

METHODS FOR THE ANALYSIS OF RNA-SEQ DATA

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Course Description

The course will provide students with theoretical and practical knowledge on how to perform bioinformatic analyses of RNA-Seq data, mainly aimed at the identification of genes differentially expressed across different conditions.

Learning outcomes

After this course participants should be able to:

- understand the theoretical principles of the analysis of RNA-Seq data
- plan and execute the main steps of a bioinformatic RNA-Seq data analysis
- use statistical approaches for the identification of differentially expressed genes
- understand the results obtained

To maximize the outcome of the course, students are encouraged to bring their own data.

Course prerequisites

Basic background knowledge on genetics, molecular biology and transcriptomics.

Program

Wednesday 17th July 2019

14:00-14:30 Opening and Welcome. Participants' self-presentation

14:30-15:30 Introduction to the R programming language – Part 1

15:30-16:00 Coffee break

16:00-17:30 Introduction to the R programming language – Part 2

Thursday 18th July 2019

10:00-11:00 Theoretical principles in the analysis of RNA-Seq data.

11:00-12:00 Good practices for designing your RNA-Seq experiment

12:00-12:30 Coffee break

12:30-14:00 Hands-on: analyzing RNA-Seq data using R – Part 1

14:00-15:00 Lunch Break

15:00-17:30 Hands-on: analyzing RNA-Seq data using R – Part 2

Friday 19th July 2019

10:00-11:00 Functional characterization of differentially expressed genes

11:00-12:00 Guidelines and strategies for post-processing the results

12:00-12:30 Wrap-up and feedback