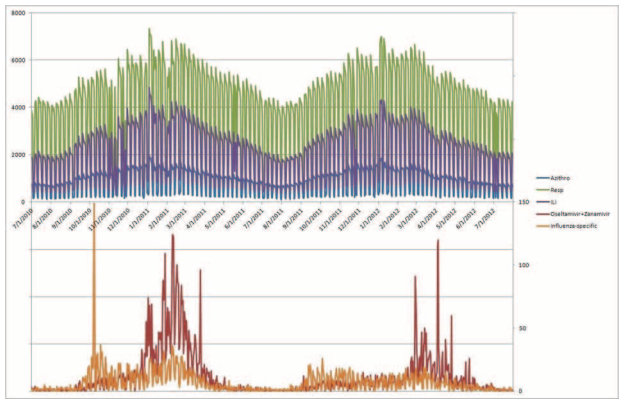


Figure 1: Daily respiratory (Resp) [green], Influenza-like Illness (ILI) [purple], and Influenza-specific [yellow] encounters compared to azithromycin (Azithro) [blue] and oseltamivir and zanamivir [red] orders in VA facilities nationally from July 1, 2010-July 31, 2012.

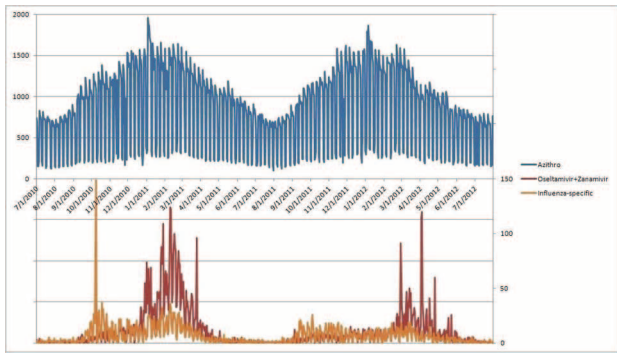


Figure 2: Detailed view of daily influenza-specific coded encounters [yellow] and azithromycin (azithro) [blue], oseltamivir and zanamivir [red] orders in VA facilities nationally from July 1, 2010-July 31, 2012.

Keywords

ESSENCE; Surveillance; Influenza; Veterans; Antimicrobials

*Patricia Schirmer
E-mail: patricia.schirmer@va.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Utilization of Various Data Sources to Locate West Nile Clusters in Tulsa County

Nicole Schlaefli*[2], Kiran Duggirala[2] and Scott Meador[1]

[1]Tulsa City-County Health Department, Enviromental Health Program, Tulsa, OK, USA; [2]Tulsa City-County Health Department, Health, Data, and Evaluation Divison, Tulsa, OK, USA

Objective

Identify, analyze, and summarize WNV in Tulsa County, Oklahoma

Introduction

As the summer temperatures soared to their highest ever recorded, Oklahoma experienced its highest disease count ever since the disease had been discovered in New York in 1999. Tulsa County is the second most populous county in Oklahoma and accounted for over one-fourth of the West Nile Cases in Oklahoma. Tulsa City County Health Department is also the only funded mosquito control program in the state that regularly reports to CDC's AborNet.

Methods

As part of the mosquito surveillance program run by TCCHD's Environmental Health Program, 75 mosquito traps are placed around the county. The traps are tested once a week during the season which runs May to November. The areas that the traps are located in are then sprayed with mosquito repellent. The EHP also gathers addresses of the West Nile positive persons that are reported to the Epidemiology Department. The positive trap locations and the human case addresses are then mapped onto a geographic representation map of Tulsa County using ArcGIS ArcMap 10.0 software.Historical trend analysis data of past West Nile cases by year, age, location and climate are then compared to the current year.

Results

From interviews conducted with West Nile positive human cases, the majority of cases reported the likelihood of being bitten on their property. Once the human case locations were overlaid with positive trap locations and a map of the storm drain system in Tulsa County, clusters formed and areas that needed to be sprayed were identified.

Conclusions

Recommendations are made throughout the season to community officials based on analysis and results found. Lessons learned from the outbreak response conducted included:

Addition of larvacidal treatment of Tulsa County Storm drainage system

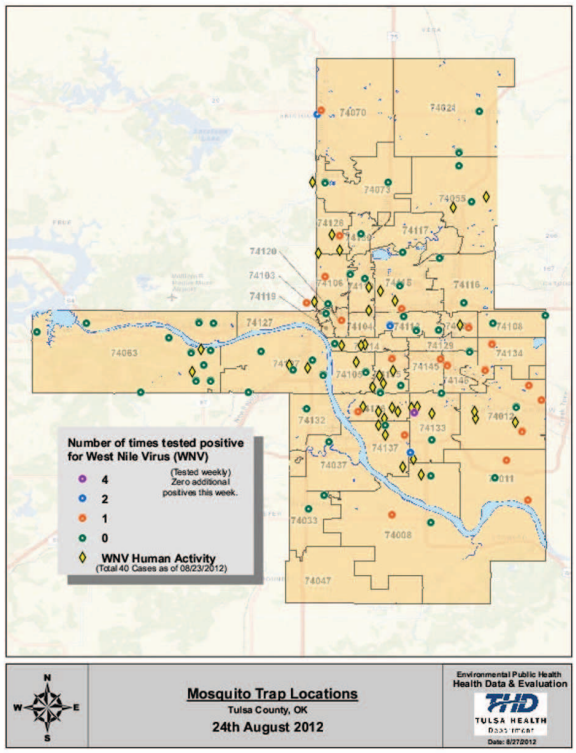
Aggressive marketing campaign in regards to prevention methods

Purpose and role of Long Term Acute Care centers in regards to human recovery

Proposed creation of a West Nile Survivors Group

West Nile Virus Disease

	Mosquito Traps	Positive Mosquito Traps (%)	WNV Fever	WNV Neuroinvasive	Total # (Rate per 100,000)	Hospitalizations Due to WNV	Deaths Due to WNV	WNV Blood Donors
Oklahoma			47	71	118 (3.1)	74	7	35
Tulsa County	75	55 (73%)	8	21	29 (4.8)	16	2	6



Keywords

Surveillance; West Nile; Mosquito

Acknowledgments

Christie McDonald-Hamm, MPH; Surveillance Officer, Department of Informatics; Oklahoma State Department of Health

References

Tulsa County, Oklahoma Public Works Department

Public Health Investigation of Disease Database in Oklahoma (PHIDDO)

Mosquito Database, Environmental Health Program, Tulsa City County Health Department

http://www.cdc.gov/ncdod/dvbid/westnile/index.htm

Centers for Disease Control and Prevention, U.S. Environmental Protection Agency, National Oceanic and Atmospheric Agency, and American Water Works Association. 2010. When every drop counts: protecting public health during drought conditions— a guide for public health professionals. Atlanta: U.S. Department of Health and Human Services.

*Nicole Schlaefli
E-mail: nschlaefli@tulsa-health.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Detecting Changes in Chief Complaint Word Count: Effects on Syndromic Surveillance

Jessica Sell*, Robert Mathes and Marc Paladini

NYC Department of Health and Mental Hygiene, Long Island City, NY, USA

Objective

To identify changes in emergency department (ED) syndromic surveillance data by analyzing trends in chief complaint (CC) word count; to compare these changes to coding changes reported by EDs; and to examine how these changes might affect the ability of syndromic surveillance systems to identify syndromes in a consistent manner.

Introduction

The New York City (NYC) Department of Health and Mental Hygiene (DOHMH) receives daily ED data from 49 of NYC's 52 hospitals, representing approximately 95% of ED visits citywide. Chief complaint (CC) is categorized into syndrome groupings using text recognition of symptom key-words and phrases. Hospitals are not required to notify the DOHMH of any changes to procedures or health information systems (HIS). Previous work noticed that CC word count varied over time within and among EDs. The variations seen in CC word count may affect the quality and type of data received by the DOHMH, thereby affecting the ability to detect syndrome visits consistently.

Methods

The daily mean number of words in the chief complaint field were examined by hospital from 2008-2011. Spectral analyses were performed on daily CC word count by hospital to explore temporal trends. Change Point Analysis (CPA) using Taylor's Method with a maximum change level of four was conducted on the CC field by hospital using 1,000 bootstrap samples. According to Taylor, a level one change is the most important change detected on the program's first pass through the data. For this analysis, a change point was considered significant if it was level 1, detected an average change of more than 0.50 words per day, and was sustained for at least 6 months before a level 2 change of at least 0.50 words occurred. Results of the CPA were compared to reported changes identified by a survey conducted by DOHMH staff of 49 hospitals that collected information about their HIS and coding practices, including any recent system changes.

When a significant level one change was identified, time series graphs for six months before and after the change were created for five syndromes (cold, diarrhea, fever-flu, influenza-like-illness, and respiratory) and the syndrome's constituent symptom categories (e.g. cough fever, etc.). Changes in syndrome count and composition at the level one change in word count were noted.

Results

The mean chief complaint word count across all hospitals from 2008 – 2011 in NYC was 3.14, with a range of 0 to 18 words. CPA detected a significant level 1 change in 21 hospitals, with a mean change of 0.60 words, with 9 increases (mean= 0.71 words) and 12 decreases (mean= 0.53 words). According to the results of a survey of 49 NYC EDs, 19 have changed coding practices or Health Information Systems since 2008. CPA identified a coincident and significant shift in word count for 8 of these hospitals. CPA also detected significant shifts in word count for 13 hospitals that did not report any changes. Figure 1 shows the results of CPA from one ED in NYC

We observed immediate changes in daily syndrome count after the detected change in CC word count. For example, respiratory syndrome count increased with increased word count and decreased with decreased word count for 10 of the 21 EDs with a significant change in word count. Only 2 EDs saw an opposite effect on respiratory syndrome count. Meanwhile, 9 EDs saw no obvious change in respiratory syndrome count. Furthermore, these changes in daily CC word count coincided with subsequent changes in syndrome composition, the breakdown of syndromes into constituent symptoms.

Conclusions

Change Point Analysis may be a useful method for prospectively detecting shifts in CC word count, which might represent a change in ED practices. In some instances changes to CC word count had an apparent effect on both syndrome capture and syndrome composition. Further studies are required to determine how often these changes happen and how they may affect the quality of syndromic surveillance.

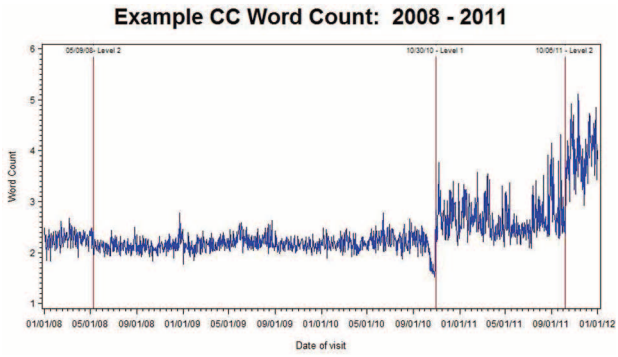


Figure 1: Mean daily CC word count with CPA results marked.

Keywords

Chief Complaint; Word Count; Change Point Analysis

References

Taylor, W. A. (2000)."Change-Point Analysis: A Powerful Tool for Detecting Changes". Retrieved July 5, 2012, from http://www.variation.com/cpa/tech/changepoint.html

*Jessica Sell
E-mail: jsell@health.nyc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Survey of Data Recording Procedures at New York City Emergency Departments

Jessica Sell*[1] and Alyssa Wong[2]

[1]NYC Department of Health and Mental Hygiene, Long Island City, NY, USA; [2]Columbia University, Mailman School of Public Health, New York, NY, USA

Objective

To describe the development, implementation, and analysis of a hospital based emergency department (ED) survey and site visit project conducted by the New York City (NYC) Department of Health and Mental Hygiene (DOHMH).

Introduction

Data is collected daily by the DOHMH from 49 of the 52 NYC EDs, representing approximately 95% of all ED visits in NYC. Variability in data fields between and within EDs has been noticed for some time. Differences in chief complaint (CC) characteristics and inconsistent availability of data elements, such as disposition and diagnosis, suggest that procedures, coding practices and health information systems (HIS) are not standardized across all NYC EDs, and may change within EDs. These differences may have an unapparent effect on the DOHMH's ability to consistently categorize ED visits into syndrome groupings, which may alter how syndromic trends are analyzed. Prior to this project, the DOHMH had no method in place to regularly capture, evaluate or utilize this level of ED-specific information.

Methods

A member of the DOHMH contacted all 49 EDs to request a brief interview with the ED director, administrator and/or appropriate staff. A questionnaire was designed to collect the following information about each ED: the clinical and administrative HIS used to collect patient information and report it to the DOHMH (including any recent system changes); CC coding practices (i.e. who records the CC, and into which HIS, and in what format); disposition and diagnosis recording practices and availability. Questions regarding hospital specific trends and characteristics were also included. Interviews were conducted in person by two members of the DOHMH.

Information from the survey was compiled into a Microsoft Excel spreadsheet by the interviewers. A descriptive analysis was performed comparing and detailing HIS used, CC coding practices, and recording procedures for disposition and diagnosis. A member of the DOHMH followed up with ED staff and IT personnel to resolve any outstanding data quality issues.

Results

All 49 EDs were contacted and interviewed. A median of 43 days (ranging from 7 to 167) elapsed between the initial attempt to contact the ED director, and the completion of the interview. All interviews lasted approximately 40 minutes.

According to the results of the survey, the DOHMH receives information from the clinical HIS from approximately 20% of EDs, from the administrative HIS from approximately 70% of the EDs, and approximately 10% of the EDs did not know which system was used to generate the daily reports sent to the DOHMH. Nearly 100% of the EDs reported that the chief complaint was entered into the clinical HIS by a triage nurse. However, it is not known who records the CC into the administrative system. Four EDs reported that a drop-down menu is used to record CC into the clinical HIS, 23 EDs CC is in free-text format, and 22 EDs CC is a combination of free-text and drop-down format.

Diagnosis was recorded by the physician at 45% of the EDs, and by other staff, including nurses and clerks, at 55% of the EDs. Two thirds of the EDs reported a lag time of less than one week between the visit and assignment of diagnosis codes. Disposition is recorded by the physician at 80% of EDs. Discharge disposition is often required for a patients chart to be considered complete.

As a result of the visits the DOHMH was able to better understand problems that cause routine data quality problems (e.g. missing data or unusable data) by hospital and identify methods to improve those problems. Missing and up to date disposition codebooks were obtained from hospitals. Current hospital contacts were identified for follow up.

Discussions with hospital personnel regarding specific trends, characteristics and interests helped to strengthen the relationship the DOHMH has with the hospital ED staff.

Conclusions

Differences in practices, procedures, and HIS used can lead to variability in data quality and characteristics which may affect the ability to categorize visits into effective syndrome groupings and understand trends. Further research is needed to develop an improved method for analyzing ED data that takes ED-specific characteristics into consideration. Additionally, it is important to establish good working relationships with key members of each ED's staff in the event of a possible outbreak, and in keeping up to date on any changes within each ED that may affect data quality.

Keywords

Emergency Department; Syndromic Surveillance; Coding Practices

Acknowledgments

NYC DOHMH
Alfred P. Sloan Foundation

*Jessica Sell
E-mail: jsell@health.nyc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Bayesian Contact Tracing for Communicable Respiratory Disease

Ayman Shalaby* and Daniel Lizotte

University of Waterloo, Waterloo, ON, Canada

Objective

The purpose of our work is to develop a system for automatic contact tracing with the goal of identifying individuals who are most likely infected, even if we do not have direct diagnostic information on their health status. Control of the spread of respiratory pathogens (e.g. novel influenza viruses) in the population using vaccination is a challenging problem that requires quick identification of the infectious agent followed by large-scale production and administration of a vaccine. This takes a significant amount of time. A complementary approach to control transmission is contact tracing and quarantining, which are currently applied to sexually transmitted diseases (STDs). For STDs, identifying the contacts that might have led to disease transmission is relatively easy; however, for respiratory pathogens, the contacts that can lead to transmission include a huge number of face-to-face daily social interactions that are impossible to trace manually.

Introduction

The evolution of novel influenza viruses in humans is a bio- logical phenomenon that can not be stopped. All existing data suggest that vaccination against the morbidity and mortality of the novel influenza viruses is our best line of defence. Unfortunately, vaccination requires that the infectious agent to be quickly identified and a safe vaccine in large quantities is produced and administered. As was witnessed with the 2009 H1N1 influenza pandemic, these steps took a frustratingly long period during which the novel influenza virus continued its unstoppable and rapid global spreading.

In addition to the different vaccination strategies (e.g. random mass vaccination, age structured vaccination), isolation and quarantining of infected individuals is another effective method used by the public health agencies to control the spreading of infectious diseases. Isolation is effective against any infectious disease, however it can be very hard to detect infectious individuals in the population when:

1. Symptoms are ambiguous or easily misdiagnosed (e.g. 2009 H1N1 influenza outbreak shared many symptoms with many other influenza like illnesses)

2. When the symptoms emerge after the individual become infectious.

Methods

We developed a dynamic Bayesian network model to process sensor information from users' cellphones together with (possibly incomplete) diagnosis information to track the spread of disease in a population. Our model tracks real-time proximity contacts and can provide public health agencies with the probability of infection for each individual in the model.

For testing our algorithm, we used a real-world mobile sensor dataset with 120 individuals collected over a period of 9 months, and we simulated an outbreak.

Results

We ran several experiments where different sub-populations were "infected" and "diagnosed." By using the contact information, our model was able to automatically identify individuals in the population who were likely to be infected even though they were not directly "diagnosed" with an illness.

Conclusions

Automatic contact tracing for respiratory pathogens is a powerful idea, however we have identified several implementation challenges. The first challenge is scalability: we note that a contact tracing system with a hundred thousand individuals requires a Bayesian model with a billion nodes. Bayesian inference on models of this scale is an open problem and an active area of research. The second challenge is privacy protection: although the test data were collected

in an academic setting, deploying any system will require appropriate safeguards for user privacy. Nonetheless, our work llustrates the potential for broader use of contact tracing for modeling and controlling disease transmission.

Keywords

Outbreak Detection; Syndromic Surveillance; Mobile; Contact Tracing; Bayesian Algorithms

*Ayman Shalaby
E-mail: aymanshalaby11@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

ISDS 2012 Conference Abstracts

SAGES Update: Electronic Disease Surveillance in Resource-Limited Settings

Lewis L. Sheri, Timothy C. Campbell, Jacqueline S. Coberly, Richard A. Wojcik, Shraddha V. Patel and Brian Feighner*

Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA

Objective

The Suite for Automated Global Electronic bioSurveillance (SAGES) is a collection of modular, flexible, open-source software tools for electronic disease surveillance in resource-limited settings. This demonstration will illustrate several new innovations and update attendees on new users in Africa and Asia.

Introduction

The new 2005 International Health Regulations (IHR), a legally binding instrument for all 194 WHO member countries, significantly expanded the scope of reportable conditions and are intended to help prevent and respond to global public health threats. SAGES aims to improve local public health surveillance and IHR compliance with particular emphasis on resource-limited settings. More than a decade ago, in collaboration with the US Department of Defense (DoD), the Johns Hopkins University Applied Physics Laboratory (JHU/APL) developed the Electronic Surveillance System for the Early Notification of Community-based Epidemics (ESSENCE). ESSENCE collects, processes, and analyzes non-traditional data sources (i.e. chief complaints from hospital emergency departments, school absentee data, poison control center calls, over-the-counter pharmaceutical sales, etc.) to identify anomalous disease activity in a community. The data can be queried, analyzed, and visualized both temporally and spatially by the end user. The current SAGES initiative leverages the experience gained in the development of ESSENCE, and the analysis and visualization components of SAGES are built with the same features in mind.

Methods

SAGES tools are organized into four categories: 1) data collection, 2) analysis & visualization, 3) communications, and 4) modeling / simulation / evaluation. Within each category, SAGES offers a variety of tools compatible with surveillance needs and different types or levels of information technology infrastructure. SAGES tools are built in a modular nature, which allows for the user to select one or more tools to enhance an existing surveillance system or use the tools *en masse* for an end-to-end electronic disease surveillance capability. Thus, each locality can select tools from SAGES based upon their needs, capabilities, and existing systems to create a customized electronic disease surveillance system. New OpenESSENCE developments include improved data query ability, improved mapping functionality, and enhanced training materials. New cellular phone developments include the ability to concatenate single SMS messages sent by simple or Smart Android cell phones. This 'multiple-SMS' message ability allows use of SMS technology to send and receive health information exceeding normal SMS message length in a manner transparent to the users.

Conclusions

The SAGES project is intended to enhance electronic disease surveillance capacity in resource-limited settings around the world. We have combined electronic disease surveillance tools developed at JHU/APL with other freely-available, interoperable software tools to create SAGES. We believe this suite of tools will facilitate local and regional electronic disease surveillance, regional public health collaborations, and international disease reporting. SAGES development, funded by the US Armed Forces Health Surveillance Center, continues as we add new international collaborators. SAGES tools are currently deployed in locations in Africa, Asia and South America, and are offered to other interested countries around the world.

Keywords

software; surveillance; electronic; open-source

*Brian Feighner
E-mail: brian.feighner@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Novel Syndrome Definition Validation Approach for Rarely Occurring Diseases

Julio C. Silva[1], Shital C. Shah[1], Dino P. Rumoro[1], Marilyn M. Hallock[1], Gillian S. Gibbs*[1] and Michael J. Waddell[2]

[1]Rush University, Chicago, IL, USA; [2]Pangaea Information Technologies, Chicago, IL, USA

Objective

To develop and test a novel syndrome definition validation approach for rarely occurring diseases.

Introduction

Early detection of rarely occurring but potentially harmful diseases such as bio-threat agents (e.g., anthrax), chemical agents (e.g., sarin), and naturally occurring diseases (e.g., meningitis) is critical for rapid initiation of treatment, infection control measures, and emergency response plans. To facilitate clinicians' ability to detect these diseases, various syndrome definitions have been developed. Due to the rarity of these diseases, standard statistical methodologies for validating syndrome definitions are not applicable.

Methods

Syndrome definitions were developed by researchers for the Geographic Utilization of Artificial Intelligence in Real-Time for Disease Identification and Alert Notification (GUARDIAN) surveillance system (1). The main steps for validation of the syndrome definitions were:

1) Partition of literature articles: Literature articles that described positive cases were randomly divided to generate detection (75% of articles) and testing (25% of articles) syndrome definitions.

2) Synthetic case generation: Syndrome definitions and associated statistical measures were reverse engineered using probability of occurrence and inverse Gaussian function to generate potentially infinite positive artificial cases.

3) Clinical filter application: To avoid clinically incompatible combinations of newly generated symptoms, rules based on clinically guided knowledge from emergency department (ED) physicians were applied. Steps 2 and 3 were repeated for both detection and testing syndrome definitions.

4) Detection phase validation:

a. ED negative case sample: Detection syndrome definitions were tested using a random sample of negative ED cases. Knowledge gained through false positive cases was utilized to modify the surveillance algorithms and system thresholds.

b. 10-fold cross-validation: Standard 10-fold cross-validation on detection articles of positive cases and ED negative cases was utilized to generate performance metrics. Suspected cases were reviewed by ED clinicians for threshold enhancement.

c. Literature articles (n=1): The ability of syndrome definitions to correctly flag literature articles with n=1 case was documented.

5) Testing phase validation:

a. Testing sample: Synthetic positive cases generated from the testing articles along with another set of ED negative cases were evaluated by the respective syndrome definition. Suspected cases were clinically evaluated.

b. Literature articles (n=1): Similar to detection step 4c, articles with n=1 were tested using syndrome definitions.

c. True positive samples: When available, true positive cases from an ED were identified and sent through the GUARDIAN system.

6) Multi-syndrome validation: A combined sample of positive cases of multiple syndromes and ED negative cases were evaluated for detection of individual syndromes among other similar syndromes.

Results

To demonstrate the validation approach, the anthrax syndrome definition was utilized. This syndrome definition was developed with 25 articles containing positive anthrax cases used for detection, and the remaining 11 articles used for testing. With a 10-fold cross validation of the detection phase, the initial results showed accuracy was 99.4% (false positive rate of 0.65% and false negative rate of 0.00%). The testing phase initial validation revealed 99.2% accuracy for the anthrax syndrome definition.

Conclusions

Syndrome specific synthetic samples that are validated through clinical filters allowed the generation of an unlimited number of positive cases. Correct identification by GUARDIAN of these cases indicates robust and reliable syndrome definitions. Utilization of these cases, in conjunction with adherence to a methodological process, was the cornerstone of the GUARDIAN syndrome definition validation approach. The validation approach was successfully demonstrated on anthrax and can be applied to other bio-threat agents, chemical agents, and naturally occurring diseases.

Keywords

syndromic surveillance; bioterrorism; infectious diseases

Acknowledgments

GUARDIAN is funded by US Department of Defense, Telemedicine and Advanced Technology Research Center, Award numbers W81XWH-09-1-0662 and W81XWH-11-1-0711.

References

1. J. Silva, D. Rumoro, M. Hallock, S. Shah, G. Gibbs, M. Waddell, K. Thomas, Disease profile development methodology for syndromic surveillance of biological threat agents, Emerging Health Threats Journal, 2011, 4:11129.

*Gillian S. Gibbs
E-mail: Gillian_Gibbs@rush.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Adaptation of GUARDIAN for Syndromic Surveillance During the NATO Summit

Julio C. Silva[1], Dino P. Rumoro[1], Shital C. Shah[1], Gillian S. Gibbs*[1], Marilyn M. Hallock[1], Michael Waddell[2] and Shon Doseck[2]

[1]Rush University, Chicago, IL, USA; [2]Pangaea Information Technologies, Chicago, IL, USA

Objective

To develop and implement a framework for special event surveillance using GUARDIAN, as well as document lessons learned post-event regarding design challenges and usability.

Introduction

Special event driven syndromic surveillance is often initiated by public health departments with limited time for development of an automated surveillance framework, which can result in heavy reliance on frontline care providers and potentially miss early signs of emerging trends. To address timelines and reliability issues, automated surveillance system are required.

Methods

The North Atlantic Treaty Organization (NATO) summit was held in Chicago, IL, May 19-21, 2012. During the NATO summit, the Chicago Department of Public Health (CDPH) was charged with collecting and analyzing syndromic surveillance data from emergency department (ED) visits that may indicate a man-made or naturally occurring infectious disease threat.

Ten days prior to the NATO summit surveillance period, Rush University Medical Center (RUMC) received a guidance document from CDPH outlining the syndromes for systematic surveillance, specifically febrile rash illness, localized cutaneous lesion, acute febrile respiratory illness, gastrointestinal illness, botulism-like illness, hemorrhagic illness, along with unexplained deaths or severe illness potentially due to infectious disease and cases due to toxins or suspected poisoning. RUMC researchers collected relevant ICD-9 codes for each syndrome category.

GUARDIAN (1), an automated surveillance system, was programmed to scan patient charts and match free text using National Library of Medicine free-text term to unique medical concept, which were further mapped to relevant ICD-9 codes. The baselines were developed using ED patient data from 1/1/2010 to 12/31/2011. Statistical references were established for unsmoothed, 24 hour counts (Baseline = Average; Threshold = +2 standard deviations).

During the NATO surveillance timeframe (May 13- 26, 2012) automated results with prior reporting period's counts, reference statistics, and charts were electronically sent to CDPH. In addition, ED charge nurses made manual surveillance reports by telephone at least daily. Open lines of communication were maintained between RUMC and CDPH during the event to discuss potential positive cases. In addition, a post-event debriefing was conducted to document lessons learned.

Results

The automated GUARDIAN surveillance reports not only provided timely counts of potentially positive cases for each syndrome but also provided trend analysis with baseline measures. The GUARDIAN User Interface was used to explain what data points could trigger positive cases. The Epic system was used to review patient charts, if further explanation was necessary. The observed counts never exceeded +2 standard deviations during the NATO surveillance period for any of the syndromes.

Based on the debriefing meeting between RUMC and CDPH, the top three achievements and lessons learned were as follows:

1. Quick turnaround time (~ 10 days) from surveillance concept development to automated implementation using GUARDIAN
2. Surveillance data was timely and reliable
3. Additional statistical information was beneficial to put trends in context
4. System may be too sensitive resulting in false alarms and additional investigative burden on public health departments
5. Need for development of user-interfaces with drill down capabilities to patient level data
6. Clinicians don't necessarily utilize exact terminology used in ICD-9 codes which could result in undetected cases.

Conclusions

This exercise successfully highlights rapid development and implementation of special event driven automated surveillance as well as collaborative approach between front-line entities such as emergency departments, surveillance researchers, and the department of public health. In addition, valuable lessons learned with potential solutions are documented for further refinements of such surveillance activities.

Keywords

Emergency department; NATO Summit; automated surveillance

Acknowledgments

GUARDIAN is funded by US Department of Defense, Telemedicine and Advanced Technology Research Center, Award numbers W81XWH-09-1-0662 and W81XWH-11-1-0711.

References

J. Silva, D. Rumoro, M. Hallock, S. Shah, G. Gibbs, M. Waddell, K. Thomas, Disease profile development methodology for syndromic surveillance of biological threat agents, Emerging Health Threats Journal, 2011, 4:11129.

*Gillian S. Gibbs
E-mail: Gillian_Gibbs@rush.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using Search Volume for Surveillance of Medication Prescribing

Jacob E. Simmering*, Linnea A. Polgreen and Philip M. Polgreen

University of Iowa, Iowa City, IA, USA

Objective

To validate search volume estimation for outpatient medication prescribing.

Introduction

Investigators have used the volume of internet search queries to model disease incidence, especially influenza and general consumer behavior [1]. Our group has used search volume to model interest in FDA safety alerts and adverse drug event incidence. We found evidence of changes in search behavior following warnings and the expected relationship between search volume and adverse drug event incidence. Thus, search volume may help provide near real time surveillance of drug use patterns to help monitor and mitigate risk to the population from adverse drug events. However, the use of search query volume as a proxy for drug use has yet to be validated.

We attempt to validate search volume estimation of drug utilization in three ways: 1) explore seasonal variations in search volume and outpatient utilization, 2) monitor change between substitute drugs following patent expirations and 3) use search volume estimation methods to estimate TB incidence.

Methods

Google Insights normalized search share was used to characterize interest in a drug. The estimates of drug utilization were derived from the Medical Expenditure Panel Survey (MEPS), a nationally representative sample of the US population. Substitute drugs and notable patent expirations between 2004 and 2011 were obtained via pharmacist review. TB incidence was derived from the MMWR yearly Summary of Notifiable Diseases.

To validate the assumption that search volume relates to drug utilization, we estimated weekly utilization for 9 drugs (amoxicillin, azelastine, azithromycin, benzomatate, cefdinir, ciprofloxacin, levofloxacin, moxifloxacin and olopatadine) using MEPS for 2004-2009. The weekly utilization volume was cross-correlated with the Google Insights series with lags ranging from -6 to +6 months.

To compare the rate of substitution between name brand and generic drugs following the expiration of a patent, we treated the generic drug search volume as the independent variable and the name brand as the dependent variable. Using OLS, we calculated the marginal rate of substitution between the name brand and generic search queries. Preliminary work has focused on substitution of generic simvastatin for branded Zocor.

As TB treatment regimens usually include a fixed set of medications (isoniazid, rifampin, pyrazinamide, ethambutol), the utilization of these drugs should correspond with TB incidence. We modeled national TB incidence using OLS with search volume and an indicator for the month of December. The number of reported cases in December is inconsistent with the seasonality of TB in the US and is a significant departure from the expected value given the rest of the series. We suspect this is due to a reporting artifact and include the indicator variable in our model to mitigate the effects of this inconsistency.

Results

The seasonality of drug use is reflected in search volume. Only 3 of the 9 drugs (33%, amoxicillin, azithromycin and cefdinir) had enough volume in the MEPS to create a reasonable time series. All 3 drugs had statistically significant positive correlations at lags near 0 and significant negative correlations at lags of +/- 6 months. Amoxicillin, for example, had a significant correlation at lags around 0 of 0.55-0.60 and correlations at a lag of -5 or +5 months of -0.4. The magnitude of this correlation coefficient would suggest that the two series track closely.

Patent expirations (and the resulting emergence of generic medications with new names) are apparent in search volume as well. We find a strong negative relationship between search volume for simvastatin and Zocor. Specifically, a one unit increase in search volume for 'simvastatin' is associated with a 0.96 ($p < 0.0001$) unit decrease in the search volume for 'Zocor.'

The simple model for TB incidence demonstrates the utility of using drugs as queries for disease. Search volume was a significant ($p = 0.006$) and positive predictor of TB incidence controlling for the December aberrations.

Conclusions

The Google Insights search volume for a set of highly seasonal drugs is highly correlated with community utilization as measured by seasonal variance in utilization, change in search and prescribing patterns and expected prescribing following TB. The ability to estimate use of drugs from search volume presents a new method for keyword selection in search based incidence models and a method to monitor changes in the pharmaceutical market.

Keywords

pharmacovigilance; web search; prescribing behavior

References

1. Goel, S. et al. (2010) Predicting Consumer Behavior with Web Search. PNAS 104:17486-17490

*Jacob E. Simmering
E-mail: jacob-simmering@uiowa.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Can Novel Flu Surveillance Be Conducted With Limited Resources?

Alan Siniscalchi*[1] and Amanda Schulte[2]

[1]State of CT Dept of Public Health, Hartford, CT, USA; [2]International Society for Disease Surveillance, Boston, MA, USA

Objective

This project was organized to facilitate discussions on whether successful novel flu surveillance can be conducted by jurisdictions with limited resources. The discussions will focus on gathering opinions regarding the best combination of surveillance systems to quickly and efficiently identify the presence of influenza A (H3N2)v and other novel influenza viruses in circulation.

Introduction

The past decade has witnessed rapid development and implementation of numerous syndromic and other advanced surveillance systems to supplement traditional laboratory testing to identify the presence of novel influenza strains and track the impact on local populations. While much of the development and widespread implementation of these systems had been supported by public health preparedness funding, the loss of these monies has greatly constrained the ability of public health agencies to staff and maintain these systems. The periodic appearance of novel flu viruses, such as H3N2v, requires agencies to carefully choose which systems will provide the most cost-effective data to support their public health practice.

Methods

This project will be facilitated by an experienced public health practitioner who has conducted surveillance for a variety of disease agents. Additional public health practitioners are being recruited among members of the International Society for Disease Surveillance (ISDS) Public Health Practice Committee (PHPC) to contribute information on comparative approaches to cost effective surveillance. Questions were selected for discussion and responses will be collected from influenza surveillance coordinators using a web-based survey tool managed by ISDS staff on behalf of the PHPC. Survey responses and subsequent recommendations will be presented at a PHPC meeting.

Results

Initial questions selected for the survey tool and subsequent discussions include:

What surveillance systems does your agency use for conducting influenza surveillance?

Which surveillance systems require trained and experienced public health and informatics staff to maintain?

Is your agency having difficulties in recruiting and retaining trained surveillance staff?

Has influenza A (H3N2)v been identified in your state or jurisdiction?

Does your agency have sufficient staff and other resources to be able to conduct targeted surveillance of novel influenza strains, such as identifying H3N2v cases associated with agricultural fairs or school surveillance for ILI cases?

Which surveillance systems provide useful data for monitoring health impact during seasons with highly pathological influenza strains?

Which surveillance systems provide useful data for identifying the presence of novel influenza strains and conducting situational awareness?

Keywords

situational awareness; influenza surveillance; H3N2v; resource limitations

*Alan Siniscalchi
E-mail: alan.siniscalchi@ct.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Applying Zero-inflated Mixed Model to School Absenteeism Surveillance in Rural China

Xiaoxiao Song[1], Tao Tao[1], Qi Zhao[1], Fuqiang Yang[2], Palm Lars[3], Diwan Vinod[4], Hui Yuan[2] and Biao* Xu[1]

[1]School of Public Health, Fudan University, Shanghai, China; [2]Jiangxi Provincial Center for Disease Prevention and Control, nanchang, China; [3]Future Position X, Gavle, Sweden; [4]ICHAR, Karolinska Instituet, Stockholm, Sweden

Objective

To describe and explore the spatial and temporal variability via ZIMM for absenteeism surveillance in primary school for early detection of infectious disease outbreak in rural China.

Introduction

Absenteeism has great advantages in promoting the early detection of epidemics1. Since August 2011, an integrated syndromic surveillance project (ISSC) has been implemented in China2. Distribution of the absenteeism generally are asymmetry, zero inflation, truncation and non-independence3. For handling these encumbrances, we should apply the Zero-inflated Mixed Model (ZIMM).

Methods

Data for this study was obtained from the web-based data of ISSC in 62 primary schools in two counties of Jiangxi province, China from April 1th, 2012 to June 30st, 2012. The ZIMM was used to explore: 1)the temporal and spatial variability regarding occurrence and intensity of absenteeism simultaneously, and 2) the heterogeneity among the reporting primary schools by introducing random effects into the intercepts. The analyse was processed in the SAS procedure NLMIXED4.

Results

The total 4914 absenteeism events were reported in the 62 primary schools in the study period. The rate of zero report was 49.88% (Fig.1). According to ZIMM, there are fixed and random effect parameters in this model (Table 1). Firstly, for the fixed parameters, the spatial variable (county) was not significantly different both the occurrence and intensity model, while for the temporal variable (month), the probability of absenteeism occurrence was significantly different over three months (β=-0.165, p =0.026), suggesting a decreasing of school absenteeism from April to June. Meanwhile, a statistical significant difference in the intensity of absenteeism was also found over the three months (β=-0.073, p=0.007). Secondly, the random effect of intensity model was statistically significance (p=0.008), which strongly indicated a heterogeneity in intensity of absenteeism among the surveillance schools. Whereas the random effect of occurrence model by logistic regression showed a non-statistical difference (p=0.774) among the schools suggesting the homogeneity in the occurrence of absenteeism.

Conclusions

School absenteeism data has greater uncertain than many other sources and easier fluctuate by some factors such as holiday, season, family status and geographic distribution. Thus, the spatial and temporal dynamics should be taken into account in controlling fluctuate of absenteeism. Moreover, school absenteeism data are correlated within each school due to repeated measures. Applying the ZIMM, the occurrences and intensity of absenteeism could be evaluated to reduce the bias and improve the prediction precision. The ZIMM is an appropriate tool for health authorities in decision making for public health events.

Table 1 Fixed parameters and variance components estimates for the absenteeism using ZIMM

		Logistic regression parameter with occurrence			lognormal regression parameter with intensity		
parameters		β	Std Err	p value	β	Std Err	p value
Fixed parameters	Intercept	-0.733	0.262	0.005	0.718	0.039	0.000
	county	-0.188	0.103	0.068	-0.020	0.042	0.632
	month	-0.165	0.074	0.026	-0.073	0.027	0.007
Variance components	Var(Randdm Effect)	0.548	1.906	0.774	0.316	0.120	0.009
	Residual				0.120	0.119	0.313

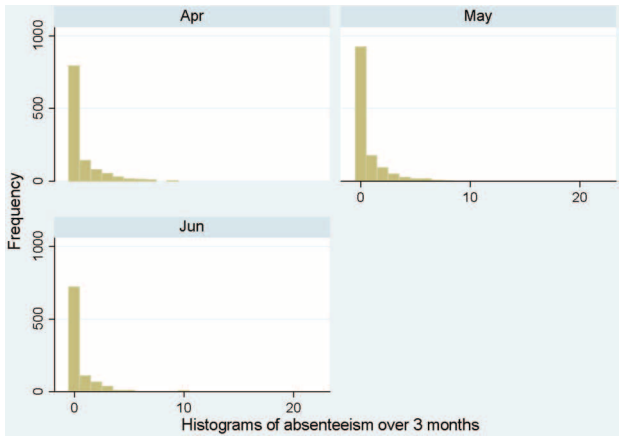


Fig. 1 Absenteeism from Apr. 1st to Jun. 30th 2012

Keywords

surveillance; absenteeism; zero-inflated mixed model; occurrence; intensity

References

1. Lenert L, Kirsh D, Johnson J, Aryel RM. Absenteeism. In: Wagner MM, Moore AW, Aryel RM, editors. Handbook of Biosurveillance Burlington: Academic Press, 2006:361-68.
2. Yan W-r, Nie S-f, Xu B, Dong H-j, Palm L, Diwan VK. Establishing a web-based integrated surveillance system for early detection of infectious disease epidemic in rural China: a field experimental study. Bmc Medical Informatics and Decision Making 2012;12.
3. Calama R, Mutke S, Tome J, Gordo J, Montero G, Tome M. Modelling spatial and temporal variability in a zero-inflated variable: The case of stone pine (Pinus pinea L.) cone production. Ecological Modelling 2011;222(3):606-18.
4. Tooze JA, Grunwald GK, Jones RH. Analysis of repeated measures data with clumping at zero. Statistical Methods in Medical Research 2002;11(4):341-55.

*Biao Xu
E-mail: bxu@shmu.edu.cn

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

When it Rains it Pours: Real-time Situational Awareness for Two Weather Emergencies in Connecticut

Kristen Soto*, Jaime Krasnitski, Therese Rabatsky-Ehr and Matthew Cartter

Epidemiology, Connecticut Department of Public Health, Hartford, CT, USA

Objective

To characterize the utility of the Connecticut Hospital Emergency Department Syndromic Surveillance (HEDSS) system for real-time situational awareness during two weather-related emergencies.

Introduction

On August 28, 2011 Tropical Storm Irene made landfall in Connecticut. On October 29, 2011 Connecticut was impacted by Winter Storm Alfred. Both of these storms included high winds and heavy precipitation which resulted in prolonged power outages, disruption of public drinking water systems, property damage, and widespread debris throughout the state. The HEDSS System was utilized to provide real-time situational awareness during the response and recovery phases of both storm events.

Methods

The HEDSS System receives electronic patient abstract data from 21 of 32 emergency departments on a daily basis. Free-text chief complaint data are characterized into syndrome categories. ED visits for carbon monoxide exposure (CO), gastrointestinal illness (GI), injury, hypothermia, motor vehicle accidents (MVA), and asthma syndromes were monitored throughout the response and recovery periods of both storm. Odds Ratios were calculated using the two weeks pre- and post-storm as reference dates. CO visits were further assessed for geographic and demographic trends to target public health messages. The HEDSS system was evaluated to make recommendations for event monitoring during future public health emergencies.

Results

Following both storms there was a high completeness of daily HEDSS reporting despite extensive power outages (96% post-tropical storm, 91% post-winter storm). Increased emergency department utilization for CO (OR: 26.20, 95% CI: 3.57-192.64) was observed post-tropical storm. Increased emergency department utilization for CO (OR: 14.61, 95% CI: 7.43-28.72), hypothermia (OR: 17.02, 95% CI: 3.01-359.30), and asthma (OR: 1.17, 95% CI: 1.05-1.30) were observed following the winter storm. Regional increases in ED utilization for injuries and MVA were observed following both storm events; no increase in GI was associated with either storm event.

During the 2 weeks post-tropical storm 28 cases of CO exposure were reported through HEDSS and 5 cases through laboratory surveillance; during the winter storm 131 cases were reported through HEDSS and 162 through reportable disease surveillance. Of the 167 cases reported through laboratory surveillance, 111 (66%) were from hospitals that sent data to HEDSS hospitals and 94(56%) were able to be matched to a specific ED record; of these 22(20%) were characterized as visiting the ED for CO syndrome, 13(14%) had symptoms consistent with CO as their chief complaint, 11(12%) had smoke/gasoline inhalation exposures as their chief complaint and 2(2%) had unrelated chief complaints. During the post-storm period the HEDSS systems detected 137 potential CO exposures that were not reported through laboratory surveillance.

Conclusions

Tropical Storm Irene and Winter Storm Alfred both had significant health impacts, particularly increased ED utilization for CO due to prolonged power outages. The HEDSS system is the only all-hazards surveillance system that was able to provide near-real time information during the storm response phase. In addition to the current CO syndrome definition, where the chief complaint must specifically mention the term CO, a broader definition should also be used in the future to better assess the magnitude of CO-related exposures. The broad definition should include symptomology and related exposures, such as smoke inhalation, to improve case detection. The HEDSS system should continue to be used in conjunction with reportable disease surveillance for situational monitoring during public health emergencies.

Keywords

emergency department; public health practice; syndromic surveillance; carbon monoxide; weather

Acknowledgments

Patricia Przysiecki, MPH; Brian Toal, MSPH

References

1. Witt Associates. Connecticut October 2011 Snowstorm Power Restoration Report. December 21, 2011.http://www.wittassociates.com/assets/860/CTPowerRestorationReport20111201_FINAL_1_.pdf

*Kristen Soto
E-mail: kristen.soto@ct.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Spatial Scan Statistics for Models with Excess Zeros and Overdispersion

Max Sousa de Lima[2], Luiz H. Duczmal*[1] and Letícia P. Pinto[1]

[1]Universidade Federal de Minas Gerais, Belo Horizonte, Brazil; [2]Universidade Federal do Amazonas, Manaus, Brazil

Objective

To propose a more realistic model for disease cluster detection, through a modification of the spatial scan statistic to account simultaneously for inflated zeros and overdispersion.

Introduction

Spatial Scan Statistics [1] usually assume Poisson or Binomial distributed data, which is not adequate in many disease surveillance scenarios. For example, small areas distant from hospitals may exhibit a smaller number of cases than expected in those simple models. Also, underreporting may occur in underdeveloped regions, due to inefficient data collection or the difficulty to access remote sites. Those factors generate excess zero case counts or overdispersion, inducing a violation of the statistical model and also increasing the type I error (false alarms). Overdispersion occurs when data variance is greater than the predicted by the used model. To accommodate it, an extra parameter must be included; in the Poisson model, one makes the variance equal to the mean.

Methods

Tools like the Generalized Poisson (GP) and the Double Poisson [2] may be a better option for this kind of problem, modeling separately the mean and variance, which could be easily adjusted by covariates. When excess zeros occur, the Zero Inflated Poisson (ZIP) model is used, although ZIP's estimated parameters may be severely biased if nonzero counts are too dispersed, compared to the Poisson distribution. In this case the Inflated Zero models for the Generalized Poisson (ZIGP), Double Poisson (ZIDP) and Negative Binomial (ZINB) could be good alternatives to the joint modeling of excess zeros and overdispersion. By one hand, Zero Inflated Poisson (ZIP) models were proposed using the spatial scan statistic to deal with the excess zeros [3]. By the other hand, another spatial scan statistic was based on a Poisson-Gamma mixture model for overdispersion [4]. In this work we present a model which includes inflated zeros and overdispersion simultaneously, based on the ZIDP model. Let the parameter p indicate the zero inflation. As the the remaining parameters of the observed cases map and the parameter p are not independent, the likelihood maximization process is not straightforward; it becomes even more complicated when we include covariates in the analysis. To solve this problem we introduce a vector of latent variables in order to factorize the likelihood, and obtain a facilitator for the maximization process using the E-M (Expectation-Maximization) algorithm. We derive the formulas to maximize iteratively the likelihood, and implement a computer program using the E-M algorithm to estimate the parameters under null and alternative hypothesis. The p-value is obtained via the Fast Double Bootstrap Test [5].

Results

Numerical simulations are conducted to assess the effectiveness of the method. We present results for Hanseniasis surveillance in the Brazilian Amazon in 2010 using this technique. We obtain the most likely spatial clusters for the Poisson, ZIP, Poisson-Gamma mixture and ZIDP models and compare the results.

Conclusions

The Zero Inflated Double Poisson Spatial Scan Statistic for disease cluster detection incorporates the flexibility of previous models, accounting for inflated zeros and overdispersion simultaneously.

The Hanseniasis study case map, due to excess of zero cases counts in many municipalities of the Brazilian Amazon and the presence of overdispersion, was a good benchmark to test the ZIDP model. The results obtained are easier to understand compared to each of the previous spatial scan statistic models, the Zero Inflated Poisson (ZIP) model and the Poisson-Gamma mixture model for overdispersion, taken separetely. The E-M algorithm and the Fast Double Bootstrap test are computationally efficient for this type of problem.

Keywords

Scan statistics; Zero inflated; Overdispersion; Expectation-Maximization algorithm

Acknowledgments

The authors acknowledge the grants provided by FAPEAM and CNPq.

References

[1] Kulldorff, M. (1999). Spatial scan statistics: Models, calculations and applications, in J. Glaz & N. Balakrishnan (eds), Scan Statistics and Applications, Springer Netherlands, pp. 303–322.

[2] Efron, B. (1986) Double Exponential Families and Their Use in Generalized Linear Regression, Journal of the American Statistical Association, 81, pp. 709-721.

[3] Cançado A., da Silva C. and da Silva M.(2011) A zero-inflated Poisson-based spatial scan statistic. Emerging Health Threats Journal, 2011;4:

[4] Zhang T., Zhang Z.; Lin G.(2012) Spatial scan statistics with overdispersion. Statistics in Medicine,31(8):762-774.

[5] Davidson, R. and J. G. MacKinnon (2001). "Improving the reliability of bootstrap tests", Queen's University Institute for Economic Research Discussion Paper No. 995, revised.

*Luiz H. Duczmal
E-mail: duczmal@ufmg.br

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Tracking Dynamic Water-borne Outbreaks with Temporal Consistency Constraints

Skyler Speakman*, Yating Zhang and Daniel B. Neill

Carnegie Mellon University, Pittsburgh, PA, USA

Objective

We describe a novel graph-based event detection approach which can accurately identify and track dynamic outbreaks (where the affected region changes over time). Our approach enforces soft constraints on temporal consistency, allowing detected regions to grow, shrink, or move while penalizing implausible region dynamics. Using simulated contaminant plumes diffusing through a water distribution system, we demonstrate that our method improves both detection time and spatial-temporal accuracy when tracking dynamic water-borne outbreaks.

Introduction

Space-time scan statistics are often used to identify emerging spatial clusters of disease cases [1,2]. They operate by maximizing a score function (likelihood ratio statistic) over multiple spatio-temporal regions. The temporal component is typically incorporated by aggregating counts across a given time window, thus assuming that the affected region does not change over time. To relax this hard constraint on spatial-temporal "shape" and increase detection power and accuracy when tracking spreading outbreaks, we implement a new graph-based event detection approach which enables identification of dynamic clusters while enforcing temporal consistency constraints between temporally-adjacent spatial regions.

Methods

In the subset scanning framework, temporal consistency constraints may be interpreted as influencing the prior probability p_i^t of location i being included in the optimal spatial subset at time t. We model this prior probability for each location as

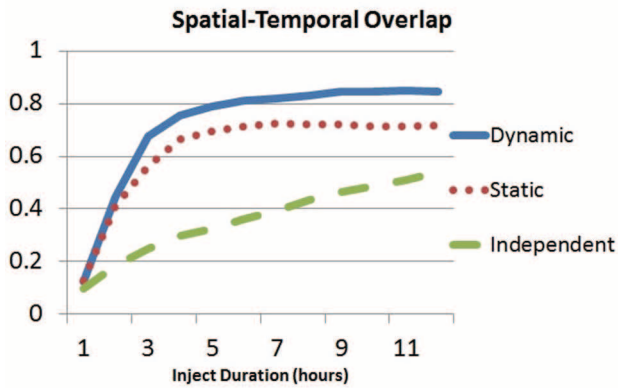
$\log(p_i^t/(1-p_i^t)) = B_0 + B_1 X_i^{t-1}$ where X_i^{t-1} is 1 if location i was included in the previous time step and 0 otherwise, and maximize the penalized log-likelihood ratio over dynamic spatio-temporal regions. Our efficient algorithm incorporates these constraints into the Graph-Scan method [3] by iteratively optimizing the spatial subset for each time slice conditioned on the previous and next slices. Each individual optimization step is made possible by expressing the score function as an additive function (conditioned on the relative risk), which enables the priors to be included while maintaining computational efficiency.

Results

Outbreak plumes were simulated in a water distribution system for 12 one-hour periods. We assumed noisy binary sensors (with 10% false positive and 90% true positive rates) observed hourly at each pipe junction. Our method ("Dynamic") was compared to the "Static" method, which aggregates counts across time for each spatial region and is therefore constrained to only return temporal cylinders, and the "Independent" method, which separately optimizes the spatial subset for each time slice without taking temporal consistency into account. The methods were evaluated on spatial-temporal overlap (Figure 1), defined as the number of sensors contained in both the detected and affected space-time regions divided by the number of sensors in either the detected or affected space-time regions. A measure of 1 is a perfect match of spatial subsets across each time window and 0 would reflect disjoint space-time regions. Additionally, average time to detect an outbreak (at a fixed false positive rate of 1/month) was 4.24, 4.56, and 6.65 hours for the dynamic, static, and independent methods respectively.

Conclusions

Relaxing constraints on spatial-temporal region shape must be done carefully. Allowing independent selection of spatial regions loses important temporal information while hard constraints on the spatial-temporal region will fail to capture the dynamics of the outbreak. Our approach for detecting dynamic space-time clusters, while incorporating temporal consistency constraints, addresses these issues and results in higher spatial-temporal accuracy and detection power.



Spatial-temporal overlap for three competing detection methods.

Keywords

outbreak detection; space-time scan statistics; dynamic event tracking; penalized likelihood ratio

Acknowledgments

This work was partially supported by NSF grants IIS-0916345, IIS-0911032, and IIS-0953330.

References

[1] Kulldorff M. A spatial scan statistic. Communications in Statistics: Theory and Methods, 1997, 26(6): 1481-1496.

[2] Neill DB. Fast subset scan for spatial pattern detection. Journal of the Royal Statistical Society (Series B), 2012, 74(2):337–360.

[3] Speakman S and Neill DB. Fast graph scan for scalable detection of arbitrary connected clusters. Advances in Disease Surveillance, 2010.

*Skyler Speakman
E-mail: skylerspeakman@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Geographical Information Systems: A Tool to Map and Analyze Disease Spread

Indumathi Srinath*[1], Barbara Szonyi[1], Maria Esteve-Gassent[1], Blanca Lupiani[1], Raju Gautam[1], Alfonso Clavijo[2], Sang-shin Park[1] and Renata Ivanek-Miojevic[1]

[1]Texas A &M, College station, TX, USA; [2]Texas Veterinary Medical Diagnostic Laboratories, College station, TX, USA

Objective

Use GIS to illustrate and understand the association between environmental factors and spread of infectious diseases.

Introduction

Spatial methods are an important component of epidemiological research motivated by a strong correlation between disease spread and ecological factors (1). Our case studies examine the relationship between environmental conditions, such as climate and location, and vector distribution and abundance. Therefore, GIS can be used as a platform for integrating local environmental and meteorological variables into the analysis of disease spread, which would help in surveillance and decision making.

Methods

Case study 1- Lyme disease -Lyme disease is a tickborne infection caused by the bacterium Borrelia burgdorferi. The goal of this study was to analyze the association between meteorological factors and Lyme disease risk in humans in Texas. A total of 1,212 cases reported from 138 counties in Texas from Jan 2000 to Dec 2010 were analyzed. We used temperature and precipitation raster grids to generate humidity maps for Texas region. Our results indicated that there is a strong positive association between Lyme disease incidence and humidity, with western cross timbers region having a higher risk then the low plains.

Case study 2- Spinach – Motivated by the recent increase in foodborne outbreaks related to fresh produce, one of the objectives for this study was to use the geospatial analysis to elucidate factors that contribute to contamination of produce at preharvest. We collected 955 spinach samples from 13 produce farms in Colorado and Texas during 2010-2011 and tested the samples for Listeria monocytogenes, Escherichia coli O157:H7 and Salmonella contamination. The spinach contamination results were then used in conjunction with the National Resource Information (NRI) databases along with the SSURGO database to predict environmental and meteorological factors contributing to spinach contamination. Our findings would help to reduce frequency of human foodborne illnesses related to fresh produce.

Case study 3- Valley fever Coccidioidomycosis or Valley Fever (VF) is a fungal zoonosis affecting humans and a variety of animal species. In this study, we used Texas Veterinary Medical Diagnostic Laboratories (TVMDL) data of all dog sera tested for coccidioidomycosis from July 1999 - December 2009. Census data on human population density for Texas were used to determine the dog population density and identify disease clusters for the 5,871 submitted dog sera over a period of 10.5 years. Both the isopleth map of the VF seropositive rates in dogs across Texas and the identified spatial and spatio-temporal clusters of the disease suggested that VF occurs in the western and southwestern part of Texas at a much higher rate than in other areas of the state (2). Since VF is not a reportable disease in TX, dogs could be used as a sentinel for human infection.

Results

The above studies illustrate the utility of GIS as a tool in integrating different ecological factors to understand disease occurrence and spread. The geographical and temporal patterns found in these studies provide benchmark to support disease control activities in Texas. Additionally, the identification of high-risk areas may be useful for decision makers to improve and prevent future disease spread.

Conclusions

Spatial epidemiological research has challenges, such as dealing with coarse level and aspatial datasets. Testing laboratories provide limited spatial information up to the zip code level due to the confidentiality concerns. Spatial analysis of such dataset prevents research at finer resolutions (Census block or block group). Despite these limitations, spatial epidemiology continues to be an invaluable field in the research and surveillance of infectious disease.

Keywords

Geospatial analysis; Disease mapping; Environmental variables

References

1. Auchincloss AH, Gebreab SY, Mair C and Diez Roux AV. A Review of Spatial Methods in Epidemiology, 2000–2010. Annu. Rev. Public Health. 2012; 33:107-22.
2. Gautam R, Srinath I, Clavijo A, Szonyi B, Bani-Yaghoub B, et al. Identifying Areas of High Risk of Human Exposure to Coccidioidomycosis in Texas Using Serology Data from Dogs. Zoonoses and Public Health. Article first published online: 1Aug,2012

*Indumathi Srinath
E-mail: isrinath@webmail.cvm.tamu.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Enabling ESSENCE to Process and Export Meaningful Use Syndromic Surveillance Data

Miles Stewart[1], Wayne Loschen*[1] and Taha Kass-Hout[2]

[1]Johns Hopkins University Applied Physics Laboratory, Laurel, MD, USA; [2]Public Health Surveillance and Informatics Program Office, Office of Surveillance, Epidemiology, & Laboratory Services, Centers for Disease Control and Prevention, Atlanta, GA, USA

Objective

The objective of this project is to enable the ESSENCE system to read in, utilize, and export out meaningful use syndromic surveillance data using the Health Level 7 (HL7) v2.5 standard. This presentation will detail the technical hurdles with reading a meaningful use syndromic surveillance data feed containing multiple sources, deriving a common meaning from the varying uses of the standard and writing data out to a meaningful use HL7 2.5 format that can be exported to other tools, such as BioSense 2.0 (2). The presentation will also describe the technologies employed for facilitating this, such as Mirth, and will discuss how other systems could utilize these tools to also support processing meaningful use syndromic surveillance data.

Introduction

In order to utilize the new meaningful use syndromic surveillance data sets (3) that many public health departments are now receiving, modifications to their systems must be made. Typically this involves enabling the storage and processing of the extra fields the new standard contains. Open source software exists, such as Mirth Connect, to help with reading and interpreting the standard. However, issues with reliably reading data from one source to another arise when the standard itself is misunderstood. Systems that process this data must understand that while the data they receive is in the HL7 v2.5 standard format, the meaning of the data fields might be different from provider to provider. Additional work is necessary to sift through the similar yet disjoint fields to achieve a consistent meaning.

Methods

This project utilized 3 separate instances of ESSENCE and BioSense 2.0. For both importing and exporting HL7 v2.x standard files, the project used the open source tool Mirth Connect. For importing data the project adapted versions of Tarrant County and Cook County ESSENCE systems in the Amazon GovCloud to receive meaningful use syndromic surveillance data files sent from BioSense 2.0. For exporting data to BioSense 2.0, the project used Mirth Connect to poll the local version of Cook County's ESSENCE database and export the data into an HL7 v2.5 file. The resultant file was sent over secure file transfer protocol (SFTP) to BioSense 2.0. The team then evaluated the process by comparing the data in the local instances of ESSENCE and the corresponding instances hosted on the Internet cloud.

Results

Many issues were encountered during the reading of the HL7. While the standard suggests that hospitals and hospital systems would all send data in the same fields for the same data, the reality was far different. Although HL7 v2.5 is a standard and there is a defined use for each field, it can be interpreted in many ways. A large portion of time was spent communicating with the local health department to determine exactly what each field meant for a particular hospital. Comparing the Internet cloud and local versions did have some difficulties due to local filtration rules that eliminated non-ER related records from the local Tarrant County system. The project was able to utilize new query features in ESSENCE to filter down to only ER related records on the Internet cloud version to support the comparisons. The project was able to re-use much of the configuration that was created when moving from one jurisdiction to the other. This will help when describing how others may use the same technology in their own systems.

Conclusions

Reading and interpreting the data consistently from a data feed containing multiple sources can be challenging. Confusion with the HL7 v2.3 or 2.5 standards causes many health organizations to transmit data in inconsistent ways that betrays the notion of a messaging standard. However, with the tools this project have created and the lessons we have learned, the pain of implementing meaningful use syndromic surveillance data into a system can be reduced.

Keywords

Analytics; Electronic Medical Records for Public Health; Interoperability; Meaningful Use; Internet Cloud

Acknowledgments

The ESSENCE in the Cloud initiative is supported by the CDC's Division of Notifiable Diseases and Healthcare Information (DNDHI) BioSense Program.

References

1) Kass-Hout, et al, CDC's BioSense 2.0: Bringing Together the Science and Practice of Public Health Surveillance, AJPM Prevention In Practice, November 15, 2011.
2) PHIN Messaging Guide for Syndromic Surveillance: Emergency Department and Urgent Care Data. Accessed August 30, 2012: http://www.cdc.gov/ehrmeaningfuluse/Syndromic.html.

*Wayne Loschen
E-mail: wayne.loschen@jhuapl.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Evaluation of Electronic Ambulatory Care Data for Use in the Influenza-like Illness Surveillance Network (ILINet)

Kathleen Stigi*[1], Atar Baer[2] and Kathy Lofy[1]

[1]Communicable Disease Epidemiology, Washington State Department of Health, Shoreline, WA, USA; [2]Public Health Seattle King County, Seattle, WA, USA

Objective

To determine if a syndromic influenza-like illness (ILI) definition previously validated for emergency department (ED) data accurately identified ILI visits in electronic ambulatory care data.

Introduction

During summer 2012, Washington State Department of Health (WA DOH) surveyed ILINet providers and found that more than half either utilize their electronic medical record system (EMRS) to gather and report weekly ILINet data, or intend to implement queries to do so in the future. There are a variety of EMRS being used state-wide, and providers that currently utilize these systems to report ILINet data apply a wide range of methods to query their data. There exists great interest in the evaluation of ambulatory care data within the context of Meaningful Use and little research is published in this area. WA DOH sought to evaluate electronic data from WA outpatient clinic networks in order to determine if a syndromic ILI definition previously validated for emergency department (ED) data accurately identified ILI visits in electronic ambulatory care data.

Methods

Public Health Seattle King County (PHSKC) receives electronic health data from the University of Washington Physicians Network (UWPN), comprised of ten outpatient clinics, on an automated basis. Data are sent daily for all outpatient visits that occurred the previous day and include clinic name, visit date and time, patient age, sex, zip code, chief complaint and diagnoses, and both a visit and patient key. Outpatient data from August 2007 through August 2012 were queried for ILI visits using the syndromic category for ILI previously validated for ED syndromic surveillance data: (1) ICD codes for influenza or mention of "flu" in chief complaint or diagnosis, or (2) a chief complaint or diagnosis of fever plus cough, or (3) a chief complaint or diagnosis of fever plus sore throat.

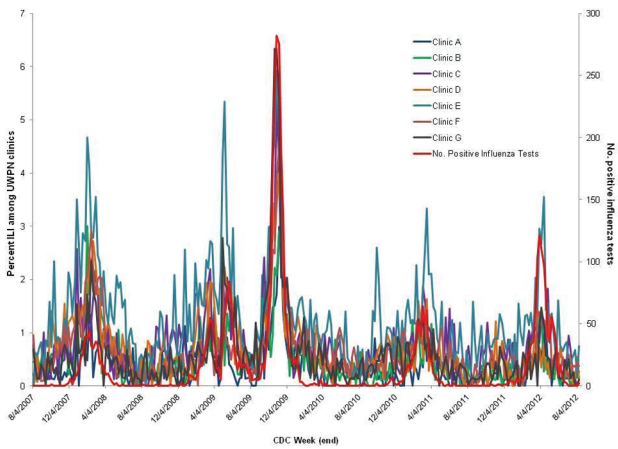
Using this definition, we assessed the correlation between the proportion of visits for ILI in the UWPN data and number and percentage of positive influenza laboratory tests reported by the University of Washington (UW) Virology Laboratory. We plan to apply this methodology to evaluate outpatient data from an additional clinic network, with statewide locations, and present these findings.

Results

The median number of weekly visits captured in the data was 6,622. Three clinics were excluded from further analyses due to insufficient data, leaving seven clinics remaining in the dataset (median number of weekly visits: 6,167). Overall, the proportion of ILI visits in the UWPN data strongly correlated with the number and percentage of positive influenza tests reported by the UW Laboratory during August 2007 through August 2012 (correlation coefficients 0.85 and 0.77, respectively). The correlation between proportion of ILI visits and number positive influenza tests among individual clinics ranged from 0.62 — 0.83. Overall, the proportion of ILI visits among the age category 5 to 24 years most strongly correlated with number positive influenza tests (correlation coefficient: 0.86).

Conclusions

During August 2007 through August 2012, the percentage of ILI visits detected in UWPN data using a previously validated definition for ILI in ED syndromic surveillance data strongly correlated with influenza activity in the community. Based on these findings, data from the UWPN network will be incorporated into ILINet during the 2012-2013 Influenza season. Findings from our analysis support the validity of using syndromic ambulatory data for ILI surveillance. Furthermore, we plan to use these results to formulate guidance for ILINet providers who want to utilize EMRS for weekly ILINet reporting.



Proportion of ILI visits within electronic clinic network data and number positive influenza tests, August 2007 - August 2012, Washington State

Keywords

Influenza; ILINet; Influenza-like Illness (ILI); Electronic Medical Records (EMR); Ambulatory data

Acknowledgments

University of Washington Physicians Network, University of Washington Virology Laboratory, WA State ILINet providers, Natasha Close (WA DOH)

*Kathleen Stigi
E-mail: Katie.Stigi@doh.wa.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Framing the Use of Social Media Tools in Public Health

Jennifer Stoll*, Richard Quartarone and Miguel Torres-Urquidy

Centers for Disease Control and Prevention, Atlanta, GA, USA

Objective

Recent scholarship has focused on using social media (e.g., Twitter, Facebook) as a secondary data stream for disease event detection. However, reported implementations such as (4) underscore where the real value may lie in using social media for surveillance. We provide a framework to illuminate uses of social media beyond passive observation, and towards improving active responses to public health threats.

Introduction

User-generated content enabled by social media tools provide a stream of data that augment surveillance data. Current use of social media data focuses on identification of disease events. However, once identification occurs, the leveraging of social media in monitoring disease events remains unclear (2, 3). To clarify this, we constructed a framework mapped to the surveillance cycle, to understand how social media can improve public health actions.

Methods

This framework builds on extant literature on surveillance and social media found in PubMed, Science Direct, and Web of Science, using keywords: "public health", "surveillance", "outbreak", and "social media". We excluded articles on online tools that were not interactive e.g., aggregated web-search results. Of 2,064 articles, 23 articles were specifically on the use of social media in surveillance work. Our review yielded five categories of social media use within the surveillance cycle (Table 1). This framing within surveillance illuminates a range of roles for social media tools beyond disease event detection. [Insert Image #1 here]

Finally, we used the 1918 Influenza Pandemic to illustrate an application of this framework (Fig 1), if it were part of the public health toolkit. In 1918, America was already becoming a "mass media" society. Yet a key difference in mass communications today is the enabling of public health to be more adaptive through the interactivity of social media.

Results

We used this "pre-social media" disease event to underscore where the real value of social media may lie in the surveillance cycle. Thus for 1918, early detection of disease could have occurred with many, e.g., sailors aboard ships in New York City's port sharing their "status updates" with the world. [Insert Image #2 here]

After detection, social media use could have shifted to help connect and inform. In 1918, this could include identifying and advising the infected on current hygiene practices and how to protect themselves. Social media would have enabled the rapid sharing of this information to friends and family, allowing public health officials to monitor the response. Then, to support multiple intervention efforts, public health officials could have rapidly messaged on local school closures; they could also have encouraged peer behavior by posting via Twitter or by "Pinning" handkerchiefs on Pinterest to encourage respiratory etiquette, and then monitored responses to these interventions, adjusting messaging accordingly.

Conclusions

The interactivity of social media moves us beyond using these tools solely as uni-directional, mass-broadcast channels. Beyond messaging about disease events, these tools can simultaneously help inform, connect, and intervene because of the user-generated feedback. These tools enable richer use beyond a noisy data stream for detection.

Surveillance Cycle Steps	Categories of Social Media Use
Detect: Identify disease event *(collection of data and consolidation and interpretation of data)*	**1. Utilize as secondary data stream** for disease event detection *(passive)*
Connect & Inform: Provide resources and information e.g. status updates *(dissemination of information)*	**2. Disseminate** links to information/resources and status updates *(active)* **3. Monitor response** to the information *(passive)*
Intervene: Respond to disease event *(take action to control and prevent)*	**4. Utilize as intervention** *(active)* **5. Monitor response** to intervention *(passive)*

Table 1. Social media use in supporting information for action

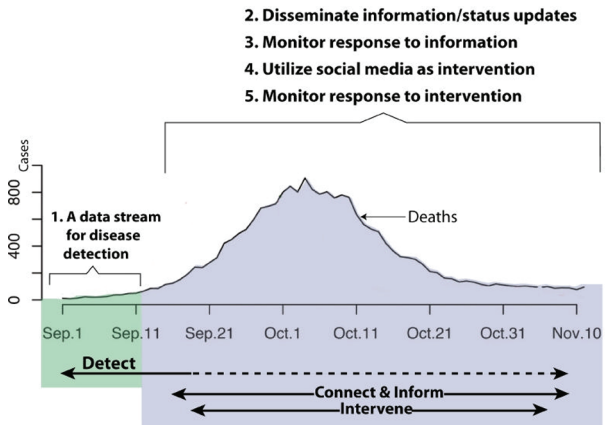


Fig. 1. Social media mapping to 1918 epi curves for NY State (1).

Keywords

Surveillance; Public Health; Social Media

References

1. Goldstein E. et al. Reconstructing influenza incidence by deconvolution of daily mortality time series. Natl Acad Sci U S A. 2009 Dec 22;106(51):21825-9
2. Heaivilin N. et al. Public health surveillance of dental pain via Twitter. J Dent Res. 2011 Sep;90(9):1047-51
3. Luck, J. et al. Using Local Health Information to Promote Public Health. Health Affairs 2006;25(4): 979-991
4. Napolitano MA. et al. Using Facebook and Text Messaging to Deliver a Weight Loss Program to College Students. Obesity 2012

*Jennifer Stoll
E-mail: jstoll@cdc.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Novel Emergency Department High Utilizer Surveillance In New Hampshire

David J. Swenson*[1], Cole Zanetti[2], Elizabeth R. Daly[1] and Jose T. Montero[1]

[1]State of NH, Concord, NH, USA; [2]NH Dartmouth Family Medicine Residency, Concord, NH, USA

Objective

To develop a manageable surveillance methodology to detect Emergency Department (ED) patients with the highest healthcare utilization, and monitor their targeted treatment improvement and medical health cost reductions over time for overall improvements in statewide health.

Introduction

Researchers have demonstrated benefits to identifying and developing interventions for patients that frequently seek healthcare services in the ED. The New Yorker Magazine, recently published an article titled The Hot Spotters, summarizing work being done in the United States to lower medical costs by giving the neediest patients better healthcare (1). In Camden, NJ, Physician Jeffrey Brenner closed his regular practice to focus on Hot Spotter patients (directing resources and brainpower to help their improvement) and measured a 40% reduction in hospital inpatient and ED visits and a 56% medical cost reduction for the first 36 Hot Spotters. A 2008 NH Office of Medicaid Business and Policy (OMBP) outpatient Medicaid ED frequency visit study was conducted, which cited that frequent ED users were more likely to have higher costs and rates of illness or disease than all Medicaid members (2). It was noted that increased prevention and wellness could reduce frequent ED use and increase cost savings (5% of the NH Medicaid population contributed to approximately 38% of ED costs). The NH Division of Public Health Services initiated a pilot project to examine NH Emergency Department (ED) surveillance data to identify high utilizer patients and realize improved health benefits and medical cost reductions.

Methods

This pilot focused first on identifying 2010 ED high utilizers in one hospital. A high utilizer was defined as a patient with 9 or more ED visits (top 10%) and were identified using Medical Record Number followed by sorting number of visits in descending order. Visit diagnosis codes were identified for the top 10% of high utilizers, along with the date of admission, resident town, age, and gender. Finally, the top 10% over utilizers were mapped, identifying the total number of utilzers in each town. We overlaid this information on a map of NH's social vulnerability index to provide comparative data. Plans for future expansion include: Creating a GIS system that trends data over 10 years; Identifying ED high utilizers by location (visits by town, number of diagnosis codes per visit, date of visits, and summative data); and Creating hospital and total state-wide breakdown of highest utilizers, most common state-wide diagnosis for ED high utilizers, and specific data from each hospital in relation to state-wide social vulnerability index data.

Results

Over 56,000 ED visits at one pilot hospital were analyzed targeting 2,005 high utilizer visits for 158 patients. Identification by location, age, gender and ICD-9-CM diagnosis coding was determined for each ED over utilizer. Mapping of the high utilizers showed that 142 of the 158 patients resided in the city where the hospital was located. The most frequent diagnosis codes for the top 10% ED high utilizers included mental health, substance abuse, and chronic disease conditions (such as diabetes mellitus).

Conclusions

This pilot project provides a manageable approach for identifying ED high utilizers for both health improvement and cost reduction surveillance efficiencies, and is a model for other surveillance management monitoring applications. Potentially, 2.1 million dollars per year could be saved, if each over utilizer used the ED one less time (2).

Keywords

Surveillance; Informatics; Chronic Disease

References

1. The Hot Spotters, Can we lower medical costs by giving the neediest patients better care? Gawande A, The New Yorker, Medical Report, January 24, 2011.
2. Office Of Medicaid Business And Policy, NH Comprehensive Health Care Information System (CHIS). Frequent Outpatient Emergency Department Use by New Hampshire Medicaid Members (An Evaluation of Prevalence, Diagnoses, Utilization, and Payments). Concord; October 2008.

*David J. Swenson
E-mail: dswenson@dhhs.state.nh.us

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Selecting Targeted Symptoms/Syndromes for Syndromic Surveillance in Rural China

Li Tan[1], Jie Zhang[1], Liwei Cheng[1], Weirong Yan[1, 2], Vinod K. Diwan[2], Lu Long[1] and Shaofa Nie*[1]

[1]Tongji Medical College, Wuhan City, China; [2]Karolinska Institutet, Stockholm, Sweden

Objective

To select the potential targeted symptoms/syndromes as early warning indicators for epidemics or outbreaks detection in rural China.

Introduction

Patients' chief complaints (CCs) as a common data source, has been widely used in syndromic surveillance due to its timeliness, accuracy and availability (1). For automated syndromic surveillance, CCs always classified into predefined syndromic categories to facilitate subsequent data aggregation and analysis. However, in rural China, most outpatient doctors recorded the information of patients (e.g. CCs) into clinic logs manually rather than computers. Thus, more convenient surveillance method is needed in the syndromic surveillance project (ISSC). And the first and important thing is to select the targeted symptoms/syndromes.

Methods

Epidemiological analysis was conducted on data from case report system in Jingmen City (one study site in ISSC) from 2004 to 2009. Initial symptoms/syndromes were selected by literature reviews. And finally expert consultation meetings, workshops and field investigation were held to confirm the targeted symptoms/syndromes.

Results

10 kinds of infectious diseases, 6 categories of emergencies, and 4 bioterrorism events (i.e. plague, anthrax, botulism and hemorrhagic fever) were chose as specific diseases/events for monitoring (Table 1). Two surveillance schemes were developed by reviewing on 565 literatures about clinical conditions of specific diseases/events and 14 literatures about CCs based syndromic surveillance. The former one was to monitor symptoms (19 initial symptoms), and then aggregation or analysis on single or combined symptom(s); and the other one was to monitor syndromes (9 initial syndromes) directly (Table 2). The consultation meeting and field investigation identified three issues which should be considered: 1) the abilities of doctors especially village doctors to understand the definitions of symptoms/syndromes; 2) the workload of data collection; 3) the sensitive and specific of each symptom/syndrome. Finally, Scheme 1 was used and 10 targeted symptoms were determined (Table 2).

Conclusions

We should take the simple, stability and feasibility of operation, and also the local conditions into account before establishing a surveillance system. Symptoms were more suitable for monitoring compared to syndromes in resource-poor settings. Further evaluated and validated would be conducted during implementation. Our study might provide methods and evidences for other developing countries with limited conditions in using automated syndromic surveillance system, to construct similar early warning system.

Table 1. Epidemiological analysis on cases and emergencies data

Respiratory cases		Gastrointestinal cases		Emergencies	
Name	%	Name	%	Name	Events (No.)
*Pulmonary tuberculosis	82.38	†Hand-foot-mouth diseases	41.73	†A(H1N1)	10
†Mumps	9.14	†Bacillary dysentery	28.56	†Mumps	5
†Measles	3.35	†Hepatitis A	15.36	†Hand-foot-mouth diseases	1
†Varicella	2.00	†Infectious diarrhea	6.58	†Bacillary dysentery	1
†Influenza/A(H1N1)	1.79	†Hepatitis E	4.30	†Food poisoning	2
†Rubella	0.72	Typhoid	3.03	†Unknown reason dermatitis	1
Scarlet fever	0.44	Paratyphoid	0.22		
Pertussis	0.15	Amebic dysentery	0.22		
Meningococcal meningitis	0.03				
Total	100.00	Total	100.00	Total	20

* Chronic infectious diseases (excluded).
† Selected specific diseases (top 5) or events (non-infectious excluded).

Table 2 List of symptoms/syndromes

*Scheme 1				**Scheme 2	
No.	Symptoms	No.	Symptoms	No.	Syndromes
1	Abdominal pain	11	†Headache	1	Coma/sudden death
2	Bone/muscle/joint Pain	12	Hematochezia	2	Fever
3	Chills	13	Jaundice	3	Gastrointestinal
4	Conjunctival hyperemia	14	†Mucocutaneous hemorrhage	4	Hemorrhagic
5	†Convulsion	15	Nasal congestion/Rhinorrhea	5	Influenza like illness
6	†Cough	16	†Nausea/Vomitting	6	Neurological
7	†Diarrhea	17	†Rach	7	Rash
8	†Disturbance of consciousness	18	†Sore throat	8	Respiratory
9	Fatigue	19	Tenesmus		
10	†Fever				

* The incidence of symptom was >= 20% of specific disease(s)/event(s).
** The number of times of syndromes monitored was >= 4 times. Asthma (4 times) and diarrhea (5 times) were excluded due to study objectives.
† Final targeted symptoms.

Keywords

Syndromic surveillance; Chief complaint; Early warning

Acknowledgments

This study was funded by [European Union's] [European Atomic Energy Community's] Seventh Framework Programme ([FP7/2007-2013] [FP7/2007-2011]) under grant agreement no. [241900].

References

1.Chapman WW, Dowling JN, Wagner MM. Generating a reliable reference standard set for syndromic case classification. J Am Med Inform Assoc. 2005;12:618-29.

*Shaofa Nie
E-mail: sf_nie@mails.tjmu.edu.cn

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Use of Control Bar Matrix for Outbreak Detection in Syndromic Surveillance System

Tao Tao[1], Qi Zhao[1], Huijian Cheng[2], Lars Palm[3], Xin Lu[4, 5], Hui Yuan[2], Xiaoxiao Song[1] and Biao Xu*[1]

[1]School of Public Health, Fudan University, Shanghai, China; [2]Jiangxi Provincial Center for Disease Control and Prevention, Nanchang, China; [3]Future Position X, Gävle, Sweden; [4]Division of Global Health (IHCAR), Department of Public Health Sciences, Karolinska Institutet, Stockholm, Sweden; [5]College of Information Systems and Management, National University of Defense Technology, Changsha, China

Objective

To develop and test the method of incorporating different control bars for outbreak detection in syndromic surveillance system.

Introduction

Aberration detection methods are essential for analyzing and interpreting large quantity of nonspecific real-time data collected in syndromic surveillance system. However, the challenge lies in distinguishing true outbreak signals from a large amount of false alarm (1). The joint use of surveillance algorithms might be helpful to guide the decision making towards uncertain warning signals.

Methods

A syndromic surveillance project (ISSC) has been implemented in rural Jiangxi Province of China since August 2011. Doctors in the healthcare surveillance units of ISSC used an internet-based electronic system to collect information of daily outpatients, which included 10 infectious related symptoms. From ISSC database, we extracted data of fever patients reported from one township hospital in GZ town between August 1st and December 31st, 2011 to conduct an exploratory study. Six different control bar algorithms, which included Shewart, Moving Average (MA), Exponentially Weighted Moving Average (EWMA) and EARS' C1, C2, C3, were prospectively run among historical time series of daily fever count to simulate a real-time outbreak detection. Each control bar used 7 days' moving baseline with a lag of 2 days [the baseline for predicting Day(t) starts from Day(t-9) to Day(t-3), C1 method used a lag of zero day]. We set the threshold of $\mu+2\sigma$ for Shewart and MA, and 2.1 for EWMA C1, C2 and C3. An alarm was triggered when the observed data exceeded threshold, and the detailed information of each patient were checked for signal verification. Microsoft Excel 2007 was used to calculate the simulation results.

Results

During the 5 months, GZ township hospital reported 514 outpatients with fever symptom, with an average of 3.4 per day. All control bars were simultaneously operated among daily counts of fever cases. Of the 153 days on surveillance, 29 triggered alarms by at least one of the control bars. Nine days triggered alarms from >= 3 control bars while on one day (12/30) all 6 algorithms raised alarms. Figure 1 shows the date, fever count, algorithm and warning level (color) of each alarm, which we called a control bar matrix. It can be seen that C3 and EWMA present a higher sensitiveness towards tiny data change whereas C1, C2 and MA focus on large increase of data. C3 also had a memory effect on recent alarms. No infectious disease epidemic or outbreak event was confirmed within the signals. Most fever patients on the nine high-warning days (red and purple) were diagnosed as upper level respiratory infection. However, we discovered that the sharp increase of fever cases on 12/30 was attributed to 5 duplicate records mistakenly input by the staff in GZ hospital.

Conclusions

By combining control bars with different characteristics, the matrix has potential ability to improve the specificity of detection while maintaining a certain degree of sensitivity. With alarms categorized into hierarchical warning levels, public health staffs can decide which alarm to investigate according to the required sensitivity of surveillance system and their own capacity of signal verification. Though we did not find any outbreak event in the study, the possibility of localized influenza epidemic on high-warning days cannot be wiped out, and the matrix's ability to detect abnormal data change was apparent. The proper combination, baseline and threshold of control bars will be further explored in the real-time surveillance situation of ISSC.

Figure 1: Detailed information of alarm signals generated by control bar matrix (No-alarm days were omitted).

Keywords

Syndromic surveillance; matrix; control bar; signal

Acknowledgments

This study was funded by [European Union's] [European Atomic Energy Community's] Seventh Framework Programme ([FP7/2007-2013] [FP7/2007-2011]) under grant agreement no. [241900].

References

1. Fearnley L: Signals come and go: syndromic surveillance and styles of biosecurity. Environment and Planning A 2008, 40(7):1615-1632.

*Biao Xu
E-mail: bxu@shmu.edu.cn

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Risk and Protective Factors for Arthritis Status and Severity

Masaru Teramoto*[1], Fred Breukelman[2], Ferdinando A. Gatto[2] and Sheniz Moonie[3]

[1]Health Sciences, Drexel University, Philadelphia, PA, USA; [2]Delaware Health and Social Services, Dover, DE, USA; [3]University of Nevada, Las Vegas, Las Vegas, NV, USA

Objective

To examine how cigarette smoking, alcohol consumption, obesity, and physical activity are associated with the risk and severity of arthritis among adults living in Delaware.

Introduction

Research has indicated several risk and protective factors for arthritis, including cigarette smoking, alcohol consumption, obesity, and physical activity (1–4). However, it is not well understood how all these factors interact to increase/decrease the risk of arthritis.

Methods

Data from the 2009 Delaware Behavioral Risk Factor Surveillance System (BRFSS) were analyzed in the current study. Potential risk and protective factors for arthritis status and severity examined in this study included: smoking status, alcohol consumption, weight status, and physical activity level. Weighted percentages were calculated for the risk and protective factors by arthritis status and activity limitation due to arthritis/joint symptoms, and were analyzed using a Rao-Scott $\chi 2$ test. A logistic regression analysis was performed to determine an odds ratio (OR) while adjusting for gender, age, race/ethnicity, and education.

Results

Adults living in Delaware self-reporting arthritis were more likely to be former and current smokers than those without self-reported arthritis ($p < 0.001$, OR = 1.64–1.70). Moderate and heavy alcohol drinking was associated with lower prevalence and severity of arthritis ($p < 0.001$, OR = 0.45–0.74). There was a significant relationship between obesity and arthritis status or activity limitation due to arthritis/joint symptoms ($p < 0.01$, OR = 1.62–2.14). Furthermore, people with arthritis having activity limitation due to arthritis/joint symptoms were more likely to not meet the current physical activity recommendations (5) ($p = 0.013$, OR = 1.49).

Conclusions

Cigarette smoking, alcohol consumption, obesity, and physical activity are all associated with the prevalence and severity of arthritis. It is possible that smoking and obesity have a negative impact on the risk and severity of arthritis, whereas alcohol consumption and physical activity may reduce its risk and severity. Further research, including prospective cohort studies, is necessary to determine the true absolute risk of developing arthritis, so that we can design the effective prevention strategies.

Table 1. Risk and protective factors by arthritis status and severity

	Arthritis status (N = 3969)			Activity limitation due to arthritis/joint symptoms (N = 1512)		
	Yes	No		Yes	No	
Potential risk/protective factor	27.5 (0.9)	72.5 (0.9)	p-value*	39.1 (1.7)	60.9 (1.7)	p-value*
Smoking status			< 0.001			0.382
Non-smoker	42.1 (1.8)	57.7 (1.5)		40.6 (2.6)	43.0 (2.4)	
Former smoker	39.3 (1.7)	24.1 (1.2)		38.4 (2.6)	39.9 (2.3)	
Current smoker	18.6 (1.4)	18.2 (1.2)		21.0 (2.2)	17.1 (1.9)	
Alcohol consumption			< 0.001			< 0.001
No drinking	52.4 (1.8)	38.8 (1.5)		61.8 (2.6)	46.5 (2.4)	
Moderate drinking	27.2 (1.6)	34.3 (1.5)		24.9 (2.3)	28.5 (2.2)	
Heavy drinking	20.4 (1.6)	26.9 (1.4)		13.3 (1.8)	25.0 (2.2)	
Weight status (body mass index [a])			< 0.001			0.008
Not overweight/obese	26.3 (1.6)	41.0 (1.6)		21.0 (2.2)	29.7 (2.3)	
Overweight	36.3 (1.7)	35.3 (1.5)		36.0 (2.6)	36.5 (2.3)	
Obese	37.4 (1.8)	23.7 (1.2)		43.0 (2.6)	33.8 (2.4)	
Recommended physical activity [b]			< 0.001			0.013
Yes	43.7 (1.8)	53.7 (1.6)		38.2 (2.7)	47.3 (2.5)	
No	56.3 (1.8)	46.3 (1.6)		61.8 (2.7)	52.7 (2.5)	

Notes: Values given as % (SE).
[a]Not overweight/obese: < 25.0 kg/m2, Overweight: 25.0–29.9 kg/m2, Obese: ≥ 30 kg/m2.
[b]Moderate physical activity for ≥ 30 minutes/day on ≥ 5 days/week, or vigorous physical activity for ≥ 20 minutes/day on ≥ 3 days/week (5).
*Rao-Scott $\chi 2$ test.

Keywords

alcohol; smoking; arthritis; Behavioral Risk Factor Surveillance

References

1. Albano SA, Santana-Sahagun E, Weisman MH. Cigarette smoking and rheumatoid arthritis. Semin Arthritis Rheum 2001; 31:146–159.
2. Maxwell JR, Gowers IR, Moore DJ, et al. Alcohol consumption is inversely associated with risk and severity of rheumatoid arthritis. Rheumatology 2010; 49:2140–2146.
3. Anandacoomarasamy A, Caterson I, Sambrook P, et al. The impact of obesity on the musculoskeletal system. Int J Obes 2008; 32:211–222.
4. Manninen P, Riihimaki H, Heliovaara M, et al. Physical exercise and risk of severe knee osteoarthritis requiring arthroplasty. Rheumatology 2001; 40:432–437.
5. Haskell WL, Lee IM, Pate RR, et al. Physical activity and public health: updated recommendation for adults from the American College of Sports Medicine and the American Heart Association. Circulation 2007; 116:1081–1093.

*Masaru Teramoto
E-mail: Masaru.Teramoto@drexel.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

On the implementation of the Biological Threat Reduction Program in the Republic of Uzbekistan

Laziz Tuychiev*[1] and Marifjon Madaminov[2]

[1]Sanitary-Epidemiological Department of Ministry of Health, Tashkent, Uzbekistan; [2]Center for Prophilaxis and Quarantine of Most Hazardous Infections of Uzbekistan, Tashkent, Uzbekistan

Objective

To review the implementation of the Biological Threat Reduction Program (BTRP) of the U.S. Defense Threat Reduction Agency in the Republic of Uzbekistan since 2004.

Introduction

The Biological Threat Reduction Program (BTRP) has been being implemented in the Republic of Uzbekistan since 2004 within the framework of the Agreement between the Government of the Republic of Uzbekistan and the Government of the United States of America Concerning Cooperation in the Area of the Promotion of Defense Relations and the Prevention of Proliferation of Weapons of Mass Destruction of 06.05.2001. Threat agent detection and response activities that target a list of especially dangerous pathogens are being carried out under the BTRP within the health care system of Uzbekistan. This presentation reviews some of the achievements of the program to date.

Results

BTRP, in partnership with the Government of Uzbekistan, has funded the establishment of five Regional Diagnostic Laboratories (RDL) and ten Epidemiological Support Units (ESU), operated by the Ministry of Health of Uzbekistan, which are intended to improve the diagnosis of quarantine and especially dangerous infections, and to ensure timely preventive and anti-epidemic measures.

RDLs provide a high level of biosafety and biosecurity to conduct rapid laboratory diagnostics (PCR, ELISA) of especially dangerous infections. RDLs are equipped with up-to-date diagnostic laboratory equipment that conforms to internationals standards, as well as with all necessary consumables.

Personnel of RDLs have been appropriately trained in epidemiology, clinical and diagnostic techniques for especially dangerous infections, including such state-of-the-art techniques as rapid PCR and ELISA diagnostics, as well as in work and equipment operation safety regulations.

Epidemiological Support Units (ESU) have been established on the basis of the Especially Dangerous Infections Divisions of Oblast, city and Rayon Centers for State Sanitary and Epidemiological Surveillance (SES) of the Ministry of Health. The BTRP ESU efforts include renovation activities, supply and installation of appropriate equipment for rapid laboratory diagnostics, and vehicles.

ESUs are meant to ensure emergency notification in cases of suspected occurrence of quarantine and especially dangerous infections, for timely implementation of anti-epidemic and preventive measures.

Three Cooperative Biological Research projects on quarantine and especially dangerous infections have been implemented within BTRP with the financial support of the US Civilian Research and Development Foundation (CRDF).

To ensure the sustainability of training and availability of a pool of skilled personnel, a training laboratory is to be established at the Tashkent Institute for Post-Graduate Medical Education (TIPME) to train personnel of RDLs and ESUs. The training laboratory will fully replicate the setup of a BSL-2 Regional Diagnostic Laboratory, but will maintain no operations with live pathogens.

Conclusions

The implementation of BTRP within the health care system of the Republic of Uzbekistan contributes to the stable and sustainable well-being in the population of the country.

Keywords

Biological Threat Reduction Program; Especially dangerous pathogens; Resource-poor setting

*Laziz Tuychiev
E-mail: laziz.tyuchiev@minzdrav.uz

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Usefulness of Syndromic Surveillance for Early Outbreak Detection in Small Islands: The Case of Mayotte

Pascal Vilain*[1], Olivier Maillard[3], Julien Raslan-Loubatie[2], Mohamed Ahmed Abdou[3], Tinne Lernout[2] and Laurent Filleul[1]

[1]Regional Office of the French Institute for Public Health Surveillance of Indian Ocean, Saint-Denis, Reunion; [2]Regional Office of the French Institute for Public Health Surveillance of Indian Ocean, Mamoudzou, Mayotte; [3]Hospital Center of Mayotte, Mamoudzou, Mayotte

Objective

To present the usefulness of syndromic surveillance for the detection of infectious diseases outbreak in small islands, based on the experience of Mayotte.

Introduction

Mayotte Island, a French overseas department of around 374 km2 and 200 000 inhabitants is located in the North of Mozambique Channel in the Indian Ocean (Figure1).

In response to the threat of the pandemic influenza A(H1N1)2009 virus emergence, a syndromic surveillance system has been implemented in order to monitor its spread and its impact on public health (1). This surveillance system which proved to be useful during the influenza pandemic, has been maintained in order to detect infection diseases outbreaks.

Methods

Data are collected daily directly from patients' computerized medical files that are filled in during medical consultations at the emergency department (ED) of the hospital Center of Mayotte (2). Among the collected variables, the diagnosis coded according to ICD-10 is used to categorize the syndromes. Several syndromes are monitored including the syndromic grouping for conjunctivitis and unexplained fever.

For early outbreak detection, a control chart is used based on an adaptation of the Cusum methods developed by the CDC within the framework of the EARS program (3).

Results

Each week, about 700 patients attend the ED of the hospital. The syndromic surveillance system allowed to detect an outbreak of conjunctivitis from week 10 (Figure2). During the epidemic peak on week 12, conjunctivitis consultations represented 5% of all consultations. The data of the sentinel practitioner network confirmed this epidemic and the laboratory isolated Enterovirus (4). At the same time, an unusual increase of unexplained fever was detected.

Conclusions

Due to its geographical and socio-demographical situation, the population of Mayotte is widely exposed to infectious diseases. Even on a small island, syndromic surveillance can be useful to detect outbreak early leading to alerts and to mobilize a rapid response in addition to others systems.

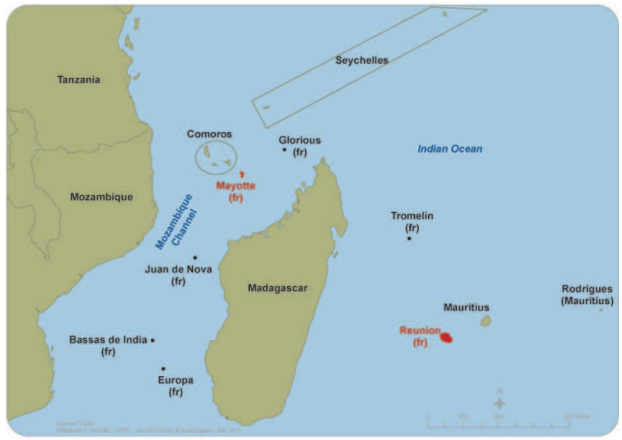


Figure1. Map of the western Indian Ocean featuring Mayotte Island

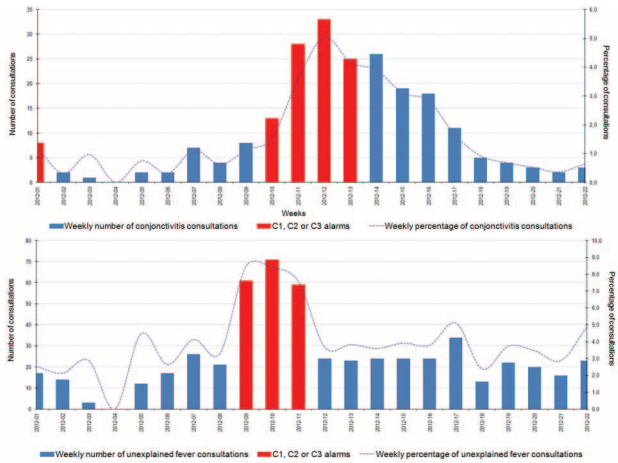


Figure2. Weekly number of conjonctivitis and unexplained fever consultations and statistical alarms detected

Keywords

Syndromic surveillance; Early outbreak detection; Mayotte Island

Acknowledgments

We are thankful to all the sentinel network practitioners and the practitioners of the emergency department.

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

References

1. Lernout T, Durquety E, Chollet P, Helleisen F, Javaudin G, Lajoinie G, Filleul L. [Influenza A (H1N1) 2009 surveillance on Mayotte island: the challenge of setting up a new system facing the pandemic]. Bull Soc Pathol Exot. 2011 May;104(2):114-8.
2. Filleul L, Durquety E, Baroux N, Chollet P, Cadivel A, Lernout T. [The development of non-specific surveillance in Mayotte and Reunion Island in the context of the epidemic influenza A(H1N1)2009] [Article in French]. Bull Epidémiol Hebd. 2010;(24-26):283-5.
3. Hutwagner L, Browne T, Seeman GM, Fleischauer AT. Comparing aberration detection methods with simulated data. Emerg Infect Dis. 2005 Feb;11(2):314-6.
4. Lernout T, Maillard O, Boireaux S, Collet L, Filleul L. A large outbreak of conjunctivitis on Mayotte Island, France, February to May 2012. Euro Surveill. 2012 Jun 7;17(23). pii: 20192.

*Pascal Vilain
E-mail: pascal.vilain@ars.sante.fr

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Syndromic Surveillance Based on Emergency Visits: A Reactive Tool for Unusual Events Detection

Pascal Vilain*[1], Arnaud Bourdé[2], Pierre-Jean Marianne dit Cassou[3], Yves Jacques-Antoine[4], Philippe Morbidelli[5] and Laurent Filleul[1]

[1]Regional Office of the French Institute for Public Health Surveillance of Indian Ocean, Saint-Denis, Reunion; [2]University hospital, Saint-Denis, Reunion; [3]University hospital, Saint-Pierre, Reunion; [4]Hopital center, Saint-Benoît, Reunion; [5]Hopital center, Saint-Paul, Reunion

Objective

To show with examples that syndromic surveillance system can be a reactive tool for public health surveillance.

Introduction

The late health events such as the heat wave of 2003 showed the need to make public health surveillance evolve in France. Thus, the French Institute for Public Health Surveillance has developed syndromic surveillance systems based on several information sources such as emergency departments (1). In Reunion Island, the chikungunya outbreak of 2005-2006, then the influenza pandemic of 2009 contributed to the implementation and the development of this surveillance system (2-3). In the past years, this tool allowed to follow and measure the impact of seasonal epidemics. Nevertheless, its usefulness for the detection of minor unusual events had yet to be demonstrated.

Methods

In Reunion Island, the syndromic surveillance system is based on the activity of six emergency departments. Two types of indicators are constructed from collected data:

- Qualitative indicators for the alert (every visit whose diagnostic relates to a notifiable disease or potential epidemic disease);
- Quantitative indicators for the epidemic/cluster detection (number of visits based on syndromic grouping).

Daily and weekly analyses are carried out. A decision algorithm allows to validate the signal and to organize an epidemiological investigation if necessary.

Results

Each year, about 150 000 visits are registered in the six emergency departments that is 415 consultations per day on average. Several unusual health events on small-scale were detected early.

In August 2011, the surveillance system allowed to detect the first autochthonous cases of measles, a few days before this notifiable disease was reported to health authorities (Figure 1). In January 2012, the data of emergency departments allowed to validate the signal of viral meningitis as well as to detect a cluster in the West of the island and to follow its trend. In June 2012, a family foodborne illness was detected from a spatio-temporal cluster for abdominal pain by the surveillance system and was confirmed by epidemiological investigation (Figure 2).

Conclusions

Despite the improvement of exchanges with health practitioners and the development of specific surveillance systems, health surveillance remains fragile for the detection of clusters or unusual health events on small scale. The syndromic surveillance system based on emergency visits has proved to be relevant for the identification of signals leading to health alerts and requiring immediate control measures. In the future, it will be necessary to develop these systems (private practitioners, sentinel schools) in order to have several indicators depending on the degree of severity.

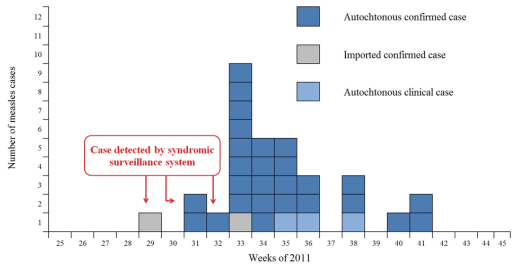


Figure 1. Epidemic curve of measles cases

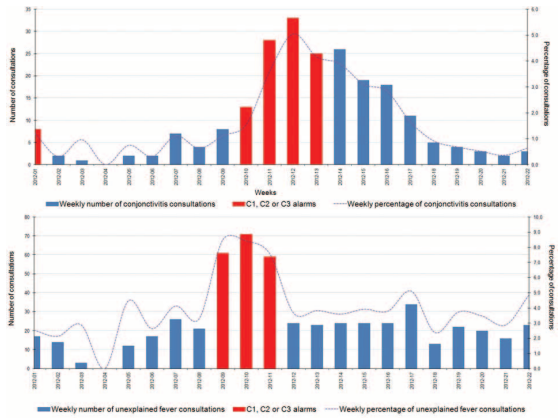


Figure 2. Line-list of patient characteristics in an abdominal pain cluster.

Keywords

Syndromic surveillance; Unusual event detection; Reunion Island

Acknowledgments

We are thankful to all the practitioners of emergency departments.

References

1. Josseran L, Nicolau J, Caillère N, Astagneau P, Brücker G. Syndromic surveillance based on emergency department activity and crude mortality: two examples. Euro Surveill. 2006;11(12):225-9.
2. D'Ortenzio E, Do C, Renault P, Weber F, Filleul L. Enhanced influenza surveillance on Réunion Island (southern hemisphere) in the context of the emergence of influenza A(H1N1)v. Euro Surveill. 2009;14(26). pii: 19257.
3. Filleul L, Durquety E, Baroux N, Chollet P, Cadivel A, Lernout T. The development of non-specific surveillance in Mayotte and Reunion Island in the contexte of the epidemic influenza A(H1N1) 2009 [Article in French]. Bull EpidemiolHebd. 2010:283.

***Pascal Vilain**
E-mail: pascal.vilain@ars.sante.fr

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Advancing Surveillance of Chronic and Non-Communicable Disease—A Path Forward

Elissa R. Weitzman[1, 3] and Nadia Waheed*[2, 4]

[1]Harvard Medical School, Boston, MA, USA; [2]Tufts University School of Medicine, Boston, MA, USA; [3]Boston Children's Hospital, Boston, MA, USA; [4]New England Eye Center, Boston, MA, USA

Objective

To characterize current and future approaches to surveillance of chronic and non-communicable diseases and establish the agenda for both methodological and condition-specific progress.

Introduction

Major global stakeholder groups including the United Nations, World Health Organization and Institute of Medicine seek to raise awareness of the threat to global health and security of chronic and non-communicable diseases. These conditions comprise 50-85% of the global annual morbidity burden and constitute a major drain on national economies. To move from awareness of this problem to action and amelioration of issues, we need effective means for monitoring and intervening with populations using approaches that span primary, secondary and tertiary prevention.

Methods

This session will begin with a discussion of key concepts and terms and their implications for defining target problems, populations and surveillance strategies. We will also begin by reviewing the epidemiologic and economic arguments for advancing surveillance in this area. The discussion will center on a critical assessment of issues related to surveillance of chronic and non-communicable diseases: how do approaches differ from established and evolving approaches to surveillance of infectious disease? Are there opportunities for synergy with current surveillance efforts and assets? Where are new methods needed? How might surveillance approaches be advanced in different regions (e.g., developing and industrialized settings)? Might new approaches predicated on "citizen science" and engaged patient and public health cohorts provide platforms for advancing surveillance of chronic and non-communicable diseases and what is required to ensure their success?

Results

Points of discussion:

1) Participants are encouraged to come prepared to share their experiences engaging patient and public health cohorts in this area, including sharing experiences engaging cohorts using online social networks, participatory research and surveys.

2) Brainstorm ideas for development of a workshop in non-communicable disease surveillance.

Sample questions:

1) What are the issues related to surveillance in the context of resource rich and poor contexts?

2) What are the special needs for establishing cost-effective and sustainable methods for longitudinal tracking?

3) How can technological advances and engaged patient and public health cohorts be used in the advancement of surveillance? What are methods to maximize engagement in both the developed and developing world?

Conclusions

Non-communicable diseases are a major and growing morbidity and mortality burden globally. This round table discussion will focus on the importance of non-communicable disease surveillance, attempt to elicit participant's experiences in the surveillance of these conditions, and outline special needs for establishing cost-effective and sustainable methods for longitudinal tracking of non-communicable diseases.

Keywords

surveillance; Non communicable diseases; chronic diseases

Acknowledgments

Dr Weitzman's work is supported by PO1HK000088-01 from the Centers for Disease Control and Prevention (CDC), National Library of Medicine grant 5R01LM007677 and 1U54RR025224-01 from NCRR/NIH.

*Nadia Waheed
E-mail: nwaheed@tuftsmedicalcenter.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Syndromic Surveillance at the New York State Veterinary Diagnostic Laboratory

Kylius Wilkins*[1], Bruce Akey[2, 3], Belinda Thompson[2, 3] and Daryl Nydam[3]

[1]Veterinary Services, USDA APHIS, Ames, IA, USA; [2]NYSVDL, Ithaca, NY, USA; [3]Cornell University, Ithaca, NY, USA

Objective

To assess the use and utility of a syndrome check list on the general submission form of a high volume veterinary diagnostic laboratory, and compare to the results of a 2009 pilot study.

Introduction

The New York State Veterinary Diagnostic Laboratory (NYSVDL) receives more than 100,000 diagnostic submissions a year that are not currently used in any formal syndromic surveillance system. In 2009, a pilot study of syndrome classification schemes was undertaken and in 2011 a new general submission form was adopted, which includes a check list of syndromes, as part of the clinical history.

Monitoring submissions to a veterinary diagnostic laboratory for increases in certain test requests is an established method of syndromic surveillance (1, 2). The new general submission form allows for clinician selected syndromes to be monitored in addition to test request.

Methods

We selected 420 "contract cases" from all submissions for bovines since the implementation of the new form, May 2011, though February 2012. Submissions were reviewed for use of the new form, use of the syndrome check list and tests requested. Test requests were assigned syndromes, if possible, to allow for comparison with the clinician selected syndromes.

The selection of cases was weighted towards the end of the period as use of the new form increased with time and to a lesser extent toward the beginning of the period in an attempt to find any early use of the form. "Contract case" refers to New York State Department of Agriculture and Markets subsidization of agricultural animal and herd health testing done under specific guidelines. The benefit of "contract cases" is the guidelines require a complete clinical history, which should include selection of syndromes. Finally, selection was limited bovine submissions as was done in the pilot study.

Results

16% (69/420) of submissions used the new form and of these 23 selected syndromes. As was seen in the pilot study the most commonly occurring syndrome in the clinical history was "Gastrointestinal/Diarrhea" 56% (13/23). The next most common syndromes were "Respiratory" (7/23), "Sudden Death" (6/23) and "Fever" (4/23).

Syndromes assigned based on test request followed a similar pattern with "Gastrointestinal/Diarrhea" (166/254) and "Respiratory" (52/254) best represented. An important difference was the syndromes "Sudden Death" and "Fever", which were never assigned to a test request. These syndromes represent a new source of information for surveillance.

These results fit well with the pilot study which found the clinical history was typically incomplete but contained additional information for syndromic surveillance that was not available from monitoring the test request alone and that monitoring syndromes or test requests alone would provide incomplete information nearly a third of the time.

Conclusions

We found monitoring syndromes, in addition to test requests, to be useful and necessary for completeness. Monitoring clinical history provided additional information not available from test requests alone. We recommend the syndromes "Sudden Death" and "Fever" be monitored as these syndromes always provided additional information not available in test requests. Other syndromes that provide new information should be investigated across species and in various clinical scenarios. Accumulating baseline data for all syndromes is recommended to create more accurate models for syndromic surveillance and improve data retrieval for retrospective studies. Despite poor use of the new general submission form and the syndrome check boxes, future compliance is likely to improve significantly with the implementation of online submission and thanks to the continuous training and consultation provided by the NYSVDL staff.

Keywords

Syndromic Surveillance; Veterinary Diagnostic Laboratory; Veterinary Surveillance

Acknowledgments

We would like to thank Dr. Robert Gilmour and the Cornell University Veterinary Investigator Program for supporting this research.

References

1. Shaffer, L., Funk, J., Rajala-Schultz, P., Wallstrom, G., Wittum, T., Wagner, M., Saville, W. (2007) Early Outbreak Detection Using an Automated Data Feed of Test Orders from a Veterinary Diagnostic Laboratory. In: D. Zeng et al. (Ed), BioSurveillance 2007, pp. 1–10
2. Glickman, L.T., Moore, G.E., Glickman, N.E., Caldanaro, R.J., Aucoin, D., Lewis, H.B. (2006) Purdue University–Banfield National Companion Animal Surveillance Program for Emerging and Zoonotic Diseases Vector-Borne and Zoonotic Diseases. 6(1), 14-23.
3. Dorea, F.C., Sanchez, J., Crawford, W.R. (2011) Veterinary syndromic surveillance: Current initiatives and potential for development. Preventive Veterinary Medicine 101, 1-17

*Kylius Wilkins
E-mail: kmw97@cornell.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

ISDS 2012 Conference Abstracts

The Black Canyon Forecast Station: Experiences And Lessons Learned

James M. Wilson*[1, 2], Bonnie Koehler[3], Kathleen Sramek[2] and Treve Henwood[2]

[1]Black Canyon Forecast Station, Delta, CO, USA; [2]Delta County Memorial Hospital, Delta, CO, USA; [3]Delta County Health and Human Services, Delta, CO, USA

Objective

To evaluate the sociological effect on indigenous biological event signature recognition and community resilience due to the operational activities of an infectious disease forecast station.

Introduction

The nation's first operational infectious disease forecast station, modeled after warning protocols developed in the meteorology community, was activated in 2011. The approach was originally pioneered in Haiti following the 2010 earthquake.

Methods

We assembled global event signature and forecast libraries that reflected locally diagnosed infectious disease activity and infrastructure impact in a rural community from a public health, veterinary, and human clinical medicine perspective. The deployment site is home to a variety of infectious disease including hantavirus, plague, tularemia, and West Nile in the context of high wildlife-livestock-human interfacing. Information derived from the issuance of forecasts coupled to situational awareness was shared with the public, local officials, public health officers, veterinarians, healthcare providers, and patients through various social media methods.

Results

Provision of 30-60-90 day forecasts for routine and non-routine endemic infectious disease activity and impact facilitated better coordination of public health messaging and daily conversation with patients in the inpatient and outpatient settings. The signature of an unusual, infrastructure-disruptive outbreak of metapneumovirus and respiratory syncytial virus was recognized and communicated with enough time to activate effective clinical mitigation protocols. Cost estimates demonstrated financial benefit at a local level to anticipating surges of infectious disease activity with enough time to mitigate patient demand. Community-wide engagement with infectious disease forecasts and live event advisories included the promotion of proactive infection control and public health surveillance and response, healthcare provider recognition of non-routine infectious disease, clinical sampling and diagnostic testing protocols, clinician and patient education, and synchronization of proactive disease reporting both in the routine daily clinical setting and in times of crisis. Collateral benefit of consistent messaging delivered to the public by the participating entities was noted. Community awareness of the repertoire of indigenous infectious disease activity was expanded beyond the official public health notification list. Neither issuance of infectious disease forecasts nor advisories issued during crises triggered an influx of anxious well phone calls or visits to the medical system that was deemed operationally relevant.

Conclusions

Activation of a local infectious disease forecast station modeled after a local weather station promotes routine communication of a broader array of infectious disease activity than that monitored by public health; facilitates proactive, cost effective healthcare; and enabled recognition of unusual, disruptive infectious activity with enough time to enable mitigation of clinical, infrastructure, and financial impact to the community. Routine communication of comprehensive infectious disease forecast and situational awareness information promotes community adaptive fitness to a wide variety of infectious hazards. The results suggest it is possible to transform the traditional public health model of data collection and analysis to one of transparent and open data availability to support innovative reduction in morbidity and mortality.

Keywords

biosurveillance; forecast; meteorology

Acknowledgments

The authors would like to acknowledge the tremendous contributions of the staff of Ascel Bio LLC for the design and management of the Black Canyon Forecast Station; the personal contributions of Mr. Michael Smith regarding meteorological warning operations; Delta County Memorial Hospital: Betty Kahrs, Janet Moore, Jason Cleckler, Bev Carlson, Randall Koehn, Johanna Roeber, and Tom Mingen; David Van Metre of Colorado State University and Delta County Colorado State University Agriculture Extension Agent Robbie B. LaValley; and Colorado Department of Agriculture Field Veterinarian, Dan Love DVM.

*James M. Wilson
E-mail: jwilson@ascelbio.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Early Detection of Influenza Activity Using Syndromic Surveillance in Missouri

Fei Wu* and Amy Kelsey

Missouri Department of Health and Senior Services, Jefferson City, MO, USA

Objective

To assess how weekly percent of influenza-like illness (ILI) reported via Early Notification of Community-based Epidemics (ESSENCE) tracked weekly counts of laboratory confirmed influenza cases in five influenza seasons in order to evaluate the early warning potential of ILI in ESSENCE and improve ongoing influenza surveillance efforts in Missouri.

Introduction

Syndromic surveillance is used routinely to detect outbreaks of disease earlier than traditional methods due to its ability to automatically acquire data in near real-time. Missouri has used emergency department (ED) visits to monitor and track seasonal influenza activity since 2006.

Methods

The Missouri ESSENCE system utilizes data from 84 hospitals, which represents up to 90 percent of all ED visits occurring in Missouri statewide each day. The influenza season is defined as starting during Centers for Disease Control and Prevention (CDC) week number 40 (around the first of October) and ending on CDC week 20 of the following year, which is usually at the end of May.

A confirmed influenza case is laboratory confirmed by viral culture, rapid diagnostic tests, or a four-fold rise in antibody titer between acute and convalescent serum samples. Laboratory results are reported on a weekly basis. To assess the severity of influenza activity, all flu seasons were compared with the 2008-09 season, which experienced the lowest influenza activity based on laboratory data. Analysis of variance (ANOVA) was applied for this analysis using Statistical Analysis Software (SAS) (version 9.2).

The standard ESSENCE ILI subsyndrome includes ED chief complaints that contain keywords such as “flu”, “flulike”, “influenza” or “fever plus cough” or “fever plus sore throat”. The ESSENCE ILI weekly percent is the number of ILI visits divided by total ED visits.

Time series of weekly percent of ILI in ESSENCE were compared to weekly counts of laboratory confirmed influenza cases. Spearman correlation coefficients were calculated using SAS. The baseline refers to the mean of three flu seasons with low influenza activity (2006-07, 2008-09 and 2010-11 seasons). The threshold was calculated as this baseline plus three standard deviations.

The early warning potential of the ESSENCE weekly ILI percent was evaluated for five consecutive influenza seasons, beginning in 2006. This was accomplished by calculating the time lag between the first ESSENCE ILI warning versus the first lab confirmed influenza warning. A warning was identified if either lab confirmed case counts or weekly percent of ILI crossed over their respective baselines.

Results

For each influenza season evaluated, weekly ILI rates reported via ESSENCE were significantly correlated with weekly counts of laboratory-confirmed influenza cases (Table 1). The baseline of ILI activity in ESSENCE was 1.8 ILI /100 ED visits/week and the threshold was set at 4.1 ILI visits per 100 ED visits/week. The ESSENCE ILI baseline provided, on average, two weeks of advanced warning for seasonal influenza activity. Figure 1 shows that two influenza seasons (2007-08 and 2009-10) were more severe than others examined based on the ESSENCE percent ILI threshold analysis, this result is consistent with the examination of severity of influenza activity based on lab confirmed influenza data ($p<0.05$).

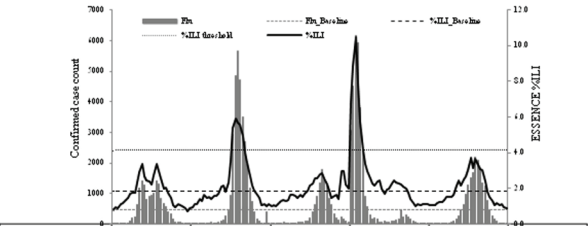
Conclusions

The significant correlation between ILI surveillance in ESSENCE and laboratory confirmed influenza cases justifies the use of weekly ILI percent in ESSENCE to describe seasonal influenza activity. The ESSENCE ILI baseline and threshold provided advanced warning of influenza and allowed for the classification of influenza severity in the community.

Table 1. Correlation between laboratory confrmed influenza cases and ESSENCE ILI weekly percent in five influenza seasons, 2006-2011

2006-2007		2007-2008		2008-2009		2009-2010		2010-2011	
r	p-value	r	p-value	r	p-value	r	p-value	r	p-value
0.936	<0.0001	0.889	<0.0001	0.773	<0.0001	0.817	<0.0001	0.889	<0.0001

Figure 1. Number and baseline of lab confirmed influenza cases, ESSENCE weekly ILI percent and baseline, and ESSENCE ILI threshold for five consecutive influenza seasons, 2006-2011.



Influenza Season	2006-07	2007-08	2008-09	2009-10	2010-11	Average
Time Lag (weeks)	0	3	3	*	2	2

*Time lag was calculated based on the difference between the first ESSENCE weekly ILI percent warning and the first lab confirmed influenza warning.
**Time lag calculation was not possible during the 2009-2010 influenza season because H1N1 Influenza A emerged prior to the regular influenza season.

Keywords

ESSENCE; syndromic surveillance; influenza-like illness (ILI); baseline; threshold

Acknowledgments

We thank Lesha Peterson, Rong He and Peggy Hartman at the Missouri Department of Health and Senior Services for providing influenza case data.

*Fei Wu
E-mail: Fei.Wu@health.mo.gov

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

An Integrated Syndromic Surveillance System for Monitoring Scarlet Fever in Taiwan

Wan-Jen Wu*, Yu-Lun Liu, Hung-Wei Kuo, Wan-Ting Huang, Shiang-Lin Yang and Jen-Hsiang Chuang

Epidemic Intelligence Center, Taiwan Centers for Disease Control, Taipei City, Taiwan

Objective

To develop an integrated syndromic surveillance system for timely monitoring and early detection of unusual situations of scarlet fever in Taiwan, since Hong Kong, being so close geographically to Taiwan, had an outbreak of scarlet fever in June 2011.

Introduction

Scarlet fever is a bacterial infection caused by group A streptococcus (GAS). The clinical symptoms are usually mild. Before October, 2007, case-based surveillance of scarlet fever was conducted through notifiable infectious diseases in Taiwan, but was removed later from the list of notifiable disease because of improved medical care capacities. In 2011, Hong Kong had encountered an outbreak of scarlet fever (1,2). In response, Taiwan developed an integrated syndromic surveillance system using multiple data sources since July 2011.

Methods

More than 99% of the Taiwan population is covered by National Health Insurance. We first retrospectively evaluated claims data from the Bureau of National Health Insurance (BNHI) by comparing with notifiable diseases reporting data from Taiwan Centers for Disease Control (TCDC). The claims data included information on scarlet fever diagnosis (ICD-9-CM code 034.1), date of visits, location of hospitals and age of patients from outpatient (OPD), emergency room (ER) and hospital admissions. Daily aggregate data of scarlet fever visits or hospitalizations were prospectively collected from BNHI since July 2011. Over 70% of the deaths in Taiwan are reported to the Office of Statistics of Department of Health electronically. We obtained daily data on electronic death certification data and used SAS Enterprise Guide 4.3 (SAS Institute Inc., Cary, NC, USA) for data management and analysis. Deaths associated with scarlet fever or other GAS infections were identified by text mining from causes of death with keywords of traditional Chinese 'scarlet fever', 'group A streptococcus' or 'toxic shock syndrome' (3).

Results

From January 2006 to September 2007, the monthly OPD data with ICD-9-CM code 034.1 from BNHI showed strong correlation with TCDC's notifiable disease data ($r=0.89$, $p<0.0001$). From July 6, 2008 (week 28) through July 28, 2012 (week 30), the average weekly numbers of scarlet fever visits to the OPD, ER and hospital admissions were 37 (range 11–70), 7 (range 0–20) and 3 (range 0–9). Eighty-five percent of the scarlet fever patients were less than 10 years old. In Taiwan, scarlet fever occurred year-round with seasonal peaks between May and July (Fig. 1). From January 2008 to July 2012, we identified 12 potential patients (9 males, age range 0–82 years) who died of GAS infections. No report had listed 'scarlet fever' as cause of death during the study period.

Conclusions

Taiwan has established an integrated syndromic surveillance system to timely monitor scarlet fever and GAS infection associated mortalities since July 2011. Syndromic surveillance of scarlet fever through BNHI correlated with number of scarlet fever cases through notifiable disease reporting system. Text mining from cause of death with the used keywords may have low sensitivities to identify patients who died of GAS infection. In Taiwan, syndromic surveillance has also been applied to other diseases such as enterovirus, influenza-like illness, and acute diarrhea. Interagency collaborations add values to existing health data in the government and have strengthened TCDC's capacity of disease surveillance.

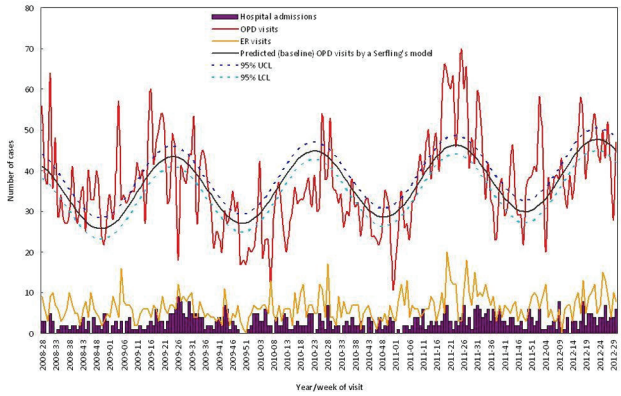


Fig. 1. Weekly numbers of nationwide scarlet fever OPD and ER visits, and hospital admissions, with baseline OPD visits and 95% confidence interval calculated by a Serfling's model, week 28 of 2008 to week 30 of 2012.

Keywords

syndromic surveillance; Taiwan; scarlet fever; claims data

Acknowledgments

We thank the Bureau of National Health Insurance and Office of Statistics of Department of Health for providing data required for this study.

References

1.Hsieh YC, Huang YC. Scarlet fever outbreak in Hong Kong, 2011. J Microbiol Immunol Infect. 2011;44:409-11.
2.Tse H, Bao JY, Davies MR, et al. Molecular characterization of the 2011 Hong Kong scarlet Fever outbreak. J Infect Dis. 2012;206:341-51.
3.Chen PJ, Wu WJ, Huang WT, Chuang JH. An early warning system for pneumonia and influenza mortality in Taiwan. Emerging Health Threats Journal 2011;4: 11024.

*Wan-Jen Wu
E-mail: teatea@cdc.gov.tw

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

The Organizational Structures and Human Resources Allocation of Infectious Disease Surveillance System in Rural China

Biao Xu*[1], Qi Zhao[1], Huijian Cheng[2], Tao Tao[1], Yipin Zhu[1], Miao Yu[1] and Hui Yuan[2]

[1]School of Public Health, Fudan University, Shanghai, China; [2]Jiangxi Provincial Center for Disease Control and Prevention, Nanchang, China

Objective

To understand the structure and capacity of current infection disease surveillance system, and to provide baseline information for developing syndromic surveillance system in rural China.

Introduction

To meet the long-term needs of public health and social development of China, it is in urgency to establish a comprehensive response system and crisis management mechanism for public health emergencies. Syndromic surveillance system has great advantages in promoting early detection of epidemics and reducing the burden of disease outbreak confirmation (1). The effective method to set up the syndromic surveillance system is to modify existing case report system, improve the organizational structures and integrate new function with the traditional system.

Methods

Since August 2011, an integrated syndromic surveillance project (ISSC) has been implemented in China. Before the launching of the project, a cross-sectional study was carried out in Fengxin County and Yongxiu County of Jiangxi province during October 11 to 18, 2010. Institution information were investigated in the county hospital, township hospital and County Center for Disease Control and Prevention (CDC) to understand the performance of existing case report system for notifiable infectious diseases with regard to its structure, capacity and data collection procedure. Health care workers from each township hospital and village health station were questionnaire interviewed for information on qualification of human resources, basic healthcare delivery condition, hardware and software needs for ISSC.

Results

An internet-based real-time (quasi real-time) case report system for notifiable infectious diseases, based on the three-tier public health service System, had been established in these two counties since 2004. The farthest end of net user in case report system was township hospital. Blood routine test, urine routine test, B ultrasound and electrocardiogram were available in all township hospitals. There was no laboratory equipment in village health stations in these two counties. All the township hospitals in these two counties were equipped with land-line telephones and desktop computers. The internet covers all township hospitals in both counties. Most clinical doctors in township hospital(TH) and village health station(VHS) were male. The age of doctors ranged from 21 to 72 years old, with the average at 42 and median at 40 years. The village health workers were significantly older, less educated and served in health care longer than the township hospital doctors. In Yongxiu County, 95.6% of the village health stations were equipped with computers, including private-owned computers, and 80.7% of them had access to the internet; while in Fengxin County, 66.5% of the village health stations possessed computers, among which most were private property of village doctors, and only 44.2% of them had access to the internet.

Conclusions

The current case report system, with full coverage and stable human resource, has established a solid basis for developing syndromic surveillance system in rural China. The syndromic surveillance system could play its role in early detection of infectious disease outbreaks in rural area where laboratory service for infectious disease diagnosis are not available. However, the lack of computerized patient registration in village and township health care facilities and incomplete internet coverage in rural area and relatively low quality of human resource in village level should be taken into consideration seriously before establishing the syndromic surveillance system in rural China.

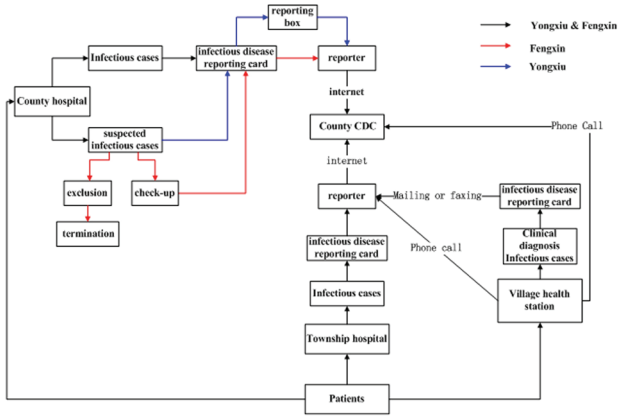


Figure1 Flowchart of case report system for notifiable infectious disease in different level of health facilities in Fengxin and Yongxiu County

Keywords

Syndromic surveillance; rural area; human resources; case report system

Acknowledgments

This study was funded by [European Union's] [European Atomic Energy Community's] Seventh Framework Programme ([FP7/2007-2013] [FP7/2007-2011]) under grant agreement no. [241900].

References

1. Heffernan R, Mostashari F, Das D, et al.Syndromic Surveillance in Public Health Practice, New York City. Emerging Infectious Diseases2004;10(5):858- 864.

*Biao Xu
E-mail: bxu@shmu.edu.cn

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Using Medications Sales from Retail Pharmacies for Syndromic Surveillance in Rural China

Weirong Yan*[1, 2], Liwei Cheng[2], Li Tan[2], Miao Yu[3], Shaofa Nie[2], Biao Xu[3], Lars Palm[4] and Vinod Diwan[1]

[1]Karolinska Institutet, Stockholm, Sweden; [2]Huazhong University of Science and Technology, Wuhan, China; [3]Fudan University, Shanghai, China; [4]Future Position X, Gavle, Sweden

Objective

To use an unconventional data - pharmaceutical sales surveillance for the early detection of respiratory and gastrointestinal epidemics in rural China.

Introduction

Drug sales data as an early indicator in syndromic surveillance has attracted particular interest in recent years (1, 2), however previous studies were mostly conducted in developed countries or areas. In China, many people (around 60%) choose self-medication as their first option when they encounter a health problem (3), and electronic sales information system is gradually used by retail pharmacies, which makes drug sales data become a promising data source for syndromic surveillance in China.

Methods

This experimental study was conducted in four rural counties in central China. From Apr. 1st 2012, there are 56 retail pharmacies joined the study, including 21 county pharmacies and 35 township pharmacies. 123 drugs were selected under surveillance based on the analysis of local historical sales volume and consultation with local pharmacists, including 19 antibiotics, 15 antidiarrheal medications, 9 antipyretics, 41 compound cold medicine, and 39 cough suppressants. Daily sales volume of the selected drugs was recorded into the database by pharmacy staff at each participating unit via electronic file importing or manual entering. Figure 1 showed the user interface for data viewing, query and export. Field training and supervision were regularly conducted to ensure the data quality.

Results

From Apr. 1st to Jun. 30th 2012, there were 103814 sales records reported in the system, including 44464 (42.83%) records from county pharmacies and 59350 (57.17%) from township pharmacies. Among all surveillance drugs, the sales of compound cold medicine accounted for the largest proportion (43.42%), followed by antibiotics (22.52 %), cough suppressants (18.50%), antidiarrheal drugs (9.49%) and antipyretics (6.06 %). More than 80% data were reported into the system within 24 hours after the sales date, and the reporting timeliness of county pharmacies improved with time (table 1). Missing report rate was less than 5% for all surveillance units. Several reporting mistakes were found during the first three-month implementation, which might be due to system bugs, data provider unfamiliar with the system especially when manual reporting, data providers' carelessness, and some pharmacies reluctant to share sales data amongst others.

Conclusions

Although the current reporting timeliness and completeness are satisfying, it is noteworthy the quality of data is not stable during the beginning phase of the implementation. Further validation of the data will be required. To ensure the accuracy of data and the effective and sustainable deployment of the system, it is imperative to establish a data sharing policy between pharmacies and public health agencies, and achieve automated data collection to avoid additional human labor involvement.

Table 1: Timeliness of reporting records from various pharmacies, Apr. 1st - Jun. 30th, 2012

Report time after sales date	April		May		June	
	County N(%)	Township N(%)	County N(%)	Township N(%)	County N(%)	Township N(%)
within 24 h	11359(75.84)	16653(85.6)	12483(81.80)	17749(87.99)	12225(85.93)	15977(81.01)
24 h-48h	1523(10.25)	1001(5.15)	1487(9.74)	1760(8.72)	1321(9.29)	2224(11.28)
later than 48h	2084(13.91)	1801(9.26)	1290(8.45)	663(3.29)	680(4.78)	1522(7.72)
Sum	14978	19455	15260	20172	14226	19723

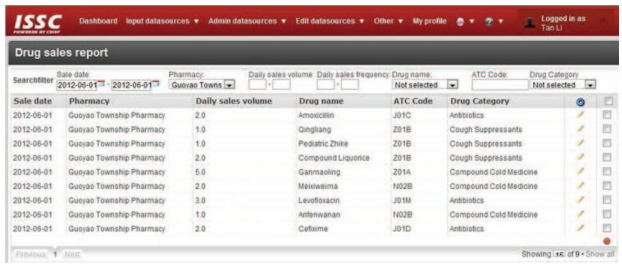


Figure 1 User interface in the system for data viewing, query and export

Keywords

Syndromic surveillance; Medication sales; Developing settings

Acknowledgments

The study is financially supported by a grant under the European Union Framework Program 7 (project no: 241900).

References

1. Magruder S. Evaluation of over - the - counter pharmaceutical sales as a possible early warning indicator of human disease. Johns Hopkins APL technical digest 2003;24(4):349-53.
2.Das D, Metzger K, Heffernan R, Balter S, Weiss D, Mostashari F. Monitoring over-the-counter medication sales for early detection of disease outbreaks—New York City. MMWR 2005;54 Suppl:41-6.
3. Wen Y, Lieber E, Wan D, Hong Y; NIMH Collaborative HIV/STD Prevention Trial Group. A qualitative study about self-medication in the community among market vendors in Fuzhou, China. Health Soc Care Community. 2011;19(5):504-13.

*Weirong Yan
E-mail: weirongy@gmail.com

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

A Bayesian Approach to Characterize Hong Kong Influenza Surveillance Systems

Ying Zhang*, Ali Arab and Michael A. Stoto

Georgetown University, Washington, DC, USA

Objective

Our goal is to develop a statistical model for characterizing influenza surveillance systems that will be helpful in interpreting multiple streams of influenza surveillance data in future outbreaks.

Introduction

Syndromic surveillance has been widely used in influenza surveillance worldwide. However, despite the potential benefits created by the large volume of data, biases due to the changes in healthcare seeking behavior and physicians' reporting behavior, as well as the background noise caused by seasonal flu epidemics, contribute to the complexity of the surveillance system and may limit its utility as a tool for early detection [1,2]. Since most current analysis methods are developed for outbreak detection, there are few tools to characterize influenza surveillance data for situational awareness purposes in a quantitative manner.

Hong Kong Centre for Health Protection (CHP) has a comprehensive influenza surveillance system based on healthcare providers, laboratories, schools, daycare centers and residential care homes for the elderly. Hong Kong usually experiences a summer peak in July and August [3], which potentially doubles the data volume and constitutes a natural experiment to assess the effect of school-age children in the influenza transmission dynamics. The richness of the available data and the unique epidemiological characteristics make Hong Kong an ideal study object to develop and evaluate our model.

Methods

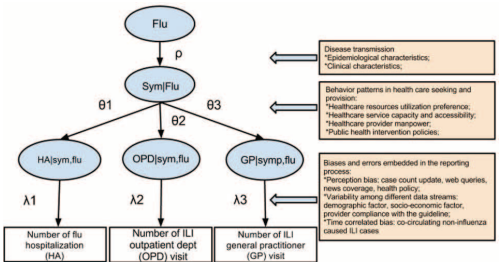
We have constructed a Bayesian statistical model for influenza surveillance data by parameterizing factors that describe disease transmission, behavior patterns in health care seeking and provision, and biases and errors embedded in the reporting process (Figure 1). The prior distributions are selected for each of the parameters to reflect knowledge of influenza epidemiology and the likely biases in each data system. Using the Markov Chain Monte-Carlo (MCMC) method in OpenBUGS, a posterior distribution can be generated for every parameter to characterize each data stream. The ratios of specific pairs of data streams are assessed in order to identify patterns in the change of ratios at different stage of the flu season.

Results

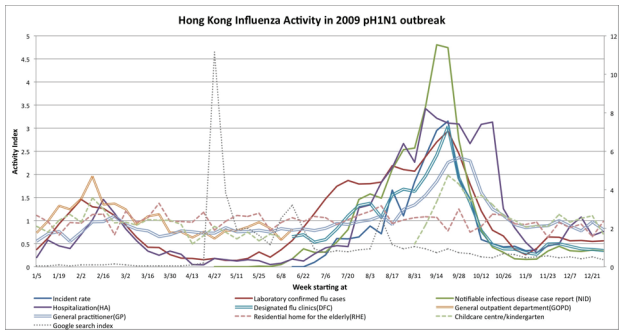
Preliminary results, as shown in Figure 2, incorporate confirmed influenza infection (solid line), influenza-like illness (double solid line), fever cases (dashed line), and Google search index (round dashed line). Although most of these data series track together, differences among them suggest reporting bias related to public awareness, which will be addressed in the statistical modeling.

Conclusions

The posterior distribution for parameters and ratios between individual data streams can be used to characterize influenza surveillance systems in terms of tendency in peak early or late, or to over or under represent actual influenza cases. To better interpret syndromic surveillance data for situational awareness purposes, behavioral data related to healthcare resource utilization, such as the percentage of intended GP visit among people with ILI, need to be collected together with the flu activity surveillance.



Conceptual model for influenza surveillance statistical model
Blue circles: unobservable true value; white boxes: observation; orange boxes: factors



Hong Kong flu activity in 2009 pH1N1 outbreak

Keywords

situational awareness; modeling; epidemiology; influenza surveillance; Bayesian

Acknowledgments

CDC, Hong Kong University
Center for Health Protection, Hong Kong SAR

References

1.Zhang, Y., May, L., & Stoto, M. A. (2011). Evaluating syndromic surveillance systems at institutions of higher education (IHEs): A retrospective analysis of the 2009 H1N1 influenza pandemic at two universities. BMC Public Health, 11, 591.

2. Stoto MA (2012) The Effectiveness of U.S. Public Health Surveillance Systems for Situational Awareness during the 2009 H1N1 Pandemic: A Retrospective Analysis. PLoS ONE 7(8): e40984.

3. Chan, P. K. S., Mok, H. Y., Lee, T. C., Chu, I. M. T., Lam, W., & Sung, J. J. Y. (2009). Seasonal influenza activity in Hong Kong and its association with meteorological variations. Journal of Medical Virology, 81(10), 1797-1806.

*Ying Zhang
E-mail: yz62@georgetown.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

The Distribution of Infectious Related Symptoms in an Internet-based Syndromic Surveillance System in Rural China

Qi Zhao[1], Fuqiang Yang[2], Lars Palm[3], Hui Yuan[2], Weirong Yan[4] and Biao Xu*[1]

[1]School of Public Health, Fudan University, Shanghai, China; [2]Jiangxi Provincial Center for Disease Control and Prevention, Nanchang, China; [3]Future Position X, Gavle, Sweden; [4]Division of Global Health (IHCAR), Department of Public Health Sciences, Karolinska Institutet, Stockholm, Sweden

Objective

To describe the distribution of the infectious related symptoms in an internet-based syndromic surveillance system reported by doctors in village health stations, township and county hospitals in rural Jiangxi Province, China, and to identify the major infectious diseases for syndromic surveillance in different levels of health facility.

Introduction

Syndromic surveillance system, which collects non-specific syndromes in the early stages of disease development, has great advantages in promoting early detection of epidemics and reducing the burden of disease confirmation (1). It is especially effective for surveillance in resource-poor settings, where laboratory confirmation is not possible or practical (2). Integrating syndromic surveillance with traditional case report system may generate timely, effective and sensitive information for early warning and control of infectious diseases in rural China (3). A syndromic surveillance system (ISSC) has been implemented in rural Jiangxi Province of China since August 2011.

Methods

Doctors and health workers in the healthcare surveillance units of ISSC, including village health station, township hospital and county hospital, used an internet-based electronic system to collect information of daily outpatients, which included 10 categories of infectious disease related symptoms, i.e., cough, fever, sore throat, diarrhea, headache, rash, nausea/vomit, mucocutaneous hemorrhage, convulsion and disturbance of consciousness. The data from August 1st to December 31st 2011 were extracted from database and analyzed using SPSS 16.0. The combination of symptoms was also analyzed to identify patients with the syndrome of influenza-like illness (ILI) and fever-gastrointestinal syndrome (FGS). ILI were composed by fever (>=38 degree centigrade) plus cough or fever plus sore throat, and FGS were defined as fever plus vomit or diarrhea.

Results

Two county hospitals (CH), 4 township hospitals (TH) and 50 village health stations (VHS) were selected as surveillance unites in the pilot study during 2011/8/1 to 2011/12/31. In total, 152270 outpatient visits were reported, and 35395 patients had a chief complain of at least one surveillance symptom. Of these symptomatic patients, 24130 (68.2%) were from VHS, 4995 (14.1%) from TH and 6810 (19.2%) from CH. The proportion of patients with targeting symptom accounted for 15.5%, 66.4% and 23.9% of total outpatients in CH, TH and VHS respectively. The first 3 reported symptoms were cough (61.8%), fever (28.4%), and sore throat (23.4%), whereas mucocutaneous hemorrhage, convulsion and disturbance of consciousness were the least frequently reported symptoms in all surveillance units. Overall 3582 ILI and 1160 FGS cases were reported accounting for 35% and 11% of fever cases respectively. Of the reported ILI and FGS cases, 75% ILI and 55.9% FGS cases were reported by health workers in the VHS.

Conclusions

Cough, fever and sore throat were the top surveillance symptoms, and the respiratory infectious diseases had more chance to be reported in syndromic surveillance system in rural Jiangxi Province. Training on infectious disease diagnosis especially respiratory diseases for village health workers should be enhanced since large numbers of patients are likely to visit the village health stations.

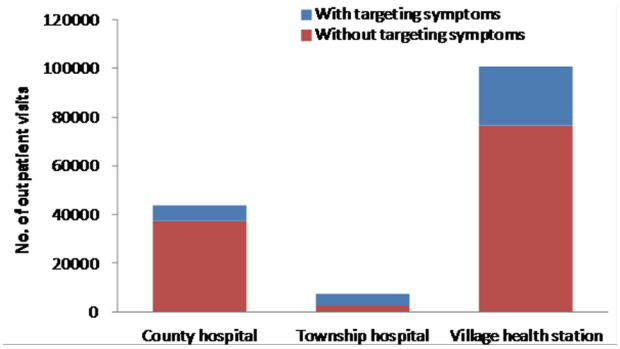


Figure1 Distributions of symptomatic patients in different level health facilities of rural China

Keywords

Syndromic surveillance; rural; influenza-likes illness; fever-gastrointestinal syndrome

Acknowledgments

This study was funded by [European Union's] [European Atomic Energy Community's] Seventh Framework Programme ([FP7/2007-2013] [FP7/2007-2011]) under grant agreement no. [241900].

References

1. Henning KJ. What is syndromic surveillance? MMWR Morb Mortal Wkly Rep 2004;53 Suppl:5-11.
2. Siswoyo H, Permana M, Larasati RP, et al. EWORS: using a syndromic-based surveillance tool for disease outbreak detection in Indonesia. BMC Proceedings 2008, 2(Suppl 3):S3
3. Reingold A. If syndromic surveillance is the answer, what is the question.Biosecur Bioterr 2003;1:1–5.

*Biao Xu
E-mail: bxu@shmu.edu.cn

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Automated Surveillance of Outpatients with Pneumonia: A Performance Evaluation

Hongzhang Zheng[1, 2], Tariq Siddiqui[1, 2] and Sylvain DeLisle*[1, 2]

[1]VA Maryland Health Care System, Baltimore, MD, USA; [2]Medicine, University of Maryland, Baltimore, MD, USA

Objective

To determine if influenza surveillance should target all patients with acute respiratory infections (ARI) or only track pneumonia cases.

Introduction

Effective responses to epidemics of infectious diseases hinge not only on early outbreak detection, but also on an assessment of disease severity. In recent work, we combined previously developed ARI case-detection algorithms (CDA) [1] with text analyses of chest imaging reports to identify ARI patients whose providers thought had pneumonia. In this work, we asked if a surveillance system aimed at patients with pneumonia would outperform one that monitors the full severity spectrum of ARI.

Methods

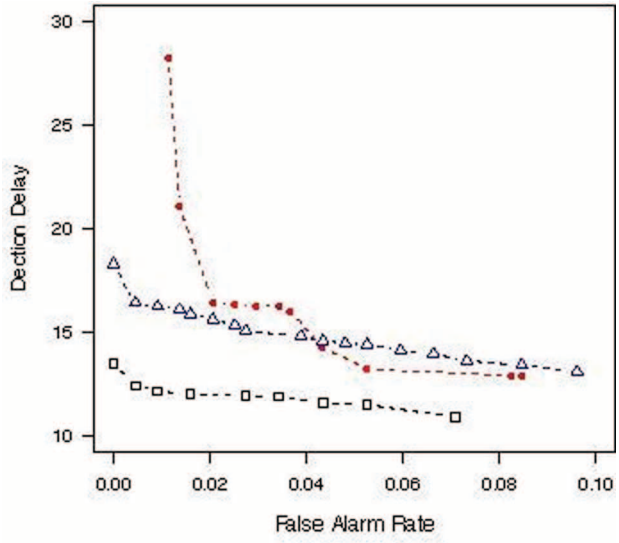
Time series of daily casecounts (backgrounds) were created by applying either an ARI CDA (ARI ICD-9 codeset [1]) or a Pneumonia CDA (ARI ICD-9 codes AND chest imaging obtained AND positive results from automated text analysis that identify those chest imaging reports that support the diagnosis of pneumonia) to electronic medical record (EMR) entries related to outpatient encounters at the VA Maryland Health Care System. We used an age-structured metapopulation influenza epidemic model for Baltimore to inject factitious influenza cases into backgrounds. Injections were discounted by the known sensitivity of the ARI CDA [1]. For injections into the pneumonia backgrounds time series, factitious ARI cases were further discounted by the expected pneumonia rate in the modeled influenza epidemic (10%). From the time of injection, EARS or CUSUM statistics [2,3] were applied on each successive day on paired background+injection vs. background-only time series. Each injection-prospective-surveillance cycle was repeated 52 times, each time with the injection shifted to a different week of the one-year study period (2010-11). We computed: 1) the "Detection Delay", the average time from injection to the first alarm present in the background+injection dataset but absent from the background-only dataset; 2) the "False-Alarm Rate" (FAR), defined as the number of unique false-alarms originating in the background-only dataset during the study year, divided by 365 days. To create activity monitoring operating characteristic (AMOC) curves, we empirically determined the corresponding Delay-FAR pairs over a wide range of alarm thresholds.

Results

The Figure compares AMOC curves for otherwise identical surveillance systems that included either any ARI outpatient visits (red circles, using the EARS W2c statistic [2] and blue triangles, using the CUSUM statistic) or pneumonia (blue triangles, using the CUSUM statistic modified for sparse data [3]). Note that Detection Delay (y-axis) is lower at any given FAR when surveillance aims at patients with pneumonia. Sensitivity analysis suggests that this advantage remains true when pneumonia complicates influenza ≥ 5% of the time.

Conclusions

Our results suggest that EMR-based influenza surveillance that targets patients with pneumonia can outperform systems that monitor all ARI patients.



Keywords

influenza; surveillance; modeling; simulations

References

[1] DeLisle S, South B, Anthony JA, Kalp E, Gundlapalli A, et al. Combining Free Text and Structured Electronic Medical Record Entries to Detect Acute Respiratory Infections. PLoS ONE (2010) 5(10): e13377

[2] Hutwagner L, Thompson W, Seeman GM, Treadwell T. The bioterrorism preparedness and response early aberration reporting system (EARS). Journal of Urban Health: Bulletin of the New York Academy of Medicine 2003; 80(2) (Suppl. 1) i89-i96.

[3] He, S., Huang, W. and Woodall, W. H. CUSUM charts for monitoring a zero-inflated Poisson process. Qual. Reliab. Engng. Int. (2012) 28: 181–192.

*Sylvain DeLisle
E-mail: sdelisle@umaryland.edu

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.

Utility of Syndromic Surveillance Using Novel Clinical Data Sources

Rebecca Zwickl*, Charles Ishikawa and Laura C. Streichert

ISDS, Brighton, MA, USA

Objective

To document the current evidence base for the use of electronic health record (EHR) data for syndromic surveillance using emergency department, urgent care clinic, hospital inpatient, and ambulatory clinical care data.

Introduction

Historically, syndromic surveillance has primarily involved the use of near real-time data sent from hospital emergency department (EDs) and urgent care (UC) clinics to public health agencies. The use of data from inpatient and ambulatory settings is now gaining interest and support throughout the United States, largely as a result of the Stage 2 and 3 Meaningful Use regulations [1]. Questions regarding the feasibility and utility of applying a syndromic approach to these data sources are hampering the development of systems to collect, analyze, and share this potentially valuable information. Solidifying the evidence base and communicating the results to the public health surveillance community may help to initiate and build support for using these data to advance surveillance functions.

Methods

We conducted a literature search in the published and grey literature that scanned for relevant articles in the Google Scholar, Pub Med, and EBSCO Information Services databases. Search terms included: "inpatient/ambulatory electronic health record"; "ambulatory/inpatient/hospital/outpatient/chronic disease syndromic surveillance"; and "EHR syndromic surveillance". Information gleaned from each article included data use, data elements extracted, and data quality indicators. In addition, several stakeholders who provided input on the September 2012 ISDS Recommendations [2] also provided articles that were incorporated into the literature review.

ISDS also invited speakers from existing inpatient and ambulatory syndromic surveillance systems to give webinar presentations on how they are using data from these novel sources.

Results

The number of public health agencies (PHAs) routinely receiving ambulatory and inpatient syndromic surveillance data is substantially smaller than the number receiving ED and UC data. Some health departments, private medical organizations (including HMOs), and researchers are conducting syndromic surveillance and related research with health data captured in these clinical settings [2].

In inpatient settings, many of the necessary infrastructure and analytic tools are already in place. Syndromic surveillance with inpatient data has been used for a range of innovative uses, from monitoring trends in myocardial infarction in association with risk factors for cardiovascular disease [3] to tracking changes in incident-related hospitalizations following the 2011 Joplin, Missouri tornado [3].

In contrast, ambulatory systems face a need for new infrastructure, as well as pose a data volume challenge. The existing systems vary in how they address data volume and what types of encounters they capture. Ambulatory data has been used for a variety of uses, from monitoring gastrointestinal infectious disease [3], to monitoring behavioral health trends in a population, while protecting personal identities [4].

Conclusions

The existing syndromic surveillance systems and substantial research in the area indicate an interest in the public health community in using hospital inpatient and ambulatory clinical care data in new and innovative ways. However, before inpatient and ambulatory syndromic surveillance systems can be effectively utilized on a large scale, the gaps in knowledge and the barriers to system development must be addressed. Though the potential use cases are well documented, the generalizability to other settings requires additional research, workforce development, and investment.

Keywords

Syndromic surveillance; EHR; Meaningful Use

Acknowledgments

We thank the ISDS Meaningful Use Workgroup for their assistance with the literature review, and all the presenters in the ISDS Meaningful Use Webinar series (http://www.syndromic.org/webinars/meaningfuluse). Work supported by CDC through ISDS contract with Task Force for Global Health.

References

1. Health Information Technology for Economic and Clinical Health (HITECH) Act. Title XIII of Division A and Title IV of Division B of the American Recovery and Reinvestment Act of 2009 2009; Pub. L. No. 111-5.
2. ISDS. Electronic Syndromic Surveillance Using Hospital Inpatient and Ambulatory Clinical Care Electronic Health Record Data: Recommendations from the ISDS Meaningful Use Workgroup. 2012. www.syndromic.org
3. Various presenters. ISDS Meaningful Use Webinar Series: 3/1-3/21/2012. http://www.syndromic.org/webinars/meaningfuluse
4. Pavlin JA, Murdock P, Elbert E, Milliken C, Hakre S. Conducting population behavioral health surveillance by using automated diagnostic and pharmacy data systems. MMWR 2004;53 (Supp.):166-172.

*Rebecca Zwickl
E-mail: bzwickl@syndromic.org

ISDS Annual Conference Proceedings 2012. This is an Open Access article distributed under the terms of the Creative Commons Attribution-Noncommercial 3.0 Unported License (http://creativecommons.org/licenses/by-nc/3.0/), permitting all non-commercial use, distribution, and reproduction in any medium, provided the original work is properly cited.