

# User manual

## Package rfbd

### Introduction

The package rfbd implements the exact computation of the distribution of the divergence times of a tree topology or a set of tree topologies sharing at least a same clade, including fossils, from the fossil ages and the origin time of diversification. Since fossil ages are given as (stratigraphic) intervals of time, it is necessary to sample them in order to obtain distributions of divergence times. We also have to sample among the possible speciation, extinction and fossilization rates. We developed an importance sampling procedure based on MCMC. The biased density used in this importance sampling procedure weights each combination of possible fossil ages and rates proportionally to the probability of the tree with these fossil ages under the fossilized birth and death model with these rates.

### Installation

Using the package rfbd first requires to install it in your R system by typing

```
>install.packages("<path_to>/rfbd_0.0.tar.gz", repos = NULL, type = "source")
```

in a R console, where `path_to` is the path to the file `'rfbd_0.0.tar.gz'`.

The package can then be loaded anytime with

```
>library(rfbd)
```

### Using the package rfbd

For technical reasons, all the functionalities of the standalone software are not implemented in the package rfbd yet. In particular, the standalone software includes graphical features which are not implemented in the the package rfbd since they require an external library. More importantly, the rfbd software does not use multithreading (parallel computations) since the library required by the standalone software is not available on all the operating systems. This point limits the availability of the package rfbd to deal with big dataset with regard to the standalone software. Notably, the Cotylasauria dataset containing the 1000 equiparsimonious trees is too large to be handled by the R package (computations took several hours with 40 threads working in parallel). We provide a smaller dataset containing only the tree of dimetrodons `'Dimetrodon.phy'` and a list of taxa defining a sub-clade of this tree `'Clade_Dimetrodon.txt'` to be used with the package rfbd.

The package rfbd includes two functions `FBDdiagnostic` and `FBDdistribution`. Both functions have numerous parameters, mainly to control the proposal of MCMC (cf their R manual). `FBDdiagnostic` does not have a return value and just write two coda files for MCMC diagnostic purposes. It runs faster than the function `FBDdistribution` and can be used in order to tune the parameters of the MCMC.

Assuming that all the files are in the R working directory, one calls `FBDdiagnostic` with

```
>FBDdiagnostic("Dimetrodon.phy", "CotylasauriaAges.csv", outName = "Dimetrodon.out", indName  
= "Dimetrodon.ind", inf_origin=-400, sup_origin=NaN, end_time=0., spec_wind_size=0.1, exti_wind_size=0  
foss_wind_size=0.02, spec_init=0.5, exti_init=0.5, foss_init=0.1, iter=1000, prop = 0.75,  
al = 0.75, burn = 25000, thin = 200, step = 0.01)
```

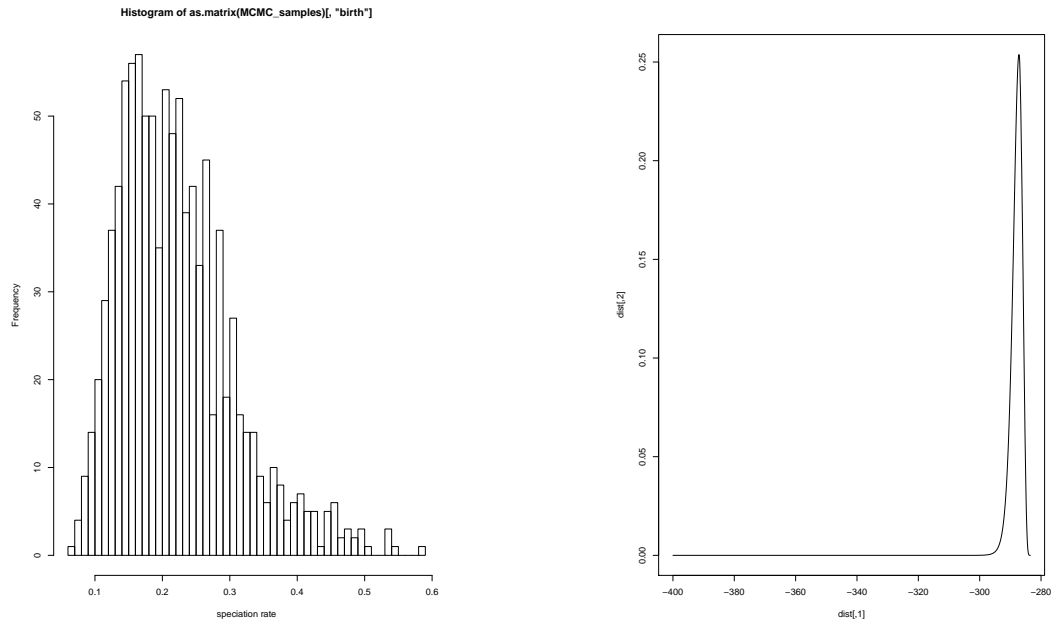


Figure 1: Left. the result of the command `hist(as.matrix(MCMC_samples)[,"birth"], xlab="speciation rate", breaks=40)`. Right. the result of the command `plot(distrib, type = 'l')`

The two files `Dimetrodon.out` and `Dimetrodon.ind` produced by the command just above can then be read for instance by using the R package `coda` with

```
>MCMC_samples = read.coda("Dimetrodon.out", "Dimetrodon.ind")
```

Various MCMC diagnostics can then be performed (see <https://cran.r-project.org/web/packages/coda/coda.pdf>).

If one is interested by the posterior distribution of the parameters of the model. In particular, their Highest Posterior Density intervals can be computed by the function `HPDinterval` of the `coda` package, i.e., with the command line:

```
>HPDinterval(MCMC_samples, 0.95)
```

Plotting the histogram of the posterior distribution of a parameter of the model, e.g., the speciation rate (Fig. 1-left), can be performed by

```
>hist(as.matrix(MCMC_samples)[,"birth"], xlab="speciation rate", breaks=40)
```

`FBDdistribution` returns the distribution or the density of the divergence times associated to the root of the smallest clade containing all the taxa in the file `Clade_Dimetrodon.txt` and still writes two `coda` files for diagnostic purposes.

```
>distrib = FBDdistribution("Clade_Dimetrodon.txt", "Dimetrodon.phy", "CotylosauriaAges.csv", outName = "Dimetrodon.out", indName = "Dimetrodon.ind", inf_origin=-400, sup_origin=NaN, endtime=0., spec_wind.size=0.1, exti_wind.size=0.1, foss_wind.size=0.02, spec_init=0.5, exti_init=0.5, foss_init=0.1, iter=1000, prop = 0.75, al = 0.75, burn = 25000, thin = 200, step = 0.01)
```

This distribution can be plotted with (Fig. 1-right)

```
>plot(distrib, type = 'l')
```