1 Installed Tools

Tool	Version	Type	Approach	Reference	Installation
Kaiju	1.7.4	Protein	FM-Index, Alignment	http://kaiju.binf.ku.dk/	Easy
Kraken2	2.0.7-beta	DNA	k-mer	http://ccb.jhu.edu/software/kraken2/	Easy
Centrifuge	1.0.4	DNA	FM-Index	https://ccb.jhu.edu/software/centrifuge/manual.shtml	Easy
taxMaps	0.2	DNA	FM-Index	https://github.com/nygenome/taxmaps	Medium/Hard
DeepMicrobes	git rev. 43b654b	DNA	Machine Learning, k-mer	https://github.com/MicrobeLab/DeepMicrobes	Easy
MetaOthello	git rev. 15ded5e	DNA	k-mer	https://github.com/xa6xa6/metaOthello	Easy
k-SLAM	1.0	DNA	k-mer	https://github.com/aindj/k-SLAM	Medium
CLARK	1.2.5	DNA	(spaced) k-mer	http://clark.cs.ucr.edu/Overview/	Easy
CCMetagen	1.2.3	DNA		https://github.com/vrmarcelino/CCMetagen	Medium
Diamond	0.9.14	Protein	Alignment	http://www.diamondsearch.org/index.php	Easy
NBC		DNA	Naive Bayes Classification	http://nbc.ece.drexel.edu/	-
CAT & BAT	5.1.2	Protein/DNA		https://github.com/dutilh/CAT	Easy

Table 1. Overview – This table shows some general information about the installed tools. The last column gives information about the installation process. Most tools are installed via conda, whereas other tools are installed from github. The difficulty *Easy* corresponds to tools that do not need troubleshooting. Tools with a *Medium* need an additional installation of some dependencies, whereas *Medium/Hard* corresponds to many additional installations.

taxMaps.

```
conda create -n taxmaps python=2.7
git clone git://github.com/nygenome/taxmaps.git
pip install numpy==1.7
conda install -c bioconda samtools
conda install -c bioconda prinseq
conda install -c bioconda gem3-mapper
conda install -c bioconda krona
conda install -c anaconda cython
python2 -m pip install --user cutadapt==1.4.1
export PERL5LIB=/home/re85gih/miniconda3/envs/taxmaps/opt/krona/lib/
export PATH=$PATH:/home/re85gih/projectClassification/taxmaps/
```

k-SLAM. Here, a specific version for `boost` was needeed, but it could be installed via `conda`.

```
conda install -c anaconda boost=1.64
conda install -c bioconda k-slam
```

CCMetagen. Here, a specific version for `ete3` was needeed, but it could be installed via `conda`.

```
conda install -c etetoolkit ete3
conda install -c bioconda ccmetagen
```

2 Not installed tools

LiME.

- installation via git and make commands

- error in `Installation_Preprocessing_Tools.sh` due to denied permission

- manually: `egsa make` did throw an error

  ```
  git clone https://github.com/veronicaguerrini/LiME
  cd LiME
  one of the follwing two make thingys; they are for different approaches
  make chose this one
  make EBWT=0
  ```

Megan-LR

- page that refers to tool does not exist anymore?

MetaMaps

- in general: bad instructions

- conda: dependency cpp-boost needs a compatibe version, but that version throws incompabilities with pther packages

- tried with conda version 4.7.5

  ```
  UnsatisfiableError: The following specifications were found to be incompatible with each other:
  conda-forge/linux-64::_openmp_mutex==4.5=1_gnu -> openmp_impl==9999
  conda-forge/linux-64::boost-cpp==1.70.0=h7b93d67_3 -> libboost[version='<0']
  conda-forge/linux-64::bzip2==1.0.8=h7f98852_4 -> libgcc-ng[version='>=9.3.0'] -> _openmp_mutex[version='>=4.5'] -> openmp_impl==9999
  conda-forge/linux-64::libgcc-ng==9.3.0=h5dbcf3e_17 -> _openmp_mutex[version='>=4.5'] -> openmp_impl==9999
  metamaps -> boost-cpp[version='>=1.70.0,<1.70.1.0a0'] -> libboost[version='<0']
  ```