

Explanation of the results of the dating analyses

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The analyses are split into the following directories:

```
|— results
|— results-calibrations
|— results-calibrations-constraints
```

Let `name` be the analysis name. In each directory, the files are structured as follows:

name.params.00.monitor Monitor file of all parameters; can be opened in Tracer.
The first 5000 iterations are burn in. Each run includes a total number of approximately 20000 iterations. The index `00` means that this is the first chain of four parallel chains, the other three chains are heated, and may be ignored.

name.ratetree.00.monitor Monitor file of the relative rate tree. Each branch stores the relative rate used on that branch.

name.timetree.00.monitor Monitor file of the absolute or relative time tree. Each branch stores the absolute or relative time between speciations.

For the following files, the burn in of 5000 iteration has already been excluded:

name.timetree.00.ages.full Table of node ages. Each row shows the ages of a specific node for all iterations. The nodes are integer indexed, and leaf names are shown when available. The indices are distributed in pre-order. That is, for a tree, we index the root first, then the sub trees from left to right (sometime called depth first). For your reference, I have created a tree with all node indices `name.meantree.index`.

name.timetree.00.ages.summary Table of node ages. Each row shows the mean age and the variance of the age of a specific node. Further, the minimum ages, the maximum ages, and the 95% confidence intervals are shown.

name.timetree.00.monitor.nex Nexus file of the tree monitor; can be directly opened with *Densitree*.

name.timetree.00.tree.mean Tree with node ages denoting the mean node age across all iterations.

name.timetree.00.tree.variance Tree with node ages denoting the variance of node ages across all iterations.

Other interesting files:

name.meantree Tree with branch lengths storing the average number of substitutions per site.

name.meantree.index Same as **name.meantree** but the node indices are printed instead of the node names.

name.timetree.00.monitor.thinned Thinned monitor file. Only every fifth iterations is printed. Used to create the Nexus file for *Densitree*.

Files related to the MCMC sampler:

name.data Internal data used by the sampler (mean branch lengths measured in average number of substitutions per site, covariance matrix, and so on).

name.mcmc.log Log file of the MCMC sampler. One can have a look at the proposals, the acceptance rates, and more.

name.mcmc.mc3 Saved state for continuing the MCMC sampler.

name.mcmc.setting Saved settings such as the analysis name, the burn in configuration and much more.

The calibration name includes the boundaries, so they can be nicely viewed in Tracer at the x-axis label. For example, when opening the file **results-calibrations-constraints/name.params.00.monitor**, the age distribution of a node calibrated by a calibration may look like this:

