

ENV-621

Hands-on bioinformatics for microbial meta-omics

Altshuler Ianina, Bell Emma, Bernier-Latmani Rizlan, Carratala Ripolles Anna

Cursus	Sem.	Type
Civil & Environmental Engineering		Opt.

Contact language	English
Credits	3
Session	
Exam	Oral presentation
Workload	90h
Hours	80
Lecture	40
Practical work	40
Number of positions	20

Frequency

Every 3 years

Remark

You will need to install software on your laptop to be able to participate in this course. The second half of the course will take place February 5-9, 2024.

Summary

This course will train doctoral students to use bioinformatic tools to analyse amplicon and metagenomic sequences. In addition, we will also touch upon meta-transcriptomics and meta-proteomics.

Content

Theory:

Introduction to Omics and DNA sequencing technologies
 DNA sequencing and uncultured microorganisms
 Reproducible research and community standards
 Metagenome sequence assembly overview
 Intro to read mapping and mapping tools
 Reconstructing genomes from metagenomes
 Intro to Annotation, databases, HMMs

Practical:

Intro to command line / computing resources
 QC reads, Adaptor Removal
 Assembly
 Assembly stats
 Gene prediction
 Mapping
 Binning
 Bin refinement
 Bin QC
 Dereplication
 Abundance
 GTDB
 Phylogenomics
 Functional Annotation

Note

Dr. Emma Bell

Resources

Moodle Link

- <https://go.epfl.ch/ENV-621>