# Package ‘pmc’

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**Version** 1.0.3

**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

**Imports** dplyr, geiger, ggplot2, parallel, ouch, tidyr

**RoxygenNote** 6.0.1.9000

**NeedsCompilation** no

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**Repository** CRAN

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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(), ..., 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**

```r
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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