

Hands-on microbiome data analysis: tools for understanding microbial communities in health and disease

December 3rd to 7th, 2018 - Institut Pasteur Montevideo (Uruguay)

This course aims to provide the theoretical and practical concepts for standard bioinformatic analysis in the field of microbiome research. The course will focus on the application of state-of-the-art software tools for the analysis of environmental and host-associated microbiomes, with particular emphasis on understanding how they change or constitute a risk for human health. The course will have expert lectures and theoretical/practical data analysis sessions with real datasets.

TOPICS

- Introduction to high-throughput sequencing data applied to microbiome research
- Microbial community profiling using amplicon sequencing (i.e 16S/18S)
- Shotgun metagenomics: strategies for binning, assembly, annotation and functional analysis
- Strain-level metagenomics: genotyping and pan-genome analysis
- Introduction to long-read sequencing for community profiling

TEACHERS

Institut Pasteur Montevideo

- **Chair: Gregorio Iraola**
- Pablo Fresia
- Daniela Costa
- Cecilia Salazar
- Verónica Antelo

- Ignacio Ferrés
- Matias Giménez

Institut Pasteur Paris

- Marie Lopez
- Amine Ghozlane
- Angèle Benard

INVITED SPEAKERS

- Gianfranco Grompone, Discovery Microbiome, Nutrition & Health Science Lead, Lesaffre, France.
- David Danko, Director of Bioinformatics, MetaSUB International Consortium, Weill Cornell Medicine, US

STUDENT'S PRE-REQUISITES

- Directed to post-graduation (M.Sc. or Ph.D.) students.
- Basic concepts of high-throughput sequencing technologies.
- Basic understanding of metagenomics and microbial ecology.
- Basic skills in the Linux terminal.

DEADLINE APPLICATIONS

October 19, 2018. Send your CV (one page) and letter of motivation to: antonio.borderia@pasteur.fr