One Health Policy Model

User Guide and Technical Description

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Acknowledgments

The development of the *One Health Policy Model* has benefited from several people and organizations. The Food and Agriculture Organization (FAO) of the United Nations in Rome helped frame the model, especially through the African Sustainable Livestock 2050 (ASL 2050) initiative. The data collection protocol developed through ASL 2050 helped inform our understanding of the types of information available to parameterize the model. The FAO staff in Rome and in the six ASL 2050 countries (Burkina Faso, Egypt, Ethiopia, Kenya, Nigeria, and Uganda) also answered questions about livestock markets and identified topics of interest for stakeholders.

Throughout the model development process, we also benefited from reviews and advice from the modeling staff at EcoHealth Alliance. Early versions of the model were used in workshops in Ethiopia, and our experience with the Ministry of Livestock and Fisheries, Ministry of Health, and FAO/Addis Ababa were invaluable. Reviews and recommendations from DAI staff at the Preparedness and Response (P&R) Project and at the Palladium Group in Washington, DC, were also useful. Finally, we gratefully acknowledge the financial support from USAID, which sponsors P&R.
Executive Summary

Livestock is an important source of household income for millions of people, especially in developing countries. It provides an important source of protein and micro-nutrients for subsistence farmers. Livestock also serve as an important source of insurance, as well as an investment instrument that can be liquidated to cover payments for routine and extraordinary costs.

As Africa continues to experience economic growth, nations are likely to see an increasing demand for and structural changes in the livestock sub-sector. As Africa develops, the increase in demand for livestock products will be linked to the substantial growth and expansion of industrialized production systems. Also, an increasingly urban and more affluent population throughout the continent will demand a more diverse diet, including a larger intake of meat, milk, and eggs. Poultry is expected to be the main source of livestock growth, with other sub-sectors (e.g., bovine, ovine, and porcine sub-sectors) showing similar growth patterns, but at a lower level. Exports to regions—for example, the Middle East—are also expected to grow, relying on high-quality livestock products.

However, several disease-related factors could influence the expected growing demand for livestock. Outbreaks of diseases, such as avian influenza, focused attention on the negative aspects of intensive livestock and poultry production. Newly emerging diseases can have substantial economic and social costs. These types of outbreaks highlight the need to have a policy and regulatory environment that anticipates and responds to these types of outbreaks. In addition, it is estimated that 60–70 percent of recently emerged infectious diseases in humans have been zoonotic. As part of managing this environment, decision-makers need to understand the relationship between animal production, veterinary public health, human public health, and the impact that zoonotic outbreaks could have on economies and societies.

A One Health approach to these issues seeks to understand the complex inter-relationships inherent between increased demand and supply for animal protein and public health risks to humans and to devise strategies and programs to mitigate those risks. This requires a multi-sector approach that brings together public health specialists and authorities, veterinary specialists, and livestock and agricultural ministries.

This technical guide describes a policy modeling tool that can be useful in understanding the complex dynamics at the country level between livestock and human populations in terms of zoonotic disease transmission and its implications. The guide is divided into two parts. Part I, a user’s guide, is an instruction manual for creating an application of the OHPM. Part II includes technical documentation that describes the calculations that underlie the model. The One Health Policy Model, Excel-based file, comprises inter-related modules for the animal population and the human population with key parameters that govern the progression of zoonotic diseases. The model has been populated with data from Kenya, but can be customized with your own data. The dynamic model can be configured for a specified animal species, up to two diseases, five production systems, and three affected human populations. Users define several parameters that govern the dynamics of disease transmission. An important feature of the model is that users can design scenarios that focus on interventions that affect spill-over, human-animal interface, and amplification. Major outputs of the model include the number of cases of the zoonotic disease in animals and humans, deaths due to the disease, disability-adjusted life years (DALYs), and the economic burden of the zoonotic disease. The model also projects the impact of the animal population on greenhouse gas emissions and water use. These outputs can be used for policy and program dialogue around priority One Health issues and to explore policy options via alternative scenarios.

The One Health Policy Model (OHPM) is designed to help decision-makers understand the nature and scale of how changes in the livestock and human populations might impact veterinary, human, and environmental health, including some of the available policy options. The model can generate analytical and scenario-based evidence that will help gain traction with country-specific stakeholders. Because the model takes a tripartite approach to modeling the human population, livestock population, and the environment, it takes a One Health approach and shows the linkages between these three sectors.
Introduction

The Livestock-Zoonosis Paradigm

According to the United Nations (UN) Food and Agriculture Organization (FAO), livestock contribute 40 percent of the global value of agricultural output and support the livelihoods and food security of approximately 1.3 billion people.¹ It provides an important source of protein and micro-nutrients for subsistence farmers and serves as an important source of insurance, as well as an investment instrument that can be liquidated to cover payments for routine and extraordinary costs.

As Africa continues to experience economic growth, nations are likely to see an increasing demand for livestock (including poultry) and structural changes in the livestock sector toward more intensive systems. Globally, it is projected that by 2050 the global production of meat will have increased from 229 tons in 2000 to more than double, to 465 tons in 2050; milk will increase from 580 tons to 1,043 tons during the same time period.² An increasingly urban, and more affluent, population throughout the African continent will demand a more diverse diet, which will include a larger intake of meat, milk, and eggs. Much of the increase for these livestock products will be in the developing countries, which are expected to experience substantial growth and expansion of industrialized production systems. Poultry is expected to be the main source of livestock growth, with other sub-sectors (e.g., bovine, ovine, and porcine) showing similar growth patterns, but at a lower level.

At the same time, human population growth, especially in Africa, will continue over the next 30–40 years. The UN population projections for Africa show an increase from 1.194 billion in 2015 to 2.527 billion in 2050.³ Increases in human numbers mean more contact with the animal population as humans begin to live increasingly closer to animal habitats.

Animal and human population growth also have important environmental consequences. Cattle require water and land for grazing or forage production; they also contribute to greenhouse gas (GHG) emissions. The human population also contributes to environmental stresses.

Briefly, changing livestock numbers and systems not only provide foods and nutrition to a growing human population, but may also have negative impacts, particularly on public health, through zoonoses and antimicrobial resistance (AMR); on the environment through the pollution of soil, water, and air; as well as, in some cases, loss of biodiversity. Impacts on animal health have direct consequences for farmers’ livelihood and, therefore, poverty is another consequence.

Figure 1 summarizes these challenges, showing what we call the livestock-zoonosis paradigm.

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² http://www.fao.org/docrep/010/a0701e/a0701e.pdf, accessed 7.2.2018
³ https://esa.un.org/unpd/wpp/DataQuery/, accessed 7.2.2018
Recent outbreaks of diseases, such as avian influenza, focused attention on the negative aspects of intensive livestock and poultry production. These outbreaks show the need for a policy and regulatory environment that anticipates and responds to these types of outbreaks. Newly emerging diseases can have substantial economic and social costs. The outbreak of H5N1 highly pathogenic avian influenza (HPAI) in Asia, beginning in 2003, resulted in billions of U.S. dollars in economic losses.\(^4\) In addition, it is estimated that 61 percent of recently emerged diseases have been zoonotic.\(^5\) As part of creating this environment, decision-makers need to understand the relationship between animal production, veterinary public health, human public health, and the impact that zoonotic disease outbreaks could have on human health, animal health, economies, and the environment.

Decision-makers also need to understand the nature and size of the threats, know what the policy and program options are, and be able to organize a multi-sector response. A useful approach to help with decision-making in the context of this paradigm is the concept of One Health, which recognizes the interconnectedness between human and animal health, as well as relationships with the environment. “One Health promotes a whole of society approach by incorporating human medicine, veterinary medicine, public health, and environmental information when developing policy and determining interventions to address current challenges threatening today’s globalized world.”\(^6\)

Modeling

It is useful to distinguish three broad categories of models:

1. Research models: answer specific questions
2. Predictive models: predict future events or indicators
3. Policy models: assist decision-makers in understanding a problem and choosing options.

*Research models* answer specific questions about the relationships between variables of interest. For example, how do changes in the interest rate affect key indicators in the economy? Or, does ambient temperature affect crop yields?

*Predictive models* are used to predict future events or indicators. For example, meteorologists use models to predict the weather and the path of large storms. Economists use models to forecast economic indicators.

*Policy models* assist decision-makers in understanding a problem and selecting options for mitigating the situation. For example, policy models have been used to show the potential impact of demographic change on the economy and policy options to change that.

The *One Health Policy Model* (OHPM) is designed to help decision-makers understand the nature and scale of how changes in the livestock and human populations might impact veterinary, human, and environmental health, including some of the available policy options. The model can generate analytical and scenario-based evidence that will help gain traction with country-specific stakeholders. Because the model takes a tripartite approach to modeling the human population, livestock population, and the environment, it takes a One Health approach and shows the linkages between these three sectors.

This guide presents a comprehensive overview of the model. The model is designed to address the following questions:

- What is the expected burden of zoonotic disease among animals and humans, if there is “business as usual?”
- What are the environmental effects of rapid livestock growth and intensification?
- How will the zoonotic disease burden in animals and humans change if the country undertakes interventions to control zoonotic diseases?
- What are the impacts of zoonotic disease on livelihoods?
- What are the costs (healthcare, as well as other) as a result of animal and human disease outbreaks under different investment or development strategies?

Model Development

Policy models, including those developed by the Palladium Group, typically address multi-sector issues that have gained prominence in the development policy dialogue, but for which the evidence base is incomplete. Recent examples include the relationship between climate change and population growth on food security\(^7\) or the relationship between population growth and economic development.\(^8\)


ownership and capacity development are important to model use, especially for providing data and information for the policy process. The OHPM is open access and is designed to be easy to use and readily trainable to diverse audiences in developing countries. It uses Microsoft Excel and does not require proprietary software. Some of the required data to run the model are pre-loaded and available from regularly updated standard international sources, but each country application is customizable for data, livestock species modeled, and other parameters—such as production systems and human populations at risk. The projection period length is usually adjustable, and national data can be used instead of pre-loaded data, at the user’s discretion.

The model development process carried out during the Preparedness and Response (P&R) project consisted of several consultations with USAID, FAO, project staff, and country counterparts. During its early stages, the model especially benefited from interactions with staff in the Ministry of Livestock in Ethiopia. We also conducted a review of the literature to identify the features and gaps of any existing models, and to identify and group relationships to be included in the model. The resulting relationships were then programmed into the user interface, which included two projection scenarios with policy inputs that the user can establish. We also worked closely with FAO’s experts whose inputs helped refine the model.

This guide is divided into two parts. Part I, a user’s guide, is an instruction manual for creating an application of the OHPM. Part II includes technical documentation that describes the calculations that underlie the model.
Part I - User Guide

Overview of Model Structure

The OHPM measures the impact on human, animal, and environmental health of zoonotic disease, as well as the economic costs. Figure 2 graphically depicts the relationships in the model. The model starts with exogenous human and animal population projections, as well as data that describe the diseases under consideration. Based on the data and projections, the number of animal and human cases of zoonotic disease are calculated; these are used to develop measures of the public health impacts of disease. Environmental indicators are calculated based on the number of animals in each scenario, and economic impacts are calculated based on animal and human health losses due to zoonotic disease.

The model compares two scenarios for one animal species. Scenarios may differ according to animal population growth rates or distribution of production systems, people exposed to zoonotic disease, and/or different levels of policy intervention. Policy interventions can affect the animal prevalence rate, the number of people exposed to disease, and the likelihood of those people contracting illness.

As currently designed, the model’s dimensions are—

- 2 zoonotic diseases
- 5 production systems
- 3 affected human populations
- 2 commodities
- 35-year time horizon.
Production Systems

Recognizing that different production systems can have drastically different implications for zoonotic disease, the framework can accommodate up to five different production systems. Often production systems vary between less intensive traditional systems and more intensive industrial systems. The user must define the characteristics of each production system, such as the animal population kept in that system, and the base year prevalence for each zoonotic disease. As zoonotic disease is managed differently in different production systems, the user can enter parameter values, such as reduced output of animal commodities per case or reduced fertility of infected animals that are specific to production systems. Production systems can also have different environmental profiles, so the parameters regarding GHG emissions and water footprint per animal may also vary by production system.

In the two different scenarios, the overall size of the livestock population changes according to user-specified growth rates. The relative sizes of the different production systems may also change over time. The user can enter different shares of the population between the production systems in the base year and the end year of each of the scenarios. These assumptions reflect programmatic ambitions to scale up livestock production, modernize, or intensify the industry.

Affected Populations at Risk

The framework enables the user to define up to three populations at risk of contracting the specific zoonotic disease. These populations are specific groups of people that interact with the livestock in question or animal products originating from them. Often, they are groups that work directly with the animals, such as herders, veterinarians, or market and slaughterhouse workers. Other affected populations that may be relevant in some circumstances are nomadic populations, small-scale farmers, general populations in specific geographic regions, and end consumers of animal protein (such as meat or dairy) for food-borne zoonotic diseases.

For each affected population, the user must enter the percentage of the population in contact with the livestock, the population forecast, and the exposure index. The exposure index is a 0–1 measure of the intensity of exposure of the people in this affected population to the livestock. Veterinarians and slaughterhouse workers would likely have a higher exposure index—for example, 0.9—than would the general population in a given geographic region with an exposure index of 0.3 because they spend a lot of time in direct contact with the animals and their bodily fluids.

Input Data

As with any model, several data inputs are necessary to configure the base year of the model and to set future values of key parameters. The OHPM requires data that vary by—

- Production system: Animal prevalence, animal fertility losses per case, and reduced production of animal products per case may all vary across production system. The user specifies the base year number of animals that are kept in each production system.

- Affected population: The human exposure index may vary by affected population. For more information about the exposure index, see the section on Affected Populations at Risk.

- Disease: For each disease, the model requires data on the human and animal health characteristics, including—
  - Number of human infections
  - Basic reproduction ratio (set to zero if human-to-human transmission does not occur)
  - Human mortality rate
In addition, the user must enter economic parameters that include—

- Base year price per animal and annual price escalation factor
- Observed reduction in animal prices due to zoonotic disease
- Off-take rate (percentage of animals sold for consumption)
- Prices of the two animal product commodities specified (such as beef and milk)
- Exchange rate to US dollars
- Per capita income measured by per capita gross domestic product (GDP) at purchasing power parity (PPP) and the growth rate of GDP.

One advantage of models is that they allow the user to create “scenarios” based on alternative assumptions and to see how these assumptions influence outputs. These assumptions pertain to the values of key inputs in the model, some of which may be amenable to control and some purely exogenous. For this model, these are the main parameters that, together, can define a scenario.

- Production system shares: The model computes the base year shares of the animal population, by production system, based on the user-provided population estimates. The user then specifies the share of the animal population in each production system in the end year, which the model uses to construct population forecasts.

- Animal population growth: The user also defines different rates of growth for the overall animal population for each scenario.

- Humans exposed to animals: The user specifies the base year percentage of the human population that falls into each affected population exposed to animals, as well as the end year percentages for each of the scenarios. For example, in a scenario in which the animal population grows faster, the user may assume that more humans become involved in keeping livestock.

- Water and GHG use per animal: These parameters can be entered by production system for the base year and end year for each scenario. This enables the user to consider trends in environmental health associated with the scenarios.
Model Walkthrough

Configuration

The OHPM begins with a welcome screen. To begin, click on the button labeled “Click to Start.”

From the welcome screen, you move to the “Configuration” step. In this step, you can define names and descriptions in the yellow cells—the country, time horizon, currency, type of livestock (such as cattle or poultry), and the two diseases under consideration. You can also define names for up to two commodities (such as beef and milk) and the units of measurement for these commodities (such as kilograms and liters).

You can enter the names for up to three affected human populations, such as consumers of animal products, herders, and market and slaughterhouse workers. You can also enter names for up to five production systems.
Scroll down the Configuration page, and you will see spaces to define the names for interventions. If you are not using interventions for the model application, skip this step. If you are using interventions, enter names for up to two animal health interventions by production system, two interventions by affected human population for both interface and spillover, and two interventions for human amplification.

To use fewer than the allotted number of populations, commodities, production systems, or interventions, enter “NA” or “None” as names in the extra spaces. When you complete the configuration step, click on the button labeled “Next” or “Continue to Step 2” to begin describing the scenarios.
Scenarios

In the next step, you define two different scenarios for animal, human, and environmental health. The scenarios require information about different hypothetical futures, including assumptions about variables that affect animal and human populations.

Following is a sample worksheet for scenario inputs for a model application with two production systems and two affected human populations. This worksheet summarizes the scenario variables available in the model and includes data for the base year. This style of worksheet may be helpful when you develop scenarios with stakeholders.

**Scenario Development Worksheet**

1. Create names for scenarios.

<table>
<thead>
<tr>
<th>Scenario Names</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Scenario 1</td>
<td>BAU Projected</td>
</tr>
<tr>
<td>Scenario 2</td>
<td></td>
</tr>
</tbody>
</table>

2. Describe future shares of each production system for each scenario.

<table>
<thead>
<tr>
<th>Animal Production System</th>
<th>2015 share</th>
<th>2050 share</th>
<th>2050 share</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Base Year</td>
<td>BAU Projected</td>
<td></td>
</tr>
<tr>
<td>Intensive</td>
<td>2.0%</td>
<td>2.0%</td>
<td>%</td>
</tr>
<tr>
<td>Extensive</td>
<td>98.0%</td>
<td>98.0%</td>
<td>%</td>
</tr>
</tbody>
</table>

3. Define animal population growth rates for each scenario.

<table>
<thead>
<tr>
<th>Animal Population growth</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>BAU Projected</td>
<td>4.2%</td>
</tr>
</tbody>
</table>

4. Describe the percentage of the population exposed to animals in the present and in the future.

<table>
<thead>
<tr>
<th>Populations exposed to animals</th>
<th>2015 share</th>
<th>2050 share</th>
<th>2050 share</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Base Year</td>
<td>BAU Projected</td>
<td></td>
</tr>
<tr>
<td>Consumers of animal products</td>
<td>11%</td>
<td>11%</td>
<td>%</td>
</tr>
<tr>
<td>Livestock keepers</td>
<td>44%</td>
<td>44%</td>
<td>%</td>
</tr>
</tbody>
</table>

5. Enter environmental data for the present and the future.

<table>
<thead>
<tr>
<th></th>
<th>2015</th>
<th>2050</th>
<th>2050</th>
</tr>
</thead>
<tbody>
<tr>
<td>Water use per animal</td>
<td>Base Year</td>
<td>BAU Projected</td>
<td></td>
</tr>
<tr>
<td>Intensive</td>
<td>68</td>
<td>68</td>
<td></td>
</tr>
<tr>
<td>Extensive</td>
<td>97</td>
<td>97</td>
<td></td>
</tr>
<tr>
<td>GHG emissions per animal</td>
<td>2015</td>
<td>2050</td>
<td>2050</td>
</tr>
<tr>
<td>Intensive</td>
<td>45</td>
<td>45</td>
<td></td>
</tr>
<tr>
<td>Extensive</td>
<td>45</td>
<td>45</td>
<td></td>
</tr>
</tbody>
</table>
After you define the scenarios to consider, you can enter the data in the Scenarios sheet. Begin by entering descriptive names for the scenarios. Next, to describe the evolution of animal production systems over the model horizon, enter values for the shares of the animal population living in each production system in the end year. This enables you to consider future scenarios in which some production systems grow faster than others, over time. The base year shares of each production system are calculated for you, based on the initial population data. In this table, enter the end year projected shares of each production system for each scenario. Check the bottom of the table to ensure that the shares equal 100 percent. By default, if the shares are constant, the model will increase all production systems at the same user-defined growth rate of the total industry. This growth rate is entered in the next table for each scenario.

<table>
<thead>
<tr>
<th>Scenario Names</th>
<th>Scenario 1</th>
<th>Scenario 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>BFA Projected</td>
<td>BFA High Growth</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Animal production systems - Shares</th>
<th>2015 share</th>
<th>2050 share</th>
<th>2050 share</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>BFA Projected</td>
<td>BFA High Growth</td>
<td></td>
</tr>
<tr>
<td>Intensive</td>
<td>2.0%</td>
<td>2.0%</td>
<td>2.0%</td>
</tr>
<tr>
<td>Extensive</td>
<td>98.0%</td>
<td>98.0%</td>
<td>98.0%</td>
</tr>
<tr>
<td>NA</td>
<td>0.0%</td>
<td>0.0%</td>
<td>0.0%</td>
</tr>
<tr>
<td>NA</td>
<td>0.0%</td>
<td>0.0%</td>
<td>0.0%</td>
</tr>
<tr>
<td>NA</td>
<td>0.0%</td>
<td>0.0%</td>
<td>0.0%</td>
</tr>
<tr>
<td>Total</td>
<td>100.0%</td>
<td>100.0%</td>
<td>100.0%</td>
</tr>
</tbody>
</table>

The next table under “Populations” describes the human populations exposed to animals. Enter the percentage of the population into each affected human population. If populations in the data overlap, select values that add up to the total exposed percentage of the population. For example, you can enter the population of animal keepers from the data; then, for consumers of animal products, enter the additional consumers that are not animal keepers.

<table>
<thead>
<tr>
<th>Animal population growth</th>
<th>BFA Projected</th>
<th>BFA High Growth</th>
</tr>
</thead>
<tbody>
<tr>
<td>Scenario growth rates</td>
<td>4.2%</td>
<td>4.2%</td>
</tr>
<tr>
<td>Source</td>
<td>sla projections - ETH|costa Asial historical</td>
<td></td>
</tr>
</tbody>
</table>

The tables labeled “Water” and “Greenhouse Gas” include data on environmental parameters by production system. These are entered for the base and end years of the model, if the scenarios require changes to the water use or GHG outputs, per animal, over time. If you do not want to change these...
values over time, enter the 2015 values in the 2050 column. After you enter all the scenario data, click “Next” or “Continue to Step 3” to enter the model parameters.

Parameters

As in the previous tables, enter values in all the yellow cells. If you did not use all the available populations (affected humans or production systems), make sure that the values of the parameters for the extra populations are set to zero or left blank. Each table in these sheets includes a column to enter the source for the data.

In the first table, enter the base year population of animals in each production system. The base year human population and population projections are displayed for your reference. For information on updating the population projection, refer to the “Population” section of the user guide.

The next table contains data used to compute the costs of zoonotic disease. Enter all values in local currency, unless instructed otherwise—for example, US dollars per capita income. The animal price escalation represents the annual price increase for healthy animals, by year. The percentage reduction in price due to disease represents the loss of value of animals because of the public perceptions of safety due to disease.

The next section of the Parameters step contains two columns of tables, each column represents one disease described in the “Configuration” step.
In the first set of tables labeled “Base Year Parameters: Humans,” enter the number of human infections from the base year data. Below this, you can enter a value for the basic reproduction ratio, which describes the number of additional people that are infected, on average, by each person who was infected by the disease. For many zoonotic diseases, human-to-human transmission is rare, and you may want to use a basic reproduction ratio value of zero. By raising the parameter, you can investigate scenarios with more virulent disease. Next, enter data about human health to be used in calculating DALYs. These include the human mortality rate for each disease, the mean duration (in years) of each illness, and the disability weight.

The exposure index summarizes the frequency, duration, and intensity of exposure to animals. Human infections are determined by the exposure index, which describes the number of people in contact with infected animals; and the spillover rate, which describes the probability that an exposed person will contract the disease. The spillover rate is calibrated to match the observed number of human cases to the user-selected basic reproduction ratio and exposure index. By changing the exposure index, you can change the relative importance of exposure and spillover.

The next set of tables describes the animal health impacts of disease. First, enter the base year animal prevalence for each production system, for each disease.
Next, enter values that are used to calculate the cost of zoonotic disease. These include the percentage of infected animals that die of disease, are culled, or are salvaged slaughtered (animals that are positive, or suspected of being positive, of a zoonotic disease that are processed for consumption, usually at a reduced price). Enter the percentage of fewer offspring produced by each animal for each production system (if relevant for the disease under consideration). Also, for each production system, enter the number of units of reduced production (such as kilograms of beef or liters of milk) per animal. The animal salvage price ratio is the percentage reduction in the sale price of carcasses that have been salvaged compared to the normal full price. This may be the same as the percentage reduction in price due to disease from above.

After entering the required data in the Parameters step, continue to the interventions by clicking the button labeled “Next” or “Continue to Interventions.” To update the population data, change the model elasticities, or change the way the DALYs are calculated, click “View Advanced Settings.”

### Advanced Settings

At the top of the Elasticities sheet are inputs that govern the DALY calculations and the associated costs. The first box enables you to choose whether to calculate the DALYs based on the average life expectancy for the country being modeled or use a standardized average life expectancy (default). Below this, you can choose to calculate the DALYs using an even distribution of infections across all ages (default) or use a distribution around the average age of infection. If using the distribution around the average, specify the average age of infection for each disease. Another cell allows you to specify the income elasticity that governs the conversion of US value of a statistical life per year (VSLY) data to international values. The default value is 1.5, but you can change this value.

Below the DALY settings is a table that includes the calculated spillover rates. If you want to change the values from these default rates, do it here (although it is not recommended).
The rest of the Elasticities step describes the elasticity values that govern the response of prevalence rates to the chosen interventions. The first two tables (in blue) define the elasticity values for each animal health intervention for each production system. You can also select upper and lower bounds on the prevalence, if desired. To the right of the second animal prevalence elasticity table is a cell labeled “Amplification Culling.” This parameter roughly describes what percentage of the disease is endemic and returns in each model year, as governed by the interventions, and what percentage is spread from animal to animal and can be eliminated by culling. Changing this parameter will change the relative impact of culling and other interventions.

The next three tables (in pink and yellow) describe similar elasticities for human health interventions that affect exposure and spillover, with possible upper and lower bounds. The first table also has a place to change the elasticities and bounds for human amplification interventions, as well. Click “Continue to Results” when complete, or click “Back” to return to the Parameters step.
Below the choice of VLSY elasticity is a button labeled “Go to Spectrum data.” Click this button to go to the raw Spectrum data used in the model. You must update four items here. First is the population forecast by age and sex for each year. Next are the population below one-year-old that must be generated in Spectrum for males and females, by year; they are used to disaggregate the population aged 0–4 for the DALY calculations. Third, update the average life expectancy in five-year increments for males and females. Last, update the age-specific total mortality (Mx), by age, in five-year increments for males and females. In this sheet, orange cells indicate where to insert the Spectrum data to be read by the OHPM. When the population forecast updates are complete, click “Back to Advanced Settings.”
Projecting the Human Population: Retrieving Data from Spectrum

Spectrum software is used to make human population projections. To create the projections needed for the OHPM, open Spectrum, choose the first option, “Run Spectrum,” and click on “New projection” under “Getting started.” In the Projection Manager that pops up, click the grey box labeled, “Projection file name,” to select the name and file location to save your projection. Next, choose as the first year the year before the OHPM model start year (this is important for generating Mx). In this example, we selected 2014 for our model that runs from 2015 to 2050. Choose the desired final year. Be sure that the box next to DemProj module is checked. At the bottom of the Projection Manager, click the grey box labeled “Default data” to select the country of interest. After entering these settings, click OK to generate the projection.

![Projection Manager](image)

Now, you can interact with the projection. In the blue ribbon at the top of the Spectrum window, click “Modules” and then the DemProj icon. This will open a grey ribbon—click “Results,” then “Age Groups,” then “All age groups.” In the pop-up window labeled “Configure – Population by age and sex” select the correct base year for the OHPM (2015 in this example) and click OK.

You will now see the population projection in five-year age groups for the total population, males and females, by year. Click on the table and select “Copy all.” This is the first population projection data needed in the “Spectrum data” sheet of the OHPM. Go back in the OHPM spreadsheet and click the first orange cell labeled “Population by age and sex” in the Spectrum data tab; paste the Spectrum data there.

You now need the populations of males and females under one-year-old in each model year. Return to Spectrum, click “Results,” then “Age Groups,” and select “Defined age group.” In the pop-up, select the following options: under Sex, choose “Male”; under Display Interval, choose “Single Year”, select the correct First year and Final year, set the Low Age and High Age both to be zero, and choose Chart type “Table.” Click OK to generate the projection. Once again, click on the table, and select “Copy all.”
This is the second population item needed for the OHPM. Paste it into the second orange cell labeled “Population aged 0-0 – (Males).” Repeat these steps to generate the forecast for females under one-year-old and paste the forecast into the appropriate cell in the OHPM.

If you are using the default calculation of the DALYs that uses standard life expectancy, you do not need to retrieve additional data from Spectrum. To use the national life expectancy, you will need two more forecasts. Next, we will retrieve forecasts of life expectancy. In Spectrum, click “Results,” “Mortality,” then “Life Expectancy.” In the pop-up window, under Sex, select “Males”; under Display Interval, select “Five year”; select the correct first and final years for the model application; and under Chart type, select “Table.” Click OK, then copy this forecast and paste it into the OHPM in the orange cell labeled “Life expectancy (Years) – (Males).” Repeat these steps to retrieve and paste in the life expectancy forecast for females.

The last item you need from Spectrum is age-specific total mortality, called Mx. In Spectrum, click “Results, Mortality,” then “Age-specific total mortality (Mx).” In the pop-up window, under Sex, select “Males”; under Display Interval, select “Five year”; and select the correct first and final years. Click OK, then copy this forecast and paste into the OHPM in the orange cell labeled “Age-specific total mortality (Mx)” for males. Repeat these steps to retrieve and paste in the Mx forecast for females.

Interventions

In the next step, you can define the levels of interventions in each scenario. Each scenario has a separate sheet, as shown at the top of the screen. The first set of interventions are for animal health. For each production system and specific intervention, you can use the arrows to increase the level of intervention, along a scale of 1–5. In this example, all interventions are set to 1 in the base year and remain at 1 through the end of the model time horizon in Scenario 1. In Scenario 2, the Intensive production system raises the level of both interventions to 3, and the Extensive production system raises the level of both interventions from 1 to 2.
The next controls enable you to change the level of interventions regarding human health for each affected population, intervention, and scenario. In this example, all interface and spillover interventions that affect the herder population increase from 1 to 3.

On the left of the sheet is an additional table that enables you to change the level of the culling intervention. The base year level is crossed out because the model uses the data entered in a previous step. You can specify different levels of culling for the final year, for each scenario, by entering the percentage of infected animals that are culled. In this example, culling increases from 0 percent to 5 percent by 2050 in Scenario 1 and to 10 percent in Scenario 2 for the Extensive production system.
After specifying the interventions, click “Next” to continue to the results pages.

The results are arranged by topic, and some graphs have drop-down menus at the top where you can select the specific indicator to view. The first results sheet displays animal health, environmental health, and economic indicators. Click “More Results” to continue to the human health indicators. At the top of each sheet, you can select the disease for which you want to view results, or view results for both diseases combined. To return to the data tables, click “Back to Inputs” at the top or click “Return to start” at the bottom to return to the home screen. See the next section for the available results.
**Description of Model Outputs**

The OHPM offers a variety of human, animal, and environmental health indicators for a specified country, animal population, and set of zoonotic diseases. Based on initial values provided by the user, the model projects these outputs for 35 years. The projection will depend on model parameters, such as the growth rate of the animal population, changes over time in the share of animals in each production system, and changes in the number of people who come into contact with livestock through their occupation or consumption of animal products.

This section briefly describes the main outputs of the model. For more details on the calculations, see the technical section of this manual.

**Animal Health**

The main animal health outputs are the *number of infected animals* per year and the *animal prevalence rate*. Without interventions, the animal prevalence rate will remain constant over time, and the number of infected animals will vary according to the population growth rate.

**Human Health**

The model calculates the *number of human infections* in each year, based on the number of people who come into contact with animals, prevalence rate among animals, interactions between people and livestock, probability of transmission from animals to humans, probability of transmission from human-to-human, and interventions used to reduce human infections. These infections can also be presented as a *human prevalence rate* or *human incidence (per 1,000)*. As with the animal prevalence rate, human prevalence will not vary significantly over time in the absence of interventions. From the number of human infections, the mortality rate of the specific disease, and the treatment of infected humans, the model computes the *number of human deaths*.

The number of cases of infection in humans and human deaths are used to compute the number of DALYs that result from zoonotic disease. DALYs are presented as a total number and as a number per 1,000 individuals. DALYs from zoonotic disease are also presented for context with the number of total DALYs for the focus country in the base year, as well as the total DALYs from infectious disease.

The human infections can be further divided into the *number of humans infected by animals* and the *number of humans infected by humans*. Human infections can also be divided by the *source of human infections* between affected human populations.

**Economic Impacts**

The model projects the annual *total cost of zoonotic disease*\(^\text{10}\) as the sum of the costs due to the loss of animals and animal products and the cost of human health impacts.

The *value of animals lost* is based on the economic value of those animals that die, are culled or slaughtered, or not born because of zoonotic disease. We assume that animals can be salvage slaughtered and sold for a reduced rate. The difference between the market price and the salvage price

\(^{10}\) To the extent possible, our methodology follows that described in the FAO presentation “Data to assess the impact of zoonoses on public health: Where do we stand?” dated October 23–27, 2017.
is included in the value of animals lost. Animal fertility can be reduced due to zoonotic disease, and the reduction in births from this impact of zoonotic disease are also considered.

The value of foregone animal production is based on the lost productivity of animals that are infected with zoonotic disease. This can occur from a reduction in the animal’s weight, resulting in lower production of meat, as well as reduced production of animal products, such as eggs or milk.

The total cost of DALYs is calculated from the DALYs and the willingness to pay for a DALY, based on the value of a statistical life (VSL, based on US estimates translated to other countries). The value of foregone household income translates lost work time due to illness into lost income based on the GDP per capita. Finally, health expenditures by households and health expenditures by government consider the average expenditures, by case of zoonotic disease, times the number of cases. The VSL, income, and health expenditures per case are inflated by the GDP growth rate minus the rate of population growth.

Environmental Health

We present two measures of the impact of livestock on the environment: water footprint of animals and GHG footprint of animals. These measures are computed from average water use or GHG emissions per animal, which can vary by production system and over time, as specified by the user. For context, these measures are presented in a percentage of total water use or GHG emissions for the entire country.
Part II – Technical Description of the OHPM

Zoonotic Disease Modeling

As already described, the OHPM begins with baseline data about the country, animal population, and zoonotic diseases being considered. The user also describes scenarios that represent two alternate future projections. The scenarios include changes to the size of the animal populations by production system, size of the exposed human populations, and environmental indicators.

In addition, the model includes interventions that the user can define. These interventions can be applied to each production system to improve animal health, to reduce the number of humans exposed to animals, to reduce the risk of transmission of disease between animals and humans, and to reduce the risk of humans infecting other humans. The user defines the types of intervention and the level at which they are applied.

First, we will look at the data needs to calibrate the baseline. Then, we will explain how these data are used to model animal, human, and environmental health impacts of zoonotic disease without interventions. We will then review how the model calculates the economic costs of zoonotic disease. Last, we will demonstrate how the interventions are applied in the model.

Animal Prevalence

The starting point for considering disease prevalence in animals is the user-input base year prevalence for each of the production systems. The model first projects the total animal population based on the overall growth rate defined by the user.

Let $t$ represent years, $t_0$ represent the initial year, and $T$ represent the terminal year. Let $p$ represent production systems, and total represent the sum over of all production systems. The total animal population in each year is calculated by—

$$\text{Animal population total, } t = \text{animal population total, } t_0 \times (1 + \text{animal growth rate total})^t$$

The annual growth rate for each production system is adjusted to reflect the changes in the shares of the total population in each scenario. The birth rate for each production system is the growth rate plus the off-take rate.

For each scenario, the user defines the percentages of the animal population in each production system at the end of the model horizon, period $T$. The annual birth rate for each production system is then calculated to match the changes in production system shares, total population growth, and off-take rate.

$$\text{Animal population } p, T = \text{animal population total, } T \times \text{production system share } p, T$$

$$\text{Animal birth rate } p = \left[ \left( \frac{\text{animal population } p, T}{\text{animal population } p, t_0} \right)^{1/T} - 1 \right] + \text{off-take rate}$$

The animal population in each year $t$ increases by the number of births; it decreases due to off-take, deaths from zoonotic disease, culling, and salvage slaughter. The number of births is also reduced due to fertility losses caused by zoonotic disease. In these calculations, we assume only one zoonotic disease for simplicity, but the model accounts for changes in populations due to both diseases simultaneously.
\[ \text{Animal population}_{p, t} = \text{Animal population}_{p, t-1} \times (1 + \text{animal birth rate}_p) \]

\[- \text{animal population}_{p, t-1} \times \text{animal prevalence}_{p, t-1} \times \text{fertility loss}_p \times (1 + \text{animal birth rate}_p) \]

\[- \text{animal population}_{p, t-1} \times \text{off-take rate} \]

\[- \text{animal population}_{p, t-1} \times \text{animal prevalence}_{p, t-1} \times \text{animal mortality rate} \]

\[- \text{animal population}_{p, t-1} \times \text{animal prevalence}_{p, t-1} \times \text{rate of culling} \]

\[- \text{animal population}_{p, t-1} \times \text{animal prevalence}_{p, t-1} \times \text{rate of salvage slaughter} \]

The model then computes the number of infected animals. In the absence of interventions, animal prevalence rates are constant, and the resulting calculated animal prevalence will also be constant.

\[ \text{Infected animals}_{p, t} = \text{animal population}_{p, t} \times \text{animal prevalence}_{p, t} \times (1 – \text{rate of culling}) \]

\[ \text{Animal prevalence}_t = \frac{\text{infected animals total, } t}{\text{animal population total, } t} \]

Human Cases

The second step in the core zoonotic modeling is to consider how many people are in contact with the livestock and, therefore, at risk of contracting the disease from animals. Interactions between humans and animals, or interface, is considered separately for each of the affected populations at risk. Similarly, to projecting animal prevalence, first the size of each human population is projected. The shares of the total population in each affected population change linearly between the base year and the end year. Let \( k \) represent the affected human populations.

\[ \text{Human population}_{k, t} = \text{Total human population}_t \times (\text{Population share}_{k, t_0} + (t – t_0) \times (\text{Population share}_{k, T} – \text{Population share}_{k, t_0}) / T) \]

These affected human populations represent the number of people in contact with animals. This animal-human interface represents the total human population at risk of infection. The animal prevalence rate is applied to the number of people in contact with livestock to determine the number of people in contact with infected animals.

\[ \text{Humans in contact with infected animals}_{k, t} = \text{Human population}_{k, t} \times \text{animal prevalence}_t \times \text{animal prevalence}_t \]

Next, we examine how many of the people in contact with animals (interface) become infected from the animals. Spillover is the transmission of pathogens from animals to humans. Like interface, spillover is considered separately for each affected population. In the absence of interventions, we use a single user-specified exposure index parameter to summarize the frequency, duration, and intensity of human exposure to animals, as well as the risk of spillover. For example, slaughterhouse workers who are regularly exposed to animal bodily fluids may be at greater risk of contracting zoonotic disease than consumers of animal products. In this case, the exposure index for the population of slaughterhouse workers should be higher than the exposure index for the consumer population.
The spillover parameter is initially calibrated to the observed human and animal prevalence data. In the Interventions section of this document, we describe how exposure indices and spillover rates can be changed in the model to represent health interventions that will prevent the spread of disease.

Humans infected by animals \( k, t \) = Humans in contact with infected animals \( k, t \) * exposure index \( k \) * spillover rate \( k, t \)

The final step in the core zoonotic modeling is amplification—the spreading of disease from person to person. The basic reproduction ratio for a specific disease is the average number of other people infected by each infected person during the course of the infection. A basic reproduction ratio of 0.05 means that 100 infected people are expected to infect five other people.

Amplification is dealt with at the national level, not the disaggregated level of the affected populations because people directly infected by animals may pass the disease to others outside their defined population, such as family members and neighbors. The total number of people infected by other people is then calculated as following:

Humans infected by humans \( t \) = Humans infected by animals total, \( t \) * basic reproduction ratio

We then calculate the total number of infected people, human prevalence, and human incidence per year.

Total infected people \( t \) = Humans infected by animals total, \( t \) + humans infected by humans \( t \)

Human prevalence \( t \) = Total infected people \( t \) / total human population \( t \)

Human incidence \( t \) = Total infected people \( t \) / (total human population \( t \) / 1,000)

From the infected people, we compute human deaths, based on the mortality rate.

Human deaths \( t \) = Total infected people \( t \) * mortality rate

Other impacts follow from this basic approach to zoonotic disease transmission. We estimate the economic impact of zoonotic disease on the livestock sector. On the human health side, we estimate the DALYs lost due to zoonotic disease.

**DALYs**

DALYs are a summary metric for the burden of disease, aggregating the number of years of life lost due to early death and a proxy for the number of years lived with disability (a weighted fraction of the number of years lived with disability). DALYs are calculated for specific diseases and causes of death or disability. They allow very different health challenges that are usually measured with different metrics to instead be measured by the same metric and then compared.

We used a DALY calculator from the World Health Organization\(^{11}\) to estimate the annual DALYs due to the zoonotic disease in question. DALYs are calculated separately for each sequelae—or

\(^{11}\) http://www.who.int/healthinfo/global_burden_disease/tools_national/en/
consequence—within a disease. For example, one estimate of the DALYs attributable to leptospirosis\textsuperscript{12} accounted for three sequelae: acute renal injury, acute lung injury, and various chronic sequelae.

Annual DALYs are calculated separately for each age (five-year age groups, up to 85+, with the exception of disaggregating the youngest group into 0 and 1–4) and sex group, then summed to determine the population total. Therefore, DALY estimates require data on the age and sex distribution of the disease being analyzed. Without such data, one neutral assumption is that the disease follows the age and sex distribution of the overall population. However, many diseases disproportionately affect certain groups—such as children, the elderly, or working age population if a disease is spread at a workplace—so age and sex distribution estimates should be made, where possible. The age distribution can have a large impact on the DALY estimates, because younger people have many more years of life remaining, which could be lost or lived with a disability, than do older people.

Because the age distribution of those who work most closely with animals does not follow the age distribution of the population as a whole, we modified the distribution of those affected by zoonotic disease. We use a Poisson distribution around the average age of infection, which concentrates the impacts of zoonotic disease around the average. The benefit of the Poisson distribution is that we can calibrate it using only the average age of infection. If the average age of infection is unknown, or the disease is expected to affect all ages uniformly, the user can assume that the infections are spread evenly across the population.

Total DALYs are the sum of Years of Life Lost (YLL) and Years Lived with Disability (YLD):

\[ \text{DALY} = \text{YLL} + \text{YLD} \]

In turn, YLL estimates the number of additional years a person would have lived in the absence of the disease. It is a function of the number of deaths (N) and the standard life expectancy at the age of death (L); the stylized formula is—

\[ \text{YLL} = N \times L \]

The full formula\textsuperscript{13} is—

\[
\text{YLL} = \frac{KCe^{a}}{(r + \beta)^{2}} \left[ e^{-(r + \beta)\alpha - \alpha} - \left( e^{-\alpha} \right) \right] + \frac{1 - K}{r} (1 - e^{-\alpha})
\]

where:
- \( a \) = age of death (years).
- \( r \) = discount rate (usually 3%).
- \( \beta \) = age weighting constant (e.g. \( \beta = 0.04 \)).
- \( K \) = age-weighting modulation constant (e.g. \( K = 1 \)).
- \( C \) = adjustment constant for age-weights (e.g. \( C = 0.1658 \)).
- \( L \) = standard life expectancy at age of death (years).


\textsuperscript{13} http://www.who.int/quantifying_ehimpacts/publications/en/9241546204chap3.pdf
Following the most recent Global Burden of Disease studies, we set the discount rate and the age weighting to zero.

Studies that use DALYs to estimate the burden of disease often use a standard human life expectancy to facilitate comparisons across diseases and countries. In this case, some users may want to calculate DALYs based on the actual life expectancy in the country representing the actual years of healthy life lost. Our model enables the user to choose this alternative calculation; however, we default to the calculation using the standard life expectancy. See the section in the user guide on Advanced Settings for information on how to change the assumptions around life expectancy and age distribution in the model.

The YLD quantifies the impact of disability on a person’s life, both for how long the person lives in less than ideal health and, also, the severity of the poor health. The YLD is a function of incidence (I), the disability weight (DW), and the average duration of the disease (L). The disability weight reflects the severity of the disease on a scale from 0 (perfect health) to 1 (dead). The stylized formula is—

\[ YLD = I \times DW \times L \]

The full formula\textsuperscript{14} is—

\[ YLD = DW \sum_{t=0}^{\infty} \frac{KCe^{a}}{(r+\beta)^{t}} \left[ e^{-(r+\beta)(L+a)} - e^{-(r+\beta)L} \right] + \frac{1-K}{r} \left(1-e^{-rL}\right) \]

\[ \text{where:} \]
\[ a = \text{age of death (years)}, \]
\[ r = \text{discount rate (usually 3%)}, \]
\[ C, \beta, K = \text{constants (see previous legend)}, \]
\[ L = \text{duration of disability (years)}, \]
\[ DW = \text{disability weight}. \]

For each year, the YLLs and YLDs are aggregated separately, across all the age and sex groups. Finally, the YLLs and YLDs are summed to get the final results, in terms of DALYs.

Because the utility of DALYs lays largely in the comparison across diseases, we compare the DALYs due to the zoonotic disease in question to total DALYs in the country, as well as the DALYs due to communicable, maternal, neonatal, and nutritional diseases. These comparisons situate the scale of the human public health impact of the zoonotic disease within the total human public health situation of the country. Note that these comparisons may not be consistent if the DALY calculation is used with local life expectancy values, because the comparison estimates for other diseases are calculated using the standard life expectancy.

The data required to compute DALYs due to zoonotic disease include—

- human mortality rates
- mean duration of each illness in years
- disability weight for each illness (examples available from the WHO\textsuperscript{15})

\textsuperscript{14} Ibid
\textsuperscript{15} Global Burden of Disease 2004 Update: Disability weights for diseases and conditions.
The OHPM also requires the following population data for the DALY calculations:

- Annual population forecasts in five-year age ranges (plus a forecast of the population under the age of one-year-old in each year)
- Male and female life expectancy in five-year intervals and age-specific total mortality (Mx) in the age of one-year-old and five-year forecast intervals (only needed if calculating DALYs using local life expectancy instead of standard assumptions).

These population data may be retrieved from the Spectrum DemProj model. Refer to the user guide section on Advanced Settings for instructions for updating population forecasts.

Environmental Impacts

The OHPM estimates the environmental impact of livestock intensification by looking at the water usage necessary to support an increase in the animal population.

\[
\text{Water use by animals}_t = \text{Animal population}_t \times \text{water use per animal}_t
\]

\[
\text{Water footprint of animals}_t = \text{Water use by animals}_t / \text{total water availability}
\]

The model does not consider the water footprint of animals as a limiting factor in the size of the animal population. In reality, the amount of water available for livestock may be limited. Drought is a constant concern in many countries and it affects livestock sector planning and development.

Greenhouse gas emissions estimates, expressed in CO\textsubscript{2} equivalents (CO\textsubscript{2}e), are also calculated based on the number of livestock. Raising livestock produces GHGs, such as methane (CH\textsubscript{4}) through digestive processes and manure decomposition. We convert the emissions into CO\textsubscript{2}e to compare emissions from livestock to the total national emissions from all sources.

\[
\text{GHG emissions from animals}_t = \text{Animal population}_t \times \text{CH}_4 \text{ emissions per animal}_t
\]

\[
* \text{kton CO}_2\text{e conversion factor}
\]

The CO\textsubscript{2}e conversion factor from CH\textsubscript{4} to CO\textsubscript{2}e equals 25. The GHG footprint of animals is calculated as a share of the total GHG emissions. The total emissions are based on user-defined assumptions about GHG emissions per capita in the base year and end year, and on the total human population.

\[
\text{Total GHG emissions}_t = \text{Human population}_t \times \text{GHG emissions per capita}_t
\]

\[
\text{GHG footprint of animals}_t = \text{GHG emissions from animals}_t / \text{Total GHG emissions}_t
\]

Economic Impacts

Zoonotic disease impacts the economy through animal and human health losses. The lost monetary value of animals includes the value of animals that die or are culled or salvage slaughtered, reductions


in output of animal products, and fertility losses caused by some zoonoses. Human health losses can be measured by lost productivity, additional healthcare expenditures, or the value that people place on healthy years of life.

Total cost of zoonotic disease \( t \) = Value of animals lost \( t \)

+ Value of reduced animal production \( t \)

+ Value of impact on lives \( t \)

+ Value of foregone household income \( t \)

+ Value of health expenditures by households and government \( t \)

The value of animals lost includes the lost value of animals that die or are culled, the value of the animals lost from decreased fertility, and some percentage of the value of the animals that are salvage slaughtered.

Animal deaths \( t \) = Infected animals total, \( t \) * animal mortality rate

Animals culled \( t \) = Infected animals total, \( t \) * rate of culling

Animals slaughtered \( t \) = Infected animals total, \( t \) * rate of salvage slaughter

Animals lost to reduced fertility \( t \) = \( \sum_p \) [Animal population \( p, t \) * animal prevalence \( p, t \) * fertility loss \( p \) * (1 + animal birth rate \( p, i \))]

The total value of animals lost is then—

Value of animals lost \( t \) =

Animal price \( t \) * (animal deaths \( t \) + animals culled \( t \) + animals lost to reduced fertility \( t \))

- animal price \( t \) * (1 – salvage price ratio) * animals slaughtered \( t \)

We assume that the price of animals and animal commodities increase over time, based on the escalation factor provided by the user. The value of reduced animal production is based on the number of animals that survive zoonotic disease and the data on production losses and commodity prices (represented by \( c \)) provided by the user.

Value of reduced animal production \( t \) = \( \sum_{c, p} \) [Animal population \( p, t \) * animal prevalence \( p, t \) * reduced production \( c, p, t \) * commodity price \( c, t \) * (1 – animal mortality rate)]

We calculate several measures of the economic losses due to the human health impacts of zoonotic disease. We calculate total healthcare expenditures as the number of human infections times the household and government expenditures to treat these illnesses. Healthcare expenses are inflated over time, based on the rate of GDP growth minus the population growth.

Value of health expenditures by households and government \( t \) = Total infected people \( t \)

* (household expenditures per case \( t \) + government expenditures per case \( t \))

We can quantify the value of lost health years of life in different ways. We measure the value of morbidity by the income lost due to missed work during an infection. This measure misses the value of
leisure time to working individuals, as well as the value of the time of children, the elderly, disabled people, and others outside the workforce.

Value of foregone household income $t = \text{Total infected people } t * \text{lost working days per infection} * \text{per capita income } t / 365$

The value of human lives lost can be measured by the VSL, which is calculated from observations about individuals’ preferences for risk and is used frequently in the US and other high-income countries to inform studies of public health and safety interventions.\textsuperscript{18,19} We can convert US estimates of VSL to estimates for other countries using the income ratio and an elasticity. Studies have shown that VSL increases with income, and that higher income populations have proportionally higher VSL.\textsuperscript{20} In this case, we assume a value of 1.5 for the elasticity, $\varepsilon$.

$$VSL = VSL_{US} \times (\text{GDP PPP / GDP PPP}_{US})^\varepsilon$$

We can use VSL to capture the impacts of mortality and morbidity by considering the VSLY. This measure annualizes the VSL based on average life expectancy to represent the willingness to pay for a healthy year of life.

$$VSLY_{US} = VSL_{US} / \sum t \text{US life expectancy} \times [(1 + r)^{-t}]$$

$$VSLY = VSLY_{US} \times (\text{GDP PPP / GDP PPP}_{US})^\varepsilon$$

We can then use the willingness to pay for DALYs as a summary measure for the value of mortality and morbidity due to zoonotic disease. We assume that the VLSY increases over time at a rate equal to GDP growth minus human population growth.

$$\text{Value of impact on lives } t = \text{DALY } t \times \text{VSLY } t$$

### Interventions

Policy interventions designed to mitigate risk or to block the transmission pathways of the infectious disease are at the heart of the zoonotic modeling. The framework is designed with flexibility to enable the user to define what interventions are most relevant to their specific situation. As shown in Figure 3, there are interventions at four stages in the framework. These interventions are designed to reduce—

1. disease prevalence in animals
2. interface (the number of humans in contact with animals)

---


3. spillover (animal-human transmission)
4. amplification (human-human transmission).

There is space for up to two interventions to affect each of these four core parameters for each animal production system and affected human population (except for amplification, which affects all human populations in the same way). For example, policy interventions designed to reduce disease prevalence in animals may include an animal vaccination campaign or an improvement in animal hygiene practices. Examples of policy interventions designed to decrease spillover—disease transmission from animals to humans—may include personal protective measures, such as gloves, or increasing post-exposure prophylaxis. Interventions can be left blank, if desired.

The framework traces zoonotic disease from animals to humans, then follows its human-to-human spread and examines the potential impact of interventions at various steps in the disease transmission pathway. Figure 4 shows how the framework moves from animal-to-human infections, divided among three populations in contact with animals.
The framework can accommodate up to eight interventions: two at each major step along the zoonotic disease pathway, including up to five different production systems for animals’ prevalence, and up to three different sub-populations for the interface and spillover steps.

Given the difficulty of measuring the level of effort of user-defined policy interventions, the framework uses a Likert scale of 1–5 to approximate the intensity or coverage of the intervention. A level 1 intervention would be a small-scale intervention—such as one with low funding levels or limited population or geographic coverage—while a level 5 intervention would have high funding, high compliance, high coverage, and high enforcement or political will. Because a Likert scale is often a subjective metric, instead of objective, it will usually be obtained through expert opinion. Each intervention requires a 1–5 rating for both the first and final years of the analysis. The final year rating may be different between the two different scenarios being analyzed. This would enable the user to examine the effects of increasing the level of effort for various policy interventions.

Each intervention also requires a user-defined elasticity. Elasticity is an economic concept that measures how sensitive an outcome is to an intervention. For example, an elasticity of less than 1 represents an intervention that is less efficient than an intervention with an elasticity of greater than 1.

The exception to this scale is the additional intervention of culling, which is specified as a percentage of infected animals that are culled, disaggregated by production system. In the base year, the level of culling should reflect the percentage of culling from the economic data. The user can then specify a culling percentage for the final year, and the model will increase the level of culling in a linear fashion
over the model horizon. Increasing culling immediately reduces the number of infected animals and additionally slows the animal population growth.

The framework initializes so that the base year parameters reflect the base year level of intervention. It does this by creating an adjustment factor for each intervention.

\[
\text{Adjustment factor} = \frac{\text{Parameter value } t_0}{\text{Intervention level } t_0^{ \varepsilon}} \div \text{Parameter value } t_0
\]

Below is an example of the initialization of an intervention designed to reduce interface (animal-human contact). In this example, 1,000,000 people are in contact with livestock in the base year, with an intervention that begins at level 2 and with an elasticity of 0.15.

\[
\text{Adjustment factor} = \frac{1,000,000}{2^{0.15}} \div 1,000,000 = 0.9
\]

This adjustment factor is then applied to future projections of the parameter.

Policy interventions shape the future path of disease prevalence. The levels and elasticities of each policy intervention are then applied to future years.

\[
\text{Animal prevalence } t = \frac{\text{animal prevalence } t-1}{\left(\text{intervention level } t-1^{ \varepsilon} \right)} \div \text{adjustment factor}
\]

To prevent unreasonable future values, animal prevalence projections may be limited by user-defined minimum and maximum values. The impacts of both interventions—if both are used—are aggregated for the final projection of animal prevalence. All calculations are done separately for the different production systems, and then aggregated (weighted by the relative population sizes in each production system) to determine the national projection of animal prevalence.

After interventions are applied to animal prevalence, the impacts of policy interventions are applied to human populations affected in the future. As with animal health interventions, human interface and spillover parameters can be limited by minimum and maximum values. The impacts of intervention are calculated separately for each affected human population, then aggregated for national projections.

\[
\text{Interface } k, t = \frac{\text{Interface } k, t-1}{\text{Intervention level } k, t-1^{ \varepsilon}} \div \text{Adjustment factor } k
\]

The spillover parameter represents the ratio between the number of humans infected and the number of humans exposed to an infected animal. So, a spillover parameter of 0.5 means that if 100 people were exposed to infected animals, 50 people would contract the disease.

\[
\text{Spillover } k, t = \frac{\text{Spillover } k, t-1}{\text{Intervention level } k, t-1^{ \varepsilon}} \div \text{Adjustment factor } k
\]

As with the other key parameters, the basic reproduction ratio for the entire human population begins in the base year with a user-defined value, which is then shaped in future years by policy interventions:

\[
\text{Basic reproduction ratio } t = \frac{\text{Basic reproduction ratio } t-1}{\text{Intervention level } t-1^{ \varepsilon}} \div \text{Adjustment factor}
\]

Limitations

The major limitation of the OHPM, as with most policy models, is that the usefulness of the projections depends on the quality of data used to calibrate the model. For our initial applications of the model, for example, we worked closely with FAO, who had collected a wide variety of data on animal populations, animal and human health, and economic values. These data were collected under an expert elicitation protocol, which aggregated data from a variety of local experts on livestock and zoonotic disease. Where detailed data are not available, regional data or expert assumptions can be used to fill in gaps.
A second limitation of the model is the application of the interventions. The model is constructed to give insight into the relative impacts of different levels and combinations of interventions. These impacts are determined based on assumptions about the response of animal and human prevalence rates to a variety of interventions, which rely heavily on user assumptions and expert opinion. The levels of interventions are quantified by a simple scale, not by dollar values of expenditure or doses of vaccine. We are working to create a smaller-scale expert elicitation protocol to collect data that summarize the effectiveness of interventions that will be used to inform elasticity values. This protocol may be used in future applications.

We do not currently have a mechanism in the model to examine an outbreak of a disease that is not currently observed, or is only observed at low levels, such as HPAI. There is global concern that the HPAI virus may increase in virulence and spread from poultry to humans and then from human to human. At this point, however, human cases are rare, so the historical data used to calibrate the model reflects few, if any, human health impacts of HPAI over the model time horizon. Additional work may include the modeling of outbreaks that represent a fundamental change in disease characteristics at a future point in time.

Our model does not account for reverse zoonosis, where humans infect animals.21 This infection pathway could be important to consider in a widespread outbreak scenario. We also do not consider the development of antimicrobial resistance (AMR) of diseases over time. We assume that parameters, such as mortality rates and treatment costs, are constant over time, although AMR is a concern because of the overuse of antibiotics in promoting the growth of livestock. In the future, we would like to develop a module that considers the impacts of AMR on the trajectory of zoonotic disease.

Photographs courtsey of (from the top): Australian Embassy Jakarta, Martin Weller and EU Civil Protection and Humanitarian Aid Operations