

# 1 Installed Tools

Tool	Version	Type	Approach	Reference	Installation
Kaiju	1.7.4	Protein	FM-Index, Alignment	<a href="http://kaiju.binf.ku.dk/">http://kaiju.binf.ku.dk/</a>	Easy
Kraken2	2.0.7-beta	DNA	k-mer	<a href="http://ccb.jhu.edu/software/kraken2/">http://ccb.jhu.edu/software/kraken2/</a>	Easy
Centrifuge	1.0.4	DNA	FM-Index	<a href="https://ccb.jhu.edu/software/centrifuge/manual.shtml">https://ccb.jhu.edu/software/centrifuge/manual.shtml</a>	Easy
taxMaps	0.2	DNA	FM-Index	<a href="https://github.com/nygenome/taxmaps">https://github.com/nygenome/taxmaps</a>	Medium/Hard
DeepMicrobes	git rev. 43b654b	DNA	Machine Learning, k-mer	<a href="https://github.com/MicrobeLab/DeepMicrobes">https://github.com/MicrobeLab/DeepMicrobes</a>	Easy
MetaOthello	git rev. 15ded5e	DNA	k-mer	<a href="https://github.com/xa6xa6/metaOthello">https://github.com/xa6xa6/metaOthello</a>	Easy
k-SLAM	1.0	DNA	k-mer	<a href="https://github.com/aindj/k-SLAM">https://github.com/aindj/k-SLAM</a>	Medium
CLARK	1.2.5	DNA	(spaced) k-mer	<a href="http://clark.cs.ucr.edu/Overview/">http://clark.cs.ucr.edu/Overview/</a>	Easy
CCMetagen	1.2.3	DNA		<a href="https://github.com/vrmarcelino/CCMetagen">https://github.com/vrmarcelino/CCMetagen</a>	Medium
Diamond	0.9.14	Protein	Alignment	<a href="http://www.diamondsearch.org/index.php">http://www.diamondsearch.org/index.php</a>	Easy
NBC		DNA	Naive Bayes Classification	<a href="http://nbc.ece.drexel.edu/">http://nbc.ece.drexel.edu/</a>	-
CAT & BAT	5.1.2	Protein/DNA		<a href="https://github.com/dutilh/CAT">https://github.com/dutilh/CAT</a>	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 cutadapt
conda install -c bioconda prinseq
conda install -c bioconda gem3-mapper
conda install -c bioconda krona
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 needed, 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 needed, but it could be installed via `conda`.

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

## 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 following two make things; 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 compatible version, but that version throws incompatibilities with other 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']
```