

Package ‘PBD’

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Type Package

Title Protracted Birth-Death Model of Diversification

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Imports deSolve, ade4, ape, DDD, phytools, graphics, stats, utils

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Description

Conducts maximum likelihood analysis and simulation of the protracted speciation model.

License GPL-2

NeedsCompilation no

R topics documented:

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Description

This package computes the (maximum) likelihood of the protracted speciation model for a given set of branching times. This package is a likelihood-based statistical package to estimate parameters under the protracted speciation model.

First version: 0.8

New in version 0.9

- Bug fix for stem age

New in version 0.91

- Reports loglik = -Inf on an error in the deSolve package (function ode)

New in version 0.92

- Correcting order of parameters of pbd_sim

New in version 0.93

- pbd_sim produces a tree, a matrix containing all events in the simulation, and a tree with one sample per species.

New in version 1.0

- Conditioning is also possible on a range of values of the number of species.

New in version 1.1

- Simulation of the protracted speciation tree has more features.

New in version 1.2

- Optimization can make use of subplex (default) and simplex (older versions).

Details

Package:	PBD
Type:	Package
Version:	1.2
Date:	2016-2-5
License:	GPL-2

pbd_loglik computes the likelihood of the protracted birth-death model of diversification, given a set of parameters and a data set of phylogenetic branching times.

pbd_ML finds the parameters that maximizes the likelihood computed by pbd_loglik.

Author(s)

Rampal S. Etienne Maintainer: Rampal S. Etienne <r.s.etienne@rug.nl>

References

- Etienne, R.S. & J. Rosindell 2012. Systematic Biology 61: 204-213.
- Lambert, A., H. Morlon & R.S. Etienne 2014. Journal of Mathematical Biology 70: 367-397. doi:10.1007/s00285-014-0767-x

- Etienne, R.S., H. Morlon & A. Lambert 2014. Evolution 68: 2430-2440 doi:10.1111/evo.12433

.

See Also

DDD

Examples

```
pbd_ML(1:10)
```

pbd_bootstrap	<i>Bootstrap analysis under protracted birth-death model of diversification</i>
---------------	---

Description

Likelihood maximization for protracted birth-death model of diversification followed by simulations of the model using the maximum likelihood parameter estimates to compute an estimate of the error in these estimates and to assess the goodness-of-fit of the model by comparing maximum likelihoods of the simulated data sets to the maximum likelihood of the real data set.

Usage

```
pbd_bootstrap(
  brts,
  initparsopt = c(0.2,0.1,1),
  idparsopt = 1:length(initparsopt),
  idparsfix = NULL,
  parsfix = NULL,
  exteq = (length(initparsopt) < 4),
  parsfunc = c(function(t,pars) {pars[1]},function(t,pars) {pars[2]},
function(t,pars) {pars[3]}, function(t,pars) {pars[4]}),
  misnumspec = 0,
  cond = 1,
  btorph = 0,
  soc = 2,
  plotltt = 1,
  methode = "lsoda",
  n_low = 0,
  n_up = 0,
  tol = c(1E-4, 1E-4, 1E-6),
  maxiter = 1000 * round((1.25)^length(idparsopt)),
  endmc = 100,
  seed = 42
)
```

Arguments

brts	A set of branching times of a phylogeny, all positive
initparsopt	The initial values of the parameters that must be optimized

idparsopt	The ids of the parameters that must be optimized, e.g. 1:4 for all parameters. The ids are defined as follows: id == 1 corresponds to b (speciation-initiation rate) id == 2 corresponds to mu_1 (extinction rate of good species) id == 3 corresponds to la_1 (speciation-completion rate) id == 4 corresponds to mu_2 (extinction rate of incipient species)
idparsfix	The ids of the parameters that should not be optimized, e.g. c(2,4) if mu_1 and mu_2 should not be optimized, but only b and la_1. In that case idparsopt must be c(1,3).
parsfix	The values of the parameters that should not be optimized
exteq	Sets whether incipient species have the same (1) or different (0) extinction rate as good species. If exteq = 0, then idparsfix and idparsopt should together have all parameters 1:4
parsfunc	Specifies functions how the rates depend on time, default functions are constant functions
missnumspec	The number of species that are in the clade but missing in the phylogeny
cond	Conditioning: cond == 0 : conditioning on stem or crown age cond == 1 : conditioning on stem or crown age and non-extinction of the phylogeny
btorph	Sets whether the likelihood is for the branching times (0) or the phylogeny (1)
soc	Sets whether the first element of the branching times is the stem (1) or the crown (2) age
plotlitt	Sets whether the lineage-through-time plot should be plotted (1) or not (0)
methode	Sets which method should be used in the ode-solver. Default is 'lsoda'. See package deSolve for details.
n_low	Sets the lower bound of the number of species on which conditioning should be done when cond = 2. Set this to 0 when conditioning should be done on precisely the number of species (default)
n_up	Sets the upper bound of the number of species on which conditioning should be done when cond = 2. Set this to 0 when conditioning should be done on precisely the number of species (default)
tol	Sets the tolerances in the optimization. Consists of: reltolx = relative tolerance of parameter values in optimization reltolf = relative tolerance of function value in optimization abstolx = absolute tolerance of parameter values in optimization
maxiter	Sets the maximum number of iterations in the optimization
endmc	Sets the number of simulations for the bootstrap
seed	Sets the seed for the simulations of the bootstrap

Value

A list of three dataframes. The first dataframe contains the maximum likelihood results of the real data set, the second contains the simulated trees, and the third dataframe, with number of rows equal to endmc, contain the maximum likelihood results for the simulated data. The columns of both frames contains the following elements for each simulated data set:

<code>ntips</code>	gives the number of tips
<code>b</code>	gives the maximum likelihood estimate of <code>b</code>
<code>mu_1</code>	gives the maximum likelihood estimate of <code>mu_1</code>
<code>la_1</code>	gives the maximum likelihood estimate of <code>la_1</code>
<code>mu_2</code>	gives the maximum likelihood estimate of <code>mu_2</code>
<code>loglik</code>	gives the maximum loglikelihood
<code>df</code>	gives the number of estimated parameters, i.e. degrees of freedom
<code>conv</code>	gives a message on convergence of optimization; <code>conv = 0</code> means convergence
<code>exp_durspec</code>	gives the expected duration of speciation
<code>median_durspec</code>	gives the median duration of speciation

Author(s)

Rampal S. Etienne

See Also

[pbdbML](#)

Examples

```
pbdbbootstrap(1:10, endmc = 2)
```

<code>pbdbrtsdensity</code>	<i>Node depth probability density for protracted birth-death model of diversification</i>
-----------------------------	---

Description

`pbdbrtsdensity` computes the probability density of node depths under the protracted speciation model given a set of parameters

Usage

```
pbdbrtsdensity(
  pars1,
  pars1f = c(function(t,pars) {pars[1]},function(t,pars) {pars[2]},
  function(t,pars) {pars[3]}, function(t,pars) {pars[4]}),
  methode = "lsoda",
  brts
)
```

Arguments

pars1	<p>Vector of parameters:</p> <p>pars1[1] corresponds to b (= la_1 in Etienne & Rosindell R2012) = speciation initiation rate</p> <p>pars1[2] corresponds to μ_1 (= μ_g in Etienne & Rosindell 2012) = extinction rate of good species</p> <p>pars1[3] corresponds to la_1 (= la_2 in Etienne & Rosindell 2012) = speciation completion rate</p> <p>pars1[4] corresponds to μ_2 (= μ_i in ER2012) = extinction rate of incipient species</p> <p>When rates depend on time this time dependence should be specified in pars1f and pars1 then becomes the parameters used in pars1f</p>
pars1f	<p>Vector of functions how the rates depend on time, default functions are constant functions of the parameters in pars1:</p> <p>pars1f[1] corresponds to time-dependence of b (= la_1 in Etienne & Rosindell R2012) = speciation initiation rate</p> <p>pars1f[2] corresponds to time-dependence of μ_1 (= μ_g in Etienne & Rosindell 2012) = extinction rate of good species</p> <p>pars1f[3] corresponds to time-dependence of la_1 (= la_2 in Etienne & Rosindell 2012) = speciation completion rate</p> <p>pars1f[4] corresponds to time-dependence of μ_2 (= μ_i in ER2012) = extinction rate of incipient species</p>
methode	sets which method should be used in the ode-solver. Default is 'lsoda'. See package deSolve for details.
brts	A set of branching times of a phylogeny, all positive, for which the density must be computed

Value

The probability density for all branching times

Author(s)

Rampal S. Etienne

See Also

[pbd_ML](#)

Examples

```
pbd_brts_density(pars1 = c(0.2,0.1,1,0.1), methode = "lsoda",brts = 1:10)
```

`pbd_durspec_cumdensity`*Cumulative density of duration of speciation under protracted birth-death model of diversification*

Description

`pbd_durspec_cumdensity` computes the cumulative density of the duration of speciation under the protracted speciation model for a given set of parameters

Usage

```
pbd_durspec_cumdensity(  
  pars,  
  tau  
)
```

Arguments

<code>pars</code>	Vector of parameters: <code>pars[1]</code> corresponds to <code>b</code> (= <code>la_3</code> in Etienne & Rosindell R2012) = speciation initiation rate <code>pars[2]</code> corresponds to <code>la_1</code> (= <code>la_2</code> in Etienne & Rosindell 2012) = speciation completion rate <code>pars[3]</code> corresponds to <code>mu_2</code> (= <code>mu_i</code> in ER2012) = extinction rate of incipient species
<code>tau</code>	Value of the duration of speciation at which the cumulative density must be computed

Value

The cumulative density of the duration of speciation

Author(s)

Rampal S. Etienne

See Also

[pbd_durspec_density](#)
[pbd_durspec_mean](#)
[pbd_durspec_mode](#)
[pbd_durspec_quantile](#)
[pbd_durspec_moment](#)
[pbd_durspec_var](#)

Examples

```
pbd_durspec_cumdensity(pars = c(0.5,0.3,0.1),3)
```

pbd_durspec_density	<i>Probability density for duration of speciation under protracted birth-death model of diversification</i>
---------------------	---

Description

pbd_durspec_density computes the probability density of the duration of speciation under the protracted speciation model for a given set of parameters

Usage

```
pbd_durspec_density(
  pars,
  tau
)
```

Arguments

pars	Vector of parameters: pars[1] corresponds to b (= la_3 in Etienne & Rosindell R2012) = speciation initiation rate pars[2] corresponds to la_1 (= la_2 in Etienne & Rosindell 2012) = speciation completion rate pars[3] corresponds to mu_2 (= mu_i in ER2012) = extinction rate of incipient species
tau	The duration of speciation for which the density must be computed

Value

The probability density

Author(s)

Rampal S. Etienne

See Also

[pbd_durspec_cumdensity](#)
[pbd_durspec_mean](#)
[pbd_durspec_mode](#)
[pbd_durspec_quantile](#)
[pbd_durspec_moment](#)
[pbd_durspec_var](#)

Examples

```
pbd_durspec_density(pars = c(0.5,0.3,0.1), tau = 1)
```

pbd_durspec_mean	<i>Mean duration of speciation under protracted birth-death model of diversification</i>
------------------	--

Description

pbd_durspec_mean computes the mean duration of speciation under the protracted speciation model for a given set of parameters

Usage

```
pbd_durspec_mean(  
  pars  
)
```

Arguments

pars Vector of parameters:

pars[1] corresponds to b (= la_3 in Etienne & Rosindell R2012) = speciation initiation rate
pars[2] corresponds to la_1 (= la_2 in Etienne & Rosindell 2012) = speciation completion rate
pars[3] corresponds to mu_2 (= mu_i in ER2012) = extinction rate of incipient species

Value

The expected duration of speciation

Author(s)

Rampal S. Etienne

See Also

[pbd_durspec_density](#)
[pbd_durspec_cumdensity](#)
[pbd_durspec_mode](#)
[pbd_durspec_quantile](#)
[pbd_durspec_moment](#)
[pbd_durspec_var](#)

Examples

```
pbd_durspec_mean(pars = c(0.5,0.3,0.1))
```

pbd_durspec_mode	<i>mode of the duration of speciation under protracted birth-death model of diversification</i>
------------------	---

Description

pbd_durspec_mode computes the mode of the duration of speciation under the protracted speciation model for a given set of parameters

Usage

```
pbd_durspec_mode(
  pars
)
```

Arguments

pars	Vector of parameters: pars[1] corresponds to b (= la_3 in Etienne & Rosindell R2012) = speciation initiation rate pars[2] corresponds to la_1 (= la_2 in Etienne & Rosindell 2012) = speciation completion rate pars[3] corresponds to mu_2 (= mu_i in ER2012) = extinction rate of incipient species
------	--

Value

The expected duration of speciation

Author(s)

Rampal S. Etienne

See Also

[pbd_durspec_density](#)
[pbd_durspec_cumdensity](#)
[pbd_durspec_mean](#)
[pbd_durspec_quantile](#)
[pbd_durspec_moment](#)
[pbd_durspec_var](#)

Examples

```
pbd_durspec_mode(pars = c(0.5, 0.3, 0.1))
```

pbd_durspec_moment	<i>Moments of duration of speciation under protracted birth-death model of diversification</i>
--------------------	--

Description

pbd_durspec_moment computes the moments of the duration of speciation under the protracted speciation model for a given set of parameters

Usage

```
pbd_durspec_moment(
  pars,
  order
)
```

Arguments

pars	Vector of parameters: pars[1] corresponds to b (= la_3 in Etienne & Rosindell R2012) = speciation initiation rate pars[2] corresponds to la_1 (= la_2 in Etienne & Rosindell 2012) = speciation completion rate pars[3] corresponds to mu_2 (= mu_i in ER2012) = extinction rate of incipient species
order	order of the moment to compute (1 is first moment, giving the mean)

Value

The moment of the duration of speciation

Author(s)

Rampal S. Etienne

See Also

[pbd_durspec_density](#)
[pbd_durspec_cumdensity](#)
[pbd_durspec_mean](#)
[pbd_durspec_mode](#)
[pbd_durspec_quantile](#)
[pbd_durspec_var](#)

Examples

```
pbd_durspec_moment(pars = c(0.5,0.3,0.1),2)
```

pbd_durspec_quantile *Quantiles of duration of speciation under protracted birth-death model of diversification*

Description

pbd_durspec_quantile computes a quantile of the duration of speciation under the protracted speciation model for a given set of parameters

Usage

```
pbd_durspec_quantile(
  pars,
  p
)
```

Arguments

pars	Vector of parameters: pars[1] corresponds to b (= la_3 in Etienne & Rosindell R2012) = speciation initiation rate pars[2] corresponds to la_1 (= la_2 in Etienne & Rosindell 2012) = speciation completion rate pars[3] corresponds to mu_2 (= mu_i in ER2012) = extinction rate of incipient species
p	Quantile (e.g. p = 0.5 gives the median)

Value

The quantil of the duration of speciation

Author(s)

Rampal S. Etienne

See Also

[pbd_durspec_density](#)
[pbd_durspec_cumdensity](#)
[pbd_durspec_mean](#)
[pbd_durspec_mode](#)
[pbd_durspec_moment](#)
[pbd_durspec_var](#)

Examples

```
pbd_durspec_quantile(pars = c(0.5,0.3,0.1),0.5)
```

pbd_durspec_var	<i>Variance in duration of speciation under protracted birth-death model of diversification</i>
-----------------	---

Description

pbd_durspec_var computes the variance in the duration of speciation under the protracted speciation model for a given set of parameters

Usage

```
pbd_durspec_var(  
  pars  
)
```

Arguments

pars Vector of parameters:

pars[1] corresponds to b (= la_3 in Etienne & Rosindell R2012) = speciation initiation rate
pars[2] corresponds to la_1 (= la_2 in Etienne & Rosindell 2012) = speciation completion rate
pars[3] corresponds to mu_2 (= mu_i in ER2012) = extinction rate of incipient species

Value

The variance in the duration of speciation

Author(s)

Rampal S. Etienne

See Also

[pbd_durspec_density](#)
[pbd_durspec_cumdensity](#)
[pbd_durspec_mean](#)
[pbd_durspec_mode](#)
[pbd_durspec_quantile](#)
[pbd_durspec_moment](#)

Examples

```
pbd_durspec_var(pars = c(0.5,0.3,0.1))
```

pbd_loglik

*Loglikelihood for protracted birth-death model of diversification***Description**

pbd_loglik computes the loglikelihood of the parameters of the protracted speciation model given a set of branching times and number of missing species

Usage

```
pbd_loglik(
  pars1,
  pars1f = c(function(t,pars) {pars[1]},function(t,pars) {pars[2]},
  function(t,pars) {pars[3]}, function(t,pars) {pars[4]}),
  pars2 = c(1,1,2,1,"lsoda",0,0),
  brts,
  misssnumspec = 0
)
```

Arguments

pars1 Vector of parameters:

pars1[1] corresponds to b (= la_1 in Etienne & Rosindell R2012) = speciation initiation rate

pars1[2] corresponds to μ_1 (= μ_g in Etienne & Rosindell 2012) = extinction rate of good species

pars1[3] corresponds to la_1 (= la_2 in Etienne & Rosindell 2012) = speciation completion rate

pars1[4] corresponds to μ_2 (= μ_i in ER2012) = extinction rate of incipient species

When rates depend on time this time dependence should be specified in pars1f and pars1 then becomes the parameters used in pars1f

pars1f Vector of functions how the rates depend on time, default functions are constant functions of the parameters in pars1:

pars1f[1] corresponds to time-dependence of b (= la_1 in Etienne & Rosindell R2012) = speciation initiation rate

pars1f[2] corresponds to time-dependence of μ_1 (= μ_g in Etienne & Rosindell 2012) = extinction rate of good species

pars1f[3] corresponds to time-dependence of la_1 (= la_2 in Etienne & Rosindell 2012) = speciation completion rate

pars1f[4] corresponds to time-dependence of μ_2 (= μ_i in ER2012) = extinction rate of incipient species

pars2 Vector of model settings:

pars2[1] set the conditioning on non-extinction of the clade (1) or not (0)

pars2[2] sets whether the likelihood is for the branching times (0) or the phylogeny (1)

pars2[3] sets whether the first element of the branching times is the stem (1) or the crown (2) age

pars2[4] sets whether the parameters and likelihood should be shown on screen (1) or not (0)

pars2[5] sets which method should be used in the ode-solver. Default is 'lsoda'. See package deSolve for details.

pars2[6]Sets the lower bound of the number of species on which conditioning should be done when cond = 2. Set this to 0 when conditioning should be done on precisely the number of species (default)

pars2[7]Sets the upper bound of the number of species on which conditioning should be done when cond = 2. Set this to 0 when conditioning should be done on precisely the number of species (default)

brts A set of branching times of a phylogeny, all positive

missnumspec The number of species that are in the clade but missing in the phylogeny

Value

The loglikelihood

Author(s)

Rampal S. Etienne

See Also

[pbid_ML](#)

Examples

```
pbid_loglik(pars1 = c(0.2,0.1,1,0.1), pars2 = c(1,1,2,0,"lsoda"),brts = 1:10)
```

pbid_ML	<i>Maximization of loglikelihood under protracted birth-death model of diversification</i>
---------	--

Description

Likelihood maximization for protracted birth-death model of diversification

Usage

```

pbd_ML(
  brts,
  initparsopt = c(0.2,0.1,1),
  idparsopt = 1:length(initparsopt),
  idparsfix = NULL,
  parsfix = NULL,
  exteq = 1,
  parsfunc = c(function(t,pars) {pars[1]},function(t,pars) {pars[2]},
function(t,pars) {pars[3]}, function(t,pars) {pars[4]}),
  misnumspec = 0,
  cond = 1,
  btorph = 1,
  soc = 2,
  methode = "lsoda",
  n_low = 0,
  n_up = 0,
  tol = c(1E-4, 1E-4, 1E-6),
  maxiter = 1000 * round((1.25)^length(idparsopt)),
  optimmethod = 'subplex'
)

```

Arguments

brts	A set of branching times of a phylogeny, all positive
initparsopt	The initial values of the parameters that must be optimized
idparsopt	The ids of the parameters that must be optimized, e.g. 1:4 for all parameters. The ids are defined as follows: id == 1 corresponds to b (speciation-initiation rate) id == 2 corresponds to mu_1 (extinction rate of good species) id == 3 corresponds to la_1 (speciation-completion rate) id == 4 corresponds to mu_2 (extinction rate of incipient species)
idparsfix	The ids of the parameters that should not be optimized, e.g. c(2,4) if mu_1 and mu_2 should not be optimized, but only b and la_1. In that case idparsopt must be c(1,3).
parsfix	The values of the parameters that should not be optimized
exteq	Sets whether incipient species have the same (1) or different (0) extinction rate as good species. If exteq = 0, then idparsfix and idparsopt should together have all parameters 1:4
parsfunc	Specifies functions how the rates depend on time, default functions are constant functions
misnumspec	The number of species that are in the clade but missing in the phylogeny
cond	Conditioning: cond == 0 : conditioning on stem or crown age cond == 1 : conditioning on stem or crown age and non-extinction of the phylogeny cond == 2 : conditioning on stem or crown age and number of extant taxa
btorph	Sets whether the likelihood is for the branching times (0) or the phylogeny (1)

soc	Sets whether the first element of the branching times is the stem (1) or the crown (2) age
methode	Sets which method should be used in the ode-solver. Default is 'lsoda'. See package deSolve for details.
n_low	Sets the lower bound of the number of species on which conditioning should be done when cond = 2. Set this to 0 when conditioning should be done on precisely the number of species (default)
n_up	Sets the upper bound of the number of species on which conditioning should be done when cond = 2. Set this to 0 when conditioning should be done on precisely the number of species (default)
tol	Sets the tolerances in the optimization. Consists of: reltolx = relative tolerance of parameter values in optimization reltolf = relative tolerance of function value in optimization abstolx = absolute tolerance of parameter values in optimization
maxiter	Sets the maximum number of iterations in the optimization
optimmethod	Method used in optimization of the likelihood. Current default is 'subplex'. Alternative is 'simplex' (default of previous versions)

Value

b	gives the maximum likelihood estimate of b
mu_1	gives the maximum likelihood estimate of mu_1
la_1	gives the maximum likelihood estimate of la_1
mu_2	gives the maximum likelihood estimate of mu_2
loglik	gives the maximum loglikelihood
df	gives the number of estimated parameters, i.e. degrees of freedom
conv	gives a message on convergence of optimization; conv = 0 means convergence

Author(s)

Rampal S. Etienne

See Also

[pbm_loglik](#)

Examples

```
pbm_ML(1:10, initparsopt = c(0.2, 0.01, 0.3), exteq = 1)
```

pbd_sim

*Function to simulate the protracted speciation process***Description**

Simulating the protracted speciation process using the Doob-Gillespie algorithm. This function differs from pbd_sim_cpp that 1) it does not require that the speciation-initiation rate is the same for good and incipient species, and 2) that it simulates the exact protracted speciation process, and not the approximation made by the coalescent point process. This function provides also the conversion to the approximation as output.

Usage

```
pbd_sim(
  pars,
  age,
  soc = 2,
  plotit = FALSE
)
```

Arguments

pars	Vector of parameters: pars[1] corresponds to b_1, the speciation-initiation rate of good species pars[2] corresponds to la_1, the speciation-completion rate pars[3] corresponds to b_2, the speciation-initiation rate of incipient species pars[4] corresponds to mu_1, the extinction rate of good species pars[5] corresponds to mu_2, the extinction rate of incipient species
age	Sets the age for the simulation
soc	Sets whether this age is the stem (1) or crown (2) age
plotit	Sets whether the various trees produced by the function should be plotted or not

Value

out	A list with the following elements: tree is the tree of extant species in phylo format stree is a tree with one sample per species in phylo format L is a matrix of all events in the simulation where - the first column is the incipient-level label of a species - the second column is the incipient-level label of the parent of the species - the third column is the time at which a species is born as incipient species - the fourth column is the time of speciation-completion of the species If the fourth element equals -1, then the species is still incipient. - the fifth column is the time of extinction of the species If the fifth element equals -1, then the species is still extant. - The sixth column is the species-level label of the species SL is a matrix like L but for stree
-----	---

`igtree.extinct` is the tree in simmap format with incipient and good flags and including extinct species
`igtree.extant` is the tree in simmap format with incipient and good flags without extinct species
`recontree` is the reconstructed tree in phylo format, reconstructed using the approximation in Lambert et al. 2014
`reconL` is the matrix corresponding to `recontree`
`L0` is a matrix where the crown age is at 0; for internal use only

Author(s)

Rampal S. Etienne

See Also

[pbd_sim_cpp](#)

Examples

```
pbd_sim(c(0.2,1,0.2,0.1,0.1),15)
```

pbd_sim_cpp

Function to simulate the approximate protracted speciation process

Description

Simulating the protracted speciation process according to the approximate model of Lambert et al. 2014. This function differs from `pbd_sim` that 1) it requires that the speciation-initiation rate is the same for good and incipient species, and 2) that it does not simulate the exact protracted speciation process, but an approximation made by the coalescent point process.

Usage

```

pbd_sim_cpp(
  pars,
  parsf = c(function(t,pars) {pars[1]},function(t,pars) {pars[2]},
function(t,pars) {pars[3]},function(t,pars) {pars[4]}),
  age,
  soc = 2,
  plotlft = 1,
  methode = "lsoda"
)

```

Arguments

`pars` Vector of parameters:

`pars[1]` corresponds to `b` (= `la_1` in Etienne & Rosindell R2012) = speciation initiation rate

`pars[2]` corresponds to `mu_1` (= `mu_g` in Etienne & Rosindell 2012) = extinction rate of good species

`pars[3]` corresponds to `la_1` (= `la_2` in Etienne & Rosindell 2012) = speciation completion rate

`pars[4]` corresponds to `mu_2` (= `mu_i` in ER2012) = extinction rate of incipient species

When rates depend on time this time dependence should be specified in `parslf` and `parsl` then becomes the parameters used in `parslf`

<code>parsf</code>	<p>Vector of functions how the rates depend on time, default functions are constant functions of the parameters in <code>parsl</code>:</p> <p><code>parsf[1]</code> corresponds to time-dependence of <code>b</code> (= <code>la_1</code> in Etienne & Rosindell R2012) = speciation initiation rate</p> <p><code>parsf[2]</code> corresponds to time-dependence of <code>mu_1</code> (= <code>mu_g</code> in Etienne & Rosindell 2012) = extinction rate of good species</p> <p><code>parsf[3]</code> corresponds to time-dependence of <code>la_1</code> (= <code>la_2</code> in Etienne & Rosindell 2012) = speciation completion rate</p> <p><code>parsf[4]</code> corresponds to time-dependence of <code>mu_2</code> (= <code>mu_i</code> in ER2012) = extinction rate of incipient species</p>
<code>age</code>	Sets the crown age for the simulation
<code>soc</code>	Determines whether the simulation should start at stem (1) or crown (2) age
<code>plotlft</code>	Sets whether the lineage-through-time plot should be plotted (1) or not (0)
<code>methode</code>	Sets which method should be used in the ode-solver. Default is 'lsoda'. See package <code>deSolve</code> for details.

Value

A set of branching times

Author(s)

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See Also

[pbd_sim](#)

Examples

```
pbd_sim_cpp(pars = c(0.2,1,0.2,0.1),age = 15)
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