

# Package ‘ppgm’

June 11, 2024

**Type** Package

**Title** PaleoPhyloGeographic Modeling of Climate Niches and Species Distributions

**Version** 1.0.3

**Description** Reconstruction of paleoclimate niches using phylogenetic comparative methods and projection reconstructed niches onto paleoclimate maps. The user can specify various models of trait evolution or estimate the best fit model, include fossils, use one or multiple phylogenies for inference, and make animations of shifting suitable habitat through time. This model was first used in Lawing and Polly (2011), and further implemented in Lawing et al (2016) and Rivera et al (2020).

Lawing and Polly (2011) <[doi:10.1371/journal.pone.0028554](https://doi.org/10.1371/journal.pone.0028554)> ``Pleistocene climate, phylogeny and climate envelope models: An integrative approach to better understand species' response to climate change"

Lawing et al (2016) <[doi:10.1086/687202](https://doi.org/10.1086/687202)> ``Including fossils in phylogenetic climate reconstructions: A deep time perspective on the climatic niche evolution and diversification of spiny lizards (Sceloporus)"

Rivera et al (2020) <[doi:10.1111/jbi.13915](https://doi.org/10.1111/jbi.13915)> ``Reconstructing historical shifts in suitable habitat of Sceloporus lineages using phylogenetic niche modelling."

**Imports** animation, ape, fields, geiger, methods, phangorn, phytools, stringi

**Depends** R (>= 4.3.0), R (>= 2.10), sp, sf

**License** GPL (>= 3)

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**LazyData** true

**LazyDataCompression** xz

**RoxygenNote** 7.3.1

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**Author** A. Michelle Lawing [aut, cph],  
Alexandra Howard [aut, cre],  
Maria-Aleja Hurtado-Materon [aut]

**Maintainer** Alexandra Howard <alexandra.howard@ag.tamu.edu>

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addFossil	<i>addFossil</i>
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## Description

Adds a fossil as a tip to a specified phylogeny given either an age range that the fossil occurs in, a specific edge that the fossil diverged from, or both. If the specific edge placement for the fossil is unknown, then this function randomly places the fossil on any edge that is within the age range.

## Usage

```
addFossil(tree, mintime = 0, maxtime = NA, name = "fossil", edge = NA)
```

**Arguments**

tree	An object of the class "phylo"
mintime	The minimum age of the fossil. If no minimum time is specified, the default value is 0.
maxtime	The maximum age of the fossil. If no maximum time is specified, the default value is the maximum tree age.
name	The name of the fossil to appear as a tip.label.
edge	The edge on the tree where the fossil presumably diverged. If no edge is specified, then the function randomly selects an edge within the age range of the fossil.

**Details**

There are several random components to this function. First, if an edge is not specified to place a fossil, then an edge is randomly selected that is within the age range of the fossil. Second, the exact placement of the node leading to the fossil is randomly selected within the age range specified. Third, the length of the edge leading to the fossil is randomly selected with constraints on the maximum length of the edge, where the maximum length of the edge cannot render the fossil younger than the minimum time of occurrence as specified in the mintime argument.

**Value**

An object of the class "phylo".

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard

**Examples**

```
mytree <- phytools::pbtree(n=20)
newtree <- addFossil(mytree, mintime = max(mytree$edge.length)/2, maxtime= max(mytree$edge.length))
plot(newtree)
```

---

getBioclimVars

*getBioclimVars*

---

**Description**

This function retrieves the bioclimatic variables described in Nix & Busby (1986) for the specified variables and the specified time period.

**Usage**

```
getBioclimVars(occurrences, which.biovars=c(1:19),
use.paleoclimate=TRUE, paleoclimateUser=NULL, layerAge=c(0:20))
```

**Arguments**

<code>occurrences</code>	a matrix or data.frame with three columns and rows to represent individuals. The first column must be species name for extant occurrences or the age in closest Ma for fossil occurrences. Second and third column must be Longitude and Latitude.
<code>which.biovars</code>	a vector of the numbers of the bioclimatic variables that should be returned. The bioclimatic variables number correspond to the table at ( <a href="https://www.worldclim.org/data/bioclim.html">https://www.worldclim.org/data/bioclim.html</a> ).
<code>use.paleoclimate</code>	if left blank, default North America paleoclimate data is used. If FALSE, user submitted paleoclimate must be provided
<code>paleoclimateUser</code>	list of data frames with paleoclimates, must be dataframes with columns: GlobalID, Longitude, Latitude, bio1, bio2,...,bio19.
<code>layerAge</code>	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data

**Details**

The occurrences argument should contain all extant or all fossils. Columns should be in the format: Species, Longitude, Latitude for extant data.

If using the provided paleoclimate data:

Modern time period uses the Hijmans et al. (2005) high resolution climate interpolations.

The time period 10 Ma uses the GCM by Micheels et al (2011) for the Tortonian.

The time period 15 Ma uses the GCM by Krapp & Jungclaus (2011) for the Middle Miocene.

For the one million year intervals outside the modern and past GCMs, the climate was interpolated based on the benthic marine foram stable oxygen isotope ratio curve from Ruddiman et al 1989. The scale of these variables is at a 50 km equidistant point grain size.

**Value**

Returns a data frame with the original occurrences input appended with columns of bioclimate variables as specified. If fossils are included, the returned bioclimate variables are from the closest 1 Ma interval of isotopically scaled climate.

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard, Maria-Aleja Hurtado-Materon

**References**

- Hijmans, R. J. et al. (2005) Very high resolution interpolated climate surfaces for global land areas
- Krapp, M. and Jungclaus, J. H. (2011) The Middle Miocene climate as modeled in an atmosphere-ocean-biosphere model. *Climate of the Past* 7(4):1169-1188
- Micheels, A. et al. (2011) Analysis of heat transport mechanisms from a Late Miocene model experiment with a fully-coupled atmosphere-ocean general circulation model. *Palaeogeography, Palaeoclimatology, Palaeoecology* 304: 337-350

Nix, H. and Busby, J. (1986) BIOCLIM, a bioclimatic analysis and prediction system. CSIRO annual report. CSIRO Division of Water and Land Resources, Canberra.

Ruddiman, W. F. et al. (1989) Pleistocene evolution: Northern hemisphere ice sheets and North Atlantic Ocean. *Paleoceanography* 4: 353-412

### Examples

```
data(occurrences)
biooccur <- getBioclimVars(occurrences,which.biovars=c(3,5))
#returns data frame with bioclimate variables 3 and 5 for occurrence data
```

---

getEnvelopes	<i>getEnvelopes</i>
--------------	---------------------

---

### Description

This function gets the bioclimate envelopes of species and nodes.

### Usage

```
getEnvelopes(treedata_min, treedata_max, node_est)
```

### Arguments

treedata_min	tree data object with min estimate of the climate envelope for each species.
treedata_max	tree data object with max estimate of the climate envelope for each species
node_est	the estimate of all the nodes, both min and max

### Details

Function derives the minimum, and maximum of each climate variable

### Value

An array containing climate envelopes for each node

### Author(s)

A. Michelle Lawing, Alexandra F. C. Howard

### See Also

ppgmESS(), nodeEstimate, geiger::treedata

**Examples**

```

data(samplerees)
data(occurrences)
tree <- samplerees[[25]]
biooccu <- getBioclimVars(occurrences, which.biovars=1)
sp_data_min<- tapply(biooccu[,4],biooccu$Species,min)
sp_data_max<- tapply(biooccu[,4],biooccu$Species,max)
treedata_min <- geiger::treedata(tree,sp_data_min,sort=TRUE,warnings=F)
treedata_max <- geiger::treedata(tree,sp_data_max,sort=TRUE,warnings=F)
full_est <- nodeEstimateEnvelopes(treedata_min,treedata_max)
node_est <- full_est$est
example_getEnvelopes <- getEnvelopes(treedata_min, treedata_max, node_est)

```

---

getGeoRate

*getGeoRate*


---

**Description**

This function calculates the change in suitable habitat through time in geographic space.

**Usage**

```

getGeoRate(envelope, tree, which.biovars, use.paleoclimate=TRUE,
paleoclimateUser=NULL, layerAge=c(0:20))

```

**Arguments**

envelope	the min and max climate envelope of each lineage for each time slice, as outputted by getEnvelopes()
tree	the phylogeny of all species. An object of class phylo
which.biovars	a vector of the numbers of the bioclimate variables to be included. The bioclimate variables number correspond to the table at ( <a href="https://www.worldclim.org/data/bioclim.html">https://www.worldclim.org/data/bioclim.html</a> ).
use.paleoclimate	if left blank, default North America paleoclimate data is used. If FALSE, user submitted paleoclimate must be provided
paleoclimateUser	list of data frames with paleoclimates, must be dataframes with columns: GlobalID, Longitude, Latitude, bio1, bio2,...,bio19. (see getBioclimvars()).
layerAge	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data

**Details**

Calculates rate of geographic change of all lineages. Outputs both the geographic center change, and the geographic size change.

**Value**

`geo_center` change in geographic center of suitable climate envelope

`geo_size` change in geographic size of suitable climate envelope

`time_int` time intervals

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard, Maria A. Hurtado-Materon

**See Also**

`getEnvelopes()`

**Examples**

```
data(samplertrees)
data(occurrences)
data(paleoclimate)
tree <- samplertrees[[25]]
occu <- getBioclimVars(occurrences, which.biovars=1)
sp_data_min<- tapply(occu[,4],occu$Species,min)
sp_data_max<- tapply(occu[,4],occu$Species,max)
treedata_min <- geiger::treedata(tree,sp_data_min,sort=TRUE,warnings=F)
treedata_max <- geiger::treedata(tree,sp_data_max,sort=TRUE,warnings=F)
full_est <- nodeEstimateEnvelopes(treedata_min,treedata_max)
node_est <- full_est$est
example_getEnvelopes <- getEnvelopes(treedata_min, treedata_max, node_est)
example_getGeoRate <- getGeoRate(example_getEnvelopes, tree, which.biovars=1)
```

---

`getLineageClimate`      *getLineageClimate*

---

**Description**

This function calculates the suitable climate for each specific lineage, starting at the tips and going back through time to the root.

**Usage**

```
getLineageClimate(envelope, tree, which.biovars,
use.paleoclimate=TRUE, paleoclimateUser=NULL, layerAge=c(0:20))
```

**Arguments**

<code>envelope</code>	the min and max climate envelope of each lineage for each time slice, as outputted by <code>getEnvelopes()</code>
<code>tree</code>	the phylogeny of all species. An object of class <code>phylo</code>
<code>which.biovars</code>	a vector of the numbers of the bioclimate variables to be included. The bioclimate variables number correspond to the table at ( <a href="https://www.worldclim.org/data/bioclim.html">https://www.worldclim.org/data/bioclim.html</a> ).
<code>use.paleoclimate</code>	if left blank, default North America paleoclimate data is used. If <code>FALSE</code> , user submitted paleoclimate must be provided
<code>paleoclimateUser</code>	list of data frames with paleoclimates, must be dataframes with columns: <code>GlobalID</code> , <code>Longitude</code> , <code>Latitude</code> , <code>bio1</code> , <code>bio2</code> , ..., <code>bio19</code> . (see <code>getBioclimvars()</code> ).
<code>layerAge</code>	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data

**Details**

Calculates rate of geographic change of all lineages. Outputs both the geographic center change, and the geographic size change.

**Value**

`matchedClim` list of occurrences points for each lineage, for each time slice of paleoclimate data  
`lineage` list of lineage specific nodes, as output from `phangorn::Ancestors`

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard, Maria A. Hurtado-Materon

**See Also**

`getEnvelopes()` `getGeoRate()`

**Examples**

```
data(sampletrees)
data(occurrences)
data(paleoclimate)
occu <- getBioclimVars(occurrences, which.biovars=1)
tree <- sampletrees[[25]]
#species minimum for biovariable 1
sp_data_min<- tapply(occu[,4],occu$Species,min)
#species maximum for biovariable 1
sp_data_max<- tapply(occu[,4],occu$Species,max)
#convert to treedata object
treedata_min <- geiger::treedata(tree,sp_data_min,sort=TRUE,warnings=F)
treedata_max <- geiger::treedata(tree,sp_data_max,sort=TRUE,warnings=F)
#estimate node values using Brownian Motion
```



```

full_est <- nodeEstimateEnvelopes(treedata_min,treedata_max)
node_est <- full_est$est #extract only node estimates
#calculate climate envelopes
example_getEnvelopes <- getEnvelopes(treedata_min, treedata_max, node_est)
#calculate lineage specific climate
example_getLinClim <- getLineageClimate(example_getEnvelopes, tree, which.biovars=1)

```

---

getTimeSlice

*getTimeSlice*


---

### Description

This function extracts estimated ancestral reconstructions for continuous characters any time specified along a phylogeny for all lineages present at the specified time.

### Usage

```
getTimeSlice(timeSlice, tree, trait, model = "BM", plot.est = FALSE)
```

### Arguments

timeSlice	single numeric or a vector with the time (or times) to extract the estimated ancestor reconstructions.
tree	an object of the class "phylo" that should be dated
trait	a vector of both tip values and node estimates that correspond to tree
model	if model = "estimate", the best fit model of evolution. If the model was specified, then model is the specified model, passes to <code>geiger::fitContinuous()</code> . Model options currently supported are: "BM", "OU", "EB", "lambda", "kappa", "delta"
plot.est	a conditional stating whether or not to plot the results

### Details

The estimated reconstruction relies on an interpolation between node or between tip and node estimates of the trait. This method assumes a constant rate of evolution along the lineage where the interpolation is taking place.

### Value

edge for each time specified, a vector of edges that are present during that time are returned  
est for each time specified, a vector of estimates of the ancestral reconstruction along each edge

### Author(s)

A. Michelle Lawing, Alexandra F. C. Howard

**See Also**

```
geiger::fitContinuous(), nodeEstimate()
```

**Examples**

```
data(sampletrees)
data(occurrences)
occurrences <- getBioclimVars(occurrences, which.biovars=1)
sp_data_min<- tapply(occurrences[,4],occurrences$Species,min)
treedata_min <- geiger::treedata(sampletrees[[1]], sp_data_min)
ex_est <- nodeEstimate(treedata_min, 1, model = 'BM') #runs BM model
ex_timeSlice <- getTimeSlice(10,treedata_min$phy,c(treedata_min$data[,1],ex_est$est))
```

---

nodeEstimate

*nodeEstimate*


---

**Description**

This function estimates the ancestral character states for continuous characters given a model of evolution or using the best fit model of evolution from the fitContinuous function in the geiger package. The ancestral states are estimated using GLS described in Martins and Hansen (1997).

**Usage**

```
nodeEstimate(treedata.obj, traitnum, model = "BM", bounds = list(),
control = list(), plot.est = FALSE)
```

**Arguments**

treedata.obj	an object of the class "treedata".
traitnum	the column number of the trait within the treedata object to be reconstructed.
model	the model of evolution to use in the ancestral state reconstruction. Options are "estimate", "BM", "OU", "EB", "lambda", "kappa", "delta".
bounds	bounds used for the model, passes to fitContinuous(), uses default if none specified.
control	setting used for optimization of the model likelihood. Passes to fitContinuous().
plot.est	logical. whether or not to plot the traitgram of the estimated ancestor states.

**Details**

See the fitContinuous() details for descriptions of the models of evolution and parameter estimation. nodeEstimate() currently supports the following models of evolution: Brownian motion (Felsenstein, 1973), Ornstein-Uhlenbeck (Butler and King, 2004), early-burst (Harmon et al., 2010), lambda (Pagel, 1999), kappa (Pagel, 1999), and delta (Pagel, 1999).

**Value**

an object of the class "nodeEstimate".

model if model = "estimate", the best fit model of evolution. If the model was specified, then model is the specified model.

est the ancestral node estimates of the continuous character.

phy the phylogeny used for the estimates, which might be transformed depending on the evolutionary model.

BM if model = "BM", returned values from fitContinuous() where the model is "BM"

OU if model = "OU", returned values from fitContinuous() where the model is "OU"

EB if model = "EB", returned values from fitContinuous() where the model is "EB"

lambda if model = "lambda", returned values from fitContinuous() where the model is "lambda"

kappa if model = "kappa", returned values from fitContinuous() where the model is "kappa"

delta if model = "delta", returned values from fitContinuous() where the model is "delta"

fitted if model = "estimate", returned values from the best fit model of evolution.

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard

**References**

Butler, M. A. and King, A. A. (2004) Phylogenetic comparative analysis: a modeling approach for adaptive evolution. *American Naturalist*, 164:683-695.

Felsenstein, J. (1973) Maximum likelihood estimation of evolutionary trees from continuous characters. *American Journal of Human Genetics*, 25:471-492

Harmon, L. J. et al. (2010) Early bursts of body size and shape evolution are rare in comparative data. *Evolution*, 64:2385-2396

Martins, E. P. and Hansen, T. F. (1997) Phylogenies and the comparative method: a general approach to incorporating phylogenetic information into the analysis of interspecific data. *American Naturalist*, 149, 646-667.

Pagel M. (1999) Inferring the historical patterns of biological evolution. *Nature*, 401:877-884

**See Also**

fitContinuous()

**Examples**

```
data(sampletrees)
data(occurrences)
occurrences <- getBioclimVars(occurrences, which.biovars=1)
sp_data_min<- tapply(occurrences[,4],occurrences$Species,min)
ex <- geiger::treedata(sampletrees[[1]], sp_data_min)
nodeEstimate(ex, 1, model = 'OU') #runs OU model
```

---

nodeEstimateEnvelopes *nodeEstimateEnvelopes*

---

### Description

This function estimates climate envelopes at nodes with the optional placement of fossils on randomly assigned or specified edges on a tree.

### Usage

```
nodeEstimateEnvelopes(treedata_min, treedata_max, fossils=FALSE,
  fossils.edges=FALSE, model="BM", bounds=list(), control=list(),
  use.paleoclimate = TRUE, paleoclimateUser = NULL, layerAge = c(0:20),
  which.biovars = which.biovars)
```

### Arguments

treedata_min	tree data object with min estimate of the climate envelope – list where first object is phylogeny, and second object is array of species with climate data variables (species must match)
treedata_max	tree data object with max estimate of the climate envelope
fossils	a matrix with three columns of age, longitude, and latitude, in that order, and rows that are entries for fossil occurrences.
fossils.edges	the edge number that the fossil occurs on
model	the model of evolution to use in the ancestral state reconstruction. Options are "estimate", "BM", "OU", "EB", "lambda", "kappa", "delta".
bounds	bounds used for the model, passes to fitContinuous(), uses default if none specified.
control	setting used for optimization of the model likelihood. Passes to fitContinuous().
use.paleoclimate	if left blank, default North America paleoclimate data is used. If FALSE, user submitted paleoclimate must be provided
paleoclimateUser	list of data frames with paleoclimates, must be dataframes with columns: GlobalID, Longitude, Latitude, bio1, bio2,...,bio19. (see getBioclimvars()).
layerAge	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data
which.biovars	A vector of the numbers of the bioclimate variables that should be returned. The bioclimate variables number correspond to the Hijmans table at ( <a href="https://www.worldclim.org/data/bioclim">https://www.worldclim.org/data/bioclim</a> ).

### Details

function adds fossils to trees according to addFossil(), then passes to nodeEstimate().

**Value**

an object of the class "nodeEstimate".

model if model = "estimate", the best fit model of evolution. If the model was specified, then model is the specified model.

est the ancestral node estimates of the continuous character.

phy the phylogeny used for the estimates, which might be transformed depending on the evolutionary model.

BM if model = "BM", returned values from fitContinuous() where the model is "BM"

OU if model = "OU", returned values from fitContinuous() where the model is "OU"

EB if model = "EB", returned values from fitContinuous() where the model is "EB"

lambda if model = "lambda", returned values from fitContinuous() where the model is "lambda"

kappa if model = "kappa", returned values from fitContinuous() where the model is "kappa"

delta if model = "delta", returned values from fitContinuous() where the model is "delta"

fitted if model = "estimate", returned values from the best fit model of evolution.

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard

**See Also**

nodeEstimate, fitContinuous

**Examples**

```
data(sampletrees)
sampletrees <- sample(sampletrees,5)
data(occurrences)
occu <- getBioclimVars(occurrences, which.biovars=c(1,2))
sp_data_min<-sapply(4:5,function(x) tapply(occu[,x],occu$Species,min))
sp_data_max<-sapply(4:5,function(x) tapply(occu[,x],occu$Species,max))
ex_min <- geiger::treedata(sampletrees[[1]], sp_data_min, sort=TRUE)
ex_max <- geiger::treedata(sampletrees[[1]], sp_data_max, sort=TRUE)
colnames(ex_min$data)<- colnames(ex_max$data)<-c("bio1","bio2") #labels biovars
nodeest<- nodeEstimateEnvelopes(treedata_min=ex_min,treedata_max=ex_max,
model="BM",which.biovars=c(1,2),
bounds=list(sigsq = c(min = 0, max = 1000000)))
```

---

 occurrences
*Sceloporus occurrence data*


---

**Description**

Occurrences for *Sceloporus*, as collected for Lawing et al 2016. Occurrence records from GBIF, and vetted using expert range maps from IUCN. See reference for further details Lawing et al (2015) Including fossils in phylogenetic climate reconstructions: A deep time perspective on the climatic niche evolution and diversification of spiny lizards (*Sceloporus*)

**Usage**

occurrences

**Format**'occurrences' A data frame of *Sceloporus* occurrence records**Species** Species name**Longitude** Longitude of occurrence**Latitude** Latitude of occurrence**Source**<<https://www.journals.uchicago.edu/doi/10.1086/687202>>

---

 paleoclimate
*Paleoclimate Data for ppgm examples*


---

**Description**

North America paleoclimate data used for running ppgm

**Usage**

paleoclimate

**Format**

'paleoclimate' A large list of paleoclimates for North America, each element in the list contains a data frame for one time period, from present to 20mya

**GlobalID** Global ID references for location**Longitude** Longitude of location**Latitude** Latitude of location

- bio1** Value for bioclimatic variable 1: annual mean temperature
- bio2** Value for bioclimatic variable 2: mean diurnal range
- bio3** Value for bioclimatic variable 3: isothermality
- bio4** Value for bioclimatic variable 2: temperature seasonality
- bio5** Value for bioclimatic variable 2: max temp of warmest month
- bio6** Value for bioclimatic variable 2: min temp of coldest month
- bio7** Value for bioclimatic variable 2: temperature annual range
- bio8** Value for bioclimatic variable 2: mean temp of wettest quarter
- bio9** Value for bioclimatic variable 2: mean temp of driest quarter
- bio10** Value for bioclimatic variable 2: mean temp of warmest quarter
- bio11** Value for bioclimatic variable 2: mean temp of coldest quarter
- bio12** Value for bioclimatic variable 2: annual precipitation
- bio13** Value for bioclimatic variable 2: precipitation of wettest month
- bio14** Value for bioclimatic variable 2: precipitation of the driest month
- bio15** Value for bioclimatic variable 2: precipitation seasonality
- bio16** Value for bioclimatic variable 2: precipitation of the wettest quarter
- bio17** Value for bioclimatic variable 2: precipitation of the driest quarter
- bio18** Value for bioclimatic variable 2: precipitation of the warmest quarter
- bio19** Value for bioclimatic variable 2: precipitation of the coldest quarter

---

plotAnimatedPPGM      *plotAnimatedPPGM*

---

## Description

This function creates an animated gif showing the change in modelled suitable habitat through time in geographic space.

## Usage

```
plotAnimatedPPGM(envelope, tree, filename="ppgm.gif", which.biovars,
path="", use.paleoclimate=TRUE, paleoclimateUser=NULL, layerAge=c(0:20))
```

## Arguments

- |               |  |
|---------------|--|
| envelope      | the min and max envelope of each lineage for each time slice   |
| tree          | the phylogeny or multiple phylogenies that show the relationship between species   |
| filename      | desired filename of output   |
| which.biovars | A vector of the numbers of the bioclimate variables that should be returned. The bioclimate variables number correspond to the Hijmans table at ( <a href="https://www.worldclim.org/data/bioclim">https://www.worldclim.org/data/bioclim</a> ). |

<code>path</code>	path to the directory where the results should be saved
<code>use.paleoclimate</code>	if left blank, default North America paleoclimate data is used. If FALSE, user submitted paleoclimate must be provided
<code>paleoclimateUser</code>	list of data frames with paleoclimates, must be dataframes with columns: GlobalID, Longitude, Latitude, bio1, bio2,...,bio19. (see <code>getBioclimvars()</code> ).
<code>layerAge</code>	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data

**Details**

Requires ImageMagick or GraphicsMagick to be installed on the operating system. This is easy to do if you have macports. Just type `sudo port install ImageMagick` into terminal.

**Value**

An animated gif of species through time

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard, Maria-Aleja Hurtado-Materon

**Examples**

```
data(samplerees)
data(occurrences)
tree <- samplerees[[25]]
biooccu <- getBioclimVars(occurrences, which.biovars=1)
sp_data_min<- tapply(biooccu[,4],biooccu$Species,min)
sp_data_max<- tapply(biooccu[,4],biooccu$Species,max)
treedata_min <- geiger::treedata(tree,sp_data_min,sort=TRUE,warnings=F)
treedata_max <- geiger::treedata(tree,sp_data_max,sort=TRUE,warnings=F)
## Not run: full_est <- nodeEstimateEnvelopes(treedata_min,treedata_max)
node_est <- full_est$est
example_getEnvelopes <- getEnvelopes(treedata_min, treedata_max, node_est)
animatedplot <- plotAnimatedPPGM(example_getEnvelopes,tree,which.biovars=1,path=tempdir())
## End(Not run)
```

---

`plotAnimatedPPGMMultiPhylo`

*plotAnimatedPPGMMultiPhylo*

---

**Description**

This function creates an animated gif showing the change in modeled suitable habitat through time in geographic space. It requires ImageMagick or GraphicsMagick to be previously installed in the operating system. This is easy to do if you have macports. Just type `sudo port install ImageMagick` into terminal.



**Usage**

```
plotAnimatedPPGMMultiPhylo(envelope, tree, filename="ppgm.gif",
  which.biovars, path="", use.paleoclimate=TRUE, paleoclimateUser=NULL, layerAge=c(0:20))
```

**Arguments**

envelope	the min and max envelope of each lineage for each time slice
tree	the phylogeny or multiple phylogenies that show the relationship between species
filename	filename of output
which.biovars	A vector of the numbers of the bioclimate variables that should be returned. The bioclimate variables number correspond to the Hijmans table at ( <a href="https://www.worldclim.org/data/bioclim">https://www.worldclim.org/data/bioclim</a> ).
path	path to the directory where the results should be saved
use.paleoclimate	if left blank, default North America paleoclimate data is used. If FALSE, user submitted paleoclimate must be provided
paleoclimateUser	list of data frames with paleoclimates, must be dataframes with columns: GlobalID, Longitude, Latitude, bio1, bio2,...,bio19. (see <code>getBioclimvars()</code> ).
layerAge	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data

**Details**

Requires ImageMagick or GraphicsMagick to be installed on the operating system. This is easy to do if you have macports. Just type `sudo port install ImageMagick` into terminal.

**Value**

An animated gif of species through time

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard

**Examples**

```
data(sampletrees)
data(occurrences)
sampletrees <- sample(sampletrees,5)
biooccu <- getBioclimVars(occurrences, which.biovars=1)
sp_data_min<- tapply(biooccu[,4],biooccu$Species,min)
sp_data_max<- tapply(biooccu[,4],biooccu$Species,max)
treedata_min <- treedata_max <- node_est <- envelope <- list()
## Not run: for (tr in 1:length(sampletrees)){
  treedata_min[[tr]] <- geiger::treedata(sampletrees[[tr]],sp_data_min,sort=TRUE,warnings=F)
  treedata_max[[tr]] <- geiger::treedata(sampletrees[[tr]],sp_data_max,sort=TRUE,warnings=F)
  full_est <- nodeEstimateEnvelopes(treedata_min[[tr]],treedata_max[[tr]])
  node_est[[tr]] <- full_est$est
```

```

  envelope[[tr]] <- getEnvelopes(treedata_min[[tr]], treedata_max[[tr]], node_est[[tr]])
}
animatedplot <- plotAnimatedPPGMMultiPhylo(envelope,samplertrees,which.biovars=1, path=tempdir())
## End(Not run)

```

---

plotGeoRates

*plotGeoRates*


---

### Description

plotGeoRates

### Usage

```
plotGeoRates(geo_center, geo_size, time_int, trees, path="")
```

### Arguments

geo_center	change in geographic center of suitable climate envelope, see
geo_size	change in geographic size of suitable climate envelope
time_int	time intervals to plot
trees	distribution of phylogenies
path	path to the directory where the results to be saved

### Details

Creates plot with gray background of all pairwise comparisons of change in geo center and area through time. Blue points on top show the sequential change in geo center and expansion/contraction for all lineages

### Value

plots of geo rate

### Author(s)

A. Michelle Lawing, Alexandra F. C. Howard

### See Also

getGeoRates

**Examples**

```

data(sampletrees)
data(occurrences)
sampletrees <- sample(sampletrees,5)
biooccu <- getBioclimVars(occurrences, which.biovars=1)
sp_data_min<- tapply(biooccu[,4],biooccu$Species,min)
sp_data_max<- tapply(biooccu[,4],biooccu$Species,max)
treedata_min <- treedata_max <- node_est <- envelope <- list()
geo_center<-array(NA,dim=c(100,53,21,21))
geo_size<-array(NA,dim=c(100,53,21,21))
for (tr in 1:length(sampletrees)){
  treedata_min[[tr]] <- geiger::treedata(sampletrees[[tr]],sp_data_min,sort=TRUE,warnings=F)
  treedata_max[[tr]] <- geiger::treedata(sampletrees[[tr]],sp_data_max,sort=TRUE,warnings=F)
  full_est <- nodeEstimateEnvelopes(treedata_min[[tr]],treedata_max[[tr]])
  node_est[[tr]] <- full_est$est
  envelope[[tr]] <- getEnvelopes(treedata_min[[tr]], treedata_max[[tr]], node_est[[tr]])
  temp <- getGeoRate(envelope[[tr]], sampletrees[[tr]], which.biovars=1)
  geo_center[tr,,,<-temp$geo_center
  geo_size[tr,,,<-temp$geo_size
}

## Not run: plotGeoRates(geo_center, geo_size, temp$time_int, sampletrees, path="tempdir()")

```

---

plotGeoRatesCon

*plotGeoRatesCon*


---

**Description**

plotGeoRatesCon

**Usage**

plotGeoRatesCon(geo\_center, geo\_size, time\_int, trees, path="")

**Arguments**

geo_center	change in geographic center of suitable climate envelope
geo_size	change in geographic size of suitable climate envelope
time_int	time intervals to plot
trees	distribution of phylogenies
path	path to the directory where the results to be saved

**Details**

Creates plot with gray background of all pairwise comparisons of change in geo center and area through time. Blue points on top show the sequential change in geo center and expansion/contraction for all lineages

**Value**

plots of geo rate

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard

**See Also**

getGeoRates

**Examples**

```

data(samplertrees)
data(occurrences)
tree <- samplertrees[[25]]
occurrences <- getBioclimVars(occurrences, which.biovars=1)
sp_data_min<- tapply(occurrences[,4],occurrences$Species,min)
sp_data_max<- tapply(occurrences[,4],occurrences$Species,max)
treedata_min <- geiger::treedata(tree,sp_data_min,sort=TRUE,warnings=F)
treedata_max <- geiger::treedata(tree,sp_data_max,sort=TRUE,warnings=F)
full_est <- nodeEstimateEnvelopes(treedata_min,treedata_max)
node_est <- full_est$est
example_getEnvelopes <- getEnvelopes(treedata_min, treedata_max, node_est)
example_getGeoRate <- getGeoRate(example_getEnvelopes, tree,which.biovars=1)

## Not run: plotGeoRatesCon(example_getGeoRate$geo_center,example_getGeoRate$geo_size,
example_getGeoRate$time_int, trees = trees[[1]], path=tempdir())
## End(Not run)

```

---

plotTraitGram

*plotTraitGram*

---

**Description**

Combine the node estimates based on random or specified fossil placement and plot them on a phylotraitgram in a specified directory.

**Usage**

```

plotTraitGram(treedata_min, treedata_max, node_est, fossils=FALSE,
which.biovars, path="", use.paleoclimate=TRUE, paleoclimateUser=NULL,
layerAge=c(0:20))

```

**Arguments**

treedata_min	a tree data object with the min estimate of the climate envelope
treedata_max	a tree data object with the max estimate of the climate envelope
node_est	the estimate of all the nodes, both min and max
fossils	a matrix with four columns of min age, max age, longitude, and latitude, in that order, and rows that are entries for fossil occurrences.
which.biovars	A vector of the numbers of the bioclimate variables that should be returned. The bioclimate variables number correspond to the Hijmans table at ( <a href="https://www.worldclim.org/data/bioclim">https://www.worldclim.org/data/bioclim</a> ).
path	path to the directory where the results should be saved
use.paleoclimate	if left blank, default North America paleoclimate data is used. If FALSE, user submitted paleoclimate must be provided
paleoclimateUser	list of data frames with paleoclimates, must be dataframes with columns: GlobalID, Longitude, Latitude, bio1, bio2,...,bio19. (see getBioclimvars()).
layerAge	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data

**Value**

a trait gram for minimum and maximum of biovariables

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard

**See Also**

plotTraitGramMultiPhylo

**Examples**

```
data(sampletrees)
data(occurrences)
bounds <- list(sigsq = c(min = 0, max = 1000000))
ex_mytree <- sampletrees[[3]] #single tree
test_con <- ppgmConsensus(occurrences = occurrences, trees = ex_mytree,
which.biovars = 1, bounds = bounds, control = list(niter = 20))
## Not run: plotTraitGram(test_con$treedata_min, test_con$treedata_max, test_con$node_est)
```

---

```
plotTraitGramMultiPhylo
```

```
plotTraitGramMultiPhylo
```

---

### Description

Combine the node estimates based on random or specified fossil placement and plot them on a phylotrait gram in a specified directory.

### Usage

```
plotTraitGramMultiPhylo(treedata_min, treedata_max, node_est,
  fossils=FALSE, use.paleoclimate=TRUE, paleoclimateUser=NULL,
  layerAge=c(0:20), which.biovars, path="")
```

### Arguments

treedata_min	tree data object with min estimate of the climate envelope
treedata_max	tree data object with max estimate of the climate envelope
node_est	the estimate of all the nodes, both min and max. Must be in format <code>[[trees]][[permut]][2,species,trait]</code>
fossils	a matrix with four columns of min age, max age, longitude, and latitude, in that order, and rows that are entries for fossil occurrences.
use.paleoclimate	if left blank, default North America paleoclimate data is used. If FALSE, user submitted paleoclimate must be provided
paleoclimateUser	list of data frames with paleoclimates, must be dataframes with columns: GlobalID, Longitude, Latitude, bio1, bio2,...,bio19. (see <code>getBioclimvars()</code> ).
layerAge	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data
which.biovars	A vector of the numbers of the bioclimate variables that should be returned. The bioclimate variables number correspond to the Hijmans table at ( <a href="https://www.worldclim.org/data/bioclim">https://www.worldclim.org/data/bioclim</a> ).
path	path to the directory where the results should be saved

### Details

plots a traitgram over multiple phylogenetic trees

### Value

a trait gram for minimum and maximum of biovariables over a distribution of phylogenetic trees

### Author(s)

A. Michelle Lawing, Alexandra F. C. Howard

**See Also**

plotTraitGram

**Examples**

```

data(sampletrees)
data(occurrences)
bounds <- list(sigsq = c(min = 0, max = 1000000))
sample <- sample(sampletrees,5)
test_ppgm <- ppgm(occurrences = occurrences, trees = sample,
model = "BM", which.biovars = c(1), bounds = bounds,
control = list(niter = 20))
## Not run: plotTraitGramMultiPhylo(test_ppgm$treedata_min,
test_ppgm$treedata_max, test_ppgm$node_est)
## End(Not run)

```

ppgm

*ppgm***Description**

ppgm makes a paleophylogeographic species distribution model using the bioclimate envelope method for a specified time period. Currently, models are only available for North America.

**Usage**

```

ppgm(occurrences, fossils = FALSE, trees, fossils.edges = FALSE,
model = "BM", permut = 1, only.biovars = TRUE, which.biovars = c(1:19),
path = "", plot.TraitGram = FALSE, plot.AnimatedMaps = FALSE,
plot.GeoRates = FALSE, bounds = list(), control = list(),
use.paleoclimate = TRUE, paleoclimateUser = NULL, layerAge=c(0:20),
verbose = TRUE)

```

**Arguments**

occurrences	a matrix with three columns of species name, longitude, and latitude, in that order, and rows that are entries for species occurrences. The bioclimate variables can be included for each occurrence in following columns. They must be in order 1 through 19.
fossils	a matrix with four columns of min age, max age, longitude, and latitude, in that order, and rows that are entries for fossil occurrences. The bioclimate variables can be included for each occurrence in following columns. They must be in order 1 through 19. All 19 variables must be included at this stage, variable selection is done with the argument: "which.biovars".
trees	phylogenies of species from first column of occurrences argument. Object of class multiphylo.

<code>fossils.edges</code>	a vector of edges that the fossils belong to. Must be in the same order of the fossils argument. If <code>fossils.edges</code> is false, the the function randomly assigns the location of the fossils depending on the age (see details for more information).
<code>model</code>	the model of evolution to use to estimate ancestor nodes. Argument is passed onto to function <code>nodeEstimate</code> .
<code>permut</code>	the number of times to randomly place fossils in phylogeny and estimate ancestor states.
<code>only.biovars</code>	logical. If FALSE, user must include biovariables in occurrence object.
<code>which.biovars</code>	a vector with the biovars to include in model (see <a href="http://www.worldclim.org">www.worldclim.org</a> for a list of biovars). If "ALL", then all 19 biovars are included in analysis.
<code>path</code>	path to the directory where the results should be saved.
<code>plot.TraitGram</code>	logical. Whether to plot a TraitGram
<code>plot.AnimatedMaps</code>	logical. Whether to plot AnimatedMaps. Requires ImageMagick to be installed on the system.
<code>plot.GeoRates</code>	logical. Whether to plot GeoRates
<code>bounds</code>	parameters for the evolutionary model selected. If none are supplied the default is used
<code>control</code>	settings used for optimisation of model likelihood. Passes to <code>geiger::fitContinuous</code>
<code>use.paleoclimate</code>	if left blank, default North America paleoclimate data is used. If FALSE, user submitted paleoclimate must be provided
<code>paleoclimateUser</code>	list of data frames with paleoclimates, must be dataframes with columns: GlobalID, Longitude, Latitude, bio1, bio2,...,bio19.
<code>layerAge</code>	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data
<code>verbose</code>	default true, returns all outputs. If FALSE then returns only climate envelopes and geographic data

## Details

If the 19 bioclimate variables are not supplied with the occurrences or with the fossils, they will be extracted from the closest 50km point location in the modern or paleoclimate maps that are loaded in with this function. The paleoclimate maps are isotopically scaled between general circulation models (see Lawing and Polly 2011; Rodder et al. 2013) and modern climate (see Hijmans et al. 2005). The fossils paleoclimate data is extracted to the closest million year paleoclimate map. Paleoclimate maps are derived at one million year intervals for the past 20 Ma. The tree (phylogeny) should be dichotomous and the species names should match the names in the first column of the occurrences argument.

## Value

`cem` Estimate of climate envelope for each species in present time. A data frame containing species and min mean and max of biovars specified with `which.biovars`.



geo\_move data frame of RateGeoCenter and RateGeoSize  
 change\_geo\_center array of change in geographic center of suitable climate for each lineage  
 change\_geo\_size array of change in geographic size of suitable climate for each lineage  
 time\_int matrix array of time intervals  
 treedata\_min list of trees with minimum bioclimatic variables  
 treedata\_max list of trees with maximum bioclimatic variables  
 model\_min list of trees with minimum fitted model as specified in model  
 model\_max list of trees with maximum fitted model as specified in model  
 node\_est list of traits at each node for all trees, min and max for each species. As estimated by nodeEstimate and nodeEstimateEnvelopes  
 aicmin if model is estimated, table of aic values for minimum trait values for all trees  
 aicmax if model is estimated, table of aic values for maximum trait values for all trees

### Author(s)

A. Michelle Lawing, Alexandra F. C. Howard, Maria A. Hurtado-Materon

### Examples

```

data(sampletrees)
data(occurrences)
bounds <- list(sigsq = c(min = 0, max = 1000000))
test_ppgm <- ppgm(occurrences = occurrences, trees = sampletrees,
model = "BM", which.biovars = c(1), bounds = bounds,
control = list(niter = 20))

```

---

ppgmConsensus

*ppgmConsensus*

---

### Description

ppgm makes a paleophylogeographic species distribution model using the bioclimate envelope method for a specified time period. consensus version

### Usage

```

ppgmConsensus(occurrences, fossils = FALSE, trees,
fossils.edges = FALSE, model = "BM", permut = 1, only.biovars = TRUE,
which.biovars = c(1:19), path = "", plot.TraitGram = FALSE,
plot.AnimatedMaps = FALSE, plot.GeoRates = FALSE, bounds = list(),
control = list(), use.paleoclimate = TRUE, paleoclimateUser = NULL,
layerAge = c(0:20), verbose = TRUE)

```

**Arguments**

occurrences	a matrix with three columns of species name, longitude, and latitude, in that order, and rows that are entries for species occurrences. The bioclimate variables can be included for each occurrence in following columns. They must be in order 1 through 19.
fossils	a matrix with four columns of min age, max age, longitude, and latitude, in that order, and rows that are entries for fossil occurrences. The bioclimate variables can be included for each occurrence in following columns. They must be in order 1 through 19. All 19 variables must be included at this stage, variable selection is done with the argument: "which.biovars".
trees	phylogeny of species from first column of occurrences argument. Object of class phylo.
fossils.edges	a vector of edges that the fossils belong to. Must be in the same order of the fossils argument. If fossils.edges is false, the the function randomly assigns the location of the fossils depending on the age (see details for more information).
model	the model of evolution to use to estimate ancestor nodes. Argument is passed onto to function nodeEstimate.
permut	the number of times to randomly place fossils in phylogeny and estimate ancestor states.
only.biovars	logical. If FALSE, user must include biovariables in occurrence object.
which.biovars	a vector with the biovars to include in model (see <a href="http://www.worldclim.org">www.worldclim.org</a> for a list of biovars). If "ALL", then all 19 biovars are included in analysis.
path	path to the directory where the results should be saved.
plot.TraitGram	logical. Whether to plot a TraitGram
plot.AnimatedMaps	Logical. Whether to plot AnimatedMaps. Requires ImageMagick to be installed on the system.
plot.GeoRates	logical. Whether to plot GeoRates
bounds	parameters for the evolutionary model selected. If none are supplied the default is used
control	settings used for optimisation of model likelihood. Passes to <code>geiger::fitContinuous</code>
use.paleoclimate	if left blank, default North America paleoclimate data is used. If FALSE, user submitted paleoclimate must be provided
paleoclimateUser	list of data frames with paleoclimates, must be dataframes with columns: GlobalID, Longitude, Latitude, bio1, bio2,...,bio19.
layerAge	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data
verbose	default true, returns all outputs. If FALSE then returns only climate envelopes and geographic data

## Details

If the 19 bioclimate variables are not supplied with the occurrences or with the fossils, they will be extracted from the closest 50km point location in the modern or paleoclimate maps that are loaded in with this function. The paleoclimate maps are isotopically scaled between general circulation models (see Lawing and Polly 2011; Rodder et al. 2013) and modern climate (see Hijmans et al. 2005). The fossils paleoclimate data is extracted to the closest million year paleoclimate map. Paleoclimate maps are derived at one million year intervals for the past 20 Ma. The tree (phylogeny) should be dichotomous and the species names should match the names in the first column of the occurrences argument.

## Value

`cem` Estimate of climate envelope for each species in present time. A data frame containing species and min mean and max of biovars specified with `which.biovars`.

`geo_move` data frame of `RateGeoCenter` and `RateGeoSize`

`change_geo_center` array of change in geographic center of suitable climate for each lineage

`change_geo_size` array of change in geographic size of suitable climate for each lineage

`time_int` matrix array of time intervals

`treedata_min` list of trees with minimum bioclimatic variables

`treedata_max` list of trees with maximum bioclimatic variables

`node_est` list of traits at each node for all trees, min and max for each species. As estimated by `nodeEstimate` and `nodeEstimateEnvelopes`

`aicmin` if model is estimated, table of aic values for minimum trait values

`aicmax` if model is estimated, table of aic values for maximum trait values

## Author(s)

A. Michelle Lawing, Alexandra F. C. Howard, Maria A. Hurtado-Materon

## Examples

```
data(sampletrees)
data(occurrences)
data(scel_fossils)
bounds <- list(sigsq = c(min = 0, max = 1000000))
ex_mytree <- sampletrees[[3]] #single tree
test_fossil_con <- ppgmConsensus(occurrences = occurrences,
fossils = scel_fossils, trees = ex_mytree, fossils.edges = FALSE, model = "BM",
permut = 5, which.biovars = 1, bounds = bounds, control = list(niter = 20))
```

ppgmMESS

*ppgmMESS***Description**

This creates a MESS map for given time slices, climate envelopes, and paleoclimate models.

**Usage**

```
ppgmMESS(cem_min, cem_max, est, tree, fossils=NULL, timeslice,
which.biovars, path = "", use.paleoclimate=TRUE, paleoclimateUser = NULL,
layerAge=c(0:20), which.plot = c("all","mess","none"))
```

**Arguments**

<code>cem_min</code>	the cem min output from the ppgm function. <code>cbind()</code> if there are multiple variables.
<code>cem_max</code>	the cem max output from the ppgm function. <code>cbind()</code> if there are multiple variables.
<code>est</code>	the <code>node_est</code> output from the ppgm function, in list format. <code>[tree][1][min and max][no.of species]</code>
<code>tree</code>	the phylogeny or multiple phylogenies that show the relationship between species
<code>fossils</code>	a matrix with four columns of age to the closest million year integer, longitude, and latitude, in that order, and rows that are entries for fossil occurrences.
<code>timeslice</code>	the time in million of years ago to project MESS maps (0 to 20). can handle single timeslice or vector of times.
<code>which.biovars</code>	the biovariable number(s) between 1 and 19.
<code>path</code>	directory where plots should be stored
<code>use.paleoclimate</code>	if left blank, default North America paleoclimate data is used. If FALSE, user submitted paleoclimate must be provided
<code>paleoclimateUser</code>	list of data frames with paleoclimates, must be dataframes with columns: GlobalID, Longitude, Latitude, bio1, bio2,...,bio19.
<code>layerAge</code>	vector with the ages of the paleoclimate dataframes, if using user submitted paleoclimate data
<code>which.plot</code>	"all" plots trait maps and MESS, "mess" plots MESS map, "none" does not plot

**Details**

plots MESS maps of climate envelope model for specific time slices. Can either plot individual biovariables, or combined.

**Value**

list containing array of MESS scores for bioclimatic variables

**Author(s)**

A. Michelle Lawing, Alexandra F. C. Howard, Maria-Aleja Hurtado-Materon

**See Also**

ppgm()

**Examples**

```
data(sampletrees)
data(occurrences)
sampletrees <- sample(sampletrees,5)
bounds <- list(sigsq = c(min = 0, max = 1000000))
test_ppgm <- ppgm(occurrences = occurrences,trees = sampletrees,
model = "BM", which.biovars = c(1,4,15), bounds = bounds,
control = list(niter = 20))
#extract min climate envelope for species
cem_min <- cbind(test_ppgm$cem[, 1], test_ppgm$cem[, 2], test_ppgm$cem[, 3])
cem_max <- cbind(test_ppgm$cem[, 7], test_ppgm$cem[, 8], test_ppgm$cem[, 9])
rownames(cem_min) <- rownames(cem_max) <- rownames(test_ppgm$cem)
mess <- ppgmMESS(cem_min,cem_max,test_ppgm$node_est,tree=sampletrees,timeslice=10,
which.biovars=c(1,4,15), path=tempdir(), which.plot="none")
```

---

sampletrees

*Sample of Sceloporus phylogenies*

---

**Description**

A sample of 100 dated phylogenies from Leache & Sites (2010), trimmed for analysis by Lawing et al (2016) Lawing et al (2016) Including fossils in phylogenetic climate reconstructions: A deep time perspective on the climatic niche evolution and diversification of spiny lizards (Sceloporus) Leache & Sites (2010) Chromosome evolution and diversification in North American Spiny Lizards (Genus Sceloporus)

**Usage**

sampletrees

**Format**

'sampletrees' 100 trees as class multiPhylo

**Source**

<<https://www.journals.uchicago.edu/doi/10.1086/687202>>

<<https://karger.com/cgr/article/127/2-4/166/62387/Chromosome-Evolution-and-Diversification-in-North>>

---

scel\_fossils

*Sceloporus fossil data*

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**Description**

Fossil occurrences for Sceloporus, as collected for Lawing et al 2016. Occurrence records from Paleobiology Database. See reference for further details Lawing et al (2016) Including fossils in phylogenetic climate reconstructions: A deep time perspective on the climatic niche evolution and diversification of spiny lizards (Sceloporus)

**Usage**

scel\_fossils

**Format**

'scel\_fossils' A data frame where each row is a single fossil

**MinAge** Minimum age of fossil

**MaxAge** Maximum age of fossil

**Longitude** Longitude of occurrence

**Latitude** Latitude of occurrence

**Source**

<<https://www.journals.uchicago.edu/doi/10.1086/687202>>

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