

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) Installing 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 -i example_input/ -f p_`

The `-f` option determines the type of analysis, of which you want to have a visualisation:

- `-f p_` phylogenetic analysis (i.e. the results have been placed on the phylogenetic reference tree of MLTreeMap)
- `-f g_` phylogenetic analysis based on the GEBA tree
- `-f n_` functional analysis (placements on the nifD reference tree).
- `-f h_` functional analysis (placements on the nifH reference tree).
- `-f r_` functional analysis (placements on the RuBisCo reference tree).
- `-f m_` functional analysis (placements on the MMO reference tree).

The `-i` option is the input directory. The MLTreeMap imagemaker will concatenate all files in this directory, which belong to the analysis type defined with the `-f` option (it also works, if there is only one file).

The concatenated file and the visualisations will be placed in the output directory.