

Core Facility Computational Bioanalytics

Short introduction to Linux and command line data analysis

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 or German

Target audience: PhD students, technicians, medical doctors and researchers

Entrance qualifications: No

Costs: free of charge

Registration: Website [Medical Research Academy | \(medunigraz.at\)](https://www.medunigraz.at)

Lecturer: Slave Trajanoski

As the number of participants is limited (min. 2 and max. 8), please register early to confirm your seat!

November 25th 2021 (14.00 to 16.00)

Location: SR EG-086/087

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