

Linux and basic scripting

Introduction

This course is designed for researchers, including PhD students and postdocs, who frequently handle large datasets or large numbers of files and who need a more efficient way of working with such data. The course is equally suitable for those working with Windows, Mac OS X or Linux. No prior knowledge of operating systems is needed.

The goal of the course is to empower students and researchers with backgrounds in biology or biomedicine to navigate, manage and perform operations on files and data and metadata in tabular text formats. The data may be microscopy images, FASTA sequences, gene ontology files, chromatograms, mass spectra or tables with data on genes or proteins.

Day one, Monday, January 26

9:30	Operating system basics	Jeroen Laros
10:00	File systems, users, ownership and permissions	Maarten van Iterson
10:30	Pause	
11:00	Practical 1	
12:00	Lunch	
13:00	The Bash shell and common command line tools	Rob Marissen
13:30	Connecting to other machines	Martijn Vermaat
14:00	Practical 2	
15:00	Pause	
15:30	Installing and updating software	Zuotian Tatum

Practical 1

In this practical, we navigate through the filesystem, move and copy files, set permissions on files, etc.

Practical 2

In this practical, we connect to a remote machine and explore various common command line tools.

Day two, Tuesday, January 27

9:30	Regular expressions	Tugce Güler
10:00	Introduction to AWK	Magnus Palmblad
10:30	Pause	
11:00	Practical 3	
12:00	Lunch	
13:00	sed, grep, rename	Martijn Vermaat
13:30	Shell scripting	Zuotian Tatum
14:00	Practical 4	
15:00	Pause	
15:30	Evaluation, wrap up	Jeroen Laros

Practical 3

In this practical, we write a number of small AWK scripts.

Practical 4

In this practical, we make a shell script that combines some of our previous work.