

Dating with constraints

A tutorial on McmcDate

Dominik Schrempf

January 13, 2023

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

1. Prepare a multi sequence alignment, and decide on a rooted tree.
2. Estimate the distributions of branch lengths measured in substitutions per unit time.
3. Prepare auxiliary data such as node age calibrations or node order constraints.
4. Date the phylogenetic tree using McmcDate.

1 Provision of sequence data and a rooted tree

Here, we are going to use data from eukaryotes (Strassert et al. [2021](#)).

2 Phylogenetic inference with Phylobayes

3 Preparation of node calibrations and node order constraints

McmcDate can also brace nodes (Appendix [A](#)).

4 Dating with McmcDate

McmcDate is a Haskell program (Appendix [B](#)).

A Node braces

B Internals of McmcDate

- Based on [mcmc](#).

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

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](#).