Package 'labdsv'

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Title Ordination and Multivariate Analysis for Ecology

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Depends R (>= 2.10), mgcv, MASS, cluster

Suggests optpart

Description A variety of ordination and community analyses
useful in analysis of data sets in community ecology.
Includes many of the common ordination methods, with
graphical routines to facilitate their interpretation,
as well as several novel analyses.

License GPL (>= 2)

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R topics documented:

abuocc 2
brycesite 4
bryceveg 4
compspec 5
concov 6
const 7
dematrify 9
dga 10
disana 11
dropplt 13
dropspc 14

dsvdis . . . 15
envrtest . . . 17
euclidify . . . 18
homoteneity . . . 19
importance . . . 20
indval . . . 21
isamic . . . 23
matrify . . . 24
metrify . . . 25
nmds . . . 27
ordcomp . . . 28
orddist . . . 30
ordpart . . . 31
ordtaxa . . . 32
ordtest . . . 33
pca . . . 34
pco . . . 36
plot.nmds . . . 37
plot.pca . . . 40
plot.pco . . . 42
plot.thull . . . 45
raretaxa . . . 46
reconcile . . . 47
rnddist . . . 48
rndtaxa . . . 49
spcdisc . . . 50
vegtab . . . 51
vegtrans . . . 52

Index **54**

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abuocc *Abundance/Occurrence Graphical Analysis*

Description

Calculates and plots summary statistics about species occurrences in a data frame

Usage

```
abuocc(taxa,minabu=0,panel='all')
```

Arguments

`taxa`	a taxon data.frame with samples as rows and species as columns
`minabu`	a minimum abundance threshold species must exceed to be included in the calculations (default=0)
`panel`	controls which of three graphs is drawn, and can be 'all' or integers 1-4

Details

This functions calculates and plots four data summaries about the occurrence of species:

Plots:

1) the number of samples each species occurs in on a log scale, sorted from maximum to minimum

2) the number of species in each sample plot (species richness) from highest to lowest

3) the mean abundance of non-zero values (on a log scale) as a function of the number of plots a species occurs in

4) the total abundance/sample as a function of the plot-level species richness

The third plot allows you to identify individual species with the mouse; the fourth plot allows you to identify individual samples with the mouse.

Value

Returns an (invisible) list composed of:

`spc.plt`	number of species/sample
`plt.spc`	number of samples each species occurs in
`mean`	mean abundance of each species when present (excluding values smaller than minabu)

Note

It's common in niche theory analyses to calculate the rank abundances of taxa in a sample. This function is similar, but works on multiple samples simultaneously. The spc.plt vector in the returned list can be used anywhere species richness is desired. The plt.spc vector in the returned list can be used to mask out rare species in calculations of sample similarity using `dsvdis` among other purposes.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab1/lab1.html

See Also

`fisherfit`, `prestonfit`, `radfit`

Examples

```
data(bryceveg) # produces a data.frame called bryceveg
abuocc(bryceveg)
```

brycesite *Site Data for Bryce Canyon National Park*

Description

Environmental variables recorded at or calculated for each of 160 sample plots in Bryce Canyon National Park, Utah, U.S.A.

Usage

```
data(brycesite)
```

Format

a data.frame with plots as rows and site variables as columns. Variables are:

plotcode original plot codes

annrad annual direct solar radiation in Langleys

asp slope aspect in degrees

av aspect value = (1+cosd(asp-30))/2

depth soil depth = "deep" or "shallow"

east UTM eastingin meters

elev elevation in feet

grorad growing season radiation in Langleys

north UTM northing in meters

pos topographic position

quad USGS 7.5 minute quad sheet

slope percent slope

bryceveg *Bryce Canyon Vegetation Data*

Description

Estimates of cover class for all non-tree vascular plant species in 160 $375m^2$ circular sample plots. Species codes are first three letters of genus + first three letters of specific epithet.

Usage

```
data(bryceveg)
```

Format

a data.frame of 160 samples (rows) and 169 species (columns). Cover is estimated in codes as follows:

0.2 present in the stand but not the plot

0.5 0-1%

1.0 1-5%

2.0 5-25%

3.0 25-50%

4.0 50-75%

5.0 75-95%

6.0 95-100%

---

compspec *Compositional Specificity Analysis*

Description

Calculates the mean similarity of all plots in which a species occurs

Usage

```
compspec(taxa, dis, numitr=100, drop=FALSE, progress=FALSE)
## S3 method for class 'compspec'
plot(x,spc=NULL,...)
```

Arguments

taxa	a data frame of taxa, samples as rows, species as columns
dis	an object of class 'dist' from dist, vegdist, or dsvdis
numitr	the number of iterations to use to establish the quantiles of the distribution
drop	a switch to determine whether to drop species out when calculating their compspec value
progress	a switch to control printing out progress
x	an object of class compspec
spc	an integer code to specify exactly which species drop-out to plot
...	additional arguments to the plot function

Value

a list with several data.frames: 'vals' with species name, mean similarity, number of occurrences, and probaability of observing as high a mean similarity as observed, and 'quantiles' with the distribution of the quantiles of mean similarity for given numbers of occurrences. If drop=TRUE, results specific to dropping out each species in turn are added to the list by taxon name.

Note

One measure of the habitat specificity of a species is the degree to which a species only occurs in communities that are similar to each other. This function calculates the mean similarity of all samples in which each species occurs, and compares that value to the distribution of mean similarities for randomly generated sets of the same size. The mean similarity of species which only occur once is set to 0, rather than NA.

If drop=TRUE each species is deleted in turn and a new dissimilarity matrix minus that species is calculated for the analysis. This eliminates the bias that part of the similarity of communities being anayzed is due to the known joint occurrence of the species being analyzed.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R

See Also

indval,isamic

Examples

```
data(bryceveg) # returns a vegetation data.frame
dis.bc <- dsvdis(bryceveg,'bray/curtis')
    # returns a Bray/Curtis dissimilarity matrix
compspec(bryceveg,dis.bc)
```

---

concov *Constancy-Coverage Table for Ecological Community Data*

Description

Produces a table of combined species constancy and importance

Usage

```
concov(taxa,clustering,digits=1,width=5,typical=TRUE,thresh=10)
```

Arguments

taxa	a taxon data.frame, samples as rows and species as columns
clustering	(1) an object of class 'clustering', class 'partana', or class 'partition', (2) a vector of integer cluster memberships, (3) a factor vector, or (4) a character vector
digits	the number of digits for the importance value of species
width	controls the formatting of columns

typical	an argument passed to importance to control how mean abundance is calculated
thresh	a theshold parameter to control the suppression of small details in the output. Species must have >= thresh constancy in at least one type to appear in the output table

Details

concov calls const and importance and then combines the output in a single table.

Value

a data.frame with factors (combined constancy and coverage) as columns

Note

Constancy-coverage tables are an informative and concise representation of species in classified types. The output format [constancy(mean cover)] follows the convention of the US Forest Service vegetation classifications.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab3/lab3.html

See Also

const, importance

Examples

```
data(bryceveg)  # returns a vegetation data.frame
data(brycesite) # returns a site data.frame
concov(bryceveg,brycesite$quad) # calculates the constance and coverage of
                                # species by USGS quad map location
```

---

const *Constancy Table*

Description

For a classified set of vegetation samples, lists for each species the fraction of samples in each class the species occurs in.

Usage

```
const(taxa, clustering, minval = 0, show = minval, digits = 2,
             sort = FALSE, spcord = NULL)
```

Arguments

taxa	a data.frame of species abundances with samples as rows and species as columns
clustering	(1) an object of class 'clustering', class 'partana', or class 'partition', (2) a vector of numeric cluster memberships, (3) a factor vector, or (4) a character vector.
minval	the minimum constancy a species must have in at least one class to be included in the output
show	the minimum constancy a species must have to show a printed value
digits	the number of digits to report in the table
sort	a switch to control interactive re-ordering of the output table
spcord	a vector of integers to specify the order in which species should be listed in the table

Details

Produces a table with species as rows, and species constancy in clusters as columns.

The 'clustering' vector represents a classification of the samples that the table summarizes. It may result from a cluster analysis, partitioning an ordination, subjective partitioning of a vegetation table, or other source.

The 'minval' argument is used to emphasize the dominant species and suppress the rare species. Vegetation tables are often very sparse, and this argument simplifies making them more compact.

The 'digits' argument limits the reported precision of the calculations. Generally, relatively low precision is adequate and perhaps more realistic.

The 'spcord' argument specifies the order species are listed in a table. You can use the reverse of the number of occurrences to get dominant species at the top to rarer at the bottom, use fidelity values for the ordered clusters, or possibly the order of species centroids in an ordination.

Value

a data.frame with species as rows, classes as columns, with fraction of occurrence of species in classes.

Note

Constancy tables are often used in vegetation classification to calculate or present characteristic species for specific classes or types. 'const' may be combined with 'importance' and 'vegtab' to achieve a vegetation table-oriented analysis.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab3/lab3.html

See Also

importance, vegtab, vegemite

Examples

```
data(bryceveg) # returns a data.frame called bryceveg
class <- sample(1:10,nrow(bryceveg),replace=TRUE)
const(bryceveg,class,minval=0.25)
```

`dematrify` *Create Three Column Database Form Data Frame from Sparse Data Frames*

Description

Takes a sparse matrix data frame (typical of ecological abundance data) and converts it into three column database format.

Usage

```
dematrify(taxa, filename, sep = ",", thresh = 0)
```

Arguments

`taxa`	a sparse data.frame or matrix, with samples as rows and taxa as columns
`filename`	the name of the filename to produce
`sep`	the separator to use in separating columns
`thresh`	the minimum abundance to be included in the output

Details

The routine is pure R code to convert data from sparse matrix form to three column database form for export or reduced storage

Value

a data.frame with the first column the sample ID, the second column the taxon ID, and the third column the abundance.

Note

Typically, large ecological data sets are characterized by sparse matrices of taxon abundance in samples with many zeros in the matrix. Because these datasets may be many columns wide, they are difficult to work with in text editors or spreadsheets, and require excessive amount of space for storage. The reduced three column form is suitable for input to databases, and more easily edited.

Author(s)

David W. Roberts <droberts@montana.edu>

See Also

matrify

Examples

```
library(labdsv)
data(bryceveg)
x <- dematrify(bryceveg)
```

---

dga *Direct Gradient Analysis*

Description

Direct gradient analysis is a graphical representation of the abundance distribution of (typically) species along opposing environmental gradients

Usage

```
dga(z,x,y,step=25,pres="+",abs="-",labcex=1,
    xlab = deparse(substitute(x)), ylab = deparse(substitute(y)),
    pch = 1, title = "", ...)
```

Arguments

z	the variable (typically a species abundance) to be plotted
x	the variable to use as the x axis
y	the variable to use as the y axis
step	controls the grid density fed to the GAM surface fitter
pres	the symbol to print when a species is present (presence/absence mode)
abs	the symbol to print when a species is absent (presence/absence mode)
labcex	the character size for contour labels
xlab	the x axis legend
ylab	the y axis legend

pch	the symbol to print in continuous abundance plots
title	the title to print
...	miscellaneous arguments to pass to par

Details

'dga' interpolates a grid of x,y values from the supplied data and fits a GAM (from mgcv) of the z variable to the grid. The GAM surface is then represented by a contour map and abundance symbols as described above.

Value

a graph of the distribution of the z variable on a grid of x and y is displayed on the current active device.

Note

Direct gradient analysis was promoted by Robert Whittaker and followers as a preferred method of vegetation analysis.

Author(s)

David W. Roberts <droberts@montana.edu>

See Also

gam

Examples

```
data(bryceveg) # returns a data.frame called bryceveg
x <- c(0.2,0.5,1.0,2.0,3.0,4.0,5.0,6.0)
y <- c(0.2,0.5,3.0,15.0,37.5,62.5,85.0,97.5)
cover <- vegtrans(bryceveg,x,y)
data(brycesite)
dga(round(cover$arcpat),brycesite$elev,brycesite$av)
```

---

disana *Dissimilarity Analysis*

Description

Dissimilarity analysis is a graphical analysis of the distribution of values in a dissimilarity matrix

Usage

```
disana(x, panel='all')
```

Arguments

x	an object of class 'dist' such as returned by dist, vegdist or dsvdis
panel	a switch to specify which panel of graphics should be displayed. Can be either an integer from 1 to 3, or the word 'all'.

Details

Calculates three vectors: the minimum, mean, and maximum dissimilarity for each sample in a dissimilarity matrix. By default it produces three plots: the sorted dissimilarity values, the sorted min, mean, and maximum dissimilarity for each sample, and the mean dissimilarity versus the minimum dissimilarity for each sample. Optionally, you can identify sample plots in the last panel with the mouse.

Value

Plots three graphs to the current graphical device, and returns an (invisible) list with four components:

min	the minimum dissimilarity of each sample to all others
mean	the mean dissimilarity of each sample to all others
max	the maximum dissimilarity of each sample to all others
plots	a vector of samples identified in the last panel

Note

Dissimilarity matrices are often large, and difficult to visualize directly. 'disana' is designed to highlight aspects of interest in these large matrices. If the first panel shows a long limb of constant maximum value, you should consider recalculating the dissimilarity with a step-across adjustment. The third panel is useful for identifying outliers, which are plots more than 0.5 dissimilar to their nearest neighbor.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab8/lab8.html

Examples

```
data(bryceveg) # returns a data.frame called veg
dis.bc <- dsvdis(bryceveg,'bray/curtis')
disana(dis.bc)
```

`dropplt` *Dropping Plots with Missing Values From Taxon and Site Data Frames*

Description

Looks for plots which have missing values in site or environment data, and deletes those plots from both the taxon and site data frames.

Usage

```
dropplt(taxa,site,which=NULL)
```

Arguments

`taxa`	a taxon data frame with samples as rows and species as columns
`site`	a site or environment data frame with samples as rows and variables as columns
`which`	a switch to dpecify specific plots to drop from both data.frames

Details

First looks to see that the row names of the taxon data frame and the site or environment data frame are identical. If not, it prints an error message and exits. if which is NULL, It then looks at the site or environment data frame for plots or samples that have missing values, and deletes those plots from both the taxon and site data frames. Alternatively, if which is a numeric scalar or vector it deletes the specified plots from both the taxon and site data.frames.

Value

produces a list with two components:

`taxa`	the new taxon data frame
`site`	the new site data frame

Note

This is a VERY heavy-handed approach to managing missing values. Most R routines (including most of the labdsv package functions) have ways of handling missing values that are fairly graceful. This function simply maintains the correspondence between the taxon and site data frames while eliminating ALL missing values, and all plots that have missing values.

Author(s)

David W. Roberts <droberts@montana.edu>

Examples

```
data(bryceveg)  # returns a data frame called bryceveg
data(brycesite) # returns a data frame called brycesite
demo <- dropplt(bryceveg,brycesite)
newveg <- demo$taxa
newsite <- demo$site
```

---

dropspc *Dropping Species with Few Occurrences*

Description

Eliminates species from the taxon data frame that occur fewer than or equal to a threshold number of occurrences.

Usage

```
dropspc(taxa,minocc=0,minabu=0)
```

Arguments

taxa	a taxon data frame
minocc	the threshold number of occurrences to be dropped
minabu	the threshold minimum abundance to be dropped

Details

The function is useful for eliminating species (columns) from taxon data frames which never occur, which often happens if you eliminate plots, and those plots are the only ones that contain that species. In addition, many species are rare in data frames, and some algorithms (especially dissimilarity functions and table sorting routines) benefit from smaller simpler data frames.

Value

produces a new taxon data frame

Note

This is a heavy-handed approach to managing rare species in data.frames. It is often possible to write a mask (logical vector) that suppresses the influence of rare species and keeps the original data.frame intact, but this function simplifies data management for some purposes.

Author(s)

David W. Roberts <droberts@montana.edu>

Examples

```
data(bryceveg) # returns a data frame called bryceveg
newveg <- dropspc(bryceveg,5) # deletes species which occur 5 or fewer times
```

---

dsvdis *Dissimilarity Indices and Distance Measures*

Description

This function provides a set of alternative dissimilarity indices and distance metrics for classification and ordination, including weighting by species (columns) and shortest-path adjustment for dissimilarity indices.

Usage

```
dsvdis(x,index,weight=rep(1,ncol(x)),step=0.0,
       diag=FALSE, upper=FALSE)
```

Arguments

x	a matrix of observations, samples as rows and variables as columns
index	a specific dissimilarity or distance index (see details below)
weight	a vector of weights for species (columns)
step	a threshold dissimilarity to initiate shortest-path adjustment (0.0 is a flag for no adjustment)
diag	a switch to control returning diagonal (default=FALSE)
upper	a switch to control returning upper (TRUE) or lower (FALSE) triangle

Details

The function calculates dissimilarity or distance between rows of a matrix of observations according to a specific index. Three indices convert the data to presence/absence automatically. In contingency table notation, they are:

steinhaus	$1 - a/(a+b+c)$
sorensen	$1 - 2a/(2a+b+c)$
ochiai	$1 - a/\sqrt{(a+b) \times (a+c)}$

Others are quantitative. For variable i in samples x and y:

ruzicka	$1 - \sum min(x_i, y_i) / \sum max(x_i, y_i)$
bray/curtis	$1 - \sum [2 * min(x_i, y_i)] / \sum x_i + y_i$
roberts	$1 - [(x_i + y_i) * min(x_i, y_i) / max(x_i, y_i)] / (x_i + y_i)$
chisq	$(exp - obs)/\sqrt{exp}$

The weight argument allow the assignment of weights to individual species in the calculation of plot-to-plot similarity. The weights can be assigned by life-form, indicator value, or for other investigator specific reasons. For the presence/absence indices the weights should be integers; for the quantitative indices the weights should be in the interval [0,1]. The default (rep(1,ncol(x)) is to set all species = 1.

The threshold dissimilarity 'step' sets all values greater than "step" to 9999.9 and then solves for the shortest path distance connecting plots to other non-9999.9 values in the matrix. Step = 0.0 (the default) is a flag for "no shortest-path correction".

Value

Returns an object of class "dist", equivalent to that from `dist`.

Note

Ecologists have spent a great deal of time and effort examining the properties of different dissimilarity indices and distances for ecological data. Many of these indices should have more general application however. Dissimilarity indices are bounded [0,1], so that samples with no attributes in common cannot be more dissimilar than 1.0, regardless of their separation along hypothetical or real gradients. The shortest-path adjustment provides a partial solution. Pairs of samples more dissimilar than a specified threshold are set to 9999.9, and the algorithm solves for their actual dissimilarity from the transitive closure of the triangle inequality. Essentially, the dissimilarity is replaced by the shortest connected path between points less than the threshold apart. In this way it is possible to obtain dissimilarities much greater than 1.0.

The chi-square distance is not usually employed directly in cluster analysis or ordination, but is provided so that you can calculate correspondence analysis as a principal coordinates analysis (using `cmdscale`) from a simple distance matrix.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu:/labdsv/R/labs/lab8/lab8.html

See Also

`dist`, `vegdist`

Examples

```
data(bryceveg)   # returns a data.frame called "bryceveg"
dis.ochiai <- dsvdis(bryceveg,index="ochiai")
dis.bc <- dsvdis(bryceveg,index="bray/curtis")
```

envrtest *Environmental Distribution Test*

Description

Calculates whether the value of a specified environmental variable has an improbable distribution with respect to a specified vector

Usage

```
envrtest(set,env,numitr=1000,minval=0,replace=FALSE,
     plotit = TRUE, main = paste(deparse(substitute(set)),
     " on ", deparse(substitute(env))))
```

Arguments

set	a vector of logical or quantitative values
env	the quantitative variable whose distribution is to be tested
numitr	the number of randomizations to iterate to calculate probabilities
minval	the threshold to use to partition the data into a logical if set is quantitative
replace	whether to permute (replace=FALSE) or bootstrap (replace=TRUE) the values in the permutation test
plotit	logical; plot results if TRUE
main	title for plot if plotted

Details

Calculates the maximum within-set difference in the values of vector 'env', and the distribution of the permuted random within-set differences. It then plots the observed difference as a red line, and the sorted permuted differences as a black line and prints the probability of getting such a limited distribution. The probability is calculated by permuting numitr-1 times, counting the number of times the permuted maximum difference is as small or smaller than observed (n), and calculating (n+1)/numitr. To get three-digit probabilities, set numitr=1000 (the default)

Value

Produces a plot on the current graphics device, and an invisible list with the components observed within-set difference and the p-value.

Note

The plot is based on the concept of constraint, or limiting value, and checks to see whether the distribution of a particular variable within a cluster is constrained in an improbable way.

Author(s)

David W. Roberts <droberts@montana.edu>

Examples

```
data(bryceveg) # returns a vegetation data.frame
data(brycesite) # returns and environmental data.frame
envrtest(bryceveg$berrep>0,brycesite$elev)
```

`euclidify` *Nearest Euclidean Space Representation of a Dissimilarity Object*

Description

Calculates the nearest Euclidean space representation of a dissimilarity object by iterating the transitive closure of transitive property (triangle inequality or Pythagoras' theorem)

Usage

```
euclidify(x,upper=FALSE,diag=FALSE)
```

Arguments

`x`	a distance or dissimilarity object returned from `dist`, `vegdist`, or `dsvdis`
`upper`	a logical switch to control whether to return the lower triangle (upper=FALSE) or upper triangle (upper=TRUE) of the distance matrix
`diag`	a logical switch to control whether to return the diagonal of the distance matrix

Details

Implements a constrained iteration of the transitive closure of Pythagoras' theorem, such that the squared distance between any two objects is less than or equal to the sum of the squared distances from the two objects to all possible third objects.

Value

an object of class 'dist'

Note

Many multivariate statistical methods are designed for euclidean spaces, and yet the direct calculation of euclidean distance is often inappropriate due to problems with joint absences. euclidify takes any dissimilarity matrix and converts it to the closest euclidean representation, generally to avoid negative eigenvalues in an eigenanalysis of the matrix.

Author(s)

David W. Roberts <droberts@montana.edu>

See Also

`metrify`

Examples

```
data(bryceveg) # returns a vegetation data.frame
dis.bc <- dsvdis(bryceveg,'bray/curtis') # calculate a Bray/Curtis
          #     dissimilarity matrix
dis.euc <- euclidify(dis.bc) # calculate the nearest euclidean representation
## Not run: plot(dis.bc,dis.euc)
```

`homoteneity` *Homoteneity Analysis of Classified Ecological Communities*

Description

Homoteneity is defined as 'the mean constancy of the S most constant species, expressed as a fraction, where S is the mean species richness of a type.'

Usage

```
homoteneity(taxa,clustering)
```

Arguments

`taxa`	a data.frame of species abundances with samples as rows and species as columns
`clustering`	a vector of (integer) class memberships, or an object of class 'clustering', class 'partana', of class `partition`

Value

a data.frame of homoteneity values

Note

This function was adapted from the Virginia Heritage Program at

http://www.dcr.virginia.gov/natural_heritage/ncstatistics.shtml

Author(s)

David W. Roberts <droberts@montana.edu>

See Also

`const`, `concov`

Examples

```
data(bryceveg) # returns a data.frame of species in sample plots
data(brycesite) # returns a data.frame of site variables
homoteneity(bryceveg,brycesite$quad) # analysis of species constancy
                                     # by USGS quad location
```

`importance` *Importance Table*

Description

For a classified set of vegetation samples, a importance table lists for each species the average or typical abundance of each species in each class.

Usage

```
importance(taxa,clustering,minval=0,digits=2,show=minval,
       sort=FALSE,typical=TRUE,spcord)
```

Arguments

`taxa`	a data.frame of species abundances with samples as rows and species as columns
`clustering`	a vector of (integer) class memberships, or an object of class 'clustering', class 'partana', of class `partition`
`minval`	the minimum importance a species must have in at least one class to be included in the output
`digits`	the number of digits to report in the table
`show`	the minimum value a species must have to print a value
`sort`	a switch to control interactive re-ordering
`typical`	a swith to control how mean abundance is calculated. Typical=TRUE divides the sum of species abundance by the number of plots in which it occurs; typical=FALSE divides by the number of plots in the type
`spcord`	a vector of integers to specify the order in which species should be listed in the table

Value

a data.frame with species as rows, classes as columns, with average abundance of species in classes.

Note

Importance tables are often used in vegetation classification to calculate or present characteristic species for specific classes or types. Importance may be combined with `const`, `concov` and `vegtab` to achieve a vegetation table-oriented analysis.

Author(s)

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References

http://ecology.msu.montana.edu/labdsv/R/labs/lab3/lab3.html

See Also

const, vegtab, concov

Examples

```
data(bryceveg) # returns a data.frame called bryceveg
class <- sample(1:10,nrow(bryceveg),replace=TRUE)
importance(bryceveg,class,minval=0.25)
```

---

indval *Dufrene-Legendre Indicator Species Analysis*

Description

Calculates the indicator value (fidelity and relative abundance) of species in clusters or types.

Usage

```
indval(x, ...)
## Default S3 method:
indval(x,clustering,numitr=1000,...)
## S3 method for class 'stride'
indval(x,taxa,numitr=1,...)
## S3 method for class 'indval'
summary(object, p=0.05, type='short', digits=2, show=p,
       sort=FALSE, too.many=100, ...)
```

Arguments

x	a matrix or data.frame of samples with species as columns and samples as rows, or an object of class 'stride' from function stride
clustering	a vector of numeric cluster memberships for samples, or a classification object returned from pam, or optpart, slice, or archi
numitr	the number of randomizations to iterate to calculate probabilities
taxa	a dataframe with samples as rows and species as columns
object	an object of class 'indval'
p	the maximum probability for a species to be listed in the summary
type	a switch to choose between 'short' and 'long' style summary
digits	the number of significant digits to show
show	the threshold to show values as opposed to a dot column place-holder
sort	a switch to control user-managed interactive table sorting
too.many	a threshold reduce the listing for large data sets
...	additional arguments to the summary or generic function

Details

Calculates the indicator value 'd' of species as the product of the relative frequency and relative average abundance in clusters. Specifically,

where:
$p_{i,j}$ = presence/absence (1/0) of species i in sample j;
$x_{i,j}$ = abundance of species i in sample j;
n_c = number of samples in cluster c;
for cluster c in set K;

$$f_{i,c} = \frac{\sum_{j \in c} p_{i,j}}{n_c}$$

$$a_{i,c} = \frac{(\sum_{j \in c} x_{i,j})/n_c}{\sum_{k=1}^{K}((\sum_{j \in k} x_{i,j})/n_k)}$$

$$d_{i,c} = f_{i,c} \times a_{i,c}$$

Calculated on a 'stride' the function calculates the indicator values of species for each of the separate partitions in the stride.

Value

The default function returns a list of class 'indval' with components:

`relfrq`	relative frequency of species in classes
`relabu`	relative abundance of species in classes
`indval`	the indicator value for each species
`maxcls`	the class each species has maximum indicator value for
`indcls`	the indicator value for each species to its maximum class
`pval`	the probability of obtaining as high an indicator values as observed over the specified iterations

The stride-based function returns a data.frame with the number of clusters in the first column and the mean indicator value in the second.

The 'summary' function has two options. In 'short' mode it presents a table of indicator species whose probability is less then 'p', giving their indicator val;ue and the identity of the cluster they indicate, along with the sum of probabilities for the entire data set. In 'long' mode, the indicator value of each species in each class is shown, with values less than 'show' replaced by a place-holder dot to emphasize larger values.

If 'sort==TRUE', a prompt is given to re-order the rows of the matrix interactively.

Note

Indicator value analysis was proposed by Dufrene and Legendre (1997) as a possible stopping rule for clustering, but has been used by ecologists for a variety of analyses. Dufrene and Legendre's nomenclature in the paper is somewhat ambiguous, but the equations above are taken from the worked example in the paper, not the equations on page 350 which appear to be in error. Dufrene and Legendre, however, multiply d by 100; this function does not.

Author(s)

David W. Roberts <droberts@montana.edu>

References

Dufrene, M. and Legendre, P. 1997. Species assemblages and indicator species: the need for a flexible asymmetrical approach. Ecol. Monogr. 67(3):345-366.

See Also

isamic

Examples

```
data(bryceveg) # returns a vegetation data.frame
dis.bc <- dsvdis(bryceveg,'bray/curtis') # returns a dissimilarity matrix
clust <- sample(1:5,nrow(bryceveg),replace=TRUE)
indval(bryceveg,clust)
```

---

isamic *Indicator Species Analysis Minimizing Intermediate Occurrences*

Description

Calculates the degree to which species are either always present or always absent within clusters or types.

Usage

```
isamic(taxa,clustering,sort=FALSE)
```

Arguments

taxa	a matrix or data.frame of samples, species as columns, samples as rows
clustering	a vector of numeric cluster memberships for samples, or a classification object returned from pam, partana, or slice
sort	if TRUE, return in order of highest value to lowest rather than input order

Details

Calculates the constancy (fractional occurrence of each species in every type), and then calculates twice the the sum of the absolute values of the constancy - 0.5, normalized to the number of clusters (columns).

Value

a data.frame of species indicator values

Note

This function was previously called 'duarm', a horrible pun on the name duleg, which is an abbreviation for Dufrene and Legendre who defined an alternative indicator species algorithm. Following publication of Aho et al. 2008, it was renamed 'isamic' as decribed in that paper.

Author(s)

David W. Roberts <droberts@montana.edu>

References

Aho, K., D.W. Roberts, and T.W.Weaver. 2008. Using geometric and non-geometric internal evaluators to compare eight vegetation classification methods. J. Veg. Sci. In press.

See Also

indval

Examples

```
data(bryceveg)
dis.bc <- dsvdis(bryceveg,'bray/curtis')
clust <- sample(1:5,nrow(bryceveg),replace=TRUE)
isamic(bryceveg,clust)
```

---

matrify *Create Taxon Data.Frames From Three Column Database Form*

Description

Takes a data.frame in three column form (sample.id, taxon, abundance) and converts it into full matrix form, and then exports it as data.frame with the appropriate row.names and column names.

Usage

```
matrify(data)
```

Arguments

data	a data.frame or matrix in three column format (or database format), where the first column is the sample ID, the second column is the taxon ID, and the third sample is the abundance of that taxon in that sample.

Details

The routine is pure R code to convert data from database form to the sparse matrix form required by multivariate analyses in packages 'labdsv' and 'vegan', as well as `dist` and other routines.

Value

a data.frame with samples as rows, taxa as columns, and abudance values for taxa in samples.

Note

Typically, the source of the data will be an ASCII file of a dbase database or a CSV file from an Excel file in three column format. That file can be read into a data.frame with `read.table` or `read.csv` and then that data.frame can be matrified by this function.

Author(s)

David W. Roberts <droberts@montana.edu>

See Also

dematrify

Examples

```
x <- cbind(c('a','a','b','b','b','c','c'),
           c('x','y','x','z','w','y','z'),
           c(1,2,1,3,2,2,1))
matrify(x)
```

---

metrify *Nearest Metric Space Representation of a Dissimilarity Object*

Description

Calculates the nearest metric space representation of a dissimilarity object by iterating the transitive closure of the triangle inequality rule

Usage

```
metrify(x,upper=FALSE,diag=FALSE)
```

Arguments

x	a distance or dissimilarity object returned from dist, vegdist, or dsvdis
upper	a logical switch to control whether to return the lower triangle (upper=FALSE) or upper triangle (upper=TRUE) of the distance matrix
diag	a logical switch to control whether to return the diagonal of the distance matrix

Details

Implements a constrained iteration of the transitive closure of the triangle inequality, such that the distance between any two objects is less than or equal to the sum of the distances from the two objects to a third.

Value

a object of class 'dist'

Note

Many multivariate statistical methods are designed for metric spaces, and yet the direct calculation of distance is often inappropriate due to problems with joint absences. metrify takes any dissimilarity matrix and converts it to the closest metric space representation, generally to avoid negative eigenvalues in an eigenanalysis of the matrix.

Author(s)

David W. Roberts <droberts@montana.edu>

See Also

euclidify

Examples

```
data(bryceveg) # returns a vegetation data.frame
dis.bc <- dsvdis(bryceveg,'bray/curtis') # calculate a Bray/Curtis
            #  dissimilarity matrix
dis.met <- metrify(dis.bc) # calculate the nearest euclidean
            #  representation
```

`nmds` *Nonmetric Multidimensional Scaling*

Description

This function is simply a wrapper for the isoMDS function in the MASS package by Venables and Ripley. The purpose is to establish a 'nmds' class to simplify plotting and additional graphical analysis as well as a summary.

Usage

```
nmds(dis,k=2,y=cmdscale(d=dis,k=k),maxit=50)
bestnmds(dis,k=2,itr=20,maxit=100)
```

Arguments

`dis`	a dist object returned from `dist` or a full symmetric dissimilarity or distance matrix
`k`	the desired number of dimensions for the result
`y`	a matrix of initial locations (objects as rows, coordinates as columns, as many columns as specified by k). If none is supplied, `cmdscale` is used to generate them
`maxit`	the maximum number of iterations in the isoMDS routine
`itr`	number of random starts to find best result

Details

The nmds function simply calls the `isoMDS` function of the MASS library, but converts the result from a list to an object of class 'nmds'. The only purpose for the function is to allow 'plot', 'identify', 'surf', and other additional methods to be defined for the nmds class, to simplify the analysis of the result.

The 'bestnmds' function runs 'itr' number of random initial locations and returns the best result of the set.

Value

an object of class 'nmds', with components:

`points`	the coordinates of samples along axes
`stress`	the "goodness-of-fit" computed as stress in percent

Note

nmds is included as part of the LabDSV package to provide a consistent interface and utility for vegetation ordination methods. Other analyses included with the same interface at present include principal components analysis (pca), and principal coordinates analysis (pco).

Author(s)

Venables and Ripley for the original isoMDS function included in the MASS package.

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References

Kruskal, J.B. (1964) Multidimensional scaling by optimizing goodness of fit to nonmetric hypothesis. Psychometrics 29:1-27.

Kruskal, J.B. (1964) Nonmetric multidimensional scaling: a numerical method. Psychometrics 29:115-129.

T.F. Cox and M.A.A. Cox. (1994) *Multidimensional Scaling.* Chapman and Hall.

http://ecology.msu.montana.edu:/labdsv/R/labs/lab9/lab9.html

See Also

isoMDS for the original function

plot.nmds for the 'plot' method, the 'plotid' method to identify points with a mouse, the 'points' method to identify points meeting a logical condition, the 'hilight' method to color-code points according to a factor, the 'chullord' method to add convex hulls for a factor, or the the 'surf' method to add surface contours for continuous variables.

initMDS for an alternative way to automate random starts

postMDS for a post-solution rescaling

metaMDS for a full treatment of variations

Examples

```
data(bryceveg)
data(brycesite)
dis.man <- dist(bryceveg,method="manhattan")
demo.nmds <- nmds(dis.man,k=4)
plot(demo.nmds)
points(demo.nmds,brycesite$elev>8000)
plotid(demo.nmds,ids=row.names(brycesite))
```

---

ordcomp *Ordination to Dissimilarity Comparison*

Description

Plots the distribution of pair-wise distances of all points in an ordination over the distances in the dissimilarity or distance matrix the ordination was calculated from. Prints the correlation between the two on the graph.

Usage

```
ordcomp(x,dis,dim,xlab="Computed Distance",ylab="Ordination Distance",
            title="",pch=1)
```

Arguments

x	an ordination object from pca, pco, nmds, fso or ordiplot
dis	an object of class dist
dim	the number of dimensions in the ordination to use (default=all)
xlab	the X axis label for the graph
ylab	the Y axis label for the graph
title	a title for the plot
pch	the symbol to plot

Value

A plot is created on the current graphics device. Returns the (invisible) correlation.

Note

Ordinations are low dimensional representations of multidimensional spaces. This function attempts to portray how well the low dimensional solution approximates the full dimensional space.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab9/lab9.html

Examples

```
data(bryceveg) # produces a vegetation data.frame
dis.bc <- dsvdis(bryceveg,'bray/curtis') # creates a Bray/Curtis dissimilarity matrix
pco.bc <- pco(dis.bc,2) # produces a two-dimensional Principal Coordinates Ordination object
ordcomp(pco.bc,dis.bc)
```

orddist *Ordination Point Pair-Wise Distance Calculation*

Description

Calculates the pair-wise distances of all points in an ordination. The function is simply a wrapper for the 'dist' function, but simplifies managing ordinations that store their coordinates under different names, as well as managing the desired dimensionality of the calculations.

Usage

```
orddist(x,dim)
```

Arguments

x	an ordination object from pca, pco, nmds, fso
dim	the desired dimensionality to be included in the calculations (must be <= number of dimensions of the ordinations)

Value

an object of class 'dist' is produced

Note

Ordinations are low dimensional representations of multidimensional spaces. This function produces data on the low-dimensional distances for other analyses.

Author(s)

David W. Roberts <droberts@montana.edu>

Examples

```
data(bryceveg) # produces a vegetation data.frame
dis.bc <- dsvdis(bryceveg,'bray/curtis') # creates a Bray/Curtis
                                         #dissimilarity matrix
pco.bc <- pco(dis.bc,2) # produces a two-dimensional Principal Coordinates
                        #Ordination object
orddist(pco.bc,dim=2)
```

ordpart *Ordination Partitioning*

Description

This function allows users to partition or classify the points in an ordination by identifying clusters of points with a mouse

Usage

```
ordpart(ord, ax = 1, ay = 2)
```

Arguments

ord	an ordination of class 'pca', 'pco', or 'nmds'
ax	the first axis number in the ordination plot
ay	the second axis number in the ordination plot

Details

Given a plot of an ordination, you assign plots to clusters by drawing a polygon with the first mouse button to include all points in a given cluster. To end that cluster, click the right mouse button to close the polygon. Plots included in that cluster will be color-coded to indicate membership. Start the next cluster by drawing another polygon. To end, click the right mouse button again after closing the last polygon. Plots within more than one polygon are assigned membership in the last polygon which includes them; plots which are not within any polygon are assigned membership in cluster zero.

Value

A integer vector of cluster membership values

Note

Although the routine could easily be adapted for any scatter plot, it is currently only designed for objects of class 'pca', 'pco', or 'nmds'

Author(s)

David W. Roberts <droberts@montana.edu>

Examples

```
data(bryceveg)
data(brycesite)
dis.bc <- dsvdis(bryceveg,'bray/curtis')
nmds.1 <- nmds(dis.bc,5)
plot(nmds.1)
## Not run: clustering <- ordpart(nmds.1)
```

ordtaxa *Re-Order the Rows and Columns of a Taxon Data Frame*

Description

Allows analysts to interactively re-order a taxon data frame to achieve a 'structured' table following phytosociological principles.

Usage

```
ordtaxa(taxa,site)
```

Arguments

taxa	a taxon data frame
site	a site or environment data frame

Details

Prints a copy of the taxon data frame, and then prompts for plots to move in front of another plot. It then prompts for species to move in front of a specified species. Multiple plots or species can be moved in a single move, with plot or species IDs separated by commas with no blanks. The program cycles between prompting for plots to move, and then species to move, until both prompts are responded to with blank lines.

Value

produces a list with two components:

taxa	the new taxon data frame
site	the new site data frame

Note

This is a a fairly simple means to sort a table. For large tables, it is often possible (and preferable) to sort the tables with ordination coordinates or other indices, but this function allows analysts to order the table arbitrarily into any form.

Author(s)

David W. Roberts <droberts@montana.edu>

See Also

summary.indval,const,importance

Examples

```
## Not run: data(bryceveg) # returns a data frame called bryceveg
## Not run: data(brycesite) # returns a data frame called brycesite
## Not run: demo <- ordtaxa(bryceveg,brycesite)
## Not run: newveg <- demo$taxon
## Not run: newsite <- demo$site
```

---

ordtest *Ordination Distribution Test*

Description

Testing the distribution of points in an ordination

Usage

```
ordtest(ord, var, dim=1:ncol(ord$points), index = 'euclidean',
   nitr = 1000)
```

Arguments

ord	an object of class 'pca', 'pco', or 'nmds'
var	a logical or factor vector used to organize the calculation of within-set distances
dim	the number of dimensions to use in the calculation
index	the distance metric for the calculation of within-set distances. Currently only euclidean is accepted
nitr	the number of iterations to perform to establish p-values

Details

Calculates the sum of within-set pair-wise distances and compares to 'nitr' permutations of the same distribution to calculate the probability of observing clusters as tight as observed or tighter. The p-value is calculated by running nitr-1 permutations and counting the number of cases where the sum of pair-wise distances is as small as smaller than observed. That count is increased by one and divided by nitr to estimate p.

Value

Produces a list with components:

obs	the observed sum of within-set distances
p	the probability of obtaining a value that small
reps	the sum of within-set pairwise distances for all permutations

Author(s)

David W. Roberts <droberts@montana.edu>

See Also

anosim

Examples

```
data(bryceveg)
data(brycesite)
dis.bc <- dsvdis(bryceveg,'bray/curtis')
pco.bc <- pco(dis.bc)
plot(pco.bc)
demo <- ordtest(pco.bc,brycesite$quad)
demo$p
```

---

pca *Principal Components Analysis*

Description

Principal components analysis is a eigenanalysis of a correlation or covariance matrix used to project a high-dimensional system to fewer dimensions.

Usage

```
pca(mat, cor = FALSE, dim = min(nrow(mat),ncol(mat)))
## S3 method for class 'pca'
summary(object, dim = length(object$sdev), ...)
## S3 method for class 'pca'
scores(x, labels = NULL, dim = length(x$sdev))
## S3 method for class 'pca'
loadings(x, dim = length(x$sdev), digits = 3, cutoff = 0.1)
```

Arguments

mat	a matrix or data.frame of interest, samples as rows, attributes as columns
cor	logical: whether to use a correlation matrix (if TRUE), or covariance matrix (if FALSE)
dim	the number of dimensions to return
object	an object of class 'pca'
x	an object of class 'pca'
labels	an (optional) vector of labels to identify points
digits	number of digits to report
cutoff	threshold to suppress printing small values
...	arguments to pass to function summary

Details

PCA is a common multivariate technique. The version here is simply a wrapper for the `prcomp` function to make its use and plotting consistent with the other LabDSV functions.

Value

an object of class "pca", a list with components:

`scores`	a matrix of the coordinates of the samples in the reduced space
`loadings`	a matrix of the contributions of the variables to the axes of the reduced space.
`sdev`	a vector of standard deviations for each dimension

Note

The current version of pca is based on the `prcomp` function, as opposed to the `princomp` function. Nonetheless, it maintains the more conventional labels "scores" and "loadings", rather than x and rotation. prcomp is based on a singular value decomposition algorithm, as has worked better in our experience. In the rare cases where it fails, you may want to try `princomp`.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab7/lab7.html

See Also

princomp, prcomp, pco, nmds, fso, cca

Examples

```
data(bryceveg) # returns a vegetation data.frame
data(brycesite)
x <- pca(bryceveg,dim=10)  # returns the first 10 eigenvectors and loadings
plot(x)
surf(x,brycesite$elev)
points(x,brycesite$depth=='deep')
```

pco *Principal Coordinates Analysis*

Description

Principal coordinates analysis is an eigenanalysis of distance or metric dissimilarity matrices.

Usage

```
pco(dis, k=2)
```

Arguments

dis	the distance or dissimilarity matrix object of class "dist" returned from dist, vegdist, or dsvdis
k	the number of dimensions to return

Details

pco is simply a wrapper for the cmdscale function of Venebles and Ripley to make plotting of the function similar to other LabDSV functions

Value

an object of class 'pco' with components:

points	the coordinates of samples on eigenvectors

Note

Principal Coordinates Analysis was pioneered by Gower (1966) as an alternative to PCA better suited to ecological datasets.

Author(s)

of the 'cmdscale' function: Venebles and Ripley

of the wrapper function David W. Roberts <droberts@montana.edu>

References

Gower, J.C. (1966) Some distance properties of latent root and vector methods used in multivariate analysis. Biometrika 53:325-328.

http://ecology.msu.montana.edu/labdsv/R/labs/lab8/lab8.html

See Also

cmdscale, pca, nmds, cca

Examples

```
data(bryceveg) # returns a vegetation data.frame
dis.bc <- dsvdis(bryceveg,'bray/curtis')
          # returns an object of class dist'
veg.pco <- pco(dis.bc,k=4) # returns first 4 dimensions
```

`plot.nmds` *Plotting Routines For Nonmetric Multi-Dimensional Scaling Ordinations*

Description

A set of routines for plotting, highlighting points, or adding fitted surfaces to NMDSs.

Usage

```
## S3 method for class 'nmds'
plot(x, ax = 1, ay = 2, col = 1, title = "", pch = 1, ...)
## S3 method for class 'nmds'
points(x, which, ax = 1, ay = 2, col = 2, pch = 1, cex = 1,
                      breaks=FALSE, ...)
## S3 method for class 'nmds'
plotid(ord, ids = seq(1:nrow(ord$points)), ax = 1, ay = 2,
    col = 1, ...)
## S3 method for class 'nmds'
hilight(ord, overlay, ax = 1, ay = 2, title="", cols=c(2,3,4,5,6,7),
                      glyph=c(1,3,5), ...)
## S3 method for class 'nmds'
chullord(ord, overlay, ax = 1, ay = 2, cols=c(2,3,4,5,6,7),
                        ltys = c(1,2,3), ...)
## S3 method for class 'nmds'
surf(ord, var, ax = 1, ay = 2, thinplate = TRUE, col = 2, labcex = 0.8,
    family = gaussian, gamma=1, grid=50, ...)
## S3 method for class 'nmds'
thull(ord,var,grain,ax=1,ay=2,col=2,grid=50,nlevels=5,levels=NULL,lty=1,
     numitr=100,...)
## S3 method for class 'nmds'
density(ord, overlay, ax = 1, ay = 2, cols = c(2, 3, 4, 5,
    6, 7), ltys = c(1, 2, 3), numitr, ...)
```

Arguments

`x`	an object of class 'nmds'
`ax`	the dimension to use for the X axis
`ay`	the dimension to use for the Y axis
`title`	a title for the plot

which	a logical variable to specify points to be highlighted
breaks	a logical switch to control using variable glyph sizes in 'points'
ord	an object of class 'nmds'
overlay	a factor or integer vector to hilight or distinguish
cols	the sequence of color indices to be used
glyph	the sequence of glyphs (pch) to be used
ltys	the sequence of line types to be used
var	a variable to be surfaced or tension hulled
thinplate	a logical variable to control the fitting routine: thinplate=TRUE (the default) fits a thinplate spline, thinplate=FALSE fits independent smooth splines. If you have too few data points you may have to specify thinplate=FALSE
family	controls the link function passed to 'gam': one of 'gaussian', 'binomial', or 'poisson'
gamma	controls the smoothness of the fit from gam
grid	the number of X and Y values to use in establishing a grid for use in surf
grain	the size of cell to use in calculating the tensioned hull
nlevels	the number of contours to draw in representing the tensioned hull
lty	the line type to use in drawing tensioned hull contours
ids	identifier labels for samples. Defaults to 1:n
col	color index for points or contours
labcex	size of contour interval labels
pch	plot character: glyph to plot
cex	character expansion factor: size of plotted characters
numitr	the number of iterations to use in estimating the probability of the observed density
levels	specific levels for contours in thull
...	arguments to pass to the plot function

Details

Function 'plot' produces a scatter plot of sample scores for the specified axes, erasing or over-plotting on the current graphic device. Axes dimensions are controlled to produce a graph with the correct aspect ratio. Functions 'points', 'plotid', and 'surf' add detail to an existing plot. The axes specified must match the underlying plot exactly.

Function 'plotid' identifies and labels samples (optionally with values from a third vector) in the NMDS, and requires interaction with the mouse: left button identifies, right button exits.

Function 'points' is passed a logical vector to identify a set of samples by color of glyph. It can be used to identify a single set meeting almost any criterion that can be stated as a logical expression.

Function 'hilight' is passed a factor vector or integer vector, and identifies factor values by color and glyph.

Function 'chullord' is passed a factor vector or integer vector, and plots a convex hull around all points in each factor class. By specifying values for arguments 'cols' and 'ltys' it is possible to control the sequence of colors and linetypes of the convex hulls.

Function 'density' calculates the fraction of points within the convex hull that belong to the specified type.

Function 'surf' calculates and plots fitted surfaces for logical or quantitative variables. The function employs the gam function to fit a variable to the ordination coordinates, and to predict the values at all grid points. The grid is established with the 'expand.grid' function, and the grid is then specified in a call to 'predict.gam'. The predicted values are trimmed to the the convex hull of the data, and the contours are fit by 'contour'. The default link function for fitting the GAMs is 'gaussian', suitable for unbounded continuous variables. For logical variables you should specify 'family = binomial' to get a logistic GAM, and for integer counts you should specify 'family = poisson' to get a Poisson GAM.

Function 'thull' calculates a tensioned hull for a specific variable on the NMDS. A tensioned hull is a minimum volume container. The grain size must be specified as a fraction of the units of the NMDS, with larger values generating smoother representations, and smaller numbers a more resolved container. 'thull' returns an invisible object of class 'thull' which has an associated plot function. Plotting the thull object produces a colored surface representation of the thull with optional contour lines.

Value

Function 'plotid' returns a vector of row numbers of identified plots

Note

Previous versions of surf relied on the 'interp' function of package akima. The revised routine using predict.gam was suggested by Jari Oksanen as used in ordisurf.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab9/lab9.html

Examples

```
data(bryceveg)
data(brycesite)
dis.bc <- dsvdis(bryceveg,'bray/curtis')
nmds.1 <- nmds(dis.bc,5)
plot(nmds.1)
points(nmds.1,brycesite$elev>8000)
surf(nmds.1,brycesite$elev)
## Not run: plotid(nmds.1,ids=row.names(bryceveg))
```

plot.pca *Plotting Routines For Principal Components Ordinations*

Description

A set of routines for plotting, highlighting points, or adding fitted surfaces to PCAs.

Usage

```
## S3 method for class 'pca'
plot(x, ax = 1, ay = 2, col = 1, title = "", pch = 1, ...)
## S3 method for class 'pca'
points(x, which, ax = 1, ay = 2, col = 2, pch = 1, cex = 1, ...)
## S3 method for class 'pca'
plotid(ord, ids = seq(1:nrow(ord$scores)), ax = 1, ay = 2,
    col = 1, ...)
## S3 method for class 'pca'
hilight(ord, overlay, ax = 1, ay = 2, cols=c(2,3,4,5,6,7),
                      glyph=c(1,3,5), ...)
## S3 method for class 'pca'
chullord(ord, overlay, ax = 1, ay = 2, cols=c(2,3,4,5,6,7),
                       ltys = c(1,2,3), ...)
## S3 method for class 'pca'
surf(ord, var, ax = 1, ay = 2, col = 2, labcex = 0.8,
    family = gaussian, thinplate=TRUE, grid=50, gamma=1, ...)
varplot.pca(x, dim=length(x$sdev))
```

Arguments

x	an object of class 'pca'
ax	the dimension to use for the X axis
ay	the dimension to use for the Y axis
title	a title for the plot
which	a logical variable to specify points to be highlighted
ord	an object of class 'pca'
overlay	a factor or integer vector to hilight or distinguish
cols	the sequence of color indices to be used
glyph	the sequence of glyphs (pch) to be used
ltys	the sequence of line types to be used
var	a variable to be surfaced
family	controls the link function passed to 'gam': one of 'gaussian', 'binomial', or 'poisson'
ids	identifier labels for samples. Defaults to 1:n

dim	number of dimensions to include in barplot
col	color index for points or contours
labcex	size of contour interval labels
thinplate	a logical switch to control using thinplate splines versus independent additive fits
gamma	controls the smoothness of the fit from gam
grid	the number of X and Y values used in establishing a grid
pch	plot character: glyph to plot
cex	character expansion factor: size of plotted characters
...	arguments to pass to the plot function

Details

Function 'plot' produces a scatterplot of sample scores for the specified axes, erasing or over-plotting

Functions 'points', 'plotid', 'hilight', 'chullord', and 'surf' add detail to an existing plot. The axes specified must match the underlying plot exactly.

Function 'plotid' identifies and labels samples (optionally with values from a third vector) in the PCA, and requires interaction with the mouse: left button identifies, right button exits.

Function 'points' is passed a logical vector to identify a set of samples by color of glyph. It can be used to identify a single set meeting almost any criterion that can be stated as a logical expression.

Function 'hilight' is passed a factor vector or integer vector, and identifies factor values by color and glyph. By specifying values for arguments 'cols' and 'glyph' it is possible to control the sequence of colors and pch glyphs used in the hilight.

Function 'chullord' is passed a factor vector or integer vector, and plots a convex hull around all points in each factor class. By specifying values for arguments 'cols' and 'ltys' it is possible to control the sequence of colors and linetypes of the convex hulls.

Function 'surf' calculates and plots fitted surfaces for logical or quantitative variables. The function employs the gam function to fit a variable to the ordination coordinates, and to predict the values at all grid points. The grid is established with the 'expand.grid' function, and the grid is then specified in a call to 'gam.predict'. The predicted values are trimmed to the the convex hull of the data, and the contours are fit by 'contour'. The default link function for fitting the GAMs is 'gaussian', suitable for unbounded continuous variables. For logical variables you should specify 'family = binomial' to get a logistic GAM, and for integer counts you should specify 'family = poisson' to get a Poisson GAM.

Value

Function 'plotid' returns a vector of row numbers of identified plots.

Function 'varplot.pca' produces two plots: (1) the variance accounted for by eigenvector up to the specified number of dimensions (default = all), and (2) the cumulative variance accounted for by dimension.

Note

Previous versions of surf relied on the 'interp' function of package akima. The revised routine using predict.gam was suggested by Jari Oksanen as used in package vegan.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab7/lab7.html

Examples

```
data(bryceveg)
data(brycesite)
pca.1 <- pca(bryceveg)
plot(pca.1)
points(pca.1,brycesite$elev>8000)
surf(pca.1,brycesite$elev)
## Not run: plotid(pca.1,ids=row.names(bryceveg))
```

---

plot.pco *Plotting Routines For Principal Coordinates Ordinations*

Description

A set of routines for plotting, highlighting points, or adding fitted surfaces to PCOs.

Usage

```
## S3 method for class 'pco'
plot(x, ax = 1, ay = 2, col = 1, title = "", pch = 1, ...)
## S3 method for class 'pco'
points(x, which, ax = 1, ay = 2, col = 2, pch = 1, cex = 1, ...)
## S3 method for class 'pco'
plotid(ord, ids = seq(1:nrow(ord$points)), ax = 1, ay = 2,
    col = 1, ...)
## S3 method for class 'pco'
hilight(ord, overlay, ax = 1, ay = 2, title="", cols=c(2,3,4,5,6,7),
    glyph=c(1,3,5), ...)
## S3 method for class 'pco'
chullord(ord, overlay, ax = 1, ay = 2, cols=c(2,3,4,5,6,7),
    ltys = c(1,2,3), ...)
## S3 method for class 'pco'
density(ord, overlay, ax = 1, ay = 2, cols = c(2, 3, 4, 5,
    6, 7), ltys = c(1, 2, 3), numitr=100, ...)
## S3 method for class 'pco'
```

```
surf(ord, var, ax = 1, ay = 2, thinplate=TRUE, col = 2, labcex = 0.8,
    family = gaussian, grid=50, gamma=1, ...)
## S3 method for class 'pco'
thull(ord,var,grain,ax=1,ay=2,col=2,grid=50,nlevels=5,levels=NULL,
    lty=1,numitr=100,...)
```

Arguments

x	an object of class 'pco'
ax	the dimension to use for the X axis
ay	the dimension to use for the Y axis
title	a title for the plot
which	a logical variable to specify points to be highlighted
ord	an object of class 'pco'
overlay	a factor or integer vector to hilight or distinguish
cols	the sequence of color indices to be used
glyph	the sequence of glyphs (pch) to be used
ltys	the sequence of line types to be used
numitr	number of iterations to use in estimating the probability of obtaining the observed density
var	a variable to be surfaced
thinplate	a logical variable to control how the surface is fit: thinplate = TRUE (the default) fits a thinplate spline, thinplate = FALSE fits independent smooth splines. If you have too few data points you may have to specify thinplate-FALSE
family	controls the link function passed to 'gam': one of 'gaussian', 'binomial', or 'poisson'
gamma	controls the smoothness of the fit from gam
grid	the number of X and Y points to use in establishing a grid for surf
ids	identifier labels for samples. Defaults to 1:n
col	color index for points or contours
labcex	size of contour interval labels
pch	plot character: glyph to plot
cex	character expansion factor: size of plotted characters
grain	the size of moving window to use in calculating the tensioned hull
nlevels	the number of contour intervals to draw on the tensioned hull
levels	specific levels to use in drawing the tensioned hull
lty	the line type to use in drawing the tensioned hull contours
...	arguments to pass to the plot function

Details

Function 'plot' produces a scatterplot of sample scores for the specified axes, erasing or over-plotting on the current graphic device. Axes dimensions are controlled to produce a graph with the correct aspect ratio.

Functions 'points', 'plotid', 'hilight', 'chullord', and 'surf' add detail to an existing plot. The axes specified must match the underlying plot exactly.

Function 'plotid' identifies and labels samples (optionally with values from a third vector) in the PCO, and requires interaction with the mouse: left button identifies, right button exits.

Function 'points' is passed a logical vector to identify a set of samples by color of glyph. It can be used to identify a single set meeting almost any criterion that can be stated as a logical expression.

Function 'hilight' is passed a factor vector or integer vector, and identifies factor values by color and glyph. By specifying values for arguments 'cols' and 'glyph' it is possible to control the sequence of colors and pch glyphs used in the hilight.

Function 'chullord' is passed a factor vector or integer vector, and plots a convex hull around all points in each factor class. By specifying values for arguments 'cols' and 'ltys' it is possible to control the sequence of colors and linetypes of the convex hulls.

Function 'density' calculates the fraction of points within the convex hull that belong to the specified type.

Function 'surf' calculates and plots fitted surfaces for logical or quantitative variables. The function employs the gam function to fit a variable to the ordination coordinates, and to predict the values at all grid points. The grid is established with the 'expand.grid' function, and the grid is then specified in a call to 'predict.gam'. The predicted values are trimmed to the the convex hull of the data, and the contours are fit by 'contour'. The default link function for fitting the GAMs is 'gaussian', suitable for unbounded continuous variables. For logical variables you should specify 'family = binomial' to get a logistic GAM, and for integer counts you should specify 'family = poisson' to get a Poisson GAM.

Value

Function 'plotid' returns a vector of row numbers of identified plots

Note

Previous versions of surf relied on the 'interp' function of package akima. The revised routine using predict.gam was suggested by Jari Oksanen as used in packageordisurf.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab8/lab8.html

Examples

```
data(bryceveg)
data(brycesite)
dis.bc <- dsvdis(bryceveg,'bray/curtis')
pco.1 <- pco(dis.bc,5)
plot(pco.1)
points(pco.1,brycesite$elev>8000)
surf(pco.1,brycesite$elev)
## Not run: plotid(pco.1,ids=row.names(bryceveg))
```

`plot.thull` *Plotting a Tensioned Hull*

Description

A tensioned hull is a minimum volume container for specified elements of an ordination. A 'thull' object is returned as an invisible object by plotting a thull of an NMDS or PCO (or MFSO). Subsequently plotting the returned thull results in an 'image' of the representation.

Usage

```
## S3 method for class 'thull'
plot(x,col=rainbow(20),levels=NULL,cont=TRUE,
          xlab=x$xlab,ylab=x$ylab,main=x$main,...)
```

Arguments

`x`	an object of class 'thull' from function thull
`col`	the color to use plotting the contours
`levels`	the specific levels desired for the contours
`cont`	a logical variable to control plotting contours on the image representation of the tensioned hull
`xlab`	the X axis label
`ylab`	the Y axis label
`main`	the main title
`...`	other graphics parameters

Details

Tensioned hull analysis fits a minimum volume envelope to specific points in an ordination. A tensioned hull object is returned from function `thull` of a PCO, NMDS or MFSO. This function plots the resulting tensioned hull as an image, with optional overlays of contours.

Value

Produces a plot on the current graphic device.

Author(s)

David W. Roberts <droberts@montana.edu>

Examples

```
data(bryceveg) # returns a dataframe called bryceveg
dis.bc <- dsvdis(bryceveg,'bray') # calculates a Bray-Curtis
                                  # dissimilarity matrix
nmds.bc <- nmds(dis.bc) # calculates an NMDS ordination
plot(nmds.bc) # plots the ordination on the current device
demo.thull <- thull(nmds.bc,bryceveg$arcpat,0.25) # calculates
                   # the tensioned hull representing the distribution
                   # of a species
plot(demo.thull) # portrays the image version of the tensioned hull
```

---

raretaxa *Identify Rare Taxa in a Data Set*

Description

Identifes the distribution of rare taxa in a taxon dataframe, using a specified rareness threshold.

Usage

```
raretaxa(taxa,min=1,log=FALSE,type='b', panel='all')
```

Arguments

taxa	a taxon dataframe with samples as rows and species as columns
min	the minimum number of occurrences for a species to be considered rare
log	controls whether or not the Y axis on some graphs should be log scaled
type	the plot type. 'b' = both points and lines
panel	a switch to control which graphic is displayed. Can be either an integer from 1 to 3 or the word 'all'.

Details

Rare species are an issue in ecological data sets. This function produces three graphs identifying (1) the distribution of rare species/plot, (2) the mean abundance (when present) of rare species, and (3) the total abundance or rare species/plot.

Value

Produces only graphs and returns no output

Author(s)

David W. Roberts <droberts@montana.edu>

Examples

```
data(bryceveg)
## Not run: raretaxa(bryceveg,min=3,log=TRUE)
```

`reconcile` *Reconcile Taxa and Site Data.Frames*

Description

reconcile takes two data frames (taxa and site) and sorts both into the same order, and then deletes any rows unique to either of the two data.frames, achieving perfect correspondence of the two.

Usage

```
reconcile(taxa,site)
```

Arguments

`taxa`	a taxon abundance data.frame with samples as rows and species as columns
`site`	a data.frame of site or environmental varialbles with samples as rows and variables as columns

Details

reconcile sorts each data.frame alphabetically by row.name, and then compares the list of row.names to identify sample plots common to both data.frames. Sample plots which occur in only one of the data.frames are deleted.

Value

a list object with two elements: taxa and site, which are the sorted and reconciled data.frames.

Note

package labdsv (and many other packages in ecological data analysis) require two data.frames to structure the data. One contains the abundance of taxa within samples with samples as rows and taxa as columns. This data.frame I refer to as the taxa data.frame. The other data.frame contains all the environmental or site data collected at the same samples. This data.frame I refer to as the site data.frame. Due to independent subsampling, sorting or editing of the data (often outside of R) the two data.frames often lose the necessary requirement of the identical number of rows, with the rows in exactly the same order. The reconcile() function is a simple remedy to correct this situation while maintaining the maximum amount of data.

Author(s)

David W. Roberts <droberts@montana.edu>

Examples

```
data(bryceveg)   # returns a data.frame of taxon abundance
data(brycesite)  # returns a data.frame of site variables
test <- reconcile(bryceveg,brycesite)
```

---

rnddist *Random Distance*

Description

Calculates a random distance matrix for use in null model analysis.

Usage

```
rnddist(size, method='metric', sat = 1.0, upper=FALSE, diag=FALSE)
```

Arguments

size	the number of items to calculate the distances for
method	the desired properties of the matrix. Must be either 'metric' or 'euclidean'
sat	a saturation coefficient to set an upper limit less than 1.0 that truncates maximum values to simulate a dissimilarity rather than a distance
upper	logical: whether to print the upper triangle (default=FALSE)
diag	logical: whether to print the diagonal (default=FALSE)

Details

Generates a matrix of $size^2$ uniform random numbers and passes the matrix to metrify or euclidify to ensure the metric or euclidean properties of the distances. Values are normalized to a maximum of 1.0.

Author(s)

David W. Roberts <droberts@montana.edu>

See Also

metrify, euclidify

Examples

```
x <- rnddist(100)
pco.x <- pco(x)
plot(pco.x)
```

rndtaxa *Randomize a Taxa Data.Frame*

Description

Permutes a vegetation (or other) data.frame to establish a basis for null model tests in vegetation ecology.

Usage

```
rndtaxa(taxa,replace=FALSE,species=FALSE,plots=FALSE)
```

Arguments

taxa	the vegetation (or other taxon) data.frame, samples as rows, species as columns
replace	a switch for permuting (if FALSE) or boostrapping (if TRUE)
species	a switch to control randomizing by species (if TRUE), maintaining species occurrence distributions
plots	a switch to control randomizing by samples (if TRUE), maintaining plot-level species richness

Details

Permutes or bootstraps a vegetation data frame for input to dist, vegdist, dsvdis, or other routines. Can randomize by columns (species=TRUE), samples (plots=TRUE), or fully (neither species nor plots = TRUE).

Value

a data.frame with samples as rows and species as columns of the same dimensions as entered.

Note

Randomizing vegetation often leads to unrealistic data distributions, but this function attempts to preserve either species occurrence distributions or plot-level species richness. It is probably worth examining the output of this function with abuocc to see its characteristics before engaging in extensive analysis.

Author(s)

David W. Roberts <droberts@montana.edu>

Examples

```
data(bryceveg) # returns a vegetation data.frame called bryceveg
test <- rndtaxa(bryceveg,species=TRUE) # preserves species abundance
        # distribution
test2 <- rndtaxa(bryceveg,plots=TRUE) # preserves plot-level
                                      # species richness
```

---

spcdisc *Species Discrimination Analysis*

Description

Calculates the degree to which species are restricted to certain classes of classified vegetation

Usage

```
spcdisc(x,sort=FALSE)
```

Arguments

x	a classified vegetation table returned by 'const', or 'importance'
sort	return in sorted order if TRUE

Details

Calculates a Shannon-Weiner information statistic on the relative abundance of species within classes.

Value

A vector of discrimination values.

Author(s)

David W. Roberts <droberts@montana.edu>

See Also

const, importance, indval, isamic

Examples

```
data(bryceveg)
data(brycesite)
test <- const(bryceveg,brycesite$quad)
spcdisc(test)
```

vegtab *Vegetation Table*

Description

Produces an ordered table of abundance of species in samples, sub-sampled by (an optional) classification of the samples

Usage

```
vegtab(taxa,set,minval=1,pltord,spcord,pltlbl,trans=FALSE)
```

Arguments

taxa	a vegetation (or other taxon) data.frame
set	a logical variable specifying which samples to include
minval	a minimum abundance threshold to include in the table
pltord	a numeric vector specifying the order of rows in the output
spcord	a numeric vector specifying the order of columns in the output
pltlbl	a vector specifying an alternative row label (must be unique!)
trans	a logical variable to control transposing the table

Details

Subsets a vegetation data.frame according to specified plots or minimum species abundances, optionally ordering in arbitrary order.

Value

a data.frame with specified rows, columns, and row.names

Note

Vegetation tables are a common tool in vegetation analysis. In recent years analysis has tended to become more quantitative, and less oriented to sorted tables, but even still presenting the results from these analyses often involves a sorted vegetation table.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab3/lab3.html

See Also

vegemite

Examples

```
data(bryceveg) # returns a vegetation data frame called bryceveg
data(brycesite) # returns an environmental data frame called brycesite
vegtab(bryceveg,minval=10,pltord=brycesite$elev)
    # produces a sorted table for species whose abundance sums
    # to 10, with rows in order of elevation.
```

---

vegtrans *Vegetation Data Transformation*

Description

Transforms vegetation abundances according to an arbitrary specified vector

Usage

```
vegtrans(taxa,code,value)
```

Arguments

taxa	the original vegetation (or other taxon) data.frame
code	a vector containing the set of values appearing in the original data.frame
value	a vector containing the set of respective values to substitute

Details

Performs a respective substitution to transform specific values in an initial data.frame to other specified values.

Value

a data.frame of transformed vegetation

Note

Vegetation data are often collected in arbitrary abundance schemes (e.g. Braun-Blanquet, Domin, etc.) which have no direct algebraic transformation (e.g. log). This function transforms coded abundances to arbitrary importance values as specified.

Author(s)

David W. Roberts <droberts@montana.edu>

References

http://ecology.msu.montana.edu/labdsv/R/labs/lab1/lab1.html

See Also

decostand, wisconsin

Examples

```
data(bryceveg)
old <- c(0.2,0.5,1.0,2.0,3.0,4.0,5.0,6.0)
new <- c(0.2,0.5,3.0,15.0,37.5,62.5,85.0,97.5)
newveg <- vegtrans(bryceveg,old,new)
```

Index

∗Topic **IO**
dematrify, 9
matrify, 24
∗Topic **aplot**
ordpart, 31
plot.nmds, 37
plot.pca, 40
plot.pco, 42
plot.thull, 45
∗Topic **arith**
vegtrans, 52
∗Topic **cluster**
envrtest, 17
indval, 21
isamic, 23
ordpart, 31
∗Topic **datagen**
rnddist, 48
rndtaxa, 49
∗Topic **datasets**
brycesite, 4
bryceveg, 4
∗Topic **data**
ordtaxa, 32
∗Topic **hplot**
ordcomp, 28
orddist, 30
ordpart, 31
plot.nmds, 37
plot.pca, 40
plot.pco, 42
raretaxa, 46
∗Topic **iplot**
ordpart, 31
plot.nmds, 37
plot.pca, 40
plot.pco, 42
∗Topic **manip**
dropplt, 13
dropspc, 14
reconcile, 47
∗Topic **multivariate**
abuocc, 2
compspec, 5
concov, 6
const, 7
dga, 10
disana, 11
dsvdis, 15
euclidify, 18
homoteneity, 19
importance, 20
metrify, 25
nmds, 27
ordcomp, 28
orddist, 30
ordtest, 33
pca, 34
pco, 36
spcdisc, 50
vegtab, 51

abuocc, 2, *49*
anosim, *34*
archi, *21*

bestnmds *(*nmds*)*, 27
brycesite, 4
bryceveg, 4

cca, *35, 36*
chullord.nmds *(*plot.nmds*)*, 37
chullord.pca *(*plot.pca*)*, 40
chullord.pco *(*plot.pco*)*, 42
compspec, 5
concov, 6, *19–21*
const, *7*, 7, *19–21*, *50*

decostand, *53*

dematrify, 9, *25*
density.nmds *(*plot.nmds*)*, 37
density.pco *(*plot.pco*)*, 42
dga, 10
disana, 11
dist, *12*, *18*, *26*, *29*, *49*
dropplt, 13
dropspc, 14
dsvdis, *3*, *5*, *12*, 15, *18*, *26*, *36*, *49*
duarm *(*isamic*)*, 23
duleg *(*indval*)*, 21

envrtest, 17
euclidify, 18, *26*, *48*

fisherfit, *3*
fso, *29, 30*, *35*

gam, *11*, *38, 39*, *41*, *43, 44*

hilight.nmds *(*plot.nmds*)*, 37
hilight.pca *(*plot.pca*)*, 40
hilight.pco *(*plot.pco*)*, 42
homoteneity, 19

importance, *7*, *9*, 20, *50*
indspc *(*compspec*)*, 5
indval, 21, *24*, *50*
initMDS, *28*
isamic, *23*, 23, *50*

loadings.pca *(*pca*)*, 34

matrify, *10*, 24
metaMDS, *28*
metrify, *18*, 25, *48*
mgcv, *11*

nmds, 27, *29, 30*, *35, 36*

optpart, *21*
ordcomp, 28
orddist, 30
ordiplot, *29*
ordisurf, *39*, *44*
ordpart, 31
ordtaxa, 32
ordtest, 33

pam, *21*, *23*
partana, *23*
partition, *19, 20*
pca, *29, 30*, 34, *36*
pco, *29, 30*, *35*, 36
plot.compspec *(*compspec*)*, 5
plot.nmds, *28*, 37
plot.pca, 40
plot.pco, 42
plot.thull, 45
plotid.nmds *(*plot.nmds*)*, 37
plotid.pca *(*plot.pca*)*, 40
plotid.pco *(*plot.pco*)*, 42
points.nmds *(*plot.nmds*)*, 37
points.pca *(*plot.pca*)*, 40
points.pco *(*plot.pco*)*, 42
postMDS, *28*
predict.gam, *39*, *42*, *44*
prestonfit, *3*

radfit, *3*
raretaxa, 46
reconcile, 47
rnddist, 48
rndtaxa, 49

scores.pca *(*pca*)*, 34
slice, *21*, *23*
spcdisc, 50
stride, *21*
summary.indval *(*indval*)*, 21
summary.pca *(*pca*)*, 34
surf.nmds *(*plot.nmds*)*, 37
surf.pca *(*plot.pca*)*, 40
surf.pco *(*plot.pco*)*, 42

thull, *45*
thull *(*plot.thull*)*, 45
thull.nmds *(*plot.nmds*)*, 37
thull.pco *(*plot.pco*)*, 42

varplot.pca *(*plot.pca*)*, 40
vegdist, *5*, *12*, *16*, *18*, *26*, *36*, *49*
vegemite, *9*, *52*
vegtab, *9*, *20, 21*, 51
vegtrans, 52

wisconsin, *53*