### Omics-based Biomarkers Detection
Fernando Gordillo González  

**Overview**

Which genes or microRNAs are most expressed in my sequencing data? Do I have a metabolomic signature associated with my study disease? Which protein biomarkers are relevant for my study? Using web tools and starting from normalized omics data, we will learn about different strategies to identify biomarkers of interest for our studies (Babelomics, eVITTA).

**No prerequisites**

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### Web-based Functional Profiling Analysis: How to make sense of gene lists
Borja Gómez Cabañes  

**Overview**

What pathways are involved in our set of significant genes? Are the proteins I have selected in my work highly functionally related? What biological processes are most overrepresented in our transcriptomic results? What do the genes in which I have identified mutations that may cause a particular disease have in common? In this session, we will learn about the main functional characterization methods to understand and interpret the results of our omics data analysis, using a selection of web tools (eVITTA, String, REVIGO, GeneMANIA).

**No prerequisites**

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### Analysis of Single-cell RNA-seq Data using Web Tools
Irene Soler Sáez  

**Overview**

The application of omics techniques to single cells allows to address biological questions taking into account the specificity of each cell type. In this seminar, the participants will learn the peculiarities of the data generated with single-cell RNA sequencing (scRNA-seq) technologies. Moreover, we will cover both the theoretical and practical understanding of the different phases of scRNA-seq data. Using the web tool ASAP, we will delve into the steps quality control, normalization, selection of highly variable genes, clustering, cell type annotation, differential expression analysis and functional profiling.

**No prerequisites**
Visualization of Omics Data with R
Rubén Grillo Risco

Overview
The large volume of results in omics studies can be problematic when we want to summarize and represent them graphically. In this course we will learn about the main graphical representations of omics data and how to improve their presentation in our papers and publications.

Prerequisites
A working knowledge of R/RStudio

How to Determine the Sample Size for Your Experiments
Cristina Galiana Roselló/Francisco García García

Overview
What sample size do I need in my experiments to assess the identification of a biological signal? Could I reduce the number of animals used and optimize the available resources? What is power, significance level and effect size?
The aim of this activity is to answer all these questions by introducing participants to sample size calculations for common experimental designs in a practical way, through examples and using web resources (GRANMO).

No prerequisites

A Practical Lipidomic Data Analysis Session
Carla Perpiñá Clérigues

Overview
Lipidomics is gaining importance due to the structural role of lipids and their influence on signaling and inflammatory processes, opening new perspectives in clinical and biomedical research. For this reason, this course aims to introduce the participants to this field. The course will consist of two parts: i) a brief introduction to the nature of the data, and ii) the implementation of a bioinformatics pipeline with a practical component to be carried out in R software (exploratory analysis, differential abundance, annotation, class enrichment and lipid networks).

Prerequisites
A working knowledge of R/RStudio
Why?

Hands-on bioinformatics training is a great way to learn how to analyze your own omics data using user-friendly web-based tools without requiring advanced programming skills. Using these tools, we can identify sets of functionally related genes and apply a complete bioinformatics analysis pipeline. The goal is to learn how to perform bioinformatics analysis in the simplest way. However, for those with a basic knowledge of the R programming language, several sessions are offered to develop R skills in the analysis of omics data.

Who?

This course is open to any CIPF researcher (PI, postdocs, PhD students, technicians) who generates, plans to generate, or works with omics data and wants to learn the basics of bioinformatics analysis.

How?

- Registration will be done through a shared registration list
- Limited to 25 participants per course.
- If a participant is unable to attend the course, it is recommended to notify it by email at least 3 days in advance so that the place can be covered.
- Participants should bring their own laptops, although some spare computers will be available for those who cannot bring their own.
- The courses will taught in Spanish or English, depending on the preferences of the participants.

Contact us: bioinfo.seminars@cipf.es

Organizers: CBL Computational Biomedicine Laboratory

Coordinators:
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Cristina Galiana Roselló