

# Package ‘SADISA’

April 22, 2017

**Type** Package

**Title** Species Abundance Distributions with Independent-Species Assumption

**Version** 1.0

**Author** Rampal S. Etienne & Bart Haegeman

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

**Description** Computes the probability of a set of species abundances of a single or multiple samples of individuals under a mainland-island model. One must specify the mainland (metacommunity) model and the island (local) community model. It assumes that species fluctuate independently. See Haegeman, B. & R.S. Etienne (2017). A general sampling formula for community structure data. *Methods in Ecology & Evolution*. In press.

**License** GPL-3

**LazyData** FALSE

**RoxygenNote** 5.0.1

**Imports** subplex, pracma, DDD

**Suggests** testthat, knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2017-04-21 23:08:31 UTC

## R topics documented:

datasets . . . . .	2
fitresults . . . . .	3
integral_peak . . . . .	4
SADISA_loglik . . . . .	5
SADISA_ML . . . . .	6
SADISA_test . . . . .	7

<b>Index</b>	<b>9</b>
--------------	----------

---

datasets

*Data sets of various tropical forest communities*

---

### **Description**

Various tree community abundance data sets to test and illustrate the Independent Species approach.

- `dset1.abunvec` contains a list of 6 samples of tree abundances from 6 tropical forest plots (BCI, Korup, Pasoh, Sinharaja, Yasuni, Lambir).
- `dset2.abunvec` contains a list of 11 lists with one of 11 samples from BCI combined with samples from Cocoli and Sherman.
- `dset3.abunvec` contains a list of 6 lists with 2 samples, each from one dispersal guild, for 6 tropical forest communities (BCI, Korup, Pasoh, Sinharaja, Yasuni, Lambir).
- `dset4a.abunvec` contains a list of 6 samples from 6 censuses of BCI (1982, 1985, 1990, 1995, 200, 2005) with  $dbh > 1$  cm.
- `dset4b.abunvec` contains a list of 6 samples from 6 censuses of BCI (1982, 1985, 1990, 1995, 200, 2005) with  $dbh > 10$  cm.

### **Usage**

```
data(datasets)
```

### **Format**

A list of 5 data sets. See description for information on each of these data sets.

### **Author(s)**

Rampal S. Etienne & Bart Haegeman

### **Source**

Condit et al. (2002). Beta-diversity in tropical forest trees. *Science* 295: 666-669.

---

fitresults	<i>Maximum likelihood estimates and corresponding likelihood values for various fits to various tropical forest communities</i>
------------	---

---

## Description

Maximum likelihood estimates and corresponding likelihood values for various fits to various tropical forest communities, to test and illustrate the Independent Species approach.

- fit1a.llikopt contains maximum likelihood values of fit of pm-dl model to dset1.abunvec
- fit1a.parsopt contains maximum likelihood parameter estimates of fit of pm-dl model to dset1.abunvec
- fit1b.llikopt contains maximum likelihood values of fit of pmc-dl model to dset1.abunvec
- fit1b.parsopt contains maximum likelihood parameter estimates of fit of pmc-dl model to dset1.abunvec
- fit2.llikopt contains maximum likelihood values of fit of rf-dl model to dset1.abunvec
- fit2.parsopt contains maximum likelihood parameter estimates of fit of rf-dl model to dset1.abunvec
- fit3.llikopt contains maximum likelihood values of fit of dd-dl model to dset1.abunvec
- fit3.parsopt contains maximum likelihood parameter estimates of fit of dd-dl model to dset1.abunvec
- fit4.llikopt contains maximum likelihood values of fit of pm-dl model to dset2.abunvec (multiple samples)
- fit4.parsopt contains maximum likelihood parameter estimates of fit of pm-dl model to dset1.abunvec (multiple samples)
- fit5.llikopt contains maximum likelihood values of fit of pm-dl model to dset3.abunvec (multiple guilds)
- fit5.parsopt contains maximum likelihood parameter estimates of fit of pm-dl model to dset3.abunvec (multiple guilds)
- fit6.llikopt contains maximum likelihood values of fit of pr-dl model to dset1.abunvec
- fit6.parsopt contains maximum likelihood parameter estimates of fit of pr-dl model to dset1.abunvec
- fit7.llikopt contains maximum likelihood values of fit of pm-dd model to dset1.abunvec
- fit7.parsopt contains maximum likelihood parameter estimates of fit of pm-dd model to dset1.abunvec
- fit8a.llikopt contains maximum likelihood values of fit of pm-dd model to dset4a.abunvec
- fit8a.parsopt contains maximum likelihood parameter estimates of fit of pm-dd model to dset4a.abunvec
- fit8b.llikopt contains maximum likelihood values of fit of pm-dd model to dset4b.abunvec
- fit8b.parsopt contains maximum likelihood parameter estimates of fit of pm-dd model to dset4b.abunvec

## Usage

```
data(fitresults)
```

**Format**

A list of 20 lists, each containing either likelihood values or the corresponding parameter estimates. See description.

**Author(s)**

Rampal S. Etienne & Bart Haegeman

**Source**

Condit et al. (2002). Beta-diversity in tropical forest trees. *Science* 295: 666-669.

---

integral_peak	<i>Computes integral of a very peaked function</i>
---------------	--

---

**Description**

# computes the logarithm of the integral of exp(logfun) from 0 to Inf under the following assumptions:

**Usage**

```
integral_peak(logfun, xx = seq(-100, 10, 2), xcutoff = 2, ycutoff = 40,
  ymaxthreshold = 1e-12)
```

**Arguments**

logfun	the logarithm of the function to integrate
xx	the initial set of points on which to evaluate the function
xcutoff	when the maximum has been found among the xx, this parameter sets the width of the interval to find the maximum in
ycutoff	set the threshold below which (on a log scale) the function is deemed negligible, i.e. that it does not contribute to the integral)
ymaxthreshold	sets the deviation allowed in finding the maximum among the xx

**Value**

the result of the integration

**References**

Haegeman, B. & Etienne, R.S. (2016). A general sampling formula for community abundance data. *Methods in Ecology & Evolution*. In review.

---

SADISA\_loglik

*Computes loglikelihood for requested model*


---

**Description**

Computes loglikelihood for requested model using independent-species approach

**Usage**

```
SADISA_loglik(abund, pars, model, mult = "mg")
```

**Arguments**

abund	abundance vector or a list of abundance vectors. When a list is provided and mult = 'mg' (the default), it is assumed that the different vectors apply to different guilds. When mult = 'ms' then the different vectors apply to multiple samples. from the same metacommunity. In this case the vectors should have equal lengths and may contain zeros because there may be species that occur in multiple samples and species that do not occur in some of the samples.
pars	a vector of model parameters or a list of vectors of model parameters. When a list is provided and mult = 'mg' (the default), it is assumed that the different vectors apply to different guilds. Otherwise, it is assumed that they apply to multiple samples.
model	the chosen combination of metacommunity model and local community model as a vector, e.g. c('pm','dl') for a model with point mutation in the metacommunity and dispersal limitation. The choices for the metacommunity model are: 'pm' (point mutation), 'rf' (random fission), 'pr' (protracted speciation), 'dd' (density-dependence). The choices for the local community model are: 'dl' (dispersal limitation), 'dd' (density-dependence).
mult	When set to 'mg' (the default) the loglikelihood for multiple guilds is computed. When set to 'ms' the loglikelihood for multiple samples from the same metacommunity is computed.

**Details**

Not all combinations of metacommunity model and local community model have been implemented yet. because this requires checking for numerical stability of the integration. The currently available model combinations are, for a single sample, c('pm','dl'), c('pm','rf'), c('dd','dl'), c('pr','dl'), c('pm','dd'), and for multiple samples, c('pm','dl').

**Value**

loglikelihood

## References

Haegeman, B. & Etienne, R.S. (2016). A general sampling formula for community abundance data. *Methods in Ecology & Evolution*. In review.

## Examples

```
data(datasets);
abund_bci <- datasets$dset1.abunvec[[1]];
data(fitresults);
data.paropt <- fitresults$fit1a.parsopt[[1]];
result <- SADISA_loglik(abund = abund_bci,pars = data.paropt,model = c('pm','dl'));
cat('The difference between result and the value in fitresults.RData is:',
result - fitresults$fit1a.llikopt[[1]]);
```

---

SADISA_ML	<i>Performs maximum likelihood parameter estimation for requested model</i>
-----------	---

---

## Description

Computes maximum loglikelihood and corresponding parameters for the requested model using the independent-species approach. For optimization it uses various auxiliary functions in the DDD package.

## Usage

```
SADISA_ML(abund, initpars, labelpars, model = c("pm", "dl"), mult = "mg",
  tol = c(1e-06, 1e-06, 1e-06), maxiter = 1000 *
  round((1.25)^length(which(labelpars == 1))), optimmethod = "subplex")
```

## Arguments

abund	abundance vector or a list of abundance vectors. When a list is provided and mult = 'mg' (the default), it is assumed that the different vectors apply to different guilds. When mult = 'ms' then the different vectors apply to multiple samples. from the same metacommunity. In this case the vectors should have equal lengths and may contain zeros because there may be species that occur in multiple samples and species that do not occur in some of the samples.
initpars	a vector, or - when there are multiple samples or multiple guilds - a matrix of parameter values
labelpars	a vector, or - when there are multiple samples or multiple guilds - a matrix indicating whether the parameters in initpars must remain fixed (0) during optimization, optimized (1), or - in the case of multiple samples or guilds - set equal to the parameter of the first sample/guild (2).

model	the chosen combination of metacommunity model and local community model as a vector, e.g. <code>c('pm','dl')</code> for a model with point mutation in the metacommunity and dispersal limitation. The choices for the metacommunity model are: 'pm' (point mutation), 'rf' (random fission), 'pr' (protracted speciation), 'dd' (density-dependence). The choices for the local community model are: 'dl' (dispersal limitation), 'dd' (density-dependence).
mult	When set to 'mg' (the default) the loglikelihood for multiple guilds is computed. When set to 'ms' the loglikelihood for multiple samples from the same metacommunity is computed.
tol	a vector containing three numbers for the relative tolerance in the parameters, the relative tolerance in the function, and the absolute tolerance in the parameters.
maxiter	sets the maximum number of iterations
optimmethod	sets the optimization method to be used, either subplex (default) or an alternative implementation of simplex.

### Details

Not all combinations of metacommunity model and local community model have been implemented yet. because this requires checking for numerical stability of the integration. The currently available model combinations are, for a single sample, `c('pm','dl')`, `c('pm','rf')`, `c('dd','dl')`, `c('pr','dl')`, `c('pm','dd')`, and for multiple samples, `c('pm','dl')`.

### References

Haegeman, B. & Etienne, R.S. (2016). A general sampling formula for community abundance data. *Methods in Ecology & Evolution*. In review.

### Examples

```
utils::data(datasets);
utils::data(fitresults);
result <- SADISA_ML(
  abund = datasets$dset1.abunvec[[1]],
  initpars = fitresults$fit1a.parsopt[[1]],
  labelpars = c(1,1),
  model = c('pm','dl'),
  tol = c(1E-1, 1E-1, 1E-1)
);
# Note that tolerances should be set much lower than 1E-1 to get the best results.
```

---

SADISA\_test

*Tests SADISA for data sets included in the paper by Haegeman & Etienne*

---

### Description

Tests SADISA for data sets included in the paper by Haegeman & Etienne

**Usage**

SADISA\_test()

**References**

Haegeman, B. & Etienne, R.S. (2016). A general sampling formula for community abundance data. *Methods in Ecology & Evolution*. In review.



# Index

\*Topic **datasets**

datasets, [2](#)

fitresults, [3](#)

\*Topic **model**

SADISA\_loglik, [5](#)

SADISA\_ML, [6](#)

SADISA\_test, [7](#)

\*Topic **species-abundance-  
distribution**

SADISA\_loglik, [5](#)

SADISA\_ML, [6](#)

SADISA\_test, [7](#)

datasets, [2](#)

fitresults, [3](#)

integral\_peak, [4](#)

SADISA\_loglik, [5](#)

SADISA\_ML, [6](#)

SADISA\_test, [7](#)