

Core Facility Computational Bioanalytics

Microbiome data analysis with R

The advent of next-generation sequencing (NGS) enabled the study of microbial communities to reach a new level. Examining large number of ecology samples has become common routine. On the other hand researches have to cope with analysis of large and very complex datasets.

Using standard data analysis pipelines in QIIME or Mothur it is very fast and convenient to generate abundancies tables and phylogenetic trees of the microbial communities found in the samples. Further analysis, like alpha and beta diversity for example is very well supported and often used in the popular statistical programming language R. During this course we will present different procedures to analyze the data and generate publication ready graphics.

Upon successful completion of this course, participants will be able to understand and analyse Microbiome data with R.

Teaching and learning method: 20% lecture and 80% interactive

Languages of instruction: English or German

Target audience: PhD students, technicians and researchers

Entrance qualifications: basic computer skills

Costs: 150 Euro (University)/ 300 Euro (Company)

Registration: zmf-sekretariat@medunigraz.at (deadline: October, 11th 2017)

As the number of participants is limited (min. 3 and max. 8), please register early to confirm your seat!

DFP: 7-Points

October 18th 2017 (9 am - 4 pm)

ZMF seminar room ground floor EG-086

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