

# Prerequisites for the bioinformatics-part

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## 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](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:

## Reading

Please make sure that you have read through the PDF document 'Unix Tools for Bioinformatics' before the 8th of May.

## Programming languages:

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

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## Trimming and quality control:

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