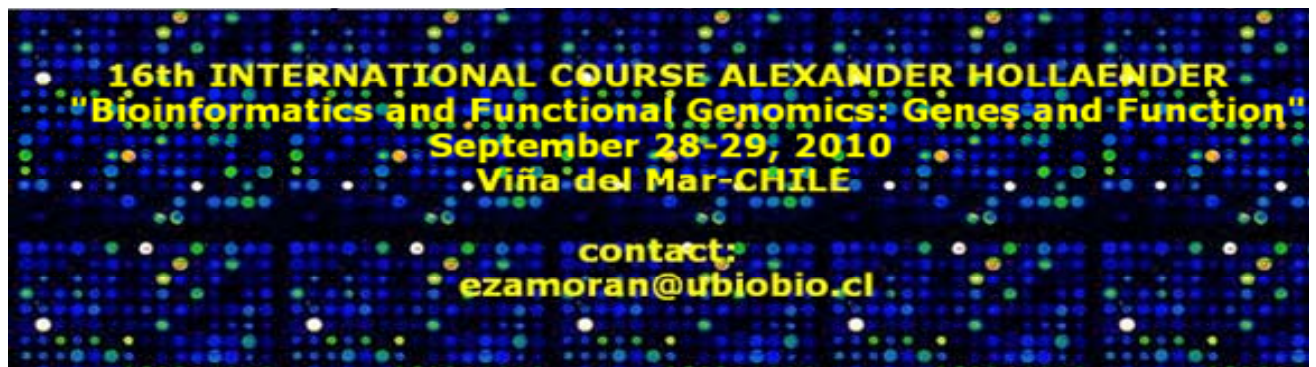


US-Environmental Mutagen Society



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DESCRIPTION:

Bioinformatics and DNA microarrays analysis constitute a paradigm among post-genomic technologies, which are characterized for producing large amounts of data, whose analysis and interpretation is not trivial. Microarray technologies allows querying living systems in a completely new way, but at the same time present new challenges in the way hypotheses must be tested and results have to be analyzed.

This course covers the state-of-the-art in the above mentioned topics, which are of major relevance in today's gene expression data analysis. Through sessions of theory and practical examples, the students will acquire the experience necessary to address scientific questions to gene expression array datasets and solve them

OBJECTIVES:

1. to provide hands-on training for young Latin American researchers on some of the recently developed techniques for the study of functional genomics
2. To acquaint the course participants with recent developments, experimental models and techniques being employed in genomics and bioinformatics

DIRECTED TO:

The 16th International course Alexander Hollaender, has been programmed for two days. It's a theoretical and practical course focused on microarray data analysis oriented to, 20 Students for the practical part (10 from Chile and 10 from other Latin American Countries) and open for the theoretical sessions. The course is designed for doctoral or post-doctoral trainees that already have some training in molecular biology and that need to apply techniques of genomics and bioinformatics to their specific research topics. Applicants should have a working knowledge of English as well as familiarity with the use of web-based tools and knowledge of basics notions of statistics

GENERAL TOPICS:

Bioinformatics Data mining of genomics
The possibilities and limitations of the micro array technology
Gene Annotations
Use of genomic analysis in Human Epidemiological studies

VENUE:

The course is being programmed as a satellite course at the ALAMCTA meeting in 2010 in Reñaca - Viña del Mar, September 28-29,2010.

INVITED LECTURERS/SPEAKERS

(in alphabetical order):

1. Stefano Bonassi, Ph.D.

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PROGRAM (Day 1)

08:00-09:30	Registration
09:30-09:45	Welcome address to the course Dr. Enrique Zamorano-Ponce GENETOX – UBB - Chile Chair
09:45- 10:15	“Bioinformatics: Tools and methods for functional genomics” Dr. Mario A. Bueno
10:15- 10:30	Break
10:30-11:30	“Genomics and transcriptomics: microarray data analysis” ¿Why microarrays? The possibilities and limitations of the micro array technology. Data preprocessing and normalization. Unsupervised analysis (clustering). Supervised analysis (gene selection, predictors). Functional annotation. Dr. Mario A. Bueno
11:30 -12:00	Break /snack
12:00 – 13:00	From SNPs to Functional polymorphism: Overview of techniques to SNP discovery and detection. Phenotypes linked to SNPs variations and its applications to the biotechnology industry, challenges and the future. Dr. Cristian Gallardo
13:00 – 14:30	Lunch
14:30 -18:00	(Practical session) Hands on microarray's data analysis. Web and programming techniques. Dr. Mario A. Bueno

PROGRAM (Day 2)

- 9:00 -10:00** High-throughput technologies in human population studies: Overview, techniques, and perspectives.
Dr. Stefano Bonassi
- 10:00 -11:00** Proteomics: a complementary approach to functional genomics. Overview of experimental and bioinformatics methodologies. Example: Discovery of biomarkers through nutritional proteomics
Dr. Andrea Mahn
- 11:00 -11:30** **Break / Snack**
- 11:30-13:00** An overview of different clustering methods: hierarchical clustering, SOM, SOTA and k-means. Gene clustering, gene neighbors, phylogenetic tree construction.
Dr. Mario A. Bueno
- 13:00-14:30** **Lunch**
- 14:30–17:30** Hands-on in clustering methods and phylogenetic tree construction. Web and programming techniques.
Dr. Mario A. Bueno
- 17:30-18:00** Concluding Remarks