

## A Guide to the MLTreeMap imagemaker:

MLTreeMap is a software framework, designed for phylogenetic and functional analysis of metagenomics data. It searches for instances of marker genes on nucleotide sequences and deduces their most likely origin in a set of reference phylogenies. The MLTreeMap imagemaker has been designed to visualize your placements within the reference phylogenies. It is not part of the MLTreeMap stand-alone package and has to be installed individually.

### A) Installation of the MLTreeMap imagemaker

The MLTreeMap imagemaker is based on Perl scripts and has the following dependencies:

```
GD
Math::Trig
```

If these dependencies are satisfied, the MLTreeMap imagemaker is ready to use.

### B) Usage of the MLTreeMap imagemaker

The MLTreeMap imagemaker has to be accessed on the command line and needs MLTreeMap output files as input. An example for valid input files is given in the directory "example\_input".

An example for a valid input command is: `./mltreemap_imagemaker.pl -i example_input`

This will concatenate all files of the same analysis type into one file and then generate the pictures (they will be written to the standard output directory `MLTreeMap_imagemaker_2_03/output/`).

If you want to enter a single file as input, this is also possible:

```
./mltreemap_imagemaker.pl -i
example_input/p_Aeropyrum_ernix_b.txt_contig158_RAxML_parsed.txt
```

Optional input option:

- o use this option if you want to write the output to another directory than the default.
- b parameter for the size of the placement bubbles (default: 0.9).

**Note:** In the previous version of the MLTreeMap imagemaker, the type of MLTreeMap analysis had to be indicated with the "-f" option (p: phylogenetic analysis, g: phylogenetic analysis based on the GEBA tree, n: functional analysis nifD, h: functional analysis nifH, r: functional analysis RuBisCo, m: functional analysis MMO). This is not necessary anymore. The MLTreeMap imagemaker now detects the analysis type automatically.