An empirical guide to producing a dated phylogeny with treePL in a maximum likelihood framework

List of the files in the Supplementary Material folder

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BL = branch lengths, BS = bootstrap, ML = maximum likelihood. Blue bars at the nodes of the trees represent 95% high posterior densities and 95% confidence intervals on the ages of the nodes for BEAST2 trees and treePL trees respectively. All trees are provided in individual PDF files to facilitate comparison between them.

RAxML files for building the *Pennantia* phylogeny with treePL

* **Pennantia\_alignment.phy:** alignment of chloroplast DNA genes for the *Pennantia* phylogeny.
* **Pennantia\_partitions.txt:** provides the delimitation of the partitions of the alignment.

I provide these files so you can go through the protocol from Step 1, following the example of the *Pennantia* phylogeny.

treePL configuration files

* **Divaricate\_treePLconfig.txt:** treePL configuration file for the divaricatephylogeny.
* **Pennantia\_treePLconfig.txt:** treePL configuration file for the *Pennantia* phylogeny.

Divaricate phylogeny trees

* **Divaricate\_BEAST2.log:** log of the BEAST2 2.6.2 run; I used a burnin of 50% when generating the consensus.
* **Divaricate\_BEAST2\_dates.pdf:** divaricatephylogeny built with BEAST2 v. 2.6.2, mean node ages and HPDs.
* **Divaricate\_BEAST2\_posteriors.pdf:** divaricatephylogeny built with BEAST2 v. 2.6.2, posterior values.
* **Divaricate\_RAxML\_BSvalues.pdf:** best ML tree produced by RAxML for the divaricatephylogeny, with BS values.
* **Divaricate\_treePL\_BLx100\_10-8.pdf:** dated divaricatephylogeny built with treePL, with BL x100 and a smoothing value of 10-8.
* **Divaricate\_treePL\_BLx100\_10-14.pdf:** dated divaricatephylogeny built with treePL, with BL x100 and a smoothing value of 10-14.
* **Divaricate\_treePL\_originalBL\_10-6.pdf:** dated divaricatephylogeny built with treePL, with unmodified BL x100 and a smoothing value of 10-14.

Please note that because the divaricate phylogeny is a work in progress in my PhD thesis, I do not display tip names in the treePL and BEAST2 phylogenies. The BEAST2 phylogeny was built under the following settings:

* Birth-Death tree model [1].
* bModelTest for each partition (same partitions as for the treePL analysis; [2]).
* Relaxed clock with rates drawn from a log-normal distribution for each partition [3].
* Calibrations set as exponential distributions with an offset equal to the same minimum ages as the ones used with treePL, except for the crown age of Eudicots, for which I set an offset of 125 My corresponding to fossils of Eudicots (see [4] and references therein). The means of those exponential distributions were chosen so that the 97.5% quantile was roughly equal to 125% of the offset.
* MCMC chain run for 250 million generations sampled once every 25,000 generations.

*Pennantia* phylogeny trees

* **Pennantia\_RAxML\_BSvalues.pdf:** best ML tree produced by RAxML for the *Pennantia* phylogeny, with BS values.
* **Pennantia\_treePL\_BLx100\_10-6.pdf:** dated *Pennantia* phylogeny built with treePL, with BL x100 and a smoothing value of 10-6.
* **Pennantia\_treePL\_BLx100\_10-8.pdf:** dated *Pennantia* phylogeny built with treePL, with BL x100 and a smoothing value of 10-8.
* **Pennantia\_treePL\_originalBL\_10-3.pdf:** dated *Pennantia* phylogeny built with treePL, with unmodified BL and a smoothing value of 10-3.

Please note that the BEAST2-built phylogeny of *Pennantia* is available in Fig. 2 of [5].

R script

* **Step4-5\_Rscript.R:** R script of the Step 4.5 of the protocol.

References

1. Gernhard T. The conditioned reconstructed process. *J. Theor. Biol.* 2008; **253**:769–778.

2. Bouckaert RR, Drummond AJ. bModelTest: Bayesian phylogenetic site model averaging and model comparison. *BMC Evol. Biol.* 2017; **17**:42.

3. Drummond AJ, Ho SY, Phillips MJ, et al. Relaxed phylogenetics and dating with confidence. *PLoS Biol.* 2006; **4**:e88.

4. Magallón S, Gómez‐Acevedo S, Sánchez‐Reyes LL, et al. A metacalibrated time‐tree documents the early rise of flowering plant phylogenetic diversity. *New Phytol*. 2015; **207**:437–453.

5. Maurin KJL. A dated phylogeny of the genus *Pennantia* (Pennantiaceae) based on whole chloroplast genome and nuclear ribosomal 18S–26S repeat region sequences. *PhytoKeys* 2020; **155**:15–32.