

Package ‘DAMOCLES’

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Type Package

Title Dynamic Assembly Model of Colonization, Local Extinction and Speciation

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License GPL-2

Description Simulates and computes (maximum) likelihood of a dynamical model of community assembly that takes into account phylogenetic history.

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DAMOCLES-package

Dynamic Assembly Model Of Colonization, Local Extinction and Speciation

Description

Simulation and likelihood methods for a dynamical community assembly that accounts for phylogenetic history

New in version 1.1:

- Function added to do bootstrap

Details

Package: DAMOCLES

Type: Package

Version: 1.1

Date: 2015-03-05

License: GPL 2.0

DAMOCLES_loglik computes the likelihood of presence-absence data in a local community given a set of parameters and a phylogeny under an immigration-extinction model

DAMOCLES_ML finds the parameters that maximizes the likelihood computed by DAMOCLES_loglik.

DAMOCLES_sim simulates presence-absence data for a given phylogeny

DAMOCLES_bootstrap computes the maximum likelihood estimates of colonisation and local extinction rate for a given phylogeny and presence-absence data under the DAMOCLES model. These rate estimates are used to simulate null communities under the DAMOCLES model. Standardized effect size of mean nearest taxon distance (mntd), mean phylogenetic distance (mpd) and loglikelihood are calculated. For comparison, standardised effect sizes are also calculated relative to a "Random-Draw" null model i.e. presence absence randomised across tips.

Author(s)

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References

Pigot, A.L. & R.S. Etienne (2015). A new dynamic null model for phylogenetic community structure. *Ecology Letters* 18: 153-163.

Examples

```
DAMOCLES_ML()
```

DAMOCLES_bootstrap *Phylogenetic community structure hypothesis test*

Description

This function computes the maximum likelihood estimates of colonisation and local extinction rate for a given phylogeny and presence-absence data under the DAMOCLES model. These rate estimates are used to simulate null communities under the DAMOCLES model. Standardized effect size of mean nearest taxon distance (mntd), mean phylogenetic distance (mpd) and loglikelihood are calculated. For comparison, standardised effect sizes are also calculated relative to a "Random-Draw" null model i.e. presence absence randomised across tips

Usage

```
DAMOCLES_bootstrap(
  phy = rcoal(10),
  pa = matrix(c(phy$tip.label, sample(c(0,1), Ntip(phy), replace = T)),
    nrow = Ntip(phy), ncol = 2),
  initparsopt = c(0.1, 0.1),
  idparsopt = 1:length(initparsopt),
  parsfix = 0,
  idparsfix = (1:3)[-idparsopt],
  pars2 = c(1E-3, 1E-4, 1E-5, 1000),
  pchoice = 0,
  runs = 999,
  estimate_pars = FALSE,
  conf.int = 0.95
)
```

Arguments

phy	phylogeny in phylo format
pa	presence-absence table. The first column contains the labels of the species (corresponding to the tip labels in the phylogeny). The second column contains the presence (1) or absence (0) of species in the local community.
initparsopt	The initial values of the parameters that must be optimized
idparsopt	The ids of the parameters that must be optimized, e.g. 1:2 for extinction rate, and offset of immigration rate. The ids are defined as follows: id == 1 corresponds to mu (extinction rate) id == 2 corresponds to gamma_0 (offset of immigration rate)

<code>parsfix</code>	The values of the parameters that should not be optimized. See <code>idparsfix</code> .
<code>idparsfix</code>	The ids of the parameters that should not be optimized, e.g. <code>c(1)</code> if <code>mu</code> should not be optimized, but only <code>gamma_0</code> . In that case <code>idparsopt</code> must be <code>c(2)</code> . The default is to fix the parameters not specified in <code>idparsopt</code> .
<code>pars2</code>	Vector of settings: <code>pars2[1]</code> sets the relative tolerance in the parameters <code>pars2[2]</code> sets the relative tolerance in the function <code>pars2[3]</code> sets the absolute tolerance in the parameters <code>pars2[4]</code> sets the maximum number of iterations
<code>pchoice</code>	sets which p-value to optimize and with which root state to simulate (default <code>pchoice = 0</code>) <code>pchoice == 0</code> correspond to optimizing sum of <code>p_0f</code> + <code>p_1f</code> , and simulating with an equal number of root states being 0 or 1 <code>pchoice == 1</code> correspond to optimizing <code>p_0f</code> , and simulating with root state being 0 <code>pchoice == 2</code> correspond to optimizing <code>p_1f</code> , and simulating with root state being 1
<code>runs</code>	the number null communities to generate.
<code>estimate_pars</code>	Whether to estimate parameters on the simulated datasets (default = FALSE).
<code>conf.int</code>	The width of the confidence intervals calculated on bootstrapped parameter estimates

Details

The output is a list of two dataframes. The first dataframe, `summary_table`, contains the summary results. The second dataframe, `null_community_data`, contains descriptive statistics for each null community.

Value

`summary_table` `mu` gives the maximum likelihood estimate of `mu` and confidence intervals in brackets if `estimate_pars = TRUE` `gamma_0` gives the maximum likelihood estimate of `gamma_0` and confidence intervals in brackets if `bootstrap=TRUE` `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 `n.obs` gives the number of species locally present in the observed community `mntd.obs` gives the MNTD of the observed community `mpd.obs` gives the MPD of the observed community `runs` gives the number of null communities simulated `mntd.mean.RD` mean of MNTD from null communities generated by a "Random Draw" model `mntd.sd.RD` standard deviation of MNTD from null communities generated by a "Random Draw" model `mntd.obs.z.RD` standardized effect size of MNTD compared to null communities generated by a "Random Draw" model (= $-1*(mntd.obs -$

$\text{mntd.mean.RD} / \text{mntd.sd.RD}$ mntd.obs.rank.RD rank of observed MNTD compared to null communities generated by a "Random Draw" model mntd.obs.q.RD quantile of observed MNTD vs. null communities ($= \text{mntd.obs.rank.RD} / \text{runs} + 1$) mpd.mean.RD mean of MPD from null communities generated by a "Random Draw" model mpd.sd.RD standard deviation of MPD from null communities generated by a "Random Draw" model mpd.obs.z.RD standardized effect size of MPD compared to null communities generated by a "Random Draw" model ($= -1 * (\text{mpd.obs} - \text{mpd.mean.RD}) / \text{mpd.sd.RD}$) mpd.obs.rank.RD rank of observed MPD compared to null communities generated by a "Random Draw" model mpd.obs.q.RD quantile of observed MPD vs. null communities ($= \text{mpd.obs.rank.RD} / \text{runs} + 1$) n.mean.DAMOCLES mean number of species locally present in the null communities generated by DAMOCLES $\text{mntd.mean.DAMOCLES}$ mean of MNTD from null communities generated by DAMOCLES mntd.sd.DAMOCLES standard deviation of MNTD from null communities generated by DAMOCLES $\text{mntd.obs.z.DAMOCLES}$ standardized effect size of MNTD compared to null communities generated by DAMOCLES ($= -1 * (\text{mntd.obs} - \text{mntd.mean.DAMOCLES}) / \text{mntd.sd.DAMOCLES}$) $\text{mntd.obs.rank.DAMOCLES}$ rank of observed MNTD compared to null communities generated by DAMOCLES $\text{mntd.obs.q.DAMOCLES}$ quantile of observed MNTD vs. null communities ($= \text{mntd.obs.rank.DAMOCLES} / \text{runs} + 1$) mpd.mean.DAMOCLES mean of MPD from null communities generated by DAMOCLES mpd.sd.DAMOCLES standard deviation of MPD from null communities generated by DAMOCLES $\text{mpd.obs.z.DAMOCLES}$ standardized effect size of MPD compared to null communities generated by DAMOCLES ($= -1 * (\text{mpd.obs} - \text{mpd.mean.DAMOCLES}) / \text{mpd.sd.DAMOCLES}$) $\text{mpd.obs.rank.DAMOCLES}$ rank of observed MPD compared to null communities generated by DAMOCLES $\text{mpd.obs.q.DAMOCLES}$ quantile of observed MPD vs. null communities ($= \text{mpd.obs.rank.DAMOCLES} / \text{runs} + 1$) $\text{loglik.mean.DAMOCLES}$ mean of loglikelihoods from null communities generated by DAMOCLES $\text{loglik.sd.DAMOCLES}$ standard deviation of loglikelihoods from null communities generated by DAMOCLES $\text{loglik.obs.z.DAMOCLES}$ standardized effect size of loglikelihood compared to null communities generated by DAMOCLES ($= -1 * (\text{loglik.obs} - \text{loglik.mean.DAMOCLES}) / \text{loglik.sd.DAMOCLES}$) $\text{loglik.obs.rank.DAMOCLES}$ rank of observed loglikelihood compared to null communities generated by DAMOCLES $\text{loglik.obs.q.DAMOCLES}$ quantile of observed loglikelihoods vs. null communities ($= \text{loglik.obs.rank.DAMOCLES} / \text{runs} + 1$)

null_community_data

run gives the simulation run root.state.print gives the state of the ancestral species in the local community assumed in the simulation, i.e. present (1) or absent (0) n gives the number of species locally present in the observed community n.RD gives the number of species locally present in the null community generated by a "Random Draw" model mntd.RD gives the MNTD of the null community generated by a "Random Draw" model mpd.RD gives the MPD of the null community generated by a "Random Draw" model n.DAMOCLES gives the number of species locally present in the null community generated by DAMOCLES mntd.DAMOCLES gives the MNTD of the null community generated by DAMOCLES mpd.DAMOCLES gives the MPD of the null community generated by DAMOCLES loglik.DAMOCLES gives the maximum loglikelihood for the null community generated by DAMOCLES mu.DAMOCLES gives the maximum

likelihood estimate of mu for the null community generated by DAMOCLES
gamma_0. DAMOCLES gives the maximum likelihood estimate of gamma_0 for
the null community generated by DAMOCLES

Author(s)

Rampal S. Etienne

References

Pigot, A.L. & R.S. Etienne (2015). A new dynamic null model for phylogenetic community structure. *Ecology Letters* 18: 153-163.

See Also

[DAMOCLES_ML](#) [DAMOCLES_sim](#)

Examples

```
data(NWPrimates_data)
out = DAMOCLES_bootstrap(
  phy = NWPrimates_data[[1]],
  pa = NWPrimates_data[[2]],
  initparsopt = c(0.01,1.8),
  idparsopt = c(1,2),
  pars2 = c(1E-3,1E-4,1E-5,1000),
  pchoice = 1,
  runs = 2,
  estimate_pars = TRUE,
  conf.int = 0.95)
```

DAMOCLES_loglik

Likelihood for DAMOCLES model

Description

Computes likelihood for the presence-absence data of species in a local community for a given phylogeny of species in the region.

Usage

```
DAMOCLES_loglik(
  phy,
  pa,
  pars,
  pchoice = 0,
  edgeTList = compute_edgeTList(phy)
)
```

Arguments

phy	phylogeny in phylo format
pa	presence-absence table with the first column the species labels and the second column the presence (1) or absence (0) of the species
pars	Vector of model parameters: pars[1] corresponds to mu (extinction rate in local community) pars[2] corresponds to gamma_0 in formula $\gamma(t) = \gamma_0 / (1 + \gamma_1 * t)$ where gamma(t) is immigration rate into local community) pars[3] corresponds to gamma_1 in formula $\gamma(t) = \gamma_0 / (1 + \gamma_1 * t)$ where gamma(t) is immigration rate into local community)
pchoice	sets the p-value to optimize: pchoice == 0 corresponds to the sum of p_0f + p_1f pchoice == 1 corresponds to p_0f pchoice == 2 corresponds to p_1f
edgeTList	list of edge lengths that need to be successively pruned; if not specified, it will be computed using compute_edgeTList

Value

The loglikelihood

Author(s)

Rampal S. Etienne

References

Pigot, A.L. & R.S. Etienne (2015). A new dynamic null model for phylogenetic community structure. *Ecology Letters* 18: 153-163.

See Also

[DAMOCLES_ML](#) [DAMOCLES_sim](#)

Examples

```
#TEST IT WORKS
phy = rcoal(100)
pars = c(0.5,0.1,0.1)
pa = rbinom(100,c(0,1),0.5)
pa = matrix(c(phy$tip.label,pa),nrow = length(phy$tip.label),ncol = 2)

# - without a root edge
loglik = DAMOCLES_loglik(phy,pa,pars)
loglik

# - with a root edge
phy$root.edge = 2
```

```
loglik = DAMOCLES_loglik(phy,pa,pars)
loglik
```

DAMOCLES_ML

Maximization of the loglikelihood under the DAMOCLES model

Description

This function computes the maximum likelihood estimates of the parameters of the DAMOCLES model for a given phylogeny and presence-absence data. It also outputs the corresponding loglikelihood that can be used in model comparisons.

Usage

```
DAMOCLES_ML(
  phy = rcoal(10),
  pa = matrix(c(phy$tip.label,sample(c(0,1),Ntip(phy),replace = T)),
    nrow = Ntip(phy),ncol = 2),
  initparsopt = c(0.1,0.1),
  idparsopt = 1:length(initparsopt),
  parsfix = 0,
  idparsfix = (1:3)[-idparsopt],
  pars2 = c(1E-3,1E-4,1E-5,1000),
  pchoice = 0
)
```

Arguments

phy	phylogeny in phylo format
pa	presence-absence table. The first column contains the labels of the species (corresponding to the tip labels in the phylogeny). The second column contains the presence (1) or absence (0) of species in the local community.
initparsopt	The initial values of the parameters that must be optimized
idparsopt	The ids of the parameters that must be optimized, e.g. 1:2 for extinction rate, and offset of immigration rate The ids are defined as follows: id == 1 corresponds to mu (extinction rate) id == 2 corresponds to gamma_0 (offset of immigration rate) id == 3 corresponds to gamma_1 (parameter controlling decline in immigration rate with time)
parsfix	The values of the parameters that should not be optimized. See idparsfix.
idparsfix	The ids of the parameters that should not be optimized, e.g. c(1,3) if mu and gamma_1 should not be optimized, but only gamma_0. In that case idparsopt must be c(2). The default is to fix all parameters not specified in idparsopt.

pars2	Vector of settings: pars2[1] sets the relative tolerance in the parameters pars2[2] sets the relative tolerance in the function pars2[3] sets the absolute tolerance in the parameters pars2[4] sets the maximum number of iterations
pchoice	sets which p-value to optimize (default 0) pchoice == 0 correspond to the sum of p_0f + p_1f pchoice == 1 correspond to p_0f pchoice == 2 correspond to p_1f

Details

The output is a dataframe containing estimated parameters and maximum loglikelihood.

Value

mu	gives the maximum likelihood estimate of mu
gamma_0	gives the maximum likelihood estimate of gamma_0
gamma_1	gives the maximum likelihood estimate of gamma_1
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

References

Pigot, A.L. & R.S. Etienne (2015). A new dynamic null model for phylogenetic community structure. *Ecology Letters* 18: 153-163.

See Also

[DAMOCLES_loglik](#) [DAMOCLES_sim](#)

Examples

```
data(NWPrimates_data)
out = DAMOCLES_ML(
  phy = NWPrimates_data[[1]],
  pa = NWPrimates_data[[2]],
  initparsopt = c(0.01,1.8),
  idparsopt = c(1,2),
  parsfix = c(0),
  idparsfix = c(3),
```

```
pars2 = c(1E-3,1E-4,1E-5,1000),
pchoice = 0)
```

DAMOCLES_sim

Simulating DAMOCLES

Description

Simulates DAMOCLES

Usage

```
DAMOCLES_sim(
  phy,
  gamma_0,
  gamma_td,
  mu,
  sigma,
  psiBranch,
  psiTrait,
  z,
  phi,
  traitOpt,
  br0,
  br_td,
  nTdim,
  root.state,
  root.trait.state,
  plotit = FALSE,
  keepExtinct = FALSE
)
```

Arguments

phy	phylogeny in phylo format
gamma_0	initial per lineage rate of immigration (gamma)
gamma_td	time dependency in gamma
mu	per lineage rate of local extinction
sigma	probability of local (i.e. in-situ) speciation
psiBranch	phylogenetic distance at which gamma is half gamma_0
psiTrait	trait distance at which gamma is half gamma_0
z	shape of increase in gamma with increasing trait or phylogenetic distance
phi	rate of decline in gamma with distance from trait optima
traitOpt	trait value at which gamma = gamma_0

<code>br0</code>	Brownian rate parameter
<code>br_td</code>	rate of temporal decline in Brownian rate parameter
<code>nTdim</code>	number of independent trait dimensions
<code>root.state</code>	geographic state of ancestor i.e. present (1) or absent(0)
<code>root.trait.state</code>	trait value of ancestor
<code>plotit</code>	whether to plot the phylogeny and timing of immigration/local extinction events
<code>keepExtinct</code>	whether to retain data for extinct lineages

Value

A list of two tables. The first table contains the following columns: The first column contains the vector of tip labels in the phylogeny The last column contains the presence (1) or absence (0) of the species The second table has dimensions $d \times N$ where d is the number of trait dimensions and N is the number of species. It contains the trait values.

Author(s)

Alex L. Pigot

References

Pigot, A.L. & R.S. Etienne (2015). A new dynamic null model for phylogenetic community structure. *Ecology Letters* 18: 153-163.

See Also

[DAMOCLES_ML](#) [DAMOCLES_loglik](#)

Examples

```
#create random phylogeny
phy = rcoal(10)

#run DAMOCLES
out = DAMOCLES_sim(
  phy,
  gamma_0 = 1.5,
  gamma_td = 0,
  mu = 0,
  sigma = 0,
  psiBranch = 0,
  psiTrait = 0,
  z = 10,
  phi = 0,
  traitOpt = 1,
  br0 = 0.1,
  br_td = -0.1,
  nTdim = 2,
```

```

root.state = 1,
root.trait.state = 0,
plotit = FALSE,
keepExtinct = FALSE
)

#the output consists of a list
patable = out[[1]] # the first element is the presence absence table
traits = out[[2]] # this is a matrix of traits values

#show presence/absence on the tree
patable$col = rep("black",dim(patable)[1])
patable$col[which(patable$state == 1)] = "red"
plot(phy,tip.col = patable$col)

```

NWPrimates_data	<i>Dated phylogenetic tree of the New World Primates in nexus format and presence-absence matrix for species in Manu</i>
-----------------	--

Description

A list with two elements.

. phy is a dated molecular phylogeny for 94 species of New World Primates extracted from the maximum likelihood tree (AUTOsoft dated) of Springer et al. (2012). 1 time unit = 100 million years.

pa is the presence-absence matrix of NW Primates in Manu from Solari et al. (2006). The first column indicate the species tip labels and the second column indicates presence (1) and absence (0).

Usage

```
data(NWPrimates_data)
```

Format

A list with two elements. The first element (phy) is the primate phylogeny in nexus format. The second element (pa) is the presence-absence matrix with 94 rows and 2 columns.

Source

Solari, S., Pacheco, V., Luna, L., Velazco, P.M. & Patterson, B.D. 2006 Mammals of the manu biosphere reserve. *Fieldiana Zoology* 110, 13-22.

Springer, M.S., Meredith, R.W., Gatesy, J., Emerling, C.A., Park, J., Rabosky, D.L., Stadler, T., Steiner, C., Ryder, O.A., Janecka, J.E., et al. 2012 Macroevolutionary dynamics and historical biogeography of primate diversification inferred from a species supermatrix. *Plos One* 7. (doi:ARTN e49521 DOI 10.1371/journal.pone.0049521).

See Also

[DAMOCLES_sim](#), [DAMOCLES_ML](#), [DAMOCLES_loglik](#)

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