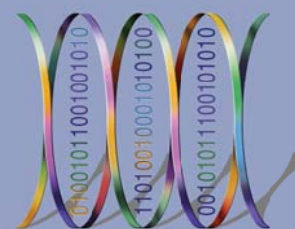




Computational and Statistical Aspects of MicroArray Analysis (CSAMA08)

June 15-20, 2008 in Bressanone, Italy



This one week intensive course is intended to give insights into recent advances in statistical and computational aspects of the design and interpretation of microarray experiments. The topics will include all aspects of the data analysis of microarray experiments for transcript profiling and ChIP-chip. The course is intended mainly for researchers with a basic understanding of microarray technology and its statistical and computational challenges. The four practical sessions of the course will be most beneficial for participants that are able to converse in a programming language such as R.

Lectures:

- Introduction to R and Bioconductor
- Microarray preprocessing, quality assessment and normalization
- Introduction to chromatin biology and experimental techniques
- Normalisation, differential enrichment and region finding in tiling array data
- Accessing and using gene annotations and metadata
- Differential expression
- Graph Methods for regulatory and protein interaction networks
- Gene set enrichment analysis, category analysis
- Introduction to high throughput sequencing data analysis and ChIP-Seq
- Machine Learning

Lecturers:

- Robert Gentleman (Fred Hutchinson Cancer Research Center, USA)
- Denise Scholtens (Northwestern University, USA)
- Wolfgang Huber (European Bioinformatics Institute, UK)
- Andreas Ladurner (European Molecular Biology Laboratory, Germany)
- Richard Bourgon (European Bioinformatics Institute, UK)



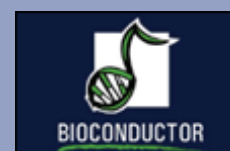
University of Milan



University of Padua



The R Foundation for Statistical Computing



The Bioconductor Project



Centro ADAMSS

Open registration from March 2008

www.economia.unimi.it/marray/

Travel awards offered through the Chromatin Plasticity Network

Application deadline: January 31, 2008

www.chromatin-plasticity.org/go.php?page=travelawards



Marie Curie Research Training Network