

INTOMED and ARISTO Course on Bioinformatic Analysis

Course Overview

The enormous microbial diversity found in most habitats is currently acknowledged. Sequencing of amplicons of phylogenetic marker genes currently comprises the dominant methodology for analyzing microbial diversity in such habitats, owing to its high-resolution ability and its capacity to capture most of the existing diversity as opposed to methodologies of the past era. Two EU projects, INTOMED (PRIMA project <https://intomed.bio.uth.gr>) and ARISTO (MSCA-ITN-EID-H2020, <https://aristo.bio.uth.gr>) will join forces in providing a training course in bioinformatic analysis of amplicon sequencing data. During the workshop, the students will be introduced to past and current methodologies for studying environmental microbial diversity, building the case around the need for high throughput sequencing of phylogenetic marker gene amplicons (currently, commonly referred as “metabarcoding” methodology) in such studies. A thorough description of all necessary steps for designing and performing microbial diversity analysis with metabarcoding will be provided. Students will also be introduced to computational tools of the field of big-data science, like the R programming/statistical environment, necessary for handling the volume of sequencing data generated in such approaches. Then, they will be walked through strategies in statistical analysis, suitable for extracting important and reliable information from “noisy” environmental datasets. Finally, the students will obtain hands on experience with the aforementioned tools and statistical strategies that will facilitate the design and execution of their future experiments.

Cost?

No fees apply

Physical presence or remote?

The workshop will be done with physical presence of the participants (12 positions). Positions for remote participation are also available (12 positions)

Who is this course for?

Young/not-so-young (Molecular) Microbial Ecology and Environmental Microbiology researchers.

What will I learn?



- Familiarize with basic and advanced concepts of diversity analysis with metabarcoding
- Obtain basic knowledge about the R platform
- Be able to use R for performing all necessary quality control and bioinformatics steps during the processing of metabarcoding data
- Be able to perform basic descriptive statistical analysis on metabarcoding datasets
- Comprehend important strategies for winnowing primary datasets to shake-off environmental noise and extract important for phenotypic traits microbial taxa

What resources do I need?

Laptop, internet connection (will be provided), positive mood, will to learn methods in molecular microbial ecology

Course Format

Theoretical modules

Computational analysis

Programme

Apr 20th Background on microbiome analysis with high metabarcoding & R/RStudio basics

Apr 21st R/RStudio basics hands on, and hands on at microbiome analysis with R

Apr 22nd Microbiome analysis with R (hands on continue)

Apr 23rd (break... for the tutor only)

Apr 24th Microbiome analysis with R (hands on and wrapping up)

Organisers/Trainers

Sotirios Vasileiadis

Email: sovasileiadis (at) uth.gr



INTOMED is PRIMA project supported under Horizon 2020, the European Union's Framework Programme for Research and Innovation.



Link for registration can be found: <https://intomed.bio.uth.gr/primer-on-microbiome-analysis/>



ARISTO is funded by the European Union Horizon 2020 Research and Innovation Program under the Grant Agreement No. 956496, and in the frame of the MSCA-ITN-EID-H2020 call. This document reflects the opinion of the authors' and the European Union cannot be held responsible for any use which may be made of the information contained in this document