**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

2.051 23.06.11 - Bugfix: plus/minus rRNA hits with “n” or “x” in their   
 sequence could not be parsed.

- MLTreeMap\_imagemaker\_2\_051: Visualizations are now  
 in SVG format. Please see the documentation for more  
 details.

2.06 01.11.11 Update:   
 - Inclusion of the pufM tree.   
 - New fungi phylogeny:  
 use the “–t i” option to search for fungi sequences and  
 have them placed in a detailed fungi phylogeny.  
 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.

2.061 21.11.11 Update:

- Inclusion of the mcrA and bssA reference trees.

- Improvement of the ‘-d’ option of the MLTreeMap  
 imagemaker. Use now the ‘-t 0’ option of the  
 imagemaker to displays trees without text labels.  
 For more details please see the documentation.