Package ‘pmc’

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**anoles**  
*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

```r
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
pmc_fit

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**

```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

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tree

*The phylogeny for the anoles data set*

**Description**

The bimaculus phylogeny, as from the ouch package

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update.gfit

**Description**

update method for gfit objects

**Usage**

```r
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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