

Prerequisites for the bioinformatics-part

Alexander Jueterbock, Martin Jakt*

PhD course: High throughput sequencing of non-model organisms

For the practical bioinformatics-part of the HTS course, we will work remotely on UNIX computers. To connect to these remote computers, you need to bring your own laptop. **MAC and Linux users** generally don't need to install any additional software to connect to a remote computer. However, please install the program [filezilla](#). This program works on all platforms and helps to transfer files between computers.

MAC users also need to install [XQuartz](#) for opening applications with a graphical user interface.

You will have internet access either via eduroam; or, if you bring your mobile phone, you will get a guest-account password via SMS.

Windows users: To connect remotely to a UNIX-based system, download [Putty](#) and [Xming](#) and follow the configuration guidelines on http://www.geo.mtu.edu/geoschem/docs/putty_install.html. Alternatively, you can use [X2Go](#).

All required programs will be available on our local UNIX computers and you are not required to install them on your own laptops. However, if you would like to try them out on your own private computer, here is a list of programs and scripts that we will use:

Programming languages:

- [R](#)
- [Python](#)
- [Perl](#)

Trimming and quality control:

- [Fastqc](#)
- [TrimGalore!](#)

*University of Nordland, Norway

- `fastx_collapser` from FASTX-Toolkit
- `fastqduplicatecounter.py` in the scripts from the Simple Fools Guide

Genome browser:

- IGV

Genome assembly:

- Mira

Mapping and variant calling:

- Bowtie2
- `Bowtie2Filtering.py`
- `samtools`
- `bcftools` (with `vcfutils.pl`)
- Picard command line tools
- `bgzip` from `tabix`