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R topics documented:

RPANDA-package	4
ancestral	5
Anolis.data	7
Balaenopteridae	8
BGB.examples	8
BICompare	9
Calomys	10
Caprimulgidae	11
Caprimulgidae_ClaDS2	11
Cetacea	12
ClaDS0_example	13
co2	14
co2_res	15
coccolithophore	16
CreateClassObject	16
CreateGeobyClassObject	18
CreateGeoObject	20
CreateGeoObject_BioGeoBEARS	21
createModel	23
createModelCoevolution	24
d13c	25
fitTipData	26
fitTipData-methods	27
fit_bd	27
fit_ClaDS	31
fit_ClaDS0	33
fit_coal_cst	35
fit_coal_var	37
fit_env	39
fit_sgd	42
fit_t_comp	43
fit_t_comp_subgroup	45
fit_t_env	48
fit_t_pl	52
foraminifera	54
getDataLikelihood	55
getDataLikelihood-methods	56
getMAPS_ClaDS	56

getMAPS_ClaDS0	58
getTipDistribution	59
getTipDistribution-methods	60
GIC.fit_pl.rpanda	61
gic_criterion	62
greenalgae	64
InfTemp	65
JSDtree	65
JSDtree_cluster	66
JSDt_cluster	67
landplant	69
likelihood_bd	69
likelihood_coal_cst	71
likelihood_coal_var	72
likelihood_sgd	73
likelihood_subgroup_model	74
likelihood_t_DD	77
likelihood_t_DD_geog	78
likelihood_t_env	79
likelihood_t_MC	81
likelihood_t_MC_geog	82
lines.fit_t.env	84
modelSelection	85
modelSelection-methods	86
MPhiFFT	86
ostracoda	87
PhenotypicACDC-class	87
PhenotypicADiag-class	89
PhenotypicBM-class	90
PhenotypicDD-class	91
PhenotypicGMM-class	92
PhenotypicModel-class	93
PhenotypicOU-class	94
PhenotypicPM-class	96
Phocoenidae	97
phyl.pca_pl	97
Phyllostomidae	99
Phyllostomidae_genera	100
plot.fit_t.env	100
plot_BICcompare	102
plot_ClaDS0_chains	103
plot_ClaDS_chains	104
plot_ClaDS_phylo	105
plot_dtt	106
plot_fit_bd	107
plot_fit_env	108
plot_prob_dtt	109
plot_spectR	111

Posdef	112
prob_dtt	113
radiolaria	115
redalgae	116
sealevel	116
silica	117
sim.convergence.geo	118
sim.divergence.geo	119
simulateTipData	120
simulateTipData-methods	121
sim_ClaDS	122
sim_env_bd	126
sim_sgd	128
sim_t_comp	129
sim_t_env	130
spectR	132
spectR_t	134

Index	135
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RPANDA-package	<i>RPANDA</i>
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Description

Implements macroevolutionary analyses on phylogenetic trees

Details

Package: RPANDA
 Type: Package
 Version: 1.5
 Date: 2018-01-29
 License: GPL (>= 2)

More information on the RPANDA package and worked examples can be found in [Morlon et al. \(2016\)](#)

Author(s)

Hélène Morlon <morlon@biologie.ens.fr>
 Julien Clavel <clavel@biologie.ens.fr>
 Fabien Condamine <fabien.condamine@gmail.com>
 Jonathan Drury <jonathan.p.drury@gmail.com>
 Eric Lewitus <elewitus@hivresearch.org>

Marc Manceau <marc.manceau@gmail.com>
 Olivier Billaud <olivier.billaud@agroparistech.fr>

References

- Morlon, H., Potts, M.D., Plotkin, J.B. (2010) Inferring the dynamics of diversification: a coalescent approach, PLoS B 8(9): e1000493
- Morlon, H., Parsons, T.L. and Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record, Proc Nat Acad Sci 108: 16327-16332
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- Manceau, M., Lambert, A., Morlon, H. (2015) Phylogenies support out-of-equilibrium models of biodiversity, Eco Lett 18: 347-356
- Lewitus, E., Morlon, H. (2016) Characterizing and comparing phylogenies from their Laplacian spectrum, Syst Biol 65: 495-507
- Morlon, H., Lewitus, E., Condamine, F.L., Manceau, M., Clavel, J., Drury, J. (2016) RPANDA: an R package for macroevolutionary analyses on phylogenetic trees, MEE 7: 589-597
- Drury, J., Clavel, J., Manceau, M., Morlon, H. (2016) Estimating the Effect of Competition on Trait Evolution Using Maximum Likelihood Inference, Syst Biol 65: 700-710
- Manceau, M., Lambert, A., Morlon, H. (2017) A Unifying Comparative Phylogenetic Framework Including Traits Coevolving Across Interacting Lineages, Syst Biol 66: 551-568
- Clavel, J., Morlon, H. (2017) Accelerated body size evolution during cold climatic periods in the Cenozoic, Proc Nat Acad Sci 114: 4183-4188
- Drury, J., Tobias, J., Burns, K., Mason, N., Shultz, A., and Morlon, H. (2018) Contrasting impacts of competition on ecological and social trait evolution in songbirds. PLOS Biolog 16: e2003563
- Clavel, J., Aristide, L., Morlon, H. (2019). A Penalized Likelihood framework for high-dimensional phylogenetic comparative methods and an application to new-world monkeys brain evolution. Syst Biol 68: 93-116

ancestral

Estimation of traits ancestral states.

Description

Reconstruct the ancestral states at the root (and possibly for each nodes) of a phylogenetic tree from models fit obtained using the `fit_t_XX` functions.

Usage

`ancestral(object)`

Arguments

object A model fit object obtained by the `fit_t_XX` class of functions.

Details

`ancestral` is an S3 method that reconstruct the ancestral states at the root and possibly for each nodes of a phylogenetic tree from the models fit obtained by the `fit_t_XX` class of functions (e.g., `fit_t_pl`, `fit_t_comp` and `fit_t_env`). Ancestral states are estimated using generalized least squares (GLS; Martins & Hansen 1997, Cunningham et al. 1998).

Value

a list with the following components

root the reconstructed ancestral states at the root
 nodes the reconstructed ancestral states at each nodes (not yet implemented for all the methods)

Note

The function is used internally in `phyl.pca_pl`.

Author(s)

J. Clavel

References

Clavel, J., Aristide, L., Morlon, H., 2019. A Penalized Likelihood framework for high-dimensional phylogenetic comparative methods and an application to new-world monkeys brain evolution. *Syst. Biol.* 68: 93-116.

Cunningham C.W., Omland K.E., Oakley T.H. 1998. Reconstructing ancestral character states: a critical reappraisal. *Trends Ecol. Evol.* 13:361-366.

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

See Also

[fit_t_pl](#), [fit_t_env](#), [phyl.pca_pl](#), [GIC](#), [gic_criterion](#)

Examples

```
require(mvMORPH)
set.seed(1)
n <- 32 # number of species
p <- 31 # number of traits
```

```
tree <- pbtree(n=n) # phylogenetic tree
R <- Posdef(p)      # a random symmetric matrix (covariance)

# simulate a dataset
Y <- mvSIM(tree, model="BM1", nsim=1, param=list(sigma=R))

# fit a multivariate BM with Penalized likelihood
fit <- fit_t_pl(Y, tree, model="BM", method="RidgeAlt")

# Perform the ancestral states reconstruction
anc <- ancestral(fit)

# retrieve the scores
head(anc$nodes)
```

Anolis.data

Anolis dataset

Description

Phylogeny, trait data, and geography.object for a subclade of Greater Antillean *Anolis* lizards.

Usage

```
data(Anolis.data)
```

Details

Illustrative phylogeny trimmed from the maximum clade credibility tree of Mahler et al. 2013, corresponding phylogenetic principal component data from Mahler et al. 2013, and biogeography data from Mahler & Ingram 2014 (in the form of a geography object, as detailed in the CreateGeoObject help file).

References

- Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020
- Mahler, D.L., Ingram, T., Revell, L., and Losos, J. 2013. Exceptional convergence on the macroevolutionary landscape in island lizard radiations. *Science*. 341:292-295.
- Mahler, D.L. and Ingram, T. 2014. Phylogenetic comparative methods for studying clade-wide convergence. In *Modern Phylogenetic Comparative Methods and Their Application in Evolutionary Biology*, ed. L. Garamszegi. pp.425-450.

See Also

[CreateGeoObject](#)

Examples

```
data(Anolis.data)
plot(Anolis.data$phylo)
print(Anolis.data$data)
print(Anolis.data$geography.object)
```

Balaenopteridae *Balaenopteridae phylogeny*

Description

Ultrametric phylogenetic tree of the 9 extant Balaenopteridae species

Usage

```
data(Balaenopteridae)
```

Details

This phylogeny was extracted from Steeman et al. Syst Bio 2009 cetacean phylogeny

References

- Steeman, M.E., et al. (2009) Radiation of extant cetaceans driven by restructuring of the oceans *Syst Biol* 58:573-585
- Morlon, H., Parsons, T.L., Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record *Proc Nat Acad Sci* 108: 16327-16332

Examples

```
data(Balaenopteridae)
print(Balaenopteridae)
plot(Balaenopteridae)
```

BGB.examples *BioGeoBEARS stochastic maps*

Description

Phylogenies and example stochastic maps for Canidae (from an unstratified BioGeoBEARS analysis) and Ochotonidae (from a stratified BioGeoBEARS analysis)

Usage

```
data(BGB.examples)
```


References

- Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020
- Matzke, N. 2014. Model selection in historical biogeography reveals that founder-event speciation is a crucial process in island clades. *Systematic Biology* 63:951-970.

See Also

[CreateGeoObject_BioGeoBEARS](#)

Examples

```
data(BGB.examples)
par(mfrow=c(1,2))
plot(BGB.examples$Canidae.phylo)
plot(BGB.examples$Ochotonidae.phylo)
```

BICcompare

Identify modalities in a phylogeny

Description

Computes the BIC values for a specified number of modalities in the distance matrix of a phylogenetic tree and that of randomly bifurcating trees; identifies these modalities using k-means clustering.

Usage

```
BICcompare(phylo,t,meth=c("ultrametric"))
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
t	the number of modalities to be tested
meth	whether the randomly bifurcating "control" tree should be ultrametric or non-ultrametric

Value

a list with the following components:

BIC_test	BIC values for finding t modalities in the distance matrix of a tree and the lowest five percent of 1000 random ("control") trees
clusters	a vector specifying which nodes in the tree belong to each of t modalities
BSS/TSS	the ratio of between-cluster sum of squares over total sum of squares

Author(s)

E Lewitus

References

Lewitus, E., Morlon, H., Characterizing and comparing phylogenies from their Laplacian spectrum, bioRxiv doi: <http://dx.doi.org/10.1101/026476>

See Also[plot_BICcompare](#), [spectR](#), [JSDtree](#)**Examples**

```
data(Cetacea)
#BICcompare(Cetacea, 5)
```

Calomys

Calomys phylogeny

Description

Ultrametric phylogenetic tree of 11 of the 13 extant Calomys species

Usage

```
data(Calomys)
```

Details

This phylogeny is from Pigot et al. PLoS Biol 2012

References

Pigot et al.(2012) Speciation and extinction drive the appearance of directional range size evolution in phylogenies and the fossil record *PLoS Biol* 10:1-9

Manceau, M., Lambert, A., Morlon, H. (submitted)

Examples

```
data(Calomys)
print(Calomys)
plot(Calomys)
```

Caprimulgidae *The Caprimulgidae phylogeny.*

Description

The MCC phylogeny for the *Caprimulgidae*, from Jetz et al. (2012).

Usage

```
data("Caprimulgidae")
```

Source

Jetz, W., G. Thomas, J. Joy, K. Hartmann, and A. Mooers. 2012. The global diversity of birds in space and time. *Nature* 491:444.

Examples

```
data("Caprimulgidae")
```

```
plot(Caprimulgidae)
```

Caprimulgidae_ClaDS2 *An example run of ClaDS2.*

Description

An example of the run on the inference of ClaDS2 on the *Caprimulgidae* phylogeny, thinned every 10 iterations.

Usage

```
data("Caprimulgidae_ClaDS2")
```

Format

A list object with fields :

`tree` The *Caprimulgidae* phylogeny on which we ran the model.

`sample_fraction` The sample fraction for the clade.

`sampler` The chains obtained by running ClaDS2 on the *Caprimulgidae* phylogeny.

Details

The *Caprimulgidae* phylogeny was obtained from Jetz et al. (2012)

Author(s)

O. Maliet

Source

Jetz, W., G. Thomas, J. Joy, K. Hartmann, and A. Mooers. 2012. The global diversity of birds in space and time. *Nature* 491:444.

References

Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0

See Also

[fit_ClaDS](#), [plot_ClaDS_chains](#), [getMAPS_ClaDS0](#)

Examples

```
data("Caprimulgidae_ClaDS2")

# plot the mcmc chains
plot_ClaDS_chains(Caprimulgidae_ClaDS2$sampler)

# extract the Maxima A Posteriori for each parameter
maps = getMAPS_ClaDS(Caprimulgidae_ClaDS2$sampler, thin = 1)
print(paste0("sigma = ", maps[1], " ; alpha = ",
  maps[2], " ; epsilon = ", maps[3], " ; l_0 = ", maps[4] ))

# plot the inferred branch specific speciation rates
plot_ClaDS_phylo(Caprimulgidae_ClaDS2$tree, maps[-(1:4)])
```

Cetacea

Cetacean phylogeny

Description

Ultrametric phylogenetic tree for 87 of the 89 extant cetacean species

Usage

```
data(Cetacea)
```

Details

This phylogeny was constructed by Bayesian phylogenetic inference from six mitochondrial and nine nuclear genes. It was calibrated using seven paleontological age constraints and a relaxed molecular clock approach. See Steeman et al. (2009) for details.

Source

Steeman ME et al.(2009) Radiation of extant cetaceans driven by restructuring of the oceans, *Syst Biol* 58:573-585

References

Steeman ME et al.(2009) Radiation of extant cetaceans driven by restructuring of the oceans *Syst Biol* 58:573-585

Morlon, H., Parsons, T.L., Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record *Proc Nat Acad Sci* 108: 16327-16332

Condamine, F.L., Rolland, J., Morlon, H. (2013) Macroevolutionary perspectives to environmental change *Eco Lett* 16: 72-85

Examples

```
data(Cetacea)
print(Cetacea)
plot(Cetacea)
```

ClaDS0_example

An example run of ClaDS0.

Description

An example of the run on the inference of ClaDS0 on a simulated phylogeny, thinned every 10 iterations.

Usage

```
data("ClaDS0_example")
```

Format

A list object with fields :

tree The simulated phylogeny on which we ran the model.

speciation_rates The simulated speciation rates.

Cl0_chains The output of the run_ClaDS0 run.

References

Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0

See Also

[fit_ClaDS0](#)

Examples

```

data(ClaDS0_example)

# plot the resulting chains for the first 4 parameters
plot_ClaDS0_chains(ClaDS0_example$Cl0_chains, param = 1:4)

# extract the Maximum A Posteriori for each of the parameters
MAPS = getMAPS_ClaDS0(ClaDS0_example$tree,
                      ClaDS0_example$Cl0_chains,
                      thin = 10)

# plot the simulated (on the left) and inferred speciation rates (on the right)
# on the same color scale
plot_ClaDS_phylo(ClaDS0_example$tree,
                 ClaDS0_example$speciation_rates,
                 MAPS[-(1:3)])

```

co2

co2 data since the Jurassic

Description

Atmospheric co2 data since the Jurassic

Usage

```
data(co2)
```

Details

Atmospheric co2 data since the Jurassic taken from Mayhew et al., (2008, 2012) and derived from the GeoCarb-III model (Berner and Kothavala, 2001). The data are reported as the ratio of the mass of co2 at time t to that at present. The format is a dataframe with the two following variables:

age a numeric vector corresponding to the geological age, in Myrs before the present

co2 a numeric vector corresponding to the estimated co2 at that age

References

Mayhew, P.J., Jenkins, G.B., Benton, T.G. (2008) A long-term association between global temperature and biodiversity, origination and extinction in the fossil record *Proceedings of the Royal Society B* 275:47-53

Mayhew, P.J., Bell, M.A., Benton, T.G, McGowan, A.J. (2012) Biodiversity tracks temperature over time *109:15141-15145*

Berner R.A., Kothavala, Z. (2001) GEOCARB III: A revised model of atmospheric CO2 over Phanerozoic time *Am J Sci* 301:182-204

Examples

```
data(co2)
plot(co2)
```

co2_res

co2 data since the beginning of the Cenozoic

Description

Atmospheric co2 data since the beginning of the Cenozoic

Usage

```
data(co2_res)
```

Details

Implied co2 data since the beginning of the Cenozoic taken from Hansen et al., (2013). The data are the amount of co2 in ppm required to yield observed global temperature throughout the Cenozoic:

age a numeric vector corresponding to the geological age, in Myrs before the present

co2 a numeric vector corresponding to the estimated co2 at that age

Source

Steeman ME et al.(2009) Radiation of extant cetaceans driven by restructuring of the oceans, *Syst Biol* 58:573-585

References

Steeman ME et al.(2009) Radiation of extant cetaceans driven by restructuring of the oceans *Syst Biol* 58:573-585

Morlon, H., Parsons, T.L., Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record *Proc Nat Acad Sci* 108: 16327-16332

Condamine, F.L., Rolland, J., Morlon, H. (2013) Macroevolutionary perspectives to environmental change *Eco Lett* 16: 72-85

Examples

```
data(Cetacea)
print(Cetacea)
plot(Cetacea)
```

coccolithophore	<i>Coccolithophore diversity since the Jurassic</i>
-----------------	---

Description

Coccolithophore fossil diversity since the Jurassic

Usage

```
data(coccolithophore)
```

Details

Coccolithophore fossil diversity since the Jurassic compiled from the Neptune Database (Lazarus, 1994) and Paleobiology Database (<https://paleobiodb.org/>). Diversity curves are estimated at the genus level using shareholder quorum subsampling (Alroy, 2010) at two-million-year bins. The format is a dataframe with the two following variables:

age a numeric vector corresponding to the geological age, in Myrs before the present

coccolithophore a numeric vector corresponding to the estimated coccolithophore change at that age

References

Lazarus, D. (1994) Neptune: A marine micropaleontology database *Mathematical Geology* 26:817–832

Alroy, J. (2010) Geographical, environmental and intrinsic biotic controls on Phanerozoic marine diversification: Controls on phanerozoic marine diversification *Palaeontology* 53:1211–1235

Examples

```
data(coccolithophore)
plot(coccolithophore)
```

CreateClassObject	<i>Create class object</i>
-------------------	----------------------------

Description

This function returns names of internode intervals, named descendants of each node, and a class object formatted in a way that can be passed to [CreateGeobyClassObject](#)

Usage

```
CreateClassObject(simmap, rnd=5)
```


Arguments

simmap	stochastic map from make.simmap in phytools
rnd	integer indicating the number of decimal places to which times should be rounded (default value is 5) (see round)

Details

This function formats the class object so that it can be correctly passed to the numerical integration performed in [fit_t_comp_subgroup](#).

Value

a list with the following components:

class.object	a list of matrices specifying the state of each branch during each internode interval (see Details)
times	a vector containing the time since the root of the tree at which nodes or changes in biogeography occur (used internally in other functions)
spans	a vector specifying the distances between times (used internally in other functions)

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com

References

Drury, J., Tobias, J., Burns, K., Mason, N., Shultz, A., and Morlon, H. in review. Contrasting impacts of competition on ecological and social trait evolution in songbirds. *PLOS Biology*.

Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020

See Also

[fit_t_comp_subgroup](#), [CreateGeobyClassObject](#)

Examples

```
data(Analis.data)

#Create a make.simmap object
require(phytools)
geo<-c(rep("cuba",7),rep("hispaniola",9),"puerto_rico")
names(geo)<-Analis.data$phylo$tip.label
stochastic.map<-phytools::make.simmap(Analis.data$phylo,
geo, model="ER", nsim=1)
CreateClassObject(stochastic.map)
```

 CreateGeobyClassObject

Create merged biogeography-by-class object

Description

Create a merged biogeography-by-class object to be passed to `fit_t_comp_subgroup` using a stochastic map created from any model in BioGeoBEARS (see documentation in BioGeoBEARS package) and a `simmap` object from `phytools` (see documentation in `phytools` package).

Usage

```
CreateGeobyClassObject(phylo, simmap, trim.class, ana.events, clado.events,
  stratified=FALSE, rnd=5)
```

Arguments

<code>phylo</code>	the object of type 'phylo' (see ape documentation) used to build ancestral range stochastic maps in BioGeoBEARS
<code>simmap</code>	a phylo object created using <code>make.simmap</code> in <code>phytools</code>
<code>trim.class</code>	category in the <code>simmap</code> object that represents the subgroup of interest (see Details and Examples)
<code>ana.events</code>	the "ana.events" table produced in BioGeoBEARS that lists anagenetic events in the stochastic map
<code>clado.events</code>	the "clado.events" table produced in BioGeoBEARS that lists cladogenetic events in the stochastic map
<code>stratified</code>	logical indicating whether the ancestral biogeography stochastic map was built from a stratified analysis in BioGeoBEARS
<code>rnd</code>	an integer value indicating the number of decimals to which values should be rounded in order to reconcile class and geo.objects (default is 5)

Details

This function merges a class object (which reconstructs group membership through time) and a stochastic map of ancestral biogeography (to reconstruct sympatry through time), such that lineages can only interact when they belong to the same subgroup AND are sympatric.

This allows fitting models of competition where only sympatric members of a subgroup can compete (e.g., all lineages that share similar diets or habitats).

This function should be used to format the geography object so that it can be correctly passed to the numerical integration performed in `fit_t_comp_subgroup`.

Value

Returns a list with the following components:

map	a simmap object with phylogeny trimmed to subgroup of interest (including all branches determined to belong to that subgroup)
geography.object	a list with the following components:
geography.matrix	a list of matrices specifying both sympatry & group membership (==1) or allopatry and/or non-membership in the focal subgroup (==0) for each species pair for each internode interval (see Details)
times	a vector containing the time since the root of the tree at which nodes or changes in biogeographyXsubgroup membership occur (used internally in other functions)
spans	a vector specifying the distances between times (used internally in other functions)

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com

References

Drury, J., Tobias, J., Burns, K., Mason, N., Shultz, A., and Morlon, H. in review. Contrasting impacts of competition on ecological and social trait evolution in songbirds. *PLOS Biology*.

Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020

See Also

[fit_t_comp_subgroup](#), [CreateGeoObject_BioGeoBEARS](#), [CreateClassObject](#)

Examples

```
data(BGB.examples)

Canidae.phylo<-BGB.examples$Canidae.phylo
dummy.group<-c(rep("B",3),rep("A",12),rep("B",2),rep("A",6),rep("B",5),rep("A",6))
names(dummy.group)<-Canidae.phylo$tip.label

Canidae.simmap<-phytools::make.simmap(Canidae.phylo,dummy.group)

#build GeobyClass object with "A" as the focal group

Canidae.geobyclass.object<-CreateGeobyClassObject(phylo=Canidae.phylo,simmap=Canidae.simmap,
trim.class="A",ana.events=BGB.examples$Canidae.ana.events,
```

```
clado.events=BGB.examples$Canidae.clado.events, stratified=FALSE, rnd=5)
phytools::plotSimmap(Canidae.geobyclass.object$map)
```

CreateGeoObject *Create biogeography object*

Description

This function returns names of internode intervals, named descendants of each node, and a geography object formatted in a way that can be passed to [fit_t_comp](#)

Usage

```
CreateGeoObject(phylo, map)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
map	either a matrix modified from phylo\$edge or a phylo object created using make.simmap (see Details and Examples)

Details

This function should be used to format the geography object so that it can be correctly passed to the numerical integration performed in [fit_t_comp](#).

The map can either be a matrix formed by specifying the region in which each branch specified by phylo\$edge existed, or a stochastic map stored as a phylo object output from [make.simmap](#) (see Examples).

Value

a list with the following components:

geography.object	a list of matrices specifying sympatry (1) or allopatry (0) for each species pair for each internode interval (see Details)
times	a vector containing the time since the root of the tree at which nodes or changes in biogeography occur (used internally in other functions)
spans	a vector specifying the distances between times (used internally in other functions)

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com

References

Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020

See Also

[fit_t_comp](#)

Examples

```
data(Anolis.data)
#Create a geography.object with a modified edge matrix
#First, specify which region each branch belonged to:
Anolis.regions<-c(rep("cuba",14),rep("hispaniola",17),"puerto_rico")
Anolis.map<-cbind(Anolis.data$phylo$edge,Anolis.regions)
CreateGeoObject(Anolis.data$phylo,map=Anolis.map)

#Create a geography.object with a make.simmmap object
#First, specify which region each branch belonged to:
require(phytools)
geo<-c(rep("cuba",7),rep("hispaniola",9),"puerto_rico")
names(geo)<-Anolis.data$phylo$tip.label
stochastic.map<-phytools::make.simmmap(Anolis.data$phylo,
geo, model="ER", nsim=1)
CreateGeoObject(Anolis.data$phylo,map=stochastic.map)
```

CreateGeoObject_BioGeoBEARS

Create biogeography object using a stochastic map from Bio-GeoBEARS

Description

Create biogeography object using a stochastic map created from any model in BioGeoBEARS (see documentation in BioGeoBEARS package).

Usage

```
CreateGeoObject_BioGeoBEARS( full.phylo, trimmed.phylo = NULL, ana.events,
clado.events, stratified=FALSE)
```

Arguments

<code>full.phylo</code>	the object of type 'phylo' (see ape documentation) that was used to construct the stochastic map in BioGeoBEARS
<code>trimmed.phylo</code>	if the desired biogeography object excludes some species that were initially included in the stochastic map, this specifies a phylo object for the trimmed set of species
<code>ana.events</code>	the "ana.events" table produced in BioGeoBEARS that lists anagenetic events in the stochastic map
<code>clado.events</code>	the "clado.events" table produced in BioGeoBEARS that lists cladogenetic events in the stochastic map
<code>stratified</code>	logical indicating whether the stochastic map was built from a stratified analysis in BioGeoBEARS

Value

a list with the following components:

<code>geography.object</code>	a list of matrices specifying sympatry (1) or allopatry (0) for each species pair for each internode interval (see Details)
<code>times</code>	a vector containing the time since the root of the tree at which nodes or changes in biogeography occur (used internally in other functions)
<code>spans</code>	a vector specifying the distances between times (used internally in other functions)

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com

References

- Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020
- Matzke, N. 2014. Model selection in historical biogeography reveals that founder-event speciation is a crucial process in island clades. *Systematic Biology* 63:951-970.

See Also

[fit_t_comp](#) [CreateGeoObject](#)

Examples

```
data(BGB.examples)
```

```
##Example with a non-stratified tree

Canidae.geography.object<-CreateGeoObject_BioGeoBEARS(full.phylo=BGB.examples$Canidae.phylo,
ana.events=BGB.examples$Canidae.ana.events, clado.events=BGB.examples$Canidae.clado.events)

#on a subclade
Canidae.trimmed<-drop.tip(BGB.examples$Canidae.phylo
,BGB.examples$Canidae.phylo$tip.label[1:9])

Canidae.trimmed.geography.object<-CreateGeoObject_BioGeoBEARS(
full.phylo=BGB.examples$Canidae.phylo, trimmed.phylo=Canidae.trimmed,
ana.events=BGB.examples$Canidae.ana.events, clado.events=BGB.examples$Canidae.clado.events)

##Example with a stratified tree

Ochotonidae.geography.object<-CreateGeoObject_BioGeoBEARS(
full.phylo = BGB.examples$Ochotonidae.phylo, ana.events = BGB.examples$Ochotonidae.ana.events,
clado.events = BGB.examples$Ochotonidae.clado.events, stratified = TRUE)

#on a subclade
Ochotonidae.trimmed<-drop.tip(BGB.examples$Ochotonidae.phylo,
BGB.examples$Ochotonidae.phylo$tip.label[1:9])

Ochotonidae.trimmed.geography.object<-CreateGeoObject_BioGeoBEARS(
full.phylo=BGB.examples$Ochotonidae.phylo, trimmed.phylo=Ochotonidae.trimmed,
ana.events=BGB.examples$Ochotonidae.ana.events,
clado.events=BGB.examples$Ochotonidae.clado.events, stratified=TRUE)
```

createModel

Creation of a PhenotypicModel

Description

Creates an object of class PhenotypicModel, intended to represent a model of trait evolution on a specific tree. Distinct keywords correspond to different models, using one phylogenetic tree.

Usage

```
createModel(tree, keyword)
```

Arguments

tree	an object of class 'phylo' as defined in the R package 'ape'.
keyword	a string specifying the model. Available models include "BM", "BM_from0", "BM_from0_driftless", "OU", "OU_from0", "ACDC", "DD", "PM", "PM_OUless".

Value

the object of class "PhenotypicModel".

Author(s)

M Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*

Examples

```
#Loading an example tree
newick <- "(((A:1,B:0.5):2,(C:3,D:2.5):1):6,E:10.25):2,(F:6.5,G:8.25):3):1;"
tree <- read.tree(text=newick)

#Creating the models
modelBM <- createModel(tree, 'BM')
modelOU <- createModel(tree, 'OU')

#Printing basic or full informations on the model definitions
show(modelBM)
print(modelOU)
```

createModelCoevolution

Creation of a PhenotypicGMM

Description

Creates an object of class PhenotypicGMM, a subclass of the class PhenotypicModel intended to represent the Generalist Matching Mutualism model of trait evolution on two specific trees.

Usage

```
createModelCoevolution(tree1, tree2, keyword)
```

Arguments

tree1	an object of class 'phylo' as defined in the R package 'ape'.
tree2	an object of class 'phylo' as defined in the R package 'ape'.
keyword	a string object. Default value "GMM" returns an object of class PhenotypicGMM, which takes advantage of faster distribution computation. Otherwise, a "PhenotypicModel" is returned, and the computation of the tip distribution will take much longer.

Value

an object of class "PhenotypicModel" or "PhenotypicGMM".

Author(s)

M Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*

Examples

```
#Loading example trees
newick1 <- "(((A:1,B:1):3,(C:3,D:3):1):2,E:6);"
tree1 <- read.tree(text=newick1)
newick2 <- "((X:1.5,Y:1.5):3,Z:4.5);"
tree2 <- read.tree(text=newick2)

#Creating the model
modelGMM <- createModelCoevolution(tree1, tree2)

#Printing basic or full informations on the model definitions
show(modelGMM)
print(modelGMM)

#Simulates tip trait data
dataGMM <- simulateTipData(modelGMM, c(0,0,5,-5, 1, 1), method=2)
```

d13c

d13c data since the Jurassic

Description

Benthic d13c weathering ratio since the Jurassic

Usage

```
data(d13c)
```

Details

Ratio of stable carbon isotopes since the Jurassic calculated by Hannisdal and Peters (2011) and Lazarus et al. (2014) from marine carbonates. The format is a dataframe with the two following variables:

age a numeric vector corresponding to the geological age, in Myrs before the present

d13c a numeric vector corresponding to the estimated d13c at that age

References

- Hannisdal, B., Peters, S.E. (2011) Phanerozoic Earth system evolution and marine biodiversity *Science* 334:1121-1124
- Lazarus, D., Barron, J., Renaudie, J., Diver, P., Turke, A. (2014) Cenozoic Planktonic Marine Diatom Diversity and Correlation to Climate Change *PLoS ONE* 9:e84857

Examples

```
data(d13c)
plot(d13c)
```

<code>fitTipData</code>	<i>Maximum likelihood estimators of a model's parameters</i>
-------------------------	--

Description

Finds the maximum likelihood estimators of the parameters, returns the likelihood and the inferred parameters.

Usage

```
fitTipData(object, data, params0, GLSstyle, v)
```

Arguments

<code>object</code>	an object of class 'PhenotypicModel'.
<code>data</code>	vector of tip trait data.
<code>params0</code>	vector of parameters used to initialize the optimization algorithm. Default value is NULL, in which case the optimization procedure starts with the vector 'params0' specified within the 'model' object.
<code>GLSstyle</code>	boolean specifying the way the mean trait value at the root is estimated. Default value is FALSE in which case the mean at the root is considered as any other parameter. If TRUE, the mean value at the root is estimated with the GLS method, as explained, e.g. in Hansen 1997.
<code>v</code>	boolean specifying the verbose mode. Default value : FALSE.

Details

Warning : This function uses the standard R optimizer "optim". It may not always converge well. Please double check the convergence by trying distinct parameter sets for the initialisation.

Value

<code>value</code>	A numerical value : the lowest $-\log(\text{likelihood})$ value found during the optimization procedure.
<code>inferredParams</code>	The maximum likelihood estimators of the model's parameters.
<code>convergence</code>	An integer code specifying the convergence of the optim function. Please refer to the optim function help files.

Author(s)

M Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*

Examples

```
#Loading an example tree
newick <- "(((A:1,B:0.5):2,(C:3,D:2.5):1):6,E:10.25):2,(F:6.5,G:8.25):3):1;"
tree <- read.tree(text=newick)

#Creating the models
modelBM <- createModel(tree, 'BM')

#Simulating tip traits under the model :
dataBM <- simulateTipData(modelBM, c(0,0,0,1))

#Fitting the model to the data
fitTipData(modelBM, dataBM, v=TRUE)
```

fitTipData-methods *~~ Methods for Function fitTipData ~~*

Description

~~ Methods for function fitTipData ~~

Methods

signature(object = "PhenotypicModel") This is the only method available for this function. Same behaviour for any PhenotypicModel.

fit_bd *Maximum likelihood fit of the general birth-death model*

Description

Fits the birth-death model with potentially time-varying rates and potentially missing extant species to a phylogeny, by maximum likelihood. Notations follow Morlon et al. PNAS 2011.

Usage

```
fit_bd(phylo, tot_time, f.lamb, f.mu, lamb_par, mu_par, f = 1,
       meth = "Nelder-Mead", cst.lamb = FALSE, cst.mu = FALSE,
       expo.lamb = FALSE, expo.mu = FALSE, fix.mu = FALSE,
       dt=0, cond = "crown")
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
tot_time	the age of the phylogeny (crown age, or stem age if known). If working with crown ages, tot_time is given by max(node.age(phylo)\$ages).
f.lamb	a function specifying the hypothesized functional form (e.g. constant, linear, exponential, etc.) of the variation of the speciation rate λ with time. Any functional form may be used. This function has two arguments: the first argument is time; the second argument is a numeric vector of the parameters of the time-variation (to be estimated).
f.mu	a function specifying the hypothesized functional form (e.g. constant, linear, exponential, etc.) of the variation of the extinction rate μ with time. Any functional form may be used. This function has two arguments: the first argument is time; the second argument is a numeric vector of the parameters of the time-variation (to be estimated).
lamb_par	a numeric vector of initial values for the parameters of f.lamb to be estimated (these values are used by the optimization algorithm). The length of this vector is used to compute the total number of parameters in the model, so to fit a model with constant speciation rate (for example), lamb_par should be a vector of length 1. Otherwise aic values will be wrong.
mu_par	a numeric vector of initial values for the parameters of f.mu to be estimated (these values are used by the optimization algorithm). The length of this vector is used to compute the total number of parameters in the model, so to fit a model without extinction (for example), mu_par should be empty (vector of length 0). Otherwise aic values will be wrong.
f	the fraction of extant species included in the phylogeny
meth	optimization to use to maximize the likelihood function, see <i>optim</i> for more details.
cst.lamb	logical: should be set to TRUE only if f.lamb is constant (i.e. does not depend on time) to use analytical instead of numerical computation in order to reduce computation time.
cst.mu	logical: should be set to TRUE only if f.mu is constant (i.e. does not depend on time) to use analytical instead of numerical computation in order to reduce computation time.
expo.lamb	logical: should be set to TRUE only if f.lamb is exponential to use analytical instead of numerical computation in order to reduce computation time.
expo.mu	logical: should be set to TRUE only if f.mu is exponential to use analytical instead of numerical computation in order to reduce computation time.
fix.mu	logical: if set to TRUE, the extinction rate μ is fixed and will not be optimized.

dt	the default value is 0. In this case, integrals in the likelihood are computed using R "integrate" function, which can be quite slow. If a positive dt is given as argument, integrals are computed using a piece-wise constant approximation, and dt represents the length of the intervals on which functions are assumed to be constant. For an exponential dependency of the speciation rate with time, we found that dt=1e-3 gives a good trade-off between precision and computation time.
cond	conditioning to use to fit the model: <ul style="list-style-type: none"> • FALSE: no conditioning (not recommended); • "stem": conditioning on the survival of the stem lineage (use when the stem age is known, in this case tot_time should be the stem age); • "crown" (default): conditioning on a speciation event at the crown age and survival of the 2 daughter lineages (use when the stem age is not known, in this case tot_time should be the crown age).

Details

The lengths of `lamb_par` and `mu_par` are used to compute the total number of parameters in the model, so to fit a model with constant speciation rate (for example), `lamb_par` should be a vector of length 1. Otherwise aic values will be wrong. In the `f.lamb` and `f.mu` functions, the first argument (time) runs from the present to the past. Hence, if the parameter controlling the variation of λ with time is estimated to be positive (for example), this means that the speciation rate decreases from past to present.

Value

a list with the following components

<code>model</code>	the name of the fitted model
<code>LH</code>	the maximum log-likelihood value
<code>aicc</code>	the second order Akaike's Information Criterion
<code>lamb_par</code>	a numeric vector of estimated <code>f.lamb</code> parameters, in the same order as defined in <code>f.lamb</code>
<code>mu_par</code>	a numeric vector of estimated <code>f.mu</code> parameters, in the same order as defined in <code>f.mu</code> (if <code>fix.mu</code> is FALSE)

Author(s)

H Morlon

References

- Morlon, H., Parsons, T.L. and Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record *Proc Nat Acad Sci* 108: 16327-16332
- Morlon, H. (2014) Phylogenetic approaches for studying diversification, *Eco Lett* 17:508-525

See Also

[plot_fit_bd](#), [plot_dtt](#), [likelihood_bd](#)

Examples

```
# Some examples may take a little bit of time. Be patient!

data(Cetacea)
tot_time<-max(node.age(Cetacea)$ages)

# Fit the pure birth model (no extinction) with a constant speciation rate
f.lamb <-function(t,y){y[1]}
f.mu<-function(t,y){0}
lamb_par<-c(0.09)
mu_par<-c()
#result_cst <- fit_bd(Cetacea,tot_time,f.lamb,f.mu,lamb_par,mu_par,
#                    f=87/89,cst.lamb=TRUE,fix.mu=TRUE,dt=1e-3)
#result_cst$model <- "pure birth with constant speciation rate"

# Fit the pure birth model (no extinction) with exponential variation
# of the speciation rate with time
f.lamb <-function(t,y){y[1] * exp(y[2] * t)}
f.mu<-function(t,y){0}
lamb_par<-c(0.05, 0.01)
mu_par<-c()
#result_exp <- fit_bd(Cetacea,tot_time,f.lamb,f.mu,lamb_par,mu_par,
#                    f=87/89,expo.lamb=TRUE,fix.mu=TRUE,dt=1e-3)
#result_exp$model <- "pure birth with exponential variation in speciation rate"

# Fit the a pure birth model (no extinction) with linear variation of
# the speciation rate with time
f.lamb <-function(t,y){y[1] + y[2] * t}
f.mu<-function(t,y){0}
lamb_par<-c(0.09, 0.001)
mu_par<-c()
#result_lin <- fit_bd(Cetacea,tot_time,f.lamb,f.mu,lamb_par,mu_par,f=87/89,fix.mu=TRUE,dt=1e-3)
#result_lin$model <- "pure birth with linear variation in speciation rate"

# Fit a birth-death model with exponential variation of the speciation
# rate with time and constant extinction
f.lamb<-function(t,y){y[1] * exp(y[2] * t)}
f.mu <-function(t,y){y[1]}
lamb_par <- c(0.05, 0.01)
mu_par <-c(0.005)
#result_bexp_dcst <- fit_bd(Cetacea,tot_time,f.lamb,f.mu,lamb_par,mu_par,
#                          f=87/89,expo.lamb=TRUE,cst.mu=TRUE,dt=1e-3)
#result_bexp_dcst$model <- "birth-death with exponential variation in speciation rate
#                          and constant extinction"

# Find the best model
#index <- which.min(c(result_cst$aiicc, result_exp$aiicc, result_lin$aiicc,result_bexp_dcst$aiicc))
#rbind(result_cst, result_exp, result_lin, result_bexp_dcst)[index,]
```

fit_ClaDS

Fit ClaDS to a phylogeny

Description

Performs the inference of branch-specific speciation rates and the model's hyper parameters for the model with constant extinction rate (ClaDS1) or constant turnover rate (ClaDS2).

Usage

```
fit_ClaDS(tree, sample_fraction, iterations, thin = 50, file_name = NULL, it_save = 1000,
          model_id="ClaDS2", nCPU = 1, mcmcSampler = NULL, ...)
```

Arguments

tree	An object of class 'phylo'
sample_fraction	The sampling fraction for the clade on which the inference is performed.
iterations	Number of steps in the MCMC, should be a multiple of thin.
thin	Number of iterations between two chain state's recordings.
file_name	Name of the file in which the result will be saved. Use file_name = NULL (the default) to disable this option.
it_save	Number of iteration between each backup of the result in file_name.
model_id	"ClaDS1" for constant extinction rate, "ClaDS2" (the default) for constant turnover rate.
nCPU	The number of CPUs to use. Should be either 1 or 3.
mcmcSampler	Optional output of fit_ClaDS to continue an already started run.
...	Optional arguments, see details.

Details

This function uses a blocked Differential Evolution (DE) MCMC sampler, with sampling from the past of the chains (Ter Braak, 2006; ter Braak and Vrugt, 2008). This sampler is self-adaptive because proposals are generated from the past of the chains. In this sampler, three chains are run simultaneously. Block updates is implemented by first drawing the number of parameters to be updated from a truncated geometric distribution with mean 3, drawing uniformly which parameter to update, and then following the normal DE algorithm.

The available optional arguments are :

Nchain Number of MCMC chains (default to 3).

res_ClaDS0 The output of ClaDS0 to use as a startpoint. If NULL (the default) a random startpoint is used for the branch-specific speciation rates for each chain.

- l0** The starting value for lambda_0 (not used if res_ClaDS0 != NULL).
- s0** The starting value for sigma (not used if res_ClaDS0 != NULL).
- nlambda** Number of subdivisions for the rate space discretization (use in the likelihood computation). Default to 1000.
- nt** Number of subdivisions for the time space discretization (use in the likelihood computation). Default to 30.

Value

A 'list' object with fields :

post	The posterior function.
startvalue	The starting value for the MCMC.
numPars	The number of parameter in the model, including the branch-specific speciation rates.
Nchain	The number of MCMC chains ran simultaneously.
currentLPs	The current values of the logposterior for th Nchains chains.
proposalGenerator	The proposal distribution for the MCMC sampler.
former	The last output of post for each of the chains.
thin	Number of iterations between two chain state's recordings.
alpha_effect	A vector of size nrow(tree\$edge), where the ith element is the number of branches on the path from the crown of the tree and branch i (used internally in other functions).
consoleupdates	The frequency at which the sampler state should be printed.
likelihood	The likelihood function, used internally.
relToAbs	A function mapping the relative changes in speciation rates to the absolute speciation rates for the object phylo, used internally.

Author(s)

O. Maliet

References

- Ter Braak, C. J. 2006. A markov chain monte carlo version of the genetic algorithm differential evolution: easy bayesian computing for real parameter spaces. *Statistics and Computing* 16:239-249.
- ter Braak, C. J. and J. A. Vrugt. 2008. Differential evolution markov chain with snooker updater and fewer chains. *Statistics and Computing* 18:435-446.
- Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0

See Also

[fit_ClaDS0](#), [plot_ClaDS_chains](#).

Examples

```

data("Caprimulgidae")

sample_fraction = 0.61

sampler = fit_ClaDS(Caprimulgidae, sample_fraction, 1000, thin = 50,
                    file_name = NULL, model_id="ClaDS2", nCPU = 1)
plot_ClaDS_chains(sampler)

# continue the same run
sampler = fit_ClaDS(Caprimulgidae, sample_fraction, 50, mcmcSampler = sampler)

# plot the result of the analysis (saved in "Caprimulgidae_ClaDS2", after thinning)

data("Caprimulgidae_ClaDS2")

# plot the mcmc chains
plot_ClaDS_chains(Caprimulgidae_ClaDS2$sampler)

# extract the Maxima A Posteriori for each parameter
maps = getMAPS_ClaDS(Caprimulgidae_ClaDS2$sampler, thin = 1)
print(paste0("sigma = ", maps[1], " ; alpha = ",
            maps[2], " ; epsilon = ", maps[3], " ; l_0 = ", maps[4] ))

# plot the inferred branch specific speciation rates
plot_ClaDS_phylo(Caprimulgidae_ClaDS2$tree, maps[-(1:4)])

```

fit_ClaDS0

Infer ClaDS0's parameter on a phylogeny

Description

Infer branch-specific speciation rates and the model's hyper parameters for the pure-birth model

Usage

```

fit_ClaDS0(tree, name, pamhLocalName = "pamhLocal",
            iteration = 1e+07, thin = 20000, update = 1000,
            adaptation = 10, seed = NULL, nCPU = 3)

```

Arguments

tree	An object of class 'phylo'.
name	The name of the file in which the results will be saved. Use name = NULL to disable this option.
pamhLocalName	The function is writing in a text file to make the execution quicker, this is the name of this file.
iteration	Number of iterations after which the gelman factor is computed and printed. The function stops if it is below 1.05
thin	Number of iterations between two chain state's recordings.
update	Number of iterations between two adjustments of the proposal parameters during the adaptation phase of the sampler.
adaptation	Number of times the proposal is adjusted during the adaptation phase of the sampler.
seed	An optional seed for the MCMC run.
nCPU	The number of CPUs to use. Should be either 1 or 3.

Details

This function uses a Metropolis within Gibbs MCMC sampler with a bactrian proposal (ref) with an initial adaptation phase. During this phase, the proposal is adjusted "adaptation" times every "update" iterations to reach a goal acceptance rate of 0.3.

To monitor convergence, 3 independant MCMC chains are run simultaneously and the Gelman statistics is computed every "iteration" iterations. The inference is stopped when the maximum of the one dimensional Gelman statistics (computed for each of the parameters) is below 1.05.

Value

A mcmc.list object with the three MCMC chains.

Author(s)

O. Maliet

References

Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0

See Also

[getMAPS_ClaDS0](#), [plot_ClaDS0_chains](#), [fit_ClaDS](#)

Examples

```

set.seed(1)

obj= sim_ClaDS( lambda_0=0.1,
                mu_0=0.5,
                sigma_lamb=0.7,
                alpha_lamb=0.90,
                condition="taxa",
                taxa_stop = 20,
                prune_extinct = TRUE)

tree = obj$tree
speciation_rates = obj$lamb[obj$rates]
extinction_rates = obj$mu[obj$rates]

plot_ClaDS_phylo(tree,speciation_rates)

sampler = fit_ClaDS0(tree=tree,
                    name="ClaDS0_example.Rdata",
                    nCPU=1,
                    pamhLocalName = "local",
                    iteration=500000,
                    thin=2000,
                    update=1000, adaptation=5)

# extract the Maximum A Posteriori for each of the parameters
MAPS = getMAPS_ClaDS0(tree, sampler, thin = 10)

# plot the simulated (on the left) and inferred speciation rates (on the right)
# on the same color scale
plot_ClaDS_phylo(tree, speciation_rates, MAPS[-(1:3)])

```

fit_coal_cst

Maximum likelihood fit of the equilibrium model

Description

Fits the equilibrium diversity model with potentially time-varying turnover rate and potentially missing extant species to a phylogeny, by maximum likelihood. The implementation allows only exponential time variation of the turnover rate, although this could be modified using expressions in Morlon et al. PLoSB 2010. Notations follow Morlon et al. PLoSB 2010.

Usage

```

fit_coal_cst(phylo, tau0 = 1e-2, gamma = 1, cst.rate = FALSE,
             meth = "Nelder-Mead", N0 = 0)

```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
tau0	initial value of the turnover rate at present (used by the optimization algorithm)
gamma	initial value of the parameter controlling the exponential variation in turnover rate (used by the optimization algorithm)
cst.rate	logical: should be set to TRUE to fit an equilibrium diversity model with time-constant turnover rate (known as the Hey model, model 1 in Morlon et al. PLoSB 2010). By default, a model with exponential time-varying rate exponential is fitted (model 2 in Morlon et al. PLoSB 2010).
meth	optimization to use to maximize the likelihood function, see <i>optim</i> for more details.
N0	Number of extant species. With default value(0), N0 is set to the number of tips in the phylogeny. That is, the phylogeny is assumed to be 100% complete.

Details

This function fits models 1 (when `cst.rate=TRUE`) and 2 (when `cst.rate=FALSE`) from the PLoSB 2010 paper. Likelihoods arising from these models are directly comparable to likelihoods from the `fit_coal_var` function, thus allowing to test support for equilibrium versus expanding diversity scenarios. Time runs from the present to the past. Hence, if `gamma` is estimated to be positive (for example), this means that the speciation rate decreases from past to present.

Value

a list with the following components

model	the name of the fitted model
LH	the maximum log-likelihood value
aicc	the second order Akaike's Information Criterion
tau0	the estimated turnover rate at present
gamma	the estimated parameter controlling the exponential variation in turnover rate (if <code>cst.rate</code> is FALSE)

Author(s)

H Morlon

References

- Hey, J. (1992) Using phylogenetic trees to study speciation and extinction, *Evolution*, 46: 627-640
- Morlon, H., Potts, M.D., Plotkin, J.B. (2010) Inferring the dynamics of diversification: a coalescent approach, *PLoS B*, 8(9): e1000493
- Morlon, H., Kemp, B., Plotkin, J.B., Brisson, D. (2012) Explosive radiation of a bacterial species group, *Evolution*, 66: 2577-2586
- Morlon, H. (2014) Phylogenetic approaches for studying diversification, *Eco Lett*, 17:508-525

See Also

[likelihood_coal_cst](#), [fit_coal_var](#)

Examples

```
data(Cetacea)
result <- fit_coal_cst(Cetacea, tau0=1.e-3, gamma=-1, cst.rate=FALSE, N0=89)
print(result)
```

fit_coal_var

Fit birth-death model using a coalescent approach

Description

Fits the expanding diversity model with potentially time-varying rates and potentially missing extant species to a phylogeny, by maximum likelihood. The implementation allows only exponential time variation of the speciation and extinction rates, although this could be modified using expressions in Morlon et al. PloSB 2010. Notations follow Morlon et al. PLoSB 2010.

Usage

```
fit_coal_var(phylo, lamb0 = 0.1, alpha = 1, mu0 = 0.01, beta = 0,
             meth = "Nelder-Mead", N0 = 0, cst.lamb = FALSE, cst.mu = FALSE,
             fix.eps = FALSE, mu.0 = FALSE, pos = TRUE)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
lamb0	initial value of the speciation rate at present (used by the optimization algorithm)
alpha	initial value of the parameter controlling the exponential variation in speciation rate (used by the optimization algorithm)
mu0	initial value of the extinction rate at present (used by the optimization algorithm)
beta	initial value of the parameter controlling the exponential variation in extinction rate.
meth	optimization to use to maximize the likelihood function, see <i>optim</i> for more details.
N0	Number of extant species. With default value(0), N0 is set to the number of tips in the phylogeny. That is, the phylogeny is assumed to be 100% complete.
cst.lamb	logical: should be set to TRUE only if f.lamb is constant (i.e. does not depend on time, models 3, 4b & 5 in Morlon et al. PloSB 2010) to use analytical instead of numerical computation in order to reduce computation time.
cst.mu	logical: should be set to TRUE only if f.mu is constant (i.e. does not depend on time, models 3 & 4a in Morlon et al. PloSB 2010) to use analytical instead of numerical computation in order to reduce computation time.

<code>fix.eps</code>	logical: should be set to TRUE only if the extinction fraction is constant (i.e. does not depend on time, model 4c in Morlon et al. PloSB 2010)
<code>mu.0</code>	logical: should be set to TRUE to force the extinction rate to 0 (models 5 & 6 in Morlon et al. PloSB 2010)
<code>pos</code>	logical: should be set to FALSE only to not enforce positive speciation and extinction rates

Details

The function fits models 3 to 6 from the PloSB 2010 paper. Likelihoods arising from these models are computed using the coalescent approximation and are directly comparable to likelihoods from the `fit_coal_cst` function, thus allowing to test support for equilibrium versus expanding diversity scenarios.

These models can be fitted using the options specified below:

- model 3:
with `cst.lamb=TRUE` & `cst.mu=TRUE`
- model 4a:
with `cst.lamb=FALSE` & `cst.mu=TRUE`
- model 4b:
with `cst.lamb=TRUE` & `cst.mu=FALSE`
- model 4c:
with `cst.lamb=FALSE`, `cst.mu=FALSE` & `fix.eps=TRUE`
- model 4d:
with `cst.lamb=FALSE`, `cst.mu=FALSE` & `fix.eps=FALSE`
- model 5:
with `cst.lamb=TRUE` & `mu.0=TRUE`
- model 6:
with `cst.lamb=FALSE` & `mu.0=TRUE`

Time runs from the present to the past. Hence, if alpha is estimated to be positive (for example), this means that the speciation rate decreases from past to present.

Value

a list with the following components

<code>model</code>	the name of the fitted model
<code>LH</code>	the maximum log-likelihood value
<code>aicc</code>	the second order Akaike's Information Criterion
<code>model.parameters</code>	the estimated parameters

Author(s)

H Morlon

References

- Morlon, H., Potts, M.D., Plotkin, J.B. (2010) Inferring the dynamics of diversification: a coalescent approach, PLoS B 8(9): e1000493
- Morlon, H., Kemp, B., Plotkin, J.B., Brisson, D. (2012) Explosive radiation of a bacterial species group, Evolution, 66: 2577-2586
- Morlon, H. (2014) Phylogenetic approaches for studying diversification, Eco Lett, 17:508-525

See Also

[likelihood_coal_var](#), [fit_coal_cst](#)

Examples

```
data(Cetacea)
result <- fit_coal_var(Cetacea, lamb0=0.01, alpha=-0.001, mu0=0.0, beta=0, N0=89)
print(result)
```

fit_env

Maximum likelihood fit of the environmental birth-death model

Description

Fits the environmental birth-death model with potentially missing extant species to a phylogeny, by maximum likelihood. Notations follow Morlon et al. PNAS 2011 and Condamine et al. ELE 2013.

Usage

```
fit_env(phylo, env_data, tot_time, f.lamb, f.mu, lamb_par, mu_par, df= NULL, f = 1,
meth = "Nelder-Mead", cst.lamb = FALSE, cst.mu = FALSE,
expo.lamb = FALSE, expo.mu = FALSE, fix.mu = FALSE,
dt=0, cond = "crown")
```

Arguments

- | | |
|----------|--|
| phylo | an object of type 'phylo' (see ape documentation) |
| env_data | environmental data, given as a data frame with two columns. The first column is time, the second column is the environmental data (temperature for instance). |
| tot_time | the age of the phylogeny (crown age, or stem age if known). If working with crown ages, tot_time is given by max(node.age(phylo)\$ages). |
| f.lamb | a function specifying the hypothesized functional form of the variation of the speciation rate λ with time and the environmental variable. Any functional form may be used. This function has three arguments: the first argument is time; the second argument is the environmental variable; the third argument is a numeric vector of the parameters controlling the time and environmental variation (to be estimated). |

f.mu	a function specifying the hypothesized functional form of the variation of the extinction rate μ with time and the environmental variable. Any functional form may be used. This function has three arguments: the first argument is time; the second argument is the environmental variable; the second argument is a numeric vector of the parameters controlling the time and environmental variation (to be estimated).
lamb_par	a numeric vector of initial values for the parameters of f.lamb to be estimated (these values are used by the optimization algorithm). The length of this vector is used to compute the total number of parameters in the model, so to fit a model with constant speciation rate (for example), lamb_par should be a vector of length 1. Otherwise aic values will be wrong.
mu_par	a numeric vector of initial values for the parameters of f.mu to be estimated (these values are used by the optimization algorithm). The length of this vector is used to compute the total number of parameters in the model, so to fit a model without extinction (for example), mu_par should be empty (vector of length 0). Otherwise aic values will be wrong.
df	the degree of freedom to use to define the spline. As a default, smooth.spline(env_data[,1], env_data[,2])\$df is used. See <i>sm.spline</i> for details.
f	the fraction of extant species included in the phylogeny
meth	optimization to use to maximize the likelihood function, see <i>optim</i> for more details.
cst.lamb	logical: should be set to TRUE only if f.lamb is constant (i.e. does not depend on time or the environmental variable) to use analytical instead of numerical computation in order to reduce computation time.
cst.mu	logical: should be set to TRUE only if f.mu is constant (i.e. does not depend on time or the environmental variable) to use analytical instead of numerical computation in order to reduce computation time.
expo.lamb	logical: should be set to TRUE only if f.lamb is an exponential function of time (and does not depend on the environmental variable) to use analytical instead of numerical computation in order to reduce computation time.
expo.mu	logical: should be set to TRUE only if f.mu is an exponential function of time (and does not depend on the environmental variable) to use analytical instead of numerical computation in order to reduce computation time.
fix.mu	logical: if set to TRUE, the extinction rate μ is fixed and will not be optimized.
dt	the default value is 0. In this case, integrals in the likelihood are computed using R "integrate" function, which can be quite slow. If a positive dt is given as argument, integrals are computed using a piece-wise constant approximation, and dt represents the length of the intervals on which functions are assumed to be constant. We found that 1e-3 generally provides a good trade-off between precision and computation time.
cond	conditioning to use to fit the model: <ul style="list-style-type: none"> • FALSE: no conditioning (not recommended); • "stem": conditioning on the survival of the stem lineage (use when the stem age is known, in this case tot_time should be the stem age);

- "crown" (default): conditioning on a speciation event at the crown age and survival of the 2 daughter lineages (use when the stem age is not known, in this case tot_time should be the crown age).

Details

The lengths of `lamb_par` and `mu_par` are used to compute the total number of parameters in the model, so to fit a model with constant speciation rate (for example), `lamb_par` should be a vector of length 1. Otherwise aic values will be wrong. In the `f.lamb` and `f.mu` functions, time runs from the present to the past.

Value

a list with the following components

<code>model</code>	the name of the fitted model
<code>LH</code>	the maximum log-likelihood value
<code>aicc</code>	the second order Akaike's Information Criterion
<code>lamb_par</code>	a numeric vector of estimated <code>f.lamb</code> parameters, in the same order as defined in <code>f.lamb</code>
<code>mu_par</code>	a numeric vector of estimated <code>f.mu</code> parameters, in the same order as defined in <code>f.mu</code> (if <code>fix.mu</code> is FALSE)

Note

The speed of convergence of the fit might depend on the degree of freedom chosen to define the spline.

Author(s)

H Morlon and F Condamine

References

- Morlon, H., Parsons, T.L. and Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record *Proc Nat Acad Sci* 108: 16327-16332
- Condamine, F.L., Rolland, J., and Morlon, H. (2013) Macroevolutionary perspectives to environmental change, *Eco Lett* 16: 72-85
- Morlon, H. (2014) Phylogenetic approaches for studying diversification, *Eco Lett*, 17:508-525

See Also

[plot_fit_env](#), [fit_bd](#), [likelihood_bd](#)

Examples

```

data(Cetacea)
tot_time<-max(node.age(Cetacea)$ages)
data(InfTemp)
dof<-smooth.spline(InfTemp[,1], InfTemp[,2])$df

# Fits a model with lambda varying as an exponential function of temperature
# and mu fixed to 0 (no extinction). Here t stands for time and x for temperature.
f.lamb <-function(t,x,y){y[1] * exp(y[2] * x)}
f.mu<-function(t,x,y){0}
lamb_par<-c(0.10, 0.01)
mu_par<-c()
#result_exp <- fit_env(Cetacea,InfTemp,tot_time,f.lamb,f.mu,lamb_par,mu_par,
#                      f=87/89,fix.mu=TRUE,df=dof,dt=1e-3)

```

fit_sgd

*Maximum likelihood fit of the SGD model***Description**

Fits the SGD model with exponential growth of the metacommunity, by maximum likelihood. Notations follow Manceau et al. (2015)

Usage

```
fit_sgd(phylo, tot_time, par, f=1, meth = "Nelder-Mead")
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
tot_time	the age of the phylogeny (crown age, or stem age if known). If working with crown ages, tot_time is given by max(node.age(phylo)\$ages)
par	a numeric vector of initial values for the parameters (b,d,nu) to be estimated (these values are used by the optimization algorithm)
f	the fraction of extant species included in the phylogeny
meth	optimization to use to maximize the likelihood function, see <i>optim</i> for more details.

Value

a list with the following components

model	the name of the fitted model
LH	the maximum log-likelihood value
aicc	the second order Akaike's Information Criterion
par	a numeric vector of estimated values of b (birth), b-d (growth) and nu (mutation)

Note

While b-d and nu can in general be well estimated, the likelihood surface is quite flat with respect to b, such that the estimated b can vary a lot depending on the choice of the initial parameter values. Estimates of b should not be trusted.

Author(s)

M Manceau

References

Manceau, M., Lambert, A., Morlon, H. (2015) Phylogenies support out-of-equilibrium models of biodiversity Ecology Letters 18: 347-356

See Also

[likelihood_sgd](#)

Examples

```
# Some examples may take a little bit of time. Be patient!
data(Calomys)
tot_time <- max(node.age(Calomys)$ages)
par_init <- c(1e7, 1e7-0.5, 1)
#fit_sgd(Calomys, tot_time, par_init, f=11/13)
```

fit_t_comp

Fits models of trait evolution incorporating competitive interactions

Description

Fits matching competition (MC), diversity dependent linear (DDlin), or diversity dependent exponential (DDexp) models of trait evolution to a given dataset and phylogeny.

Usage

```
fit_t_comp(phylo, data, model=c("MC", "DDexp", "DDlin"), pars=NULL, geography.object=NULL)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
data	a named vector of trait values with names matching phylo\$tip.label
model	model chosen to fit trait data, "MC" is the matching competition model of Nuismer & Harmon 2014, "DDlin" is the diversity-dependent linear model, and "DDexp" is the diversity-dependent exponential model of Weir & Mursleen 2013.
geography.object	a list of sympatry through time created using CreateGeoObject
pars	vector specifying starting parameter values for maximum likelihood optimization. If unspecified, default values are used (see Details)

Details

If unspecified, `par` takes the default values of `var(data)/max(nodeHeights(phylo))` for `sig2` and 0 for either `S` for the matching competition model, `b` for the linear diversity dependence model, or `r` for the exponential diversity dependence model. Values can be manually entered as a vector with the first element equal to the desired starting value for `sig2` and the second value equal to the desired starting value for either `S`, `b`, or `r`. Note: since likelihood optimization uses `sig` rather than `sig2`, and since the starting value for `sig` is exponentiated to stabilize the likelihood search, if you input a `par` value, the first value specifying `sig2` should be the `log(sqrt())` of the desired `sig2` starting value.

Value

a list with the following elements:

LH	maximum log-likelihood value
aic	Akaike Information Criterion value
aicc	AIC value corrected for small sample size
free.parameters	number of free parameters from the model
sig2	maximum-likelihood estimate of <code>sig2</code> parameter
S	maximum-likelihood estimate of <code>S</code> parameter of matching competition model (see Note)
b	maximum-likelihood estimate of <code>b</code> parameter of linear diversity dependence model
r	maximum-likelihood estimate of <code>r</code> parameter of exponential diversity dependence model
z0	maximum-likelihood estimate of <code>z0</code> , the value at the root of the tree
convergence	convergence diagnostics from <code>optim</code> function (see <code>optim</code> documentation)

Note

In current version, the `S` parameter is restricted to take on negative values in MC + geography ML optimization.

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com
Julien Clavel

References

- Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020
- Nuismer, S. & Harmon, L. 2015. Predicting rates of interspecific interaction from phylogenetic trees. *Ecology Letters* 18:17-27.
- Weir, J. & Mursleen, S. 2012. Diversity-dependent cladogenesis and trait evolution in the adaptive radiation of the auks (Aves: Alcidae). *Evolution* 67:403-416.

See Also

[sim_t_comp](#) [CreateGeoObject](#) [likelihood_t_MC](#) [likelihood_t_MC_geog](#) [likelihood_t_DD](#) [likelihood_t_DD_geog](#)

Examples

```
data(Anolis.data)
geography.object<-Anolis.data$geography.object
pPC1<-Anolis.data$data
phylo<-Anolis.data$phylo

#Fit three models without biogeography to pPC1 data
MC.fit<-fit_t_comp(phylo, pPC1, model="MC")
DDlin.fit<-fit_t_comp(phylo, pPC1, model="DDlin")
DDexp.fit<-fit_t_comp(phylo, pPC1, model="DDexp")

#Now fit models that incorporate biogeography, NOTE these models take longer to fit
MC.geo.fit<-fit_t_comp(phylo, pPC1, model="MC", geography.object=geography.object)
DDlin.geo.fit<-fit_t_comp(phylo, pPC1,model="DDlin", geography.object=geography.object)
DDexp.geo.fit<-fit_t_comp(phylo, pPC1, model="DDexp", geography.object=geography.object)
```

fit_t_comp_subgroup	<i>Fits models of trait evolution incorporating competitive interactions, restricting competition to occur only between members of a subgroup</i>
---------------------	---

Description

Fits matching competition (MC), diversity dependent linear (DDlin), or diversity dependent exponential (DDexp) models of trait evolution to a given dataset, phylogeny, and stochastic maps of both subgroup membership and biogeography.

Usage

```
fit_t_comp_subgroup(full.phylo, ana.events, clado.events, stratified=FALSE, map,data,
trim.class, model=c("MC","DDexp","DDlin"), par=NULL, method="Nelder-Mead",
bounds=NULL)
```

Arguments

full.phylo	an object of type 'phylo' (see ape documentation) containing all of the tips used to estimate ancestral biogeography in BioGeoBEARS
ana.events	the "ana.events" table produced in BioGeoBEARS that lists anagenetic events in the stochastic map

clado.events	the "clado.events" table produced in BioGeoBEARS that lists cladogenetic events in the stochastic map
stratified	logical indicating whether the stochastic map was built from a stratified analysis in BioGeoBEARS
map	a phylo object created using <code>make.simmap</code> in phytools that contains reconstructed subgroup membership
data	a named vector of trait values for subgroup members with names matching <code>full.phylo\$tip.label</code>
trim.class	subgroup whose members are competing
model	model chosen to fit trait data, "MC" is the matching competition model of Nuismer & Harmon 2014, "DDlin" is the diversity-dependent linear model, and "DDexp" is the diversity-dependent exponential model of Weir & Mursleen 2013.
par	vector specifying starting parameter values for maximum likelihood optimization. If unspecified, default values are used (see Details)
method	optimization algorithm to use (see <code>optim</code>)
bounds	(optional) list of bounds to pass to optimization algorithm (see details at <code>optim</code>)

Details

If unspecified, `par` takes the default values of `var(data)/max(nodeHeights(phylo))` for `sig2` and 0 for either `S` for the matching competition model, `b` for the linear diversity dependence model, or `r` for the exponential diversity dependence model. Values can be manually entered as a vector with the first element equal to the desired starting value for `sig2` and the second value equal to the desired starting value for either `S`, `b`, or `r`. Note: since likelihood optimization uses `sig` rather than `sig2`, and since the starting value for `sig` is exponentiated to stabilize the likelihood search, if you input a `par` value, the first value specifying `sig2` should be the `log(sqrt())` of the desired `sig2` starting value.

Value

a list with the following elements:

LH	maximum log-likelihood value
aic	Akaike Information Criterion value
aicc	AIC value corrected for small sample size
free.parameters	number of free parameters from the model
sig2	maximum-likelihood estimate of <code>sig2</code> parameter
S	maximum-likelihood estimate of <code>S</code> parameter of matching competition model (see Note)
b	maximum-likelihood estimate of <code>b</code> parameter of linear diversity dependence model
r	maximum-likelihood estimate of <code>r</code> parameter of exponential diversity dependence model
z0	maximum-likelihood estimate of <code>z0</code> , the value at the root of the tree
convergence	convergence diagnostics from <code>optim</code> function (see <code>optim</code> documentation)

Note

In current version, the S parameter is restricted to take on negative values in MC + geography ML optimization.

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com

References

Drury, J., Tobias, J., Burns, K., Mason, N., Shultz, A., and Morlon, H. in review. Contrasting impacts of competition on ecological and social trait evolution in songbirds. *PLOS Biology*.

Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020

Nuismer, S. & Harmon, L. 2015. Predicting rates of interspecific interaction from phylogenetic trees. *Ecology Letters* 18:17-27.

Weir, J. & Mursleen, S. 2012. Diversity-dependent cladogenesis and trait evolution in the adaptive radiation of the auks (Aves: Alcidae). *Evolution* 67:403-416.

See Also

[likelihood_subgroup_model CreateGeobyClassObject](#)

Examples

```
data(BGB.examples)
```

```
Canidae.phylo<-BGB.examples$Canidae.phylo
dummy.group<-c(rep("B",3),rep("A",12),rep("B",2),rep("A",6),rep("B",5),rep("A",6))
names(dummy.group)<-Canidae.phylo$tip.label
```

```
Canidae.simap<-phytools::make.simap(Canidae.phylo,dummy.group)
```

```
set.seed(123)
Canidae.data<-rnorm(length(Canidae.phylo$tip.label))
names(Canidae.data)<-Canidae.phylo$tip.label
Canidae.A<-Canidae.data[which(dummy.group=="A")]
```

```
fitA<-fit_t_comp_subgroup(full.phylo=Canidae.phylo,ana.events=BGB.examples$Canidae.ana.events,
clado.events=BGB.examples$Canidae.clado.events,stratified=FALSE,map=Canidae.simap,
data=Canidae.A,trim.class="A",model="DDexp")
```

fit_t_env

*Maximum likelihood fit of the environmental model of trait evolution***Description**

Fits model of trait evolution for which evolutionary rates depends on an environmental function, or more generally a time varying function.

Usage

```
fit_t_env(phylo, data, env_data, error=NULL, model=c("EnvExp", "EnvLin"),
          method="Nelder-Mead", control=list(maxit=20000), ...)
```

Arguments

phylo	An object of class 'phylo' (see ape documentation)
data	A named vector of phenotypic trait values.
env_data	Environmental data, given as a time continuous function (see, e.g. splinefun) or a data frame with two columns. The first column is time, the second column is the environmental data (temperature for instance).
error	A named vector with standard error (SE) for each species. Default is NULL, if NA, then the SE is estimated from the data.
model	The model describing the functional form of variation of the evolutionary rate σ^2 with time and the environmental variable. Default models are "EnvExp" and "EnvLin" (see details). An user defined function of any functional form may be used (forward in time). This function has three arguments: the first argument is time; the second argument is the environmental variable; the third argument is a numeric vector of the parameters controlling the time and environmental variation (to be estimated). See the example below.
method	Methods used by the optimization routine (see ?optim for details).
control	Max. bound for the number of iteration of the optimizer; other options can be fixed on the list (see ?optim).
...	Arguments to be passed to the function. See details.

Details

fit_t_env allows fitting environmental models of trait evolution. The default models *EnvExp* and *EnvLin* represents models for which the evolutionary rates are changing as a function of environmental changes though times as defined below.

EnvExp:

$$\sigma^2(t) = \sigma_0^2 e^{(\beta T(t))}$$

EnvLin:

$$\sigma^2(t) = \sigma_0^2 + \beta T(t)$$

Users defined models should have the following form (see also examples below):

```
fun <-function(t,env,param){ param*env(t)}
```

t: is the time parameter.

env: is a time function of an environmental variable. See for instance object created by `splinefun` when interpolating coordinate of points.

param: is a vector of parameters to estimate.

For instance, the `EnvExp` function can be coded as:

```
fun <-function(t,env,param){ param[1]*exp(param[2]*env(t))}
```

where `param[1]` is the σ^2 parameter and `param[2]` is the β parameter. Note that in this later case, two starting values should be provided in the `param` argument.

e.g.:

```
sigma=0.1
```

```
beta=0
```

```
fit_t_env(tree,data,env_data=InfTemp,model=fun,param=c(sigma,beta))
```

The various options are passed through "...".

-`param`: The starting values used for the model. Must match the total number of parameters of the specified models. If "error=NA", a starting value for the SE to be estimated must be provided with user-defined models.

-`scale`: scale the amplitude of the environmental curve between 0 and 1. This may improve the parameters search in some situations.

-`df`: the degree of freedom to use for defining the spline. As a default, `smooth.spline(env_data[,1],env_data[,2])$df` is used. See *sm.spline* for details.

-`upper`: the upper bound for the parameter search when the "L-BFGS-B" method is used. See *optim* for details.

-`lower`: the lower bound for the parameter search when the "L-BFGS-B" method is used. See *optim* for details.

-`sig2`: can be used instead of `param` to define the starting sigma value only

-`beta`: can be used instead of `param` to define the beta starting value only

-`maxdiff`: difference in time between tips and present day for phylogenetic trees with no contemporaneous species (default is 0)

Value

a list with the following components

<code>LH</code>	the maximum log-likelihood value
<code>aic</code>	the Akaike's Information Criterion
<code>aicc</code>	the second order Akaike's Information Criterion
<code>free.parameters</code>	the number of estimated parameters

param	a numeric vector of estimated parameters, sigma and beta respectively for the defaults models. In the same order as defined by the user if a customized model is provided
root	the estimated root value
convergence	convergence status of the optimizing function; "0" indicates convergence (See ?optim for details)
hess.value	reliability of the likelihood estimates calculated through the eigen-decomposition of the hessian matrix. "0" means that a reliable estimate has been reached
env_func	the environmental function
tot_time	the root age of the tree
model	the fitted model (default models or user specified)
SE	the estimated SE for species mean when "error=NA"

Note

The users defined function is evaluated forward in time i.e.: from the root to the tips (time = 0 at the (present) tips). The speed of convergence of the fit might depend on the degree of freedom chosen to define the spline.

Author(s)

J. Clavel

References

Clavel, J. & Morlon, H., 2017. Accelerated body size evolution during cold climatic periods in the Cenozoic. *Proceedings of the National Academy of Science*, 114(16): 4183-4188.

See Also

[plot.fit_t.env](#), [likelihood_t.env](#)

Examples

```
data(Cetacea)
data(InfTemp)

# Simulate a trait with temperature dependence on the Cetacean tree
set.seed(123)

trait <- sim_t_env(Cetacea, param=c(0.1,-0.2), env_data=InfTemp, model="EnvExp",
root.value=0, step=0.001, plot=TRUE)

## Fit the Environmental-exponential model
# Fit the environmental model
result1=fit_t_env(Cetacea, trait, env_data=InfTemp, scale=TRUE)
plot(result1)

# Add to the plot the results from different smoothing of the temperature curve
```

```

result2=fit_t_env(Cetacea, trait, env_data=InfTemp, df=10, scale=TRUE)
lines(result2, col="red")

result3=fit_t_env(Cetacea, trait, env_data=InfTemp, df=50, scale=TRUE)
lines(result3, col="blue")

## Fit the environmental linear model

fit_t_env(Cetacea, trait, env_data=InfTemp, model="EnvLin", df=50, scale=TRUE)

## Fit user defined model (note that several other environmental variables
## can be simultaneously encapsulated in this function through the env argument)

# We define the function for the model
my_fun<-function(t, env_cont, param){
  param[1]*exp(param[2]*env_cont(t))
}

res<-fit_t_env(Cetacea, trait, env_data=InfTemp, model=my_fun,
               param=c(0.1,0), scale=TRUE)
# Retrieve the parameters and compare to 'result1'
res
plot(res, col="red")

## Fit user defined environmental function

require(apspline)
spline_result <- sm.spline(x=InfTemp[,1],y=InfTemp[,2], df=50)
env_func <- function(t){predict(spline_result,t)}
t<-unique(InfTemp[,1])

# We build the interpolated smoothing spline function
env_data<-splinefun(t,env_func(t))

# We then fit the model
fit_t_env(Cetacea, trait, env_data=env_data)

## Various parameterization (box constraints, df, scaling of the curve...) example
fit_t_env(Cetacea, trait, env_data=InfTemp, model="EnvLin", method="L-BFGS-B",
          scale=TRUE, lower=-30, upper=20, df=10)

## A very general model...

# We define the function for the Early-Burst/AC model:
maxtime = max(branching.times(Cetacea))

#  $\sigma^2 e^{(r \cdot t)}$ 
my_fun_ebac <- function(t, env_cont, param){
  time = (maxtime - t)
  param[1]*exp(param[2]*time)
}

```

```
res<-fit_t_env(Cetacea, trait, env_data=InfTemp, model=my_fun_ebac,
              param=c(0.1,0), scale=TRUE)
res # note that "r" is positive: it's the AC model (~OU model on ultrametric tree)
```

fit_t_pl

High-dimensional phylogenetic models of trait evolution

Description

Fits high-dimensional model of trait evolution on trees through penalized likelihood. A phylogenetic Leave-One-Out Cross-Validated log-likelihood (LOOCV) is used to estimate model parameters.

Usage

```
fit_t_pl(Y, tree, model=c("BM", "OU", "EB", "lambda"),
         method=c("RidgeAlt", "RidgeArch", "RidgeAltapprox",
                  "LASSO", "LASSOapprox"), targM=c("null", "Variance",
          "unitVariance"), REML=TRUE, up=NULL, low=NULL,
         tol=NULL, starting=NULL, SE=NULL,
         scale.height=TRUE, ...)
```

Arguments

Y	A matrix of phenotypic traits values (the variables are represented as columns)
tree	An object of class 'phylo' (see ape documentation)
model	The evolutionary model, "BM" is Brownian Motion, "OU" is Ornstein-Uhlenbeck, "EB" is Early Burst, and "lambda" is Pagel's lambda transformation.
method	The penalty method. "RidgeArch": Archetype (linear) Ridge penalty, "RidgeAlt": Quadratic Ridge penalty, "LASSO": Least Absolute Selection and Shrinkage Operator. "RidgeAltapprox" and "LASSOapprox" are fast approximations of the LOOCV for the Ridge quadratic and LASSO penalties
targM	The target matrix used for the Ridge regularizations. "null" is a null target, "Variance" for a diagonal unequal variance target, "unitVariance" for an equal diagonal target. Only works with "RidgeArch", "RidgeAlt", and "RidgeAltapprox" methods.
REML	Use REML (default) or ML for estimating the parameters.
up	Upper bound for the parameter search of the evolutionary model (optional).
low	Lower bound for the parameter search of the evolutionary model (optional).

tol	minimum value for the regularization parameter. Singularities can occur with a zero value in high-dimensional cases. (default is NULL)
starting	Starting values for the parameter search (optional).
SE	Standard errors associated with values in Y. If TRUE, SE will be estimated.
scale.height	Whether the tree should be scaled to unit length or not. (default is TRUE)
...	Options to be passed through. (e.g., echo=FALSE to stop printing messages)

Details

`fit_t_pl` allows fitting various multivariate evolutionary models to high-dimensional datasets (where the number of variables p is larger than n). Models estimates are more accurate than maximum likelihood methods. Models fit can be compared using the GIC criterion (see `?GIC`). Details about the methods are described in *Clavel et al. (2019)*.

Value

a list with the following components

loocv	the (negative) cross-validated penalized likelihood
model.par	the evolutionary model parameter estimates
gamma	the regularization/tuning parameter of the penalized likelihood
corrstruct	a list with the transformed variables and the phylogenetic tree with branch length stretched to the model estimated parameters
model	the evolutionary model
method	the penalization method
p	the number of traits
n	the number of species
targM	the target used for Ridge Penalization
R	a list with the estimated evolutionary covariance matrix and it's inverse
REML	logical indicating if the REML (TRUE) or ML (FALSE) method has been used
variables	Y is the input dataset and tree is the input phylogenetic tree
SE	the estimated standard error

Note

The LASSO is computationally intensive. Please wait! For highly-dimensional datasets you should favor the "RidgeArch" method to speed up the computations. The Ridge penalties with "null" or "unitVariance" targets are rotation invariants.

Author(s)

J. Clavel

References

Clavel, J., Aristide, L., Morlon, H., 2019. A Penalized Likelihood framework for high-dimensional phylogenetic comparative methods and an application to new-world monkeys brain evolution. *Syst. Biol.* 68: 93-116.

See Also

[ancestral](#), [phyl.pca_pl](#), [GIC.fit_pl.rpanda](#), [gic_criterion mvgl](#)s

Examples

```
require(mvMORPH)
set.seed(1)
n <- 32 # number of species
p <- 31 # number of traits

tree <- pbtree(n=n) # phylogenetic tree
R <- Posdef(p)      # a random symmetric matrix (covariance)

# simulate a dataset
Y <- mvSIM(tree, model="BM1", nsim=1, param=list(sigma=R))

# fit the model
fit_t_pl(Y, tree, model="BM", method="RidgeAlt")

# try on rotated axis (using PCA)
trans <- prcomp(Y, center=FALSE)
fit_t_pl(trans$x, tree, model="BM", method="RidgeAlt")

# Estimate the SE (similar to Pagel's lambda for BM).
# Advised with empirical datasets
fit_t_pl(Y, tree, model="BM", method="RidgeAlt", SE=TRUE)
```

foraminifera

Foraminifera diversity since the Jurassic

Description

Foraminifera fossil diversity since the Jurassic

Usage

```
data(foraminifera)
```

Details

Foraminifera fossil diversity since the Jurassic compiled from the Neptune Database (Lazarus, 1994) and Paleobiology Database (<https://paleobiodb.org/>). Diversity curves are estimated at the genus level using shareholder quorum subsampling (Alroy, 2010) at two-million-year bins. The format is a dataframe with the two following variables:

age a numeric vector corresponding to the geological age, in Myrs before the present

foraminifera a numeric vector corresponding to the estimated foraminifera change at that age

References

Lazarus, D. (1994) Neptune: A marine micropaleontology database *Mathematical Geology* 26:817–832

Alroy, J. (2010) Geographical, environmental and intrinsic biotic controls on Phanerozoic marine diversification: Controls on phanerozoic marine diversification *Palaeontology* 53:1211–1235

Examples

```
data(foraminifera)
plot(foraminifera)
```

getDataLikelihood *Likelihood of tip trait values.*

Description

Computes $-\log(\text{likelihood})$ of tip trait data under a given set of parameters, and for a specified model of trait evolution.

Usage

```
getDataLikelihood(object, data, params, v)
```

Arguments

object	an object of class 'PhenotypicModel'.
data	vector of tip trait data.
params	vector of parameters, given in the same order as in the 'model' object.
v	boolean specifying the verbose mode. Default value : FALSE.

Value

A numerical value : $-\log(\text{likelihood})$ of the model.

Author(s)

M Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*

Examples

```
#Loading an example tree
newick <- "(((A:1,B:0.5):2,(C:3,D:2.5):1):6,E:10.25):2,(F:6.5,G:8.25):3):1;"
tree <- read.tree(text=newick)

#Creating the models
modelBM <- createModel(tree, 'BM')

#Simulating tip traits under the model :
dataBM <- simulateTipData(modelBM, c(0,0,0,1))

#Likelihood of the data :
getDataLikelihood(modelBM, dataBM, c(0,0,0,1))
```

getDataLikelihood-methods

~~ *Methods for Function* getDataLikelihood ~~

Description

~~ *Methods for function* getDataLikelihood ~~

Methods

signature(object = "PhenotypicModel") This is the only method available for this function. Same behaviour for any PhenotypicModel.

getMAPS_ClaDS

Gets the Maximum A Posteriori for each ClaDS parameter

Description

Extract the MAPs (Maximum A Posteriori) for the marginal posterior distributions estimated with fit_ClaDS

Usage

```
getMAPS_ClaDS(sampler, burn = 1/2, thin = 1)
```


Arguments

sampler	The output of a fit_ClaDS run.
burn	Number of iterations to drop in the beginning of the chains.
thin	Thinning parameter, one iteration out of "thin" is kept to compute the MAPs.

Value

A vector MAPS containing the MAPs for the marginal posterior distribution for each of the model's parameters.

MAPS[1:4] are the estimated hyperparameters, with MAPS[1] the sigma parameter (new rates stochasticity), MAPS[2] the alpha parameter (new rates trend), MAPS[3] the turnover rate epsilon, and MAPS[4] the initial speciation rate lambda_0.

MAPS[-(1:4)] are the estimated branch-specific speciation rates, given in the same order as the edges of the phylogeny on which the inference was performed.

Author(s)

O. Maliet

References

Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0

See Also

[fit_ClaDS](#), [plot_ClaDS_chains](#), [getMAPS_ClaDS0](#)

Examples

```
data("Caprimulgidae_ClaDS2")

MAPS = getMAPS_ClaDS(Caprimulgidae_ClaDS2$sampler, thin = 1)

print(paste0("sigma = ", MAPS[1], " ; alpha = ",
  MAPS[2], " ; epsilon = ", MAPS[3], " ; l_0 = ", MAPS[4] ))
plot_ClaDS_phylo(Caprimulgidae_ClaDS2$tree, MAPS[-(1:4)])
```

`getMAPS_ClaDS0`*Gets the Maximum A Posteriori for each ClaDS0 parameter*

Description

Extract the MAPs (Maximum A Posteriori) for the marginal posterior distributions estimated with `run_ClaDS0`.

Usage

```
getMAPS_ClaDS0(phylo, sampler, burn=1/2, thin=1)
```

Arguments

<code>phylo</code>	An object of class <code>'phylo'</code> .
<code>sampler</code>	The output of a <code>run_ClaDS0</code> run.
<code>burn</code>	Number of iterations to drop in the beginning of the chains.
<code>thin</code>	Thinning parameter, one iteration out of "thin" is kept to compute the MAPs.

Value

A vector MAPS containing the MAPs for the marginal posterior distribution for each of the model's parameters.

MAPS[1:3] are the estimated hyperparameters, with MAPS[1] the sigma parameter (new rates stochasticity), MAPS[2] the alpha parameter (new rates trend), and MAPS[3] the initial speciation rate `lambda_0`.

MAPS[-(1:3)] are the estimated branch-specific speciation rates, given in the same order as the `phylo$edges`.

Author(s)

O. Maliet

References

Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0

See Also

[fit_ClaDS0](#), [plot_ClaDS0_chains](#), [getMAPS_ClaDS](#)

Examples

```

set.seed(1)

obj= sim_ClaDS( lambda_0=0.1,
               mu_0=0.5,
               sigma_lamb=0.7,
               alpha_lamb=0.90,
               condition="taxa",
               taxa_stop = 20,
               prune_extinct = TRUE)

tree = obj$tree
speciation_rates = obj$lamb[obj$rates]
extinction_rates = obj$mu[obj$rates]
data("ClaDS0_example")

# extract the Maximum A Posteriori for each of the parameters
MAPS = getMAPS_ClaDS0(ClaDS0_example$tree,
                    ClaDS0_example$Cl0_chains,
                    thin = 10)

# plot the simulated (on the left) and inferred speciation rates (on the right)
# on the same color scale
plot_ClaDS_phylo(ClaDS0_example$tree,
                ClaDS0_example$speciation_rates,
                MAPS[-(1:3)])

```

getTipDistribution *Distribution of tip trait values.*

Description

Computes the mean and variance of the tip trait distribution under a specified model of trait evolution.

Usage

```
getTipDistribution(object, params, v)
```

Arguments

object	an object of class 'PhenotypicModel'
params	vector of parameters, given in the same order as in the 'model' object.
v	boolean specifying the verbose mode. Default value : FALSE.

Value

mean	Expectation vector of the tip trait distribution.
Sigma	Variance-covariance matrix of the tip trait distribution.

Author(s)

M Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*

Examples

```
#Loading an example tree
newick <- "(((A:1,B:0.5):2,(C:3,D:2.5):1):6,E:10.25):2,(F:6.5,G:8.25):3):1;"
tree <- read.tree(text=newick)

#Creating a BM model
modelBM <- createModel(tree, 'BM')

#Tip trait distribution under the model :
getTipDistribution(modelBM, c(0,0,0,1))
```

getTipDistribution-methods

Distribution of tip trait values.

Description

Computes the mean and variance of the tip trait distribution under a specified model of trait evolution.

Methods

signature(object = "PhenotypicModel") In the most general case, this function computes the expectation vector and the variance-covariance matrix using a numerical integration procedure that may take time.

signature(object = "PhenotypicACDC") The function has been optimized for this subclass.

signature(object = "PhenotypicADiag") The function has been optimized for this subclass.

signature(object = "PhenotypicBM") The function has been optimized for this subclass.

signature(object = "PhenotypicDD") The function has been optimized for this subclass.

signature(object = "PhenotypicGMM") The function has been optimized for this subclass.

signature(object = "PhenotypicOU") The function has been optimized for this subclass.

signature(object = "PhenotypicPM") The function has been optimized for this subclass.

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*

GIC.fit_pl.rpanda	<i>Generalized Information Criterion (GIC) to compare models fit by Maximum Likelihood (ML) or Penalized Likelihood (PL).</i>
-------------------	---

Description

The GIC allows comparing models fit by Maximum Likelihood (ML) or Penalized Likelihood (PL).

Usage

```
## S3 method for class 'fit_pl.rpanda'
GIC(object, ...)
```

Arguments

object	An object of class "fit_pl.rpanda". See ?fit_t_pl
...	Options to be passed through.

Details

GIC allows comparing the fit of various models estimated by Penalized Likelihood (see ?fit_t_pl). It's a wrapper to the `gic_criterion` function.

Value

a list with the following components

LogLikelihood	the log-likelihood estimated for the model with estimated parameters
GIC	the GIC criterion
bias	the value of the bias term estimated to compute the GIC

Author(s)

J. Clavel

References

Konishi S., Kitagawa G. 1996. Generalised information criteria in model selection. *Biometrika*. 83:875-890.

Clavel, J., Aristide, L., Morlon, H., 2019. A Penalized Likelihood framework for high-dimensional phylogenetic comparative methods and an application to new-world monkeys brain evolution. *Syst. Biol.* 68: 93-116.

See Also

[gic_criterion](#), [fit_t_pl](#) [mvgl](#)s

Examples

```

require(mvMORPH)
set.seed(1)
n <- 32 # number of species
p <- 40 # number of traits

tree <- pbtree(n=n) # phylogenetic tree
R <- Posdef(p)      # a random symmetric matrix (covariance)
# simulate a dataset
Y <- mvSIM(tree, model="BM1", nsim=1, param=list(sigma=R))

fit1 <- fit_t_pl(Y, tree, model="BM", method="RidgeAlt")
fit2 <- fit_t_pl(Y, tree, model="OU", method="RidgeAlt")

GIC(fit1); GIC(fit2)

```

gic_criterion	<i>Generalized Information Criterion (GIC) to compare models fit by Maximum Likelihood (ML) or Penalized Likelihood (PL).</i>
---------------	---

Description

The GIC allows comparing models fit by Maximum Likelihood (ML) or Penalized Likelihood (PL).

Usage

```

gic_criterion(Y, tree, model="BM", method=c("RidgeAlt", "RidgeArch", "LASSO", "ML",
"RidgeAltapprox", "LASSOapprox"), targM=c("null",
"Variance", "unitVariance"), param=NULL,
tuning=0, REML=TRUE, ...)

```

Arguments

Y	A matrix of phenotypic traits values (the variables are represented as columns)
tree	An object of class 'phylo' (see ape documentation)
model	The evolutionary model, "BM" is Brownian Motion, "OU" is Ornstein-Uhlenbeck, "EB" is Early Burst, and "lambda" is Pagel's lambda transformation.
method	The penalty method. "RidgeArch": Archetype (linear) Ridge penalty, "RidgeAlt": Quadratic Ridge penalty, "LASSO": Least Absolute Selection and Shrinkage Operator, "ML": Maximum Likelihood.

targM	The target matrix used for the Ridge regularizations. "null" is a null target, "Variance" for a diagonal unequal variance target, "unitVariance" for an equal diagonal target. Only works with "RidgeArch","RidgeAlt" methods.
param	Parameter for the evolutionary model (see "model" above).
tuning	The tuning/regularization parameter.
REML	Use REML (default) or ML for estimating the parameters.
...	Additional options. Not used yet.

Details

`gic_criterion` allows comparing the fit of various models estimated by Penalized Likelihood (see `?fit_t_pl`). Use the wrapper GIC instead for models fit with `fit_t_pl`.

Value

a list with the following components

LogLikelihood	the log-likelihood estimated for the model with estimated parameters
GIC	the GIC criterion
bias	the value of the bias term estimated to compute the GIC

Note

The tuning parameter is assumed to be zero when using the "ML" method.

Author(s)

J. Clavel

References

- Konishi S., Kitagawa G. 1996. Generalised information criteria in model selection. *Biometrika*. 83:875-890.
- Clavel, J., Aristide, L., Morlon, H., 2019. A Penalized Likelihood framework for high-dimensional phylogenetic comparative methods and an application to new-world monkeys brain evolution. *Syst. Biol.* 68: 93-116.

See Also

[GIC.fit_pl.rpanda](#), [fit_t_pl](#)

Examples

```
require(mvMORPH)
set.seed(123)
n <- 32 # number of species
p <- 2 # number of traits
```

```

tree <- pbtree(n=n) # phylogenetic tree
R <- Posdef(p)      # a random symmetric matrix (covariance)

# simulate a dataset
Y <- mvSIM(tree, model="BM1", nsim=1, param=list(sigma=R))

# Compute the GIC for ML
gic_criterion(Y, tree, model="BM", method="ML", tuning=0) # ML

# Compare with PL?
#test <- fit_t_pl(Y, tree, model="BM", method="RidgeAlt")
#GIC(test)

```

greenalgae

Green algae diversity since the Jurassic

Description

Green algae fossil diversity since the Jurassic

Usage

```
data(greenalgae)
```

Details

Green algae fossil diversity since the Jurassic compiled from the Neptune Database (Lazarus, 1994) and Paleobiology Database (<https://paleobiodb.org/>). Diversity curves are estimated at the genus level using shareholder quorum subsampling (Alroy, 2010) at two-million-year bins. The format is a dataframe with the two following variables:

age a numeric vector corresponding to the geological age, in Myrs before the present

greenalgae a numeric vector corresponding to the estimated green algae change at that age

References

Lazarus, D. (1994) Neptune: A marine micropaleontology database *Mathematical Geology* 26:817–832

Alroy, J. (2010) Geographical, environmental and intrinsic biotic controls on Phanerozoic marine diversification: Controls on phanerozoic marine diversification *Palaeontology* 53:1211–1235

Examples

```
data(greenalgae)
plot(greenalgae)
```

InfTemp

Paleotemperature data across the Cenozoic

Description

Paleotemperature data across the Cenozoic inferred from delta O18 measurements

Usage

```
data(InfTemp)
```

Details

Paleotemperature data inferred from delta O18 measurements using the equation of Epstein et al. (1953). The format is a dataframe with the two following variables:

Age a numeric vector corresponding to the geological age, in Myrs before the present

Temperature a numeric vector corresponding to the inferred temperature at that age

References

Epstein, S., Buchsbaum, R., Lowenstam, H.A., Urey, H.C. (1953) Revised carbonate-water isotopic temperature scale *Geol. Soc. Am. Bull.* 64: 1315-1326

Zachos, J.C., Dickens, G.R., Zeebe, R.E. (2008) An early Cenozoic perspective on greenhouse warming and carbon-cycle dynamics *Nature* 451: 279-283

Condamine, F.L., Rolland, J., Morlon, H. (2013) Macroevolutionary perspectives to environmental change *Eco Lett* 16: 72-85

Examples

```
data(InfTemp)
plot(InfTemp)
```

JSDtree

Jensen-Shannon distance between phylogenies

Description

Computes the Jensen-Shannon distance metric between spectral density profiles of phylogenies.

Usage

```
JSDtree(phylo, meth=c("standard"))
```

Arguments

phylo	a list of objects of type 'phylo' (see ape documentation)
meth	the method used to compute the spectral density, which can either be "standard", "normal1", or "normal2". if set to "normal1", computes the spectral density normalized to the degree matrix. if set to "normal2", computes the spectral density normalized to the number of eigenvalues. if set to "standard", computes the unnormalized version of the spectral density (see the associated paper for an explanation)

Value

a matrix providing the Jensen-Shannon distance values between phylogeny pairs

Author(s)

E Lewitus

References

Lewitus, E., Morlon, H., Characterizing and comparing phylogenies from their Laplacian spectrum, bioRxiv doi: <http://dx.doi.org/10.1101/026476>

See Also

[JSDtree_cluster](#), [spectR](#), [BICompare](#)

Examples

```
trees<-TESS::tess.sim.age(n=20,age=10,0.15,0.05,MRCA=TRUE)
JSDtree(trees)
```

JSDtree_cluster *Clustering of phylogenies*

Description

Clusters phylogenies using hierarchical and k-medoids clustering

Usage

```
JSDtree_cluster(JSDtree,alpha=0.9,draw=T)
```

Arguments

JSDtree	a matrix of distances between phylogenie pairs, typically the output of the JS-Dtree function when the distance is measured as the Jensen-Shannon distance
alpha	the confidence value for demarcating clusters in the hierarchical clustering plot; the default is 0.9
draw	plot heatmap and hierarchical cluster in new windows

Value

plots a heatmap and a hierarchical cluster with bootstrap support, and outputs results of the k-medoids clustering in the form of a list with the following components

`clusters` the optimal number of clusters around medoids (see pamk documentation)

`cluster_assignments`
assignments of trees to clusters

`cluster_support`
a list with the following components: `widths`: a table specifying the cluster to which each tree belongs, the neighbor (i.e. most similar) cluster, and the silhouette width of the observation (see silhouette documentation); `clus.avg.widths`: average silhouette width for each cluster; `vg.width`: average silhouette width across all clusters

Note

The k-medoids clustering may not work with fewer than 10 trees

Author(s)

E Lewitus

References

Lewitus, E., Morlon, H., Characterizing and comparing phylogenies from their Laplacian spectrum, bioRxiv doi: <http://dx.doi.org/10.1101/026476>

See Also

[JSDtree](#)

Examples

```
trees<-TESS::tess.sim.age(n=20,age=10,0.15,0.05,MRCA=TRUE)
res<-JSDtree(trees)
#JSDtree_cluster(res,alpha=0.9,draw=T)
```

JSDt_cluster

Clustering on the Jensen-Shannon distance between phylogenetic trait data

Description

Computes the Jensen-Shannon distance metric between spectral density profiles of phylogenetic trait data and clusters on those distances.

Usage

```
JSDt_cluster(phylo,mat,plot=F)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
mat	a matrix of trait data with one trait per column and rows aligned to phylo tips
plot	plot hierarchical cluster in a new window

Value

plots a heatmap and hierarchical cluster with bootstrap support (>0.9) and outputs results of the k-medoids clustering on the optimal number of clusters in the form of a list with the following components

clusters	a list with the following components: size, max_diss, av_diss, diameter, and separation
J-S matrix	a matrix providing the Jensen-Shannon distance values between pairs of phylogenetic trait data
cluster assignment	a table that lists for each trait its cluster assignment and silhouette width

Author(s)

E Lewitus

References

Lewitus, E., Morlon, H. (2019) Characterizing and comparing phylogenetic trait data from their normalized Laplacian spectrum, bioRxiv doi: <https://doi.org/10.1101/654087>

See Also

[spectR_t](#)

Examples

```
data(Cetacea)
n<-length(Cetacea$tip.label)
mat<-replicate(20, rnorm(n))
colnames(mat)<-1:dim(mat)[2]
JSDt_cluster(Cetacea,mat)
```

landplant	<i>Land plant diversity since the Jurassic</i>
-----------	--

Description

Land plant fossil diversity since the Jurassic

Usage

```
data(landplant)
```

Details

Land plant fossil diversity since the Jurassic compiled from the Neptune Database (Lazarus, 1994) and Paleobiology Database (<https://paleobiodb.org/>). Diversity curves are estimated at the genus level using shareholder quorum subsampling (Alroy, 2010) at two-million-year bins. The format is a dataframe with the two following variables:

age a numeric vector corresponding to the geological age, in Myrs before the present

landplant a numeric vector corresponding to the estimated land plant change at that age

References

Lazarus, D. (1994) Neptune: A marine micropaleontology database *Mathematical Geology* 26:817–832

Alroy, J. (2010) Geographical, environmental and intrinsic biotic controls on Phanerozoic marine diversification: Controls on phanerozoic marine diversification *Palaeontology* 53:1211–1235

Examples

```
data(landplant)
plot(landplant)
```

likelihood_bd	<i>Likelihood of a phylogeny under the general birth-death model</i>
---------------	--

Description

Computes the likelihood of a phylogeny under a birth-death model with potentially time-varying rates and potentially missing extant species. Notations follow Morlon et al. PNAS 2011.

Usage

```
likelihood_bd(phylo, tot_time, f.lamb, f.mu, f, cst.lamb = FALSE, cst.mu = FALSE,
              expo.lamb = FALSE, expo.mu = FALSE, dt=0, cond = "crown")
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
tot_time	the age of the phylogeny (crown age, or stem age if known). If working with crown ages, tot_time is given by <code>max(node.age(phylo)\$ages)</code> .
f.lamb	a function specifying the time-variation of the speciation rate λ . This function as a single argument (time). Any function may be used.
f.mu	a function specifying the time-variation of the speciation rate μ . This function as a single argument (time). Any function may be used.
f	the fraction of extant species included in the phylogeny
cst.lamb	logical: should be set to TRUE only if f.lamb is constant (i.e. does not depend on time) to use analytical instead of numerical computation in order to reduce computation time.
cst.mu	logical: should be set to TRUE only if f.mu is constant (i.e. does not depend on time) to use analytical instead of numerical computation in order to reduce computation time.
expo.lamb	logical: should be set to TRUE only if f.lamb is exponential to use analytical instead of numerical computation in order to reduce computation time.
expo.mu	logical: should be set to TRUE only if f.mu is exponential to use analytical instead of numerical computation in order to reduce computation time.
dt	the default value is 0. In this case, integrals in the likelihood are computed using R "integrate" function, which can be quite slow. If a positive dt is given as argument, integrals are computed using a piece-wise constant approximation, and dt represents the length of the intervals on which functions are assumed to be constant. For an exponential dependency of the speciation rate with time, we found that <code>dt=1e-3</code> gives a good trade-off between precision and computation time.
cond	conditioning to use to fit the model: <ul style="list-style-type: none"> • FALSE: no conditioning (not recommended); • "stem": conditioning on the survival of the stem lineage (use when the stem age is known, in this case tot_time should be the stem age); • "crown" (default): conditioning on a speciation event at the crown age and survival of the 2 daughter lineages (use when the stem age is not known, in this case tot_time should be the crown age).

Details

When specifying f.lamb and f.mu, time runs from the present to the past (hence if the speciation rate decreases with time, f.lamb must be a positive function of time).

Value

the loglikelihood value of the phylogeny, given f.lamb and f.mu

Author(s)

H Morlon

References

Morlon, H., Parsons, T.L. and Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record *Proc Nat Acad Sci* 108: 16327-16332

Examples

```
data(Cetacea)
tot_time <- max(node.age(Cetacea)$ages)
# Compute the likelihood for a pure birth model (no extinction) with
# an exponential variation of speciation rate with time
lamb_par <- c(0.1, 0.01)
f.lamb <- function(t){lamb_par[1] * exp(lamb_par[2] * t)}
f.mu <- function(t){0}
f <- 87/89
lh <- likelihood_bd(Cetacea,tot_time,f.lamb,f.mu,f,cst.mu=TRUE,expo.lamb=TRUE, dt=1e-3)
```

likelihood_coal_cst *Likelihood of a phylogeny under the equilibrium diversity model*

Description

Computes the likelihood of a phylogeny under the equilibrium diversity model with potentially time-varying rates and potentially missing extant species. Notations follow Morlon et al. PloSB 2010.

Usage

```
likelihood_coal_cst(Vtimes, ntips, tau0, gamma, N0)
```

Arguments

Vtimes	a vector of branching times (sorted from present to past)
ntips	the number of tips in the phylogeny
tau0	the turnover rate at present
gamma	the parameter controlling the exponential variation in turnover rate. With gamma=0, the turnover rate is constant over time.
N0	the number of extant species

Details

Time runs from the present to the past. Hence, a positive gamma (for example) means that the turnover rate declines from past to present.

Value

a list containing the following components:

res	the loglikelihood value of the phylogeny, given tau0 and gamma
all	vector of all the individual loglikelihood values corresponding to each branching event

Author(s)

H Morlon

References

Morlon, H., Potts, M.D., Plotkin, J.B. (2010) Inferring the dynamics of diversification: a coalescent approach, PLoS B 8(9): e1000493

Examples

```
data(Cetacea)
Vtimes <- sort(branching.times(Cetacea))
tau0 <- 0.1
gamma <- 0.001
ntips <- Ntip(Cetacea)
N0 <- 89
likelihood <- likelihood_coal_cst(Vtimes,ntips,tau0,gamma,N0)
```

likelihood_coal_var *Likelihood of a birth-death model using a coalescent approach*

Description

Computes the likelihood of a phylogeny under the expanding diversity model with potentially time-varying rates and potentially missing extant species to a phylogeny. Notations follow Morlon et al. PloSB 2010.

Usage

```
likelihood_coal_var(Vtimes, ntips, lamb0, alpha, mu0, beta, N0, pos = TRUE)
```

Arguments

Vtimes	a vector of branching times (sorted from present to past)
ntips	number of species in the phylogeny
lamb0	the speciation rate at present
alpha	the parameter controlling the exponential variation in speciation rate.
mu0	the extinction rate at present

beta	the parameter controlling the exponential variation in extinction rate.
N0	the number of extant species
pos	logical: should be set to FALSE only to not enforce positive speciation and extinction rates

Details

Time runs from the present to the past. Hence, a positive alpha (for example) means that the speciation rate declines from past to present.

Value

a list containing the following components:

res	the loglikelihood value of the phylogeny, given the parameters
all	vector of all the individual loglikelihood values corresponding to each branching event

Author(s)

H Morlon

References

Morlon, H., Potts, M.D., Plotkin, J.B. (2010) Inferring the dynamics of diversification: a coalescent approach, PLoS B 8(9): e1000493

Examples

```
data(Cetacea)
Vtimes <- sort(branching.times(Cetacea))
lamb0 <- 0.1
alpha <- 0.001
mu0 <- 0
beta <- 0
ntips <- Ntip(Cetacea)
N0 <- 89
likelihood <- likelihood_coal_var(Vtimes, ntips, lamb0, alpha, mu0, beta, N0)
```

likelihood_sgd

Likelihood of a phylogeny under the SGD model

Description

Computes the likelihood of a phylogeny under the SGD model with exponential increasing of the metacommunity, and potentially missing extant species. Notations follow Manceau et al. (2015).

Usage

```
likelihood_sgd(phylo, tot_time, b, d, nu, f)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
tot_time	the age of the phylogeny (crown age, or stem age if known). If working with crown ages, tot_time is given by <code>max(node.age(phylo)\$ages)</code> .
b	the (constant) birth rate of individuals in the model.
d	the (constant) death rate of individuals in the model.
nu	the (constant) mutation rate of individuals in the model.
f	the fraction of extant species included in the phylogeny

Value

the likelihood value of the phylogeny, given the model and the parameter values b, d, nu.

Author(s)

M Manceau

References

Manceau M., Lambert A., Morlon H. (2015) Phylogenies support out-of-equilibrium models of biodiversity *Ecology Letters* 18: 347-356

Examples

```
data(Cetacea)
tot_time <- max(node.age(Cetacea)$ages)
b <- 1e6
d <- 1e6-0.5
nu <- 0.6
f <- 87/89
#lh <- likelihood_sgd(Cetacea, tot_time, b, d, nu, f)
```

```
likelihood_subgroup_model
```

Likelihood of a dataset under models with biogeography fit to a subgroup.

Description

Computes the likelihood of a dataset under either the linear or exponential diversity dependent model with specified `sigma2` and `slope` values and with a `geography` object formed using [CreateGeoObject](#).

Usage

```
likelihood_subgroup_model(data, phylo, geography.object, model=c("MC", "DDexp", "DDlin"),
  par, return.z0=FALSE, maxN=NULL)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation) produced as "map" from CreateGeobyClassObject. NB: the length of this object need not match number of items in data, since map may include tips outside of group with some part of their branch in the group
data	a named vector of continuous data for a subgroup of interest with names corresponding to phylo\$tip.label
geography.object	a list of sympatry/group membership through time created using CreateGeobyClassObject
model	model chosen to fit trait data. "DDlin" is the diversity-dependent linear model, and "DDexp" is the diversity-dependent exponential model of Weir & Mursleen 2013.
par	a vector listing a value for $\log(\text{sig}^2)$ (see Note) and either b (for the linear diversity dependent model) or r (for the exponential diversity dependent model), in that order.
return.z0	logical indicating whether to return an estimate of the trait value at the root given the parameter values (if TRUE, function returns root value rather than negative log-likelihood)
maxN	when fitting DDlin model, it is necessary to specify the maximum number of sympatric lineages to ensure that the rate returned does not correspond to negative sig^2 values at any point in time (see Details).

Details

When specifying par, $\log(\text{sig}^2)$ (see Note) must be listed before the slope parameter (b or r).

maxN can be calculated using `maxN=max(vapply(geo.object$geography.object, function(x)max(rowSums(x)), 1))`, where geo.object is the output of [CreateGeoObject](#)

Value

The negative log-likelihood value of the dataset (accordingly, the negative of the output should be recorded as the likelihood), given the phylogeny, sig^2 and slope values, and geography.object.

If return.z0=TRUE, the estimated root value for the par values is returned instead of the negative log-likelihood.

Note

To stabilize optimization, this function exponentiates the input sig^2 value, thus the user must input the $\log(\text{sig}^2)$ value to compute the correct log likelihood (see example).

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com

Julien Clavel

References

Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020

Weir, J. & Mursleen, S. 2012. Diversity-dependent cladogenesis and trait evolution in the adaptive radiation of the auks (Aves: Alcidae). *Evolution* 67:403-416.

See Also

[fit_t_comp](#) [CreateGeoObject](#) [likelihood_t_DD](#)

Examples

```
data(BGB.examples)

Canidae.phylo<-BGB.examples$Canidae.phylo
dummy.group<-c(rep("B",3),rep("A",12),rep("B",2),rep("A",6),rep("B",5),rep("A",6))
names(dummy.group)<-Canidae.phylo$tip.label

Canidae.simap<-phytools::make.simap(Canidae.phylo, dummy.group)

set.seed(123)
Canidae.data<-rnorm(length(Canidae.phylo$tip.label))
names(Canidae.data)<-Canidae.phylo$tip.label
Canidae.A<-Canidae.data[which(dummy.group=="A")]
Canidae.geobyclass.object<-CreateGeobyClassObject(phylo=Canidae.phylo,
simap=Canidae.simap, trim.class="A", ana.events=BGB.examples$Canidae.ana.events,
clado.events=BGB.examples$Canidae.clado.events,stratified=FALSE, rnd=5)

par <- c(log(0.01),-0.0005)
maxN<-max(vapply(Canidae.geobyclass.object$geography.object$geography.object,
function(x)max(rowSums(x)),1))

lh <- -likelihood_subgroup_model(data=Canidae.A, phylo=Canidae.geobyclass.object$map,
geo.object=Canidae.geobyclass.object$geography.object, model="DDlin", par=par,
return.z0=FALSE, maxN=maxN)
```

likelihood_t_DD	<i>Likelihood of a dataset under diversity-dependent models.</i>
-----------------	--

Description

Computes the likelihood of a dataset under either the linear or exponential diversity dependent model with specified σ^2 and slope values.

Usage

```
likelihood_t_DD(phylo, data, par,model=c("DDlin","DDexp"))
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
data	a named vector of continuous data with names corresponding to phylo\$tip.label
par	a vector listing a value for $\log(\sigma^2)$ (see Note) and either b (for the linear diversity dependent model) or r (for the exponential diversity dependent model), in that order.
model	model chosen to fit trait data, "DDlin" is the diversity-dependent linear model, and "DDexp" is the diversity-dependent exponential model of Weir & Mursleen 2013.

Details

When specifying par, $\log(\sigma^2)$ must be listed before the slope parameter (b or r).

Value

the negative log-likelihood value of the dataset (accordingly, the negative of the output should be recorded as the likelihood), given the phylogeny and σ^2 and slope values

Note

To stabilize optimization, this function exponentiates the input σ^2 value, thus the user must input the $\log(\sigma^2)$ value to compute the correct log likelihood (see example).

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com
Julien Clavel

References

Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020
Weir, J. & Mursleen, S. 2012. Diversity-dependent cladogenesis and trait evolution in the adaptive radiation of the auks (Aves: Alcidae). *Evolution* 67:403-416.

See Also

[fit_t_comp likelihood_t_DD_geog](#)

Examples

```
data(Anolis.data)
phylo <- Anolis.data$phylo
pPC1 <- Anolis.data$data

# Compute the likelihood that the r value is twice the ML estimate for the DDexp model
par <- c(0.08148371, (2*-0.3223835))
lh <- -likelihood_t_DD(phylo,pPC1,par,model="DDexp")
```

likelihood_t_DD_geog *Likelihood of a dataset under diversity-dependent models with biogeography.*

Description

Computes the likelihood of a dataset under either the linear or exponential diversity dependent model with specified `sigma2` and slope values and with a `geography` object formed using [CreateGeoObject](#).

Usage

```
likelihood_t_DD_geog(phylo, data, par, geo.object, model=c("DDlin", "DDexp"), maxN=NA)
```

Arguments

<code>phylo</code>	an object of type 'phylo' (see ape documentation)
<code>data</code>	a named vector of continuous data with names corresponding to <code>phylo\$tip.label</code>
<code>par</code>	a vector listing a value for $\log(\sigma^2)$ (see Note) and either <code>b</code> (for the linear diversity dependent model) or <code>r</code> (for the exponential diversity dependent model), in that order.
<code>geo.object</code>	a list of sympatry through time created using CreateGeoObject
<code>model</code>	model chosen to fit trait data, "DDlin" is the diversity-dependent linear model, and "DDexp" is the diversity-dependent exponential model of Weir & Mursleen 2013.
<code>maxN</code>	when fitting DDlin model, it is necessary to specify the maximum number of sympatric lineages to ensure that the rate returned does not correspond to negative σ^2 values at any point in time (see Details).

Details

When specifying `par`, $\log(\sigma^2)$ (see Note) must be listed before the slope parameter (`b` or `r`).

`maxN` can be calculated using `maxN=max(vapply(geo.object$geography.object,function(x)max(rowSums(x)),1))`, where `geo.object` is the output of [CreateGeoObject](#)

Value

the negative log-likelihood value of the dataset (accordingly, the negative of the output should be recorded as the likelihood), given the phylogeny, sig2 and slope values, and geography.object.

Note

To stabilize optimization, this function exponentiates the input sig2 value, thus the user must input the $\log(\text{sig}2)$ value to compute the correct log likelihood (see example).

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com

Julien Clavel

References

Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020

Weir, J. & Mursleen, S. 2012. Diversity-dependent cladogenesis and trait evolution in the adaptive radiation of the auks (Aves: Alcidae). *Evolution* 67:403-416.

See Also

[fit_t_comp](#) [CreateGeoObject](#) [likelihood_t_DD](#)

Examples

```
data(Anolis.data)
phylo <- Anolis.data$phylo
pPC1 <- Anolis.data$data
geography.object <- Anolis.data$geography.object

# Compute the likelihood with geography using ML parameters for fit without geography
par <- c(log(0.01153294), -0.0006692378)
maxN <- max(vapply(geography.object$geography.object, function(x) max(rowSums(x)), 1))
lh <- -likelihood_t_DD_geog(phylo, pPC1, par, geography.object, model="DDlin", maxN=maxN)
```

likelihood_t_env

Likelihood of a dataset under environmental models of trait evolution.

Description

Computes the likelihood of a dataset under either the linear or exponential environmental model, or an user defined environmental model. This function is used internally by fit_t_env.

Usage

```
likelihood_t_env(phylo, data, model=c("EnvExp", "EnvLin"), ...)
```

Arguments

phylo	an object of class 'phylo' (see ape documentation)
data	a named vector of continuous data with names corresponding to phylo\$tip.label
...	"param", "fun", "times", "mtot" and "error" arguments. -param: a vector with the parameters used in the environmental function. The first value is sig2 and the second is beta. -fun: a time continuous function of an environmental variable (see e.g. ?fit_t_env) -times: a vector of branching times starting at zero (e.g. max(branching.times(phylo))-branching.times(phylo)) -mtot: root age of the tree (e.g. max(branching.times(phylo))) -error: a vector of standard error (se) for each species If the "times" argument is not provided, the "phylo" object is used to compute it as well as "mtot". Note that the argument "mu" can be used to specify the root state (e.g. when using an mcmc sampler)
model	model chosen to fit trait data, "EnvExp" is the exponential-environmental model, and "EnvLin" is the linear-environmental model. Otherwise, an user specified model can be provided.

Details

the "fun" argument can be filled by an environmental dataframe.

Value

the log-likelihood value of the environmental model

Author(s)

Julien Clavel

References

Clavel, J. & Morlon, H., 2017. Accelerated body size evolution during cold climatic periods in the Cenozoic. *Proceedings of the National Academy of Science*, 114(16): 4183-4188.

See Also

[fit_t_env](#)

Examples

```
data(Cetacea)
data(InfTemp)

# Simulate a trait with temperature dependence on the Cetacean tree
set.seed(123)
```



```

trait <- sim_t_env(Cetacea, param=c(0.1,-0.2), env_data=InfTemp, model="EnvExp",
root.value=0, step=0.001, plot=TRUE)

# Compute the likelihood
likelihood_t_env(Cetacea, trait, param=c(0.1, 0), fun=InfTemp, model="EnvExp")

# Provide the times
brtime<-branching.times(Cetacea)
mtot<-max(brtime)
times<-mtot-brtime

likelihood_t_env(Cetacea,trait,param=c(0.1, 0), fun=InfTemp,
times=times, mtot=mtot, model="EnvExp")

# Provide the environmental function rather than the dataset (faster if used recursively)

spline_result <- sm.spline(InfTemp[,1],InfTemp[,2], df=50)
env_func <- function(t){predict(spline_result,t)}
t<-unique(InfTemp[,1])
# We build the interpolated smoothing spline function
env_data<-splinefun(t,env_func(t))

likelihood_t_env(Cetacea, trait, param=c(0.1, 0), fun=env_data,
times=times, mtot=mtot, model="EnvExp")

```

likelihood_t_MC

Likelihood of a dataset under the matching competition model.

Description

Computes the likelihood of a dataset under the matching competition model with specified σ^2 and S values.

Usage

```
likelihood_t_MC(phylo, data, par)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
data	a named vector of continuous data with names corresponding to phylo\$tip.label
par	a vector listing a value for $\log(\sigma^2)$ (see Note) and S (parameters of the matching competition model), in that order

Details

When specifying par, $\log(\sigma^2)$ must be listed before S .

Value

the negative log-likelihood value of the dataset (accordingly, the negative of the output should be recorded as the likelihood), given the phylogeny and sig2 and S values

Note

To stabilize optimization, this function exponentiates the input sig2 value, thus the user must input the $\log(\text{sig}2)$ value to compute the correct log likelihood (see example).

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com

Julien Clavel

References

Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020

Nuismer, S. & Harmon, L. 2015. Predicting rates of interspecific interaction from phylogenetic trees. *Ecology Letters* 18:17-27.

See Also

[fit_t_comp likelihood_t_MC_geog](#)

Examples

```
data(Anolis.data)
phylo <- Anolis.data$phylo
pPC1 <- Anolis.data$data

# Compute the likelihood that the S value is twice the ML estimate
par <- c(0.0003139751, (2*-0.06387258))
lh <- -likelihood_t_MC(phylo,pPC1,par)
```

likelihood_t_MC_geog *Likelihood of a dataset under the matching competition model with biogeography.*

Description

Computes the likelihood of a dataset under the matching competition model with specified sigma2 and S values and with a geography.object formed using [CreateGeoObject](#).

Usage

```
likelihood_t_MC_geog(phylo, data, par, geo.object)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
data	a named vector of continuous data with names corresponding to phylo\$tip.label
par	a vector listing a value for $\log(\text{sig}2)$ (see Note) and S (parameters of the matching competition model), in that order
geo.object	a geography object indicating sympatry through time, created using CreateGeoObject

Details

When specifying par, $\log(\text{sig}2)$ must be listed before S.

Value

the negative log-likelihood value of the dataset (accordingly, the negative of the output should be recorded as the likelihood), given the phylogeny, sig2 and S values, and geography.object.

Note

S must be negative (if it is positive, the likelihood function will multiply input by -1).

To stabilize optimization, this function exponentiates the input sig2 value, thus the user must input the $\log(\text{sig}2)$ value to compute the correct log likelihood (see example).

Author(s)

Jonathan Drury jonathan.p.drury@gmail.com

Julien Clavel

References

Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020

Nuismer, S. & Harmon, L. 2015. Predicting rates of interspecific interaction from phylogenetic trees. *Ecology Letters* 18:17-27.

See Also

[fit_t_comp](#) [CreateGeoObject](#) [likelihood_t_MC](#)

Examples

```
data(Anolis.data)
phylo <- Anolis.data$phylo
pPC1 <- Anolis.data$data
geography.object <- Anolis.data$geography.object

# Compute the likelihood with geography using ML parameters for fit without geography
par <- c(0.0003139751, -0.06387258)
lh <- -likelihood_t_MC_geog(phylo,pPC1,par,geography.object)
```

lines.fit_t.env *Add to a plot line segments joining the phenotypic evolutionary rate through time estimated by the fit_t_env function*

Description

Plot estimated evolutionary rate as a function of the environmental data and time.

Usage

```
## S3 method for class 'fit_t.env'
lines(x, steps = 100, ...)
```

Arguments

x an object of class 'fit_t.env' obtained from a *fit_t_env* fit.

steps the number of steps from the root to the present used to compute the evolutionary rate σ^2 through time.

... further arguments to be passed to plot. See ?plot.

Value

lines.fit_t.env returns invisibly a list with the following components used to add the line segments to the current plot:

time_steps the times steps where the climatic function was evaluated to compute the rate. The number of steps is controlled through the argument steps.

rates the estimated evolutionary rate through time estimated at each time_steps

Note

All the graphical parameters (see [par](#)) can be passed through (e.g. line type: lty, line width: lwd, color: col ...)

Author(s)

J. Clavel

References

Clavel, J. & Morlon, H., 2017. Accelerated body size evolution during cold climatic periods in the Cenozoic. *Proceedings of the National Academy of Science*, 114(16): 4183-4188.

See Also

[plot.fit_t.env](#), [likelihood_t_env](#)

Examples

```

data(Cetacea)
data(InfTemp)

# Plot estimated evolutionary rate as a function of the environmental data and time.
set.seed(123)
trait <- sim_t_env(Cetacea, param=c(0.1,-0.2), env_data=InfTemp, model="EnvExp",
root.value=0, step=0.01, plot=TRUE)

## Fit the Environmental-exponential model with different smoothing parameters

result1=fit_t_env(Cetacea, trait, env_data=InfTemp, scale=TRUE)
result2=fit_t_env(Cetacea, trait, env_data=InfTemp, scale=TRUE, df=10)

# first plot result1
plot(result1, lwd=3)

# add result2 to the current plot
lines(result2, lty=2, lwd=3, col="red")

```

modelSelection

Phenotypic model selection from tip trait data.

Description

For each model taken as input, fits the model and returns its AIC value in a recap table.

Usage

```
modelSelection(object, data)
```

Arguments

object	a vector of objects of class 'PhenotypicModel'.
data	vector of tip trait data.

Details

Warning : This function relies on the standard R optimizer "optim". It may not always converge well. Please double check the convergence by trying distinct parameter sets for the initialisation.

Value

A recap table presenting the AIC value of each model.

Author(s)

M Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*

modelSelection-methods

~~ *Methods for Function modelSelection* ~~

Description

~~ Methods for function modelSelection ~~

Methods

signature(object = "PhenotypicModel") This is the only method available for this function. Same behaviour for any PhenotypicModel.

MPhiFFT

A class used internally to compute ClaDS's likelihood

Description

This class represents a matrix $A = (1/\text{rowSums}(\text{Toep})) * \text{Toep}$ where Toep is a Toeplitz matrix.

References

Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0

See Also

[fit_ClaDS](#)

 ostracoda

Ostracod diversity since the Jurassic

Description

Ostracod fossil diversity since the Jurassic

Usage

```
data(sealevel)
```

Details

Ostracod fossil diversity since the Jurassic compiled from the Neptune Database (Lazarus, 1994) and Paleobiology Database (<https://paleobiodb.org/>). Diversity curves are estimated at the genus level using shareholder quorum subsampling (Alroy, 2010) at two-million-year bins. The format is a dataframe with the two following variables:

age a numeric vector corresponding to the geological age, in Myrs before the present

ostracoda a numeric vector corresponding to the estimated ostracod change at that age

References

Lazarus, D. (1994) Neptune: A marine micropaleontology database *Mathematical Geology* 26:817–832

Alroy, J. (2010) Geographical, environmental and intrinsic biotic controls on Phanerozoic marine diversification: Controls on phanerozoic marine diversification *Palaeontology* 53:1211–1235

Examples

```
data(ostracoda)
plot(ostracoda)
```

 PhenotypicACDC-class *Class "PhenotypicACDC"*

Description

Subclass of the PhenotypicModel class intended to represent the model of ACcelerating or DeCeLerating phenotypic evolution.

Objects from the Class

Objects can be created by calls of the form `new("PhenotypicACDC", ...)`.

Slots

matrixCoalescenceTimes: Object of class "matrix" ~~
name: Object of class "character" ~~
period: Object of class "numeric" ~~
aAGamma: Object of class "function" ~~
numbersCopy: Object of class "numeric" ~~
numbersPaste: Object of class "numeric" ~~
initialCondition: Object of class "function" ~~
paramsNames: Object of class "character" ~~
constraints: Object of class "function" ~~
params0: Object of class "numeric" ~~
tipLabels: Object of class "character" ~~
tipLabelsSimu: Object of class "character" ~~
comment: Object of class "character" ~~

Extends

Class "[PhenotypicModel](#)", directly.

Methods

getTipDistribution signature(object = "PhenotypicACDC"): ...

Author(s)

Marc Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages Systematic Biology, and the associated Supplementary material.

Examples

```
showClass("PhenotypicACDC")
```

PhenotypicADiag-class *Class* "PhenotypicADiag"

Description

A subclass of the PhenotypicModel class, intended to represent models of phenotypic evolution with a "A" matrix diagonalizable.

Objects from the Class

Objects can be created by calls of the form `new("PhenotypicADiag", ...)`.

Slots

name: Object of class "character" ~~
period: Object of class "numeric" ~~
aAGamma: Object of class "function" ~~
numbersCopy: Object of class "numeric" ~~
numbersPaste: Object of class "numeric" ~~
initialCondition: Object of class "function" ~~
paramsNames: Object of class "character" ~~
constraints: Object of class "function" ~~
params0: Object of class "numeric" ~~
tipLabels: Object of class "character" ~~
tipLabelsSimu: Object of class "character" ~~
comment: Object of class "character" ~~

Extends

Class "[PhenotypicModel](#)", directly.

Methods

getTipDistribution signature(object = "PhenotypicADiag"): ...

Author(s)

Marc Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages Systematic Biology, and the associated Supplementary material.

Examples

```
showClass("PhenotypicADiag")
```

```
PhenotypicBM-class    Class "PhenotypicBM"
```

Description

A subclass of the PhenotypicModel class, intended to represent the model of Brownian phenotypic evolution.

Objects from the Class

Objects can be created by calls of the form `new("PhenotypicBM", ...)`.

Slots

```
matrixCoalescenceTimes: Object of class "matrix" ~~
name: Object of class "character" ~~
period: Object of class "numeric" ~~
aAGamma: Object of class "function" ~~
numbersCopy: Object of class "numeric" ~~
numbersPaste: Object of class "numeric" ~~
initialCondition: Object of class "function" ~~
paramsNames: Object of class "character" ~~
constraints: Object of class "function" ~~
params0: Object of class "numeric" ~~
tipLabels: Object of class "character" ~~
tipLabelsSimu: Object of class "character" ~~
comment: Object of class "character" ~~
```

Extends

Class "[PhenotypicModel](#)", directly.

Methods

```
getTipDistribution signature(object = "PhenotypicBM"): ...
```

Author(s)

Marc Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*, and the associated Supplementary material.

Examples

```
showClass("PhenotypicBM")
```

```
PhenotypicDD-class    Class "PhenotypicDD"
```

Description

A subclass of the PhenotypicModel class, intended to represent the model of Density-Dependent phenotypic evolution.

Objects from the Class

Objects can be created by calls of the form `new("PhenotypicDD", ...)`.

Slots

```
matrixCoalescenceJ: Object of class "matrix" ~~
nLivingLineages: Object of class "numeric" ~~
name: Object of class "character" ~~
period: Object of class "numeric" ~~
aAGamma: Object of class "function" ~~
numbersCopy: Object of class "numeric" ~~
numbersPaste: Object of class "numeric" ~~
initialCondition: Object of class "function" ~~
paramsNames: Object of class "character" ~~
constraints: Object of class "function" ~~
params0: Object of class "numeric" ~~
tipLabels: Object of class "character" ~~
tipLabelsSimu: Object of class "character" ~~
comment: Object of class "character" ~~
```

Extends

Class "[PhenotypicModel](#)", directly.

Methods

getTipDistribution signature(object = "PhenotypicDD"): ...

Author(s)

Marc Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*, and the associated Supplementary material.

Examples

```
showClass("PhenotypicDD")
```

```
PhenotypicGMM-class  Class "PhenotypicGMM"
```

Description

A subclass of the PhenotypicModel class, intended to represent the Generalist Matching Mutualism model of phenotypic evolution. This is a model of phenotypic evolution with interactions between two clades, running on two trees.

Objects from the Class

Objects can be created by calls of the form `new("PhenotypicGMM", ...)`.

Slots

```
n1: Object of class "numeric" ~~
n2: Object of class "numeric" ~~
name: Object of class "character" ~~
period: Object of class "numeric" ~~
aAGamma: Object of class "function" ~~
numbersCopy: Object of class "numeric" ~~
numbersPaste: Object of class "numeric" ~~
initialCondition: Object of class "function" ~~
paramsNames: Object of class "character" ~~
constraints: Object of class "function" ~~
params0: Object of class "numeric" ~~
tipLabels: Object of class "character" ~~
tipLabelsSimu: Object of class "character" ~~
comment: Object of class "character" ~~
```

Extends

Class "[PhenotypicModel](#)", directly.

Methods

getTipDistribution signature(object = "PhenotypicGMM"): ...

Author(s)

Marc Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*, and the associated Supplementary material.

Examples

```
showClass("PhenotypicGMM")
```

PhenotypicModel-class *Class* "PhenotypicModel"

Description

This class describes a model of phenotypic evolution running on a phylogenetic tree, with or without interactions between lineages.

Objects from the Class

Objects can be created by calls of the form `new("PhenotypicModel", ...)`. Alternatively, you may just want to use the "createModel" function for predefined models.

Slots

```
name: Object of class "character" ~~
period: Object of class "numeric" ~~
aAGamma: Object of class "function" ~~
numbersCopy: Object of class "numeric" ~~
numbersPaste: Object of class "numeric" ~~
initialCondition: Object of class "function" ~~
paramsNames: Object of class "character" ~~
constraints: Object of class "function" ~~
params0: Object of class "numeric" ~~
```

tipLabels: Object of class "character" ~~
 tipLabelsSimu: Object of class "character" ~~
 comment: Object of class "character" ~~

Methods

[<- signature(x = "PhenotypicModel", i = "ANY", j = "ANY", value = "ANY"): ...
 [signature(x = "PhenotypicModel", i = "ANY", j = "ANY", drop = "ANY"): ...
fitTipData signature(object = "PhenotypicModel"): ...
getDataLikelihood signature(object = "PhenotypicModel"): ...
getTipDistribution signature(object = "PhenotypicModel"): ...
modelSelection signature(object = "PhenotypicModel"): ...
print signature(x = "PhenotypicModel"): ...
show signature(object = "PhenotypicModel"): ...
simulateTipData signature(object = "PhenotypicModel"): ...

Author(s)

Marc Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*, and the associated Supplementary material.

Examples

```
showClass("PhenotypicModel")
```

PhenotypicOU-class *Class "PhenotypicOU"*

Description

A subclass of the PhenotypicModel class, intended to represent the Ornstein-Uhlenbeck model of phenotypic evolution.

Objects from the Class

Objects can be created by calls of the form `new("PhenotypicOU", ...)`.

Slots

matrixCoalescenceTimes: Object of class "matrix" ~~
name: Object of class "character" ~~
period: Object of class "numeric" ~~
aAGamma: Object of class "function" ~~
numbersCopy: Object of class "numeric" ~~
numbersPaste: Object of class "numeric" ~~
initialCondition: Object of class "function" ~~
paramsNames: Object of class "character" ~~
constraints: Object of class "function" ~~
params0: Object of class "numeric" ~~
tipLabels: Object of class "character" ~~
tipLabelsSimu: Object of class "character" ~~
comment: Object of class "character" ~~

Extends

Class "[PhenotypicModel](#)", directly.

Methods

getTipDistribution signature(object = "PhenotypicOU"): ...

Author(s)

Marc Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages Systematic Biology, and the associated Supplementary material.

Examples

```
showClass("PhenotypicOU")
```

PhenotypicPM-class *Class "PhenotypicPM"*

Description

A subclass of the PhenotypicModel class, intended to represent the Phenotypic Matching model of phenotypic evolution, by Nuismer and Harmon (Eco Lett, 2014).

Objects from the Class

Objects can be created by calls of the form `new("PhenotypicPM", ...)`.

Slots

name: Object of class "character" ~~
 period: Object of class "numeric" ~~
 aAGamma: Object of class "function" ~~
 numbersCopy: Object of class "numeric" ~~
 numbersPaste: Object of class "numeric" ~~
 initialCondition: Object of class "function" ~~
 paramsNames: Object of class "character" ~~
 constraints: Object of class "function" ~~
 params0: Object of class "numeric" ~~
 tipLabels: Object of class "character" ~~
 tipLabelsSimu: Object of class "character" ~~
 comment: Object of class "character" ~~

Extends

Class "[PhenotypicModel](#)", directly.

Methods

getTipDistribution signature(object = "PhenotypicPM"): ...

Author(s)

Marc Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages Systematic Biology, and the associated Supplementary material.

Examples

```
showClass("PhenotypicPM")
```

Phocoenidae	<i>Phocoenidae phylogeny</i>
-------------	------------------------------

Description

Ultrametric phylogenetic tree of the 6 extant Phocoenidae (porpoise) species

Usage

```
data(Phocoenidae)
```

Details

This phylogeny was extracted from Steeman et al. Syst Bio 2009 cetacean phylogeny

References

Steeman ME et al.(2009) Radiation of extant cetaceans driven by restructuring of the oceans *Syst Biol* 58:573-585

Morlon, H., Parsons, T.L., Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record *Proc Nat Acad Sci* 108: 16327-16332

Examples

```
data(Phocoenidae)  
print(Phocoenidae)  
plot(Phocoenidae)
```

phyl.pca_pl	<i>Regularized Phylogenetic Principal Component Analysis (PCA).</i>
-------------	---

Description

Performs a principal component analysis (PCA) on a regularized evolutionary variance-covariance matrix obtained using the `fit_t_pl` function.

Usage

```
phyl.pca_pl(object, plot=TRUE, ...)
```

Arguments

object	A penalized likelihood model fit obtained by the <code>fit_t_pl</code> function.
plot	Plot of the PC's axes. Default is TRUE (see details).'
...	Options to be passed through. (e.g., <code>axes=c(1,2)</code> , <code>col</code> , <code>pch</code> , <code>cex</code> , <code>mode="cov"</code> or <code>"corr"</code> , etc.)

Details

`phyl.pca_pl` allows computing a phylogenetic principal component analysis (following Revell 2009) using a regularized evolutionary variance-covariance matrix from penalized likelihood models fit to high-dimensional datasets (where the number of variables p is potentially larger than n ; see details for the models options in `fit_t_pl`). Models estimates are more accurate than maximum likelihood methods, particularly in the high-dimensional case. Plotting options, the number of axes to display (`axes=c(1, 2)` is the default), and whether the covariance (`mode="cov"`) or correlation (`mode="corr"`) should be used can be specified through the ellipsis `"..."` argument.

Value

a list with the following components

values	the eigenvalues of the evolutionary variance-covariance matrix
scores	the PC scores
loadings	the component loadings
nodes_scores	the scores for the ancestral states at the nodes (projected on the space of the tips)
mean	the mean/ancestral value used to center the data
vectors	the eigenvectors of the evolutionary variance-covariance matrix

Note

Contrary to conventional PCA, the principal axes of the phylogenetic PCA are not orthogonal, they represent the main axes of (independent) evolutionary changes.

Author(s)

J. Clavel

References

- Revell, L.J., 2009. Size-correction and principal components for intraspecific comparative studies. *Evolution*, 63:3258-3268.
- Clavel, J., Aristide, L., Morlon, H., 2019. A Penalized Likelihood framework for high-dimensional phylogenetic comparative methods and an application to new-world monkeys brain evolution. *Syst. Biol.* 68: 93-116.

See Also

[fit_t_pl](#), [ancestral](#), [GIC.fit_pl.rpanda](#), [gic_criterion](#)

Examples

```
require(mvMORPH)
set.seed(1)
n <- 32 # number of species
p <- 31 # number of traits

tree <- pbtree(n=n) # phylogenetic tree
R <- Posdef(p)      # a random symmetric matrix (covariance)

# simulate a dataset
Y <- mvSIM(tree, model="BM1", nsim=1, param=list(sigma=R))

# fit a multivariate Pagel lambda model with Penalized likelihood
fit <- fit_t_pl(Y, tree, model="lambda", method="RidgeAlt")

# Perform a phylogenetic PCA using the model fit (Pagel lambda model)
pca_results <- phyl.pca_pl(fit, plot=T)

# retrieve the scores
head(pca_results$scores)
```

Phyllostomidae

Phyllostomidae phylogeny

Description

Ultrametric phylogenetic tree of 150 of the 165 extant known Phyllostomidae species

Usage

```
data(Phyllostomidae)
```

Details

This phylogeny is the maximum clade credibility tree used in Rolland et al. (2014), which originally comes from the Bininda-Emonds tree (Bininda-Emonds et al. 2007)

References

Bininda-Emonds, O. R., et al. (2007) The delayed rise of present-day mammals *Nature* 446: 507-512

Rolland, J., Condamine, F. L., Jiguet, F., & Morlon, H. (2014) Faster speciation and reduced extinction in the tropics contribute to the mammalian latitudinal diversity gradient. *PLoS Biol*, 12(1): e1001775.

See Also

[Phyllostomidae_genera](#)

Examples

```
data(Phyllostomidae)
print(Phyllostomidae)
#plot(Phyllostomidae)
```

Phyllostomidae_genera *Phylogenies of Phyllostomidae genera*

Description

List of 25 ultrametric phylogenetic trees corresponding to 25 Phyllostomidae genera

Usage

```
data(Phyllostomidae_genera)
```

See Also

[Phyllostomidae](#)

Examples

```
data(Phyllostomidae_genera)
print(Phyllostomidae_genera)
```

plot.fit_t.env *Plot the phenotypic evolutionary rate through time estimated by the fit_t_env function*

Description

Plot estimated evolutionary rate as a function of the environmental data and time.

Usage

```
## S3 method for class 'fit_t.env'
plot(x, steps = 100, ...)
```

Arguments

x	an object of class 'fit_t.env' obtained from a <i>fit_t_env</i> fit.
steps	the number of steps from the root to the present used to compute the evolutionary rate σ^2 through time.
...	further arguments to be passed to plot. See ?plot.

Value

plot.fit_t.env returns invisibly a list with the following components used in the current plot:

time_steps	the times steps where the climatic function was evaluated to compute the rate. The number of steps is controlled through the argument steps.
rates	the estimated evolutionary rate through time estimated at each time_steps

Note

All the graphical parameters (see [par](#)) can be passed through (e.g. line type: lty, line width: lwd, color: col ...)

Author(s)

J. Clavel

References

Clavel, J. & Morlon, H., 2017. Accelerated body size evolution during cold climatic periods in the Cenozoic. *Proceedings of the National Academy of Science*, 114(16): 4183-4188.

See Also

[lines.fit_t.env](#), [likelihood_t_env](#)

Examples

```
data(Cetacea)
data(InfTemp)

# Simulate a trait with temperature dependence on the Cetacean tree
set.seed(123)

trait <- sim_t_env(Cetacea, param=c(0.1,0.2), env_data=InfTemp, model="EnvExp",
root.value=0, step=0.01, plot=TRUE)

## Fit the Environmental-exponential model

result1=fit_t_env(Cetacea, trait, env_data=InfTemp, scale=TRUE)
plot(result1)
```

```
# further options  
plot(result1, lty=2, lwd=2, col="red")
```

plot_BICompare	<i>Display modalities on a phylogeny.</i>
----------------	---

Description

Plot a phylogeny with branches colored according to modalities

Usage

```
plot_BICompare(phylo,BICompare)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
BICompare	an object of class 'BICompare', output of the 'BICompare' function

Value

a plot of the phylogeny with branches colored according to which modalities they belong to.

Author(s)

E Lewitus

References

Lewitus, E., Morlon, H., Characterizing and comparing phylogenies from their Laplacian spectrum, bioRxiv doi: <http://dx.doi.org/10.1101/026476>

See Also

[BICompare](#)

Examples

```
data(Cetacea)  
#result <- BICompare(Cetacea,5)  
#plot_BICompare(Cetacea,result)
```

plot_ClaDS0_chains *Plot the MCMC chains obtained when inferring ClaDS0 parameters*

Description

Plot the MCMC chains obtained with run_ClaDS0.

Usage

```
plot_ClaDS0_chains(sampler, burn = 1/2, thin = 1,  
                  param = c("sigma", "alpha", "l_0", "LP"))
```

Arguments

sampler	The output of a run_ClaDS0 run.
burn	Number of iterations to drop in the beginning of the chains.
thin	Thinning parameter, one iteration out of "thin" is plotted.
param	Either a vector of "character" elements with the name of the parameter to plot, or a vector of integers indicating what parameters to plot.

Author(s)

O. Maliet

References

Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0

See Also

[fit_ClaDS0](#), [getMAPS_ClaDS0](#), [plot_ClaDS_chains](#)

Examples

```
data("ClaDS0_example")  
  
plot_ClaDS0_chains(ClaDS0_example$Cl0_chains)  
plot_ClaDS0_chains(ClaDS0_example$Cl0_chains, param = paste0("lambda_", c(1,10,5)))
```

plot_ClaDS_chains *Plot the MCMC chains obtained when inferring ClaDS parameters*

Description

Plot the MCMC chains obtained with fit_ClaDS.

Usage

```
plot_ClaDS_chains(sampler, burn = 1/2, thin = 1,
                  param = c("sigma", "alpha", "mu", "LP"))
```

Arguments

sampler	The output of a fit_ClaDS run.
burn	Number of iterations to drop in the beginning of the chains.
thin	Thinning parameter, one iteration out of "thin" is plotted.
param	Either a vector of "character" elements with the name of the parameter to plot, or a vector of integers indicating what parameters to plot.

Author(s)

O. Maliet

References

Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0

See Also

[fit_ClaDS](#), [getMAPS_ClaDS](#), [plot_ClaDS0_chains](#)

Examples

```
data("Caprimulgidae_ClaDS2")

plot_ClaDS_chains(Caprimulgidae_ClaDS2$sampler)

plot_ClaDS_chains(Caprimulgidae_ClaDS2$sampler, burn = 1/4,
                  param = c("sigma", "alpha", "l_0", "LP"))

plot_ClaDS_chains(Caprimulgidae_ClaDS2$sampler, burn = 1/5, thin = 5, param = c(1,5,6,15))
```

plot_ClaDS_phylo *Plot a phylogeny with branch-specific values*

Description

Plot a phylogeny with branches colored according to branch-specific rate values

Usage

```
plot_ClaDS_phylo(phylo, rates, rates2 = NULL,  
                 same.scale = T, main = NULL, lwd = 2, log = T, show.tip.label = F, ...)
```

Arguments

phylo	An object of class 'phylo'.
rates	A vector containing the branch-specific rates, in the same order as phylo\$edges.
rates2	An optional second vector containing the branch-specific rates, in the same order as phylo\$edges. If NULL (the default), the tree is only plotted once with the rate values from rates. If not, the tree is plotted twice, with the rate values from rates in the left panel and those from rates2 in the right panel.
same.scale	A boolean specifying whether the values from rates and rates2 are plotted with the same colorscale. Default to TRUE.
main	A title for the plot.
lwd	Width of the tree branch lengths. Default to 2.
log	A boolean specifying whether the rates values are plotted on a log scale. Default to TRUE.
show.tip.label	A boolean specifying whether the labels of the phylogeny should be displayed. Default to FALSE.
...	Optional arguments for plot.phylo.

Author(s)

O. Maliet

References

Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0

See Also

[sim_ClaDS](#)

Examples

```

set.seed(1)

obj= sim_ClaDS( lambda_0=0.1,
                mu_0=0.5,
                sigma_lamb=0.7,
                alpha_lamb=0.90,
                condition="taxa",
                taxa_stop = 20,
                prune_extinct = TRUE)

tree = obj$tree
speciation_rates = obj$lamb[obj$rates]
extinction_rates = obj$mu[obj$rates]

plot_ClaDS_phylo(tree,speciation_rates)

plot_ClaDS_phylo(tree,speciation_rates, lwd = 4, log = FALSE)

```

plot_dtt

Plot diversity through time

Description

Plot the estimated number of species through time

Usage

```
plot_dtt(fit.bd, tot_time, N0)
```

Arguments

fit.bd	an object of class 'fit.bd', output of the 'fit_bd' function
tot_time	the age of the underlying phylogeny (crown age, or stem age if known). If working with crown ages, tot_time is given by <code>max(node.age(phylo)\$ages)</code> .
N0	number of extant species. If all extant species are represented in the phylogeny, N0 is given by <code>length(phylo\$tip.label)</code>

Value

Plot representing how the estimated number of species vary through time

Author(s)

H Morlon

References

- Morlon, H., Parsons, T.L. and Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record *Proc Nat Acad Sci* 108: 16327-16332
- Morlon, H. (2014) Phylogenetic approaches for studying diversification, *Eco Lett* 17:508-525

See Also

[fit_bd](#)

Examples

```
data(Balaenopteridae)
tot_time<-max(node.age(Balaenopteridae)$ages)

# Fit the pure birth model (no extinction) with exponential variation of the speciation rate
# with time
f.lamb <-function(t,y){y[1] * exp(y[2] * t)}
f.mu<-function(t,y){0}
lamb_par<-c(0.08, 0.01)
mu_par<-c()
result <- fit_bd(Balaenopteridae,tot_time,f.lamb,f.mu,lamb_par,mu_par,f=1,
                 expo.lamb = TRUE, fix.mu=TRUE)

# plot estimated number of species through time
# plot_dtt(result, tot_time, N0=9)
```

plot_fit_bd	<i>Plot speciation, extinction & net diversification rate functions of a fitted model</i>
-------------	---

Description

Plot estimated speciation, extinction & net diversification rates through time

Usage

```
plot_fit_bd(fit.bd, tot_time)
```

Arguments

fit.bd	an object of class 'fit.bd', output of the 'fit_bd' function
tot_time	the age of the phylogeny (crown age, or stem age if known). If working with crown ages, tot_time is given by max(node.age(phylo)\$ages).

Value

Plots representing how the estimated speciation, extinction & net diversification rate functions vary through time

Author(s)

H Morlon

See Also[fit_bd](#)**Examples**

```

data(Balaenopteridae)
tot_time<-max(node.age(Balaenopteridae)$ages)

# Fit the pure birth model (no extinction) with exponential variation of the speciation rate
# with time
f.lamb <-function(t,y){y[1] * exp(y[2] * t)}
f.mu<-function(t,y){0}
lamb_par<-c(0.08, 0.01)
mu_par<-c()
result <- fit_bd(Balaenopteridae,tot_time,f.lamb,f.mu,lamb_par,mu_par,
                 expo.lamb = TRUE, fix.mu=TRUE)

# plot fitted rates
#plot_fit_bd(result, tot_time)

```

plot_fit_env

Plot speciation, extinction & net diversification rate functions of a fitted environmental model

Description

Plot estimated speciation, extinction & net diversification rates as a function of the environmental data and time

Usage

```
plot_fit_env(fit.env, env_data, tot_time)
```

Arguments

fit.env	an object of class 'fit.env', output of the 'fit_env' function
env_data	environmental data, given as a data frame with two columns. The first column is time, the second column is the environmental data (temperature for instance).
tot_time	the age of the phylogeny (crown age, or stem age if known). If working with crown ages, tot_time is given by max(node.age(phylo)\$ages).

Value

Plots representing how the estimated speciation, extinction & net diversification rate functions vary as a function of the environmental data & time

Author(s)

H Morlon and FL Condamine

See Also[fit_env](#)**Examples**

```

data(Balaenopteridae)
tot_time<-max(node.age(Balaenopteridae)$ages)
data(InfTemp)
dof<-smooth.spline(InfTemp[,1], InfTemp[,2])$df

# Fit the pure birth model (no extinction) with exponential variation of the speciation rate
# with time
f.lamb <-function(t,x,y){y[1] * exp(y[2] * x)}
f.mu<-function(t,x,y){0}
lamb_par<-c(0.10, 0.01)
mu_par<-c()
#result <- fit_env(Balaenopteridae,InfTemp,tot_time,f.lamb,f.mu,
#      lamb_par,mu_par,f=1, fix.mu=TRUE, df=dof, dt=1e-3)

# plot fitted rates
#plot_fit_env(result, InfTemp, tot_time)

```

plot_prob_dtt

*Plot diversity through time with confidence intervals.***Description**

Plots confidence intervals of the estimated number of species through time using a matrix of probabilities given by the function 'prob_dtt'.

Usage

```

plot_prob_dtt(mat, grain = 0.1, plot.prob = TRUE,
              plot.mean = TRUE, int = TRUE, plot.bound=FALSE,
              conf = 0.95, add = FALSE, col.mean = "red", col.bound = "blue",
              lty="solid", lwd=1)

```

Arguments

mat matrix of probabilities, with species numbers as rows and times as columns with rownames and colnames set to the values of each.

grain the upper limit of a range of probabilities plotted in a gray scale (lower limit is zero). Higher probabilities are plotted in black. Default value is 0.1.

<code>plot.prob</code>	logical: set to TRUE (default value) to plot the probabilities.
<code>plot.mean</code>	logical: set to TRUE (default value) to plot a line for the mean.
<code>plot.bound</code>	logical: set to TRUE to plot the bounds of the confidence interval, <code>int</code> must be set to TRUE.
<code>int</code>	logical: set to TRUE (default value) to plot a confidence interval.
<code>conf</code>	confidence level. The default value is 0.95.
<code>add</code>	logical: set to TRUE to add the plot on an existing graph.
<code>col.mean</code>	color of the line for the mean.
<code>col.bound</code>	color of the confidence interval bounds
<code>lty</code>	style of the line for the mean (if added on a current plot)
<code>lwd</code>	the line width, a positive number (default to 1)

Details

The function assumes that the matrix of probabilities 'mat' has species numbers as rows and times as columns with rownames and colnames set to the values of each.

'Grain' must be between 0 and 1. If the plot is too pale 'grain' should be diminished (and inversely if the plot is too dark)

Value

Plot representing how the estimated number of species vary through time with confidence intervals. The darker is the plot, the higher is the probability.

Author(s)

O.Billaud, T.L.Parsons, D.S.Moen, H.Morlon

References

Morlon, H., Parsons, T.L. and Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record. *Proc. Nat. Acad. Sci.* 108: 16327-16332.

Billaud, O., Moen, D. S., Parsons, T. L., Morlon, H. (under review) Estimating Diversity Through Time using Molecular Phylogenies: Old and Species-Poor Frog Families are the Remnants of a Diverse Past.

See Also

[fit_bd](#), [plot_dtt](#), [prob_dtt](#)

Examples

```
data(Balaenopteridae)
tot_time<-max(node.age(Balaenopteridae)$ages)

# Fit the pure birth model (no extinction) with exponential variation of the speciation rate
# with time
```

```
f.lamb <-function(t,y){y[1] * exp(y[2] * t)}
f.mu<-function(t,y){0}
lamb_par<-c(0.08, 0.01)
mu_par<-c()
result <- fit_bd(Balaenopteridae,tot_time,f.lamb,f.mu,lamb_par,mu_par,f=1,
                 expo.lamb = TRUE, fix.mu=TRUE)

# Compute the matrix of probabilities
prob <- prob_dtt(result, tot_time, 1:tot_time, N0=9, type="crown")

# Check that the sums of probabilities are equal to 1
colSums(prob)

# Plot Diversity through time
plot_prob_dtt(prob)
```

plot_spectR

Spectral density plot of a phylogeny.

Description

Plot the spectral density of a phylogeny and all eigenvalues ranked in descending order.

Usage

```
plot_spectR(spectR)
```

Arguments

spectR an object of class 'spectR', output of the 'spectR' function

Value

A 2-panel plot with the spectral density profile on the first panel and the eigenvalues ranked in descending order on the second panel

Author(s)

E Lewitus

References

Lewitus, E., Morlon, H., Characterizing and comparing phylogenies from their Laplacian spectrum, bioRxiv doi: <http://dx.doi.org/10.1101/026476>

See Also

[spectR](#)

Examples

```
data(Cetacea)
result <- spectR(Cetacea)
#plot_spectR(result)
```

Posdef

Positive definite symmetric matrices

Description

Generates a positive definite and symmetric matrix with specified eigen-values

Usage

```
Posdef(p, ev = rexp(p, 1/100))
```

Arguments

p	The dimension of the matrix
ev	The eigenvalues. If not specified, eigenvalues are taken from an exponential distribution.

Details

Posdef generates random positive definite covariance matrices with specified eigen-values that can be used to simulate multivariate datasets (see Uyeda et al. 2015 - and supplied R codes).

Value

Returns a symmetric positive-definite matrix with eigen-values = ev.

Author(s)

J. Clavel

References

Uyeda J.C., Caetano D.S., Pennell M.W. 2015. Comparative Analysis of Principal Components Can be Misleading. *Syst. Biol.* 64:677-689.

Clavel, J., Aristide, L., Morlon, H., 2019. A Penalized Likelihood framework for high-dimensional phylogenetic comparative methods and an application to new-world monkeys brain evolution. *Syst. Biol.* 68:93-116.

See Also

[GIC.fit_pl.rpanda](#), [fit_t_pl.phyl.pca_pl](#)

Examples

```
require(mvMORPH)
set.seed(123)
n <- 32 # number of species
p <- 40 # number of traits

tree <- pbtree(n=n) # phylogenetic tree
R <- Posdef(p) # a random symmetric matrix (covariance)
# simulate a dataset
Y <- mvSIM(tree, model="BM1", nsim=1, param=list(sigma=R))

test <- fit_t_pl(Y, tree, model="BM", method="RidgeAlt")
GIC(test)
```

 prob_dtt

Confidence intervals of diversity through time

Description

Returns a matrix of probabilities to have 'm' species at a given time 't' with 'n' observed extant species (complete sampling or not) and 's' species at the root of the phylogeny (s=1 if the tree has a stem, otherwise s=2)

Usage

```
prob_dtt(fit.bd, tot_time, time, N0, l=N0, f = 1/N0,
         m = seq(N0), method="simple", lin = FALSE,
         prec = 1000, type = "stem", logged = TRUE)
```

Arguments

fit.bd	an object of class 'fit.bd', output of the 'fit_bd' function.
tot_time	the age of the underlying phylogeny (crown age, or stem age if known). If working with crown ages, tot_time is given by max(node.age(phylo)\$ages).
time	vector of times on which the function calculates the probabilities of 'm' species. The function goes forward in time, so that $t = 0$ is the time of the most recent common ancestor.
N0	number of extant species. If all extant species are represented in the phylogeny, N0 is given by length(phylo\$tip.label).
l	number of extant species sampled. Default value is N0 (complete sampling).

f	the fraction of extant species included in the phylogeny, given by $1/N_0$.
m	a vector of integers for which we want to know the probability of each value.
method	reflects which way of computing is chosen. A 'simple' one (quicker) is used when the number of extant species (N_0) is known exactly or when the whole phylogeny is sampled ($f=1$). A 'hard one', much longer, is used when N_0 is not known without doubt and $f < 1$. The default value is "simple" (the other possibility is "hard")
lin	logical: set to TRUE if λ & μ are fitted with a linear model.
prec	precision (number of bits used) of the computation. The default value is 1000.
type	reflects whether the clade has a stem or not. Options are the default "stem" and the alternative "crown", which means the tree starts with two species at time 0.
logged	logical: set to TRUE to log probabilities and factorials as much as possible (required, except perhaps for very small, young clades).

Details

If the sampling fraction is not equal to 1, the function computes with very high numbers. To be sufficiently accurate, the package 'Rmpfr' is used and "prec" is the precision of the computation. Hence, the calculation may take a lot of time. In case of wrong probabilities (negatives or higher than 1 for instance) you should increase the precision.

If the sampling fraction is equal to 1, the function doesn't need the package 'Rmpfr' and simply uses the log of probabilities and factorials (argument "logged"). Thus, computation is faster.

The matrix columns names go backward in time.

Value

Matrix of probabilities to have 'm' species at a given time 't' with 'n' observed extant species (complete sampling or not).

Author(s)

O.Billaud, T.L.Parsons, D.S.Moen, H.Morlon

References

Morlon, H., Parsons, T.L. and Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record. Proc. Nat. Acad. Sci. 108: 16327-16332.

Billaud, O., Moen, D. S., Parsons, T. L., Morlon, H. (under review) Estimating Diversity Through Time using Molecular Phylogenies: Old and Species-Poor Frog Families are the Remnants of a Diverse Past.

See Also

[fit_bd](#), [plot_dtt](#), [plot_prob_dtt](#)

Examples

```

data(Balaenopteridae)
tot_time<-max(node.age(Balaenopteridae)$ages)

# Fit the pure birth model (no extinction) with exponential variation of the speciation rate
# with time
f.lamb <-function(t,y){y[1] * exp(y[2] * t)}
f.mu<-function(t,y){0}
lamb_par<-c(0.08, 0.01)
mu_par<-c()
result <- fit_bd(Balaenopteridae,tot_time,f.lamb,f.mu,lamb_par,mu_par,f=1,
                 expo.lamb = TRUE, fix.mu=TRUE)

# Compute the matrix of probabilities
prob <- prob_dtt(result, tot_time, 1:tot_time, N0=9, type="crown")

# Check that the sums of probabilities are equal to 1
colSums(prob)

```

radiolaria

Radiolaria diversity since the Jurassic

Description

Radiolaria fossil diversity since the Jurassic

Usage

```
data(sealevel)
```

Details

Radiolaria fossil diversity since the Jurassic compiled from the Neptune Database (Lazarus, 1994) and Paleobiology Database (<https://paleobiodb.org/>). Diversity curves are estimated at the genus level using shareholder quorum subsampling (Alroy, 2010) at two-million-year bins. The format is a dataframe with the two following variables:

age a numeric vector corresponding to the geological age, in Myrs before the present

radiolaria a numeric vector corresponding to the estimated ostracod change at that age

References

- Lazarus, D. (1994) Neptune: A marine micropaleontology database *Mathematical Geology* 26:817–832
- Alroy, J. (2010) Geographical, environmental and intrinsic biotic controls on Phanerozoic marine diversification: Controls on phanerozoic marine diversification *Palaeontology* 53:1211–1235

Examples

```

data(radiolaria)
plot(radiolaria)

```

`redalgae`*Red algae diversity since the Jurassic*

Description

Red algae fossil diversity since the Jurassic

Usage

```
data(redalgae)
```

Details

Red algae fossil diversity since the Jurassic compiled from the Neptune Database (Lazarus, 1994) and Paleobiology Database (<https://paleobiodb.org/>). Diversity curves are estimated at the genus level using shareholder quorum subsampling (Alroy, 2010) at two-million-year bins. The format is a dataframe with the two following variables:

`age` a numeric vector corresponding to the geological age, in Myrs before the present

`redalgae` a numeric vector corresponding to the estimated Red algae change at that age

References

Lazarus, D. (1994) Neptune: A marine micropaleontology database *Mathematical Geology* 26:817–832

Alroy, J. (2010) Geographical, environmental and intrinsic biotic controls on Phanerozoic marine diversification: Controls on phanerozoic marine diversification *Palaeontology* 53:1211–1235

Examples

```
data(redalgae)
plot(redalgae)
```

`sealevel`*Sea level data since the Jurassic*

Description

Global sea level change since the Jurassic

Usage

```
data(sealevel)
```

Details

Eustatic sea level change since the Jurassic calculated by Miller et al. (2005) from satellite measurements, tide gauges, shoreline markers, reefs, atolls, oxygen isotopes, the flooding history of continental margins, cratons. The format is a dataframe with the two following variables:

age a numeric vector corresponding to the geological age, in Myrs before the present

sea level a numeric vector corresponding to the estimated sea level change at that age

References

Miller, K.G., Kominz, M.A., Browning, J.V., Wright, J.D., Mountain, G.S., Katz, M.E., Sugarman, P.J., Cramer, B.S., Christie-Blick, N., Pekar, S.F. (2005) The Phanerozoic Record of Global Sea-Level Change *Science* 310:1293-1298

Examples

```
data(sealevel)
```

```
plot(sealevel)
```

silica

Silica data across the Cenozoic

Description

Silica weathering ratio across the Cenozoic

Usage

```
data(silica)
```

Details

Silica weathering ratio across the Cenozoic calculated by Cermeno et al. (2015) using the lithium isotope record of seawater from Misra and Froelich (2012). The format is a dataframe with the two following variables:

age a numeric vector corresponding to the geological age, in Myrs before the present

silica weathering ratio a numeric vector corresponding to the estimated CO2 at that age

References

Misra, S., Froelich, P.N. (2012) Lithium isotope history of Cenozoic seawater: Changes in silicate weathering and reverse weathering. *Science* 335(6070):818–823

Cermeno, P., Falkowski, P.G., Romero, O.E., Schaller, M.F., Vallina, S.M. (2015) Continental erosion and the Cenozoic rise of marine diatoms *Proceedings of the National Academy of Sciences* 112:4239-244

Examples

```
data(silica)
plot(silica)
```

sim.convergence.geo *Simulation of trait data under the model of convergent character displacement described in Drury et al. 2017*

Description

Simulates the evolution of a continuous character that evolves depending on pairwise similarity in another, OU-evolving trait (e.g., a trait that covaries with resource use). `sig2` and `z0` are shared between two traits, `max` and `alpha` are for focal trait, OU parameters for non-focal trait

Usage

```
sim.convergence.geo(phylo,pars, Nsegments=2500, plot=FALSE, geo.object)
```

Arguments

<code>phylo</code>	an object of type 'phylo' (see ape documentation)
<code>pars</code>	A matrix with a number of rows corresponding to the desired number of simulations, columns containing values for <code>sig2</code> in [, 1], <code>m</code> in [, 2], <code>alpha</code> in [, 3], <code>root.value</code> in [, 4], <code>psi</code> of the OU model for the non-focal, resource use trait in [, 5], and <code>theta</code> in the OU model for the non-focal resource use trait in [, 6]
<code>Nsegments</code>	the minimum number of time steps to simulate
<code>plot</code>	if TRUE, returns two plots: the top plot is focal trait undergoing convergence, the bottom plot is non-focal trait evolving under BM or OU
<code>geo.object</code>	geography object created using CreateGeoObject

Details

Adjusting `Nsegments` will impact the length of time the simulations take. The length of each segment ($\max(\text{nodeHeights}(\text{phylo}))/\text{Nsegments}$) should be much smaller than the smallest branch ($\min(\text{phylo}\$edge.length)$).

Value

A list of two matrices with the simulated values for each lineage (one simulation per row; columns correspond to species) for `trait1` (focal trait undergoing convergence) and `non.focal` (resource-use trait that determines strength of convergence in `trait1`)

Author(s)

J.P. Drury jonathan.p.drury@gmail.com

References

Drury, J., Grether, G., Garland Jr., T., and Morlon, H. 2017. A review of phylogenetic methods for assessing the influence of interspecific interactions on phenotypic evolution. *Systematic Biology*

See Also

[CreateGeoObject](#)

Examples

```
data(Anlis.data)
phylo<-Anlis.data$phylo
geo.object<-Anlis.data$geography.object

#simulate with the OU process present and absent
pars<-expand.grid(0.05,-0.1,1,0,c(2,0),0)
sim.convergence.geo(phylo,pars,Nsegments=2500, plot=FALSE, geo.object)
```

sim.divergence.geo	<i>Simulation of trait data under the model of divergent character displacement described in Drury et al. 2017</i>
--------------------	--

Description

Simulates the evolution of a continuous character under a model of evolution where trait values are repelled according to between-species similarity in trait values, taking into account biogeography using a biogeo.object formatted from RPANDA (see CreateGeoObject function in RPANDA package)

Usage

```
sim.divergence.geo(phylo,pars, Nsegments=2500, plot=FALSE, geo.object)
```

Arguments

phylo	a phylogenetic tree
pars	A matrix with a number of rows corresponding to the desired number of simulations, columns containing values for <i>sig2</i> in [, 1], <i>m</i> in [, 2], <i>alpha</i> in [, 3], <i>root.value</i> in [, 4], <i>psi</i> of the OU model in [, 5], and <i>theta</i> in the OU model in [, 6]
Nsegments	the minimum number of time steps to simulate
plot	logical indicating whether to plot the simulated trait values at each time step
geo.object	geography object created using CreateGeoObject

Details

Adjusting `Nsegments` will impact the length of time the simulations take. The length of each segment ($\max(\text{nodeHeights}(\text{phylo}))/\text{Nsegments}$) should be much smaller than the smallest branch ($\min(\text{phylo}\$edge.length)$).

Value

A matrix with the simulated values for each lineage (one simulation per row; columns correspond to species)

Author(s)

J.P. Drury jonathan.p.drury@gmail.com F. Hartig

References

Drury, J., Grether, G., Garland Jr., T., and Morlon, H. 2017. A review of phylogenetic methods for assessing the influence of interspecific interactions on phenotypic evolution. *Systematic Biology*

See Also

[CreateGeoObject](#)

Examples

```
data(Anolis.data)
phylo<-Anolis.data$phylo
geo.object<-Anolis.data$geography.object

#simulate with the OU process present and absent
pars<-expand.grid(0.05,2,1,0,c(2,0),0)
sim.divergence.geo(phylo,pars,Nsegments=2500, plot=FALSE, geo.object)
```

simulateTipData

Tip trait simulation under a model of phenotypic evolution.

Description

Simulates tip trait data under a specified model of phenotypic evolution, with three distinct behaviours specified with the 'method' argument.

Usage

```
simulateTipData(object, params, method, v)
```


Arguments

object	an object of class 'PhenotypicModel'.
params	vector of parameters, given in the same order as in the 'model' object.
method	an integer specifying the behaviour of the function. If method = 1 (default value), the tip distribution is first computed, before returning a simulated dataset drawn in this distribution. If method = 2, the whole trajectory is simulated step by step, plotted, and returned. Otherwise, the whole trajectory is simulated step by step, and then returned without being plotted.
v	boolean specifying the verbose mode. Default value : FALSE.

Value

a vector of trait values at the tips of the tree.

Author(s)

M Manceau

References

Manceau M., Lambert A., Morlon H. (2017) A unifying comparative phylogenetic framework including traits coevolving across interacting lineages *Systematic Biology*

Examples

```
#Loading an example tree
newick <- "(((A:1,B:0.5):2,(C:3,D:2.5):1):6,E:10.25):2,(F:6.5,G:8.25):3):1;"
tree <- read.tree(text=newick)

#Creating the models
modelBM <- createModel(tree, 'BM')
modelOU <- createModel(tree, 'OU')

#Simulating tip traits under both models with distinct behaviours of the functions :
dataBM <- simulateTipData(modelBM, c(0,0,0,1))
dataOU <- simulateTipData(modelOU, c(0,0,1,5,1), method=1)
dataBM2 <- simulateTipData(modelBM, c(0,0,0,1), method=2)
```

simulateTipData-methods

~~ *Methods for Function simulateTipData* ~~

Description

~~ Methods for function simulateTipData ~~

Methods

`signature(object = "PhenotypicModel")` This is the only method available for this function. Same behaviour for any `PhenotypicModel`.

sim_ClaDS

Simulation of the ClaDS model

Description

Simulate a birth-death phylo-h-geny with rate shifts happening at speciation events.

Usage

```
sim_ClaDS(lambda_0, mu_0,
           new_lamb_law="lognormal*shift", new_mu_law="turnover",
           condition="time", time_stop = 0, taxa_stop = Inf,
           sigma_lamb=0.1, alpha_lamb=1, lamb_max=1, lamb_min=0,
           sigma_mu=0, alpha_mu=1, mu_min=mu_0, mu_max=mu_0,
           theta=1, nShiftMax=Inf,
           return_all_extinct=FALSE, prune_extinct=TRUE,
           maxRate=Inf)
```

Arguments

<code>lambda_0</code>	Initial speciation rate.
<code>mu_0</code>	Initial extinction rate, or turnover rate if <code>new_mu_law == "turnover"</code> .
<code>new_lamb_law</code>	Distribution in which the new speciation rates are drawn at a speciation event. See details.
<code>new_mu_law</code>	Distribution in which the new extinction rates are drawn at a speciation event. See details.
<code>condition</code>	Stopping condition. Can be "time" (the default) or "taxa".
<code>time_stop</code>	Stopping time if <code>condition == "time"</code> .
<code>taxa_stop</code>	Final number of species if <code>condition == "taxa"</code> . If <code>condition == "time"</code> , the process is stopped if the number of species exceeds <code>taxa_stop</code> . This can be useful for some parametrizations of the model for which the number of species can reach very large number very quickly, leading to computation time and memory issues. To disable this option, use <code>taxa_stop = Inf</code> (the default).
<code>sigma_lamb</code>	Parameter of the new speciation rates distribution, see details.
<code>alpha_lamb</code>	Parameter of the new speciation rates distribution, see details.
<code>lamb_max</code>	Parameter of the new speciation rates distribution, see details.
<code>lamb_min</code>	Parameter of the new speciation rates distribution, see details.

sigma_mu	Parameter of the new extinction rates distribution, see details.
alpha_mu	Parameter of the new extinction rates distribution, see details.
mu_min	Parameter of the new extinction rates distribution, see details.
mu_max	Parameter of the new extinction rates distribution, see details.
theta	Probability to have a rate shift at speciation. Default to 1.
nShiftMax	Maximum number of rate shifts. If nShiftMax < Inf, theta is set to 0 as soon as there has been nShiftMax rate shifts. Set nShiftMax = Inf (the default) to disable this option.
return_all_extinct	Boolean specifying whether the function should return extinct phylogenies. Default to FALSE.
prune_extinct	Boolean specifying whether extinct species should be removed from the resulting phylogeny. Default to TRUE.
maxRate	The process is stopped if one of the lineage has a speciation rate that exceeds maxRate. This can be useful for some parametrizations of the model for which the rates can reach very large values, leading to numerical overflows. To disable this option, use maxRate = Inf (the default).

Details

Available options for new_lamb_law are :

- "uniform", the new speciation rates are drawn uniformly in [lamb_min, lamb_max].
- "normal", the new speciation rates are drawn in a normal distribution with parameters (sigma_lamb^2, parent_lambda), truncated in 0.
- "lognormal", the new speciation rates are drawn in a lognormal distribution with parameters (sigma_lamb^2, parent_lambda).
- "lognormal*shift", the new speciation rates are drawn in a lognormal distribution with parameters (sigma_lamb^2, parent_lambda * alpha_lamb). This is the default option as it corresponds to the ClaDS model.
- "lognormal*t", the new speciation rates are drawn in a lognormal distribution with parameters (sigma_lamb^2 * t^2, parent_lambda), where t is the age of the mother species.
- "logbrownian", the new speciation rates are drawn in a lognormal distribution with parameters (sigma_lamb^2 * t, parent_lambda), where t is the age of the mother species. This is used to approximate the case where speciation rates are evolving as the log of a brownian motion, as is done in Beaulieu, J. M. and B. C. O'Meara. (2015).
- "normal+shift", the new speciation rates are drawn in a normal distribution with parameters (sigma_lamb^2, parent_lambda + alpha_lamb), truncated in 0.
- "normal*shift", the new speciation rates are drawn in a normal distribution with parameters (sigma_lamb^2, parent_lambda * alpha_lamb), truncated in 0.

Available options for new_mu_law are :

- "uniform", the new extinction rates are drawn uniformly in [mu_min, mu_max].

- "normal", the new extinction rates are drawn in a normal distribution with parameters (σ_{μ}^2 , μ_{parent}), truncated in 0.
- "lognormal", the new extinction rates are drawn in a lognormal distribution with parameters (σ_{μ}^2 , μ_{parent}).
- "lognormal*shift", the new extinction rates are drawn in a lognormal distribution with parameters (σ_{μ}^2 , $\mu_{\text{parent}} * \alpha_{\mu}$).
- "normal*t", the new speciation rates are drawn in a normal distribution with parameters ($\sigma_{\lambda}^2 * t^2$, μ_{parent}), where t is the age of the mother species.
- "turnover", the turnover rate is constant (in that case μ_0 is the turnover rate), so the new extinction rates are μ_0 times the new speciation rates. This is the default option, corresponding to ClaDS2.

Value

A list with :

tree	The resulting phylogeny.
times	A vector with the times of all speciation and extinction events.
nblineages	A vector in which <code>nblineages[i]</code> is the number of species in the clade after the event happening at time <code>times[i]</code> .
lamb	A vector with all the different speciation rates resulting from the simulation.
mu	A vector with all the different extinction rates resulting from the simulation.
rates	A vector of integer mapping the elements of <code>lamb</code> and <code>mu</code> to the branches of <code>tree</code> .
maxRate	A boolean indicating whether the process was ended before reaching the specified stopping criterion because one of the speciation rates exceeded <code>maxRate</code> (see the "arguments" section).
root_length	The time before the first speciation event.

Author(s)

O. Maliet

References

- Maliet O., Hartig F. and Morlon H. 2019, A model with many small shifts for estimating species-specific diversification rates, *Nature Ecology and Evolution*, doi 10.1038/s41559-019-0908-0
- Beaulieu, J. M. and B. C. O'Meara. 2015. Extinction can be estimated from moderately sized molecular phylogenies. *Evolution* 69:1036-1043.

See Also

[plot_ClaDS_phylo](#)

Examples

```
# Simulation of a ClaDS2 phylogeny
set.seed(1)

obj= sim_ClaDS( lambda_0=0.1,
                mu_0=0.5,
                sigma_lamb=0.7,
                alpha_lamb=0.90,
                condition="taxa",
                taxa_stop = 20,
                prune_extinct = TRUE)

tree = obj$tree
speciation_rates = obj$lamb[obj$rates]
extinction_rates = obj$mu[obj$rates]

plot_ClaDS_phylo(tree,speciation_rates)

# Simulation of a phylogeny with constant extinction rate and speciation
# rates evolving as a logbrownian
set.seed(4321)

obj= sim_ClaDS( lambda_0=0.1,
                mu_0=0.2,
                new_mu_law = "uniform",
                new_lamb_law = "logbrownian",
                sigma_lamb=0.4,
                condition="taxa",
                taxa_stop = 20,
                prune_extinct = FALSE)

tree = obj$tree
speciation_rates = obj$lamb[obj$rates]
extinction_rates = obj$mu[obj$rates]

plot_ClaDS_phylo(tree,speciation_rates)

# Simulation of a phylogeny with constant extinction rate and at most one shift
# in speciation rates
set.seed(1221)

obj= sim_ClaDS( lambda_0=0.1,
                mu_0=0.05,
                new_mu_law = "uniform",
                new_lamb_law = "uniform",
                lamb_max = 0.5, lamb_min = 0,
                theta = 0.1, nShiftMax = 1,
                condition="taxa",
                taxa_stop = 100,
```

```

        prune_extinct = TRUE)

tree = obj$tree
speciation_rates = obj$lamb[obj$rates]
extinction_rates = obj$mu[obj$rates]

plot_ClaDS_phylo(tree,speciation_rates)

```

sim_env_bd

Simulate birth-death tree dependent on an environmental curve

Description

Simulates a birth-death tree (starting with one lineage) with speciation and/or extinction rate that varies as a function of an input environmental curve. Notations follow Morlon et al. PNAS 2011 and Condamine et al. ELE 2013.

Usage

```

sim_env_bd(env_data, f.lamb, f.mu, lamb_par, mu_par, df=NULL, time.stop=0,
return.all.extinct=TRUE, prune.extinct=TRUE)

```

Arguments

env_data	environmental data, given as a data frame with two columns. The first column is time, the second column is the environmental data (temperature for instance).
time.stop	the age of the phylogeny.
f.lamb	a function specifying the hypothesized functional form of the variation of the speciation rate λ with time and the environmental variable. Any functional form may be used. This function has three arguments: the first argument is time; the second argument is the environmental variable; the third argument is a numeric vector of the parameters controlling the time and environmental variation (to be estimated).
f.mu	a function specifying the hypothesized functional form of the variation of the extinction rate μ with time and the environmental variable. Any functional form may be used. This function has three arguments: the first argument is time; the second argument is the environmental variable; the second argument is a numeric vector of the parameters controlling the time and environmental variation (to be estimated).
lamb_par	a numeric vector of initial values for the parameters of f.lamb to be estimated (these values are used by the optimization algorithm). The length of this vector is used to compute the total number of parameters in the model, so to fit a model with constant speciation rate (for example), lamb_par should be a vector of length 1. Otherwise aic values will be wrong.

mu_par	a numeric vector of initial values for the parameters of f.mu to be estimated (these values are used by the optimization algorithm). The length of this vector is used to compute the total number of parameters in the model, so to fit a model without extinction (for example), mu_par should be empty (vector of length 0). Otherwise aic values will be wrong.
df	the degree of freedom to use to define the spline. As a default, smooth.spline(env_data[,1], env_data[,2])\$df is used. See <i>sm.spline</i> for details.
return.all.extinct	return all extinction lineages in simulated tree.
prune.extinct	prune extinct lineages in simulated tree.

Details

In the f.lamb and f.mu functions, time runs from the present to the past.

Value

a list with the following components

tree	the simulated tree with number tips
times	the times of speciation events starting from the past
nblineages	the labels of surviving lineages and total number of surviving lineages

Note

The speed of convergence of the fit might depend on the degree of freedom chosen to define the spline.

Author(s)

E Lewitus and H Morlon

References

Morlon, H., Parsons, T.L. and Plotkin, J.B. (2011) Reconciling molecular phylogenies with the fossil record *Proc Nat Acad Sci* 108: 16327-16332

Condamine, F.L., Rolland, J., and Morlon, H. (2013) Macroevolutionary perspectives to environmental change, *Eco Lett* 16: 72-85

See Also

[fit_env](#), [fit_bd](#)

Examples

```

data(InfTemp)
dof<-smooth.spline(InfTemp[,1], InfTemp[,2])$df
# Simulates a tree with lambda varying as an exponential function of temperature
# and mu fixed to 0 (no extinction). Here t stands for time and x for temperature.
f.lamb <-function(t,x,y){y[1] * exp(y[2] * x)}
f.mu<-function(t,x,y){0}
lamb_par<-c(0.10, 0.01)
mu_par<-c()
#result_exp <- sim_env_bd(InfTemp,f.lamb,f.mu,lamb_par,mu_par,time.stop=10)

```

sim_sgd

Algorithm for simulating a phylogenetic tree under the SGD model

Description

Simulates a phylogeny arising from the SGD model with exponentially increasing metapopulation size. Notations follow Manceau et al. (2015).

Usage

```
sim_sgd(tau, b, d, nu)
```

Arguments

tau	the simulation time, which corresponds to the length of the phylogeny
b	the (constant) per-individual birth rate
d	the (constant) per-individual death rate
nu	the (constant) per-individual mutation rate

Value

a phylogenetic tree of class "phylo" (see ape documentation)

Author(s)

M Manceau

References

Manceau M., Lambert A., Morlon H. (2015) Phylogenies support out-of-equilibrium models of biodiversity Ecology Letters 18: 347-356

Examples

```
tau <- 10
b <- 1e6
d <- b-0.5
nu <- 0.6
tree <- sim_sgd(tau,b,d,nu)
plot(tree)
```

sim_t_comp

*Recursive simulation (root-to-tip) of competition models***Description**

Simulates datasets for a given phylogeny under matching competition (MC), diversity dependent linear (DDlin), or diversity dependent exponential (DDexp) models of trait evolution. Simulations are carried out from the root to the tip of the tree.

Usage

```
sim_t_comp(phylo,pars,root.value,Nsegments=1000,model="MC,DDexp,DDlin")
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
pars	a vector containing the two parameters for the chosen model; all models require sig2, and additionally, the MC model requires S, specifying the level of competition (larger negative values correspond to higher levels of competition), the DDlin model requires b and DDexp require r, the slope parameters (negative in cases of decline in evolutionary rates with increasing diversity). sig2 must be listed first.
root.value	a number specifying the trait value for the ancestor
Nsegments	a value specifying the total number of time segments to simulate across for the phylogeny (see Details)
model	model chosen to fit trait data, "MC" is the matching competition model of Nuismer & Harmon 2014, "DDlin" is the diversity-dependent linear model, and "DDexp" is the diversity-dependent exponential model of Weir & Mursleen 2013.

Details

Adjusting Nsegments will impact the length of time the simulations take. The length of each segment ($\max(\text{nodeHeights}(\text{phylo}))/\text{Nsegments}$) should be much smaller than the smallest branch ($\min(\text{phylo}\$edge.length)$).

Value

a named vector with simulated trait values for n species in the phylogeny

Author(s)

J Drury jonathan.p.drury@gmail.com

References

Drury, J., Clavel, J., Manceau, M., and Morlon, H. 2016. Estimating the effect of competition on trait evolution using maximum likelihood inference. *Systematic Biology* doi 10.1093/sysbio/syw020

Nuismer, S. & Harmon, L. 2015. Predicting rates of interspecific interaction from phylogenetic trees. *Ecology Letters* 18:17-27.

Weir, J. & Mursleen, S. 2012. Diversity-dependent cladogenesis and trait evolution in the adaptive radiation of the auks (Aves: Alcidae). *Evolution* 67:403-416.

See Also

[fit_t_comp](#)

Examples

```
data(Cetacea)

# Simulate data under the matching competition model
MC.data<-sim_t_comp(Cetacea,pars=c(sig2=0.01,S=-0.1),root.value=0,Nsegments=1000,model="MC")

# Simulate data under the diversity dependent linear model
DDlin.data<-sim_t_comp(Cetacea,pars=c(sig2=0.01,b=-0.0001),root.value=0,Nsegments=1000,
model="DDlin")

# Simulate data under the diversity dependent linear model
DDexp.data<-sim_t_comp(Cetacea,pars=c(sig2=0.01,r=-0.01),root.value=0,Nsegments=1000,model="DDexp")
```

sim_t_env

Recursive simulation (root-to-tip) of the environmental model

Description

Simulates datasets for a given phylogeny under the environmental model (see `?fit_t_env`)

Usage

```
sim_t_env(phylo, param, env_data, model, root.value=0, step=0.001, plot=FALSE, ...)
```

Arguments

phylo	An object of class 'phylo' (see ape documentation)
param	A numeric vector of parameters for the user-defined climatic model. For the <i>EnvExp</i> and <i>EnvLin</i> , there is only two parameters. The first is sigma and the second beta.
env_data	Environmental data, given as a time continuous function (see, e.g. splinefun) or a data frame with two columns. The first column is time, the second column is the environmental data (temperature for instance).
model	The model describing the functional form of variation of the evolutionary rate σ^2 with time and the environmental variable. Default models are "EnvExp" and "EnvLin" (see details). An user defined function of any functional form can be used (forward in time). This function has three arguments: the first argument is time; the second argument is the environmental variable; the third argument is a numeric vector of the parameters controlling the time and environmental variation (to be estimated). See the example below.
root.value	A number specifying the trait value for the ancestor
step	This argument describe the length of the segments to simulate across for the phylogeny. The smaller is the segment, the greater is the accuracy of the simulation at the expense of the computation time.
plot	If TRUE, the simulated process is plotted.
...	Arguments to be passed through. For instance, "col" for plot=TRUE.

Details

The users defined function is simulated forward in time i.e.: from the root to the tips. The speed of the simulations might depend on the value used for the "step" argument. It's possible to estimate the traits with the MLE from another fitted object (see the example below).

Value

A named vector with simulated trait values for n species in the phylogeny

Author(s)

J. Clavel

References

Clavel, J. & Morlon, H., 2017. Accelerated body size evolution during cold climatic periods in the Cenozoic. *Proceedings of the National Academy of Science*, 114(16): 4183-4188.

See Also

[plot.fit_t.env](#), [likelihood_t.env](#)

Examples

```

data(Cetacea)
data(InfTemp)

set.seed(123)
# define the parameters
param <- c(0.1, -0.5)
# define the environmental function
my_fun <- function(t, env, param){ param[1]*exp(param[2]*env(t))}

# simulate the trait
trait <- sim_t_env(Cetacea, param=param, env_data=InfTemp, model=my_fun, root.value=0,
                  step=0.001, plot=TRUE)

# fit the model to the simulated trait.
fit <- fit_t_env(Cetacea, trait, env_data=InfTemp, model=my_fun, param=c(0.1,0))
fit

# Then use the results from the previous fit to simulate a new dataset
trait2 <- sim_t_env(Cetacea, param=fit, step=0.001, plot=TRUE)
fit2 <- fit_t_env(Cetacea, trait2, env_data=InfTemp, model=my_fun, param=c(0.1,0))
fit2

# When providing the environmental function:
require(apspline)
spline_result <- sm.spline(x=InfTemp[,1],y=InfTemp[,2], df=50)
env_func <- function(t){predict(spline_result,t)}
t<-unique(InfTemp[,1])

# We build the interpolated smoothing spline function
env_data<-splinefun(t,env_func(t))

# provide the environmental function to simulate the traits
trait3 <- sim_t_env(Cetacea, param=param, env_data=env_data, model=my_fun,
                  root.value=0, step=0.001, plot=TRUE)
fit3 <- fit_t_env(Cetacea, trait3, env_data=InfTemp, model=my_fun, param=c(0.1,0))
fit3

```

Description

Computes the spectra of eigenvalues for the modified graph Laplacian of a phylogenetic tree, identifies the spectral gap, then convolves the eigenvalues with a Gaussian kernel, and plots them alongside all eigenvalues ranked in descending order.

Usage

```
spectR(phylo, meth=c("standard"), zero_bound=F)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
meth	the method used to compute the spectral density, which can either be "standard" or "normal". If set to "standard", computes the unnormalized version of the spectral density. If set to "normal", computes the spectral density normalized to the degree matrix (see the associated paper for an explanation)
zero_bound	if false, eigenvalues less than one are discarded

Details

Note that the eigengap should in principle be computed with the "standard" option

Value

a list with the following components:

eigenvalues	the vector of eigenvalues
principal_eigenvalue	the largest (or principal) eigenvalue of the spectral density profile
asymmetry	the skewness of the spectral density profile
peak_height	the largest y-axis value of the spectral density profile
eigengap	the position of the largest difference between eigenvalues, giving the number of modalities in the tree

Author(s)

E Lewitus

References

Lewitus, E., Morlon, H., Characterizing and comparing phylogenies from their Laplacian spectrum, bioRxiv doi: <http://dx.doi.org/10.1101/026476>

See Also

[plot_spectR](#), [JSDtree](#), [BICcompare](#)

Examples

```
data(Cetacea)
spectR(Cetacea, meth="standard", zero_bound=FALSE)
```

 spectR_t

Spectral density plot of phylogenetic trait data

Description

Computes the spectra of eigenvalues for the modified graph Laplacian of a phylogenetic tree with associated tip data, convolves the eigenvalues with a Gaussian kernel and plots the density profile of eigenvalues, and estimates the summary statistics of the profile.

Usage

```
spectR_t(phylo, dat, draw=F)
```

Arguments

phylo	an object of type 'phylo' (see ape documentation)
dat	a vector of trait data associated with the tips of the phylo object; tips and trait data should be aligned
draw	if true, the spectral density profile of the phylogenetic trait data is plotted

Value

a list with the following components:

eigenvalues	the vector of eigenvalues
splitter	the largest (or principal) eigenvalue of the spectral density profile
fragmenter	the skewness of the spectral density profile
tracer	the largest y-axis value of the spectral density profile

Author(s)

E Lewitus

References

Lewitus, E., Morlon, H. (2019) Characterizing and comparing phylogenetic trait data from their normalized Laplacian spectrum, bioRxiv doi: <https://doi.org/10.1101/654087>

Examples

```
tr<-rtree(10)
dat<-runif(10,1,2)
spectR_t(tr, dat, draw=TRUE)
```

Index

*Topic **classes**

PhenotypicACDC-class, [87](#)
PhenotypicADiag-class, [89](#)
PhenotypicBM-class, [90](#)
PhenotypicDD-class, [91](#)
PhenotypicGMM-class, [92](#)
PhenotypicModel-class, [93](#)
PhenotypicOU-class, [94](#)
PhenotypicPM-class, [96](#)

*Topic **datasets**

Balaenopteridae, [8](#)
Calomys, [10](#)
Cetacea, [12](#)
co2, [14](#)
co2_res, [15](#)
coccolithophore, [16](#)
d13c, [25](#)
foraminifera, [54](#)
greenalgae, [64](#)
InfTemp, [65](#)
landplant, [69](#)
ostracoda, [87](#)
Phocoenidae, [97](#)
Phyllostomidae, [99](#)
Phyllostomidae_genera, [100](#)
radiolaria, [115](#)
redalgae, [116](#)
sealevel, [116](#)
silica, [117](#)

*Topic **methods**

fitTipData-methods, [27](#)
getDataLikelihood-methods, [56](#)
getTipDistribution-methods, [60](#)
modelSelection-methods, [86](#)
simulateTipData-methods, [121](#)

[,PhenotypicModel,ANY,ANY,ANY-method
(PhenotypicModel-class), [93](#)

[<-,PhenotypicModel,ANY,ANY,ANY-method
(PhenotypicModel-class), [93](#)

ancestral, [5](#), [54](#), [98](#)

Anolis.data, [7](#)

Balaenopteridae, [8](#)

BGB.examples, [8](#)

BICompare, [9](#), [66](#), [102](#), [133](#)

Calomys, [10](#)

Caprimulgidae, [11](#)

Caprimulgidae_ClaDS2, [11](#)

Cetacea, [12](#)

ClaDS0_example, [13](#)

co2, [14](#)

co2_res, [15](#)

coccolithophore, [16](#)

CreateClassObject, [16](#), [19](#)

CreateGeobyClassObject, [16](#), [17](#), [18](#), [47](#), [75](#)

CreateGeoObject, [7](#), [20](#), [22](#), [43](#), [45](#), [74–76](#),
[78](#), [79](#), [82](#), [83](#), [118–120](#)

CreateGeoObject_BioGeoBEARS, [9](#), [19](#), [21](#)

createModel, [23](#)

createModelCoevolution, [24](#)

d13c, [25](#)

fit_bd, [27](#), [41](#), [107](#), [108](#), [110](#), [114](#), [127](#)

fit_ClaDS, [12](#), [31](#), [31](#), [34](#), [57](#), [86](#), [104](#)

fit_ClaDS0, [13](#), [33](#), [33](#), [58](#), [103](#)

fit_coal_cst, [35](#), [39](#)

fit_coal_var, [37](#), [37](#)

fit_env, [39](#), [109](#), [127](#)

fit_sgd, [42](#)

fit_t_comp, [20–22](#), [43](#), [76](#), [78](#), [79](#), [82](#), [83](#), [130](#)

fit_t_comp_subgroup, [17–19](#), [45](#)

fit_t_env, [6](#), [48](#), [80](#)

fit_t_pl, [6](#), [52](#), [61](#), [63](#), [98](#), [113](#)

fitTipData, [26](#)

fitTipData,PhenotypicModel-method
(fitTipData-methods), [27](#)

fitTipData-methods, [27](#)

- foraminifera, [54](#)
- getDataLikelihood, [55](#)
- getDataLikelihood, PhenotypicModel-method
(getDataLikelihood-methods), [56](#)
- getDataLikelihood-methods, [56](#)
- getMAPS_ClaDS, [56](#), [58](#), [104](#)
- getMAPS_ClaDS0, [12](#), [34](#), [57](#), [58](#), [103](#)
- getTipDistribution, [59](#)
- getTipDistribution, PhenotypicACDC-method
(getTipDistribution-methods),
[60](#)
- getTipDistribution, PhenotypicADiag-method
(getTipDistribution-methods),
[60](#)
- getTipDistribution, PhenotypicBM-method
(getTipDistribution-methods),
[60](#)
- getTipDistribution, PhenotypicDD-method
(getTipDistribution-methods),
[60](#)
- getTipDistribution, PhenotypicGMM-method
(getTipDistribution-methods),
[60](#)
- getTipDistribution, PhenotypicModel-method
(getTipDistribution-methods),
[60](#)
- getTipDistribution, PhenotypicOU-method
(getTipDistribution-methods),
[60](#)
- getTipDistribution, PhenotypicPM-method
(getTipDistribution-methods),
[60](#)
- getTipDistribution-methods, [60](#)
- GIC, [6](#)
- GIC.fit_pl.rpanda, [54](#), [61](#), [63](#), [98](#), [113](#)
- gic_criterion, [6](#), [54](#), [61](#), [62](#), [98](#)
- greenalgae, [64](#)
- InfTemp, [65](#)
- JSDt_cluster, [67](#)
- JSDtree, [10](#), [65](#), [67](#), [133](#)
- JSDtree_cluster, [66](#), [66](#)
- landplant, [69](#)
- likelihood_bd, [30](#), [41](#), [69](#)
- likelihood_coal_cst, [37](#), [71](#)
- likelihood_coal_var, [39](#), [72](#)
- likelihood_sgd, [43](#), [73](#)
- likelihood_subgroup_model, [47](#), [74](#)
- likelihood_t_DD, [45](#), [76](#), [77](#), [79](#)
- likelihood_t_DD_geog, [45](#), [78](#), [78](#)
- likelihood_t_env, [50](#), [79](#), [84](#), [101](#), [132](#)
- likelihood_t_MC, [45](#), [81](#), [83](#)
- likelihood_t_MC_geog, [45](#), [82](#), [82](#)
- lines.fit_t.env, [84](#), [101](#)
- make.simmap, [17](#), [18](#), [20](#), [46](#)
- modelSelection, [85](#)
- modelSelection, PhenotypicModel-method
(modelSelection-methods), [86](#)
- modelSelection-methods, [86](#)
- MPhiFFT, [86](#)
- mvgls, [54](#), [61](#)
- optim, [44](#), [46](#)
- ostracoda, [87](#)
- par, [84](#), [101](#)
- PhenotypicACDC-class, [87](#)
- PhenotypicADiag-class, [89](#)
- PhenotypicBM-class, [90](#)
- PhenotypicDD-class, [91](#)
- PhenotypicGMM-class, [92](#)
- PhenotypicModel, [88–91](#), [93](#), [95](#), [96](#)
- PhenotypicModel-class, [93](#)
- PhenotypicOU-class, [94](#)
- PhenotypicPM-class, [96](#)
- Phocoenidae, [97](#)
- phyl.pca_pl, [6](#), [54](#), [97](#), [113](#)
- Phyllostomidae, [99](#), [100](#)
- Phyllostomidae_genera, [100](#), [100](#)
- plot.fit_t.env, [50](#), [84](#), [100](#), [132](#)
- plot_BICcompare, [10](#), [102](#)
- plot_ClaDS0_chains, [34](#), [58](#), [103](#), [104](#)
- plot_ClaDS_chains, [12](#), [33](#), [57](#), [103](#), [104](#)
- plot_ClaDS_phylo, [105](#), [124](#)
- plot_dtt, [30](#), [106](#), [110](#), [114](#)
- plot_fit_bd, [30](#), [107](#)
- plot_fit_env, [41](#), [108](#)
- plot_prob_dtt, [109](#), [114](#)
- plot_spectR, [111](#), [133](#)
- Posdef, [112](#)
- print, PhenotypicModel-method
(PhenotypicModel-class), [93](#)
- prob_dtt, [110](#), [113](#)
- radiolaria, [115](#)

redalgae, [116](#)
round, [17](#)
RPANDA (RPANDA-package), [4](#)
RPANDA-package, [4](#)

sealevel, [116](#)
show, PhenotypicModel-method
 (PhenotypicModel-class), [93](#)
silica, [117](#)
sim.convergence.geo, [118](#)
sim.divergence.geo, [119](#)
sim_ClaDS, [105](#), [122](#)
sim_env_bd, [126](#)
sim_sgd, [128](#)
sim_t_comp, [45](#), [129](#)
sim_t_env, [130](#)
simulateTipData, [120](#)
simulateTipData, PhenotypicModel-method
 (simulateTipData-methods), [121](#)
simulateTipData-methods, [121](#)
spectR, [10](#), [66](#), [111](#), [132](#)
spectR_t, [68](#), [134](#)