About

postpb can be used to evaluate the results of Bayesian phylogentics software packages (such as *Phylobayes* and *MrBayes*) in an interactive and graphical way. Although both programmes come with built-in methods for assessing convergence and mixing of parameters, additional analyses are often helpful when interpreting the outcomes of Bayesian phylogenetics software. *postpb* bundles a number of common post-analyses and exploratory plotting approaches in one shiny app.

Notes

postpb is optimized and tested for usage with *Phylobayes* and *MrBayes* output files, but should work for any other Bayesian phylogenetic software that produces tabulated parameter files and tree files in Newick or Nexus format. It currently supports analysis of up to 4 chains, which should have been run under identical models and the same dataset.

Installation

To run *postpb* locally on your machine, open `R` and follow these instructions:

```r
# Install required libraries (skip if already installed)
install.packages(c( "distory",
                    "doParallel",
                    "dplyr",
                    "DT",
                    "foreach"
                    "gridExtra",
                    "markdown",
                    "phytools",
                    "rwty",
                    "shinycssloaders",
                    "shinyjs",
                    "shinythemes",
                    "shinyWidgets"),
                    dependencies = TRUE)

# Run Shiny app
library(shiny)
shiny::runGitHub("postpb","gerthmicha")
```

postpb is also hosted on shinyapps.io and can be accessed without installation. This is only recommended for testing though, as it will be slow for bigger files. There is also usage limit of 25h per month and if this is used up the app will be offline.

A commandline version of the app with reduced functionality can be found on github.

Usage

There are two modules in *postpb*, accessible through the tabs in the navbar on top of this page: **Traces** and **Trees**. Global options can be found on the sidebar on the left, and options specific for each analysis type will be in the main window. Usage is fairly self-explanatory. For a quick start, load one of the examples (see below), and click through the interface to explore the different plots and statistics.

Traces

Here, parameter files from *Phylobayes* or *MrBayes* can be summarized (file name ending in `.trace` or `.p`). Upload 1–4 of trace files from mcmc chains that were run under identical options. Click through the tabs to access the different funtions. Use the sliders in the sidebar to adjust the options. Currently implemented:

Global options for all tabs (in sidebar)

- Upload and select which trace files to analyse
- Thinning interval [default: consider every 10th generation]
- burnin adjustment [default: 20% of shortest chain]
- Plot adjustments (size of plot area, size of lines & points)
- Download of all plots in single PDF

XY tab

- XY plots of all parameters over mcmc generation

Violin tab

- Violin plots of all parameters

Density tab

- Density plots of all parameters

Summary statistics tab

- Various statistics for assessing convergence, stationarity, and mixing of chains
- Export in several formats

Trees

Here, tree samples obtained with *Phylobayes* or *MrBayes* can be analysed (file name ending in `.treelist` or `.t`). Typically, one would upload 2–4 tree sample files from mcmc chains run under identical options, although loading a single tree sample file is also possible. Click through the tabs to access the different funtions. Check the sidebar for options. Currently implemented:

Global options for all tabs (in sidebar)

- Upload and select which tree files to analyse
- Thinning interval [default: consider every 10th generation]
- Burnin adjustment [default: 20% of shortest chain]
- Select outgroup(s) for rooting, reroot with outgroup, midpoint, or unroot
- Highlighting taxa (three different colors)
- Formating of tree labels
- Plot adjustments (size of plot area, size of lines & points)
- Download of currently displayed tree plot

Trees tab

- Plot trees for chains side by side, browse through mcmc generations (can be animated)

Consensus tab

- Consensus tree including branch lengths and posterior probabilities (pp)
- Collapse branches below interactively chosen pp
- Export in newick file format
- Interactively chose outgroup with mouse (experimental)

Difference * Highlight conflicting nodes between consensus trees of all chains (requires at least 2 tree files)

Pairwise Robinson-Foulds * Plot Robinson-Foulds distances of trees within and between chains over generation

Bipartition support * Posterior probabilities for any taxonomic group in posterior sample of trees.

Examples

postpb comes with two sets of example data that can be loaded by clicking the buttons under the file selection dialogs in the trace and tree tabs.

Example 1 is taken from Kocot et al. (2017), and it contains the first 5,000 iterations of their *Phylobayes* analysis of the "LB_106" matrix under the CAT+GTR model. The example contains traces and trees for 4 chains. Please refer to the paper for details on how the dataset was compiled. All data associated with this paper is accessible under https://doi.org/10.5061/dryad.30k4v.2.

Example 2 is a *MrBayes* analysis of the "primates" alignment that is distributed with *MrBayes* (https://github.com/NBISweden/MrBayes/tree/develop/examples) and is originally from Hayasaka et al. (1988). The analysis was run under a HKY+G model using 2x4 chains for 1,000,000 generations with a sampling frequency of 50.

Citation

If you use *postpb* in your research, I would appreciate if you could cite it as

- Michael Gerth (2019) Postpb. Available under https://github.com/gerthmicha/postpb

A preprint describing *postpb* is in preparation. Please also cite the appropriate R packages listed below:

Tree plots, RF and consensus calculations:

- Paradis, E., Claude, J. and Strimmer, K. (2004) APE: analyses of phylogenetics and evolution in R language. Bioinformatics, 20, 289–290. https://cran.r-project.org/package=ape
- Revell, L. J. (2012) phytools: An R package for phylogenetic comparative biology (and other things). Methods Ecol. Evol., 3, 217-223. https://cran.r-project.org/package=phytools
- Chakerian, J. and Holmes, S. P. Computational Tools for Evaluating Phylogenetic and Heirarchical Clustering Trees. arXiv:1006.1015v1. https://cran.r-project.org/package=distory

MCMC diagnostics:

- Plummer, M., Best, N., Cowles, K. and Vines, K. (2006) CODA: convergence diagnosis and output analysis for MCMC. R News, 6, 7–11. https://cran.r-project.org/package=coda

Questions, comments, bugs

Please raise an issue at github.