

PRDATR: PRobabilistic Distances under models of Adaptive Trait evolution in R

NOTE See the file https://github.com/radamsRHA/PRDATR/PRDATR_Manual.pdf for detailed instructions

Installing R package PRDATR from github

The R package PRDATR is freely available to download and distribute from github <https://github.com/radamsRHA/PRDATR/>. To install and load PRDATR, you must first install the R package devtools, Additionally, make sure the most updated version of R is installed

```
install.packages("devtools")
```

Now using devtools we can install PRDATR from github:

```
library(devtools)
install_github("radamsRHA/PRDATR")
library(PRDATR) # Load package
```

PRDATR also requires the following dependencies to be installed:

- `install.packages('geiger')`
- `install.packages('ape')`
- `install.packages('gaussDiff')`

To begin using PRDATR try using the examples associated with each function.

Example: compute probabilistic distances between evolutionary models

We can use `Function_ComputeDistances` to compute the probabilistic distance between a BM and an OU model for an example dataset. First, let's load the R package PRDATR and its dependancies:

```
#####
# Load depends #
#####
library(ape)
library(geiger)
library(gaussDiff)
library(PRDATR)
```

Now, let's specify the phylogenetic tree we want to use as a framework (here we are using the tree from Felsenstein 1985)

```
#####
# Specifity example tree (Fig. 8, Felsenstein 1985) used for demonstrating model distances #
#####
string.Figure01_Felsenstein1985_Tree <- "(((Species_7:1.635983031,Species_8:0.8079384444):1.801052391,(
handle.Figure01_Felsenstein1985_Tree <- read.tree(text = string.Figure01_Felsenstein1985_Tree)
```

Next, we specify two lists, each representing the two models:

```
#####
# Construct a list for Model 01 #
#####
vector.Model_01_Theta <- c(1) # using a rate of 1
names(vector.Model_01_Theta) <- c("Sig2")
```

```
list.Model01_BM <- list(handle.Phylogeny = handle.Figure01_Felsenstein1985_Tree,
                        string.Model = "BM",
                        vector.Z = rep(0, length(handle.Figure01_Felsenstein1985_Tree$tip.label)), # me
                        vector.Theta = vector.Model_01_Theta)
```

```
#####
# Construct a list for Model 02 #
#####
```

```
vector.Model_02_Theta <- c(1, 1) # rate of 1, alpha of 1
names(vector.Model_02_Theta) <- c("Sig2", "alpha")
```

```
list.Model02_OU <- list(handle.Phylogeny = handle.Figure01_Felsenstein1985_Tree,
                        string.Model = "OU",
                        vector.Z = rep(0, length(handle.Figure01_Felsenstein1985_Tree$tip.label)), # me
                        vector.Theta = vector.Model_02_Theta)
```

After the two models have been specified in their respective lists (Model01_BM and list.Model02_OU), we can compute the probabilistic distances between the two:

```
Function_ComputeDistances(list.Model_01 = list.Model01_BM, list.Model_02 = list.Model02_OU)
```

```
      dH      dKL
0.9991598 15.5200103
```

As you can see, the two distances (dH and dKL) are 0.9991598 and 15.5200103, respectively. In practice, the specific values of the model parameters can be specified as shown above, to represent maximum likelihood or Bayesian inferences, for example.