

Dating with constraints

A tutorial on McmcDate

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In this tutorial, we are going to date a phylogeny with constraints. That is, we are going to estimate the ages of the ancestral nodes of a phylogeny with node age calibrations and node order constraints. In general, the rough pipeline is:

1. Get a multi sequence alignment, and decide on a rooted tree. Here, we are going to use data from eukaryotes (Strassert et al. [2021](#)).
2. Perform a Bayesian analysis using Phylobayes to estimate the distributions of branch lengths measured in substitutions per unit time.
3. Get auxiliary data such as node age calibrations, node order constraints or node braces.
4. Use the branch length distributions Perform a Bayesian analysis using McmcDate to estimate.

1 Provision of sequence data and a rooted tree

2 Phylogenetic inference with Phylobayes

3 Preparation of node calibrations and node order constraints

4 Dating with McmcDate

A Internals of McmcDate

- Based on [mcmc](#).
- Based on [elynx-tree](#).
- Explain code a bit (I guess mostly proposals).

B Node braces

References

Strassert, J. F. H., I. Irisarri, T. A. Williams, and F. Burki (2021). “A molecular timescale for eukaryote evolution with implications for the origin of red algal-derived plastids.” In: *Nature Communications* 12.1. DOI: [10.1038/s41467-021-22044-z](https://doi.org/10.1038/s41467-021-22044-z).