Package ‘pmc’

January 7, 2021

Version 1.0.4
Title Phylogenetic Monte Carlo

URL https://github.com/cboettig/pmc
BugReports https://github.com/cboettig/pmc/issues
License CC0
LazyData true
VignetteBuilder knitr
Suggests covr, gridExtra, knitr, testthat, rmarkdown
Imports dplyr, geiger, ggplot2, parallel, ouch, tidyr
RoxygenNote 7.1.1
NeedsCompilation no
Author Carl Boettiger [aut, cre]
Maintainer Carl Boettiger <cboettig@gmail.com>
Repository CRAN
Date/Publication 2021-01-07 18:10:12 UTC

R topics documented:

anoles ................................................................. 2
pmc ................................................................. 2
pmc_fit ........................................................... 3
simulate.gfit ....................................................... 4
tree ................................................................. 4
update.gfit ........................................................ 4

Index 6
The anoles data set

Description

as from ouch with additional regimes added and minor formatting changes

pmc

Description

Performs a phylogenetic monte carlo between modelA and modelB

Usage

pmc(
  tree,
  data,
  modelA,
  modelB,
  nboot = 500,
  optionsA = list(),
  optionsB = list(),
  ...
  mc.cores = parallel::detectCores()
)

Arguments

tree  A phylogenetic tree. Can be phylo (ape) or ouch tree
data   The data matrix
modelA a model from the list, or a custom model, see details
modelB any other model from the list, or custom model, see details
nboot number of bootstrap replicates to use
optionsA additional arguments to modelA
optionsB additional arguments to modelB
...   additional arguments to both fitting methods
mc.cores number of parallel cores to use

Details

Simulates data under each model and returns the distribution of likelihood ratio, L(B)/L(A), under for both simulated datasets.
**Value**

list with the nboot likelihood ratios obtained from fitting both models to data simulated by model A, and the nboot likelihood ratios obtained by fitting both models to simulations from model B, and the likelihood ratio between the original MLE estimated models from the data.

**Examples**

```r
library("geiger")
geo=get(data(geospiza))
tmp=treedata(geo$phy, geo$dat)
phy=tmp$phy
dat=tmp$data[,1]

pmc(phy, dat, "BM", "lambda", nboot = 20, mc.cores=1)
```

---

**pmc_fit**  
*Fit any model used in PMC*

**Description**

The fitting function used by pmc to generalize fitting to both geiger and ouch models.

**Usage**

```r
pmc_fit(tree, data, model, ...)
```

**Arguments**

- `tree`  
a phylogenetic tree. can be ouch or ape format
- `data`  
trait data in ape or ouch format
- `model`  
the name of the model to fit,
- `...`  
whatever additional options would be provided to the model fit

**Value**

the object returned by the model fitting routine (gfit for geiger, hansen/brown for ouch)
**simulate.gfit  simulate gfit**

**Description**

simulate method for gfit objects

**Usage**

simulate.gfit(object, nsim = 1, seed = NULL, ...)

**Arguments**

- **object**: a gfit object
- **nsim**: number of sims
- **seed**: an optional seed for the simulations (not implemented)
- **...**: additional arguments, not implemented for gfit simulations

**Value**

simulated dataset

**tree**

*The phylogeny for the anoles data set*

**Description**

The bimaculus phylogeny, as from the ouch package

**update.gfit  update gfit**

**Description**

update method for gfit objects

**Usage**

update.gfit(object, ...)

**Arguments**

- **object**: a gfit object
- **...**: additional arguments, such as the data to use to update
update.gfit

Value

updated gfit object
Index

* data
  anoles, 2
  tree, 4

anoles, 2

pmc, 2
pmc_fit, 3

simulate.gfit, 4

tree, 4

update.gfit, 4