

Core Facility Computational Bioanalytics

Short Introduction to Linux and command line data analysis on HPC cluster

Most tasks of bioinformatics are processed using the Linux operating system (OS). Therefore, familiarity with and understanding of basic Linux command lines is essential for bioinformatics analysis. This course will provide you an introduction to the Linux OS and its basic command line tools. Material will cover logging into remote machines, filesystem organization and file manipulation. During the course participants will also learn how to use and submit jobs with SLURM on the cluster.

Upon successful completion of this course, you will be familiar with:

- Basic Linux commands (including grep, sort, find, etc.)
- Running tools over SLURM (cluster management and job scheduling system)

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

Languages of instruction: English

Target audience: PhD students, technicians and researchers

Entrance qualifications: No

Registration: zmf-sekretariat@medunigraz.at (deadline: September, 25th 2019)

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

October 3rd 2019 (2 pm - 4 pm)

ZMF seminar room ground floor EG 086

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