Unix a práce s genomickými daty
Unix and genomic data

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:

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 pursuit their scientific goals.

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