

Core Facility Computational Bioanalytics

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, and installing and using software.

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

- Basic Linux commands (including grep, sort, awk, sed, etc.)
- Basic regular expressions - useful syntax for matching and substituting string and sequence data
- Conda package manager and sourcing different environments
- 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

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

Registration: zmf-sekretariat@medunigraz.at (deadline: April, 13th 2018)

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

April 18th 2018 (9 am - 4 pm)

ZMF seminar room EG 086

Contact: zmf-sekretariat@medunigraz.at
Tel: +43 (0)316 385-73001

Center for Medical Research (ZMF)
Stiftingtalstrasse 24, A-8010 Graz
<https://zmf.medunigraz.at>

DFP: 7-Points