

## Version history:

Version	date	comments
2.01	12.01.10	First stable release of MLTreeMap. - Implementation in ANSI-C. - Usage of RAxML for maximum likelihood calculations.
2.011	05.07.10	Minor code revision: - Bugfix: the return value of int main() is now 0. - Optimization of the AA model for the different gene families in the RAxML step.
2.03	12.08.10	Major code revision: - Re-implementation in Perl. - Runtime Improvement of the BLAST step. - Improved output handling. - Minimum Blast bitscore and minimum sequence length after Gblocks are now user definable.
2.031	31.08.10	Bugfix: Prevents the pipeline from crashing due to some non-word characters in input sequence names.
2.032	09.09.10	Improvements of the "sungrid cluster mode" -c s. MLTreeMap_imagemaker: introduction of a new mode (-d 1), which allows to print different datasets into one picture in different colors.
2.033	06.10.10	Bugfix: Corrected a minor error, which could lead to a segmentation fault in Gblocks. Compatibility note: MLTreeMap imagemaker 2.032 is fully compatible with MLTreeMap 2.033.
2.034	11.10.10	Bugfix: Prevents RAxML from crashing due to overlong sequence names. Compatibility note: MLTreeMap imagemaker 2.032 is fully compatible with MLTreeMap 2.034.
2.04	21.12.10	Major update: - Inclusion of 16s & 18s rRNA data. - Improvement of the MMO tree. - New dsrAB tree (based on sequences from Loy et al. 2009). - New photolyase/cryptochrome tree - Improved output format (note: because of this, MLTreeMap 2.04 also needs the MLTreeMap imagemaker 2.04)
2.05	16.06.11	Major update: - Inclusion of the HZO/HAO tree. - Improved 16S & 18S rRNA trees. - Bugfix: Version 2.04 lost plus/minus strand BLAST hits. - Bugfix in the sungrid mode. - Note: MLTreeMap 2.05 also needs the MLTreeMap imagemaker 2.05

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| 2.051 | 23.06.11 | <ul style="list-style-type: none"><li>- Bugfix: plus/minus rRNA hits with “n” or “x” in their sequence could not be parsed.</li><li>- MLTreeMap_imagemaker_2_051: Visualizations are now in SVG format. Please see the documentation for more details.</li></ul>  |
| 2.06  | 01.11.11 | <p>Update:</p> <ul style="list-style-type: none"><li>- Inclusion of the pufM tree.</li><li>- New fungi phylogeny:<br/>use the “-t i” option to search for fungi sequences and have them placed in a detailed fungi phylogeny.<br/>Note: this tree allows a more accurate and detailed analysis of fungi sequences. Nevertheless the assignment accuracy of eukaryotic sequences is still below the one for prokaryotes.</li></ul> |
| 2.061 | 21.11.11 | <p>Update:</p> <ul style="list-style-type: none"><li>- Inclusion of the mcrA and bssA reference trees.</li><li>- Improvement of the ‘-d’ option of the MLTreeMap imagemaker. Use now the ‘-t 0’ option of the imagemaker to displays trees without text labels.<br/>For more details please see the documentation.</li></ul>  |