Package ‘dave’

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R topics documented:

aocc ......................................................... 2
ccost ......................................................... 4
centroid ...................................................... 6
dave ........................................................... 7
davesil ....................................................... 8
dircor ......................................................... 10
EKs ............................................................ 11
EKv ............................................................ 12
fitmarkov ...................................................... 13
fspa ............................................................ 14
ltim ............................................................ 16
lveg ............................................................ 17
Mtabs .......................................................... 18
mveg ........................................................... 20
<table>
<thead>
<tr>
<th>Term</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>mxplot</td>
<td>21</td>
</tr>
<tr>
<td>nsit</td>
<td>22</td>
</tr>
<tr>
<td>nveg</td>
<td>23</td>
</tr>
<tr>
<td>orank</td>
<td>24</td>
</tr>
<tr>
<td>outlier</td>
<td>26</td>
</tr>
<tr>
<td>overly</td>
<td>27</td>
</tr>
<tr>
<td>pcaser</td>
<td>29</td>
</tr>
<tr>
<td>pcobiplot</td>
<td>30</td>
</tr>
<tr>
<td>pcovar</td>
<td>31</td>
</tr>
<tr>
<td>psit</td>
<td>33</td>
</tr>
<tr>
<td>pveg</td>
<td>34</td>
</tr>
<tr>
<td>sn59sit</td>
<td>35</td>
</tr>
<tr>
<td>sn59veg</td>
<td>35</td>
</tr>
<tr>
<td>sn6sit</td>
<td>36</td>
</tr>
<tr>
<td>sn6veg</td>
<td>37</td>
</tr>
<tr>
<td>sn7sit</td>
<td>38</td>
</tr>
<tr>
<td>sn7veg</td>
<td>39</td>
</tr>
<tr>
<td>SNPsm</td>
<td>40</td>
</tr>
<tr>
<td>SNPtm</td>
<td>41</td>
</tr>
<tr>
<td>speedprof</td>
<td>42</td>
</tr>
<tr>
<td>srank</td>
<td>43</td>
</tr>
<tr>
<td>ssind</td>
<td>45</td>
</tr>
<tr>
<td>ssit</td>
<td>46</td>
</tr>
<tr>
<td>sspft</td>
<td>47</td>
</tr>
<tr>
<td>sveg</td>
<td>48</td>
</tr>
<tr>
<td>tsit</td>
<td>49</td>
</tr>
<tr>
<td>tveg</td>
<td>50</td>
</tr>
<tr>
<td>vsrsv</td>
<td>51</td>
</tr>
<tr>
<td>vrveg</td>
<td>52</td>
</tr>
<tr>
<td>vvelocity</td>
<td>57</td>
</tr>
<tr>
<td>wetsit</td>
<td>59</td>
</tr>
<tr>
<td>wetveg</td>
<td>62</td>
</tr>
<tr>
<td>ws200</td>
<td>62</td>
</tr>
<tr>
<td>ws30</td>
<td>63</td>
</tr>
<tr>
<td>ws500</td>
<td>64</td>
</tr>
<tr>
<td>wsssit</td>
<td>64</td>
</tr>
</tbody>
</table>

**Index**

66

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**aocc**  
*Analysis of concentration (AOC)*
Description

Given a two-dimensional matrix of vegetation data the function derives a contingency table of counts (scores presence-absence transformed) based on input classification of rows (the vegetation releves) and columns (the species). The cells of the contingency table are then adjusted to equal weight, followed by correspondence analysis (cca). Concentration of counts is measured and an ordination plotted.

Usage

```r
aocc(veg, o.rgr, o.sgr,...)  
aoc(veg, o.rgr, o.sgr)
```

```r
## Default S3 method:  
aocc(veg, o.rgr, o.sgr,...)  
## S3 method for class 'aocc'  
plot(x,...)
```

Arguments

- `veg` A data frame of vegetation releves (rows) by species (columns)
- `o.rgr` Group membership of rows given upon input
- `o.sgr` Group membership of columns given upon input
- `x` An object of class "aocc"
- `...` Further variables used for plotting

Details

These input parameters are typically generated by functions clust() and cutree() in the cluster package. See example below.

Value

An output list of class "aocc" with at least the following items:

- `rgrscores` Ordination scores of releve groups
- `sgrscores` Ordination scores of species groups
- `eigvar` Eigenvalues of correspondence analysis
- `grand.total` Grand total of contingency table
- `MSCC` Mean square contingency coefficient, a measure of concentration
- `new.relorder` Order of rows after ordering groups according to 1. axis
- `new.sporder` Order of columns after ordering groups according to 1. axis
- `cont.table` The contingency table

Note

The analysis of lattice structure, described in some of the references, is not included in this function.
Author(s)
Otto Wildi

References

Examples
# First, groups of releves are formed
require(vegan)
dr<- vegdist(nveg*0.5,method="bray")       # dr is distance matrix of rows
o.clr<- hclust(dr,method="ward.D2")       # this is clustering
o.rgr<- cutree(o.clr,k=3)                 # 3 row groups formed
# Now I group the columns of nveg (the species)
# the same way as for rows
ds<- vegdist(t(nveg*0.25),method="euclid")
o.cls<- hclust(ds,method="ward.D2")
o.sgr<- cutree(o.cls,k=4)                  # 4 column groups formed

o.aocc<- aocc(nveg,o.rgr,o.sgr)
plot(o.aocc)                               # double scatter plot
                                      # 3 row-, 4 column goups as points.

# If cluster analysis is not used but classification is input by row and
# column to be processed by aocc():
o.rgr<- c(1,2,1,3,2,3,1,2,3,1,3)
o.sgr<- c(1,1,2,2,1,3,4,3,1,1,1,3,3,1,1,4,4,4,1,3)
o.aocc<- aocc(nveg,o.rgr,o.sgr)
plot(o.aocc)

ccost  Cost function of 2 alternative classifications of rows in vegetation data

Description
Given 2 alternative classifications (g groups) of rows in a data frame of vegetation data, confusion matrix, C, is derived first. Using the first classification a matrix of row centroids is derived (using function centroid) of which a g by g distance matrix, W, is computed (correlation transformed to distance). Cost factor, cf, is the sum of element by element multiplication of C and W respectively, cf=\sum(CW).
Usage

ccost(veg, oldgr, newgr, y, ...)
ccost2(veg, oldgr, newgr, y)

## Default S3 method:
ccost(veg, oldgr, newgr, y, ...)
## S3 method for class 'ccost'
print(x, ...)

Arguments

veg A data frame of vegetation releves (rows) by species (columns)
oldgr Initial classification, e.g., derived by hclust()
newgr Final classification, e.g., result of a model
y Transformation of species scores: x’= x exp(y)
x An object of class "ccost"
... Further variables used for printing

Details

Cost factor cf has range 0 (both classifications identical) to n (number of rows), where n is the worst case of misclassification.

Value

An output list of class "ccost" with at least the following items:
dimension Dimension of confusion matrix (n by n)
ccost Cost factor, cf
old.groups Initial classification
new.groups Final classification
conf.matrix Confusion matrix
weight.matrix Weighth matrix
transf Transformation applied to scores, y-value

Author(s)

Otto Wildi

References

Examples

# First, groups of releves are formed by cluster analysis require(vegan)

dr <- vegdist(nveg * 0.5, method = "bray")  # dr is distance matrix of rows

o.clr <- hclust(dr, method = "ward")  # this is clustering

oldgr <- cutree(o.clr, k = 3)  # 3 row groups formed

oldgr  # this displays initial classification:

# 2 4 6 9 10 18 25 27 39 49 50
# 1 2 1 3 2 3 1 2 3 1 3

# For simplicity we assume that row "2" and "50" change membership:

newgr <- c(2, 2, 1, 3, 2, 3, 1, 2, 3, 1, 1)

o.ccost <- ccost(nveg, oldgr, newgr, y = 0.5)  # does square root transformation

# Default method releasing cf

o.ccost  # displays C and W (see above)

centroid

Centroids of row groups (vegetation releves)

Description

Given a two-dimensional data frame or matrix of vegetation data and group membership of rows (releve classification) a new matrix is derived with relative species frequency (0 to 1 scale) within groups. The matrix of centroids has as many rows as there are row groups in the vegetation matrix and the same number of columns (species).

Usage

centroid(nveg, grel, y, ...)

## Default S3 method:
centroid(nveg, grel, y, ...)  
## S3 method for class 'centroid'

print(x, ...)

Arguments

nveg A data frame of vegetation releves (rows) by species (columns)
grel A vector containing group membership of releves (rows), typically generated by

hclust and cutree

y Transformation of species scores: x' = x exp(y)

... Further variables used for printing

x A list of class "centroid" generated by centroid
Value
An output list of class "centroid" with at least the following items:

- `nrelgroups`: Number of rows of centroid table
- `nspec`: Number of columns of centroid table
- `freq.table`: A table of species frequencies within groups, unadjusted
- `prob.table`: A table of species frequencies within groups, adjusted (0-1)
- `dist.mat`: An nrelgroups by nrelgroups distance matrix of centroids

Note
In function Mtabs() built in as summary method

Author(s)
Otto Wildi

References

Examples

```r
# This generates a typical artificial vegetation data frame `aveg`
aveg <- matrix(rep(0, 200), nrow=10)
aveg[1:4, 1:3] <- 1
aveg[5:8, 9:11] <- 0

# First, groups of relevés are formed by cluster analysis
require(vegan)
dr <- vegdist(aveg, method="bray")
do.clr <- hclust(dr, method="ward")
grel <- cutree(d.o.clr, k=3)
d.o.centroid <- centroid(d.o.aveg, d.o.grel, y=0.5)
do.centroid
```
The use of all functions included is explained in "Data Analysis in Vegetation Ecology" (see reference below). Version 2.0 includes various new data frames, sspt and ssind, plant functional types and indicator values respectively to be used in conjunction with sveg. Also new is a somewhat longer time series, sn7veg and sn7sit and the new "Vraconnaz" time series in vrveg and vrsit.

Author(s)

Otto Wildi, otto.wildi@wsl.ch

References


Examples

# A typical and probably the most complex function is Mtab() that re-arranges
# the rows and columns within a vegetation data frame and through plotting it
# illustrates the presumably emerging pattern:
y.r<- 0.5 ; y.s<- 0.2 # defining transformations used
k.r <- 3 ; k.s <- 4 # row- and column numbers
ndiffs <- 18 # no. of columns used to show pattern
o.Mt<-Mtabs(nveg,"mulva",y.r,y.s,k.r,k.s,ndiffs)
plot(o.Mt,method="normal")
# to see the original order simply replace "mulva" by "raw"

davesil

Modified version of silhouette plotting

Description

This is a wrapper for function silhouette in the cluster package. It also relies on the output of hclust and cutree.

Usage

davesil(ddist, o.hclr, o.relgr, ...)
dsil(ddist, o.hclr, o.relgr)

# Default S3 method:
davesil(ddist, o.hclr, o.relgr, ...)
## S3 method for class 'davesil'
plot(x, ..., range=NULL)

Arguments

- **ddist**: A distance matrix, probably the same as used for clustering
- **o.hclr**: Output object of function hclust()
- **o.relgr**: Output object of function cutree()
- **...**: Plot parameter range(a,b) can be specified to limit plot to the subsed specified by a (begin) and b (end).
- **x**: An object of class "davesil"
- **range**: A vector of length 2, allows to plot a portion of the silhouette, e.g., range=c(1,5) plots the first 5.

Details

See function silhouette in the cluster package.

Value

An output list of class "davesil" with at least the following items:

- **sil**: Data for drawing the silhouette, computed by silhouette()
- **names**: The names of the items clustered, first 15 characters, used for plotting

Author(s)

Otto Wildi

References


Examples

```r
# An ordinary cluster analysis
ddr<- as.dist(1-cor(t(nveg)))/2  # distance matrix, correlation as distance
o.hclr<- hclust(ddr,method="complete")
o.relgr<- cutree(o.hclr,k=3)
# Getting silhouette plot
o.davesil<- davesil(ddr,o.hclr,o.relgr)
plot(o.davesil)
```
**dircor**

_DIRctional mantel correlation_

**Description**

Given a two-dimensional vegetation data frame and the x- and y-coordinates of the releves (the rows in the data frame) in geographical space, mantel correlation (function `mantel` in the vegan package) is evaluated at regular intervals of direction. Direction versus correlation is plotted including 95 percent confidence interval.

**Usage**

```r
dircor(veg, x.axis, y.axis, step,...)
dircor2(veg, x.axis, y.axis, step = 5)
```

```r
## Default S3 method:
dircor(veg, x.axis, y.axis, step,...)
## S3 method for class 'dircor'
plot(x,...)
```

**Arguments**

- `veg` A data frame of vegetation releves (rows) by species (columns)
- `x.axis` This is the x-coordinate in geographical space
- `y.axis` This is the y-coordinate in geographical space
- `step` The step length in degrees, used to draw the above mentioned function
- `x` An object of class "dircor"
- `...` Further variables used for printing

**Details**

The method presently uses correlation as distance, as.dist((1-cor(t(sveg^2.0)))/2), as distance measure for vegetation releves.

**Value**

An output list of class "dircor" with at least the following items:

- `steps` The explicit steps used in degrees, 0 - 180 degrees
- `mean.correlation` Mantel correlation at each step
- `lower.limit` The lower confidence limits
- `upper.limit` The upper confidence limits
Note

Computation time is fairly long because function mantel() evaluates the confidence limits for each directional step between 0 and 180 degrees. See also mantel in the vegan package.

Author(s)

Otto Wildi

References


Examples

```r
# vegetation data is taken from sveg
# the x- and y-axes are stored in object ssit
o.dircor<- dircor(sveg,ssit$x.axis,ssit$y.axis,step=40)
plot(o.dircor)
```

---

**Eks**

*Swiss forest vegetation data base 1972, site information*

Description

Swiss forest vegetation data base 1972, site information. Vegetation data is in data frame **EKv**.

Usage

data(EKs)

Format

A data frame with 2533 observations on the following 11 variables.

**Autor**  a factor with author names as levels  
**Jahr**  a numeric vector with year of survey  
**Tabellennr.**  a numeric vector  
**Laufnr.**  a numeric vector  
**Gesellschaftsnr**  a factor with name of vegetation unit as levels  
**Hoehe_u.M.**  a numeric vector, elevation a.s.l.  
**Neigung_in_Prozent**  a numeric vector  
**Exposition**  a factor with exposure of plot as levels  
**Y.Koordinate**  y coordinate, a numeric vector  
**X.Koordinate**  x coordinate, a numeric vector  
**EK.Gesellschaftsnr**  number (label) of vegetation unit the releve belongs to, a numeric vector
Details

Classification used in 1972 is in variable "EK.Gesellschaftsnr"

Source


References


Examples

summary(HeksI)

<table>
<thead>
<tr>
<th>EKv</th>
</tr>
</thead>
<tbody>
<tr>
<td>Swiss forest vegetation data base 1972, vegetation information</td>
</tr>
</tbody>
</table>

Description

Swiss forest vegetation data base 1972, vegetation information. Site data is in data frame EKs.

Usage
data(EKv)

Format

A data frame with 2533 observations on 1259 species, the variables on a numerical scale from 0 to 7.

Details

Old taxonomy, not updated.

Source


References


Examples

summary(EKv)

fitmarkov

Approximating a Markov chain

Description

Given a vegetation data frame considered a time series with relevées as rows and species as columns transition matrices are derived for each time step based on some simple assumptions. These are averaged and a model series is derived through scalar products. Time steps are given in a separate vector \( t \). Missing steps are properly processed.

Usage

```r
fitmarkov(veg, t, adjust = FALSE, ...) 
rfitmarkov(veg, t, adjust)
```

## Default S3 method:
```r
fitmarkov(veg, t, adjust = FALSE, ...) 
```

## S3 method for class 'fitmarkov'
```r
plot(x,...)
```

Arguments

- `veg` This is a vegetation data frame, relevées are rows, species columns
- `t` The time step scale of length according with rows in \( x \)
- `x` An object of class "fitmarkov"
- `adjust` A logical vector adjusting the sum of species scores to 1.0. Default is adjust=FALSE
- `...` Vector colors of any length for line colors, vector widths for line widths. See example below.

Details

This method yields a possible solution for fitting a Markov series. The true process may be very different.
Value

An output list of class "fitmarkov" with at least the following items:

- fitted.data: The fitted time series’
- raw.data: The input time series’
- transition.matrix: The mean transition matrix’
- t.measured: The time steps upon input where time steps may be missing’
- t.modeled: The time steps upon output, no missing steps’

Note

The aim of this method is to provide a smooth curve based on input data. Because this relies on incomplete information, it is just one out of many solutions.

Author(s)

Otto Wildi

References


Examples

```r
# data frame ltim is Lippe's data (see references)
# ltim just contains the time scale of the same
o.fm<-fitmarkov(1veg,ltim$Year)
plot(o.fm)
```

Description

Flexible shortest path adjustment is a heuristic ordination method attempting to adjust pattern to ecological situations. It erases long distances in the resemblance matrix and replaces these by the sum of intermediate steps. Subsequent ordination uses function `pco`. 
Usage

fspa(veg, method, d.rev, n.groups, ...)
fspa2(veg, method, d.rev=0.5, n.groups=3)

## Default S3 method:
fspa(veg, method, d.rev, n.groups, ...)
## S3 method for class 'fspa'
plot(x, ..., axes=c(1,2))

Arguments

veg            A data frame of vegetation releves (rows) by species (columns)
method         The method used for calculating distance as available in function vegdist of
                package vegan, for instance method = "bray".
d.rev           The percentage of distances revised, for instance 0.5 (50 percent, the default).
n.groups       This classifies the data points for illustrative purposes (uses Ward’s method).
                ... Variable axes=c(1,2) (default), the axes to be plotted
x              An object of class "fspa".
axes           A vector of length two, assessing the axes used for plotting. Default is c(1,2).

Value

An output list of class "fspa" with at least the following items:

oldpoints     Ordination scores before adjustment
newpoints     Ordination scores after adjustment
symbols       The symbols used for classified plot
nline         The number of lines to be drawn in the graph
startline     Coordinates where the lines start
endline       Coordinates where the lines end
dmat.before   Distance matrix before analysis
dmat.after    Distance matrix after analysis
endline       Coordinates where the lines end
d.rev         proportion of distances revised

Author(s)

Otto Wildi

References


Examples

```r
o.fspa<- fspa(sveg,method="euclid",d.rev=0.75,n.groups=6)  # sveg is vegetation data
plot(o.fspa,axes=c(1,2))  # plots axis 1, 2
```

---

**ltim**

Lippe et al. 1985 data set, yr of observation

---

**Description**

Lippe et al. 1985 data set, yr of observation. Vegetation data is in data frame `lveg`.

**Usage**

```r
data(ltim)
```

**Format**

A data frame with 19 observations on the following variable.

- **Year** a numeric vector containing the year of sampling

**Source**


**References**


**Examples**

```r
summary(ltim)
```
Description

Lippe et al. 1985 data set, vegetation data. Year of observation is in data frame `ltim`.

Usage

data(lveg)

Format

A data frame with 19 observations on the following 9 variables, the species.

- `open.soil` a numeric vector
- `Empetrum.nigrum` a numeric vector
- `Calluna.vulgaris` a numeric vector
- `Erica.tetralix` a numeric vector
- `Molinia.coeurea` a numeric vector
- `Carex.pilulifera` a numeric vector
- `Juncus.squarrosus` a numeric vector
- `Rumex.acetosella` a numeric vector
- `other.species` a numeric vector

Source


References


Examples

summary(lveg)
Description

Mimics traditional manual ordering of vegetation data table by (i) clustering rows and columns (hclust), (ii) rearranging the resulting groups according to the first AOC axis (aocc), (iii) rearranging rows and columns inside groups based on CA (cca), (iv) Putting high resolving species on top of the table (aoc). Also offers variants for ordering.

Usage

```r
Mtabs(veg, method = "raw", y.r, y.s, k.r, k.s, ndiffs, ...)
mtab(veg, method = "raw", y.r, y.s, k.r, k.s, ndiffs)
plottab(veg, rorder=NULL, sorder=NULL, grr=NULL, gcs=NULL, y=0.5)
plottabl(veg, rorder=NULL, sorder=NULL, grr=NULL, gcs=NULL, y=0.5)
setgroupsize(vec)

## Default S3 method:
Mtabs(veg, method, y.r, y.s, k.r, k.s, ndiffs, ...)
## S3 method for class 'Mtabs'
plot(x, ..., method="normal")
## S3 method for class 'Mtabs'
summary(object, ..., range=NULL)
```

Arguments

- `veg` This is a vegetation data frame, releves are rows, species columns
- `method` The method used for ordering: "raw", "sort", "ca", "clust", "aoc" or "mulva"
- `y.r` Transformation of species scores when clustering releves (rows): $x' = x \exp(y.r)$
- `y.s` Transformation of species scores when clustering species (columns): $x' = x \exp(y.s)$
- `k.r` The number of releve groups
- `k.s` The number of species groups
- `ndiffs` The number of (high resolving) species used for top portion of the table
- `...` Use method="normal" for conventional display, "compressed" for very large tables
- `rorder` The order of releves (rows) for printing
- `sorder` The order of species (columns) for printing
- `grr` The group labels of releves (rows) for printing
- `grs` The group labels of species (columns) for printing
- `x` An object of class "Mtabs"
- `object` An object of class "Mtabs"
### range
A subset of species to be displayed in summary table, e.g., c(1,10) for the first 10.

### vec
A vector of group labels, analyzed similar to function table(), but without sorting.

### y
Transformation of species scores: \( x' = x \exp(y) \)

### Details
Function plottab() and plottabl() are for internal use only.

### Value
An object of class "Mtabs" with at least the following items:

- **method**: The method used for ordering
- **transf.r**: Argument y.r
- **transf.s**: Argument y.s
- **order.rel**: The resulting order of rows
- **order.sp**: The resulting order of columns
- **order.relgr**: The resulting order of releve groups
- **order.spgr**: The resulting order of species groups
- **MCC**: Mean square contingency coefficient
- **CAeig.rel**: Eigenvalues of correspondence analysis
- **AOCeig.rel**: Eigenvalues of analysis of concentration
- **veg**: The input vegetation data frame
- **centroids**: The matrix of groups centroids (see summary.Mtabs)

### Note
This extremely complex procedure accords with conventions used in vegetation ecology. It assumes that the vegetation data frame has many zero entries (plots in which species are not found). The summary method displays a frequency table (relative frequency of all species within the releve groups, centroid).

### Author(s)
Otto Wildi

### References

Examples

```r
y.r <- 0.5; y.s <- 0.2  # defining transformations used
k.r <- 3; k.s <- 4       # row- and column numbers
ndiffs <- 18            # no. of columns used to show pattern
o.Mt <- Mtabs(mveg,"mulva",y.r,y.s,k.r,k.s,ndiffs)
plot(o.Mt, method="normal")
# to see the original order simply replace "mulva" by "raw"
```

---

**mveg**  
*Ellenberg’s 1956 meadow data*

**Description**

Ellenberg’s 1956 meadow data. No site factors available.

**Usage**

```r
data(mveg)
```

**Format**

A data frame with 25 observations on the 94 species, the variables (cover percentages). Species names are abbreviations.

**Details**

No site factors available for this data frame.

**Source**


**References**


**Examples**

```r
summary(mveg)
```
mxplot

Matrixplot of groups similarities

Description

This calculates and plots average similarities of rows (releves) in a square, classified matrix. Cor-
relation coefficient is used as similarity, upon plotting proportionas to the surface of circles. Hence,
diagonal elements exhibit similarity of groups, off-diagonals all similarities to the remaining groups.

Usage

mxplot(veg, rmember, use, y=1, ...)
matrixplot(veg, rmember, use, y=1)

## Default S3 method:
mxplot(veg, rmember, use, y=1,...)
## S3 method for class 'mxplot'
plot(x,...,capacity=100)

Arguments

veg This is a vegetation data frame, releves are rows, species columns
rmember Group membership of the rows or columns, typically taken from cluster analysis
use Either "rows" or "columns"
y Transformation of species scores: x’= x exp(y)
... Capacity. Adjusts plot size to the number of groups.
x An object of class "mxplot"
capacity The number of group symbols that fit on one page

Details

The distance measure used is "correlation used as distance". See reference.

Value

An object of class "mxplot" with at least the following items:

order Dimension of the similarity matrix (equal to the number of groups ng)
mmatrix The ng x ng matrix of average group similarity
levels The ng group names (a vector of character variables)

Note

Plot parameter capacity only affects the format of plot. Just try.
Author(s)
Otto Wildi

References

Examples
# Starts with classifying releves by cluster analysis
dd<- vegdist(sveg[,1],method="euclid") # dd is distance matrix
o.clust<- hclust(dd,method="ward") # clustering
groups<- as.factor(cutree(o.clust,k=4)) # forming 6 groups

o.mxpl<- mxplot(sveg,groups,use="rows",y=0.5)
plot(o.mxpl,capacity=30)

nsit  European beach forest data, site factors

Description
European beach forest data, site factors. Vegetation information is in data frame nveg.

Usage
data(nsit)

Format
A data frame with 11 observations on the following 8 site variables.

PH  a numeric vector
ALTITUDE  a numeric vector
SLOPE.deg  a numeric vector
X_AXIS  a numeric vector
Y_AXIS  a numeric vector
EXPOSURE  a factor with levels E N S
YEAR  a numeric vector
GROUP_NO  a numeric vector

Details
Artificial data
Source

References

Examples

```r
summary(nsit)
```

---

**nveg**

*European beach forest data, vegetation*

---

**Description**
European beach forest data, vegetation. Site factors are in data frame `nsit`.

**Usage**

data(nveg)

**Format**
A data frame with 11 observations on the following 21 species, the variables (0 to 6 scale used).

- Fagus.silvatica: a numeric vector
- Quercus.petraea: a numeric vector
- Acer.pseudoplatanus: a numeric vector
- Fraxinus.excelsior: a numeric vector
- Lonicera.xylosteum: a numeric vector
- Sambucus.racemosa: a numeric vector
- Sambucus.nigra: a numeric vector
- Vaccinium.myrtillus: a numeric vector
- Carex.silvatica: a numeric vector
- Oxalis.acetosella: a numeric vector
- Viola.silvestris: a numeric vector
- Luzula.nemorosa: a numeric vector
- Veronica.officinalis: a numeric vector
- Galium.odoratum: a numeric vector
- Lamium.galeobdolon: a numeric vector
- Primula.elatior: a numeric vector
Allium.ursinum a numeric vector
Arum.maculatum a numeric vector
Ranunculus.ficaria a numeric vector
Eurhynchium.striatum a numeric vector
Polytrichum.formosum a numeric vector

Details

Artificial data

Source


References


Examples

summary(nveg)

orank

Ranking by orthogonal components (RANK)

Description

Given a correlation matrix of rows or columns this selects the variable sharing a maximum variance with all others and declares this rank 1. Reduces the matrix (covariances, correlations) by the contribution of the variable ranked first. Repeats the process to derive consecutive ranks until no variance is left.

Usage

orank(veg, use, rlimit=5, y=1, x.axis=NULL, y.axis=NULL,...)
orank1(veg, use, rlimit=5, y=1, x.axis=NULL, y.axis=NULL)

# Default S3 method:
orank(veg, use, rlimit=5, y=1, x.axis=NULL, y.axis=NULL,...)
# S3 method for class 'orank'
plot(x,...)
# S3 method for class 'orank'
summary(object,...)
Arguments

- **veg**: This is a vegetation data frame, releves are rows, species columns
- **use**: Either "rows" or "columns"
- **rlimit**: The maximum number of ranks to be determined
- **y**: Transformation of species scores: \( x' = x \exp(y) \)
- **x.axis**: Horizontal axis used for plotting result in a sampling plan
- **y.axis**: Vertical axis used for plotting result in a sampling plan
- **x**: An object of class "orank"
- **...**: Further variables used for printing
- **object**: An object of class "orank"

Details

If x-axis=NULL or y-axis=NULL then a pcoa-ordination is computed and the first two axes used for plotting

Value

An object of class "orank" with at least the following items:

- **use**: Either "rows" or "columns"
- **n.ranks**: The number of ranks
- **var.names**: Names of the ranked variables
- **var.explained**: Explained variance of the ranked variables
- **var.percent**: Percentage of the variance explained
- **cum.var**: Cummulative variance of ranked variables, percentage
- **x.axis**: The same as input parameter x.axis
- **y.axis**: The same as input parameter y.axis

Note

The present function exclusively relies on a correlation matrix, function `cor`.

Author(s)

Otto Wildi

References

outlier

Outlier detection

Description

Identifies outliers based on the nearest neighbour criterion. It starts by computing a matrix of distances (correlation, r, used as distance, \( d_r = (1-r)/2 \)). Variables with nearest neighbour distance larger than parameter `thresh` are considered outliers.

Usage

```
outlier(veg, thresh, y,...)
outly(veg, thresh = 0.2, y = 0.5)
```

```
## Default S3 method:
outlier(veg, thresh, y,...)
## S3 method for class 'outlier'
plot(x,...)
## S3 method for class 'outlier'
print(x,...)
```

Arguments

- **veg**: This is a vegetation data frame, releves are rows, species columns
- **thresh**: Threshold nearest neighbour distance for outliers
- **y**: Transformation of species scores: \( x' = x \exp(y) \)
- **x**: An object of class "outlier"
- **...**: Parameter `out.seq`, the plotting interval

Value

An object of class "outlier" with at least the following items:

- **threshold**: Threshold nearest neighbour distance for considering outliers
- **y**: Transformation of species scores: \( x' = x \exp(y) \)
- **rel.names**: All row names
- **neigh.names**: Names of the corresponding nearest neighbours
- **neigh.dist**: Distance to the nearest neighbour

Examples

```
# Uses vegetation data frame `sveg` with vegetation data
# and `ssit` with corresponding x- and y-axes scores
x.axis=ssit$x.axis ; y.axis=ssit$y.axis
o.orank<- orank(sveg,use="rows",rlimit=5,y=0.25,x.axis,y.axis)
plot(o.orank)
```
Overly of multivariate time series

Description

This function attempts to superimpose (overlay) multivariate time series that typically stem from different locations to form one single series. Series are combined pairwise following the arrangement in a minimum spanning tree, `spantree`. The result is a time series which may be longer than the contributing series, but shorter than their length total.

Usage

```r
overly(veg, Plot.no, y, sint, ...)
overly2(veg, Plot.no, y, sint)
```

# Default S3 method:
```r
overly(veg, Plot.no, y, sint, ...)
```
# S3 method for class 'overly'
```r
plot(x,...,colors=NULL,l.widths=NULL)
```

Arguments

- **veg**: This is a vegetation data frame, relevés are rows, species columns. It is assumed that it constitutes two or more time series.
- **Plot.no**: Plot names. Rows with identical name are assumed to belong to the same time series.
- **y**: Transformation of species scores: $x' = x \exp(y)$
sint Length of time interval. Affects display only.

... Parameters colors=NULL, l.width=NULL, colors and line widths in plots.

colors A vector of colors, such as c(1,2,3). The entries are recycled upon printing.

l.widths A vector of line widths used for plotting, e.g., c=(0.5,1,1.5,2). The entries are recycled upon printing.

x An object of class "overly"

Details

In plant ecology this procedure is also known as space-for-time substitution. See also pco, spantree.

Value

An object of class "overly" with at least the following items:

plot.labels Names of plots, see Plot.no above

n.tseps The resulting (synthetic) number of time steps

tseps A vector of time steps in time units

tser.data The resulting vegetation time steps

ord.scores The pco scores of the ordination of time series

d.mat Euclidean distance matrix of time series

vegraw Input vegetation data frame veg (see above)

linex1 Starting address of the time series in the synthetic time frame

linex2 End address of the time series in the synthetic time frame

ltex The plot names

sint The time interval (see above)

vegtypes The species names involved

Author(s)

Otto Wildi

References


Examples

o.overly<- overly(sn59veg,sn59sit$Plot.no,y=0.5,sint=5)
# Plotting (i) minimum spanning tree, (ii) temporal arrangement of time series,
# (iii) synthetic multivariate time series
plot(o.overly,colors=NULL,l.width=NULL)
Description

Given a vegetation data frame containing various time series this plots a pca-ordination (pca) and connects points belonging to the same series with lines. The plots where the releves come from are identified by plotlabels (see below).

Usage

\[
\text{pcaser(} \text{veg, plotlabels, y, ...)}
\]

\text{pcaser2(} \text{veg, plotlabels, y=}1\text{)}

## Default S3 method:
\[
\text{pcaser(} \text{veg, plotlabels, y, ...)}
\]

## S3 method for class 'pcaser'
\[
\text{plot(} \text{x, lines=}TRUE, \text{arrows=}TRUE, ...\text{)}
\]

Arguments

\text{veg} \quad \text{This is a vegetation data frame, releves are rows, species columns}

\text{plotlabels} \quad \text{Plot names. Rows with identical name are assumed to belong to the same time series.}

\text{y} \quad \text{Transformation of species scores: } x'= x \exp(y)

\text{...} \quad \text{Parameter lines=}TRUE \text{ will connect the series. Otherwise they are distinguished by symbols used in plot only.}

\text{x} \quad \text{An object of class "pcaser".}

\text{lines} \quad \text{A logical variable. When TRUE then points of the same time series are connected.}

\text{arrows} \quad \text{A logical variable. When TRUE then the first and the last points of the same time series are connected.}

Value

An object of class "pcaser" with at least the following items:

\text{comp1} \quad \text{Description of 'comp1'}

\text{nrel} \quad \text{Total number of releves involved (i.e., row number)}

\text{nser} \quad \text{Total number of time series (i.e., locations where the data stem from}

\text{scores} \quad \text{The pca-ordination scores}

\text{plotlab} \quad \text{Plot labels used for plotting}

\text{plotlabels} \quad \text{Plot names}

\text{Eigv} \quad \text{Eigenvalues (percentage)}
pcobiplot

Computing and plotting a biplot ordination using principal coordinates analysis

Description

Computing a principal coordinates analysis of releves (rows, see pco) and subsequently the correlations with all species (columns). Two ordinations are plotted, one for releves and an arrow-plot for species. Species are restricted to the list given in sel.sp and species names are abbreviated upon request (see make.cepnames).

Usage

pcobiplot(veg, method, y = 1, ...)
pcoo(pveg, method, y = 1)

## Default S3 method:
pcobiplot(veg, method, y = 1, ...)
## S3 method for class 'pcobiplot'
plot(x, ..., axes = c(1, 2), sel.sp = NULL, shortnames = TRUE)

Arguments

veg This is a vegetation data frame, releves are rows, species columns
method The method used for calculating distance. See function vegdist(), package vegan.
y Transformation of species scores: x' = x exp(y)
... Plot parameters axes = c(1, 2), sel.sp = NULL (species selection), shortnames = TRUE for abbreviation of species names
shortnames A logical variable, when TRUE delivering shortnames of species (package vegan used).
axes A vector of length two, assessing the axes used for plotting. Default is c(1, 2).
x An object of class "pcobiplot"
sel.sp The species (column numbers) to be included in the plot of arrows
Value

An object of class "pcobiplot" with at least the following items:

- nrel: The number of releves
- nspe: The number of species
- rpoints: Ordination scores of releves
- spoints: Ordination scores of species
- allspnames: The full list of species names

Note

If sel.sp is not specified a random selection of 6 species is taken

Author(s)

Otto Wildi

References


Examples

```r
sel.sp <- c(3,11,23,31,39,46,72,77,96)  # selection of species
o.pco <- pco(veg, method="bray", y=0.25)  # used pco
plot(o.pco, sel=sel.sp, axes=c(1,2), shortnames=TRUE)  # plot of releves, sepecies
```

---

Description

Plotting 6 ordinations using euclidean distance, manhattan distance, chord distance, Canberra distance, Bray-Curtis distance (`vegdist`) and correlation as distance respectively. Transformation of scores can be adjusted according to $x' = x \exp(y)$. All ordinations (`pco`) superimposed to PCA solution (`pca`) by procrustes analysis.

Usage

```r
pcovar(veg, y, ...)
pcoatest(veg, y=1)
```

## Default S3 method:
pcovar(veg, y, ...)

## S3 method for class 'pcovar'
plot(x,...,reversals=c(0,0,0,0,0,0))

---
Arguments

veg A vegetation data frame, releves are rows, species columns
y Transformation of species scores: \( x' = x \exp(y) \)
... Additional plot parameters, see par.
reversals Vector reversals=c(0,0,0,0,0,0). When set to 1 the corresponding plot is mirrored vertically.
x An object of class "pcovar".

Details

\texttt{pco}, \texttt{vegdist}, \texttt{procrustes} for the main functions used

Value

An object of class "pcovar" with at least the following items:

nrel The number of releves
nspec The number of species
y Transformation of species scores: \( x' = x \exp(y) \)
euclidpca PCA coordinates, euclid used, adjusted by procrustes analysis
euclidpco PCO coordinates, euclid used, adjusted by procrustes analysis
manhpco PCO coordinates, manhattan used, adjusted by procrustes analysis
manhpca PCA coordinates, manhattan used, adjusted by procrustes analysis
cordpco PCO coordinates, chord distance used, adjusted by procrustes analysis
cordpca PCA coordinates, chord distance used, adjusted by procrustes analysis
canpco PCO coordinates, canberra dist. used, adjusted by procrustes analysis
canpca PCA coordinates, canberra dist. used, adjusted by procrustes analysis
bpco PCO coordinates, Bray-Curtis dist. used, adjusted by procrustes analysis
b pca PCA coordinates, Bray-Curtis dist. used, adjusted by procrustes analysis
cor pco PCO coord., correlation as dist. used, adjusted by procrustes analysis
cor pca PCA coord., correlation as dist. used, adjusted by procrustes analysis

Note

This function serves primarily instructional purposes

Author(s)

Otto Wildi

References

Examples

```r
o.pcovar <- pcovar(sveg, y=1)
plot(o.pcovar, reversals=c(0,0,0,0,0,0))
```

Description

Time scale (yr) for Soppensee pollen data. See details below. Vegetation is in data frame `pveg`.

Usage

```r
data(psit)
```

Format

A data frame with 145 observations on the following variable.

- **Years B.P** a numeric vector

Details

Time scale (no corrections applied for revised 14C calibration).

Source

Lotter, A.F. 1999. Late-glacial and Holocene vegetation history and dynamics as shown by pollen macrofossil analyses in annually laminated sediments from Soppensee, central Switzerland. Vegetation History and Archaeobotany 8: 165-184.

References


Examples

```r
summary(psit)
```
Soppensee pollen data

Description
Soppensee pollen data. Vegetation only (tree species). The age (year B.P) is in psit.

Usage
data(pveg)

Format
A data frame with 145 observations on the following 14 variables.
X1.Abies  a numeric vector
X2.Pinus   a numeric vector
X3.Fagus   a numeric vector
X4.Quercus a numeric vector
X5.Acer    a numeric vector
X6.Fraxinus a numeric vector
X7.Ulmus   a numeric vector
X8.Tilia   a numeric vector
X9.Betula  a numeric vector
X10.Alnus  a numeric vector
X11.Populus a numeric vector
X12.Salix  a numeric vector
X13.Sorbus a numeric vector
X14.Picea  a numeric vector

Source
Lotter, A.F. 1999. Late-glacial and Holocene vegetation history and dynamics as shown by pollen macrofossil analyses in annually laminated sediments from Soppensee, central Switzerland. Vegetation History and Archaeobotany 8: 165-184.

References

Examples
summary(pveg)
Description

Time series from the Swiss National Park, 59 plots. Site data: Plot names and yr of sampling. Vegetation data in sn59veg.

Usage

data(sn59sit)

Format

A data frame with 751 observations on the following 2 variables.

- Plot.no : a factor with 59 levels, the plot names
- Year : a numeric vector

Source


References


Examples

summary(sn59sit)

Description

Time series from the Swiss National Park, 59 plots. Vegetation data. Variables are species guilds. Site data is in sn59sit.

Usage

data(sn59veg)
Format
A data frame with 751 observations on the following 6 variables (the species guilds).

Aconitum  a numeric vector
Trisetum   a numeric vector
Deschampsia a numeric vector
Festuca    a numeric vector
Carex      a numeric vector
Pinus      a numeric vector

Source

References

Examples
summaryHsnUYvegI

sn6sit
Time series from the Swiss National Park, 6 plots. Site data.

Description
Time series from the Swiss National Park, 6 plots. Site data: Plot names and yr of sampling. Vegetation data in sn6veg.

Usage
data(sn6sit)

Format
A data frame with 81 observations on the following 2 variables.

Plot no  a factor with levels Ac9 FN2 MU21 N8 PF1 Pin3
Year     a numeric vector

Details
A subset of data frame sn59sit
Source


References


Examples

summary(sn6sit)

data(sn6veg)

Description

Time series from the Swiss National Park, 6 plots. Vegetation data. Plot names are in sn6sit.

Usage

data(sn6veg)

Format

A data frame with 81 observations on the following 6 variables (species guilds), cover percentage.

- Aconitum  a numeric vector
- Deschampsia  a numeric vector
- Trisetum  a numeric vector
- Festuca  a numeric vector
- Carex  a numeric vector
- Pinus  a numeric vector

Details

A subset of data frame sn59veg

Source


References

**Examples**

```r
summary(sn6veg)
```

---

**sn7sit**

*Time series from the Swiss National Park, 7 plots. Site data.*

---

**Description**

Time series from the Swiss National Park, 7 plots. Site data: Plot names and yr of sampling. Vegetation data in `sn7veg`.

**Usage**

```r
data("sn7sit")
```

**Format**

A data frame with 97 observations on the following 2 variables.

- `Plot.no` a factor with levels `Ac9 FN2 MU21 N8 PF1 Pin3 Tr6`
- `Year` a numeric vector

**Details**

A subset of data frame `sn59sit`

**Source**


**References**


**Examples**

```r
data(sn7sit)
str(sn7sit)
```
Description
Time series from the Swiss National Park, 6 plots. Vegetation data. Plot names are in sn6sit.

Usage
data("sn7veg")

Format
A data frame with 97 observations on the following 6 variables (species guilds).

Aconitum a numeric vector
Deschampsia a numeric vector
Trisetum a numeric vector
Festuca a numeric vector
Carex a numeric vector
Pinus a numeric vector

Details
A subset of data frame sn59veg

Source

References

Examples
data(sn7veg)
str(sn7veg)
SNPsm

The spatial and temporal model of succession in the Swiss National Park

Description

A dynamic model of succession on alp Stabelchod in the Swiss National Park using differential equations and numerical integration. 6 species guilds are considered. Space is conceived as a grid of 30 times 40 cells. Typical simulation time is around 500yr.

Usage

SNPsm(trange,tsl,diff,r6,...)
SNPsm2(trange=100,tsl=5.0,diff=0.001,r6=NULL)

## Default S3 method:
SNPsm(trange, tsl, diff, r6, ...)
## S3 method for class 'SNPsm'
plot(x, ...,out.seq=1,col=FALSE)

Arguments

trange  Time range of simulation in yr
tsl  Time range of simulation in yr
out.seq  Time interval (yr) at which maps of the state are printed
diff  A diffusion coefficient driving random spatial propagation
r6  Growth rates of 6 guilds involved, increase in cover percentage per yr
...  Parameter out.seq, the plotting interval
x  An object of class "SNPsm"
col  A logical variable to suppress color printing

Value

An object of class "SNPsm" with at least the following items:

n.time.steps  Number of time steps used for numerical integration
imax  Vertical grid count
jmax  Horizontal grid count
time.step.length  The time step length in yr
veg.types  The names of the vegetation types, i.e., the species
vegdef  A nspecies x nspecies matrix defining composition of vegetation types
growth.rates  The growth rates given upon input
**SNPtm**  

Simulated scores of all species (guilds) during simulation time

**tmap**  
The 30 x 40 grid map of types used as initial condition

**igmap**  
The same as tmap

**frame**  
A 30 x 40 grid showing initial forest edges, used for printing

**Author(s)**

Otto Wildi

**References**


**Examples**

```r
r6=NULL  # imposes default growth rates
do.stSNP<- SNPsm(trange=100,tsl=10.0,diff=0.001,r6)
plot(do.stSNP,out.seq=50)
```

---

**Description**

A dynamic model of succession in the Swiss National Park using differential equations and numerical integration. 6 species guilds are considered. Typical simulation time is around 500yr.

**Usage**

```r
SNPtm(trange, tsl, x6, r6,...)
SNPtm2(trange, tsl, x6, r6)
```

```r
## Default S3 method:
SNPtm(trange, tsl, x6, r6,...)
## S3 method for class 'SNPtm'
plot(x,...)
```

**Arguments**

- `trange`  
  Time range of simulation in yr

- `tsl`  
  Time step length used for integration (no. of yr)

- `x6`  
  Initial conditions of 6 guilds involved, cover percentage

- `r6`  
  Growth rates of 6 guilds involved, increase in cover percentage per yr

- `x`  
  An object of class "SNPtm"

- `...`  
  Parameter out.seq, the plotting interval
Value

An object of class "SNPtm" with at least the following items:

- `n.time.steps` Time step range covered by the model
- `time.step.length` Time step length used for integration, no. of yr
- `time.vector` All time steps described by the results
- `veg.types` The names of the vegetation types, i.e., the species
- `growth.rates` The growth rates given upon input
- `initial.cond` Initial conditions of 6 guilds involved, cover percentage
- `sim.data` Simulated scores of all species (guilds) during simulation time

Author(s)

Otto Wildi

References


Examples

```r
o.SNPtm<- SNPtm(trange=400,tsl=1.0,x6= NULL,r6=NULL)
plot(o.SNPtm)
```

Description

From a multivariate time series of vegetation data this first computes a distance matrix (`vegdist`, euclidean). The first plot is a graphical representation of the full distance matrix, the second a profile of change per time step of different length (velocity).

Usage

```r
speedprof(veg, timescale, orders, y = 1, adjust,...)
speedprof2(veg, timescale, orders, y = 1, adjust)
```

## Default S3 method:
speedprof(veg, timescale, orders, y = 1, adjust,...)

## S3 method for class 'speedprof'
plot(x,...)
sr ank

Arguments

veg This is a vegetation data frame, releves are rows, species columns. Releves are considered a time series.
timescale A vector of points in time of releves (rows)
orders Orders used for printing the velocity profile, i.e., the number of time steps used for calculating speed (rate of change per time unit).
y Transformation of species scores: \( x' = x \exp(y) \)
adjust Parameter adjust=TRUE re-scales releves to vector sum=100 percent (assuming cover
x An object of class "speedprof".
... Parameter out.seq, the plotting interval

Value

An object of class "SNPsm" with at least the following items:

nrel The number of releves
dmatrix The distance matrix	imescale The time scale
orders Time step lengths considered for plotting the profile

Author(s)

Otto Wildi

References


Examples

orders<- c(1,2,3,4)
o.spp<- speedprof(tveg,tsit$Year,orders,y=1.0,adjust=TRUE)
plot(o.spp)

sr ank

Ranking species by IndVal or F-value

Description

Given a vegetation data frame with grouped rows (releves) indicator value analysis (funcion indval) or analysis of variance (aov) is performed on columns (species) and these are ordered by decreasing IndVal (function indval()) or F-value (aov()) accordingly.
Usage

sr ank(veg, groups, method, y,...)
srank2(veg, groups, method, y)

## Default S3 method:
srank(veg, groups, method, y,...)
## S3 method for class 'srank'
print(x,...)

Arguments

veg This is a vegetation data frame, releves are rows, species columns

groups Group membership of rows (releves)

method Either "indval" or "jancey"

y Transformation of species scores: \( x' = x \exp(y) \)

... Further variables used for printing

x A list of class "srank" generated by centroid

Value

An object of class "srank" with at least the following items:

 rank A sequence of numbers, 1,2,3,...p where p= number of species

 species.no The corresponding species no. (i.e. the column no.

 species The corresponding species names (taken from column names

 Indval The corresponding indicator values (method "indval")

 F_value The corresponding F-values (method "jancey")

 error.probability The corresponding error probabilities

Author(s)

Otto Wildi

References


Examples

# Starts with classifying releves by cluster analysis
dd<- vegdist(nveg=0.5,method="euclid") # dd is distance matrix
o.clust<- hclust(dd,method="ward") # clustering
groups<- as.factor(cutree(o.clust,k=3)) # forming 3 groups
# Applies ranking and prints ordered table of species (the columns)
o.srank<- srank(nveg,groups,method="jancey",y=0.5)
o.srank

## ssind

**Indicator values of all species in data set "sveg"**

### Description
For each species in "sveg" all 8 indicator values are taken from the "Flora Indicativa by" Landolt et al. (2010). These are ranks on a 1 to 5 scale (except for M), but for some indicators half steps are used as well. Scores zero (0) are either undefined or unknown and must be treated as missing values.

### Usage
```r
data(ssind)
```

### Format
A data frame with 119 observations on the following 9 variables.

- **T** Temperature value (1-5, 9 steps)
- **K** Continentality value (1-5, 5 steps)
- **L** Light value (1-5, 5 steps)
- **F** Moisture value (1-5, 5 steps)
- **W** Moisture availability (1-3, 3 steps)
- **R** Reaction value (acidity, 1-5, 5 steps)
- **N** Nutrient value (1-5, 9 steps)
- **H** Humus value (1-3, 3 steps)
- **D** Soil aeration value (1-3, 3 steps)

### Details
Indicator values from vascular plants and bryophytes stem from different lists in Landolt et al. (2010). Note that this data set was not in cluded in the original dave package, but added in version 1.5 only.

### Source
References


Examples

summary(ssind)

ssit  
Schlaenggli site data

Description

Schlaenggli site data. 63 plots arranged in a square grid. Vegetation in data frame sveg.

Usage

data(ssit)

Format

A data frame with 63 observations on the following 20 site variables.

- pH.peat: a numeric vector
- log.ash.perc: a numeric vector
- Ca.peat: a numeric vector
- Mg.peat: a numeric vector
- Na.peat: a numeric vector
- K.peat: a numeric vector
- Acidity.peat: a numeric vector
- CEC.peat: a numeric vector
- Base.sat.perc: a numeric vector
- P.peat: a numeric vector
- Waterlev.max: a numeric vector
- Waterlev.av: a numeric vector
- Waterlev.min: a numeric vector
- log.peat.lev: a numeric vector
- log.slope.deg: a numeric vector
- pH.water: a numeric vector
- log.cond.water: a numeric vector
- log.Ca.water: a numeric vector
- x.axis: a numeric vector
- y.axis: a numeric vector
sspft

Source


References


Examples

summary(sspft)

sspft

Selected plant functional traits of all species in data set "sveg"

Description

For each species in "sveg" a selection of 23 traits are taken from the "Flora Indicativa by" Landolt et al. (2010). These are all nominal variables. Score 1 indicates the trait is present, score 0 it is absent. Hence, there is no such things like missing values.

Usage

data(sspft)

Format

A data frame with 119 observations on the following 23 variables.

lfNg Life form "geophyte" (plants with resting buds below ground)
lfNc Life form "herbaceous" (herbaceous plant, buds on shoots above ground)
lfNz Life form "woody chamaephyte" (dwarf shrub, buds above ground)
lfNp Life form "phanerophyte" (woody shrub or tree, > 4m)
lfNn Life form "nanophanerophyte" (woody shrub or tree, < 4m)
lfNa Life form "hydrophyte" (plants with buds submerged)
lfNh Life form "hemicryptophyte" (buds on or directly below ground, rosettes, tussocks)
lfNt Life form "therophyte" (plant dying back, surviving as seed or annual hemicryptophyte)
lfNhp Life form "hemiparasite" (plant obtaining water and nutrients from host, green leaves)
lfNk Life form "short-lived hemicryptophyte" (resting buds near ground, hapaxantic species)
lfNff Life form "carnivorous species" (consuming some nutrients from animals)
lfNmoss Life form "moss" (in separate list of Landolt et al. 2010)
lfNsph Life form "Sphagnum" (all species of genus Sphagnum)
fsNzw Reproduction "hermaphrodictic, normal sexual" (pollination necessary to reproduce)
FS.c1  Reproduction "cleistogamous" (normal flowers and self-pollinating)
FS.d1  Reproduction "unisexual and dioecious" (only male or female organs)
FS.mo  Reproduction "unisexual and monoecious" (male, female and bisexual flowers on one plant)
FS.ve  Reproduction "polysexual" (male and/or female and bisexual flowers on one individual)
FS.fa  Reproduction "facultatively apomictic" (sexual and simultaneously asexual reproduction)
FS.oa  Reproduction "obligate apomictic" (mostly bisexual, fertilization necessary for reproduction)

c  Life strategy "competitive" (competitive, long-lived), range 1-3
r  Life strategy "ruderal" (pioneer species, short-lived), range 1-3
s  Life strategy "stress-tolerant" (adapted to harsh environmental conditions), range 1-3

Details
Species traits from vascular plants and bryophytes stem from different lists in Landolt et al. (2010). Note that this data set was not included in the original dave package, but added in version 1.5 only.

Source

References

Examples
summary(sspft)

dave Package
sveg  Schlaenggli vegetation data

Description
Schlaenggli vegetation data. 63 plots arranged in a square grid. Site factors in data frame ssit.

Usage
data(sveg)

Format
A data frame with 63 observations on 119 species as variables. Species abundance measured on a 0 to 6 scale.
Source

References

Examples
summary(sveg)

---

`tsit`  
*Time series from the Swiss National Park, Plot Tr6. Site data.*

Description
Time series from the Swiss National Park, plot Tr6. Site data: Plot names and yr of sampling. Vegetation is in `tveg`.

Usage
data(tsit)

Format
A data frame with 16 observations on the following 2 variables.

- `Plot.no`  a factor with levels `Tr6`
- `Year`  a numeric vector

Details
A subset of data frame `sn59sit`.

Source

References

Examples
data(tsit)
## maybe str(tsit); plot(tsit) ...
Description

Time series from the Swiss National Park, Plot Tr6. Vegetation data. Site data is in \textit{tsit}.

Usage

data(tvec)

Format

A data frame with 16 observations on the following 6 variables, the species guilds.

\begin{itemize}
  \item Aconitum a numeric vector
  \item Deschampsia a numeric vector
  \item Trisetum a numeric vector
  \item Festuca a numeric vector
  \item Carex a numeric vector
  \item Pinus a numeric vector
\end{itemize}

Details

A subset of data frame sn59veg

Source


References


Examples

summary(tvec)
Vrsit

Vraconnaz time series data, site factors and dates

Description

A vegetation time series from 11 plots in the Vraconnaz peat bog, describing species invasion and
propagation after a bog burst in 1986. The corresponding vegetation object is `vrveg`

Usage

data("vrsit")

Format

A data frame with 231 observations on the following 26 variables.

- `nom_de_lobjet` a factor with levels La_Vraconnaz Vraconnaz
- `nom_de_la_releviste` a factor with levels E.Feldmeyer ef ef ke
- `date` a factor with levels 01.01.91 01.07.92 01.07.99 03.07.01 04.07.01 04.07.06 04.07.07
  05.07.05 05.07.06 05.07.93 06.07.04 06.07.05 06.07.06 06.07.93 07.04.07.05
  07.07.93 08.07.03 08.07.04 08.07.08 09.07.02 09.07.03 09.07.08 09.07.96 09.07.97
  10.07.00 10.07.02 10.07.03 10.07.07 10.07.08 10.07.89 10.07.90 10.07.97 11.07.00
  11.07.02 11.07.07 11.07.89 11.07.91 11.07.95 12.07.00 12.07.02 12.07.07 12.07.09
  12.07.95 13.07.89 15.07.98 16.07.98 25.07.88 26.07.88 27.06.94 27.08.88 28.06.94
  28.07.88 29.06.92 29.06.94 29.06.99 29.07.88 30.06.92 30.06.99
- `jahr` a numeric vector
- `No_du_releve` a numeric vector
- `No_du_carre` a numeric vector
- `surface_.m2.` a numeric vector
- `recouvrement_muscinal` a numeric vector
- `recouvrement_herbace` a numeric vector
- `recouvrement_sous.arbore` a numeric vector
- `recouvrement_arbore` a numeric vector
- `litiere_seche` a numeric vector
- `tourbe_nue` a numeric vector
- `eau_libre` a numeric vector
- `Artenzahl` a numeric vector
- `Feuchtezahl` a numeric vector
- `Lichtzahl` a numeric vector
- `Temperaturzahl` a numeric vector
- `Kontinentalitaetszahl` a numeric vector
Reaktionszahl a numeric vector
Naehrstoffzahl a numeric vector
Humuszahl a numeric vector
Dispersitaetszahl a numeric vector
X a numeric vector
Y a numeric vector
Z a numeric vector

Details
For processing the data as time series only variable "Jahr" is used. There are 20 states in time resulting.

Source

References

Examples
```r
data(vrsit)
str(vrsit)
```

---

### vrveg

**Vraconnaz time series data, vegetation**

**Description**
A vegetation time series from 11 plots in the Vraconnaz peat bog, describing species invasion and propagation after a bog burst in 1986. The corresponding site object is **vrsit**

**Usage**
```r
data("vrveg")
```
Format

A data frame with 231 observations on the following 154 variables (the species):

Agrostis_canina  a numeric vector
Agrostis_capillaris  a numeric vector
Agrostis_capillaris.1  a numeric vector
Agrostis_gigantea  a numeric vector
Agrostis_stolonifera  a numeric vector
Ajuga_reptans  a numeric vector
Amblystegium_riparium  a numeric vector
Angelica_sylvestris  a numeric vector
Anthoxanthum_odoratum  a numeric vector
Atrichum_undulatum  a numeric vector
Aulacomnium_palustre  a numeric vector
Betula_pubescens  a numeric vector
Brachythecium_mildeanum  a numeric vector
Brachythecium_mildeanum.1  a numeric vector
Brachythecium_rivulare  a numeric vector
Brachythecium_rutabulum  a numeric vector
Briza_media  a numeric vector
Bryum_pseudotriquetrum  a numeric vector
Calliergonella_cuspidata  a numeric vector
Caltha_palustris  a numeric vector
Campanula_rotundifolia  a numeric vector
Campylium_stellatum  a numeric vector
Cardamine_pratensis  a numeric vector
Carex_canescens  a numeric vector
Carex_davalliana  a numeric vector
Carex_echinata  a numeric vector
Carex_flava  a numeric vector
Carex_hostiana  a numeric vector
Carex_leporina  a numeric vector
Carex_nigra  a numeric vector
Carex_panicea  a numeric vector
Carex_pauciflora  a numeric vector
Carex_pulicaris  a numeric vector
Carex_rostrata  a numeric vector
Cerastium_caespitosum  a numeric vector
Cerastium_fontanum a numeric vector
Cerastium_glomeratum a numeric vector
Ceratodon_purpureus a numeric vector
Cirriphyllum_piliferum a numeric vector
Cirsium_palustre a numeric vector
Climacium_dendroides a numeric vector
Cratoneuron_filicinum a numeric vector
Crepis_mollis a numeric vector
Crepis_paludosa a numeric vector
Crepis_paludosa.1 a numeric vector
Crocus_albiflorus a numeric vector
Ctenidium_molluscum a numeric vector
Dactylorhiza_fistulosa a numeric vector
Dactylorhiza_maculata a numeric vector
Danthonia_decumbens a numeric vector
Deschampsia_cespitosa a numeric vector
Drepanocladus_revolvens_aggr. a numeric vector
Drepanocladus_vernicosus.1 a numeric vector
Eleocharis_quinqueflora a numeric vector
Epilobium_angustifolium a numeric vector
Epilobium_montanum a numeric vector
Epilobium_montanum.1 a numeric vector
Epilobium_palustre a numeric vector
Epipactis_palustris a numeric vector
Equisetum_fluviatile a numeric vector
Equisetum_palustre a numeric vector
Eriophorum_angustifolium a numeric vector
Eriophorum_latifolium a numeric vector
Eurhynchium_speciosum a numeric vector
Festuca_arundinacea a numeric vector
Festuca_pratensis a numeric vector
Festuca_rubra_aggr. a numeric vector
Filipendula_ulmaria a numeric vector
Fissidens_adianthoides a numeric vector
Fragaria_vesca a numeric vector
Galeopsis_tetrahit a numeric vector
Galium_palustre a numeric vector
Galium_uliginosum a numeric vector
Geum_rivale a numeric vector
Homalotheicum_nitens a numeric vector
Hypericum_maculatum a numeric vector
Juncus_acutiflorus a numeric vector
Juncus_alpinoarticulatus a numeric vector
Juncus_articulatus a numeric vector
Juncus_effusus a numeric vector
Lathyrus_pratensis a numeric vector
Leontodon_hispidus a numeric vector
Lophocolea_heterophylla a numeric vector
Lotus_corniculatus a numeric vector
Luzula_campestris a numeric vector
Luzula_multiflora a numeric vector
Melampyrum_pratense a numeric vector
Mnium_hornum a numeric vector
Molinia_caerulea a numeric vector
Myosotis_cespitosa a numeric vector
Myosotis_nemorosa a numeric vector
Myosotis_scorpioides a numeric vector
Myosoton_aquaticum a numeric vector
Parnassia_palustris a numeric vector
Pedicularis_palustris a numeric vector
Pellia_neesiana a numeric vector
Petasites_albus a numeric vector
Phragmites_communis a numeric vector
Picea_abies a numeric vector
Picea_excelsa a numeric vector
Pinguicula_vulgaris a numeric vector
Plagiommium_affine_aggr. a numeric vector
Pleurozium_schreberi a numeric vector
Poa_pratensis a numeric vector
Poa_trivialis a numeric vector
Polygala_amarella a numeric vector
Polygonum_bistorta a numeric vector
Polytrichum_commune a numeric vector
Polytrichum_formosum a numeric vector
Polytrichum_strictum a numeric vector
Populus_tremula a numeric vector
Potentilla_erecta a numeric vector
Potentilla_palustris a numeric vector
Prunella_vulgaris a numeric vector
Ranunculus_acris a numeric vector
Ranunculus_auricomus a numeric vector
Rhinanthus_lectorolophus a numeric vector
Rhinanthus_minor a numeric vector
Rhytidiadelphus_squarrosus a numeric vector
Rhytidiadelphus_triquetras a numeric vector
Riccardia_multifida a numeric vector
Rumex_acetosa a numeric vector
Salix_caprea a numeric vector
Salix_cinerea a numeric vector
Salix_cinerea_cf. a numeric vector
Salix_cinerea_.S a numeric vector
Salix_myrsinifolia a numeric vector
Salix_myrsinifolia_.S a numeric vector
Salix_purpurea a numeric vector
Salix_repens a numeric vector
Sanguisorba_officinalis a numeric vector
Scleropodium_purum a numeric vector
Silene_flos_cuculi a numeric vector
Stellaria_graminea a numeric vector
Stellaria_media a numeric vector
Succisa_pratensis a numeric vector
Swertia_perennis a numeric vector
Tomentypnum_nitens a numeric vector
Trichophorum_cespitosum a numeric vector
Trollius_europaeus_.cf. a numeric vector
Tussilago_farfara a numeric vector
Vaccinium_myrtillus a numeric vector
Vaccinium_uliginosum a numeric vector
Vaccinium_vitis_idaea a numeric vector
Valeriana_dioeca a numeric vector
Valeriana_officinalis a numeric vector
Valerianella_locusta a numeric vector
Veronica_beccabunga a numeric vector
Veronica_chamaedrys a numeric vector
Vicia_cracca a numeric vector
Viola_palustris a numeric vector
litiere_seche a numeric vector
tourbe_nue a numeric vector
eau_libre a numeric vector

Details
Note that this is a data frame whereas the corresponding time (years) is listed in vrsit.

Source

References

Examples
data(vrveg)
str(vrveg)

vvelocity

Printing ordinations of velocity and acceleration and differently transformed speed profiles

Description
Given a data frame of a multivariate (vegetation) time series this plots a pco ordination using circles with diameters proportional to rate of change (velocity), a pco ordination pco using circles with diameters proportional to change in velocity (acceleration) and three velocity profiles with differently transformed species scores (from quantitative to qualitative).

Usage
vvelocity(pveg, timescale, y, ...)
vvelocity2(pveg, timescale, y=1)

## Default S3 method:
vvelocity(pveg,timescale,y,....)
## S3 method for class 'vvelocity'
plot(x,tlabs,scal=1,....)
Arguments

- **pveg**: A data frame of a multivariate (vegetation) time series
- **timescale**: A vector of points in time of releves (rows)
- **y**: Transformation of species scores: \( x' = x \exp(y) \)
- **...**: Additional arguments passed to plot.
- **tlabs**: A vector of releve labels used for annotation of data points in ordinations. See example.
- **scal**: A variable for scaling the circles in the ordinations. Default is `scal=1`.
- **x**: An object of class "vvelocity".

Details

See also **pco** for the ordinations used.

Value

An object of class "vvelocity" with at least the following items:

- **pveg**: The input vegetation data frame
- **timescale**: The input time scale
- **y**: Transformation of species scores: \( x' = x \exp(y) \)

Author(s)

Otto Wildi

References


Examples

```r
tlabs <- c(1, 15, 48, 60, 100, 122, 145)
timescale <- psit$Years.B.P
o.vvel <- vvelocity(pveg, timescale, y=0.5)
plot(o.vvel, tlabs=tlabs, scal=1)
```
**Description**

Random sample of Swiss wetland vegetation, site information. Vegetation information is in `wetveg`. Note: this differs from the same file in the 2nd edition as 4 observations are erased and 16 new site factors added.

**Usage**

data(westsit)

**Format**

A data frame with 1496 observations on the following 85 variables.

- **EK2_Identifikation** a factor with levels identifying phytosociologica identity
- **Flnr_ek1** a numeric vector, a plot number
- **Flnr_ek2** a numeric vector, a plot number
- **Area** a numeric vector, surface of plot
- **ek** a numeric vector
- **Objekt_Nr** a numeric vector
- **Kanton** a factor with levels identifying canton
- **Datum** a factor with levels for date of sampling
- **Autor_Code** a factor with levels for author code
- **Det_Code** a factor with levels of author initials
- **Erhebung** a numeric vector, survey, mainly 1
- **Torfmoose** a factor with levels for Sphagnum cover
- **Uebrige_Moose** a factor with levels for cover of other mosses
- **Zwergstraeucher** a factor with levels for cover of dwarf shrubs
- **Straeucher** a factor with levels for cover of shrubs
- **Baeume** a factor with levels for cover of trees
- **Nekromasse** a factor with levels for cover of necro mass
- **Offener_Torf** a factor with levels for cover of open turf
- **Offener_Mineralboden** a factor with levels for mineral soil
- **Offene_Wasserflaeche** a factor with levels for open water surface
- **Stark_abgefressen** a factor with levels for browsing _Ja_Nein
- **Kurz_geschnitten** a factor with levels for cutting _Ja_Nein
- **X** a factor with levels for x-axis in space
Y a factor with levels for y-axis in space
Z a factor with levels for z-axis in space, elevation
humidity a numeric vector
light a numeric vector
temperature a numeric vector
continence a numeric vector
reaction a numeric vector
nutrients a numeric vector
humus a numeric vector
dispersity a numeric vector
Assoziation1_eck a factor with levels for alliance names, first choice
Assoziation2_eck a factor with levels for alliance names, second choice
Assoziation3_eck a factor with levels for alliance names, third choice
X1._Wert_eck a numeric vector
X2._Wert_eck a numeric vector
X3._Wert_eck a factor with levels (rather than a numeric vector as above)
Differenz_Wert1_Wert2 a numeric vector
Unterverband1_eck a factor with names of sub-alliance as levels, first choice
Unterverband2_eck a factor with names of sub-alliance as levels, second choice
Verband1_eck a factor with names of alliances as levels, first choice
Verband2_eck a factor with names of alliances as levels, first choice
unklassierbar_verband a factor with levels _ ja
Unterordnung1_eck a logical vector
Unterordnung2_eck a logical vector
Ordnung1_eck a factor with order as levels, first choice
Ordnung2_eck a factor with order as levels, second choice
unklassierbar_ordnung a factor with levels _ ja
Unterkasse1_eck a logical vector
Unterkasse2_eck a factor with levels Polygono-Poenea_annucae
Klasse1_eck a factor with class as levels, first choice
Klasse2_eck a factor with class as levels, second choice
BAFU.Gruppe1_eck a factor with vegetation type in german, first choice
BAFU.Gruppe2_eck a factor with vegetation type in german, second choice
Wirkungskontrolle1_eck a factor with vegetation type in german as levels
Wirkungskontrolle2_eck a factor with vegetation type in german as levels
Wirkungskontrolle_engl1_eck a factor with vegetation type in english as levels
Wirkungskontrolle_engl2_eck a factor with vegetation type in english as levels
wetsit

Moor_j.n1_ek1 a factor with levels j n
Moor_j.n2_ek1 a factor with levels j n
Assoziation_Nr a numeric vector
Unterverband_Nr a numeric vector
Verband_Nr a numeric vector
Unterordnung_Nr a logical vector
Ordnung_Nr a numeric vector
Unterklasse_Nr a logical vector
Klasse_Nr a numeric vector
slp25_d8 a numeric vector
ddeg300 a numeric vector
precyy a numeric vector
sfroyy a numeric vector
tminall a numeric vector
sraddy a numeric vector
swb a numeric vector
mind7 a numeric vector
SOILTYPE a factor with levels identifying soil type
GRUNDIGKEI a numeric vector
SKELETT a numeric vector
WASSERSPEI a numeric vector
NAHRSTOFF a numeric vector
WASSERDURC a numeric vector
VERNASS a numeric vector
GT_ID a numeric vector

Source


References


Examples

summary(wetsit)
**wetveg**

*Random sample of Swiss wetland vegetation, vegetation information.*

---

**Description**

Random sample of Swiss wetland vegetation, vegetation information. Site data is in `wetsit`. Note: this differs from the same used in the 2nd edition in that 4 observations and 1 variable are erased.

**Usage**

`data(wetveg)`

**Format**

A data frame with 1496 observations on 1163 variables, the species. A 0 to 4 step scales is used.

**Source**


**References**


**Examples**

`summary(wetveg)`

---

**ws200**

*Four kilometre grid forest data of Switzerland, 200m2 plots*

---

**Description**

Four kilometre grid forest data of Switzerland, 200m2 plots. Also see `ws30`, `ws500`. Site information is in `wssit`.

**Usage**

`data(ws200)`

**Format**

A data frame with 726 observations on 1262 variables, the species.
Details
See object wssit for corresponding site information

Source

References

Examples
summary(ws200)

Four kilometre grid forest data of Switzerland, 30m2 plots

Description
Four kilometre grid forest data of Switzerland, 30m2 plots. Also see ws200, ws500. Site information is in wssit.

Usage
data(ws30)

Format
A data frame with 726 observations on 1262 variables, the species.

Details
See object wssit for corresponding site information

Source

References

Examples
summary(ws30)
Four kilometre grid forest data of Switzerland, 500m² plots

Description

Four kilometre grid forest data of Switzerland, 500m² plots. Also see ws30, ws200. Site information is in wssit.

Usage

data(ws500)

Format

A data frame with 726 observations on 1262 variables, the species.

Details

See object wssit for corresponding site information.

Source


References


Examples

summary(ws500)

Four kilometre grid forest data of Switzerland, site information

Description

Four kilometre grid forest data of Switzerland, site information. Also see ws30, ws200 and ws500 for vegetation data.

Usage

data(ws50it)
Format

A data frame with 726 observations on the following 18 variables.

x.coord  a numeric vector
y.coord  a numeric vector
hoehe    a numeric vector
elev      a numeric vector
slp       a numeric vector
ddeg.Ø    a numeric vector
prcp.yy   a numeric vector
sfro.yy   a numeric vector
tave.cc   a numeric vector
srad.yy   a numeric vector
swb       a numeric vector
min7      a numeric vector
s.depth   a numeric vector
s.wcap    a numeric vector
s.nutrient a numeric vector
s.wperm   a numeric vector
s.wetn    a numeric vector
pH.LFI    a numeric vector

Details

Corresponding vegetation data is in ws30, ws200 and ws500 respectively.

Source


References


Examples

summary(wssit)
Index

*Topic arith
  orank, 24
  outlier, 26
  srank, 43
*Topic array
  aocc, 2
  ccost, 4
  centroid, 6
  Mtabs, 18
*Topic cluster
  davesil, 8
  overly, 27
*Topic datasets
  EKs, 11
  EKv, 12
  ltim, 16
  lveg, 17
  mveg, 20
  nsit, 22
  nveg, 23
  psit, 33
  pveg, 34
  sn59sit, 35
  sn59veg, 35
  sn6sit, 36
  sn6veg, 37
  sn7sit, 38
  sn7veg, 39
  ssind, 45
  ssit, 46
  ssspft, 47
  sveg, 48
  tsit, 49
  tveg, 50
  vrsit, 51
  vrveg, 52
  wetsit, 59
  wetveg, 62
  ws200, 62
  ws30, 63
  ws500, 64
  wssit, 64
*Topic graphs
  fspa, 14
*Topic hplot
  davesil, 8
  mxplot, 21
  pcaser, 29
  pcobiplot, 30
  pcovar, 31
*Topic misc
  ccost, 4
  centroid, 6
*Topic models
  dircor, 10
  fitmarkov, 13
  SNPsm, 40
*Topic model
  SNPtm, 41
*Topic multivariate
  aocc, 2
  dircor, 10
  fitmarkov, 13
  fspa, 14
  Mtabs, 18
  mxplot, 21
  orank, 24
  outlier, 26
  overly, 27
  pcaser, 29
  pcobiplot, 30
  pcovar, 31
  SNPsm, 40
  SNPtm, 41
  speedprof, 42
  srank, 43
  vvelocity, 57
*Topic package, dave
INDEX

sn6veg, 36, 37
sn7sit, 38
sn7veg, 38, 39
SNPsm, 40
SNPsm2 (SNPsm), 40
SNPtM, 41
SNPtM2 (SNPtM), 41
spantree, 27, 28
speedprof, 42
speedprof2 (speedprof), 42
srank, 43
srank2 (srank), 43
ssind, 45
ssit, 46, 48
sspft, 47
summary.Mtabs (Mtabs), 18
summary.orank (orank), 24
sveg, 46, 48

tsit, 49, 50
tveg, 49, 50

vegdist, 31, 32, 42
vrsit, 51, 52, 57
vrveg, 51, 52
vvelocity, 57
vvelocity2 (vvelocity), 57

wetsit, 59, 62
wetveg, 59, 62
ws200, 62, 64
ws30, 63, 64
ws500, 64, 64
wssit, 62–64, 64