



PhD Program in Plant Sciences: BIO634 - Next-generation Sequencing 2 - Continuation Course: Transcriptome and Biological Interpretation

Lecturers: Dr. Deepak Tanwar
Location: University of Zurich, BOT-P1-41
Small Lecture Hall at Botanical Garden
Dates: 12.11. & 13.11.2024
Credit Points: 1 ECTS

Course Description:

The goal is to introduce the students into data processing and analysis used in high-throughput sequencing (HTS). Based on the course BIO610 "Next-Generation Sequencing for Model and Non-Model Species" it will extend knowledge of HTS analysis and skills in computing taking a hands-on approach.

Course Objectives:

By the end of the module the students should be able to:

- Perform standard transcriptomic data analysis
- Choose and apply tools for basic HTS analysis
- Understand some possible pitfalls in HTS data analysis
- Use the Linux/Unix command line and R
- Perform exploratory data analysis

Prior Knowledge:

BIO 609 "Introduction to UNIX/Linux and Bash scripting" and BIO 610 "Next-Generation Sequencing for Model and Non-Model Species" or appropriate previous knowledge in the Linux/Unix command line and HTS technologies. A basic knowledge of R is also desired.

Students can brush-up their skills

- Bash scripting: <https://www.learnshell.org/>

- R: <https://www.codecademy.com/learn/learn-r>

Individual Performance and Assessment:

Attendance at lectures and active participation in the hands-on exercises are required.

Number of Participants: 24,

Open for PhD and MSc students. Priority will be given to the PhD programs in Plant Sciences, Science & Policy and Evolutionary Biology. Postdocs if places available.