

Instructions for students who already have machines with a UNIX system installed.

If you would like to install the packages for genome assembly yourself, please download the scripts from www.biomed.cas.cz/mbu/lbwrf/c4sys/archive/genome_assembly/scripts.zip and install the following software:

- C4sys genome assembly scripts, link above.
- Fastqc - <https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>
- Khmer (version 2.1.1) - <https://github.com/dib-lab/khmer>
- Bowtie2 (version 2.3.0) - <https://sourceforge.net/projects/bowtie-bio/files/bowtie2/>
- Velvet (Version 1.2.10) – Attention! It is necessary to compile Velvet, allowing it to use max_kmer_length longer than 32 mers. If you do not know how to compile Velvet, use the following commands:

```
sudo git clone https://github.com/dzerbino/velvet.git
cd velvet
sudo make 'CATEGORIES=32' 'MAXKMERLENGTH=181' 'BUNDLEDZLIB=1'
```

Remember to add all scripts and binaries to the path of your operating system. If you have troubles, feel free to write to:

Daniel K. Morais - daniel.morais@biomed.cas.cz
Laboratory of Environmental Microbiology
Microbiology Institute
Czech Academy of Sciences