Unix and genomic data

The recent progress of Next Generation Sequencing (NGS) technologies led to a huge increase in the amount of data that biologists have to deal with. The usual amount of generated data is far beyond the capacity of common data analysis tools on the Microsoft Windows platform. The Unix environment provides efficient tools for handling large amounts of genomic data.

Participants of the course will gain sufficient skills and confidence in the Unix environment to use it for analysis of genomic data. We will explore the possibilities of the system using the examples of NGS data manipulation, analysis and visualization. The focus of the course is not one particular NGS analysis, but to teach the participants how to comfortably use any Unix tool to pursue their scientific goals.

A new advanced course

Lecturers: Václav Janoušek, Libor Mořkovský
Date: January 8–10, 2016 (weekend)
   Winter semester
Language: English or Czech*
Limited to 24 participants
Recommended for master’s degree and PhD students
SIS: 2 credits,
   MB170C47,
link in the QR code:

* If all participants understand Czech, we will teach in Czech