



**Course: Molecular Microbiology and Virology - Academic Year 2017-2018**

## **Basic Computational Skills for Metagenomics Analysis**

**February 5-9, 2018 Room B1 – Polo Cravino - Via Ferrata, 1**

### **Course Synopsis**

The course will teach the basic computational skills required to perform analyses in metagenomics. The module will be eminently practical and hands-on, and will teach participants skills ranging from the installation and basic use of Linux systems to the building of analysis pipelines. The course will teach the basics in Next Generation Sequencing data quality assessment, metagenomic assembly and statistics, annotation process in standard and supercomputing environments.

**Course language:** English

**INSTRUCTOR: Dr. Giuseppe D'Auria**

PhD., FISABIO-SP, Coordinator of Sequencing  
and Bioinformatics Service (dauria\_giu@gva.es)



### **Course program**

**Monday 5 February 2018 14:00-18:00 – Introduction to Linux and NGS**

Next generation sequencing technologies: Introduction to metagenomics  
Linux system, installing a new distro, virtual environments  
From office automation to computation for NGS  
Unix commands, moving around the system, building pipelines

**Tuesday 6 February 2018 14:00-18:00 – Basic steps in Metagenomics**

NGS Bioinformatics formats, managing data, practice  
Metagenome assembly and quality control  
Reads mapping and ORFs finding

**Wednesday 7 February 2018 14:00-18:00 – Metagenomes validation**

Metagenomes validation  
Scaffolds analysis  
Metagenomics analysis (wrap up section)

**Thursday 8 February 2018 14:00-18:00 – Metagenomics using a computer cluster**

Bash scripting and qsub environment for computer cluster queuing system in metagenomics

**Friday 9 February 2018 14:00-18:00 – Metataxonomy analysis (16S rDNA amplicons)**

Quimera check and taxonomic annotation  
Descriptive and statistics analysis of 16S rDNA data