Package ‘DDD’

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Title Diversity-dependent diversification
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R topics documented:

DDD-package .......................................................... 1
dd_loglik ............................................................. 2
dd_loglik_choosepar ............................................... 3
dd_loglik_rhs ........................................................ 4
dd_ML ................................................................. 5

Index

DDD-package Diversity dependent diversification

Description

This package is a likelihood-based statistical package to estimate parameters under diversity-dependent diversification models.

Details
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Version: 0.2
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dd_loglik computes the likelihood of any of 4 different models of diversity-dependent diversification, given a set of parameters and a data set of phylogenetic branching times. dd_ML finds the parameters that maximizes this likelihood.

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References

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dd_loglik
loglikelihood for diversity-dependent diversification models

Description
This function computes loglikelihood of a diversity-dependent diversification model for a given set of branching times and parameter values.

Usage
dd_loglik(trpars1, pars2, brts, missnumspec)

Arguments
- trpars1: transformed vector of parameters, after transformation pars/(1+pars), e.g. trpars1 = c(0.2,0.1,100)
- pars2: pars2[1] sets the maximum number of species for which a probability must be computed, must be larger than 1 + length(brts)
- brts: a set of branching times of a phylogeny, all positive, from present to past
- missnumspec: The number of species that are in the clade but missing in the phylogeny

Value
the loglikelihood

Author(s)
Rampal S. Etienne & Bart Haegeman
References

See Also
laser

Examples

dd_loglik(trpars = c(0.2,0.1,0.98), pars2 = c(100,1), brts = 1:10, missnumspec = 0)

Description
This function reorders the parameters so that dd_loglik can be called with the correct parameters. It is called from dd_ML.

Usage

dd_loglik_choosepar(trparsopt, trparsfix, idparsopt, idparsfix, pars2, brts, missnumspec)

Arguments

trparsopt  These are the initial values of the transformed parameters that must be optimized. The transformation is trpars = pars/(1+pars). See dd_ML.
trparsfix  These are the values of the transformed parameters that must not be optimized. The transformation is trpars = pars/(1+pars). See dd_ML.
idparsopt  These are the ids of the parameters to be optimized. For example, to optimize all parameters, idparsopt = 1:3
idparsfix  These are the ids of the parameters to be fixed. For example, idparsfix = c(1,3). In that case idparsopt must be 2
brts  a set of branching times of a phylogeny, all positive, from present to past
missnumspec  The number of species that are in the clade but missing in the phylogeny

Details
This function should not be called directly from R.

Value
the loglikelihood
Author(s)
Rampal S. Etienne & Bart Haegeman

References

See Also
dd_loglik

Examples
```
dd_loglik_choosepar(c(0.15,0.10,0.99),NULL,1:3,NULL,c(100,1),1:10,0)
```

dd_loglik_rhs

**Auxiliary function to dd_loglik**

Description
This function computes the right-hand side of the master equation for the diversity-dependent model. It is called from dd_loglik.

Usage
```
dd_loglik_rhs(t, x, pars)
```

Arguments
- `t` time
- `x` the probability vector at time t

Details
This function should not be called directly from R.

Value
The function outputs the incremental probability vector needed in the master equation

Author(s)
Rampal S. Etienne & Bart Haegeman

References
**dd_ML**

See Also

dd_loglik

Examples

dd_loglik_rhs(-3,(1:10)/sum(1:10),c(0.2,0.1,100,3,1))

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**dd_ML**

Maximization of the loglikelihood under a diversity-dependent diversification model

Description

This function computes the maximum likelihood estimates of the parameters of a diversity-dependent diversification model for a given set of phylogenetic branching times. It also outputs the corresponding loglikelihood that can be used in model comparisons.

Usage

dd_ML(brts, initpars_opt = c(2, 1, 2 * length(brts)), idpars_opt = 1:3, idparsfix = ... 2 * length(brts)), res = 1/s * (1 + length(brts)), ddmodel = 1, missnums = 0)

Arguments

- **brts** a set of branching times of a phylogeny, all positive, from present to past
- **initpars_opt** the initial values of the parameters that must be optimized
- **idpars_opt** the ids of the parameters that must be optimized, e.g. 1:3 for all parameters. The ids are defined as follows: id == 1 corresponds to lambda (speciation rate) id == 2 corresponds to mu (extinction rate) id == 3 corresponds to K (clade-level carrying capacity)
- **idparsfix** the ids of the parameters that should not be optimized, e.g. c(1,3) if lambda and K should not be optimized, but only mu. In that case idpars_opt must be. The default is to fix all parameters not specified in idpars_opt.
- **parsfix** the values of the parameters that should not be optimized
- **res** sets the maximum number of species for which a probability must be computed, must be larger than 1 + length(brts)
- **ddmodel** sets the model of diversity-dependence: ddmodel == 1 : linear dependence in speciation rate ddmodel == 2 : exponential dependence in speciation rate ddmodel == 3 : linear dependence in extinction rate ddmodel == 4 : exponential dependence in extinction rate
- **missnums** The number of species that are in the clade but missing in the phylogeny

Value

- **pars** gives the list of parameter estimates
- **fvalues** gives the maximum loglikelihood
Note

The output is a dataframe where $par and $fvalues are the first elements. There are more elements that are all from the optimization algorithm, optimx. The computed loglikelihood contains the factor $N_{q,m} = (q-1)/(q + m - 1) (q + m + 1)!/(q + 1)! m!$ where $q$ is the number of species in the phylogeny and $m$ is the number of missing species, as explained in the supplementary material to Etienne et al. 2011.

Author(s)

Rampal S. Etienne & Bart Haegeman

References


See Also

dd_loglik optimx

Examples

```r
cat("This will estimate the parameters for a set of branching times brts with the default settings:")
brts = 1:20
dd_ML(brts)

cat("This will estimate the intrinsic speciation rate lambda and the carrying capacity K for a fixed extinction rate (value = 0.1):")
brts = 1:20
dd_ML(brts, initparsopt = c(0.2,100), idparsopt = c(1,3), parsfix = 0.1)

cat("This will estimate all parameters under the linear diversity-dependent extinction model:")
brts = 1:20
dd_ML(brts, ddmodel = 3)

cat("This will estimate all parameters under the default model when there are 2 missing species:")
brts = 1:20
dd_ML(brts, missnumspec = 2)
```
Index

«Topic **models**
  dd_loglik, 2
  dd_loglik_choosepar, 3
  dd_loglik_rhs, 4
  dd_ML, 5
  DDD-package, 1

dd_loglik, 2, 4–6
dd_loglik_choosepar, 3
dd_loglik_rhs, 4
dd_ML, 5
DDD (DDD-package), 1
DDD-package, 1

optimx, 6