A course on Statistical Methods for mRNA-Seq and ChIP-seq using Bioconductor.

Different solutions for the most common problems derived from the use of Next Generation Sequencing (NGS) in the study of the transcriptome and DNA-protein binding using the popular Bioconductor package.

The course will be taught by Bioconductor developeprs from the Division of Biostatistics, School of Public Health, University of California, Berkeley and has been organized in collaboration with the Department of Bioinformatics of the CIPF. The course is especially suited to bioinformaticists and advanced users of bioinformatic tools interested in dealing with NGS data. It is also strongly recommended to personnel in charge of data analysis in core facilities implementing NGS.

The course will be held in the teaching facilities located in the premises of the CIPF.

More info: http://bioinfo.cipf.es/RNA-seq2010

Venue

Centro de Investigacion Principe Felipe (CIPF), Valencia, Spain

Dates

Course: 10th to 12th November, 2010.

Registration closes: 30th October, 2010.

Program of the course

- Introduction to high-throughput sequencing
- Experimental design
- Pre-processing: Image analysis, base-calling, read-mapping
- Exploratory data analysis
- Normalization and expression quantitation
- Differential expression
- Inference of isoform expression
- Introduction to ChIP-seq
- Statistical aspects of peak-finding
- Statistical software

Teachers:

Laurent Jacob

Oleg Mayba

University of California, Berkeley.

Organised by:

Sandrine Dudoit

Joaquin Dopazo

Fees and on-line registration:

Registration fee: 500 € The price includes meals and coffees at the course location, as well as the gala dinner. On-line registration: http://bioinfo.cipf.es/RNA-seq2010-reg