Package ‘ppgm’

May 9, 2026

Type Package

Title PaleoPhyloGeographic Modeling of Climate Niches and Species Distributions

Version 1.1

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> ``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> ``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> ``Reconstructing historical shifts in suitable habitat of Sceloporus lineages using phylogenetic niche modelling.".

Imports ape, fields, geiger, gifski, methods, phangorn, phytools, stringi, parallel, doParallel, foreach

Depends R (>= 4.4.0), R (>= 2.10), sp, sf

License GPL (>= 3)

Encoding UTF-8

LazyData true

LazyDataCompression xz

RoxygenNote 7.3.2

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

Config/testthat/parallel true

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2025-03-12 16:20:02 UTC

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`addFossil` *addFossil*

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

`occurrences` 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.

`which.biovars` a vector of the numbers of the bioclimatic variables that should be returned. The bioclimatic variables number correspond to the table at (https://www.worldclim.org/data/bioclim.html).

`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

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, Palaeocology 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 *getEnvelopes*

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

ppgmMESS(), nodeEstimate, geiger::treedata

Examples

```
data(sampletrees)
data(occurrences)
tree <- sampletrees[[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 (https://www.worldclim.org/data/bioclim.html).
`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(sampletrees)
data(occurrences)
data(paleoclimate)
tree <- sampletrees[[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

- `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 (https://www.worldclim.org/data/bioclim.html).
- `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 suitable climate for each specific lineage given reconstructed climate envelopes from `getEnvelopes()`. Returns dataframe of all estimated occurrences for every lineages for every time slice of paleoclimate.

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 `geiger::fitContinuous()`. 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", "mtrend","rtrend".
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"

`mtrend` if model = "mtrend', returned values from `fitContinuous()` `where the model is "mean_trend"`

`rtrend` if model = "rtrend', returned values from `fitContinuous()` `where the model is "rate_trend"`

`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=4)
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", "mtrend","rtrend".
`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 (https://www.worldclim.org/data/bioclim.l

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"

`mtrend` if model = "mtrend', returned values from `fitContinuous()` where the model is "mean_trend"

`rtrend` if model = "rtrend', returned values from `fitContinuous()` where the model is "rate_trend"

`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 occurence

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 4: temperature seasonality

bio5 Value for bioclimatic variable 5: max temp of warmest month

bio6 Value for bioclimatic variable 6: min temp of coldest month

bio7 Value for bioclimatic variable 7: temperature annual range

bio8 Value for bioclimatic variable 8: mean temp of wettest quarter

bio9 Value for bioclimatic variable 9: mean temp of driest quarter

bio10 Value for bioclimatic variable 10: mean temp of warmest quarter

bio11 Value for bioclimatic variable 11: mean temp of coldest quarter

bio12 Value for bioclimatic variable 12: annual precipitation

bio13 Value for bioclimatic variable 13: precipitation of wettest month

bio14 Value for bioclimatic variable 14: precipitation of the driest month

bio15 Value for bioclimatic variable 15: precipitation seasonality

bio16 Value for bioclimatic variable 16: precipitation of the wettest quarter

bio17 Value for bioclimatic variable 17: precipitation of the driest quarter

bio18 Value for bioclimatic variable 18: precipitation of the warmest quarter

bio19 Value for bioclimatic variable 19: 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 (https://www.worldclim.org/data/bioclim.l

`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

`...` other parameters to pass to save_gif

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(sampletrees)
data(occurrences)
tree <- sampletrees[[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 (https://www.worldclim.org/data/bioclim.l
`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
`...`	other parameters to pass to save_gif

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,sampletrees,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(sampletrees)
data(occurrences)
tree <- sampletrees[[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 (https://www.worldclim.org/data/bioclim.
- `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 [[trees]][[permut]][2,species,trait]
`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 `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 (https://www.worldclim.org/data/bioclim.l
`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, use.parallel = FALSE)
```

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.

`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. Options are "estimate", "BM", "OU", "EB", "lambda", "kappa", "delta", "rtrend, "mtrend".

`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 www.worldclim.org 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` list of parameters for the evolutionary model selected. If none are supplied the default is used. If multiple biovars are selected, must include separate bounds for each variable.

`control` settings used for optimisation of model likelihood. Passes to `geiger::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.

`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

`use.parallel` default FALSE, select TRUE to implement parallelisation

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

`richnesscount` list for every tree, list of species richness for each geographic point at each paleoclimate slice

`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. Options are "estimate", "BM", "OU", "EB", "lambda", "kappa", "delta", "rtrend, "mtrend".

`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 www.worldclim.org 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 `geiger::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.

`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

`richnesscount` list for every tree, list of species richness for each geographic point at each paleoclimate slice

`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

cem_min	the cem min output from the ppgm function. cbind() if there are multiple variables.
cem_max	the cem max output from the ppgm function. cbind() if there are multiple variables.
est	the node_est output from the ppgm function, in list format. [tree][1][min and max][no.of species]
tree	the phylogeny or multiple phylogenies that show the relationship between species
fossils	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.
timeslice	the time in million of years ago to project MESS maps (0 to 20). can handle single timeslice or vector of times.
which.biovars	the biovariable number(s) between 1 and 19.
path	directory where plots should be stored
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
which.plot	"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 (2009), 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) The American Naturalist 188(2): 133-148
- Leache & Sites (2009) Chromosome evolution and diversification in North American Spiny Lizards (Genus Sceloporus) Cytogenetic and Genome Research 127(2-4) 166-181

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*

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 occurence

Source

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

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