May 19-21th, 2014
Board room, ground floor

Training courses

Introduction to microarray gene expression analysis

From raw data to gene selection

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Monday 19

10:00 R Basics

11:00 Data types in R

12:15 Break (15")

13:00 Plots

Tuesday 20

10:00 Microarray platforms and procedures at IBIS Genomics Unit

11:00 Accessing raw data and background correction

12:15 Break (15")

13:00 Normalization and quality check

14:00 Lunch (60")

16:00 Preprocessing

17:00 Differential Expression Analysis

Wednesday 21

10:00 Gene list functional enrichment

11:00 Gene set enrichment analysis

12:30 Break (15")

12:45 Exploring gene interactions

This introductory course on microarray analysis is targeted to people without previous knowledge on this field.

We will cover the basic steps that should be followed to obtain a list of differentially expressed genes, starting from raw expression data.

The theoretical part of the course will be comprehensive and the similarities and differences between one- and two-color arrays will be discussed.

For the practical part, an already published public dataset of Agilent two-color arrays will be used for all subsequent hands-on work.

Students will get familiar with raw data format, background subtraction and normalization procedures that are needed before any differential expression analysis.

Some notions on experimental design and statistical tests will be given, and attendees will learn the value of biological replicates and the importance of multiple testing corrections.

Finally, we will present some useful tools to visualize the results and review the clustering methods, making emphasis on the interpretation of the results.