

These trees contain **pre-computed MLEs for branch lengths** to speed the analyses.

You will want to estimate all the branch lengths via ML when you analyze your own data!

```
seqfile = seqfile.txt          * sequence data filename

* treefile = treefile_M0.txt   * SET THIS for tree file with ML branch lengths under M0
* treefile = treefile_M1.txt   * SET THIS for tree file with ML branch lengths under M1
* treefile = treefile_M2.txt   * SET THIS for tree file with ML branch lengths under M2
* treefile = treefile_M3.txt   * SET THIS for tree file with ML branch lengths under M3
* treefile = treefile_M7.txt   * SET THIS for tree file with ML branch lengths under M7
* treefile = treefile_M8.txt   * SET THIS for tree file with ML branch lengths under M8

outfile = results.txt         * main result file name
  noisy = 9                   * lots of rubbish on the screen
  verbose = 1                  * detailed output
  runmode = 0                  * user defined tree
  seqtype = 1                  * codons
CodonFreq = 2                  * F3X4 for codon frequencies
  model = 0                    * one omega ratio for all branches

* NSSites = 0                  * SET THIS for M0
* NSSites = 1                  * SET THIS for M1
* NSSites = 2                  * SET THIS for M2
* NSSites = 3                  * SET THIS for M3
* NSSites = 7                  * SET THIS for M7
* NSSites = 8                  * SET THIS for M8

  icode = 0                    * universal code
fix_kappa = 1                  * kappa fixed
  * kappa = 4.43491             * SET THIS to fix kappa at MLE under M0
  * kappa = 4.39117             * SET THIS to fix kappa at MLE under M1
  * kappa = 5.08964             * SET THIS to fix kappa at MLE under M2
  * kappa = 4.89033             * SET THIS to fix kappa at MLE under M3
  * kappa = 4.22750             * SET THIS to fix kappa at MLE under M7
  * kappa = 4.87827             * SET THIS to fix kappa at MLE under M8

fix_omega = 0                  * omega to be estimated
  omega = 5                     * initial omega

  * ncatG = 3                   * SET THIS for 3 site categories under M3
  * ncatG = 10                  * SET THIS for 10 of site categories under M7 and M8

fix_branch = 2                 * fixed branch lengths from tree file
```

These are **pre-computed MLEs for kappa** to speed the analyses.

You will want to also estimate the kappa value via ML when you analyze your own data!