International Course on Massive Data Analysis: Transcriptomics

What is MDA? A theoretical and practical course on Next Generation Sequencing Data Analysis for transcriptomic studies.

How is the course scheduled? 5-days session: 10th-14th of March, 2014

Who is the target audience? The course is oriented to experimental researchers, post-doctoral and PhD students who want to learn about the state-of-the-art of transcriptomics data analysis methodologies and carry out their own analysis.

Who organizes MDA? The course is organized by the Genomics of Gene Expression Lab of the Príncipe Felipe Research Center (CIPF) in Valencia.

Why attending this course? RNA-Seq data from next generation sequencing assays allows the study of genome-wide gene expression data at an unprecedented level of detail. However, analysing and understanding such expression data is not an easy task. Data analysis is still a major bottleneck for many researchers which are still applying inadequate statistical methods for the interpretation of their transcriptomic results. The aim of this course is to familiarize the students with the latest analysis methodologies and to provide hands-on training on the analytical approaches implemented in high-performance computing packages. Lectures and hands-on sessions are taught in the facilities of the CIPF, which provide the ideal environment for the organization of bioinformatic courses.

What else? Social activities are organised during the course to favour networking and exchange of experiences among the students, as well as to promote a fruitful dialog between teachers and students.

Language The official language of the course is English.

Registration and payment closes by 1st March
Places are limited and will be assigned on a first come first served basis.

Registration fee: 500 €

Meals, coffees and gala dinner are included.

More info at http://bioinfo.cipf.es/mda14transcriptomics/registration or eflores@cipf.es