

# Package ‘simba’

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**Type** Package

**Version** 0.3-1

**Date** 2010-07-23

**Title** A Collection of functions for similarity analysis of vegetation data

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**Depends** R (>= 2.9.0), stats, vegan

**Suggests** gplots, geoR, plotrix

**Description** Besides a function for the calculation of similarity measures with binary data (for instance presence/absence species data) the package contains some simple wrapper functions for reshaping species lists into matrices and vice versa and some other functions for further processing of similarity data (Mantel-like permutation procedures) as well as some other useful stuff.

**License** GPL (>= 2)

**URL** <http://www.r-project.org>,  
<http://www2.auf.uni-rostock.de/loe/ma/simba.html>

**LazyLoad** yes

## R topics documented:

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simba-package	<i>Calculate similarity measures for binary data</i>
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**Description**

Besides a function for the calculation of similarity measures with binary data (for instance presence/absence species data) the package contains some simple wrapper functions for reshaping species lists into matrices and vice versa and some other functions for further processing of similarity data.

**Details**

Package: simba  
Type: Package  
Version: 0.3-1  
Date: 2010-07-08  
License: GPL version 2

The functions in this package can be used to calculate similarities between species records (in binary format). Functions related to the correlation of similarity matrices and some other useful functions for the analysis of spatial patterns and their change in time are included as well.

**Author(s)**

Gerald Jurasinski <terhorab@mac.com>, with some help by Vroni Retzer <vroni.retzer@uni-bayreuth.d

**References**

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### See Also

`vegdist`, `dist.binary`, `dsvdis`, `dist`, `reshape`, `cor.test`

### Examples

```
##see functions for examples
```

---

abis	<i>Vegetation and environmental data recorded in a Tundra ecosystem in Northern Sweden (Southeast of Abisko).</i>
------	---

---

### Description

Vegetation and related data from field sites in a Tundra Ecosystem in Northern Sweden. `abis.spec` holds abundance information of 158 species on 61 sites.

### Usage

```
data(abis)
```

### Format

- `abis.env` contains some environmental variables from the Abisko field sites. These are:
  - X Numeric: The x-coordinates of the field sites (utm). The sites are arranged in a regular equidistant grid. Each site is a hexagon plot with 5m radius.
  - Y Numeric: The y-coordinates of the geographic position of the field sites.
  - alt Integer: Height a.s.l. of the field sites.
  - aspect Exposition of the sites. In degree from 0 to 180/-180. Counts negative in westward direction and positive in eastward direction.
  - slope Numeric: the inclination of the sites in degree
  - pH Numeric: pH value of soil samples taken on the sites (mixed samples from three
  - n.spec Integer: Number of species on the site.
  - shannon Numeric: Shannon index calculated from the species data.
  - even Numeric: Evenness calculated from the species data.
  - sims Numeric: Simpson diversity index for the site.

- ephwtrs1 Numeric: Cover of ephemeral waters
- ephwtrs2 Numeric: Cover of dried out ephemeral waters?
- roughn Numeric: Roughness index for the site. Obtained through calculating the ratio between the length of the straight lines dissecting the hexagonal plot and the lengths of lines along this dissections but exactly following the surface.
- stones.cov Numeric: Proportion of area of site covered by rocks which are covered with vegetation.
- stones.uncov Numeric: Proportion of area of site with uncovered, bare rocks.
- bare.soil Numeric: Open soil (most often sandy substrates).
- water Numeric: Proportion of area covered by permanent water bodies.
- bog Numeric: Proportion of area covered with boggy depressions.
- lemming Numeric: Counts of Lemming feces.
- elk Numeric: Counts of Elk feces.
- ren Numeric: Counts of Ren feces.
- ripa Numeric: Counts of Ripa feces.
- fox Numeric: Counts of Fox feces.
- grubblings Numeric: Amount of mole grubblings.
- tread Numeric: Amount of hoof tread.
- betula Numeric: Cover of *Betula*.
- CEC Numeric: Cation Exchange Capacity measured from the mixed soil sample taken in the field.
- base.satur Numeric: Base saturation.
- heath Binary: Does the site belong to the vegetation type 'heath'?
- shrubs Binary: Does the site belong to the vegetation type 'shrubby vegetation'?
- protect Binary: Does the site belong to the vegetation type 'protected snow heath'?

### Source

Jurasinski, G. and Retzer, V. (in. prep.) Measuring multi-plot similarity with presence-absence data.  
 Rettenmaier, N. 2004. Räumliche Muster der Biodiversität in der skandinavischen Tundra - Diploma thesis (unpublished), Department of Biogeography, University of Bayreuth, pp. 96.

### Examples

```
data(abis)
```

---

<code>ads.ternaries</code>	<i>Artificial data-set for studying the mathematical behavior of asymmetrical similarity coefficients</i>
----------------------------	---

---

### Description

Artificial data-set as utilized in Koleff et al. 2003, and Jurasinski 2007 to study the mathematical behavior of asymmetrical similarity indices. The corresponding values of all indices computable with `sim` are contained. See example!

### Usage

```
data(ads.ternaries)
```

## Format

- `ads.ternariesdata.frame` with the three matching components of asymmetric binary similarity measures (`a`, `b`, `c`) with all possible combinations of these components derived from a virtual data-set with 100 variables (species). These are the first three columns. The preceding columns contain the values of the similarity coefficients computable with `sim` according to the three matching components. This information can be used to study the mathematical behavior of the indices. See example

## Source

Jurasinski, G. (2007) Spatio-Temporal Patterns of Biodiversity and their Drivers - Method Development and a Case Study from Northeastern Morocco. PhD-Thesis, Department of Biogeography, University of Bayreuth

Koleff, P., Gaston, K. J. & Lennon, J. J. (2003) Measuring beta diversity for presence-absence data. *Journal of Animal Ecology* **72**: 367-382.

## Examples

```
data(ads.ternaries)
library(plotrix)
##take any index you want to study, see the help for sim() for available
##asymmetric indices or the names of the data.frame:
names(ads.ternaries)

##make a tmp from the index you want to study (we perform a transformation
##to obtain values between 0 and 1). if you want another index,
##just change the name in the next line:
tmp <- ads.ternaries$mountford
tmp <- (tmp-min(tmp))/max(tmp)
triax.plot(ads.ternaries[,c(2,3,1)], main="mountford",
col.symbols=grey(seq(0.1,1,0.1))[floor((tmp*100)/5)+1], pch=16)

##don't wonder: mountford is strange, just try another one:
##this time with rainbow-colors
tmp <- ads.ternaries$sjoerensen
tmp <- (tmp-min(tmp))/max(tmp)
triax.plot(ads.ternaries[,c(2,3,1)], main="sjoerensen",
col.symbols=rainbow(10)[floor((tmp*100)/10)+1], pch=16)

##and an interesting shape: routledge in greyscale...
tmp <- ads.ternaries$routledge
tmp <- (tmp-min(tmp))/max(tmp)
triax.plot(ads.ternaries[,c(2,3,1)], main="routledge",
col.symbols=grey(seq(0.1,1,0.1))[floor((tmp*100)/5)+1], pch=16)
```

## Description

Allows for the comparison of plots regarding the two variables slope aspect and slope inclination at once. To obtain a distance measure integrating aspect and inclination the model of a unit sphere is used and great-circle distances between virtual locations are calculated. For each plot a virtual location on the sphere is defined using the values for aspect as longitude and 90°-inclination as latitude. See `details` for more...

## Usage

```
aslopect(asp, slo, names=rownames(asp), fc=FALSE, listout = FALSE)
```

## Arguments

<code>asp</code>	Numeric vector with aspect values, given in degree. Expects values between 0° (North) and 180°/-180° (South). Eastward directions count positive, westward directions count negative. Alternatively the aspect values can be given in degrees of a full circle up to 359° starting from 0° (North). In the latter case <code>fc</code> has to be set to <code>TRUE</code> .
<code>slo</code>	Numeric vector with slope inclination values. Expects values between 0° (flat) and 90° (vertical wall).
<code>names</code>	Plot names, defaults to the rownames of <code>asp</code> , but a separate vector can be specified. Its length has to match the length of <code>asp</code> and <code>slo</code> .
<code>fc</code>	Triggers conversion from full circle degrees to half circle degrees. Set this to <code>TRUE</code> if full circle degrees (from 0° to 360°) are given in <code>asp</code> .
<code>listout</code>	Shall the results be given in list-format ( <code>data.frame</code> ). Defaults to <code>FALSE</code> which means that a matrix of class <code>dist</code> is returned.

## Details

To obtain a distance measure integrating aspect and inclination the model of a unit sphere is used and great-circle distances between virtual locations are calculated. For each plot a virtual location on the sphere is defined using the values for aspect as longitude and 90°-inclination as latitude. This means that as long as the inclination is low the virtual points are located in the pole region so that, regardless of aspect, plots with low inclination are rather close to each other regarding these qualities. The idea behind is, that solar radiation, wind or other factors highly depending on aspect and inclination are not really differing between plots with different aspect as long as the slope is low. The longitude values on the unit sphere are derived from the values of slope aspect. The equator of the sphere is thought as the compass circle. The Prime Meridian of the virtual sphere is the great circle through North and South of the compass. As in geographic terms longitude counts positive in Eastern and negative in Western direction. With  $\phi$  = latitude = 90°-inclination and  $\lambda$  = longitude = aspect the great-circle distance between A and B can be calculated with the following formula.

$$sim = \zeta = \arccos \left( \sin(\phi_A) \cdot \sin(\phi_B) + \cos(\phi_A) \cdot \cos(\phi_B) \cdot \cos(\lambda_B - \lambda_A) \right)$$

## Value

Returns a `dist` object or a `data.frame` (depending if `listout = FALSE` or `TRUE`). As a unit sphere is used, the maximum distance between two inclination/aspect pairs is `perimeter/2` of the sphere which is by definition  $\pi$ . To scale the possible distances between 0 and 1 the results are divided by  $\pi$ . Thus, a great-circle distance of 1 is rather scarce in the real world, however, two vertical rock walls with opposite aspect would share it. If `listout = TRUE` a `data.frame` with the following variables returns.

NBX	one of the compared sampling units
NBY	the other part of the pair
x	The returned aslopect value

**Author(s)**

Gerald Jurasinski

**Examples**

```
data(abis)
## identify columns with slope and aspect data
names(abis.env)

## calculate aslopect
abis.aslop <- aslopect(abis.env[,4], abis.env[,5])
```

---

auc

---

*Calculate the area under a line(curve).*

---

**Description**

Calculates the **area under a curve** (integral) by decomposing the curve (line) into rectangles and adding their area.

**Usage**

```
auc(x, y, below.zero = TRUE)
```

**Arguments**

x	Numerical vector giving the x cordinates of the points of the line (curve).
y	Numerical vector giving the x cordinates of the points of the line (curve). One can calculate the integral of a fitted line through giving a vector to x that spans xlim with small intervalls and predicting the y coordinates with <code>predict</code> and that x-vector as newdata. See example.
below.zero	How to handle y-data below zero? When below zero data represent proper data you'll want to substract the areas below the zero line from the area above the zero line to integrate the area under the curve. When below zero makes no sense for your question, you are able to set this to FALSE. Then, all 'negative' areas are just set to 0.

**Value**

Returns a numeric value that expresses the area under the curve. The unit depends from the input.

**Author(s)**

Gerald Jurasinski, <gerald.jurasinski@uni-rostock.de>

## Examples

```
## Construct a data set (Imagine 2-hourly ghg emission data
## (methane) measured during a day).
## The emission vector (data in mg CH4 / m2*h) as a time series.
ghg <- ts(c(12.3, 14.7, 17.3, 13.2, 8.5, 7.7, 6.4, 3.2, 19.8, 22.3, 24.7, 15.6, 17.4), st
## Have a look at the emission development.
plot(ghg)
## Calculate what has been emitted that day
## Assuming that emissions develop linearly between
## measurements
auc(time(ghg), ghg)

## The effect of below.zero:
## Shift data, so that we have negativ emissions (immissions)
ghg <- ghg-10
## See the difference
plot(ghg)
abline(h=0)
## With below.zero=TRUE the negative emissions are substracted
## from the positive emissions
auc(time(ghg), ghg)
## With below.zero=TRUE the negative emissions are set to 0
## and only the emissions >= 0 are counted.
auc(time(ghg), ghg, below.zero=FALSE)
```

---

bb2num

---

*Transform Braun-Blanquet scale data to percentage cover values and vice versa*


---

## Description

The function allows for an easy transformation of Braun-Blanquet (or any other phytosociological scale) data to numeric values for numerical analysis or vice versa. Be aware that this transformation is not losless regarding the information content.

## Usage

```
bb2num(dat, from = c("r", "+", "1", "2", "3", "4", "5"), to = c(0.1, 1, 5, 15, 3
```

## Arguments

dat	A species matrix.
from	Definition of the input scale. Per default the transformation is done from the classic Braun-Blanquet scale to cover percentages. For transformation from numerical values to a phytosociological scale see details and example.
to	Definition of the output scale. The default are the recommended class centers when transforming BB to percentage cover values. Can be changed according to your needs. See details.



## Details

When transforming from a phytosociological scale to Braun-Blanquet `from` and `to` have to be the same length. In case of transformation from numerical cover values to a phytosociological scale the function expects a numerical vector in `from` that, for each class, gives the lower and upper limit. Thus, `length(from) == 2*length(to)` in this case.

## Value

Returns a species matrix in the specified format.

## Author(s)

Gerald Jurasinski <gerald.jurasinski@uni-rostock.de>

## Examples

```
## Create a species that occurs on 7 plots
## with all the different possibilities of
## the BB scale
spec <- c("r", "+", "0", "1", "2", "3", "4", "5")

## Create a highly artificial species matrix.
## All species are the same for simplicity
dat.bb <- data.frame(spec, spec, spec, spec, spec, spec, spec)

## Transform from BB scale to percentage values
dat.proc <- bb2num(dat.bb)

## When transforming back the class definitions are a little
## more complicated. Just give the lower and upper limits for
## each class in the from vector class for class.
from <- c(0, 0.1, 0.1, 2, 2, 5, 5, 25, 25, 50, 50, 75, 75, 100)
to <- c("r", "+", "1", "2", "3", "4", "5")
bb2num(dat.proc, from=from, to=to)
```

---

bcoov

---

*Calculate Bray-Curtis distance for only one variable*


---

## Description

Calculates Bray-Curtis distance for only one variable: How dissimilar are the units regarding for instance pH?

## Usage

```
bcoov(x, names, listout = FALSE)
```

**Arguments**

<code>x</code>	numeric vector with quantitative data from sampling-units, standardization may be applied before
<code>names</code>	where should the names be taken from, must be a vector of the same length as <code>x</code> and should give the names of the sampling-units
<code>listout</code>	Shall the result given in list-format ( <code>data.frame</code> )? Defaults to <code>FALSE</code>

**Details**

It is just a simple way to calculate similarity based on only one variable. In the future there might be a possibility to choose from some functions. However, you could also use the difference in the data-values instead (which is the Euclidean distance in one dimensional space).

**Value**

Returns a `dist` object or a `data.frame` (in the case of `listout = TRUE`) with

<code>NBX</code>	one of the compared sampling units
<code>NBY</code>	the other part of the pair
<code>x</code>	The returned distance value. It is named like the tested variable

**Author(s)**

Gerald Jurasinski

**See Also**

[vegdist](#), [dist.quant](#), [dsvdis](#)

**Examples**

```
data(abis)
names(abis.env) ##take a look at the data
##calculate the similarity (Bray-Curtis) between the plots
##regarding pH
pH.dist <- bcoov(abis.env$pH, names=rownames(abis.env))

## directly give it as a list (data.frame)
pH.dist.ls <- bcoov(abis.env$pH, names=rownames(abis.env)
, listout=TRUE)
```

**Description**

Uses [boxplot](#) to produce a boxplot, which is then annotated with the number of observations in each group. Does allow for more flexibility compared to [boxplot.n](#). Default size of the text is bigger and per default the numbers are not plotted directly on the x-axis and their distance from the axis can be changed.

## Usage

```
boxes(..., top = FALSE, shrink = 1, textcolor = NULL, yadj = NULL)
```

## Arguments

<code>...</code>	Parameters passed to <code>boxplot</code> .
<code>top</code>	Should the numbers of observations be printed below or above the boxes? Defaults to below ( <code>top = FALSE</code> ).
<code>shrink</code>	Parameter to scale the size of the numbers of observations. Above 1 increases size, below 1 until 0 decreases size.
<code>textcolor</code>	Color of the text. Defaults to <code>NULL</code> which then uses the actual plotting colour of the graphics device.
<code>yadj</code>	Can be used to adjust the vertical plotting positions of the numbers of observations. Defaults to <code>NULL</code> - no adjustment.

## Author(s)

Gerald Jurasinski

## See Also

[boxplot](#), [plot](#), [boxplot.n](#)

## Examples

```
data(abis)

## see environmental data (see documentation on data for details)
abis.env

## calculate the difference in similarities for the three major
## vegetation types
## therefore created a vector from the data expressing belonging
## to the vegetation types:
tcs.sub <- rep(0, 61)
tcs.sub[abis.env[,29]==1] <- 1
tcs.sub[abis.env[,30]==1] <- 2
tcs.sub[abis.env[,31]==1] <- 3

## calculate similarity (Jaccard) between all pairs of plots
abis.jacc <- sim(abis.spec, method="jaccard")

## make boxplots regarding the similarities for each vegetation
## type, including the number of pairs contained in each box.
boxes(as.matrix(abis.jacc)~tcs.sub, shrink=1.2)

## prettier
boxes(as.matrix(abis.jacc)~tcs.sub, notch=TRUE, col="grey50",
      shrink=1.2, ylim=c(-0.1, 0.9))
```

com.sim

*Compare mean similarity between subsets of data***Description**

Related to [mrpp](#). Are the differences in mean similarity between data subsets significant? Function takes the whole data-set (species matrix) and a subsetting vector and computes a specified similarity between all sampling units (rows). Then subsets are compared regarding their mean similarity. Statistical inference is obtained through permutation.

**Usage**

```
com.sim(veg, subs, simil = "soerensen", binary = TRUE,
        permutations = 1000, alpha = 0.05, bonfc = TRUE, ...)
```

**Arguments**

veg	Species matrix with columns = sites, rows = species. Deliver presence/absence data or abundance data. However, <code>binary</code> has to be set accordingly.
subs	Vector containing the subset definition. Same entries are understood to indicate belonging to the same subset (can be characters, factors or numerics). For each subset similarities/distances are calculated. Then all subsets are compared regarding mean and variance of the similarities/distances.
simil	Sets the coefficient to be used for calculating similarities/distances. If <code>binary = TRUE</code> , see <a href="#">sim</a> , otherwise see <a href="#">vegdist</a> for possible choices.
binary	Changes the function used for the calculation of similarity/distance. If binary species data is provided in <code>veg</code> keep the default ( <code>binary = TRUE</code> ). In this case <a href="#">sim</a> is used to calculate the similarities. Set to <code>FALSE</code> when abundance or frequency data is provided. This calls <a href="#">vegdist</a> to calculate the distances between sites in species similarity space.
permutations	Number of permutations performed to obtain the statistical inference. See Details.
alpha	Initial alpha level to test against. Defaults to 0.05.
bonfc	Shall Bonferroni correction be applied? Defaults to true.
...	Further arguments to functions.

**Details**

Entries of similarity/distance matrices are not independent. Therefore normal statistics might fail. One possibility is the application of permutation procedures. This means that the statistical distribution against which significance is tested is derived from the data.

Here it is implemented as follows: For each subset the similarities/distances between all sites (plots) are calculated with the specified coefficient. Then the resulting similarity/distance matrices are compared with [diffmean](#). This is done for the comparison of each subset with each other subset. If specified (defaults to `TRUE`), Bonferroni correction is applied (to correct for multiple testing).

Depending on the number of subsets and the number of sites per subset it may take some seconds to be computed.

**Value**

Returns an object of class `cslist` containing the call to the function, the used method for similarity/distance calculation, a comparison matrix showing the connections between data-subsets (rows and columns connected with "\*" are significantly different), the number of subsets involved, the number of permutations and a matrix giving information about the following components for each comparison between subsets:

<code>X</code>	Subset identifier for one of the compared subsets
<code>Y</code>	Subset identifier for the other compared subset
<code>mean.x</code>	Average distance/similarity for subset X.
<code>mean.y</code>	Average distance/similarity for subset Y.
<code>diff</code>	Difference in average distance/similarity for this comparison
<code>sig</code>	Significance of the difference in mean of the similarities.
<code>sigs</code>	Significance flag for the comparison ("*" means significant differences, "ns" means that the differences are not significant).
<code>F</code>	F-value for the Comparison.
<code>sigF</code>	Is F significant?
<code>sigsF</code>	Significance flag for F.

**Author(s)**

Gerald Jurasinski

**See Also**

[mrpp](#) for an anova like approach for comparing the differences of species data subsets.

**Examples**

```
data(abis)

## see environmental data (see documentation on data for details)
abis.env

## calculate the difference in similarities for the three major
## vegetation types
## therefore create a vector from the data expressing belonging
## to the vegetation types:
tcs.sub <- rep(0, 61)
tcs.sub[abis.env[,29]==1] <- 1
tcs.sub[abis.env[,30]==1] <- 2
tcs.sub[abis.env[,31]==1] <- 3

## calculate differences with Bray-Curtis as the distance measure
com.sim(abis.spec, tcs.sub, simil="bray", binary=FALSE)

## calculate differences with Soerensen as the similarity measure
com.sim(abis.spec, tcs.sub)
```

---

dfcor	<i>Calculate permuted (Mantel) correlations between one and many variables</i>
-------	--

---

### Description

The function uses `permc2` to calculate permuted correlation on vectors. One vector is compared to various vectors of the same length. Useful e.g. if one variable has to be tested against various variables.

### Usage

```
dfcor(ox, y, method = "pearson", permutations = 1000, ...)
```

### Arguments

<code>ox</code>	Numeric vector. If it is a similarity matrix (i.e. a <code>dist</code> object, extract vector via <code>as.vector(x)</code> beforehand).
<code>y</code>	A <code>data.frame</code> containing numeric vectors to correlate <code>ox</code> with. Number of rows has to equal the length of <code>x</code>
<code>method</code>	Method for correlation. Defaults to "pearson". See <code>cor</code> for other possibilities.
<code>permutations</code>	Number of permutations. Defaults to 1000, which gives reasonable results and allows to test against $\alpha = 0.001$ .
<code>...</code>	Further arguments passed to internal functions (i.e. to <code>cor</code> ).

### Details

`dfcor` is a wrapper for `permc2`, which is usually called as a part of `pcol`. Here, the numeric vector in `x` is compared to each column vector of `y`.

### Value

A list with the following:

<code>call</code>	The function call
<code>method</code>	P-value obtained by testing the initial correlation against the permuted correlation values.
<code>out</code>	A table with statistics. See details below.
<code>gesN</code>	The included number of cases.
<code>strata</code>	The number of variables against which <code>x</code> was tested.
<code>permutations</code>	The number of permutations.
	The included printing method gives nice output (where information appears in a slightly different order) ending with the table of <code>out</code> . It is based on a <code>data.frame</code> with <code>nrow = ncol(y)</code> giving the statistics for the correlation between <code>x</code> and each column of <code>y</code> as follows.
<code>corr</code>	Correlation value (regarding to <code>method</code> ).

sig	P-value obtained by testing the initial correlation against the permuted correlation values.
nop	Number of included pairs. The function tests for complete cases before calculation starts. Pairs containing NA's are not included.
miss	Number of missing pairs.

### Note

Maybe [pcol](#) will get this functionality in future releases.

### Author(s)

Gerald Jurasinski

### References

Legendre, P. & Legendre, L. (1998) *Numerical Ecology*. 2nd English Edition. Elsevier.

### See Also

For related functions of `simba` [permcors](#), [permcors2](#), [mancors](#), [pcol](#). Further see [mantel](#) of package `vegan` for a different implementation of permuted correlation on distance matrices.

### Examples

```
## load included data
data(abis)

## obtain several similarity matrices and correlate them
## with one other matrix.
# calculate soerensen similarity for species composition data
abis.soer <- sim(abis.spec, listout = TRUE)[,3]
# calculate euclidean distances between the plot locations
abis.geodist <- dist(abis.env[,1:2])
# calculate the ecological distance according to slope and aspect
abis.aslopect <- with(abis.env, aslopect(aspect, slope))
# calculate the ecological distance according to disturbance
abis.pert <- dist(abis.env[,19:25])

# put distances according to environment together
abis.envdist <- data.frame(dist = c(abis.geodist), aslopect = c(abis.aslopect), pert = c(abis.pert))

# no mantel correlation between those constructed
# variables and the similarity in species composition
dfcor(abis.soer, abis.envdist)
```

diffmean

*Calculate the difference in Mean between two vectors***Description**

The function can be used to calculate the difference in mean between two vectors. Statistical inference is obtained through permutation. F-ratio is also calculated. For data which is not normally distributed or lacks independence. The plotting method plots the actual values of the difference in mean and F against an histogram of the results of the permuted runs.

**Usage**

```
diffmean(x, y, permutations = 1000)
## S3 method for class 'dmn':
plot(x, y, which=3, two=2, ...)
```

**Arguments**

<code>x</code>	Numeric vector. For the plotting method the <code>dmn</code> -object which should be printed (results from a <code>diffmean</code> operation). Plotting object in the plotting method.
<code>y</code>	Numeric vector. Plotting object in the plotting method, optional when <code>x</code> has appropriate structure
<code>permutations</code>	Number of permutations.
<code>which</code>	which histogram should be plotted? 1 triggers the histogram for difference in mean, 2 the one for F. It defaults to 3: both histograms are plotted. If it is changed from default, the next argument ( <code>two</code> ) is automatically set to 1!
<code>two</code>	Should the histograms be printed on a divided display? And how? Can only be set if <code>which</code> is set to 3. Defaults to 2, which means that the display is divided in two halves and the histogram-plots are plotted side by side. 3 causes histograms to be plotted one on top of the other. If <code>two = 1</code> , the display is NOT automatically divided. Might be useful if more than one <code>dmn</code> -objekt is to be plotted on one display. Otherwise the function overrides the actual display settings.
<code>...</code>	Further arguments to the plotting method.

**Details**

The two vectors do not need to share the same length but they should not be too different. Otherwise the function might give spurious results.

**Value**

Returns a list giving the function call, the difference in Mean, the mean of vector `x` and `y`, the mean of means, the F-value, the significance of the difference in Mean and the significance of F, as well as the number of permutations. The results of the permutation runs can be retrieved with `result$bootSM` (for the difference in mean) and `result$bootF` (for the F-values). There is a plot method for easily illustrating the test. The difference is plotted against an histogram displaying the distribution of the permuted values.

**Author(s)**

Gerald Jurasinski



**See Also**[diffslope](#), [diffmich](#)**Examples**

```

data(abis)

## create subsetting vector describing the belonging to different
## vegetationtypes
tcs.sub <- rep(0, 61)
tcs.sub[abis.env[,29]==1] <- 1
tcs.sub[abis.env[,30]==1] <- 2
tcs.sub[abis.env[,31]==1] <- 3

## check distribution
summary(as.factor(tcs.sub))

## compare vegetation types "shrubby vegetation" (shrub=2) and
## "protected by snowcover" (protect=3) regarding difference in
## similarities
abis2.soer <- sim(abis.spec[tcs.sub==2,])
abis3.soer <- sim(abis.spec[tcs.sub==3,])
abis.23cmp <- diffmean(abis2.soer, abis3.soer)

```

diffmich

---

*Calculate the difference in parameters of a Michaelis-Menten kinetik fitted to (PAM) data*

---

**Description**

The function can be used to calculate the difference in the two parameters of the Michaelis-Menten Kinetik  $y = \frac{a \cdot x}{b + x}$  between two datasets containg each two vectors. Through permutation it is possible to compute significance of the difference. [fitmich](#) is used to calculate the Michaelis-Menten fit to the data. With the corresponding plot method a plot of the actual difference in the parameters against a histogram of the permuted values can easily be achieved.

**Usage**

```

diffmich(x1, y1, x2, y2, permutations = 1000, a=3, b=0.5, trace=FALSE, ...)
fitmich(x, y, a=3, b=0.5)
## S3 method for class 'diffmich':
plot(x, y, which=3, two=2, ...)

```

**Arguments**

x1	Vector containing an independent variable, for instance PAR measurements.
y1	Vector containing a variable dependent on x1 (for instance ETR measurements). Must have the same length as x1.
x2	Vector containing a second independent variable (for instance PAR measurements).

<code>y2</code>	Vector containing a variable dependent on <code>x2</code> (for instance ETR measurements). Must have the same length as <code>x2</code> .
<code>permutations</code>	Number of permutations.
<code>a</code>	start value for parameter a, defaults to 3, usually there is no change necessary, but if the function gets trapped in the first run, changing the parameters might solve the problem.
<code>b</code>	Start value for parameter b, defaults to 0.5.
<code>trace</code>	set to TRUE for displaying the progress of the calculation
<code>...</code>	Arguments to other functions (for instance to <code>lm</code> , which is used to calculate the regression lines)
<code>x</code>	Vector containing an independent variable, for instance PAR measurements. Function <code>fitmich</code> is usually called only internally by <code>diffmich</code> . Plotting object in the plot method.
<code>y</code>	Vector containing a variable dependent on <code>x1</code> (for instance ETR measurements). Must have the same length as <code>x1</code> . Plotting object in the plotting method, optional when <code>x</code> has appropriate structure
<code>which</code>	Which histogram should be plotted? 1 triggers the histogram for parameter a, 2 the one for parameter b. It defaults to 3: both histograms are plotted. If it is changed from default the next argument ( <code>two</code> ) is automatically set to 1!
<code>two</code>	Should the histograms be printed on a divided display? And how? Can only be set if <code>which</code> is set to 3. Defaults to 2, which means that the display is divided in two halves and the histogram-plots are plotted side by side. 3 causes histograms to be plotted one on top of the other. If <code>two</code> = 1, the display is NOT automatically divided. Might be useful if more than one <code>diffmich</code> -objekt is to be plotted on one display. Otherwise the function overrides the actual display settings.

## Details

As the function was initially built to easily calculate the difference of parameters of the Michaelis-Menten Kinetik for PAM measurements, the independent vectors are meant to contain PAR values whereas the dependent vectors should represent ETR values. But you can use it for anything else which can be fitted with Michaelis-Menten. The vectors belonging together are formed into a `data.frame`. For each permutation run the rows are interchanged randomly between the two `data.frames` and the difference in the parameters is calculated and collected into a vector. The p-value is then computed as the ratio between the number of cases where the differences in Parameter exceed the difference in parameter of the initial configuration and the number of permutations.

As it uses a `for` loop it takes a while to calculate. So get a coffee while it is running, or set `trace` = TRUE to avoid boring moments ...

## Value

Returns a `diffmich`-object with the function call, the difference in the two parameters and their significance. Furthermore the number of permutations. If you want to change the way `fitmich` is computed you can change the starting values. Per default it is calculated with starting values `a=3` and `b=0.5`. There's no change needed unless the function gets trapped.

## Author(s)

Gerald Jurasinski

**See Also**[nls](#), [sample](#)

diffslope

*Calculate the difference in slope or intercept of two regression lines***Description**

The function can be used to calculate the difference in slope between two datasets containing each two vectors. Follows an idea of Nekola & White (1999) for calculating the statistical inference of the difference in slope between two regression lines. `diffslope2` has the same purpose as `diffslope` but implementation is without for-loop. The plot method allows easy plotting of the actual difference in slope against the distribution of permuted values.

**Usage**

```
diffslope(x1, y1, x2, y2, permutations = 1000, ic = FALSE,
  resc.x = FALSE, resc.y = TRUE, trace=FALSE, ...)

diffslope2(x1, y1, x2, y2, permutations =1000, resc.x = FALSE,
  resc.y = TRUE, ...)

diffic(x1, y1, x2, y2, permutations = 1000, resc.x = FALSE,
  resc.y = FALSE, trace=FALSE, ...)

## S3 method for class 'dsl':
plot(x, y, ...)
```

**Arguments**

<code>x1</code>	vector containing an independent variable (for instance distance between plots).
<code>y1</code>	vector containing a variable dependent on <code>x1</code> (for instance similarity between the plots. must have the same length as <code>x1</code> ).
<code>x2</code>	vector containing a second independent variable (for instance distance between plots). can be the same as in <code>x1</code> .
<code>y2</code>	vector containing a variable dependent on <code>x2</code> (for instance similarity between the plots. must have the same length as <code>x2</code> ).
<code>permutations</code>	number of permutations
<code>ic</code>	Shall the difference in intercept be tested? Defaults to <code>FALSE</code> .
<code>resc.x</code>	Shall the values of the independent variables be rescaled to a common mean? Defaults to <code>FALSE</code> .
<code>resc.y</code>	Shall the values of the dependent variables be rescaled to a common mean? Defaults to <code>TRUE</code> (Nekola & White 1999) for <code>diffslope</code> and to <code>FALSE</code> for <code>diffic</code> .
<code>trace</code>	Set to true if progress shall be printed with increasing numbers. Defaults to <code>FALSE</code>
<code>...</code>	Arguments to other functions (for instance to <a href="#">lm</a> , which is used to calculate the regression lines).
<code>x</code>	dsl-object (given back by <code>diffslope</code> or <code>diffic</code> ) which is to be plotted.
<code>y</code>	Plotting object, usually not necessary

## Details

`diffslope`: As the function was initially build to easily calculate the difference in slope between the regression lines of distance decay plots, the independent vectors are meant to contain distance values whereas the dependent vectors should represent similarity values. But you can use it for anything else, as you wish. The vectors belonging together are formed into a `data.frame`. For each permutation run the rows are interchanged randomly between the two `data.frames` and the difference in slope calculated thereafter is calculated and collected into a vector. The p-value is then computed as the ratio between the number of cases where the differences in slope exceed the difference in slope of the initial configuration and the number of permutations.

The same applies to `diffic`. However, this function tests whether the intercepts of the two relationships are significantly different. Although `resc.y` has been kept as an option, it is not wise to do so, when one is testing for differences in intercept.

If the difference in slope returns negative, the slope (distance decay) of the second relationship is less pronounced, if it returns positive, the second relationship exhibits a stronger distance decay (slope) than the first. This holds for distance decay relationships. If  $y$  increases with  $x$ , it is vice versa.

As it uses a `for` loop, it takes a while to calculate. So get a coffee while it is running, or set `trace` to `TRUE` to avoid being bored ...

## Value

Returns a list giving the function call, the difference in slope, the significance of this difference, and the number of permutations. If you want to change the way `lm` is computed you must send the arguments to `lm` via `...`. Per default it is calculated with the default arguments of `lm`.

In case of `diffic` there is still differences in slope reported (although differences in intercept have been calculated). So it's just a false label here. This will be updated soon.

## Author(s)

Gerald Jurasinski

## References

Nekola, J. C. and White, P. S. (1999) The distance decay of similarity in biogeography and ecology. *Journal of Biogeography* 26: 867-878.

Steinitz, O., Heller, J., Tsoar, A., Rotem, D. and Kadmon, R. (2005) Predicting Regional Patterns of Similarity in Species Composition for Conservation Planning. *Conservation Biology* 19: 1978-1988.

Steinitz, O., Heller, J., Tsoar, A., Rotem, D. and Kadmon, R. (2006) Environment, dispersal and patterns of species similarity. *Journal of Biogeography* 33: 1044-1054.

## See Also

`lm`, `sample`

## Examples

```
data(abis)
names(abis.env) ##take a look at the data
pert.dist <- 1-vegdist(abis.env[,19:25], "euclidean")
##calculate the distance (Euclidean) between the plots
```

```

##regarding disturbance variables

soil.dist <- 1-vegdist(abis.env[,c(6,27:28)])
##calculate the similarity (Bray-Curtis) between the plots
##regarding soil parameters

coord.dist <- dist(abis.env[,1:2]) ##calculate geographical distance between plots

##transform all distance matrices into list format:
struc.dist.ls <- liste(pert.dist, entry="BC.struc")
soil.dist.ls <- liste(soil.dist, entry="BC.soil")
coord.dist.ls <- liste(coord.dist, entry="dist")

##create a data.frame containg plot information, geographical
##distance,similarity of soil parameters, and similarity of
##structural parameters:

df <- data.frame(coord.dist.ls, soil.dist.ls[,3], struc.dist.ls[,3])
names(df) ##see names

##give better names:
names(df)[4:5] <- c("soil","struc")
attach(df)

##prepare graphics device:
par(mfrow=c(2,1))

##plot and compare distance decay (decrease of similarity with
##distance):
plot(dist, soil)
plot(dist, struc)
##remove problematic zero entries:
df <- subset(df, struc != 0)

##plot again, this time with regression lines (in red for better
##visability):
detach(df)
attach(df)
plot(dist, soil)
abline(lm(soil~dist), col="red4")
plot(dist, struc)
abline(lm(struc~dist), col="red4")
##is the slope significantly different?
res <- diffslope(dist, soil, dist, struc)
res2 <- diffic(dist, soil, dist, struc)

##go for a coffee, as it takes a while...

```

## Description

The functions calculates direction classes from geographic coordinates (not lat/lon). All possible connections between these points are established and the direction of each link is calculated. This

is followed by a designation of direction-classes.

### Usage

```
direct(coord, listout=FALSE)
direct2(coord, listout=FALSE)
```

### Arguments

coord	A <code>data.frame</code> containing coordinates. Should have the same number of points as the data for which the direction-classes are calculated.
listout	Logical value, indicating whether the result is given back in ( <code>data.frame</code> )-format instead of returning a <code>dist</code> -object.

### Value

Returns a matrix containing the direction-classes of the connections between the coordinates as a `dist`-object. If `listout = TRUE`, the result is given as a list (`data.frame`).

`direct` returns 4 directions (North-South, Northwest-Southeast, West-East, Northeast-Southwest).

`direct2` returns 6 directions.

### Note

as with `mantel` it takes a while to calculate

### Author(s)

Gerald Jurasinski

### See Also

`mantel`, `cor.test`

### Examples

```
data(abis)
dirclass <- direct(abis.env[,1:2])
dirclass
dirclass.ls <- direct(abis.env[,1:2], listout=TRUE)
dirclass.ls
```

---

dist.tmp

*Calculate the distance between the instances or variables of two similar data-sets.*

---

### Description

The function calculates the distance between the instances or variables of two data-sets, preferably two recordings from the same places/variables at different time steps. Could for example be useful to calculate the dissimilarity of species records from the same set of plots at different recording campaigns.

**Usage**

```
dist.tmp(x, y, method = "euclidean", margin = 1, adjust=TRUE)
```

**Arguments**

x	data.frame with numeric columns giving the data at time one
y	data.frame with numeric columns giving the data at time two
method	Which distance measure should be employed? The following measures are available: "manhattan", "euclidean", "bray", "canberra", "kulczynski", "gower", "jaccard". See details.
margin	Shall the distance between the instances (rows, margin = 2), or the distance between the variables (columns, margin = 1) be calculated?
adjust	The default adjust = TRUE takes care of your input data. However, instances and variable names have to be unique, as the matching relies on these names. If your data meets this requirement the function automatically detects which instances and variables can be found in both data-sets and calculates the distance based on these data.

**Details**

The function provides just an alternative to code your repeated measurements from the same plots, calculate the distances between all instances and sort out the distances between the same instances at different time steps. Here just the latter is calculated directly.

For details regarding the different distance coefficients, see [vegdist](#). The formulae behind were taken from there. However, not all choices have been implemented here.

**Value**

Returns a vector of distances. Length depends on margin. If you choose margin = 1 it equals the number of instances (plots) in your two data-sets. If you choose margin = 2 it equals the number of variables (species) in your data-sets.

**Author(s)**

Gerald Jurasinski <terhorab@mac.com>

**References**

See references in [vegdist](#)

**See Also**

[vegdist](#), [dist](#), [sim](#)

**Examples**

```
data(abis)

##just to see that the function takes care of matching instances
##and variables we compare abis.spec with a permuted version of
##itself and skip some instances and variables in the original matrix.
dist.tmp(abis.spec[5:50,3:120], apply(abis.spec, 2, sample), method="bray")
```

---

hexgrid

*Produces the nodes of an equidistant grid.*


---

### Description

Given the coordinates of a starting point (left upper point of the grid), the function produces the nodes of an equidistant grid. Extent and distance between plots can be specified.

### Usage

```
hexgrid(x, y, r = 100, nro = 10, nco = 20)
```

### Arguments

x	x-value of the starting point. Defaults to 0.
y	y-value of the starting point. Defaults to 0.
r	Distance between nodes. Defaults to 100.
nro	Number of rows in the grid. Defaults to 10
nco	Number of columns in the grid. Defaults to 20. They are doubled (see the grid) compared to the rows. That's why <code>2*nro</code> produces a quadratic grid.

### Details

If the overall shape of the grid is not square, the user has to delete by hand the superfluous units. Might get more flexible in future versions.

### Value

Returns a data.frame giving informations on the produced point/unit/plot locations with the following columns:

ROW	Number of row in the grid to which the point/unit/plot belongs.
COL	Number of column in the grid to which the point/unit/plot belongs.
X	x-coordinate of the point.
Y	y-coordinate of the point.

### Author(s)

Gerald Jurasinski

### References

<http://homepage.mac.com/terhorab/gerald/downloads/whyhexaagons.pdf>

### See Also

[spsample](#)



## Examples

```
## produces a grid with r=400:
test.grd <- hexgrid(456000, 7356700, r=400)
## for plotting the following is recommended as it preserves
## real positions:
library(geoR)
points.geodata(coords=test.grd[,3:4], data=rnorm(nrow(test.grd)))
```

liste

*Convert dist-objects and matrices to database format*

## Description

Transposes `dist` objects to database list format (where each line represents a similarity value calculated between two plots, so the list has three columns containing information on plot x, plot y and information on similarity/dissimilarity). This might be useful if further database processing is intended. If the given matrix is not of class `dist`, the whole matrix is converted. This might be handy if species matrices are to be converted to database format.

## Usage

```
liste(obj, x="NBX", y="NBY", entry=NULL, factorize=TRUE,
      splist=FALSE)
```

## Arguments

<code>obj</code>	A distance object as it is returned from <code>sim</code> , <code>dist</code> , <code>vegdist</code> or <code>dist.binary</code> or a similar matrix with class="dist". If the matrix is not of class <code>dist</code> a <code>data.frame</code> is expected and all entries are converted. Species matrices are assumed to contain sites (or plots) in rows and species in columns.
<code>x</code>	How the second column should be named, standard is that it contains "NBX" the neighbour X. Obsolete when <code>splist = TRUE</code> .
<code>y</code>	How the second column should be named, standard is that it contains "NBY" the neighbour Y. Obsolete when <code>splist = TRUE</code> .
<code>entry</code>	How the third column should be named. If there is nothing given, it is named "we" (whatever). Obsolete when <code>splist = TRUE</code> .
<code>factorize</code>	If naming (first two) columns should be given as factors. Defaults to <code>TRUE</code> .
<code>splist</code>	Set to <code>TRUE</code> if a species matrix is transformed to a database list format. Automatically removes entries with zero occurrence of the species' and names columns correspondingly (see Value).

## Details

Column x represents the column names of the input matrix. So if you want to reshape a species matrix, x will be the species names and y will be the plot names. If it is needed vice versa, you have to change column order. For convenience you can set `splist = TRUE` and you will get a species list in database format with columns representing the plot, species and occurrence information. Furthermore zero occurrences are already omitted.

**Value**

Returns a `data.frame` with three columns:

Col1	The column names of the input matrix. If it is a <code>dist</code> -object only the lower triangle is used. Named <code>plot</code> when a species matrix is transformed with <code>splist = TRUE</code> .
Col2	The row names of the input matrix. Named <code>spec</code> when a species matrix is transformed with <code>splist = TRUE</code> .
Col3	The respective matrix entries. Named <code>occ</code> when a species matrix is transformed with <code>splist = TRUE</code> .

**Author(s)**

Gerald Jurasinski

**See Also**

[reshape](#), [data.frame](#). It resembles functionality of `reshape` - which is more flexible (but also more complex).

**Examples**

```
data(abis)
## there are empty species entries:
sum(colSums(abis.spec)==0)
## remove empty species
abis.spec <- abis.spec[,colSums(abis.spec)!=0]
abis.spec.ls <- liste(abis.spec, splist=TRUE)
```

---

makead

*Create artificial data set (species matrix).*

---

**Description**

The functions allow for the automated creation of artificial data (species matrix). The user can choose between random organization or a gradient. The gradient can be defined via a gradient vector which allows for fine tuning of the gradient. [ads](#) has a different implementation and produces better results for gradients.

**Usage**

```
makead(nspec, nplots, avSR = NULL, anc = NULL, grad.v = NULL,
cf = 0.2, puq = 0.01)

ads(nspec, nplots, avSR = NULL, anc = NULL, grad.v = NULL,
reord = TRUE, cf = 0.2, puq = 0.01)

ads.hot(nspec, nplots, avSR = NULL, anc = NULL, grad.v = NULL,
frac=0.5, reord=TRUE, cf=0.2, puq=0.01)

ads.fbg(nspec, nplots, grad.v, n.iter = 100, method = "ads", ...)
```

## Arguments

<code>nspec</code>	Numbers of species you want to be in the data-set. Meaningless if <code>anc != NULL</code> .
<code>nplots</code>	Numbers of plots you want to be in the data-set. Meaningless if <code>anc != NULL</code> .
<code>avSR</code>	Average species richness. If <code>anc</code> is given, it is calculated from the data when the default is not changed. If <code>avSR != NULL</code> , the given value is taken instead. In the actual version not implemented in <code>ads</code> .
<code>anc</code>	If a model species matrix is available (either a real data-set, or another artificial data-set) on which creation should be based, give it here. Rows must be plots and columns be species. The first three parameters are then obtained from this set. However average species richness ( <code>avSR</code> ) can still be given by the user.
<code>grad.v</code>	A numeric vector describing the gradient, or - in case of <code>ads.hot</code> - the hotspot. Must have the same length as <code>nplots</code> (or <code>nrow(anc)</code> respectively). See details.
<code>cf</code>	Determines the probability of the species to occur on the plots. In other words, it changes the shape of the species accumulation curve. Set to <code>NULL</code> if no natural species accumulation should be applied (may sometimes increase the visibility of the gradient)
<code>puq</code>	Percentage of ubiquitous species. Set to <code>NULL</code> if the produced gradients seem to be unclear or if you don't want ubiquitous species to be in the data-set. Only used if a gradient vector is given (which is then not applied to the given percentage of species).
<code>reord</code>	Triggers reordering of the columns in the produced gradient matrix (see details). May considerably change the resulting matrix. Defaults to <code>TRUE</code> .
<code>frac</code>	Numeric between 0 and 1 giving the percentage of species which should occur on the hotspot-gradient only (see details).
<code>n.iter</code>	Number of iterations when <code>ads.fbg</code> is used for finding the species matrix representing best the prescribed gradient (see details).
<code>method</code>	Which method of <code>makead</code> , <code>ads</code> , <code>ads.hot</code> should be used?
<code>...</code>	Further arguments to the function specified in <code>method</code>

## Details

There are three different implementations to create an artificial species matrix and a fourth function `ads.fbg` that allows to use either of the three possibilities to find a "best" gradient.

`makead` first applies the **natural species accumulation curve**, the gradient for each species is represented by a vector containing numerics between 0 and 1. Both matrices are added so that values between 0 and 2 result. Through an iteration procedure a breakvalue is defined above which all entries are converted to 1. Values below are converted to 0 resulting in a presence/absence matrix. However the random element seems to be too strong to get evident gradient representations.

Therefore `ads` is implemented. It works different. First, a gradient is applied. As with `makead` the gradient is always applied in two directions so that half of the species are more likely to occur on plots on one side of the gradient, whereas the others are more likely to occur on the other side of the gradient. Subsequently, species occurrence for all species will oscillate around `nplots/2`.

If `puq` is specified the given percentage of species is divided from the whole matrix before the gradient is applied. With the parameter `cf` a vector is produced representing quasi-natural occurrence of the species on the plots: Most species are rare and few species are very common. This is

described by a power function  $y = \frac{1}{x^c}$  with  $x$  starting at 2 and gives a vector of length `nspec` representing the number of times each species is occurring.

These numbers are applied to the gradient matrix and from the species occurrences only as many as specified by the respective number are randomly sampled. In cases where the occurrence number given by the vector exceeds the occurrences resulting from the gradient matrix, the species in the gradient matrix is replaced by a new one for which occurrence is not following the gradient and represents the number of occurrences given by the vector. The idea behind this is, that also in nature a species occurring on more than about half of the plots will likely be independent from a specific gradient.

In both cases (`makead` and `ads`) a totally random species matrix (under consideration of natural species occurrence, see `cf`) is obtained by randomly shuffling these occurrences on the columns (species) of the "natural species occurrence" matrix.

Contrarily to the other two functions, `ads.hot` allows for the creation of an artificial data-set including a hotspot of species richness and composition. In this case, `frac` can be used to specify which proportion of the total number of species should only occur on the hotspot gradient. All other species occur randomly on the plots. However, with the hotspot-gradient (`grad.v`) you can influence the explicitness of the hotspot.

The function `ads.fbg` allows for finding the best gradient representation with one of the above functions. A gradient is considered to be represented best, when the correlation between the first axis scores of a DCA (which is calculated with `decorana` of package `vegan` and the gradient positions as described by the gradient vector `grad.v` are maximized. `ads.fbg` just runs the specified `makead` function `n.iter` times and gives out the best result matrix and the `r2.adjust` value that has been obtained.

## Value

The three functions for creating an artificial species matrix each return a presence/absence species matrix with rows representing plots/sampling units and columns representing species. `ads.fbg` returns a list with

<code>mat</code>	The species matrix as for the three artificial data set functions.
<code>r2.adjust</code>	The adjusted <code>r2</code> value for the regression of the first axis DCA scores of the resulting species matrix against the position on the prescribed gradient as described by the gradient vector <code>grad.v</code> .

## Author(s)

Gerald Jurasinski, Vroni Retzer

## Examples

```
## create a random data-set with 200 species on 60 plots
artda <- makead(200, 60, avSR=25)

## create a gradient running from North to South (therefore you
## need a spatially explicit model of your data which is obtained
## with hexgrid())
coor <- hexgrid(0, 4000, 200)
coor <- coor[order(coor$ROW),] #causes coordinates to be in order.
## then the gradient vektor can easily be generated from the ROW names
gradvek <- as.numeric(coor$ROW)
## check how many plots your array has
nrow(coor)
```

```
## create a data-set with 200 species
artda <- ads(200, 100, grad.v=gradvek)
## see the species frequency distribution curve
plot(sort(colSums(artda)))
```

---

mama

*A (convenience) wrapper function to make matrix from a data.frame*

---

## Description

The function `mama` uses [reshape](#) to transpose species data given in database list format (where each line represents a species in a plot, so the list has three columns containing information on plot, species and information on occurrence) into a plot species matrix (where rows represent plots and columns represent species) for further use with other functions on vegetational data.

## Usage

```
mama(dat)
```

## Arguments

dat	Species data in list format. The columns have to represent plot, species, occurrence information (presence/absence or abundances). Column names may differ but they must be in that order!
-----	--

## Details

You could reach the same result with [reshape](#). I was just always quite confused with this. That's why i decided to do this little wrapper for convenience. It needs quite a while to run though, but this is due to [reshape](#).

## Value

Returns a [data.frame](#) which contains the presence/absence or abundance data of the species list. Rows represent plots, columns represent species. If you want to have it vice versa you have to use the function on a list with columns `species`, `plots`, `occurrence information` (in that order).

## Author(s)

Gerald Jurasinski

## See Also

[reshape](#), [data.frame](#)

## Examples

```
data(abis)
abis.spcls <- liste(abis.spec, splist=TRUE)
## see the list, it like what you get from a database
## and return to matrix-format:
abis.test <- mama(abis.spcls)
```

---

occ.time

*Track species occurrence*

---

## Description

Calculate the change in occurrence of species on plots in general or on specific plots. Allows for the tracking of temporal changes in species abundance throughout an area or the simple quantification and comparison of species occurrences between time steps.

## Usage

```
occ.time(x, y, times = NULL, adjust = TRUE, gen.occ = FALSE,
perc = TRUE, nc.acc = FALSE, ...)
```

```
occ.tmp(x, y, adjust=TRUE, gen.occ=FALSE, perc=TRUE,
nc.acc=FALSE, ...)
```

## Arguments

- |        |   |
|--------|---|
| x      | Species data in matrix or database-format representing species occurrence at time step one or throughout a time series. The latter means that you have a table with three columns where the columns represent plots, species and occurrence information (in this order!). These are typically exported from a database. When <code>times</code> are given and data represents more than one time steps it has to be in database format. Conversion is handled automatically - if three columns are in the table it is assumed to be in database format. When there are only three species give the data in database-format. If there are many plots and/or species, internal matrix conversion might be quite slow. |
| y      | Species data in matrix or database-format representing species occurrence at time step two. Obsolete when <code>times</code> are given. Otherwise the same as for <code>x</code> applies.   |
| times  | When there are more than two timesteps. A vector describing the timesteps which has to be coercible to a factor. If your data comes from a database and contains species records for different time-steps, just export the time information with the species data. If you have single matrices for each time step, you could reshape them to database format via <a href="#">liste</a> and concatenate these or calculate each time step alone.   |
| adjust | Do not change the default behaviour (TRUE) unless you know what you do. Would spare some calculation time if set to FALSE, when your species data do not need adjustment, which means that in both or all time steps, there are exactly the same species and the same plots. However in most cases it will be more convenient to rely on the function (see details).  |

<code>gen.occ</code>	Triggers if general occurrence is regarded or specific occurrence. The latter is default ( <code>gen.occ=FALSE</code> ) and it means that it is calculated on which exact plots a species is changing. When set to <code>TRUE</code> only general occurrence is regarded and it is calculated on how many plots a species occurs more or less then before. See details.
<code>perc</code>	If output shall be in percentage of species. Defaults to <code>TRUE</code> .
<code>nc.acc</code>	Per default, species which are not changing on a plot are counted as single species (also when they do not change on more than one plot). This can be changed when setting <code>nc.acc = TRUE</code> . Then each occurrence of species which has not changed is counted.
<code>...</code>	Further arguments to functions.

## Details

If you compare species data among time steps there will be most likely different numbers of species (and often also different numbers of plots for which information is available). The function takes care of this and you can give any species matrices you want. If one plot is the same, it will calculate what changed on this plot. There will be an error message if no plot is shared. The function relies on plot and species names!! As in a database - they must be unique!!

With the resulting named vector or table it is easy to draw a barplot tracking the changing occurrence of plants. Walter et al. (2005) used such plots to illuminate the changing (and increasing) occurrence of plant species on Alpine summits due to climate change.

However they only considered change in general occurrence. We added the possibility to track changes on the specific plots. If a species is occurring on 5 plots at time one and on 4 plots at time two one can't be shure that this species changed occurrence on only one plot. If it occurs partly on different plots then before it will contribute to loss and gain respectively in this function when `gen.occ` is set to `FALSE`.

## Value

Returns a named vector or a table (when multiple time steps are evaluated at once) with information on change in species occurrence. The names tell on how many plots a certain species has changed. The values tell how many species (or percent of species) exhibit this change. Additionally the number of matching plots and species for each comparison are given back.

Per default nice output is given. However, the table can be accessed for printing with `*$bac` (see Example for Details). A plotting method will be added in the near future.

## Author(s)

Gerald Jurasinski <terhorab@mac.com> <http://homepage.mac.com/terhorab/gerald/>

## References

Walther, G.-R., Beißner, S. & Burga, C. A. 2005. Trends in the upward shift of alpine plants. *Journal of Vegetation Science* **16**: 541-548.

## See Also

to calculate similarity based on plant species occurrence between time steps see [sim.tmp](#)

## Examples

```
## load included data
data(bernina)

## how species changed occurrence between first recording
## and last recording?
# construct a species matrix that only contains the species
# that occurred on the summits at the first recording
first <- veg[summits$year=="1907",]
first <- first[,colSums(first)>0]
# make right summit names
row.names(first) <- as.character(summits$summit[summits$year=="1907"])
# construct a species matrix that only contains the species
# that occurred on the summits at the last recording
last <- veg[summits$year=="2003",]
last <- last[,colSums(last)>0]
# make right summit names
row.names(last) <- as.character(summits$summit[summits$year=="2003"])
# see that dimensions of first and last differ
dim(first)
dim(last)
# calculate change in occurrence
changed.occurrence <- occ.tmp(first, last)
barplot(changed.occurrence$bac, main="percentage of species
that changed on ... plots")
# try the same but species are not given in percentages
changed.occurrence <- occ.tmp(first, last, perc=FALSE)
barplot(changed.occurrence$bac, main="number of species that
changed on ... plots")
# there is a lot of info in the output
changed.occurrence

## how species changed occurrence between recordings?
## data has to come in list format
occ.time(veg.lst, times=years)
```

## Description

The function is a wrapper for several functions related to the permuted correlation between matrices or vectors: It calls [permcorm2](#) to calculate permuted correlation between vectors and [permcorm](#) to calculate permuted correlation on strata. This can be useful to obtain data-points for a multivariate Mantel correlogram. Two matrices or vectors and a variable dividing these vectors into strata (levels) are to be specified. If the last is not given only permuted correlation between the two matrices ([dist](#)-objects) is done. If the second matrix/vector is a subsetting object the correlation can be done on the first object for each of the strata with [manccorm](#).



## Usage

```
pcol(x, y, z = NULL, method="pearson", permutations=1000,
solo=FALSE, ...)

permcors(x, y, subsetter, method="pearson", permutations=1000,
alpha=0.05, trace=FALSE, ...)

permcors2(x, y, method="pearson", permutations=1000, subset=NULL,
complete=TRUE, loop=FALSE, ...)

mancors(dis, classes, width=NULL, method="pearson", permutations=1000,
alpha=0.05, trace=FALSE, ...)

## S3 method for class 'permcors':
plot(x, y, ...)
```

## Arguments

x	Matrix (dist-object) or vector of numeric values (atomic) containing distances or similarities returned by <a href="#">sim</a> , <a href="#">vegdist</a> , <a href="#">dist</a> , <a href="#">dist.binary</a> or a similar matrix. Conversion is done automatically and triggered by <a href="#">is.vector</a> . If it is not a vector it is assumed to be a dist-object or a similar matrix (with <code>nrow==ncol</code> ). For the plotting method a <code>permcors</code> -object.
y	If <code>solo=FALSE</code> an object of the same qualities and dimensions (or length) as x to correlate to. See <a href="#">Details</a> for the case <code>solo=TRUE</code> . For the plotting method an optional object. Not needed here.
z	Vector or dist-object of a variable which defines the strata, or levels for which the permuted correlation shall be calculated. Doesn't have to be a factor but it has to be convertible into factor. see <a href="#">Details</a> for more.
subsetter	Vector of a variable which defines the strata, or levels for which the permuted correlation shall be calculated. Usually conversion from dist-object to vector is done in <code>pcol</code> . If <code>permcors</code> is run separately it has to be a vector (same holds for x, y, and z if the background functions are run separately). Doesn't have to be a factor but it has to be convertible into factor. see <a href="#">Details</a> for more.
method	Method of correlation, as it is done by <a href="#">cor.test</a> , see help there for details. Defaults to Pearson correlation coefficients. Other options are Kendall and Spearman rank correlations.
permutations	number of permutations, defaults to 1000 to get a significance level of $p = 0.001$ .
solo	If TRUE y is assumed to be a subsetting matrix, dist-object or vector giving strata to correlate x with and calculate the data-points for a Multivariate Mantel Correlogram for one distance-matrix.
width	If <code>solo=TRUE</code> the subsetting object is assumed to contain classes already. If width is specified (defaults to NULL), the classes are defined inside the function and width gives the class width.
trace	Set to TRUE to follow the runs of the for-loops in functions <code>permcors</code> and <code>mancors</code> . See <a href="#">details</a> for when it is appropriate to set via <code>pcol</code> .
complete	Should only complete cases be considered? Defaults to TRUE.
alpha	The initial alpha-level against which should be tested. Depending on sub-function it is internally changed via Bonferroni-correction if necessary.

subset	If Case is 1 (see details) a subset of cases from <code>x</code> and <code>y</code> can be defined for correlation.
loop	Triggers the method for permutation inside the function. Shall it be looped (for-loop, <code>loop = TRUE</code> ) or be done by an <code>apply</code> method ( <code>loop = FALSE</code> )? Determines speed. For the most, reasonably huge data sets, the latter will be better.
dis	Same as <code>x</code> for <code>mancor</code> .
classes	If <code>mancor</code> shall be run, second item is a vector or <code>dist</code> -objekt of a variable which defines the strata, or levels for which the permuted correlation shall be calculated. Doesn't have to be a factor but it has to be convertible into factor. see Details for more.
permc	(In <code>plot.permcor</code> ) an object returned by <code>permc2</code> is easily plotted with <code>plot.permcor</code> . The actual correlation value is plotted against an histogram of the distribution of the permuted values.
...	Arguments to other functions, for instance to <code>cor.test</code> regarding specifications of the test, however only the correlation value is taken from this function. but here you could change from pearson to kendall for instance.

## Details

`pcol` is a wrapper for the other functions. Depending on the input and the setting of `solo` the following functions are invoked (They can also be run separately. In this case `x`, `y`, and `z` must be given as vectors).

1. If `x` and `y` are `dist`-objects, or vectors containing distance or similarity values and everything else is set to defaults a simple permuted correlation with `permc2` is run. This corresponds to a Mantel test. The two data-objects are correlated with `cor.test`, then the `y` is permuted and with `cor` the correlation is calculated again and written to a vector. This is repeated `permutation` times. Finally, the initial correlation value is compared to the permuted values. The number of times, the permuted values exceed the initial value is divided by the number of permutations to obtain a significance value. Thus, with 1000 permutations a minimum `p` of 0.001 can be tested.
2. If a `subsetter` is given in `z`, the permuted correlation is done for every stratum or level given by the subsetting object - this could e.g. be direction or distance classes flagging which plots share a similar distance and therefore fall into the same class. The resulting data-points can be used to plot a correlogram which allows for the analysis of non-stationarity in the relationships between `x` and `y`.
3. If `y` is itself a subsetting object (distance classes or so) you have to set `solo=TRUE`. Then the matrix or vector in `x` is correlated against this classes. This is handled by `mancor`. The parameter `width` allows for the calculation of classes inside the function. If for instance a distance-matrix with geographical distances is given, `width` specifies the width of the distance classes, they are computed and used to correlate the data in `x` against. This produces the data-points for a multivariate Mantel correlogram in the sense of Oden & Sokal (1986) (see also Legendre & Legendre 1998 for a comprehensive coverage of the subject).

## Value

Returns different objects, depending on given arguments and triggers.

- case 1            a `permc`-object with the following items is returned:
- call The call to the function.

- `method` The correlation method as used by `cor.test`.
- `statistic` The initial correlation value which is tested against the permuted values.
- `signif` The significance of the calculation.
- `n` The number of cases.
- `permutations` The number of permutations as specified by `permutations`.
- `perms` The result of the permuted runs. It is not printed by default but can be accessed via `result$perms`. The correlation value can be plotted against an histogram of the distribution of the permuted values to visualize the significance with the default plotting method.

`case 2` a `pclist`-object with the following items (in this case it might be nice to set `trace=TRUE` to display the progress of the calculation) is returned:

- `call` The call to the function.
- `method` The correlation method as used by `cor.test`.
- `gesN` The total number of cases.
- `strata` The number of strata (or levels) for which permutation has been done.
- `permutations` The number of permutations as specified by `permutations`.
- `out` A `data.frame` with 3 columns containing the result for each stratum in the rows: `statistic` contains the correlation values for the corresponding stratum, `sig` the obtained significance, and `nop` the number of cases found and used for permutation on this very level.

`case 3` a `pclist`-object with the same items as in Case 2 (in this case it might be as well interesting to set `trace=TRUE` to display the progress of the calculation) is returned.

### Note

Depending on the background-function and the size of the matrices or vectors it may take a while to calculate. The slowest is `mancor` (case 3).

### Author(s)

Gerald Jurasinski

### References

- Legendre, P. & Legendre, L. (1998) *Numerical Ecology*. 2nd English Edition. Elsevier.
- Oden, N. L. & Sokal, R. R. (1986) Directional Autocorrelation: An Extension of Spatial Correlograms to Two Dimensions. *Systematic Zoology* **35**: 608-617.

### See Also

`mantel` for a different implementation of Mantel tests, `cor.test`

### Examples

```
data(abis)

## calculate soerensen of species data
abis.soer <- sim(abis.spec)
```

```
## calculate distance (Euclidean) regarding some disturbance
## variables (feces counts)
abis.pert <- dist(abis.env[,19:25])
## are compositional similarity and dissimilarity of disturbance related?
pcol(abis.soer, abis.pert)
## the relationship is significant, but not very strong
```

---

plot.mrpp

*plot an mrpp-object*


---

## Description

There is no mrpp plotting function in the vegan package. For convenience it is provided here.

## Usage

```
## S3 method for class 'mrpp':
plot(x, y, ...)
```

## Arguments

x	a mrpp-object as computed with <a href="#">mrpp</a>
y	Optional plotting object, not needed here.
...	Arguments to the plotting function

## Value

Returns a histogram with the distribution of the permutation values plotted against delta: For explanations see [mrpp](#)

## Author(s)

Gerald Jurasinski

## See Also

[mrpp](#), [anosim](#)

rin

*Calculate multiple plot resemblance measures***Description**

The functions calculate several multiple plot similarity measures. In addition `rin` provides a wrapper that allows for the easy calculation of multiple plot (site) resemblance measures in neighborhoods in an automated fashion including testing whether the found resemblance patterns are significantly different from random.

**Usage**

```
mpd(x, method="simpson", all=FALSE)

mps(x, method="whittaker", all=FALSE)

mps.ave(x, method="soerensen", all=FALSE, foc=NULL, what="mean", ...)

mps.f(x, foc, d.inc=FALSE, preso=FALSE)

sos(x, method="mean", foc=NULL, normal.sp=TRUE, normal.pl=TRUE)

rin(veg, coord, dn, func, test = TRUE, permutations = 100, permute = 2, sfno = 1)
```

**Arguments**

<code>x</code>	Species composition data, a matrix-like object.
<code>method</code>	Method for the calculation of multiple plot resemblance. The possible choices depend on the function used and include (among others) Simpson based multiple plot dissimilarity, Sørensen based multiple plot dissimilarity, Nestedness based multiple plot dissimilarity, Whittaker's beta, additive partitioning, Harrison multiple plot similarity, Harrison multiple plot turnover, Williams multiple plot turnover, average pairwise similarity (with a similarity measure of your choice from <a href="#">sim</a> ), Diserud & Ødegaard multiple plot similarity. The methods of <code>mps.f</code> (a new group of multiple plot similarity measures) evolve from setting the arguments accordingly. For <code>sos</code> the choice is <code>mean</code> or <code>foc</code> . See details.
<code>all</code>	Logical. Depending on the function this argument has a different meaning. In <code>mps</code> and <code>mpd</code> it sets whether the results of all possible methods shall be given in the result, or only the method given in the <code>method</code> argument. Because some of the measures are just derived from others all methods are always calculated within the function when it is called and the <code>method</code> argument just triggers which to give back. In <code>mps.ave</code> it sets whether all statistics calculated ( <a href="#">mean</a> and <a href="#">sd</a> ) shall be given back or only the one specified by the <code>what</code> argument.
<code>foc</code>	Character vector with length one or an integer specifying which one is the focal plot. Three of the functions are/can be sensitive to the species composition in the focal plot ( <code>mps.f</code> , <code>mps.ave</code> , <code>sos</code> ). The automation function <code>rin</code> is able to automatically derive the identity of the focal plot. Just set <code>foc = foc</code> in the <code>func</code> argument (see example). When <code>mps.ave</code> or <code>mps.f</code> are used stand alone either the name of the plot in parenthesis or the index of the plot within the species matrix ( <code>x</code> ) has to be given.

what	For <code>mps.ave</code> , which statistic (mean or sd) should be given back? See details.
d.inc	Logical. Shall all species that are within <code>veg</code> but not within the plots that make up a neighborhood be regarded when computing <code>mps.f</code> . This setting dramatically changes the behaviour of <code>mps.f</code> because it then becomes a symmetric similarity coefficient. Defaults to <code>FALSE</code> so that an asymmetric multiple plot similarity coefficient is computed. Only makes sense when <code>mps.f</code> is applied within <code>rin</code> and changes nothing otherwise.
preso	Logical. Shall a presence only version of <code>mps.f</code> be computed? Default is <code>FALSE</code> . See details.
normal.sp	In case of <code>sos</code> (sum of squares of species matrix, which is a measure of beta-diversity (Legendre et al. 2005)): Shall the result be normalized with respect to the number of species.
normal.pl	In case of <code>sos</code> (sum of squares of species matrix, which is a measure of beta-diversity (Legendre et al. 2005)): Shall the result be normalized with respect to the number of plots.
veg	Species composition data, a matrix-like object that is ought to be recorded in a regular array or a similar structure and that shall be divided into neighborhoods with a moving window so that each plot becomes the focal plot with a certain neighborhood of plots around for which the multiple plot resemblance measures are then calculated.
coord	Spatial coordinates of the field plots where the data in <code>veg</code> comes from. The function expects a <code>data.frame</code> with two columns with the first column giving the x (easting) coordinate and the second giving the y (northing) coordinate in UTM or the like. These coordinates are used to calculate the neighborhoods within a moving window approach.
dn	Distance to neighbors or neighbor definition. A positive numeric or a two value vector (also positive numeric). In the first case it gives the distance from each sampling unit in m until which other sampling units should be seen as neighbours. In the second the two values define a ring around each plot. Plots that fall into the ring are considered as neighbors. See details.
func	A character string that defines the formula which shall be applied to calculate a multiple plot resemblance measure for all possible neighborhoods within an array. For instance <code>"mpd(x)"</code> to compute the Simpson multiple plot dissimilarity coefficient sensu Baselga (2010). See details.
test	Logical. Shall the significance of the calculated values of multiple plot resemblance be tested regarding its deviation from random expectations. Defaults to <code>TRUE</code> . See details.
permutations	The number of permutations run for testing the significance. Defaults to 100. And it is already slow. So test before you give much higher number of runs here.
permute	When testing with <code>rin</code> , how should the permutation of species to reflect random expectations be done: An integer of either 1, 2, or 3. With 1 the species matrix ( <code>veg</code> ) is permuted across rows. With 2 the species matrix ( <code>veg</code> ) is permuted across columns. With 3 the species in the focal plot are permuted (They are randomly drawn from the species pool).
sfno	Species from neighborhood only? Logical, that is only be set in combination with <code>permute = 3</code> . If <code>TRUE</code> , than the species are only drawn at random from the neighborhood species sub matrix. If set to <code>FALSE</code> , the species are drawn at random from the whole species matrix <code>veg</code> .

<code>p.level</code>	Significance level below which the resemblance patterns shall be considered as significantly different from random expectations. Defaults to 0.05. Enables to give asteriks and stars in the results.
<code>...</code>	Further arguments to the workhorse functions <code>mpd</code> , <code>mps</code> , <code>mps.ave</code> , <code>mps.f</code> can be passed via <code>...</code>

## Details

Several multiple plot similarity indices have been presented that cure some of the problems associated with the approaches for the calculation of compositional similarity for groups of plots by averaging pairwise similarities (Diserud and Ødegaard 2007, Baselga 2010). These indices calculate the similarity between more than two plots whilst considering the species composition on all compared plots. The resulting similarity value is true for the whole group of plots considered (called neighborhood in the following). Further, there are multiple plot similarity coefficients that are determined by the species composition on a reference plot (named focal plot in the following). All of these, can be calculated with the functions described in this help file. See vignette for an overview table. Further, the function `rin` takes all of them and provides a framework for applying the measures to an array of plots to calculate multiple plot resemblance in neighborhoods (Jurasinski et al. submitted).

`mps` stands for **m**ultiple **p**lot **s**imilarity, whereas `mpd` stands for **m**ultiple **p**lot **d**issimilarity; the letters behind the `.` further specify the class of measures that can be calculated with the respective function.

`mps.ave` calculates **average** multiple plot (dis-)similarities from pairwise (dis-)similarity calculations between the plots in the dataset or in the specified neighborhood. It has several options. With setting the `foc` argument different from `NULL`, only the pairwise (dis-)similarities between the specified focal plot and all others in the dataset (neighborhood) are taken to calculate the `mean` and `sd` from. When the specified focal plot is not existing, the function will issue a warning and stop. When run with defaults (`foc = NULL`), all pairwise similarities between the plots in the neighborhood (dataset) are considered. Any resemblance measure available via `sim` or `sim.yo` can be taken as base for calculating the average (dis-)similarity and its spread.

`mps` calculates **m**ultiple **p**lot (dis-)similarities that are either derived from other approaches to beta-diversity calculation (Whittaker's beta, additive partitioning), or have been around for quite a while (Harrison multiple plot dissimilarity, Harrison multiple plot turnover, Williams multiple plot turnover). None of these considers the actual species composition on each of the compared plots. The following methods are available ( $n$  = number of plots,  $S$  = number of species,  $\gamma$  = *gammadiversity*( $S_n$ ),  $\alpha$  = *alphadiversity*( $S_i$ )):

<code>whittaker</code>	Calculates Whittaker's beta (multiplicative partitioning, Whittaker 1960) $\beta = \gamma / \text{mean}(\alpha)$ .
<code>inverse.whittaker</code>	Inverse Whittaker's beta (multiplicative partitioning). Scales between $1/n$ (when the considered
<code>additive</code>	Additive partitioning. Following Lande (1996) and keeping it with $\alpha$ = species number, the ac
<code>harrison</code>	Harrison (1992) multiple plot dissimilarity. A transformation of Whittaker's beta to be bounde
<code>diserud</code>	Diserud & Ødegaard (2007) derived this from the pairwise Sørensen similarity measure. How
<code>harrison.turnover</code>	$\frac{\frac{\gamma}{\text{max}(\alpha)} - 1}{n-1}$ (Harrison et al. 1992)
<code>williams</code>	$1 - \frac{\text{max}(\alpha)}{\gamma}$ (Williams 1996)

`mpd` calculates **m**ultiple **p**lot **d**issimilarity indices that have been suggested by Baselga (2010). The following methods are available (The implementation differs slightly from the one offered by Baselga in the electronic appendix of his paper and is computationally more efficient):

<code>simpson</code>	<code>mps.Sim</code> in the following. Baselga et al. (2007) derive this multiple plot dissimilarity coefficient directly
----------------------	---

sorensen      mps.Sor in the following. By building multiple site equivalents of the matching components (a, b, c) Bas  
 nestedness      mps.nes in the following. Because the Sørensen based multiple plot dissimilarity coefficient accounts for

mps.f calculates **focal multiple plot similarities**. In contrast to the other functions the different outcomes can be triggered by setting the further arguments accordingly.

The indices of mps.f are the only ones whose value changes depending on the vegetation composition of the focal plot. It is therefore true and valid only for the comparison of the focal plot with the surrounding plots. Not the similarity in the neighborhood, but the similarity of the focal plot to all others in the neighborhood is calculated. The calculation is based on the occurrences and non-occurrences of species on the compared plots with the species composition on the focal plot determining which of the two is to be used for which species: For all species that occur on the focal plot the proportional frequencies of occurrence in the neighborhood are summed up. For species that do not occur on the focal plot the proportional frequencies of non-occurrence in the neighborhood are summed up.

$$\sum_{i=1}^{s_o} f_{oi} + \sum_{i=1}^{s_n} f_{ni}$$

with  $f_{oi}$  = proportional frequency of occurrences of the  $i$ th species on the compared plots, only carried out for species that do occur on the focal plot,  $f_{nj}$  = frequency of non-occurrences of the  $j$ th species on the compared plots, only carried out for species that do not occur on the focal plot). The frequencies are calculated against the total numbers of cells in the species matrix and are therefore 'proportional frequencies' (in analogy to 'proportional abundances' as in diversity indices like Shannon or Simpson). Thus, if all compared plots have an identical species composition, the resulting value of the multi-plot similarity coefficient is 1. In this rather hypothetical case the species presence absence matrix would be filled with ones only. This is the null model against which the 'proportional frequencies' are calculated. Therefore, the coefficient can be interpreted as a measure of deviation from complete uniformity. There are three versions.

preso=TRUE      In this case a presence only version is calculated (mps.fpo). Therefore the second term is skipped and  
 d.inc=FALSE      When the d.inc argument is set to FALSE, only the species in the neighborhood build the basis again

When run with defaults (preso = FALSE) and (d.inc = TRUE), a **symmetric focal multiple plot similarity** (mps.fs) index results. It is definitely meant for use in the context of rin. The 'proportional frequencies' are calculated against the whole species matrix. Thus, the index is a symmetric similarity coefficient sensu Legendre & Legendre 1998 that considers species that do not occur on the compared plots but in the whole data set. Therefore, it is more appropriate for biodiversity or conservation studies and not so much for the investigation of ecological relationships. However, it can be interpreted as an 'ordination on the spot': By calculating mps.fs for a focal plot against its surrounding plots its position along the main gradient according to its species composition is estimated immediately because the species composition in the rest of the data set is incorporated in the construction of the proportional frequencies of the species. Because of this, mps.fs can be interpreted as a measure of deviation from complete unity in species composition. When the neighborhood is increased to the full data set, mps.f and mps.fs converge.

sos calculates the **sum of squares** of a species matrix. Legendre et al. (2005) show, that this is a measure of beta-diversity. However, when you don't normalize against the number of species and/or plots the obtained values can hardly be compared across data sets (or neighborhoods). Therefore, its advisable to run this with defaults (normal.sp = TRUE and normal.pl = TRUE). For experiments, method can be set to "foc". Then, not the deviation from the mean of the species



occurrence across plots builds the basis, but the deviation from the situation on a focal plot. This makes it somewhat related to the `mps.f`-stuff.

`rin` applies the other functions to an array of plots. For each plot a neighborhood is constructed via the `dn` argument and the specified index is calculated for all plots and neighborhoods. The function to be calculated is specified simply by the `func` argument. For instance, with `func = "mpd(x, method='sorensen')"` the function `rin` calculates the Sørensen multiple plot dissimilarity for each plot and its neighborhood in an array. The functions that need the identity of a focal plot (`mps.ave` and `mps.f`) automatically derive the focal plots. However, to trigger this it has to be specified within the `func` argument: `func = "mps.f(x, foc = foc)"`.

## Value

The functions `mpd`, `mps`, `mps.ave`, `mps.f` return a single value with the calculated index (according to the `method` argument, or to the other arguments). When `all` is set to `TRUE`, `mps.ave` returns two values (the average and the standard deviation of the pairwise similarities in the neighborhood), whereas `mpd` and `mps` return a named numerical vector with the values for all indices that can be calculated with the respective function.

`rin` gives back a table (`data.frames`), that reports several values for each plot in the dataset per row. The first three columns are always returned. In case `test = TRUE`, three more columns with information on the significance test are returned.

<code>n.plots</code>	Number of plots that make up the neighborhood.
<code>n.spec</code>	Number of species that occur in the neighborhood.
<code>dis</code>	Value of the calculated (dis)similarity index per plot.
<code>p.val</code>	p value of the permutation test. According to the <code>permute</code> argument the data set is shuffled. The random data is subjected to the same calculations <code>permutations</code> times. The original value of multiple plot similarity is compared to the distribution of random values to obtain this p.
<code>sig</code>	Significance flag. Just a translation of the p value into a significance flag. There are only two possibilities: "*" value is significantly different from random, "ns" value is not significantly different from random.
<code>sig.sign</code>	The sign of the significance value. The tail which is tested is determined by the relation of the multiple plot similarity value to the average multiple plot similarity value of the random test distribution. Thus, the sign shows whether the multiple plot similarity is significantly higher than can be expected from random expectations (+) of lower (-).

## Note

`rin` is not optimized and could perhaps profit from some C code. So when `test = TRUE` it takes a while because of the permutations.

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### See Also

[sim](#), [vegdist](#), [dsvdis](#) for pairwise similarity measures.

### Examples

```
## Not run:
# load the data that comes with the package
data(abis)

# calculate a multiple plot similarity index
# (Sørensen sensu Baselga) for whole dataset
mpd(abis.spec, method="sorensen")

# calculate a multiple plot similarity index
# (Sørensen sensu Baselga) for each plot and
# its neighborhood
abis.mpd.so <- rin(abis.spec, coord=abis.env[,1:2],
dn=100, func="mpd(x, method='sorensen')")

# plot the grid of plots and show the calculated
# multiple plot dissimilarity value through the
# size of the symbol and the sign of the value
# with a superimposed "+" or "-"
with(abis.mpd.so, {
plot(abis.env[,1:2], cex=symbol.size(dis), pch=c(21,1)[sig], bg="grey50", xlab="", ylab="")
subs <- sig == "*"
points(abis.env[subs,1:2], pch=c("-", "+")[sig.prefix[subs]])
})

# calculate a multiple plot similarity index
# that takes care of the species composition
# on the focal plot
rin(abis.spec, coord=abis.env[,1:2], test=FALSE,
dn=100, func="mps.f(x, foc=foc)")

## End(Not run)
```

sim

*Calculate similarities for binary vegetation data*

## Description

One of 56 (dis)similarity measures for binary data can be set to calculate (dis)similarities. The vegetational data can be in either database (list) or matrix format. Same holds for the output. Simultaneous calculation of geographical distances between plots and the virtual position of the calculated similarity values between the parental units can be achieved if a `data.frame` with coordinates is given.

## Usage

```
sim(x, coord=NULL, method = "soer", dn=NULL, normalize = FALSE,
    listin = FALSE, listout = FALSE, ...)
```

## Arguments

- |        |   |
|--------|---|
| x      | Vegetation data, either as matrix with rows = plots and columns = species (similarities are calculated between rows!), or as <code>data.frame</code> with first three columns representing plots, species and occurrence information respectively. All further columns are dumped before calculation. Occurrence is only considered as binary. If your list or matrix contains abundances or frequencies they are transformed automatically.  |
| coord  | A <code>data.frame</code> with two columns containing the coordinate values of the sampling units. If given, it triggers the simultaneous calculation of the geographical distances between the sampling units, the coordinates of virtual centre-points between all possible pairs of plots, and the geographical distances in either x- or y-direction. If <code>coord</code> is given, output is always in database format (no matrix).  |
| method | Binary Similarity index (see Details for references and formulae), partial match to "soerensen", "jaccard", "ochiai", "mountford", "whittaker", "lande", "wilsonshmid", "cocogaston", "magurran", "harrison", "cody", "williams", "williams2", "harte", "simpson", "lennon", "weiher", "ruggiero", "lennon2", "rout1ledge", "rout2ledge", "rout3ledge", "sokal1", "dice", "kulczlinsky", "kulcz2insky", "mcconnagh", "manhattan", "simplematching", "margaleff", "pearson", "roger", "baroni", "dennis", "fossum", "gower", "legendre", "sokal2", "sokal3", "sokal4", "stiles", "yule", "michael", "hamann", "forbes", "chisquare", "peirce", "eyraud", "simpson2", "legendre2", "fager", "maarel", "lamont", "johnson", "sorgenfrei", "johnson2". See details. |
| dn     | Neighbor definition. A geographic distance represented by a numeric or a two value vector defining a ring around each plot. Only takes effect when <code>coord != NULL</code> . If specified, the output does only contain similarities between neighboring plots. A plot is a neighbour to any given plot if it is within the range of the neighbor definition. See details.   |

<code>normalize</code>	Logical value indicating whether the values for <code>a</code> , <code>b</code> and <code>c</code> which are calculated in the process should be normalized to 100% (per row, which means per plot comparison). If <code>normalize = TRUE</code> an asymmetric index must be chosen (see details).
<code>listin</code>	if <code>x</code> is given in database (list) format this must be set to <code>TRUE</code> (there is no automatic detection of the format)
<code>listout</code>	If output is wanted in database format rather than as a <code>dist</code> -object set this to <code>TRUE</code> . Output is automatically given in database-format, when <code>coord</code> is specified.
<code>...</code>	Arguments to other functions

## Details

All binary similarity indices are based on the variables `a`, `b` and `c` (or can be expressed as such). Some of them also use `d`. Where `a` is the number of species shared by two compared plots, `b` is the number of species found only in one of the compared plots, and `c` is the number of species only found in the other of the compared plots. `d` refers to species which are absent from both the compared plots but present in the whole dataset. Indices incorporating `d` are discussed critically by Legendre & Legendre (1998) and elsewhere. They are called symmetric and expose a "double zero" problem as they take species into account which are absent from both compared units. Absence of species from a sampling site might be due to various factors, it does not necessarily reflect differences in the environment. Hence, it is preferable to avoid drawing ecological conclusions from the absence of species at two sites (Legendre & Legendre 1998). The indices presented here come from various sources as indicated. Comparative reviews can be found in e.g. Huhta (1979), Wolda (1981), Janson & Vegelius (1981), Shi (1993), Koleff et al. (2003), Albatineh (2006)

The indices considerably differ in their behaviour. For classification purposes and in ecology, Jaccard and Sørensen have been found to give robust and meaningful results (e.g. Janson & Vegelius 1981, Shi 1993). For other purposes other indices might be better suited. However, you are invited to use (at least with the asymmetric indices) ternary plots as suggested by Koleff et al. 2003. The matching components `a`, `b`, and `c` can be displayed in a `ternary.plot` to evaluate the position of the plots in similarity space. When output is in database-format, the matching components are always given and `triax.plot` can be used to plot them into a triangle-plot. Koleff et al. (2003) used an artificial set of matching components including all possibilities of values that `a`, `b`, and `c` can take from 0 to 100 to display the mathematical behavior of indices. An artificial data-set with this properties - together with the values for the asymmetric indices included here - is part of this package (`ads.ternaries`) and can be used to study the behavior of the indices prior to analysis. See details and examples there.

If `coord` is given, the geographic distances between plots/sampling units are calculated automatically, which may be of value when the display or further analyses of distance decay (sensu Tobler 1970, Nekola & White 1999) is in focus. For convenience the `dn-trigger` can be used to tell the function to only return similarities calculated between neighboring plots. Similarities between neighboring plots in an equidistant array are not subjected to the problem of auto-correlation because all plots share the same distance (Jurasinski & Beierkuhnlein 2006). Therefore, any variation occurring in the data are most likely caused by environmental differences alone.

In the following formulae...

`a` = number of shared species

`b` = number of species only found on one of the compared units

`c` = number of species only found on the other of the compared units

`d` = number of species not found on the compared plots but in the dataset

$$N = a + b + c + d$$

with  $(n_1 \leq n_2)$ ...

$n_1$  = number of species of the plot with fewer species  $(a + b)$  or  $(a + c)$

$n_2$  = number of species of the plot with more species  $(a + b)$  or  $(a + c)$

Computable asymmetric indices:

soerensen	$sim = \frac{2a}{2a+b+c}$	Soerensen (1948)
jaccard	$sim = \frac{a}{a+b+c}$	Jaccard (1912)
ochiai	$sim = \frac{a}{\sqrt{(a+b)(a+c)}}$	Ochiai (1957), Shi (1993)
mountford	$sim = \frac{2a}{(a(b+c)+2bc)}$	Mountford (1962), Shi (1993)
whittaker	$sim = \frac{a+b+c}{2a+b+c} - 1$	Whittaker (1960), Magurran (1988)
lande	$sim = \frac{b+c}{2}$	Lande (1996)
wilsonshmida	$sim = \frac{b+c}{2a+b+c}$	Wilson & Shmida (1984)
cocogaston	$sim = \frac{b+c}{a+b+c}$	Colwell & Coddington (1948), Gaston et al. (2001)
magurran	$sim = (2a + b + c)(1 - \frac{a}{a+b+c})$	Magurran (1988)
harrison	$sim = \frac{\min(b,c)}{\max(b,c)+a}$	Harrison et al. (1992), Koleff et al. (2003)
cody	$sim = 1 - \frac{a(2a+b+c)}{2(a+b)(a+c)}$	Cody (1993)
williams	$sim = \frac{\min(b,c)}{a+b+c}$	Williams (1996), Koleff et al. (2003)
williams2	$\frac{(bc)+1}{(a+b+c)^2 - (a+b+c)}$	Williams (1996), Koleff et al. (2003)
harte	$1 - \frac{2a}{2a+b+c}$	Harte & Kinzig (1997), Koleff et al. (2003)
simpson	$\frac{\min(b,c)}{\min(b,c)+a}$	Simpson (1949), Koleff et al. (2003)
lennon	$\frac{2 b-c }{2a+b+c}$	Lennon et al. (2001), Koleff et al. (2003)
weiher	$sim = b + c$	Weiher & Boylen (1994)
ruggiero	$sim = \frac{a}{a+c}$	Ruggiero et al. (1998), Koleff et al. (2003)
lennon2	$sim = 1 - \left[ \frac{\log\left(\frac{2a+b+c}{a+b+c}\right)}{\log 2} \right]$	Lennon et al. (2001), Koleff et al. (2003)
rout1ledge	$sim = \frac{(a+b+c)^2}{(a+b+c)^2 - 2bc} - 1$	Routledge (1977), Magurran (1988)
rout2ledge	<i>toolong, see below</i>	Routledge (1977), Wilson & Shmida (1984)
rout3ledge	$sim = e^{rout2ledge} - 1$	Routledge (1977)
sokal1	$sim = \frac{a}{a+2(b+c)}$	Sokal & Sneath (1963)
dice	$sim = \frac{a}{\min((b+a), (c+a))}$	Association index of Dice (1945), Wolda (1981)
kulczlinsky	$sim = \frac{a}{b+c}$	Oosting (1956), Southwood (1978)
kulcz2insky	$sim = \frac{\frac{a}{2}(2a+b+c)}{(a+b)(a+c)}$	Oosting (1956), Southwood (1978)
mcconnagh	$sim = \frac{a^2 - bc}{(a+b)(a+c)}$	Hubalek (1982)
simpson2	$sim = \frac{a}{a+b}$	Simpson (1960), Shi (1993)
legendre2	$sim = \frac{3a}{3a+b+c}$	Legendre & Legendre (1998)
fager	$sim = \frac{a}{\sqrt{n_1 n_2}} - \frac{1}{2\sqrt{n_2}}$	Fager (1957), Shi (1993)
maarel	$sim = \frac{2a - (b+c)}{2a+b+c}$	van der Maarel (1969)
lamont	$sim = \frac{a}{2a+b+c}$	Lamont and Grant (1979)
johnson	$sim = \frac{a}{2b}$	Johnson (1971)
sorgenfrei	$sim = \frac{a^2}{(a+b)(a+c)}$	Sorgenfrei (1959)
johnson2	$sim = \frac{a}{a+b} + \frac{a}{a+c}$	Johnson (1967)

Computable symmetric indices (including unshared species):

manhattan	$sim = \frac{b+c}{a+b+c+d}$	Mean Manhattan, Legendre & Legendre (1998)
-----------	-----------------------------	--

simplermatching	$sim = \frac{a+d}{a+b+c+d}$	Sokal & Michener 1958
margaleff	$sim = \frac{a(a+b+c+d)}{(a+b)(a+c)}$	Clifford & Stevenson (1975)
pearson	$sim = \frac{ad-bc}{\sqrt{(a+b)(a+c)(d+b)(d+c)}}$	Phi of Pearson, Gower & Legendre (1986), Yule (1912)
roger	$sim = \frac{a+d}{a+2(b+c)+d}$	Rogers & Tanimoto (1960), Gower & Legendre (1986)
baroni	$sim = \frac{\sqrt{ad+a}}{\sqrt{ad+a+b+c}}$	Baroni-Urbani & Buser (1976), Wolda (1981)
dennis	$sim = \frac{ad-bc}{\sqrt{(a+b+c+d)(a+b)(a+c)}}$	Holliday et al. (2002), Ellis et al. (1993)
fossum	$sim = \frac{(a+b+c+d)(-\frac{a}{2})^2}{(a+b)(a+c)}$	Holliday et al. (2002), Ellis et al. (1993)
gower	$sim = \frac{a-(b+c)+d}{a+b+c+d}$	Gower & Legendre (1986)
legendre	$sim = \frac{a}{a+b+c+d}$	Gower & Legendre (1986), Russell/Rao in Ellis et al. (1993)
sokal2	$sim = \frac{ad}{\sqrt{(a+b)(a+c)(d+b)(d+c)}}$	Sokal & Sneath (1963)
sokal3	$sim = \frac{2a+2d}{(a+d)+(a+b+c+d)}$	Sokal & Sneath (1963)
sokal4	$sim = \frac{a+d}{b+c}$	Sokal & Sneath (1963)
stiles	$sim = \log \frac{(a+b+c+d)( ad-bc  - \frac{a+b+c+d}{2})^2}{(a+b)(a+c)(b+d)(c+d)}$	Stiles (1946)
yule	$sim = \frac{ad-bc}{ad+bc}$	Yule & Kendall (1973)
michael	$sim = \frac{4(ad-bc)}{(a+d)^2 + (b+c)^2}$	Michael (1920), Shi (1993)
hamann	$sim = \frac{(a+d)-(b+c)}{(a+d)^2 + (b+c)^2}$	Hamann (1961)
forbes	$sim = \frac{(aN-2n_2)}{(Nn_1-2n_2)}$	Forbes (1925), Shi (1993)
chisquare	$sim = \frac{(a+b+c+d)(ad-bc)^2}{(a+b)(a+c)(b+d)(c+d)}$	Yule & Kendall (1950)
peirce	$sim = \frac{(ad-bc)}{(a+c)(b+d)}$	Peirce (1884)
eyraud	$sim = \frac{a-(a+b)(a+c)}{(a+b)(a+c)(b+d)(c+d)}$	Eyraud (1936) in Shi (1993)
euclidean	$sim = \frac{\sqrt{b+c}}{a+b+c+d}$	Mean Euclidean in Ellis et al. (1993)
divergence	$sim = \frac{\sqrt{b+c}}{\sqrt{a+b+c+d}}$	Ellis et al. (1993)

rou2ledge formula (Routledge, 1977; Koleff et al. 2003):

$$\beta_{R2} = \log(2a+b+c) - \left( \frac{1}{2a+b+c} 2a \log 2 \right) - \left( \frac{1}{2a+b+c} ((a+b) \log(a+b) + (a+c) \log(a+c)) \right)$$

## Value

If listout = FALSE a distance matrix of class `dist` is returned. If listout = TRUE, a `data.frame` is returned with 7 columns giving the names of the compared plots in the first two and the calculated similarity measure in the third column. The rest of the columns give the values for `a`, `b`, `c`, and `d` (in this order). Naming of the first three columns can be changed but defaults to NBX (one of the compared plots), NBY (the other one), used index (the values of the calculated index). If `coord != NULL`, the following columns are given in addition and the columns `a:d` shift to the end of the `data.frame`.

distance	Geographical distance between compared plots
X	For plotting purposes, the x-coordinate of the virtual position of the calculated similarity value in the center between the two compared plots
Y	For plotting purposes, the y-coordinate of the virtual position of the calculated similarity value in the center between the two compared plots
xdist	Geographical distance between compared plots, on the x-axis only
ydist	Geographical distance between compared plots, on the y-axis only

## Note

In general, concepts of data-handling are taken from [vegdist](#) and the calculation of a, b, c and d is taken from [dist.binary](#). Thanks to Jari Oksanen for his [vegan](#) package. The indices were collected from the literature and are applicable in different fields of research.

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## See Also

[vegdist](#), [dist.binary](#), [dsvdis](#), [dist](#)

## Examples

```
data(abis)
##calculate jaccard similarity and output as dist-object
jacc.dist <- sim(abis.spec, method="jaccard")

##calculate Whittaker similarity (with prior normalisation) and
##output as data.frame
whitt.list <- sim(abis.spec, method="whittaker", normalize=TRUE,
listout=TRUE)

##calculate similarity from a database list after Harte & Kinzig (1997)
##and output as dist-object
abis.spec.ls <- liste(abis.spec, splist=TRUE)
hart.dist <- sim(abis.spec.ls, method="harte", listin=TRUE)

## calculate the geographic distances between sites simultaneously
## and return only similarities calculated between neighboring plots
abis.soer <- sim(abis.spec, coord=abis.env[,1:2], dn=100)

## in an equidistant array
## you can plot this nice between the original positions of the
## sites (with the size of the dots expressing number of species
## for the sites, and value of the Sørensen coefficient in between)
require(geoR)
```

```
points.geodata(coord=abis.env[,1:2], data=abis.env$spec,
  cex.min=1, cex.max=5)
points.geodata(coord=abis.soer[,5:6], data=abis.soer$soerensen,
  cex.min=1, cex.max=5, col="grey50", add=TRUE)
```

sim.tmp

*Calculate binary similarity in time*

## Description

The function applies one of 56 similarity measures for binary data to calculate compositional similarity of plots between time steps.

## Usage

```
sim.tmp(x, y, method = "soer", normalize = FALSE, adjust = TRUE, ...)
```

## Arguments

x	Vegetation data, either as matrix with rows = plots and columns = species, or as <code>data.frame</code> with first three columns representing plots, species and occurrence information respectively. All further columns are dumped before calculation. Occurrence is only considered as binary. If your list or matrix contains abundances or frequencies they are transformed automatically.
y	Same as x for time-step two.
method	One of 42 similarity measures for binary data. The function uses the same indices as <code>sim</code> . See details there. Per default <code>soerensen</code> similarity is calculated.
normalize	Logical value indicating whether the values for a, b and c which are calculated in the process should be normalized to 100% (per row, which means per plot comparison). If <code>normalize = TRUE</code> an asymmetric index must be chosen (for details see <code>sim</code> ).
adjust	Do not change the default behaviour (TRUE) unless you know what you do. Would spare some calculation time if set to FALSE, when your species data do not need adjustment, which means that in both or all time steps, there are exactly the same species and the same plots. However in most cases it will be more convenient to rely on the function (see details).
...	Other arguments to <code>sim</code>

## Details

If you compare species data among time steps there will be most likely different numbers of species (and often also different numbers of plots for which information is available). The function takes care of this and you can give any species matrices you want. If one plot is the same, it will calculate what changed on this plot. There will be an error message if no plot is shared. The function relies on plot and species names!! As in a database - they must be unique!!

## Value

Returns a named vector with the similarities for each site between time steps for each plot.

**Author(s)**

Gerald Jurasinski <terhorab@mac.com>

**References**

See references in [sim](#)

**See Also**

See Also as [sim](#) (where you can find a much more elaborate see also section as well).

**Examples**

```
data(bernina)
## load included data
data(bernina)

## how species changed occurrence between first recording
## and last recording?
# construct a species matrix that only contains the species
# that occurred on the summits at the first recording
first <- veg[summits$year=="1907",]
first <- first[,colSums(first)>0]
# make right summit names
row.names(first) <- as.character(summits$summit[summits$year=="1907"])
# construct a species matrix that only contains the species
# that occurred on the summits at the last recording
last <- veg[summits$year=="2003",]
last <- last[,colSums(last)>0]
# make right summit names
row.names(last) <- as.character(summits$summit[summits$year=="2003"])
# calculate similarity between time steps
sim.tmp(first, last)
```

---

sim.yo

---

*Calculate a binary similarity index you define.*


---

**Description**

Enables the calculation of any binary similarity index via the provision of a formula.

**Usage**

```
sim.yo(x, coord = NULL, method = "(2*a)/((2*a) + b + c)", dn = NULL,
normalize = FALSE, listin = FALSE, listout = FALSE, ...)
```

## Arguments

<code>x</code>	Vegetation data, either as matrix with rows = plots and columns = species (similarities are calculated between rows!), or as <code>data.frame</code> with first three columns representing plots, species and occurrence information respectively. All further columns are dumped before calculation. Occurrence is only considered as binary. If your list or matrix contains abundances or frequencies they are transformed automatically.
<code>coord</code>	A <code>data.frame</code> with two columns containing the coordinate values of the sampling units. If given, it triggers the simultaneous calculation of the geographical distances between the sampling units, the coordinates of virtual centre-points between all possible pairs of plots, and the geographical distances in either x- or y-direction. If <code>coord</code> is given, output is always in database format (no matrix).
<code>method</code>	Give the formula for a binary similarity index. Defaults to the formula of Sørensen index. See <code>sim</code> for more examples and general explanations.
<code>dn</code>	Neighbor definition. A geographic distance represented by a numeric or a two value vector defining a ring around each plot. Only takes effect when <code>coord != NULL</code> . If specified, the output does only contain similarities between neighboring plots. A plot is a neighbour to any given plot if it is within the range of the neighbor definition. See details.
<code>normalize</code>	Logical value indicating whether the values for a, b and c which are calculated in the process should be normalized to 100% (per row, which means per plot comparison). If <code>normalize = TRUE</code> an asymmetric index must be chosen (see details in <code>sim</code> ).
<code>listin</code>	if <code>x</code> is given in database (list) format this must be set to <code>TRUE</code> (there is no automatic detection of the format)
<code>listout</code>	If output is wanted in database format rather than as a <code>dist</code> -object set this to <code>TRUE</code> . Output is automatically given in database-format, when <code>coord</code> is specified.
<code>...</code>	Arguments to other functions

## Details

Presumably this function will rarely be used because `sim` already allows for the calculation of a large variety of binary similarity coefficients. But just in case you found or thought of an alternative this function is provided. For details regarding similarity indices see `sim`. You have to give your formula in quotation marks like this: `"(2*a)/((2*a) + b + c)"`.

## Value

If `listout = FALSE` a distance matrix of class `dist` is returned. If `listout = TRUE`, a `data.frame` is returned with 7 columns giving the names of the compared plots in the first two and the calculated similarity measure in the third column. The rest of the columns give the values for a, b, c, and d (in this order). Naming of the first three columns can be changed but defaults to NBX (one of the compared plots), NBY (the other one), used index (the values of the calculated index). If `coord != NULL`, the following columns are given in addition and the columns a:d shift to the end of the `data.frame`.

<code>distance</code>	Geographical distance between compared plots
<code>x</code>	For plotting purposes, the x-coordinate of the virtual position of the calculated similarity value in the center between the two compared plots

<code>y</code>	For plotting purposes, the y-coordinate of the virtual position of the calculated similarity value in the center between the two compared plots
<code>xdist</code>	Geographical distance between compared plots, on the x-axis only
<code>ydist</code>	Geographical distance between compared plots, on the y-axis only

### Note

In general, concepts of data-handling are taken from [vegdist](#) and the calculation of a, b, c and d is taken from [dist.binary](#). Thanks to Jari Oksanen for his `vegan` package and the idea to provide a custom build distance formula.

### Author(s)

Gerald Jurasinski <gerald.jurasinski@uni-rostock.de>

### References

Sørensen, T. (1948) A method of establishing groups of equal amplitude in plant sociology based on similarity of species content. *Biologiske Skrifter* **5**: 1-34.

### See Also

[vegdist](#), [designdist](#), [dist.binary](#), [dsvdis](#), [dist](#) for other dissimilarity coefficients, and [sim](#) for a variety of formulae for similarity coefficients.

### Examples

```
data(abis)

##calculate the default Sørensen index
abis.soer <- sim.yo(abis.spec)

##calculate a custom similarity index
abis.sim <- sim.yo(abis.spec, method="(2*a) / ((a) + b + c)")
```

---

simbadocs

Display Package Documentation

---

### Description

Display package documentation using the `pager` or `pdfviewer` defined in [options](#).

### Usage

```
simbadocs(doc = c("NEWS", "ChangeLog", "mps-coefficients.pdf"))
```

### Arguments

`doc` The name of the document to view (partial match, case sensitive).

**Note**

Since R does not have this facility Jari Oksanen provided a workaround for his `vegan` package ([vegandocs](#)). This here is just adapted to `simba`.

**Author(s)**

Jari Oksanen, adapted by Gerald Jurasinski

**See Also**

[vignette](#).

**Examples**

```
## Not run:
simbadocs("Change")

## End (Not run)
```

---

<code>symbol.size</code>	<i>Little helper function to obtain bubble plots with simple plot and points methods</i>
--------------------------	--

---

**Description**

Can be used within the `cex` argument of a plotting command (`plot` or `points`) to scale the symbols with regard to the values of a numeric variable. Thus, a bubble plot is computed.

**Usage**

```
symbol.size(x, cex.min = 0.2, cex.max = 5)
```

**Arguments**

<code>x</code>	A numeric vector giving the data for scaling the symbols in a scatter (however, you can scale everything that's got a <code>cex</code> argument). The vector must have the same length as <code>x</code> (and <code>y</code> ) that give the plotting positions.
<code>cex.min</code>	The minimum size (scaling) of the plotted symbols.
<code>cex.max</code>	The maximum size (scaling) of the plotted symbols.

**Details**

The same, but in a mapping context can be achieved by [bubble](#). Also [symbols](#) provides a comparable result. However, with `symbol.size` a very simple interface to bubble plots that can be used within regular scatter plot methods is given.

**Value**

A vector is returned with values between `cex.min` and `cex.max` that represent the values in the input vector `x`. After all, there is just a scaling applied. The vector is meant to be used to specify `cex` wherever appropriate.

**Author(s)**

Gerald Jurasinski

**References**

Tufte ER (1998) The visual display of quantitative information. Graphics Press. Cheshire, Connecticut.

**See Also**

[bubble](#), [symbols](#)

**Examples**

```
# load abisko data that comes with simba
data(abis)

# take the environmental data and plot species richness at the field plot positions
with(abis.env, {plot(X, Y, cex=symbol.size(n.spec))})

# make kind of a multivariate plot in 3d:
# the relation between shannon, evenness, and simpson index (bubble size)
with(abis.env, {plot(shannon, even, cex=symbol.size(simps, cex.max=8))})
```

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