

Microbiome analysis using mOTUs2

Time

15. August 2019: 9:00 – 17:30

Location

Seminar Room 105, Main Building, University of Bern

Format/Scope

Interactive course in workshop format on the use of mOTUs in microbiome analysis. Students will work individually on exercises covering an introduction to Unix, installation and basic use of the software, the effects of various parameters and understanding the output.

Learning goals

Students should be able to:

- install mOTUs2 in a suitable environment,
- run the software, including the individual steps of the pipeline,
- understand the format and effects of modifying different parameters on the output,
- understand the advantages of mOTUs over 16S and reference genome-dependent tools.

Language of instruction

English

Instructors

Prof. Dr. Shinichi Sunagawa, Dr. Chris Field, Dr. Hans Ruscheweyh

Required materials

Participants need to bring their own laptop computer

Reference material

Course: https://github.com/SushiLab/motus_course/

Website: <https://motu-tool.org/>

Paper: "Microbial abundance, activity and population genomic profiling with mOTUs2." Milanese et al., Nature Communications 10, Article number: 1014 (2019): <https://doi.org/10.1038/s41467-019-08844-4>

Workshop Schedule

9:00 – 10:00	Session 1: Introductory Lecture mOTUs motivation and method
10:00 – 10:30	<i>Coffee Break</i>
10:30 – 12:00	Session 2: Preparation and Installation Access to virtual machines and the HPC “Euler” Unix orientation mOTUs installation and testing
12:00 – 14:00	<i>Lunch Break</i>
14:00 – 15:30	Session 3: Running mOTUs Read quality control Running mOTUs on single and multiple samples Available parameters and their effects on the output
15:30 – 16:00	<i>Coffee Break</i>
16:00 – 17:30	Session 4: Working with mOTU profiles in R Brief introduction to R Comparison of samples and parameter sets Database extension demonstration Q & A