

This repository contains folders corresponding to different analyses and results. Individual code files are uploaded separately, with specific files listed in red below with what analyses they are used for.

- **Comet analyses**

The R file documents how to perform the analyses, with the COMET sub-folder containing the results. The scaled phylogenetic data are provided in a separate folder (see below).

- [comet\\_analyses.R](#)

- **LTT plot**

The necessary code and cal3 results needed to reproduce the lineage through time plot.

- [fancy\\_LTT.R](#)

- **Randomization workflow**

This folder contains the information for randomizing the placement of families placed using morphology and then re-calculating lineage through time plots. There are sub-folders for data and R scripts used in the analysis, with an overall workflow provided as a pdf file.

- [add.tip.to.clade.R](#)

- [generate.treePL.config.R](#)

- **Sampling rate ghost lineage**

This folder is for the analysis investigating how sampling a simulated fossil record under different sampling rates affects relative ghost lineage sampling between a budding and bifurcating process of evolution. The directory contains the R code used to run the analysis and the results of the analysis.

- [samplingRateGhostLineage.R](#)

- **Scaled phylogenetic data**

This folder contains four .tre files, reflecting the timescaled phylogenetic data under the different evolutionary models and taxon sampling regimes.

- **treePL config files**

The four files correspond to the four control files used to timescale the phylogenetic backbone under the different evolutionary models and taxon sampling regimes.