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   <DOI:10.1073/pnas.1102543108>, Condamine et al. (2013) <DOI:10.1111/ele.12062>,
   Lewitus & Mor-
   Manceau et al. (2016) <DOI:10.1093/sysbio/syw115>, Morlon et al. (2016) <DOI:10.1111/2041-
   210X.12526>, Clavel & Morlon (2017) <DOI:10.1073/pnas.1606868114>,
Drury et al. (2018) <DOI:10.1371/journal.pbio.2003563>, Clavel et al. (2019) <DOI:10.1093/sysbio/syy045>, Maliet et al. (2019) <DOI:10.1038/s41559-019-0908-0>,
Billaud et al. (2019) <DOI:10.1093/sysbio/syz057>, Lewitus et al. (2019) <DOI:10.1093/sysbio/syz061>,

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**Description**

Implements macroevolutionary analyses on phylogenetic trees

**Details**

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

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References


---

**add.gts**

**Geological time scale**

**Description**

Adds geological time scale (GTS) to plots.

**Usage**

```r
add.gts(thickness, quaternary = T, is.phylo = F, xpd.x = T, time.interval = 1, names = NULL, fill = T, cex = 1, padj = -0.5, direction = "rightwards")
```

**Arguments**

- **thickness** numeric < 0. Define the thickness of the scale.
- **quaternary** boolean. Whether to merge Pleistocene and Holocene into Quaternary. Default is TRUE.
- **is.phylo** boolean. Whether the plot is a phylogeny or not. Default is FALSE.
- **time.interval** numeric. Define the minimum time interval (in million years) for the geological time scale. Default is 1 and displays ticks every million year but with numbers at every five million years.
- **xpd.x** boolean. Whether to expand the last period of the geological time scale before root age (mainly for tree). Default is TRUE.
- **names** a character vector with the names of geological periods (stages). Can be used to write abbreviations. Default is NULL and display full names (except for Quaternary and Pliocene).
- **fill** boolean. If TRUE (default), background is alternatively filled with grey and white bands to distinguish geological periods. If FALSE, dashed lines are drawn to limit geological periods.
- **cex** numeric. Size of the names of geological periods.
- **padj** padj argument defining space between the axis and the values of the axis (see par() for more details).
- **direction** character. Direct the geological time scale. Can be either "rightwards" (default) of "leftwards" (NOT IMPLEMENTED YET).
Details

This function plots a geological times scale (GTS). It has been designed for adding GTS to plot of phylogeny, diversification rates and paleodiversity dynamics through time but can be used with any R plot. Time should be negative for other plots than phylogenies.

Value

Draws geological time scale on x axis.

Author(s)

Nathan Mazet

References


Examples

```r
## Not run:
# with a phylogeny
data("Cetacea")
# first plot to get the dimensions of the gts
plot(Cetacea, cex = 0.5, label.offset = 0.2, tip.color = "white")
add.gts(-3, quaternary = T, is.phylo = T, xpd.x = F,
       names = c("Q.", "Pli.", "Miocene", "Oligocene", "Eoc."))
# second plot to display the tree on the gts
par(new = T)
plot(Cetacea, cex = 0.5, label.offset = 0.2)
mtext("Time (Myrs)", side = 1, line = 3, at = 18)

# see Appendix S4 from Mazet et al. (2023) for more examples.

## End(Not run)
```

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.
ancestral

Usage

ancestral(object, ...)

Arguments

object A model fit object obtained by the fit_t_XX class of functions.
... Further arguments to be passed through (not used yet).

Details

ancestral reconstructs 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 (Clavel et al. 2019).

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.

Cunningham C.W., Omland K.E., Oakley T.H. 1998. Reconstructing ancestral character states: a

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

if(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

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


**See Also**

*CreateGeoObject*

**Examples**

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

---

**apply_prob_dtt**  
*Calculates paleodiversity dynamics with the probabilistic approach.*

**Description**

Applies prob_dtt() to outputs from shift.estimates().

**Usage**

```r
apply_prob_dtt(phylo, data, sampling.fractions, shift.res, 
combi = 1, backbone.option = "crown.shift", 
m = NULL)
```

**Arguments**

- **phylo**  
an object of type 'phylo' (see ape documentation)

- **data**  
a data.frame containing a database of monophyletic groups for which potential shifts can be investigated. This database should be based on taxonomy, ecology or traits and contain a column named "Species" with species names as in phylo.

- **sampling.fractions**  
the output resulting from get.sampling.fractions.

- **shift.res**  
the output resulting from shift.estimates.

- **backbone.option**  
type of the backbone analysis:
  - "stem.shift": for every shift, the probability of the speciation event at the stem age of the subclade is included in the likelihood of the backbone thanks to the argument spec_times.
  - "crown.shift": for every shift, both the probability of the speciation event at the stem age of the subclade and the probability that the stem of the subclade survives to the crown age are included in the likelihood of the backbone thanks to the argument branch_times.
apply_prob_dtt

combi numeric. The combination of shifts defined by its rank in the global comparison.

m NULL or numeric. The set of maximum values for m ranges. Should be as long as the number of parts in the combinaison. Default is NULL (see details).

Details

This funcion calls the function prob_dtt() to calculate paleodiversity dynamics with the probabilistic approach for the different parts of a combination of diversification shifts.

As explained in Billaud et al. (2020), all the sum of probabilities per million year must be equal to 1. However, it can be difficult to reach 1 for groups showing a paleodiversity decline because the range of paleodiversity over which we need to calculate the probabilities can be very large. To circumvent this issue, apply_prob_dtt() set the range of the paleodiversity to the maximum of the deterministic estimate from the function paleodiv() and successively multiplies this maximum by 2, 3, 5, 7 and 10 until the sums of probabilities for each million year reach a minimum of 95%. In few cases, this value of 95% is not reached for few million years. In this case, it might come from an extremely high range of m and maximum values can be manually set up with the argument m.

Value

A list of results from prob_dtt() for subclades and backbone(s).

Author(s)

Nathan Mazet

References


See Also

fit_bd, plot_prob_dtt, prob_dtt

Examples

# loading data
data("Cetacea")
data("taxo_cetacea")
data("shifts_cetacea")

taxo_cetacea_no_genus <- taxo_cetacea[!names(taxo_cetacea) == "Genus"]
```
# apply_prob_dtt() needs the sampling fractions
f_df_cetacea <- get.sampling.fractions(phylo = Cetacea,
   data = taxo_cetacea_no_genus,
   plot = TRUE, cex = 0.3, lad = FALSE)

# use of apply_prob_dtt()
prob_dtt_cetacea <- apply_prob_dtt(phylo = Cetacea,
   data = taxo_cetacea_no_genus,
   shift.res = shifts_cetacea,
   sampling.fractions = f_df_cetacea,
   combi = 1)
```

---

### Balaenopteridae

#### Balaenopteridae Phylogeny

**Description**

Ultrametric phylogenetic tree of the 9 extant Balaenopteridae species

**Usage**

```r
data(Balaenopteridae)
```

**Details**

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

**References**


**Examples**

```r
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

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

### References


### See Also

`CreateGeoObject_BioGeoBEARS`

### Examples

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

---

**BICompare**  
*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

```r
BICompare(phylo,t,meth=c("ultrametric"))
```
build_network.BipartiteEvol

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

- **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_BICompare
- spectR
- JSDtree

Examples

```r
data(Cetacea)
#BICompare(Cetacea,5)
```

Description

Build the interaction network in BipartiteEvol

Build the phylogenies from the output of BipartiteEvol and the corresponding genealogies and phylogenies

Usage

```r
build_network.BipartiteEvol( gen, spec)
```
Arguments

- **gen**: The output of a run of `make_gen.BipartiteEvol`
- **spec**: The output of a run of `define_species.BipartiteEvol`

Value

A matrix $M$ where $M[i,j]$ is the number of individuals from species $i$ (from guild P) interacting with an individual from species $j$ (from guild H)

Author(s)

O. Maliet

References


See Also

- `sim.BipartiteEvol`

Examples

```r
# run the model
set.seed(1)

if(test){

  mod = sim.BipartiteEvol(nx = 8, ny = 4, NG = 800,
                          D = 3, muP = 0.1, muH = 0.1,
                          alphaP = 0.12, alphaH = 0.12,
                          rP = 10, rH = 10,
                          verbose = 100, thin = 5)

  # build the genealogies
gen = make_gen.BipartiteEvol(mod)
plot(gen$H)

  # compute the phylogenies
phy1 = define_species.BipartiteEvol(gen, threshold=1)

  # plot the result
plot_div.BipartiteEvol(gen, phy1, 1)

  # build the network
net = build_network.BipartiteEvol(gen, phy1)

  trait.id = 1
plot_net.BipartiteEvol(gen, phy1, trait.id, net, mod, nx = nx, spatial = FALSE)

```
```r
## add time steps to a former run
seed = as.integer(10)
set.seed(seed)

mod = sim.BipartiteEvol(nx = 8, ny = 4, NG = 200,
D = 3, muP = 0.1, muH = 0.1,
alphaP = 0.12, alphaH = 0.12,
rP = 10, rH = 10,
verbose = 100, thin = 5,
P = mod$P, H = mod$H) # former run output

# update the genealogy
gen = make_gen.BipartiteEvol(mod,
  treeP = gen$P, treeH = gen$H)

# update the phylogenies...
phy1 = define_species.BipartiteEvol(gen, threshold = 1)
#... and the network
net = build_network.BipartiteEvol(gen, phy1)

trait.id = 1
plot_net.BipartiteEvol(gen, phy1, trait.id, net, mod, nx = 10, spatial = FALSE)
```

---

Calomys phylogeny

**Description**

Ultrametric phylogenetic tree of 11 of the 13 extant Calomys species

**Usage**

```r
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)
Caprimulgidae

The Caprimulgidae phylogeny.

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

Usage
data("Caprimulgidae")

Source

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

References

See Also
fit_ClaDS, plot_ClaDS_chains, getMAPS_ClaDS

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 infered 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


References

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


Examples

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

---

**Cetacea_clades**

*Stochastic map of clade membership in Cetacean phylogeny*

Description

simmap object of clade membership in Cetacean phylogeny

Usage

data(Cetacea_clades)

Details

See *Cetacea*

Source

References

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


Examples

data(Cetacea_clades)
print(Cetacea_clades)
plot(Cetacea_clades)

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


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 eported 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 tempera-
ture and biodiversity, origination and extinction in the fossil record Proceedings of the Royal Society
B 275:47-53

time 109:15141-15145

Phanerozoic time Am J Sci 301:182-204
co2_res

Examples

data(co2)
plot(co2)

c02_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


References

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


Examples

data(Cetacea)
print(Cetacea)
plot(Cetacea)
coccolithophore  Coccolithophore diversity since the Jurassic

Description
Coccolithophore fossil diversity since the Jurassic

Usage
data(coccolithophore)

data(coccolithophore)

plot(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

Examples

CreateClassObject  Create class object

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(map, rnd=5, return.mat=FALSE)
Arguments

map  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`)

return.mat  logical indicating whether to return simmap in a format to be passed to other
             internal functions (usually FALSE)

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 inter-
              val (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 func-
       tions)

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. Contrast-
ing impacts of competition on ecological and social trait evolution in songbirds. PLOS Biology.

trait evolution using maximum likelihood inference. Systematic Biology doi 10.1093/sysbio/syw020

See Also

`fit_t_comp_subgroup`, `CreateGeobyClassObject`

Examples

data(Anolis.data)

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

- **phylo**: the object of type 'phylo' (see ape documentation) used to build ancestral range stochastic maps in BioGeoBEARS
- **simmap**: a phylo object created using `make.simmap` in phytools
- **trim.class**: category in the simmap object that represents the subgroup of interest (see Details and Examples)
- **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 ancestral biogeography stochastic map was built from a stratified analysis in BioGeoBEARS
- **rnd**: 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.
CreateGeobyClassObject

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


See Also

fit_t_comp_subgroup, CreateGeoObject_BioGeoBEARS, CreateClassObject

Examples

data(BGB.examples)

Canidae.phylo<-BGB.examples$Canidae.phylo
names(dummy.group)<-Canidae.phylo$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)
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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>phylo</td>
<td>an object of type 'phylo' (see ape documentation)</td>
</tr>
<tr>
<td>map</td>
<td>either a matrix modified from phylo$edge or a phylo object created using make.simmap (see Details and Examples)</td>
</tr>
</tbody>
</table>

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)
CreateGeoObject_BioGeoBEARS

Author(s)
Jonathon Drury jonathan.p.drury@gmail.com

References

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.simmap 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.simmap(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 BioGeoBEARS

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, simmap.out=FALSE)
Arguments

- **full.phylo**: the object of type 'phylo' (see ape documentation) that was used to construct the stochastic map in BioGeoBEARS.
- **trimmed.phylo**: 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.
- **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.
- **simmap.out**: logical indicating whether output should be a stochastic map (simmap) object (see note).

Details

Note: generating a stochastic map output using `simmap.out=TRUE` and passing to `fit_t_comp` for diversity dependent models with biogeography greatly speeds up model fitting compared to output generated when `simmap.out=FALSE`. This cannot be used for matching competition or any two-regime models with biogeography.

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


See Also

`fit_t_comp` `CreateGeoObject`
**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**

```r
createModel(tree, keyword)
```
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**


**Examples**

```r
#Loading example trees
newick2 <- "((X:1.5,Y:1.5):3,Z:4.5);"

#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**

```r
data(d13c)
```
define_species.BipartiteEvol

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


Examples

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

---

define_species.BipartiteEvol

*Build the phylogenies for BipartiteEvol*

Description

Build the phylogenies from the output of BipartiteEvol and the corresponding genealogies

Usage

```r
define_species.BipartiteEvol(genealogy, threshold = 1,
    distanceH = NULL, distanceP = NULL, verbose = T,
    monophyly = TRUE, seed = NULL)
```

Arguments

- `genealogy` The output of a run of make_gen.BipartiteEvol
- `threshold` The species definition ratchet (s)
- `distanceH` Distance (ie nb of mutations) matrix between the individual of clade H
- `distanceP` Distance (ie nb of mutations) matrix between the individual of clade P
- `verbose` Should the progression of the computation be printed?
- `monophyly` Should the species delineations be strictly monophyletic species (TRUE - default) or not (FALSE)? If not, the threshold must be equal to 1.
- `seed` If monophyly==FALSE, the seed is used to pick one representative individual per (potentially non-monophyletic) species.
define_species.BipartiteEvol

Details

If monophyly==TRUE, species delineation is performed using the model of Speciation by Genetic Differentiation (Manceau et al., 2015) where the ‘threshold’ (the number of mutations needed to belong to different species) can vary. It results in monophyletic species. If monophyly==FALSE, we consider that each new mutation (i.e. each new combination of traits) gives rise to a new species (Perez-Lamarque et al., 2021). As a result, species are not necessarily formed by a monophyletic group of individuals.

Value

a list with

P The species identity of each individual in guild P
H The species identity of each individual in guild H
Pphylo The phylogeny for guild P
Hphylo The phylogeny for guild H

Author(s)

O. Maliet & B. Perez-Lamarque

References


See Also

sim.BipartiteEvol

Examples

# run the model
set.seed(1)

if(test){

mod = sim.BipartiteEvol(nx = 8,ny = 4,NG = 800,
D = 3, muP = 0.1 , muH = 0.1,
alphaP = 0.12, alphaH = 0.12,
rP = 10, rH = 10,
verbose = 100, thin = 5)
delineate_phylotypes

Automatic phylotypes delineation

Description

This function traverses a tree from the root to the tips, at every node computes the average similarity of all sequences descending from the node, and collapses the sequences into a single phylotype if
their sequence dissimilarity is lower than a given threshold. The average similarity can be computed using raw measured of the average similarity or using measures of genetic diversity (nucleotidic diversity "pi" (Nei & Li, 1979) or Watterson "theta" (Watterson, 1975)) which correct for gaps in the nucleotidic alignments (Ferretti et al., 2012).

Usage

delineate_phylotypes(tree, thresh=97, sequences, method="pi")

Arguments

tree a phylogenetic tree of all the sequences. It must be an object of class "phylo" and must be rooted.

thresh a numeric digit between 0 and 100 indicating the minimal average similarity to collapse sequences within the same phylotype. By default, the average similarity is 97.

sequences a matrix representing the nucleotidic alignment of all the sequences present in the phylogenetic tree.

method indicates which method to use to compute the average similarity: "mean" computes the average raw distances between pairs of sequences, "pi" (default) measures the nucleotidic diversity (Nei & Li, 1979) while controlling for gaps in the alignment, and "theta" measures the Watterson theta genetic diversity (Watterson, 1975) also controlling for gaps.

Value

A table with its row names corresponding to the sequence names. The first column corresponds to the phylotype assignation and the second columns indicates the name of the representative sequence of each phylotype (longest sequence available). Phylotypes are numbered starting at 1, and all the phylotypes named "0" correspond to singletons.

Author(s)

Benoît Perez-Lamarque

References


div.models

Model comparison of diversification models

Description

Applies a set of birth-death models to a phylogeny.

Usage

div.models(phylo, tot_time, f, backbone = F, spec_times = NULL, branch_times = NULL, models = c("BCST", "BCST_DCST", "BVAR", "BVAR_DCST", "BCST_DVAR", "BVAR_DVAR"), cond, verbose = T, n.max = NULL, rate.max = NULL)

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
    numeric. The sampling fraction given as the number of species in the phylogeny over the number of species described in the taxonomy.
backbone
    character. Allows to analyse a backbone. Default is FALSE and spec_times and branch_times are then ignored. Otherwise:
• "stem.shift": for every shift, the probability of the speciation event at the stem age of the subclade is included in the likelihood of the backbone thanks to the argument spec_times.
• "crown.shift": for every shift, both the probability of the speciation event at the stem age of the subclade and the probability that the stem of the subclade survives to the crown age are included in the likelihood of the backbone thanks to the argument branch_times.

**spec_times**
a numeric vector of the stem ages of subclades. Used only if backbone = "stem.shift". Default is NULL.

**branch_times**
a list of numeric vectors. Each vector contain the stem and crown ages of subclades (in this order). Used only if backbone = "crown.shift". Default is NULL.

**models**
a vector of character. Defines the set of birth-death models to applies e.g. BCST means pure-birth constant rate model, BCST_DVAR means birth constant rate and death variable rate model. Default is c("BCST", "BCST_DCST", "BVAR", "BVAR_DCST", "BCST_DVAR", "BVAR_DVAR") and applies all combinations of constant or variable rates for speciation and extinction. Time dependency is only exponential.

**cond**
conditioning to use to fit the model:
  • FALSE: no conditioning (not recommended);
  • "stem": conditioning on the survival of the stem lineage (used 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 on survival of the two daugther lineages (used when the stem age is not known, in this case tot_time should be the crown age).

**verbose**
boolean. Wether to print model names and AICc values during the calculation.

**rate.max**
numeric. Set a limit of diversificaton rates in terms of rate values.

**n.max**
numeric. Set a limit of diversificaton rates in terms of diversity estimates with the deterministic approach.

**Details**
Parameters of birth-death models are defined backward in time such as a positive alpha corresponds to a speciation rate decreasing through time from the past to the present.

**Value**
A data.frame with number of parameters, likelihood, AICc and parameter values for all models.

**Author(s)**
Nathan Mazet

**References**
div.rates

Diversification rates through time

Description

Calculates diversification rates through time from shift.estimates() output.

Usage

div.rates(phylo, shift.res, combi = 1, part = "backbone",
          time.interval = 1, backbone.option = "crown.shift")

Arguments

phylo an object of type 'phylo' (see ape documentation)
shift.res the output resulting from shift.estimates.
combi numeric. The combination of shifts defined by its rank in the global comparison.
part character. Specifies for which parts of the combination diversification rates has to be calculated. Default is "backbone" and provides only the backbone rate. Can be "all" for all the parts of a combination or "subclades" for subclades only.
backbone.option type of the backbone analysis (see backbone.option in shift.estimates for more details):
  • "stem.shift": rates are calculated from the stem age for subclades.
  • "crown.shift": rates are calculated from the crown age for subclades.
time.interval numeric. Define the time interval (in million years) at which diversification rates are calculated. Default is 1 for a value at each million year.

Value

a list of matrix with two rows (speciation and extinction) and as many columns as million years from the root to the present.

Author(s)

Nathan Mazet
References


See Also

   shift.estimates

Examples

# loading data
data("Cetacea")
data("shifts_cetacea")

# with shifts_cetacea the output from shift.estimates()
rates <- div.rates(phylo = Cetacea, shift.res = shifts_cetacea,
                   combi = 1, part = "all")

---

`fitTipData` *Maximum likelihood estimators of a model’s parameters*

Description

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

Usage

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

Arguments

   object  an object of class 'PhenotypicModel'.
   data    vector of tip trait data.
   error   vector of intraspecific (i.e., tip-level) standard error of the mean. Specify NULL if no error data are available
   params0 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.
   GLSstyle 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.
   v       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

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

Author(s)

M Manceau

References


Examples

```r
#Loading an example tree
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)
```

Description

~~ Methods for function fitTipData ~~

Methods

```r
signature(object = "PhenotypicModel")
```

This is the only method available for this function. Same behaviour for any PhenotypicModel.
**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**

```r
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 $\lambda$ 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 $\mu$ 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 `optim` 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 \( \mu \) 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 contant 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:

- 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 daugther 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 \( \lambda \) with time is estimated to be positive (for example), this means that the speciation rate decreases from past to present. Note that abs(f.lamb) and abs(f.mu) are used in the likelihood computation as speciation and extinction rates should always be positive. A consequence of this is that negative speciation/extinction rates estimates can be returned. They should be interpreted in absoslute terms. See Morlon et al. 2020 for a more detailed explanation.

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
lamb_par a numeric vector of estimated f.lamb parameters, in the same order as defined in f.lamb
mu_par a numeric vector of estimated f.mu parameters, in the same order as defined in f.mu (if fix.mu is FALSE)

Author(s)
H Morlon

References

See Also
plot_fit_bd, plot_dtt, likelihood_bd, fit_env

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 pure birth model (no extinction) with linear variation of
# the speciation rate with time
f.lamb <-function(t,y){abs(y[1] + y[2] * t)}
# alternative formulation that can be used depending on the choice made to avoid negative rates:
# f.lamb <- function(t, y) {pmax(0, y[1] + y[2] * t)}, see Morlon et al. (2020)
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$aicc, result_exp$aicc, result_lin$aicc, result_bexp_dcst$aicc))
#rbind(result_cst, result_exp, result_lin, result_bexp_dcst)[index,]

---

fit_bd_backbone

**Maximum likelihood fit of the general birth-death model (backbone)**

**Description**


**Usage**

```
fit_bd_backbone(phylo, tot_time, f.lamb, f.mu, lamb_par, mu_par, f = 1,
               backbone, spec_times, branch_times,
               meth = "Nelder-Mead", cst.lamb = FALSE, cst.mu = FALSE,
               expo.lamb = FALSE, expo.mu = FALSE, fix.mu = FALSE,
               dt=1e-3, cond = "crown", model)
```

**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;
fit_bd_backbone

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 \( \mu \) 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

backbone

character. Allows to analyse a backbone. Default is FALSE and spec_times and branch_times are then ignored. Otherwise

• "stem.shift": for every shift, the probability of the speciation event at the stem age of the subclade is included in the likelihood of the backbone thanks to the argument spec_times.

• "crown.shift": for every shift, both the probability of the speciation event at the stem age of the subclade and the probability that the stem of the subclade survives to the crown age are included in the likelihood of the backbone thanks to the argument branch_times.

spec_times

a numeric vector of the stem ages of subclades. Used only if backbone = "stem.shift". Default is NULL.

branch_times

a list of numeric vectors. Each vector contains the stem and crown ages of subclades (in this order). Used only if backbone = "crown.shift". Default is NULL.

meth

optimization to use to maximize the likelihood function, see optim 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.
fit_bd_backbone

fix.mu logical: if set to TRUE, the extinction rate $\mu$ 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:
• 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 two daughter lineages (use when the stem age is not known, in this case tot.time should be the crown age).

model character. The model name as defined in the function div.models.

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 $\lambda$ with time is estimated to be positive (for example), this means that the speciation rate decreases from past to present. Note that abs(f.lamb) and abs(f.mu) are used in the likelihood computation as speciation and extinction rates should always be positive. A consequence of this is that negative speciation/extinction rates estimates can be returned. They should be interpreted in absolute terms. See Morlon et al. 2020 for a more detailed explanation.

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
lamb_par a numeric vector of estimated f.lamb parameters, in the same order as defined in f.lamb
mu_par a numeric vector of estimated f.mu parameters, in the same order as defined in f.mu (if fix.mu is FALSE)

Author(s)

Hélène Morlon, Nathan Mazet
References


See Also

plot_fit_bd, plot_dtt, likelihood_bd, fit_env

Examples

# Some examples may take a little bit of time. Be patient!
data(Cetacea)
tot_time<-max(node.age(Cetacea)$ages)
# Fit the pure birth model (no extinction) with a constant speciation rate
f.lamb <-function(t,y){y[1]}
f.muc<-function(t,y){0}
lamb_par<-c(0.09)
mu_par<-c()
#result_cst <- fit_bd(Cetacea,tot_time,f.lamb,f.mu,lamb_par,mu_par,
# f=87/89,cst.lamb=TRUE,fix.mu=TRUE,dt=1e-3)
#result_cst$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.muc<-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$model <- "pure birth with exponential variation in speciation rate"
# Fit the pure birth model (no extinction) with linear variation of
# the speciation rate with time
f.lamb <-function(t,y){abs(y[1] + y[2] * t)}
# alternative formulation that can be used depending on the choice made to avoid negative rates:
# f.lamb <-function(t,y){pmax(0,y[1] + y[2] * t)}, see Morlon et al. (2020)
f.muc<-function(t,y){0}
lamb_par<-c(0.09, 0.001)
mu_par<-c()
#result_lin <- fit_bd(Cetacea,tot_time,f.lamb,f.mu,lamb_par,mu_par,f=87/89,fix.mu=TRUE,dt=1e-3)
#result_lin$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.muc <-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$model <- "birth-death with exponential variation in speciation rate
# and constant extinction"
# Find the best model
#index <- which.min(c(result_cst$aicc, result_exp$aicc, result_lin$aicc,result_bexp_dcst$aicc))
#rbind(result_cst, result_exp, result_lin, result_bexp_dcst)[index,]

---

**fit_bd_backbone_c**

*Maximum likelihood fit of the general birth-death model (backbone and constraints)*

**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. Modified version of fit_bd for backbones and to add constraints on rate estimates.

**Usage**

```r
fit_bd_backbone_c(phylo, tot_time, f.lamb, f.mu, lamb_par, mu_par, f = 1,
backbone, spec_times, branch_times,
meth = "Nelder-Mead", cst.lamb = FALSE, cst.mu = FALSE,
expo.lamb = FALSE, expo.mu = FALSE, fix.mu = FALSE,
dt=1e-3, cond = "crown", model, rate.max, n.max)
```

**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 \( \lambda \) 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 \( \mu \) 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

**backbone**  
a character. Allows to analyse a backbone. Default is FALSE and spec_times and branch_times are then ignored. Otherwise

- "stem.shift": the stems of subclades are included in subclade analyses;
- "crown.shift": the stems of subclades are included in the backbone analysis.

**spec_times**  
a numeric vector of the stem ages of subclades. Used only if backbone = "stem.shift". Default is NULL.

**branch_times**  
a list of numeric vectors. Each vector contains the stem and crown ages of subclades (in this order). Used only if backbone = "crown.shift". Default is NULL.

**meth**  
optimization to use to maximize the likelihood function, see *optim* 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 $\mu$ 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:

- 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).

**model**  
a character. The model name as defined in the function *div.models*.
rate.max  numeric. Set a limit of diversification rates in terms of rate values.
n.max   numeric. Set a limit of diversification rates in terms of diversity estimates with the deterministic approach.

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 $\lambda$ with time is estimated to be positive (for example), this means that the speciation rate decreases from past to present. Note that abs(f.lamb) and abs(f.mu) are used in the likelihood computation as speciation and extinction rates should always be positive. A consequence of this is that negative speciation/extinction rates estimates can be returned. They should be interpreted in absolute terms. See Morlon et al. 2020 for a more detailed explanation.

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
- lamb_par a numeric vector of estimated f.lamb parameters, in the same order as defined in f.lamb
- mu_par a numeric vector of estimated f.mu parameters, in the same order as defined in f.mu (if fix.mu is FALSE)

Author(s)

Hélène Morlon, Nathan Mazet

References


See Also

plot_fit_bd, plot_dtt, likelihood_bd, fit_env
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$model <- "pure birth with exponential variation in speciation rate"
# Fit the pure birth model (no extinction) with linear variation of
# the speciation rate with time
f.lamb<-function(t,y){abs(y[1] + y[2] * t)}
# alternative formulation that can be used depending on the choice made to avoid negative rates:
# f.lamb <-function(t,y){pmax(0,y[1] + y[2] * t)}, see Morlon et al. (2020)
f.mu<-function(t,y){0}
lamb_par<-c(0.05, 0.001)
mu_par<-c()
result_lin <- fit_bd(Cetacea,tot_time,f.lamb,f.mu,lamb_par,mu_par,f=87/89,fix.mu=TRUE,dt=1e-3)
#result_lin$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$model <- "birth-death with exponential variation in speciation rate
# and constant extinction"
# Find the best model
#index <- which.min(c(result_cst$aicc, result_exp$aicc, result_lin$aicc,result_bexp_dcst$aicc))
#rbind(result_cst, result_exp, result_lin, result_bexp_dcst)[index,]
**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**


**See Also**

*fit_ClaDS*, *plot_ClaDS_chains*. 
Examples

```r
if(test){
  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**

```r
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 independent 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**


**See Also**

getMAPS_ClaDS0, plot_ClaDS0_chains, fit_ClaDS
Examples

```r
set.seed(1)

if(test){
  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

```r
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 `optim` 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 cst.rate is FALSE)

Author(s)

H Morlon
References

See Also
likelihood_coal_cst, fit_coal_var

Examples

data(Cetacea)

if(test){
  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)
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
  - model: the name of the fitted model
  - LH: the maximum log-likelihood value
  - aicc: the second order Akaike's Information Criterion
  - model.parameters: the estimated parameters

Author(s)

H Morlon

References


See Also

- likelihood_coal_var, fit_coal_cst

Examples

```r
library(phytools)

# Cetacea data
data(Cetacea)

if(test){
  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

```r
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 $\lambda$ 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 $\mu$ 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 sm.spline for details.
- **f**: the fraction of extant species included in the phylogeny
- **meth**: optimization to use to maximize the likelihood function, see optim 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 $\mu$ 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:
  • 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.

Note that abs(f.lamb) and abs(f.mu) are used in the likelihood computation as speciation and extinction rates should always be positive. A consequence of this is that negative speciation/extinction rates estimates can be returned. They should be interpreted in absolute terms. See Morlon et al. 2020 for a more detailed explanation.

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
lamb_par a numeric vector of estimated f.lamb parameters, in the same order as defined in f.lamb
mu_par a numeric vector of estimated f.mu parameters, in the same order as defined in f.mu (if fix.mu 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


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)
fit_sgd

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 optim 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


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**

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

**Arguments**

- **phylo**: an object of type 'phylo' (see ape documentation)
- **data**: a named vector of trait values with names matching `phylo$tip.label`
- **error**: A named vector with standard errors (SE) of trait values for each species (with names matching "phylo$tip.label"). The default is NULL, in this case potential error is ignored in the fit. If set to NA, the SE is estimated from the data (to be used when there are no error measurements, a nuisance parameter is estimated). Note: When standard errors are provided, a nuisance parameter is also estimated.
- **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.
- **pars**: vector specifying starting parameter values for maximum likelihood optimization. If unspecified, default values are used (see Details)
- **geography.object**: if incorporating biogeography, a list of sympatry through time created using `CreateGeoObject`
- **regime.map**: if running two-regime versions of models, a stochastic map of the two regimes stored as a simmap object output from `make.simmap`

**Details**

Note: if including known measurement error, the model fit incorporates this known error and, in addition, estimates an unknown, nuisance contribution to measurement error. The current implementation does not differentiate between the two, so, for instance, it is not possible to estimate the nuisance measurement error without providing the known, intraspecific error values.

For single-regime fits without measurement error, `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 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.

For two-regime fits without measurement error, the second and third values for par correspond to the first and second S, b, or r value (run trial fit to see which regime corresponds to each slope).

For fits including measurement error, the default starting value for sig2 is $0.95 \times \text{var(data)}/\text{max(nodeHeights(phylo))}$, and nuisance values start at $0.05 \times \text{var(data)}/\text{max(nodeHeights(phylo))}$. In all cases, the nuisance parameter is the last in the par vector, with the order of other variables as described above.

For two-regime fits, particularly under the matching competition model, we recommend fitting with several different starting values.

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 sig2 parameter
- S: maximum-likelihood estimate of S parameter of matching competition model (see Note)
- b: maximum-likelihood estimate of b parameter of linear diversity dependence model
- r: maximum-likelihood estimate of r parameter of exponential diversity dependence model
- z0: maximum-likelihood estimate of z0, the value at the root of the tree
- nuisance: maximum-likelihood estimate of nuisance, the unknown, nuisance contribution to measurement error (see details)
- convergence: convergence diagnostics from optim function (see optim 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., Tobias, J., Rolland, J., Sheard, C., and Morlon, H. Tempo and mode of morphological evolution are decoupled from latitude in birds. *PLOS Biology* doi:10.1371/journal.pbio.3001270


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$phylo
regime.map<-Anolis.data$regime.map

# 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)

# Now fit models that estimate parameters separately according to different 'regimes'
MC.two_regime.fit<-fit_t_comp(phylo, pPC1, model="MC", regime.map=regime.map)
DDlin.two_regime.fit<-fit_t_comp(phylo, pPC1, model="DDlin", regime.map=regime.map)
DDexp.two_regime.fit<-fit_t_comp(phylo, pPC1, model="DDexp", regime.map=regime.map)

# Now fit models that estimate parameters separately according to different 'regimes', # including biogeography
MC.two_regime.geo.fit<-fit_t_comp(phylo, pPC1, model="MC", geography.object=geography.object, regime.map=regime.map)
DDlin.two_regime.geo.fit<-fit_t_comp(phylo, pPC1, model="DDlin", geography.object=geography.object, regime.map=regime.map)
DDexp.two_regime.geo.fit<-fit_t_comp(phylo, pPC1, model="DDexp", geography.object=geography.object, regime.map=regime.map)
fit_t_comp_subgroup  Fits models of trait evolution incorporating competitive interactions, restricting competition to occur only between members of a subgroup

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

```r
fit_t_comp_subgroup(full.phylo, data, subgroup, subgroup.map, 
                    model=c("MC","DDexp","DDlin"), ana.events=NULL, clado.events=NULL, 
                    stratified=FALSE, regime.map=NULL, error=NULL, 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
- `data` a named vector of trait values for subgroup members with names matching `full.phylo$tip.label`
- `subgroup` subgroup whose members are competing
- `subgroup.map` a phylo object created using `make.simmap` in phytools that contains reconstructed subgroup membership
- `model` model chosen to fit trait data, "MC" is the matching competition model of Nuismer & Harmon 2014, "DDlin" is the diversity-dependent linear model, and "DDexp" is the diversity-dependent exponential model of Weir & Mursleen 2013.
- `ana.events` the "ana.events" table produced in BioGeoBEARS that lists anagenetic events in the stochastic map
- `clado.events` the "clado.events" table produced in BioGeoBEARS that lists cladogenetic events in the stochastic map
- `stratified` logical indicating whether the stochastic map was built from a stratified analysis in BioGeoBEARS
- `regime.map` a phylo object created using `make.simmap` in phytools that contains reconstructed competitive regime membership (see Details)
- `error` A named vector with standard error (SE) for each species (with names matching "phylo$tip.label"). Default is NULL, if NA, then the SE is estimated from the data (a nuisance parameter for unknown errors). Note: When standard error are provided the nuisance parameter is also estimated.
par vector specifying starting parameter values for maximum likelihood optimization. If unspecified, default values are used (see Details).
method optimization algorithm to use (see optim; for DD models without biogeography, method="BB" is also supported, which uses spg).
bounds (optional) list of bounds to pass to optimization algorithm (see details at optim).

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 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. We recommend running ML optimization with several different starting values to ensure convergence.
Currently, this function can be used to implement the following models: 1. Subgroup pruning with biogeography: matching competition, diversity dependent 2. Subgroup pruning without biogeography: diversity dependent 3. Subgroup pruning without biogeography (two-regimes): diversity dependent (for more details, see fit_t_comp).

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 sig2 parameter
S maximum-likelihood estimate of S parameter of matching competition model (see Note)
b maximum-likelihood estimate of b parameter of linear diversity dependence model (see Note)
r maximum-likelihood estimate of r parameter of exponential diversity dependence model (see Note)
z0 maximum-likelihood estimate of z0, the value at the root of the tree
convergence convergence diagnostics from optim function (see optim documentation)
nuisance maximum-likelihood estimate of nuisance, the unknown, nuisance contribution to measurement error when error argument is used (that is NA or a vector provided by the user).

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., Clavel, J. Tobias, J., Rolland, J., Sheard, C., and Morlon, H. Tempo and mode of morphological evolution are decoupled from latitude in birds. *PLOS Biology* doi:10.1371/journal.pbio.3001270


See Also

likelihood_subgroup_model CreateGeobyClassObject fit_t_comp

Examples

data(BGB.examples)

#Prepare dataset with subgroups and biogeography
Canidae.phylo<-BGB.examples$Canidae.phylo
names(dummy.group)<-Canidae.phylo$tip.label

Canidae.simmap<-phytools::make.simmap(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")]

#Fit model with subgroup pruning and biogeography
MC.fit_subgroup_geo<-fit_t_comp_subgroup(full.phylo=Canidae.phylo, ana.events=BGB.examples$Canidae.ana.events, clado.events=BGB.examples$Canidae.clado.events, stratified=FALSE,subgroup.map=Canidae.simmap, data=Canidae.A,subgroup="A",model="MC")
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 errors (SE) of trait values for each species (with names matching 'phylo$tip.label'). The default is NULL, in this case potential error is ignored in the fit. If set to NA, the SE is estimated from the data (to be used when there are no error measurements, a nuisance parameter is estimated). Note: When standard errors are provided, a nuisance parameter is also estimated.

model
The model describing the functional form of variation of the evolutionary rate \( \sigma^2 \) 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 \( \sigma^2 \) parameter and param[2] is the \( \beta \) 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

- `LH` the maximum log-likelihood value
- `aic` the Akaike’s Information Criterion
- `aicc` the second order Akaike’s Information Criterion
- `free.parameters` 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)
- `nuisance` maximum-likelihood estimate of `nuisance`, the unknown, nuisance contribution to measurement error when `error` argument is used (i.e., NA or a vector provided by the user)
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


See Also

plot.fit_t.env, likelihood_t_env

Examples

if(test){
  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
if(require(pspline)){
  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*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)
**Description**

Fits Ornstein-Uhlenbeck (OU) model of trait evolution for which the optimum depends on an environmental function, or more generally a time varying function.

**Usage**

```r
fit_t_env_ou(phylo, data, env_data, error=NULL, model,
             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 errors (SE) of trait values for each species (with names matching `"phylo$tip.label"`). The default is NULL, in this case potential error is ignored in the fit. If set to NA, the SE is estimated from the data (to be used when there are no error measurements, a nuisance parameter is estimated). Note: When standard errors are provided, a nuisance parameter is also estimated.
- `model`: A user defined model. If not provided, a default model is used (see details)
- `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_ou` allows fitting OU-environmental models of trait evolution (Troyer et al. 2020, Goswami & Clavel 2024). Compared to model implemented in `fit_t_env` where the rate of phenotypic evolution evolves as a function of an environmental variable (Clavel & Morlon 2020), here it’s the optimum of a generalized Ornstein-Uhlenbeck (also called Hull-White model) that can changes as a function of an environmental variable T(t). More formally, the model is defined by the following process:

\[ dX(t) = \alpha(\theta(t) - X(t))dt + \sigma dB(t) \]

Note that this model works only on NON-ULTRAMETRIC trees (e.g., with fossils)

The default model has the optimum changing as a function of environmental changes though times as defined below:

\[ \theta(t) = \theta_0 + \beta T(t) \]
Users defined models should have the following form (see also examples below):

```
fun <- function(t, env, param, theta0){ theta0 + 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.

\( theta_0 \): is the state at the root of the tree.

For instance, the default model function can be coded as:

```
fun <- function(t, env, param, theta0){ theta0 + param[1]*env(t)}
```

where `param[1]` is the \( \beta \) parameter. Note that in this case, one starting value should be provided in the `param` argument.

e.g.:
```
beta=0
fit_t_env(tree, data, env_data=InfTemp, model=fun, param=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.

-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:

- `LH`: the maximum log-likelihood value
- `aic`: the Akaike’s Information Criterion
- `aicc`: the second order Akaike’s Information Criterion
- `free.parameters`: 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 custom 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)

nuisance: 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**


**See Also**

`plot.fit_t.env.ou, sim_t_env.ou`

**Examples**

data(InfTemp)

# Simulate a trait with temperature dependence of the optimum on a simulated tree

set.seed(9999) # for reproducibility

# Let's start by simulating a trait under a climatic OU
beta = 0.6 # relationship to the climate curve
sim_theta = 4 # value of the optimum if the relationship to the climate curve is 0
sim_sigma2 = 0.025 # variance of the scatter = sigma^2
sim_alpha = 0.36  # alpha value = strength of the OU; quite high here...
delta = 0.001    # time step used for the forward simulations => here its 1000y steps
tree <- phytools::pbtree(n=200, d=0.3)  # simulate a bd tree with some extinct lineages
toolage = 60  # height of the root (almost all the Cenozoic here)
tree$edge.length <- root_age*tree$edge.length/max(phytools::nodeHeights(tree))
# here - for this contrived example - I scale the tree so that the root is at 60 Ma

trait <- sim_t_env_ou(tree, sigma=sqrt(sim_sigma2), alpha=sim_alpha, theta0=sim_theta,
                        param=beta, env_data=InfTemp, step=0.01, scale=TRUE, plot=TRUE)

## Fit the Environmental model (default)
result1 <- fit_t_env_ou(phylo = tree, data = trait, env_data =InfTemp,
                         method = "Nelder-Mead", df=50, scale=TRUE)
plot(result1)

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

# We re-define the function for the OU model with linear trend to the climatic curve
# NOTE: the env(t) function should return the value at the root for t=0
my_fun<-function(t, env, param, theta0){
  theta0 + param[1]*env(t)
}

# starting value for param[1]. Here we use an arbitrary value of 0.1
beta_guess = 0.1

# fit the model
result2 <- fit_t_env_ou(phylo = tree, data = trait, env_data =InfTemp,
                         model = my_fun, param = beta_guess,
                         method = "Nelder-Mead", df=50, scale=TRUE)

# Retrieve the parameters and compare to 'result1'
result2
lines(result2, col="red", lty=2)

## Fit user defined environmental function

require(pspline)
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 (not scaled here)
env_data<splinefun(t,env_func(t))

# We then fit the model
result3 <- fit_t_env_ou(phylo = tree, data = trait, env_data = env_data,
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

```r
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
- `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 its 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


See Also

ancestral, phyl.pca_pl, GIC.fit_pl.rpanda, gic_criterion mvgl
Examples

if(test){
  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)
}

fit_t_standard

Fits standard models of trait evolution incorporating known and nuisance measurement error

Description

Fits Brownian motion (BM), Ornstein-Uhlenbeck (OU), or early burst (EB) models of trait evolution to a given dataset and phylogeny.

Usage

fit_t_standard(phylo, data, model=c("BM","OU","EB"), error=NULL, two.regime=FALSE, method="Nelder-Mead", echo=TRUE, ...)

Arguments

phylo an object of type 'phylo' (see ape documentation); if two.regime=TRUE, this must be a simmap object from make.simmap with two regimes

data a named vector of trait values with names matching phylo$tip.label

model model chosen to fit trait data, "BM" is the Brownian motion model, "OU" is the Ornstein-Uhlenbeck model, and "EB" is the early burst model.
A named vector with standard errors (SE) of trait values for each species (with names matching "phylo$tip.label"). The default is NULL, in this case potential error is ignored in the fit. If set to NA, the SE is estimated from the data (to be used when there are no error measurements, a nuisance parameter is estimated). Note: When standard errors are provided, a nuisance parameter is also estimated.

if TRUE, fits a two-regime model

optimization method from link{optim}

prints information to console during fit

Optional arguments. e.g. "upper=xx", "lower=xx" to specify bounds on the parameter search. "fixedRoot=TRUE" to use an OU model where the root state is assumed fixed (instead of sampled from the stationary distribution)

Note: if including known measurement error, the model fit incorporates this known error and, in addition, estimates an unknown, nuisance contribution to measurement error. The current implementation does not differentiate between the two, so, for instance, it is not possible to estimate the nuisance measurement error without providing the known, intraspecific error values.

a list with the following elements:

maximum log-likelihood value

Akaike Information Criterion value

AIC value corrected for small sample size

number of free parameters from the model

maximum-likelihood estimate of sig2 parameter

maximum-likelihood estimate of alpha parameter of OU model (see Note)

maximum-likelihood estimate of the slope parameter of early burst model

maximum-likelihood estimate of z0, the value at the root of the tree

maximum-likelihood estimate of nuisance, the unknown, nuisance contribution to measurement error (see details)

convergence diagnostics from optim function (see optim documentation)

Jonathan Drury jonathan.p.drury@gmail.com

Julien Clavel

fit_t_comp sim_t_tworegime
Examples

```r
if(test){
  data(Cetacea_clades)
  data<-sim_t_tworegime(Cetacea_clades,pars=c(sig2=0.01,r1=-0.01,r2=-0.02),
                        root.value=0,Nsegments=1000,model="EB")
  error<-rep(0.05,length(Cetacea_clades$tip.label))
  names(error)<-Cetacea_clades$tip.label

  #Fit single-regime models
  BM1.fit<-fit_t_standard(Cetacea_clades,data,model="BM",error,two.regime=FALSE)
  OU1.fit<-fit_t_standard(Cetacea_clades,data,model="OU",error,two.regime=FALSE)
  EB1.fit<-fit_t_standard(Cetacea_clades,data,model="EB",error,two.regime=FALSE)

  #Now fit models that incorporate biogeography, NOTE these models take longer to fit
  BM2.fit<-fit_t_standard(Cetacea_clades,data,model="BM",error,two.regime=TRUE)
  OU2.fit<-fit_t_standard(Cetacea_clades,data,model="OU",error,two.regime=TRUE)
  EB2.fit<-fit_t_standard(Cetacea_clades,data,model="EB",error,two.regime=TRUE)
}
```

---

<table>
<thead>
<tr>
<th>foraminifera</th>
<th>Foraminifera diversity since the Jurassic</th>
</tr>
</thead>
</table>

### 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


get.comb.shift

Examples

data(foraminifera)
plot(foraminifera)

Description

Provides all the combinations of nodes of a phylogeny where shifts of diversification can be tested.

Usage

get.comb.shift(phylo, data, sampling.fractions,
    clade.size = 5, Ncores = 1)

Arguments

phylo an object of type 'phylo' (see ape documentation)
data a data.frame containing a database of monophyletic groups for which potential shifts can be tested. This database should be based on taxonomy, ecology or traits and must contain a column named "Species" with species names as in phylo.
sampling.fractions the output resulting from get.sampling.fractions.
clade.size numeric. Define the minimum number of species in a subgroup. Default is 5.
Ncores numeric. Define the number of CPU cores to use for parallelizing the computation of combinations.

Details

clade.size argument should be the same value for the whole procedure (same that for get.sampling.fraction and shift.estimates).

Value

a vector of character summarizing the combination of shifts as a concatenation of node IDs separated by "." or "/". Node IDs at the left of "/" correspond to shifts at the origin of subclades (monophyletic and ultrametric subtrees) while node IDs at the right of "/" correspond to shifts at the origin of backbone(s) (pruned trees).

Author(s)

Nathan Mazet
get.sampling.fractions

References

See Also
get.sampling.fractions, shift.estimates

Examples

# loading data
data("Cetacea")
data("taxo_cetacea")

# no shifts tested at genus level
taxo_cetacea_no_genus <- taxo_cetacea[names(taxo_cetacea) != "Genus"]

f_cetacea <- get.sampling.fractions(phylo = Cetacea,
data = taxo_cetacea_no_genus)

comb.shift_cetacea <- get.comb.shift(phylo = Cetacea,
data = taxo_cetacea_no_genus,
sampling.fractions = f_cetacea,
Ncores = 4)

get.sampling.fractions

Sampling fractions of subclades

Description
Provides the sampling fractions of a phylogenetic tree from a complete database.

Usage
get.sampling.fractions(phylo, data, clade.size = 5, plot = F,
lad = T, text.cex = 1, pch.cex = 0.8, ...)

Arguments
phylo an object of type 'phylo' (see ape documentation)
data a data.frame containing a database of monophyletic groups for which potential shifts can be tested. This database should be based on taxonomy, ecology or traits and must contain a column named "Species" with species names as in phylo.
get.sampling.fractions

clade.size numeric. Define the minimum number of species in a subgroup. Default is 5.
plot bolean. If TRUE, the tree is plotted and testable nodes are highlighted with red dots. Default is FALSE.
lad bolean. Define which way the tree should be represented if plot = T. If TRUE, the smallest clade is at the bottom plot. If FALSE, it is at the top of the plot. Default is TRUE.
text.cex numeric. Defines the size of the text in legend.
pch.cex numeric. Defines the size of the red points at the crown of subclades.
...

Details

All described species should be included to properly calculate sampling fractions. The example of Cetacea uses a taxonomic database but groups can be defined on geography or traits as soon as they are monophyletic. If the taxonomy of the studied group is difficult to establish (e.i. taxonomic uncertainty, etc.), a "fake" taxonomic database can be created with random species names (Gen1_sp1, Gen1_sp2, Gen2_sp1, etc.) to circumvent taxonomic difficulties. Note that sampling fractions of the backbones are calculated in the next step of the pipeline (function get.comb.shift()).

Value

da data.frame with as many rows as nodes in the phylogeny with the following informations in columns:

- nodes the node IDs
- data the name of the subclade from data
- f the sampling fraction for this subclade
- sp_in the number of species included in the tree
- sp_tt the number of species described in the data
- to_test the node IDs for nodes that are testable according to clade.size

Author(s)

Nathan Mazet

References


See Also

getc.comb.shift, shift.estimates
Examples

# loading data
data("Cetacea")
data("taxo_cetacea")

# no shifts tested at genus level
taxo_cetacea_no_genus <- taxo_cetacea[!names(taxo_cetacea) == "Genus"]

# calculating sampling fractions with a plot
f_cetacea <- get.sampling.fractions(phylo = Cetacea, lad = FALSE,
data =taxo_cetacea_no_genus,
plot = TRUE, cex = 0.3)

getDataLikelihood

**Likelihood of tip trait values.**

Description

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

Usage

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

Arguments

- **object**: an object of class 'PhenotypicModel'.
- **data**: vector of tip trait data.
- **error**: vector of intraspecific (i.e., tip-level) standard error of the mean. Specify NULL if no error data are available.
- **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(likelihood) of the model.

Author(s)

M Manceau

References

Examples

# Loading an example tree

# Reading tree from text
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, error=NULL, c(0,0,0,1))

---

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 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

See Also
fit_ClaDS, plot_ClaDS_chains, getMAPS_ClaDS0

Examples

```r
if(test){
  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_ClaDS**

*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

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

- `phylo`: An object of class `phylo`.
- `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 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


See Also

`fit_ClaDS0`, `plot_ClaDS0_chains`, `getMAPS_ClaDS`

Examples

```r
set.seed(1)

if(test){
  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[1]
  extinction_rates = obj$mu[1]
  data("ClaDS0_example")

  # extract the Maximum A Posteriori for each of the parameters
```
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


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)])
### Examples

```r
# Loading an example tree
  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))
```

### 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

Generalized Information Criterion (GIC) to compare models fit by Maximum Likelihood (ML) or Penalized Likelihood (PL).

Description

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

Usage

```r
## 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


See Also

gic_criterion, fit_t_pl mvgl s
Examples

```r
if(require(mvMORPH)){
  if(test){
    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)
  }
}
```

**Description**

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

**Usage**

```r
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
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.

See Also
GIC.fit_pl.rpanda, fit_t_pl
Examples

```r
if(test){
  if(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 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


Examples

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

---

**InfTemp**  

*Paleotemperature data across the Cenozoic*

Description

Paleotemperature data across the Cenozoic inferred from delta O18 measurements

Usage

```r
data(InfTemp)
```

Details

Paleotemperature data inferred from delta 018 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


Examples

```r
data(InfTemp)
plot(InfTemp)
```
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)
Clusters phylogenies using hierarchical and k-medoids clustering

Usage

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

Arguments

JSDtree: a matrix of distances between phylogenetic pairs, typically the output of the JSDtree 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
**JSDt_cluster**

**See Also**

*JSDtree*

**Examples**

```r
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)
```

**Description**

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

**Usage**

```r
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


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

Land plant diversity since the Jurassic

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


Examples

data(landplant)
plot(landplant)
**likelihood_bd**  
*Likelihood of a phylogeny under the general birth-death model*

**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**

```r
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 max(node.age(phylo)$ages).
- `f.lamb`: a function specifying the time-variation of the speciation rate $\lambda$. This function as a single argument (time). Any function may be used.
- `f.mu`: a function specifying the time-variation of the speciation rate $\mu$. 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 dt=1e-3 gives a good trade-off between precision and computation time.
- `cond`: conditioning to use to fit the model:
  - 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


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)
Usage

`likelihood_bd_backbone(phylo, tot_time, f, f.lamb, f.mu,`  
`    backbone, spec_times, branch_times,`  
`    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 `max(node.age(phylo)$ages)`.
- **f.lamb**: a function specifying the time-variation of the speciation rate \(\lambda\). This function as a single argument (time). Any function may be used.
- **f.mu**: a function specifying the time-variation of the speciation rate \(\mu\). This function as a single argument (time). Any function may be used.
- **f**: the fraction of extant species included in the phylogeny
- **backbone**: character. Allows to analyse a backbone. Default is NULL and `spec_times` and `branch_times` are then ignored. Otherwise:
  - "stem.shift": for every shift, the probability of the speciation event at the stem age of the subclade is included in the likelihood of the backbone thanks to the argument `spec_times`.
  - "crown.shift": for every shift, both the probability of the speciation event at the stem age of the subclade and the probability that the stem of the subclade survives to the crown age are included in the likelihood of the backbone thanks to the argument `branch_times`.
- **spec_times**: a numeric vector of the stem ages of subclades. Used only if `backbone = "stem.shift"`. Default is NULL.
- **branch_times**: a list of numeric vectors. Each vector contains the stem and crown ages of subclades (in this order). Used only if `backbone = "crown.shift"`. Default is NULL.
- **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 $dt=1e^{-3}$ gives a good trade-off between precision and computation time.

cond conditioning to use to fit the model:

- 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)

Hélène Morlon, Nathan Mazet

References


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
# same as likelihood_bd in this case
lh <- likelihood_bd_backbone(Cetacea, tot_time, f, f.lamb, f.mu,
backbone = FALSE, spec_times = NULL, branch_times = NULL,
cst.mu = TRUE, expo.lamb = TRUE, dt = 1e-3)
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
Examples

```r
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

```r
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


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)

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 max(node.age(phylo)$ages).
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.
likelihood_subgroup_model

Likelihood of a dataset under models with biogeography fit to a sub-group.

Description

Computes the likelihood of a dataset under either the linear or exponential diversity dependent model with specified \( \sigma^2 \) and slope values and with a geography.object formed using CreateGeoObject.

Usage

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

Examples

```r
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

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.

return.z0

- Logical indicating whether to return an estimate of the trait value at the root given the parameter values (if \( \text{TRUE} \), function returns root value rather than negative log-likelihood).

maxN

- When fitting \( \text{DDlin} \) model, it is necessary to specify the maximum number of sympatric lineages to ensure that the rate returned does not correspond to negative \( \sigma^2 \) values at any point in time (see Details).

error

- A named vector with standard errors (SE) of trait values for each species (with names matching "phylo$tip.label"). The default is NULL, in this case potential error is ignored in the fit. If set to NA, the SE is estimated from the data (to be used when there are no error measurements, a nuisance parameter is estimated). Note: When standard errors are provided, a nuisance parameter is also estimated.

Details

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

- \( \text{maxN} \) can be calculated using \( \text{maxN} = \text{max(vapply(geo.object$geography.object, function(x) max(rowSums(x)), 1))} \), where geo.object is the output of \( \text{CreateGeoObject} \).

Value

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

- If \( \text{return.z0=TRUE} \), the estimated root value for the \( \text{par} \) values is returned instead of the negative log-likelihood.

Note

- To stabilize optimization, this function exponentiates the input \( \sigma^2 \) 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

See Also

fit_t_comp CreateGeoObject likelihood_t_DD

Examples

data(BGB.examples)

Canidae.phylo<-BGB.examples$Canidae.phylo
names(dummy.group)<-Canidae.phylo$tip.label

Canidae.simmap<-phytools::make.simmap(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, simmap=Canidae.simmap, 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),-0.000005)
maxN<-max(vapply(Canidae.geobyclass.object$geo.object$geography.object, function(x)max(rowSums(x)),1))

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


likelihood_t_DD Likelihood of a dataset under diversity-dependent models.

Description

Computes the likelihood of a dataset under either the linear or exponential diversity dependent model with specified sigma2 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 $log(sig2)$ (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(sig2) 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 sig2 and slope values

Note

To stabilize optimization, this function exponentiates the input sig2 value, thus the user must input the log(sig2) value to compute the correct log likelihood (see example).

Author(s)

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

References


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")
**Description**

Computes the likelihood of a dataset under either the linear or exponential diversity dependent model with specified \( \sigma^2 \) and slope values and with a geography.object formed using `CreateGeoObject`.

**Usage**

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

**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.
- `geo.object` a list of sympatry through time created using `CreateGeoObject`
- `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.
- `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 \( \sigma^2 \) 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`).

\( \text{maxN} \) can be calculated using

\[ \text{maxN} = \max(\text{vapply}(\text{geo.object}$\text{geography.object}$, \text{function}(x) \max(\text{rowSums}(x)), 1)) \]

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, \( \sigma^2 \) and slope values, and `geo.object`.

**Note**

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


### See Also

- fit_t_env

### Examples

```r
if(test){
  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)
#require(pspline)
#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 sigma2
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(sig2) (see Note) and S (parameters of the matching
     competition model), in that order

Details

When specifying par, log(sig2) 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(sig2) value to compute the correct log likelihood (see example).

Author(s)

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

References


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)

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(sig2) (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(sig2) 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(sig2) value to compute the correct log likelihood (see example).

Author(s)

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

References


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)
Description

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

Usage

```r
## 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 \( \sigma^2 \) 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


See Also

`plot.fit_t.env`, `likelihood_t_env`
Examples

if(test){

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")
}

lines.fit_t.env.ou

Add to a plot line segments joining the phenotypic evolutionary optimum through time estimated by the fit_t_env_ou function

Description

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

Usage

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

Arguments

x an object of class 'fit_t.env.ou' obtained from a fit_t_env_ou fit.
steps the number of steps from the root to the present used to compute the optimum \( \theta(t) \) through time.
... further arguments to be passed to plot. See ?plot.
Value

`lines.fit_t.env.ou` 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`.
- `values` — the estimated optimum 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


See Also

`plot.fit_t.env.ou`, `fit_t_env_ou`

Examples

```r
if(test){
  data(InfTemp)
  set.seed(9999) # for reproducibility

  # Let's start by simulating a trait under a climatic OU
  beta = 0.6       # relationship to the climate curve
  sim_theta = 4    # value of the optimum if the relationship to the climate
  # curve is 0 (this corresponds to an 'intercept' in the linear relationship used below)
  sim_sigma2 = 0.025 # variance of the scatter = sigma^2
  sim_alpha = 0.36  # alpha value = strength of the OU; quite high here...
  delta = 0.001 # time step used for the forward simulations => here its 1000y steps
  tree <- pbtree(n=200, d=0.3) # simulate a bd tree with some extinct lineages
  root_age = 60        # height of the root (almost all the Cenozoic here)
  tree$edge.length <- root_age*tree$edge.length/max(nodeHeights(tree))
```
# make_gen.BipartiteEvol

## Description

Compute the genealogies from a run of BipartiteEvol

## Usage

```r
make_gen.BipartiteEvol(out, treeP = NULL, treeH = NULL, verbose = T)
```

## Arguments

- **out**: The output of a run of sim.BipartiteEvol
- **treeP**: Optional, a previous genealogy for clade P to which the new tree will be grafted (used if out was the continuation of a former run, see in the example)
- **treeH**: Optional, a previous genealogy for clade H to which the new tree will be grafted (used if out was the continuation of a former run, see in the example)
- **verbose**: Should the progression of the computation be printed?

## Value

A list object with

- **P**: The genealogy of the clade P
- **H**: The genealogy of the clade H

## Author(s)

O. Maliet
References


See Also

sim.BipartiteEvol

Examples

```r
if(test){
  # run the model
  set.seed(1)
  mod = sim.BipartiteEvol(nx = 8, ny = 4, NG = 800,
                          D = 3, muP = 0.1, muH = 0.1,
                          alphaP = 0.12, alphaH = 0.12,
                          rP = 10, rH = 10,
                          verbose = 100, thin = 5)

  # build the genealogies
  gen = make_gen.BipartiteEvol(mod)
  plot(gen$H)

  # compute the phylogenies
  phy1 = define_species.BipartiteEvol(gen, threshold=1)

  # plot the result
  plot_div.BipartiteEvol(gen, phy1, 1)

  # build the network
  net = build_network.BipartiteEvol(gen, phy1)

  trait.id = 1
  plot_net.BipartiteEvol(gen, phy1, trait.id, net, mod, nx = nx, spatial = FALSE)

  ## add time steps to a former run
  seed=as.integer(10)
  set.seed(seed)

  mod = sim.BipartiteEvol(nx = 8, ny = 4, NG = 200,
                          D = 3, muP = 0.1, muH = 0.1,
                          alphaP = 0.12, alphaH = 0.12,
                          rP = 10, rH = 10,
                          verbose = 100, thin = 5,
                          P=mod$P, H=mod$H)  # former run output

  # update the genealogy
  gen = make_gen.BipartiteEvol(mod,
                              treeP=gen$P, treeH=gen$H)
```
# update the phylogenies...
phy1 = define_species.BipartiteEvol(gen, threshold=1)

#... and the network
net = build_network.BipartiteEvol(gen, phy1)

trait.id = 1
plot_net.BipartiteEvol(gen, phy1, trait.id, net, mod, nx = 10, spatial = FALSE)

---

**mantel_test**

**Compute Mantel test**

**Description**

This function computes a Mantel test between two dissimilarity matrices. The available correlations are Pearson, Spearman, and Kendall.

**Usage**

```r
mantel_test(formula = formula(data), data = sys.parent(),
correlation = "Pearson", nperm = 1000)
```

**Arguments**

- `formula` formula y ~ x describing the test to be conducted where y and x are distance matrices (as "dist" objects).
- `data` an optional data frame containing the variables in the model as columns of dissimilarities. By default, the variables are taken from the current environment.
- `correlation` indicates which correlation (R) must be used among Pearson (default), Spearman, and Kendall correlations.
- `nperm` a number of permutations to evaluate the significance of the correlation. By default, it equals 1000, but this can be very long for the Kendall correlation.

**Details**

This function is adapted from the function `mantel` in the R-package ecodist (Goslee & Urban, 2007).

**Value**

- `mantelr` Mantel correlation (R).
- `pval1` one-tailed p-value (null hypothesis: R <= 0).
- `pval2` one-tailed p-value (null hypothesis: R >= 0).
- `pval3` two-tailed p-value (null hypothesis: R = 0).
Author(s)

Benoît Perez-Lamarque

References


See Also

phylosignal_network
phylosignal_sub_network

Examples

# Measuring phylogenetic signal in species interactions using a Mantel test
# (do closely related species interact with similar partners?)

library(RPANDA)

# Load the data
data(mycorrhizal_network)

network <- mycorrhizal_network[[1]] # bipartite interaction matrix
tree_orchids <- mycorrhizal_network[[2]] # phylogenetic tree (phylo object)

network <- network[,tree_orchids$tip.label]

ecological_distances <- as.matrix(vegan::vegdist(t(network), "jaccard", binary=FALSE))

phylogenetic_distances <- cophenetic.phylo(tree_orchids)

mantel_test(as.dist(ecological_distances) ~ as.dist(phylogenetic_distances),
correlation="Pearson", nperm = 10000)
mantel_test_nbpartners

Compute Mantel test

Description

This function tests for phylogenetic signal in species interactions in guild A using a Mantel test that keep constant the number of partners per species.

Usage

```r
mantel_test_nbpartners(network, tree_A, tree_B = NULL, method="Jaccard_binary", nperm = 1000, correlation = "Pearson")
```

Arguments

- `network`: a matrix representing the bipartite interaction network with species from guild A in columns and species from guild B in rows. Row names (resp. columns names) must correspond to the tip labels of tree B (resp. tree A).
- `tree_A`: a phylogenetic tree of guild A (the columns of the interaction network). It must be an object of class "phylo".
- `tree_B`: (optional) a phylogenetic tree of guild B (the rows of the interaction network). It must be an object of class "phylo".
- `method`: indicates which method is used to compute the phylogenetic signal in species interactions. If you want to perform a Mantel test between the phylogenetic distances and some ecological distances (do closely related species interact with similar partners?), you can choose "Jaccard_weighted" (default) for computing the ecological distances using Jaccard dissimilarities (or "Jaccard_binary" to not take into account the abundances of the interactions), "Bray-Curtis" for computing the Bray-Curtis dissimilarity, or "GUniFrac" for computing the weighted (or generalized) UniFrac distances ("UniFrac_unweighted" to not take into account the interaction abundances).
- `correlation`: indicates which correlation (R) must be used among Pearson (default) and Spearman correlations.
- `nperm`: a number of permutations to evaluate the significance of the correlation. By default, it equals 1000.

Value

- `mantelr`: Mantel correlation (R).
- `pval1`: one-tailed p-value (null hypothesis: R <= 0).
- `pval2`: one-tailed p-value (null hypothesis: R >= 0).
- `pval3`: two-tailed p-value (null hypothesis: R = 0).
**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**

```r
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


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 $A = (1/\text{rowSums(Toep)}) \times \text{Toep}$ where Toep is a Toeplitz matrix.

References


See Also

*fit_ClaDS*

mycorrhizal_network

Mycorrhizal network from La Réunion island

Description

Mycorrhizal intercation network between orchids and mycorrhizal fungi from La Réunion island (Martos et al., 2012) along with the reconstructed phylogenetic trees of the orchids and the fungal OTUs.

Usage

`data(mycorrhizal_network)`

Details

These phylogenies were constructed by maximum likelihood inference from four plastid genes for the orchids and one nuclear gene for the fungi. See Martos et al. (2012) for details.

Source

References


Examples

```r
data(mycorrhizal_network)

network <- mycorrhizal_network[[1]] # interaction matrix
tree_orchids <- mycorrhizal_network[[2]] # phylogenetic tree (phylo object)
tree_fungi <- mycorrhizal_network[[3]] # phylogenetic tree (phylo object)
```

---

**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**


Examples

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

---

**paleodiv**  
*Paleodiversity through time*

**Description**

Calculates paleodiversity through time from shift.estimates output with the deterministic approach.

**Usage**

```r
paleodiv(phylo, data, sampling.fractions, shift.res, 
    backbone.option = "crown.shift", combi = 1, 
    time.interval = 1, split.div = F)
```

**Arguments**

- `phylo`: an object of type 'phylo' (see ape documentation)
- `data`: a data.frame containing a database of monophyletic groups for which potential shifts can be investigated. This database should be based on taxonomy, ecology or traits and contain a column named "Species" with species name as in phylo.
- `sampling.fractions`: the output resulting from get.sampling.fractions.
- `shift.res`: the output resulting from shift.estimates.
- `backbone.option`: type of the backbone analysis:
  - "stem.shift": paleodiversity dynamics are calculated from the stem age for subclades.
  - "crown.shift": paleodiversity dynamics are calculated from the crown age for subclades.
- `combi`: numeric. The combination of shifts defined by its rank in the global comparison.
- `time.interval`: numeric. Define the time interval (in million years) at which paleodiversity values are calculated. Default is 1 for a value at each million year.
- `split.div`: bolean. Specifies if paleodiversity should be plotted by parts of the selected combination (TRUE) or not.

**Value**

If split.div = FALSE, paleodiversity dynamics are returned in a matrix with as many rows as parts in the selected combination and as many column as million years from the root to the present. If split.div = TRUE, global paleodiversity dynamic is returned as a vector with a value per million year.
PhenotypicACDC-class

Author(s)

Nathan Mazet

References


See Also

shift.estimates, apply_prob_dtt

Examples

```r
# loading data
data("Cetacea")
data("taxo_cetacea")
data("shifts_cetacea")

# no shifts tested at genus level
taxo_cetacea_no_genus <- taxo_cetacea[ names(taxo_cetacea) != "Genus" ]
f_cetacea <- get.sampling.fractions( phylo = Cetacea, lad = FALSE,
                                      data = taxo_cetacea_no_genus,
                                      plot = TRUE, cex = 0.3)

# use of paleodiv
paleodiversity <- paleodiv( phylo = Cetacea,
                           data = taxo_cetacea_no_genus,
                           sampling.fractions = f_cetacea,
                           shift.res = shifts_cetacea,
                           combi = 1, split.div = FALSE)
```

---

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


Examples

d showClass("PhenotypicACDC")
PhenotypicADiag-class

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

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
PhenotypicDD-class

References


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


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" ~
PhenotypicModel-class

Extended

Class "PhenotypicModel", directly.

Methods

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

Author(s)

Marc Manceau

References


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

ame: 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" ~-
PhenotypicOU-class

Methods

\[
\begin{align*}
\text{tipLabels: Object of class } \text{"character"} & \text{ \~ ~} \\
\text{tipLabelsSimu: Object of class } \text{"character"} & \text{ \~ ~} \\
\text{comment: Object of class } \text{"character"} & \text{ \~ ~}
\end{align*}
\]

\[
\text{<- signature(x = "PhenotypicModel", i = "ANY", j = "ANY", value = "ANY"): ...}
\]

\[
[\text{ signature(x = "PhenotypicModel", i = "ANY", j = "ANY", drop = "ANY"): ...}
\]

\[
\text{fitTipData signature(object = "PhenotypicModel"): ...}
\]

\[
\text{getDataLikelihood signature(object = "PhenotypicModel"): ...}
\]

\[
\text{getTipDistribution signature(object = "PhenotypicModel"): ...}
\]

\[
\text{modelSelection signature(object = "PhenotypicModel"): ...}
\]

\[
\text{print signature(x = "PhenotypicModel"): ...}
\]

\[
\text{show signature(object = "PhenotypicModel"): ...}
\]

\[
\text{simulateTipData signature(object = "PhenotypicModel"): ...}
\]

Author(s)

Marc Manceau

References


Examples

\[
\text{showClass("PhenotypicModel")}
\]

PhenotypicOU-class

\[
\begin{align*}
\text{Class } \text{"PhenotypicOU"}
\end{align*}
\]

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 \text{new("PhenotypicOU", ...).}
**PhenotypicOU-class**

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


Examples

`showClass("PhenotypicOU")`
PhenotypicPM-class

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

**Examples**

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

---

<table>
<thead>
<tr>
<th>Phocoenidae</th>
<th>Phocoenidae phylogeny</th>
</tr>
</thead>
</table>

**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


**Examples**

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

---

**phyl.pca_pl**

*Regularized Phylogenetic Principal Component Analysis (PCA).*

**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 fit_t_pl function.

plot Plot of the PC’s axes. Default is TRUE (see details).

Options to be passed through. (e.g., axes=c(1,2), col, pch, cex, mode="cov" or "corr", 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. Ploting 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


See Also

fit_t_pl, ancestral, GIC.fit_pl.rpanda, gic_criterion
### Examples

```r
if(test){
  if(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=TRUE)

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

---

**Phyllostomidae**  
*Phyllostomidae phylogeny*

---

**Description**

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

**Usage**

```r
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**


phylosignal_network

See Also

Phyllostomidae_genera

Examples

```r
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

```r
data(Phyllostomidae_genera)
```

See Also

Phyllostomidae

Examples

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

phylosignal_network  Compute phylogenetic signal in a bipartite interaction network

Description

This function computes the phylogenetic signal in a bipartite interaction network, either the phylogenetic signal in species interactions (do closely related species interact with similar partners?) using Mantel tests, or the phylogenetic signal in the number of partners (i.e. degree; do closely related species interact with the same number of partners?) using Mantel tests or using the Phylogenetic bipartite linear model (PBLM) from Ives and Godfray (2006). Mantel tests measuring the phylogenetic signal in species interactions can be computed using quantified or binary networks, with the Jaccard, Bray-Curtis, or UniFrac ecological distances.

Usage

```r
phylosignal_network(network, tree_A, tree_B = NULL, method = "Jaccard_weighted", nperm = 10000, correlation = "Pearson", only_A = FALSE, permutation = "shuffle")
```
**Arguments**

- **network**: A matrix representing the bipartite interaction network with species from guild A in columns and species from guild B in rows. Row names (resp. column names) must correspond to the tip labels of tree B (resp. tree A).

- **tree_A**: A phylogenetic tree of guild A (the columns of the interaction network). It must be an object of class "phylo".

- **tree_B** (optional): A phylogenetic tree of guild B (the rows of the interaction network). It must be an object of class "phylo".

- **method**: Indicates which method is used to compute the phylogenetic signal in species interactions. If you want to perform a Mantel test between the phylogenetic distances and some ecological distances (do closely related species interact with similar partners?), you can choose "Jaccard_weighted" (default) for computing the ecological distances using Jaccard dissimilarities (or "Jaccard_binary" to not take into account the abundances of the interactions), "Bray-Curtis" for computing the Bray-Curtis dissimilarity, or "GUniFrac" for computing the weighted (or generalized) UniFrac distances ("UniFrac_unweighted" to not take into account the interaction abundances).

Conversely, if you want to evaluate the phylogenetic signal in the number of partners (do closely related species interact with the same number of partners?), you can choose "degree".

Alternatively (not recommended), you can use the Phylogenetic Bipartite Linear Model "PBLM" (see Ives and Godfray, 2006) or "PBLM_binary" to not consider the abundances of the interactions.

- **correlation** (optional): Indicates which correlation (R) must be used in the Mantel test, among Pearson (default), Spearman, and Kendall correlations. It only applies for the methods "Jaccard_weighted", "Jaccard_binary", "Bray-Curtis", "GUniFrac", "UniFrac_unweighted", or "degree".

- **nperm** (optional): A number of permutations to evaluate the significance of the Mantel test. By default, it equals 10,000, but this can be very long for the Kendall correlation. It only applies for the methods "Jaccard_weighted", "Bray-Curtis", "Jaccard_binary", "GUniFrac", "UniFrac_unweighted", or "degree".

- **permutation** (optional): Indicates which permutations must be performed to evaluate the significance of the Mantel correlation: either "shuffle" (by default - i.e. random shuffling of the distance matrix) or "nbpartners" (i.e. keeping constant the number of partners per species and shuffling at random their identity).

- **only_A** (optional): Indicates whether the signal should be only computed for guild A (and not for guild B). By default, it is computed for both guilds if "tree_B" is provided.

**Details**

See the tutorial on GitHub (https://github.com/BPerezLamarque/Phylosignal_network).

**Value**

For Mantel tests, the function outputs a vector of up to 8 values: the number of species in guild A ("nb_A"), the number of species in guild B ("nb_B"), the correlation for guild A ("mantel_cor_A"),
its associated upper p-value ("pvalue_upper_A", i.e. the fraction of permutations that led to higher correlation values), its associated lower p-value ("pvalue_lower_A", i.e. the fraction of permutations that led to lower correlation values), and (optional) the correlation for guild B ("mantel_cor_B"), its associated upper p-value ("pvalue_upper_B"), and its associated lower p-value ("pvalue_lower_B"),

"mantel_cor_A" (or "mantel_cor_B") indicates the strength of the phylogenetic signal in guild A (or B). The upper p-value "pvalue_upper_A" (or "pvalue_upper_B") indicates the significance of the phylogenetic signal in guild A (or B). The lower p-value "pvalue_lower_A" (or "pvalue_lower_B") indicates the significance of the anti-phylogenetic signal in guild A (or B). For instance, if "pvalue_upper_A"<0.05, there is a significant phylogenetic signal in guild A.

For the PBLM approach (Ives and Godfray, 2006), the function outputs a vector of 8 values: the number of species in guild A ("nb_A"), the number of species in guild B ("nb_B"), the phylogenetic signals in guilds A ("dA") and B ("dB"), the covariance of interaction matrix ("MSETotal"), the mean square error of the complete model ("MSEFull"), the mean square error of model run on star phylogenies ("MSEStar"), and the mean square error of the model assuming strict Brownian motion evolutions ("MSEBase"). The significance of the phylogenetic signal can be evaluated by comparing "MSEFull" and "MSEStar".

Author(s)

Benoît Perez-Lamarque

References


See Also

phylosignal_sub_network

Examples

# Load the data
data(mycorrhizal_network)
network <- mycorrhizal_network[[1]] # interaction matrix
tree_orchids <- mycorrhizal_network[[2]] # phylogenetic tree (phylo object)
tree_fungi <- mycorrhizal_network[[3]] # phylogenetic tree (phylo object)

if(test){
  # Using Mantel tests:
  # Step 1: Phylogenetic signal in species interactions
  # (do closely related species interact with similar partners?)
  phylosignal_network(network, tree_A = tree_orchids, tree_B = tree_fungi,
                      method = "GUniFrac", correlation = "Pearson", nperm = 10000) # measured for both guilds

  # Step 2: Phylogenetic signal in species interactions when accounting
  # for the signal in the number of partners
  # Mantel test with permutations that keep constant the number of partners per species
  phylosignal_network(network, tree_A = tree_orchids, tree_B = tree_fungi,
                      method = "GUniFrac", correlation = "Pearson", nperm = 1000, permutation = "nbpartners")

  # Other: Phylogenetic signal in the number of partners
  # (do closely related species interact with the same number of partners?)
  phylosignal_network(network, tree_A = tree_orchids, method = "degree",
                      correlation = "Pearson", nperm = 10000) # for guild A
  phylosignal_network(t(network), tree_A = tree_fungi, method = "degree",
                      correlation = "Pearson", nperm = 10000) # for guild B

  # Alternative using PBLM (not recommended) - very slow
  # phylosignal_network(network, tree_A = tree_orchids, tree_B = tree_fungi, method = "PBLM")
}

---

**phylosignal_sub_network**

*Compute clade-specific phylogenetic signals in a bipartite interaction network*

**Description**

This function computes the clade-specific phylogenetic signals in species interactions. For each node of tree A having a certain number of descending species, it computes the phylogenetic signal
in the resulting sub-network by performing a Mantel test between the phylogenetic distances and the ecological distances for the given sub-clade of tree A. Mantel tests can be computed using quantified or binary networks, with the Jaccard, Bray-Curtis, or UniFrac ecological distances.

Usage

phylosignal_sub_network(network, tree_A, tree_B = NULL, method = "Jaccard_weighted", nperm = 1000, correlation = "Pearson", minimum = 10, degree = FALSE, permutation = "shuffle")

Arguments

- **network**: a matrix representing the bipartite interaction network with species from guild A in columns and species from guild B in rows. Row names (resp. columns names) must correspond to the tip labels of tree B (resp. tree A).
- **tree_A**: a phylogenetic tree of guild A (the columns of the interaction network). It must be an object of class "phylo".
- **tree_B**: (optional) a phylogenetic tree of guild B (the rows of the interaction network). It must be an object of class "phylo".
- **method**: indicates which method is used to compute the phylogenetic signal in species interactions using Mantel tests. You can choose "Jaccard_weighted" (default) for computing ecological distances using Jaccard dissimilarities (or "Jaccard_binary" to not take into account the abundances of the interactions), "Bray-Curtis" for computing the Bray-Curtis dissimilarity, or "GUniFrac" for computing the weighted (or generalized) UniFrac distances ("UniFrac_unweighted" to not take into account the interaction abundances).
- **correlation**: indicates which correlation (R) must be used in the Mantel test, among Pearson (default), Spearman, and Kendall correlations.
- **nperm**: a number of permutations to evaluate the significance of the Mantel test. By default, it equals 10,000, but this can be very long for the Kendall correlation.
- **permutation**: (optional) indicates which permutations must be performed to evaluate the significance of the Mantel correlation: either "shuffle" (by default - i.e. random shuffling of the distance matrix) or "nbpartners" (i.e. keeping constant the number of partners per species and shuffling at random their identity).
- **minimum**: indicates the minimal number of descending species for a node in tree A to compute its clade-specific phylogenetic signal.
- **degree**: if degree=TRUE, Mantel tests testing for phylogenetic signal in the number of partners are additionally performed in each sub-clade.

Details

See the tutorial on GitHub (https://github.com/BPerezLamarque/Phylosignal_network).
**Value**

For Mantel tests, the function outputs a table where each line corresponds to a tested clade and which contains at least 8 columns: the name of the node ("node"), the number of species in the sub-clade A ("nb_A"), the number of species in guild B associated with the sub-clade A ("nb_B"), the Mantel correlation for guild A ("mantel_cor"), its associated upper p-value ("pvalue_upper"), its associated lower p-value ("pvalue_lower"), and the associated Bonferroni corrected p-values ("pvalue_upper_corrected" and "pvalue_lower_corrected").

"mantel_cor" indicates the strength of the phylogenetic signal in the sub-clade A. The upper p-value "pvalue_upper" indicates the significance of the phylogenetic signal in the sub-clade A. The lower p-value "pvalue_lower" indicates the significance of the anti-phylogenetic signal in the sub-clade A. Both Bonferroni p-values are corrected using the number of tested nodes. For instance, if "pvalue_upper_corrected"<0.05 for a given node, there is a significant phylogenetic signal in the corresponding sub-clade of A.

If degree=TRUE, it also indicates in each sub-clade, the phylogenetic signal in the number of partners ("degree_mantel_cor") and its significance with or without the Bonferroni correction ("degree_pvalue_upper", "degree_pvalue_lower" and "degree_pvalue_upper_corrected", "degree_pvalue_lower_corrected")

**Author(s)**

Benoît Perez-Lamarque

**References**


**See Also**

phylosignal_sub_network plot_phylosignal_sub_network

**Examples**

```r
# Load the data
data(mycorrhizal_network)
network <- mycorrhizal_network[[1]] # interaction matrix
tree_orchids <- mycorrhizal_network[[2]] # phylogenetic tree (phylo object)
tree_fungi <- mycorrhizal_network[[3]] # phylogenetic tree (phylo object)
```
if(test){

# Clade-specific phylogenetic signal in species interactions in guild A
# (do closely related species interact with similar partners in sub-clades of guild A?)
results_clade_A <- phylosignal_sub_network(network, tree_A = tree_orchids, tree_B = tree_fungi,
method = "GUniFrac", correlation = "Pearson", degree = TRUE)
plot_phylosignal_sub_network(tree_A = tree_orchids, results_clade_A, network)

# Clade-specific phylogenetic signal in species interactions in guild B
# (do closely related species interact with similar partners in sub-clades of guild B?)
results_clade_B <- phylosignal_sub_network(t(network), tree_A = tree_fungi, tree_B = tree_orchids,
method = "GUniFrac", correlation = "Pearson", degree = TRUE)
plot_phylosignal_sub_network(tree_A = tree_fungi, results_clade_B, t(network))
}

---

pi_estimator

**Compute nucleotidic diversity (Pi estimator)**

### Description

This function computes the Pi estimator of genetic diversity (Nei and Li, 1979) while controlling for the presence of gaps in the alignment (Ferretti et al, 2012), frequent in barcoding datasets.

### Usage

```r
pi_estimator(sequences)
```

### Arguments

- **sequences**
  - a matrix representing the nucleotidic alignment of all the sequences present in the phylogenetic tree.

### Value

An estimate of genetic diversity

### Author(s)

Ana C. Afonso Silva & Benoît Perez-Lamarque

### References


See Also

theta_estimator delineate_phylotypes

Examples

```r
data(woodmouse)

alignment <- as.character(woodmouse) # nucleotidic alignment

pi_estimator(alignment)
```

---

**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**

```r
## S3 method for class 'fit_t.env'
plot(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 $\sigma^2$ 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
plot.fit_t.env.ou

Note

All the graphical parameters (see \texttt{par}) can be passed through (e.g. line type: \texttt{lty}, line width: \texttt{lwd}, color: \texttt{col} ...)

Author(s)

J. Clavel

References


See Also

\texttt{lines.fit_t.env}, \texttt{likelihood_t.env}

Examples

\begin{verbatim}
if(test){
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")
}
\end{verbatim}

Description

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

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

Arguments

- `x` an object of class 'fit_t.env.ou' obtained from a `fit_t_env_ou` fit.
- `steps` the number of steps from the root to the present used to compute the optimum \( \theta(t) \) through time.
- `...` further arguments to be passed to `plot`. See `plot`.

Value

`plot.fit_t.env.ou` 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`.
- `values` the estimated optimum values 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


See Also

- `lines.fit_t.env`
- `fit_t_env_ou`
- `lines.fit_t.env.ou`
Examples

```r
if(test){
  data(InfTemp)

  set.seed(9999) # for reproducibility

  # Let's start by simulating a trait under a climatic OU
  beta = 0.6     # relationship to the climate curve
  sim_theta = 4  # value of the optimum if the relationship to the climate curve is 0
  # (this corresponds to an 'intercept' in the linear relationship used below)
  sim_sigma2 = 0.025 # variance of the scatter = sigma^2
  sim_alpha = 0.35 # alpha value = strength of the OU; quite high here...
  delta = 0.001   # time step used for the forward simulations => here its 1000y steps
  tree <- pbtree(n=200, d=0.3) # simulate a bd tree with some extinct lineages
  root_age = 60   # height of the root (almost all the Cenozoic here)
  tree$edge.length <- root_age*tree$edge.length/max(nodeHeights(tree))
  # here - for this contrived example - I scale the tree so that the root is at 60 Ma

  trait <- sim_t_env_ou(tree, sigma=sqrt(sim_sigma2), alpha=sim_alpha,
      theta0=sim_theta, param=beta, env_data=InfTemp, step=0.01,
      scale=TRUE, plot=FALSE)

  ## Fit the Environmental model (default)
  result1 <- fit_t_env_ou(phylo = tree, data = trait, env_data =InfTemp,
      method = "Nelder-Mead", df=50, scale=TRUE)
  plot(result1, lty=2, col="red")
}
```

---

**plot_BICompare**

Display modalities on a phylogeny.

**Description**

Plot a phylogeny with branches colored according to modalities.

**Usage**

```r
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


See Also

`fit_ClaDS0`, `getMAPS_ClaDS0`, `plot_ClaDS_chains`

Examples

```r
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

```r
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


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

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]

par(mar=c(1,1,0,0))
plot_ClaDS_phylo(tree, speciation_rates)
plot_ClaDS_phylo(tree, speciation_rates, lwd = 4, log = FALSE)

plot_div.BipartiteEvol

*Plot the output of BipartiteEvol*

Description
Plot the genealogies and phylogenies simulated with BipartiteEvol

Usage
plot_div.BipartiteEvol(gen, spec, trait.id, lwdgen = 1,
                       lwdsp = lwdgen, scale = NULL)

Arguments
gen The output of a run of make_gen.BipartiteEvol
spec The output of a run of define_species.BipartiteEvol
trait.id  The trait dimension used to color the genealogies, phylogenies an network with trait values

lwdgen  Width of the branches of the genealogies, default to 1

lwdsp  Width of the branches of the phylogenies, default to 1

scale  Optional, used to force the trait scale

Details

The upper line shows the genealogies colored with trait values for both guilds (the number above shows the depth of the respective genealogy).

The second line shows the phylogenies colored with trait values for both guilds (the number above shows the tip number of the respective phylogeny).

On the third line there is, from left to right, the trait distribution within individuals in guild P, trait of the individual in H as a function of the trait of the interacting individual in P, and the trait distribution within individuals in guild H (for the dimension trait.id).

The lower line shows the quantitative interaction network, with species colored according to their mean trait value (for the dimension trait.id).

Author(s)

O. Maliet

References


See Also

sim.BipartiteEvol

Examples

# run the model
set.seed(1)
if(test){
  mod = sim.BipartiteEvol(nx = 8, ny = 4, NG = 1000,
  D = 3, muP = 0.1, muH = 0.1,
  alphaP = 0.12, alphaH = 0.12,
  rP = 10, rH = 10,
  verbose = 100, thin = 5)

  # build the genealogies
  gen = make_gen.BipartiteEvol(mod)
  plot(gen$H)

  # compute the phylogenies
}
phy1 = define_species.BipartiteEvol(gen,threshold=1)

#plot the result
plot_div.BipartiteEvol(gen,phy1, 1)  

---

**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 max(node.age(phylo)$ages).
- **N0**
  - number of extant species. If all extant species are represented in the phylogeny, N0 is given by length(phylo$tip.label)

**Value**

Plot representing how the estimated number of species vary through time

**Author(s)**

H Morlon

**References**


**See Also**

fit_bd
Examples

```r
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)
```

Description

Plot estimated speciation, extinction & net diversification rates through time

Usage

```r
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

```r
if(require(pspline)){
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 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 <- 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_net.BipartiteEvol**

*Plot the output of BipartiteEvol*

**Description**

Plot the genealogies, phylogenies and interaction network simulated with BipartiteEvol

**Usage**

```r
plot_net.BipartiteEvol(gen, spec, trait.id, link,
                        out, lwdgen = 1, lwdsp = lwdgen, scale = NULL,
                        nx = NULL, cor = F, network.method = "bipartite",
                        spatial = F)
```

**Arguments**

- `gen` The output of a run of make_gen.BipartiteEvol
- `spec` The output of a run of define_species.BipartiteEvol
- `trait.id` The trait dimension used to color the genealogies, phylogenies an network with trait values
- `out` The output of a run of sim.BipartiteEvol
- `link` The output of a run of sim.BipartiteEvol
- `lwdgen` Width of the branches of the genealogies, default to 1
plot_net.BipartiteEvol

lwdsp  
Width of the branches of the phylogenies, default to 1

scale  
Optional, used to force the trait scale

nx  
Grid size parameter used in sim.BipartiteEvol. If NULL, sqrt(N) is used, where N is the number of individuals in a guild

cor  
If F (the default), the middle panel displays the interaction network with species positioned in trait space. If T, it shows all the individual's trait values.

network.method  
How should the network be plotted? Can be "bipartite" (the default) or "matrix"

spatial  
Should the grid with trait values of the individual of both guilds been shown? Default to F

Details

The upper line shows the genealogies colored with trait values for both guilds (the number above shows the depth of the respective genealogy).

The second line shows the phylogenies colored with trait values for both guilds (the number above shows the tip number of the respective phylogeny).

On the third line there is, from left to right, the trait distribution within individuals in guild P (for the dimension trait.id), the interaction network with species positioned in trait space (if cor = T), and the trait distribution within individuals in guild H (for the dimension trait.id).

The lower line shows the quantitative interaction network, with species colored according to their mean trait value (for the dimension trait.id).

Author(s)

O. Maliet

References


See Also

sim.BipartiteEvol

Examples

    # run the model
    set.seed(1)

    if(test){
    mod = sim.BipartiteEvol(nx = 8, ny = 4, NG = 1000,
                          D = 3, muP = 0.1, muH = 0.1,
                          alphaP = 0.12, alphaH = 0.12,
                          rP = 10, rH = 10,
                          verbose = 100, thin = 5)
#build the genealogies
gen = make_gen.BipartiteEvol(mod)
plot(gen$H)

#compute the phylogenies
phy1 = define_species.BipartiteEvol(gen,threshold=1)

#build the network
net = build_network.BipartiteEvol(gen, phy1)

trait.id = 1
plot_net.BipartiteEvol(gen,phy1,trait.id, net,mod, nx = 10, spatial = FALSE)

---

plot_phylosignal_sub_network

*Plot clade-specific phylogenetic signals in a bipartite interaction network*

**Description**

This function plots the clade-specific phylogenetic signals in species interactions. For each node of tree A having a certain number of descending species, it represents the phylogenetic signal in the resulting sub-network by performing a Mantel test between the phylogenetic distances and the ecological distances for the given sub-clade of tree A.

**Usage**

```r
plot_phylosignal_sub_network(tree_A, results_sub_clades, network, legend=TRUE, show.tip.label=FALSE, where="bottomleft")
```

**Arguments**

- `tree_A` a phylogenetic tree of guild A (the columns of the interaction network). It must be an object of class "phylo".
- `results_sub_clades` output of the function `phylosignal_sub_network`.
- `network` a matrix representing the bipartite interaction network with species from guild A in columns and species from guild B in rows. Row names (resp. columns names) must correspond to the tip labels of tree B (resp. tree A).
- `legend` indicates whether the legend should be plotted.
- `show.tip.label` indicates whether the tip labels should be plotted.
- `where` indicates where to put the legend (default is "bottomleft").

**Details**

See the tutorial on GitHub (https://github.com/BPerezLamarque/Phylosignal_network).
**Value**

A phylogenetic tree with nodes colored according to the clade-specific phylogenetic signals. Blue nodes are not significant (Bonferroni correction), whereas orange-red nodes present significant phylogenetic signals and their color indicates the strength of the signal (correlation R of the Mantel test).

**Author(s)**

Benoît Perez-Lamarque

**References**


**See Also**

phylosignal_network phylosignal_sub_network

**Examples**

```r
# Load the data
data(mycorrhizal_network)

network <- mycorrhizal_network[[1]] # interaction matrix
tree_orchids <- mycorrhizal_network[[2]] # phylogenetic tree (phylo object)
tree_fungi <- mycorrhizal_network[[3]] # phylogenetic tree (phylo object)

if(test){
  # Clade-specific phylogenetic signal in species interactions in guild A
  # (do closely related species interact with similar partners in sub-clades of guild A?)
  results_clade_A <- phylosignal_sub_network(network, tree_A = tree_orchids, tree_B = tree_fungi, method = "GUniFrac", correlation = "Pearson")
  plot_phylosignal_sub_network(tree_A = tree_orchids, results_clade_A, network)

  # Clade-specific phylogenetic signal in species interactions in guild B
  # (do closely related species interact with similar partners in sub-clades of guild B?)
  results_clade_B <- phylosignal_sub_network(t(network), tree_A = tree_fungi, tree_B = tree_orchids,
```

```r
  method = "GUniFrac", correlation = "Pearson")
  plot_phylosignal_sub_network(tree_A = tree_orchids, results_clade_B, network)
  ```
**plot_phylo_comb**

```r
method = "GUniFrac", correlation = "Pearson")
plot_phylosignal_sub_network(tree_A = tree_fungi, results_clade_B, t(network))
```

---

**plot_phylo_comb**  
*Plot shifts of diversification on a phylogeny*

---

**Description**

Plots the phylogeny with colored branches according to shifts of diversification.

**Usage**

```r
plot_phylo_comb(phylo, data, sampling.fractions, shift.res = NULL, combi, backbone.option = "crown.shift", main = NULL, col.sub = NULL, col.bck = "black", lty.bck = 1, tested_nodes = F, lad = T, leg = T, text.cex = 1, pch.cex = 1, ...)
```

**Arguments**

- **phylo** 
  an object of type 'phylo' (see ape documentation)

- **data** 
  a data.frame containing a database of monophyletic groups for which potential shifts can be tested. This database should be based on taxonomy, ecology or traits and must contain a column named "Species" with species names as in phylo.

- **sampling.fractions** 
  the output resulting from get.sampling.fractions.

- **shift.res** 
  the output resulting from shift.estimates or NULL (default). This latter case allows to represent combinations only from the output of `get.comb.shift` by specifying the combination (see argument combi).

- **combi** 
  character or numeric. If shift.res is provided, this argument is a numeric and corresponds to the rank of the combination in the global comparison (shift.res$total). If shift.res is NULL, this argument should be a character giving a combination of node IDs as in get.comb.shift output. This latter manner to specify combination allows to visualize a combination of shifts before having results.

- **backbone.option** 
  type of the backbone analysis (see backbone.option in shift.estimates for more details):
  - "stem.shift": the stems of subclades are included in subclade analyses;
  - "crown.shift": the stems of subclades are included in the backbone analysis (Default).

- **main** 
  Character. The name of the plot. Default is NULL and the combination rank with AICc will be printed if shift.res is not NULL.
col.sub character. A vector to specify colors of subclade(s). Can be let NULL (see details).

col.bck character. A vector to specify colors of backbone(s). Default is "black" for simple backbone (see details).

lad boolean. Allows to ladderize the tree.

leg boolean. If TRUE, legend of the selected combination is added to the plot with names from data and best model names. Default is TRUE. The position is automatically adjusted in function of lad argument.

lty.bck numeric. Define lty for the backbone.

tested_nodes boolean. If TRUE, all the tested nodes are highlighted by a red point.

text.cex numeric. Define the size of legend text.

pch.cex numeric. Define the size of points if tested_nodes = TRUE

... further arguments to be passed to plot or to plot.phylo.

Details

If col.sub is not specified, color vector for subclades is c(c(brewer.pal(8, "Dark2"), brewer.pal(8, "Set1"), "darkmagenta", "dodgerblue2", "orange", "forestgreen"))). For multiple backbone, default vector is c("blue4", "orange4", "red4", "grey40", "coral4", "deeppink4", "khaki4", "darkolivegreen", "darkslategray","black"). ... allows to set different graphical parameters from plot.phylo such as cex for size of tip labels or edge.width for the thickness of the phylogeny edges.

Value

plot the phylogeny and returns the same invisible object as plot.phylo.

Author(s)

Nathan Mazet

References


See Also

shift.estimates

Examples

# loading data
data("Cetacea")
data("taxo_cetacea")
taxo_cetacea_no_genus <- taxo_cetacea[names(taxo_cetacea) != "Genus"]
# main procedure
f_cetacea <- get.sampling.fractions(phylo = Cetacea, lad = FALSE,
data = taxo_cetacea_no_genus,
plot = TRUE, cex = 0.3)

comb.shift_cetacea <- get.comb.shift(phylo = Cetacea,
data = taxo_cetacea_no_genus,
sampling.fractions = f_cetacea,
Ncores = 4)

# use of plot_phylo_comb
# without shift.estimates results but with comb.shift_cetacea

plot_phylo_comb(phylo = Cetacea,
data = taxo_cetacea,
sampling.fractions = f_cetacea,
combi = comb.shift_cetacea[15],
label.offset = 0.3,
main = "", lad = FALSE ,cex = 0.4)

---

**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

```r
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, lty.bound=1, add.present=T, ...)
```

## 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.
- `plot.prob`: logical: set to TRUE (default value) to plot the probabilities.
- `plot.mean`: logical: set to TRUE (default value) to plot a line for the mean.
- `plot.bound`: logical: set to TRUE to plot the bounds of the confidence interval, int must be set to TRUE.
int logical: set to TRUE (default value) to plot a confidence interval.
conf confidence level. The default value is 0.95.
add logical: set to TRUE to add the plot on an existing graph.
col.mean color of the line for the mean.
col.bound color of the confidence interval bounds
lty style of the line for the mean (if added on a current plot)
lwd the line width, a positive number (default to 1)
lty.bound style of the line for the bound (if added on a current plot)
add.present whether or not to add the present diversity value to the plot. Default is TRUE.
... further arguments to be passed to plot or to plot.phylo.

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


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)

if(test){
  # 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**

```r
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**


See Also

GIC.fit_pl.rpanda, fit_t_pl, phyl.pca_pl

Examples

if(test){
  if(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**

```r
prob_dtt(fit.bd, tot_time, time, N0, l=N0, f = l/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.
prob_dtt

- **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 l/N0.
- **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 (N0) is known exactly or when the whole phylogeny is sampled (f==1). A 'hard one', much longer, is used when N0 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**


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()

if(test){
  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 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

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


Examples

data(redalgae)
plot(redalgae)
remove.model

Description

Allows to remove a model from the model comparisons of shift.estimates output.

Usage

remove.model(shift.res, model)

Arguments

shift.res  the output resulting from shift.estimates.
model      character. Specifies the model to remove from the set of model of diversification applied in shift.res.

Details

This function allow to remove model one at a time. The idea is to remove a model without having to reanalyse the phylogeny and all the combinations of shifts if a model (e.g. BVAR_DVAR) behaves strangely on the studied phylogeny.

Value

the same output resulting from shift.estimates but without the chosen model in model comparisons.

Author(s)

Nathan Mazet

References


See Also

shift.estimates
Examples

# loading data
data("shifts_cetacea")

# Removing "BVAR_DCST" model for the example
shifts_cetacea_noBVAR_DCST <- remove.model(shift.res = shifts_cetacea, 
model = "BVAR_DCST")

---

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


Examples

data(sealevel)
plot(sealevel)
shift.estimates  Estimating clade-shifts of diversification

Description

Applies models of diversification to each part of all combinations of shifts to detect the best combination of subclades and backbone(s).

Usage

```r
shift.estimates(phylo, data, sampling.fractions, comb.shift,
models = c("BCST", "BCST_DCST", "BVAR",
"BVAR_DCST", "BCST_DVAR", "BVAR_DVAR"),
backbone.option = "crown.shift",
multi.backbone = F, np.sub = 4,
rate.max = NULL, n.max = NULL, Ncores = 1)
```

Arguments

- `phylo`: an object of type 'phylo' (see ape documentation)
- `data`: a data.frame containing a database of monophyletic groups for which potential shifts can be investigated. This database should be based on taxonomy, ecology or traits and contain a column named "Species" with species name as in phylo.
- `sampling.fractions`: the output resulting from `get.sampling.fractions`.
- `comb.shift`: the output resulting from `get.comb.shift`.
- `models`: a vector of character that specifies the set of models of diversification to apply. Default is c("BCST", "BCST_DCST", "BVAR", "BVAR_DCST", "BCST_DVAR", "BVAR_DVAR").
- `backbone.option`: type of the backbone analysis:
  - "stem.shift": for every shift, the probability of the speciation event at the stem age of the subclade is included in the likelihood of the backbone thanks to the argument `spec_times`.
  - "crown.shift": for every shift, both the probability of the speciation event at the stem age of the subclade and the probability that the stem of the subclade survives to the crown age are included in the likelihood of the backbone thanks to the argument `branch_times`.
- `multi.backbone`: can be either FALSE (default), TRUE or "all":
  - FALSE: only combinations with simple backbone will be analyzed.
  - TRUE: only combinations with multiple backbones will be analyzed.
  - "all": all combinations are analyzed.
\texttt{np.sub} \hfill Defines the set of models to apply to subclade based on the number of parameters. By default \texttt{np.sub = 4} and all models from argument \texttt{models} will be applied. If \texttt{np.sub = 3}, the more complex model "BVAR DVAR" is excluded. If \texttt{np.sub = 2}, the set of models is reduced to "BCST", "BCST DCST" and "BVAR" models. \texttt{np.sub = "no_extinction"} only applies "BCST" and "BVAR" models.

\texttt{rate.max} \hfill numeric. Define a maximum value for diversification rate through time.

\texttt{n.max} \hfill numeric. Define a maximum value for diversity through time.

\texttt{Ncores} \hfill numeric. Define the number of CPU cores to use for parallelizing the computation of combinations.

\section*{Details}

The output for backbone is a list in which each element corresponds to the backbone model comparisons of a combination. This element contains a list with one table of model comparison per backbone.

We recommend to remove "BVAR DVAR" model from the models set and to lead the first analysis with \texttt{multi.backbone = F} to limit the number of combination.

\texttt{clade.size} argument should be the same value for the whole procedure (same than for \texttt{get.sampling.fraction} and \texttt{get.comb.shift}).

\section*{Value}

a list with the following components

\begin{itemize}
  \item \texttt{whole.tree} \hfill a data.frame with the model comparison for the whole tree
  \item \texttt{subclades} \hfill a list of dataframes summarizing the model comparison for all subclades (same format than \texttt{div.models} outputs)
  \item \texttt{backbones} \hfill a list with the model comparison for all backbones (see details)
  \item \texttt{total} \hfill the global comparison of combinations based on AICc
\end{itemize}

\section*{Author(s)}

Nathan Mazet

\section*{References}


\section*{See Also}

\texttt{get.sampling.fractions}, \texttt{shift.estimates}, \texttt{paleodiv}
Examples

# loading data
data("Cetacea")
data("taxo_cetacea")

# whole procedure
taxo_cetacea_no_genus <- taxo_cetacea[names(taxo_cetacea) != "Genus"]
f_cetacea <- get.sampling.fractions(phylo = Cetacea, lad = FALSE, data = taxo_cetacea_no_genus, plot = TRUE, cex = 0.3)

comb.shift_cetacea <- get.comb.shift(phylo = Cetacea, data = taxo_cetacea_no_genus, sampling.fractions = f_cetacea, Ncores = 4)

shifts_cetacea <- shift.estimates(phylo = Cetacea, data = taxo_cetacea_no_genus, sampling.fractions = f_cetacea, comb.shift = comb.shift_cetacea, models = c("BCST","BCST_DCST","BVAR","BVAR_DCST","BCST_DVAR"), backbone.option = "crown.shift", Ncores = 4)

shifts_cetacea

Cetacean shift.estimates results

Description

Results of shift.estimates applied to Cetaceans

Usage

data(shifts_cetacea)

Details

This object is the result of shifts.estimates applied to the Cetacean phylogeny as in the example of shift.estimates function.

Source

References

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


Examples

```r
data(shifts_cetacea)
print(shifts_cetacea)
```

### silica

Silica data across the Cenozoic

**Description**

Silica weathering ratio across the Cenozoic

**Usage**

```r
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**


**Examples**

```r
data(silica)
plot(silica)
```
**sim.BipartiteEvol**

*Simulation of the BipartiteEvol model*

**Description**

Simulate of the BipartiteEvol model from Maliet et al. (2020)

**Usage**

```r
sim.BipartiteEvol(nx, ny = nx, NG, dSpace = Inf, D = 1, muP,
muH, alphaP = 0, alphaH = 0, iniP = 0, iniH = 0, nP = 1, nH = 1,
rP = 1, rH = 1, effect = 1, verbose = 100, thin = 1, P = NULL, H = NULL)
```

**Arguments**

- **nx**: Size of the grid (the grid has size nx * ny)
- **ny**: Size of the grid (default to nx, the grid has size nx * ny)
- **NG**: Number of time step the model is run
- **dSpace**: Size of the dispersal kernel (default to Inf, meaning there are no restrictions on dispersion)
- **D**: Dimension of the trait space (default to 3)
- **muP**: Mutation probability at reproduction for the individuals of clade P
- **muH**: Mutation probability at reproduction for the individuals of clade H
- **alphaP**: alpha parameter for clade P (1/alpha is the niche width)
- **alphaH**: alpha parameter for clade H (1/alpha is the niche width)
- **iniP**: Initial trait value for the individuals in clade P
- **iniH**: Initial trait value for the individuals in clade P
- **nP**: Number of individuals of clade P killed at each time step
- **nH**: Number of individuals of clade H killed at each time step
- **rP**: r parameter for clade P (r is the ratio between the fitness maximum and minimum)
- **rH**: r parameter for clade H (r is the ratio between the fitness maximum and minimum)
- **effect**: Standard deviation of the trait mutation kernel
- **verbose**: The simulation
- **thin**: The number of iterations between two recording of the state of the model (default to 1)
- **P**: Optionnal, used to continue one precedent run: traits of the individuals of clade P at the end of the precedent run
- **H**: Optionnal, used to continue one precedent run: traits of the individuals of clade H at the end of the precedent run
Value

a list with

- Pgenealogy: The genealogy of clade P
- Hgenealogy: The genealogy of clade H
- xP: The trait values at each time step for clade P
- xH: The trait values at each time step for clade H
- P: The trait values at present for clade P
- H: The trait values at present for clade P
- Pmut: The number of new mutations at each time step for clade P
- Hmut: The number of new mutations at each time step for clade H
- iniP: The initial trait values for the individuals of clade P used in the simulation
- iniH: The initial trait values for the individuals of clade H used in the simulation
- thin.factor: The thin value used in the simulation

Author(s)

O. Maliet

References


Examples

# run the model
set.seed(1)

if(test){
  mod = sim.BipartiteEvol(nx = 8, ny = 4, NG = 500,
        D = 3, muP = 0.1, muH = 0.1,
        alphaP = 0.12, alphaH = 0.12,
        rP = 10, rH = 10,
        verbose = 100, thin = 5)

  # build the genealogies
  gen = make_gen.BipartiteEvol(mod)
  plot(gen$H)

  # compute the phylogenies
  phy1 = define_species.BipartiteEvol(gen, threshold=1)
  plot_div.BipartiteEvol(gen, phy1, 1)

  # build the network
net = build_network.BipartiteEvol(gen, phy1)

trait.id = 1
plot_net.BipartiteEvol(gen, phy1, trait.id, net, mod, nx = 10, spatial = FALSE)

## add time steps to a former run
seed = as.integer(10)
set.seed(seed)

mod = sim.BipartiteEvol(nx = 8, ny = 4, NG = 500,
D = 3, muP = 0.1, muH = 0.1,
alphaP = 0.12, alphaH = 0.12,
rP = 10, rH = 10,
verbose = 100, thin = 5,
P=mod$P, H=mod$H) # former ru output

# update the genealogy
gen = make_gen.BipartiteEvol(mod,
    treeP=gen$P, treeH=gen$H)

# update the phylogenies...
phy1 = define_species.BipartiteEvol(gen, threshold=1)

#... and the network
net = build_network.BipartiteEvol(gen, phy1)

trait.id = 1
plot_net.BipartiteEvol(gen, phy1, trait.id, net, mod, nx = 10, spatial = FALSE)
}

---

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

- **phylo**
  - an object of type 'phylo' (see ape documentation)

- **pars**
  - A matrix with a number of rows corresponding to the desired number of simulations, columns containing values for \( \text{sig}^2 \) in [,1], \( m \) in [,2], \( \alpha \) in [,3], \( \text{root.value} \) in [,4], \( \psi \) of the OU model for the non-focal, resource use trait in [,5], and \( \theta \) in the OU model for the non-focal resource use trait in [,6]

- **Nsegments**
  - the minimum number of time steps to simulate

- **plot**
  - 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

- **geo.object**
  - geography object created using CreateGeoObject

Details

Adjusting \( N_{\text{segments}} \) will impact the length of time the simulations take. The length of each segment (\( \frac{\text{max(nodeHeights(phylo))}}{N_{\text{segments}}} \)) should be much smaller than the smallest branch (\( \frac{\text{min(phylo$edge.length)}}{N_{\text{segments}}} \)).

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


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,-0.1,1,0,c(2,0),0)
sim.convergence.geo(phylo,pars,Nsegments=2500, plot=FALSE, geo.object)
**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 bioge.object formatted from RPANDA (see CreateGeoObject function in RPANDA package)

**Usage**

```r
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 `sig2` in [,1], `m` in [,2], `alpha` in [,3], `root.value` in [,4], `psi` of the OU model in [,5], and `theta` 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(nodeHeights(phylo))/Nsegments`) should be much smaller than the smallest branch (`min(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**

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)

simul.comb.shift

Simulating trees from shift.estimates() results to test model adequacy

Description

Simulates trees with combination of shifts from shift.estimates() output.

Usage

simul.comb.shift(n = 10000, phylo, sampling.fractions, shift.res, combi = 1, clade.size = 5)

Arguments

n numeric. Defines the number of simulations to generate (see Details).
phylo an object of type 'phylo' (see ape documentation).
sampling.fractions the output resulting from get.sampling.fractions.
shift.res the output resulting from shift.estimates.
combi numeric. Corresponds to the rank of the combination in the global comparison (shift.res$Total).
clade.size numeric. Defines the minimum number of species in a subgroup. Default is 5.
Details

Some combinations of shifts might be complex cases to simulate because the backbone needs to be rich enough to graft subclades. Some simulations will not satisfy this condition and will then be discarded. In consequence, the number of simulated phylogenies in the output will not be equal to \( n \) for complex simulations. This is why the value of \( n \) is high by default (\( n = 10000 \)), to ensure to have enough simulations (around 500) to test the presence.

clade.size argument should be the same value for the whole procedure in the empirical case (same than for get.sampling.fraction and get.comb.shift).

Value

a list of simulated phylogenies as object of type phylo. Tips of subclades are named with the letters a, b, c, etc. while tips of backbones are named with letters z, y, etc. The empirical groups are sorted from the more recent to the older one (i.e. group a will be the more recent empirical subclade, etc.).

Author(s)

Nathan Mazet

References


See Also

shift.estimates

Examples

```r
# loading data
data("Cetacea")
data("taxo_cetacea")
data("shifts_cetacea")

# with the results from shifts.estimates()

# no shifts tested at genus level
taxo_cetacea_no_genus <- taxo_cetacea[ names(taxo_cetacea) != "Genus" ]

f_cetacea <- get.sampling.fractions(phylo = Cetacea,
data = taxo_cetacea_no_genus)

all_posteriors_cetacea <- simul.comb.shift(phylo = Cetacea,
sampling.fractions = f_cetacea,
shift.res = shifts_cetacea)
```
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


Examples

#Loading an example tree
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 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-geny with rate shifts happening at speciation events.

### Usage

```r
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

- **lambda_0** Initial speciation rate.
- **mu_0** Initial extinction rate, or turnover rate if `new_mu_law` == "turnover".
- **new_lamb_law** Distribution in which the new speciation rates are drawn at a speciation event. See details.
- **new_mu_law** Distribution in which the new extinction rates are drawn at a speciation event. See details.
- **condition** Stopping condition. Can be "time" (the default) or "taxa".
time_stop  Stoping time if condition == "time".
taxa_stop  Final number of species if condition == "taxa".

If condition == "time", the process is stoped if the number of species exceeds taxa_stop. This can be usefull 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 taxa_stop = Inf (the default).

sigma_lamb  Parameter of the new speciation rates distribution, see details.
alpha_lamb  Parameter of the new speciation rates distribution, see details.
lamb_max  Parameter of the new speciation rates distribution, see details.
lamb_min  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 stoped if one of the lineage has a speciation rate that exceeds maxRate. This can be usefull 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 $(\sigma_{\lambda}^2 \cdot t, \lambda_{\text{parent}})$, 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 $(\sigma_{\lambda}^2, \lambda_{\text{parent}} + \alpha_{\lambda})$, truncated in 0.

• "normal*shift", the new speciation rates are drawn in a normal distribution with parameters $(\sigma_{\lambda}^2, \lambda_{\text{parent}} \cdot \alpha_{\lambda})$, truncated in 0.

Available options for new_mu_law are:

• "uniform", the new extinction rates are drawn uniformly in $[\mu_{\text{min}}, \mu_{\text{max}}]$.

• "normal", the new extinction rates are drawn in a normal distribution with parameters $(\sigma_{\mu}^2, \mu_{\text{parent}})$, truncated in 0.

• "lognormal", the new extinction rates are drawn in a lognormal distribution with parameters $(\sigma_{\mu}^2, \mu_{\text{parent}})$.

• "lognormal*shift", the new extinction rates are drawn in a lognormal distribution with parameters $(\sigma_{\mu}^2, \mu_{\text{parent}} \cdot \alpha_{\mu})$.

• "normal*t", the new speciation rates are drawn in a normal distribution with parameters $(\sigma_{\lambda}^2 \cdot t^2, \lambda_{\text{parent}})$, where $t$ is the age of the mother species.

• "turnover", the turnover rate is constant (in that case $\mu_0$ is the turnover rate), so the new extinction rates are $\mu_0$ 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 nblineages[i] is the number of species in the clade after the event happening at time[i].
- 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.
- maxRate: A boolean indicating whether the process was ended before reaching the specified stopping criterion because one of the speciation rates exceeded maxRate (see the "arguments" section).
- root_length: The time before the first speciation event.

Author(s)

O. Maliet
References


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]

par(mar=c(1,1,0,0))
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**

```r
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 $\lambda$ 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 $\mu$ 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 sm.spline 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


sim_MCBD

Simulation of macroevolutionary diversification under the integrated model described in Aristide & Morlon 2019

Description

Simulates the joint diversification of species and a continuous trait, where changes in both dimensions are interlinked through competitive interactions.

Usage

```r
sim_MCBD(pars, root.value = 0, age.max = 50, step.size = 0.01, bounds = c(-Inf,Inf), plot = TRUE, ylims=NULL, full.sim = FALSE)
```

Arguments

- **pars** Vector of simulation parameters:
  - `pars[1]` corresponds to $\lambda_1$, the speciation initiation rate
  - `pars[2]` corresponds to $\tau_0$, the basal speciation completion rate
  - `pars[3]` corresponds to $\beta$, the effect of trait differences on the speciation completion rate
  - `pars[4]` corresponds to $\mu_0$, the competitive extinction parameter for good species
  - `pars[5]` corresponds to $\mu_{bg}$, the background good species extinction rate
  - `pars[6]` corresponds to $\mu_{i0}$, the competitive extinction parameter for incipient species
  - `pars[7]` corresponds to $\mu_{ibg}$, the background incipient species extinction rate
  - `pars[8]` corresponds to $\alpha_1$, the competition effect on extinction (competition strength)
  - `pars[9]` corresponds to $\alpha_1$, the competition effect on trait evolution (competition strength)
```
pars[10] corresponds to \( \sigma_2 \), the variance (rate) of the Brownian motion
pars[11] corresponds to \( m \), the relative contribution of character displacement (competition) with respect to stochastic (brownian) evolution

root.value the starting trait value
age.max maximum time for the simulation (if the process doesn’t go extinct)
step.size size of each simulation step
bounds lower and upper value for bounds in trait space
plot logical indicating whether to plot the simulation
ylims y axis (trait values) limits for the simulation plot
full.sim logical indicating whether to return the full simulation (see details)

Details

It might be difficult to find parameter combinations that are sensitive. It is recommended to use the parameter settings of the examples as a starting point and from there modify them to understand the behavior of the model. If trees produced are too big, simulation can become too slow to ever finish.

Value

returns a list with the following elements:

all contains the complete tree of the process (extant and extinct good and incipient lineages) and trait values for each tip in the tree
gsp_fossil contains the extant and extinct good species tree and trait values for each tip in the tree
gsp_extant contains the reconstructed (extant only) good species tree and trait values for each tip in the tree

If full.sim = TRUE, two additional elements are returned inside all:

note: both elements are used internally to keep track of the simulation and are dynamically updated, so returned elements only reflect the last state

lin_mat a matrix with information about the diversification process. Each row represents a new lineage in the process with the following elements: - Parental node, descendent node (0 if a tip), starting time, ending time, status at end (extinct(-2); incipient(-1); good(1)), speciation completion or extinction time; speciation completion time (NA if still incipient).

trait_mat a list with trait values for each lineage at each time step throughout the simulation. Each element is a vector composed of the following: Lineage number (same as row number in lin_mat), status (as in lin_mat), sister lineage number, trait values (NA if lineage didn’t exist yet at that time step)

Author(s)

Leandro Aristide (leandroaristi@gmail.com)

References

Aristide, L., and Morlon, H. 2019. Understanding the effect of competition during evolutionary radiations: an integrated model of phenotypic and species diversification
Examples

```r
lambda1 = 0.25
tau0 = 0.01
beta = 0.6
mu0 = 0.5
mubg = 0.01
mui0 = 0.8
muibg = 0.02
alpha1 = alpha2 = 0.04
sig2 = 0.5
m = 20
```

pars <- c(lambda1, tau0, beta, mu0, mubg, mui0, muibg, alpha1, alpha2, sig2, m)

if(test){
  # 1000 steps, unbounded
  res <- sim_MCBD(pars, age.max=10, step.size=0.01)

  # asymmetric bounds
  res <- sim_MCBD(pars, age.max=10, step.size=0.01, bounds=c(-10,Inf))

  # only deterministic component
  pars <- c(lambda1, tau0, beta, mu0, mubg, mui0, muibg, alpha1, alpha2, sig2=0, m)
  res <- sim_MCBD(pars, age.max=10)

  plot(res$gsp_extant$tree)
}
```

**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**

```r
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**


**Examples**

```r
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**

```r
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(nodeHeights(phylo))/Nsegments) should be much smaller than the smallest branch (min(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**


**See Also**

*fit_t_comp*

**Examples**

```r
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 exponential 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**

```r
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 `EnvExp` and `EnvLin`, 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 \( \sigma^2 \) 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

See Also
plot.fit_t.env, likelihood_t_env

Examples

if(test){
  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:
if(require(pspline)){
  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,
sim_t_env_ou

Recursive simulation (root-to-tip) of the OU environmental model

Description
Simulates datasets for a given phylogeny under the OU environmental model (see ?fit_t_env_ou)

Usage

sim_t_env_ou(phylo, param, env_data, model, step=0.01,
plot=FALSE, sigma, alpha, theta0, ...)

Arguments

d | phylo | An object of class 'phylo' (see ape documentation) |
| param | A numeric vector of parameters for the user-defined climatic model. For the OU-environmental model, there is only one parameters (beta). If a model fit object of class 'fit_t_env.ou' is provided, the ML parameters are used to generate new datasets. |
| 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 trajectory of the optimum "theta(t)" with time and the environmental variable (see details for default model). An user defined function of any functional form can be used (forward in time). This function has four 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), and the fourth is the theta_0 value. See the example below. |
| 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. |
| sigma | The "sigma" parameter of the OU process. |
alpha  The "alpha" parameter of the OU process.
theta0  The "theta" parameter at the root of the tree (t=0).
...    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

See Also
plot.fit_t.env, fit_t_env, fit_t_env_ou, plot.fit_t.env_ou

Examples

if(test){
data(InfTemp)
set.seed(9999) # for reproducibility

# Let's start by simulating a trait under a climatic OU
beta = 0.6       # relationship to the climate curve
sim_theta = 4    # value of the optimum if the relationship to the climate
# curve is 0 (this corresponds to an 'intercept' in the linear relationship used below)
sim_sigma2 = 0.025  # variance of the scatter = sigma^2
sim_alpha = 0.36  # alpha value = strength of the OU; quite high here...
delta = 0.001     # time step used for the forward simulations => here its 1000y steps
Recursive simulation (root-to-tip) of two-regime models

Description

Simulates datasets for a given phylogeny under two-regime matching competition (MC), diversity dependent linear (DDlin), diversity dependent exponential (DDexp), or early burst (EB) models of trait evolution. Simulations are carried out from the root to the tip of the tree.

Usage

```
sim_t_tworegime(regime.map, pars, root.value, Nsegments=2500, 
    model=c("MC","DDexp","DDlin","EB"), 
    verbose=TRUE, rnd=6) 
```
Arguments

regime.map a stochastic map of the two regimes stored as a simmap object output from make.simmap
pars a vector containing the three parameters for the chosen model; all models require \( \text{sig2} \), and additionally, the MC model requires \( S1 \) and \( S2 \), specifying the level of competition in regime 1 and 2, respectively (larger negative values correspond to higher levels of competition), the DDlin model requires \( b1 \) and \( b2 \), the DDexp model requires \( r1 \), the slope parameters (negative in cases of decline in evolutionary rates with increasing diversity). \( \text{sig2} \) 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, "DDlin" is the diversity-dependent linear model, "DDexp" is the diversity-dependent exponential model, and "EB" is the early burst model.
verbose if TRUE, prints the identity of regimes corresponding to each parameter value
rnd number of digits to round timings to (see round (see Details))

Details

Adjusting Nsegments will impact the length of time the simulations take. The length of each segment (\( \max(\text{nodeHeights(phylo)})/\text{Nsegments} \)) should be much smaller than the smallest branch (\( \min(\text{phylo}$edge.length) \)).

Adjusting rnd may help if function crashes.

Value

a named vector with simulated trait values for \( n \) species in the phylogeny

Author(s)

J Drury jonathan.p.drury@gmail.com

References


See Also

fit_t_comp
Examples

data(Cetacea_clades)

# Simulate data under the matching competition model
MC_tworegime.data<-sim_t_tworegime(Cetacea_clades,pars=c(sig2=0.01,S1=-0.1,S2=-0.01),
root.value=0,Nsegments=1000,model="MC")

# Simulate data under the diversity dependent linear model
DDlin_tworegime.data<-sim_t_tworegime(Cetacea_clades,pars=c(sig2=0.01,b1=-0.0001,b2=-0.000001),
root.value=0,Nsegments=1000,model="DDlin")

# Simulate data under the diversity dependent linear model
DDexp_tworegime.data<-sim_t_tworegime(Cetacea_clades,pars=c(sig2=0.01,r1=-0.01,r2=-0.02),
root.value=0,Nsegments=1000,model="DDexp")

# Simulate data under the diversity dependent linear model
EB.data_tworegime<-sim_t_tworegime(Cetacea_clades,pars=c(sig2=0.01,r1=-0.01,r2=-0.02),
root.value=0,Nsegments=1000,model="EB")

spectR

Spectral density plot of a phylogeny

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
meth
zero_bound

an object of type 'phylo' (see ape documentation)
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)
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`, `BICompare`

Examples

data(Cetacea)
spectR(Cetacea, meth="standard", zero_bound=FALSE)

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)

taxo_cetacea  Cetacean taxonomy

Description

Taxonomy of Cetaceans

Usage

data(taxo_cetacea)

Details

This taxonomy lists all species of Cetaceans to properly calculate sampling fractions by clades. It
corresponds to the phylogeny of Steeman et al. (2009).
Source

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

Examples
```r
data(taxo_cetacea)
print(taxo_cetacea)
```

---

**theta_estimator**

*Compute Watterson genetic diversity (Theta estimator)*

**Description**
This function computes the Theta estimator of genetic diversity (Watterson, 1975) while controlling for the presence of gaps in the alignment (Ferretti et al, 2012), frequent in barcoding datasets.

**Usage**
```
theta_estimator(sequences)
```

**Arguments**

- **sequences**
  a matrix representing the nucleotidic alignment of all the sequences present in the phylogenetic tree.

**Value**
An estimate of genetic diversity.

**Author(s)**
Ana C. Afonso Silva & Benoît Perez-Lamarque
References


See Also

pi_estimator delineate_phylotypes

Examples

data(woodmouse)

alignment <- as.character(woodmouse) # nucleotide alignment

theta_estimator(alignment)
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