Package ‘pmc’

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Title Phylogenetic Monte Carlo


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

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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(),
  ...
)

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)

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**

**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

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**tree**

The phylogeny for the anoles data set

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**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
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