Package 'pmc'

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Version 1.0.6

Title Phylogenetic Monte Carlo

Description Monte Carlo based model choice for applied phylogenetics of continuous traits. Method described in Carl Boettiger, Graham Coop, Peter Ralph (2012) Is your phylogeny informative? Measuring the power of comparative methods, Evolution 66 (7) 2240-51. <doi:10.1111/j.1558-5646.2011.01574.x>.

URL https://github.com/cboettig/pmc

BugReports https://github.com/cboettig/pmc/issues

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LazyData true

VignetteBuilder knitr

Suggests covr, gridExtra, knitr, testthat, rmarkdown

Imports dplyr, geiger (>= 2.0.11), ggplot2, parallel, ouch, tidyr, phytools (>= 1.5-1)

RoxygenNote 7.2.3

Encoding UTF-8

NeedsCompilation no

Author Carl Boettiger [aut, cre]

Maintainer Carl Boettiger <cboettig@gmail.com>

Repository CRAN

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`anoles` *The anoles data set*

Description

as from ouch with additional regimes added and minor formatting changes

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`pmc` *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

```
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

```
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

Value

updated gfit object

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