Package 'shipunov'

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Description A collection of functions for data manipulation, plotting and statistical computing, to use separately or with the book ``Visual Statistics. Use R!'': Shipunov (2019) <http://ashipunov.info/shipunov/software/r/r-en.htm>. Most useful functions are probably Bclust(), Jclust() and BootA() which bootstrap hierarchical clustering; Recode...() which multiple recode in a fast, flexible and simple way; Misclass() which outputs confusion matrix even if classes are not concerted; Overlap() which calculates overlaps of convex hulls from any projection; and Pleiad() which is fast and flexible correlogram. In fact, there are much more useful functions, please see documentation.

Suggests adabag, apcluster, ape, class, cluster, dbscan, e1071, effsize, grid, ips, kernlab, MASS, mclust, meanShiftR, neuralnet, nnet, PBSmapping, randomForest, rpart, scales, smirnov, tapkee, tree, vegan

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`Adj.Rand` *Adjusted Rand index*

Description

Adjusted Rand index

Usage

```
Adj.Rand(cl1, cl2)
```

Arguments

`cl1`	First classification (character vector of group names)
`cl2`	Second classification

Details

Adjusted Rand Index.

Value

Similarity: numerical vector of length 1

Author(s)

Alexey Shipunov

References

Hubert L. and Arabie P. 1985. Comparing partitions. Journal of Classification. 2. 193–218.

See Also

Misclass

Examples

```
iris.dist <- dist(iris[, 1:4], method="manhattan")
iris.hclust <- hclust(iris.dist)
iris.3 <- cutree(iris.hclust, 3)
Adj.Rand(iris.3, iris[, 5])
```

Aggregate1 *Aggregates by one vector and uses it for row names*

Description

Aggregates by one vector and uses it for row names

Usage

```
Aggregate1(df, by, ...)
```

Arguments

df	Data frame to aggregate
by	Atomic object to use for aggregating
...	Arguments for 'aggregate()'

Details

'Aggregate1()' is an 'aggregate()' helper: aggregates only by one atomic variable and uses it for row names.

Value

Same as of 'aggregate()'

Author(s)

Alexey Shipunov

See Also

aggregate

Examples

```
trees3 <- sample(letters[1:3], nrow(trees), replace=TRUE)
Aggregate1(trees, trees3, median, na.rm=TRUE)
```

`Alldups` *Finds all duplicates*

Description

Finds duplicates from both ends, optionally returns indexes of duplicate groups

Usage

```
Alldups(v, groups = FALSE)
```

Arguments

v	vector
groups	If TRUE, uses as.numeric(as.character(v)) twice to index duplicated groups with natural numbers (and non-duplicated with 0)

Details

In short, this is extension of unique() which skips the first duplicate in each group. 'NA' count as duplicate but do not count as duplicate group.

Value

Logical vector of length equal to 'v', or numerical vector if 'groups=TRUE'

Author(s)

Alexey Shipunov

See Also

unique

Examples

```
aa <- c("one", "two", "", NA, "two", "three", "three", "three", NA, "", "four")
Alldups(aa)
data.frame(v=aa, dups=Alldups(aa), groups=Alldups(aa, groups=TRUE))
```

`atmospheres` *atmospheres*

Description

Atmospheres of Solar System.

Mercury might be easily taken out because it does not have atmosphere in strict sense.

All data in percentages.

Usage

```
atmospheres
```

Source

Data from the NASA Web site, once was available as 'planetatmoscomp.pdf' document.

`Bclabels` *Plot bootstrap values*

Description

Print (bootstrap) values on 'hclust' plot

Usage

```
Bclabels(hcl, values, coords=NULL, horiz=FALSE, method="text", threshold=NULL, ...)
```

Arguments

`hcl`	`hclust` object
`values`	`numeric`, (bootstrap) values to use
`coords`	If NULL (default), coordinates will be calculated with Hcoords(hcl)
`horiz`	Plot values for a horizontal tree?
`method`	If "text" (default), plot text values, if "points", plot points
`threshold`	If set, do not plot text or points for values < threshold
`...`	If "text" (default), additional arguments to text(), if "points", to points()

Details

This low-level plot function plots text or points in accordance with bootstrap values to the corresponding node of the plotted 'hclust' object.

Value

List with components: 'coords' for coordinates, 'labels' for (selected) values.

See Also

Bclust

Examples

```
bb <- Bclust(t(moldino)) # specify 'mc.cores=4' or similar to speed up the process
plot(bb$hclust)
Bclabels(bb$hclust, bb$values, col="red", pos=3, offset=0.1, threshold=0.5)
```

Bclust *Bootstrapped hclust*

Description

Bootstraps (or jacknife) hierarchical clustering

Usage

```
Bclust(data, method.d="manhattan", method.c="ward.D",
FUN=function(.x) hclust(dist(.x, method=method.d), method=method.c),
iter=1000, mc.cores=1, monitor=TRUE, bootstrap=TRUE)
```

Arguments

data	Data suitable for the chosen distance method
method.d	Method for dist()
method.c	Method for hclust()
FUN	Function to make 'hclust' objects
iter	Number of replicates
mc.cores	integer, number of processes to run in parallel
monitor	If TRUE (default), prints a dot for each replicate
bootstrap	If FALSE (not default), performs jacknife (and makes 'iter=ncol(data)')

Details

This function provides bootstrapping for hierarchical clustering (hclust objects). Internally, it uses Hcl2mat() which converts 'hclust' objects into binary matrix of cluster memberships.

Bclust() and companion functions were based on functions from the 'bootstrap' package of Sebastian Gibb.

Value

List with components: 'values' for bootstrapped frequencies of each node, 'hcl' for original 'hclust' object, 'consensus' which is a sum of all Hcl2mat() matrices.

References

Felsenstein, Joseph. *Confidence limits on phylogenies: an approach using the Bclust.* Evolution (1985): 783-791.

Efron, Bradley, Elizabeth Halloran, and Susan Holmes. *Bootstrap confidence levels for phylogenetic trees.* Proceedings of the National Academy of Sciences 93.23 (1996): 13429-13429.

See Also

Jclust, BootA, Hcl2mat, Bclabels, Hcoords

Examples

```
(bb <- Bclust(t(atmospheres))) # specify 'mc.cores=4' or similar to speed up the process

plot(bb$hclust)
Bclabels(bb$hclust, bb$values, col="blue", pos=3, offset=0.1)

plot(bb$hclust)
Bclabels(bb$hclust, bb$values, col="blue", pos=3, offset=0.1, threshold=0.9)

plot(bb$hclust)
Bclabels(bb$hclust, bb$values, method="points", threshold=0.9, pch=19, cex=2)

plot(bb$hclust)
Bclabels(bb$hclust, bb$values, method="points", pch=19, cex=bb$values*3)

coords1 <- Hcoords(bb$hclust)
plot(bb$hclust)
Bclabels(bb$hclust, bb$values, coords=coords1, method="points", pch=19,
 cex=bb$values*3)

oldpar <- par(mar=c(2,1,0,4))
Ploth(bb$hclust, horiz=TRUE)
Bclabels(bb$hclust, bb$values, col="blue", pos=3, offset=0.1, horiz=TRUE)
par(oldpar)

plot(hclust(dist(bb$consensus)), main="Net consensus tree") # net consensus
## majority rule is 'consensus >= 0.5', strict is like 'round(consensus) == 1'

bb1 <- Bclust(t(atmospheres), FUN=function(.x) hclust(Gower.dist(.x)), monitor=FALSE)
plot(bb1$hclust)
Bclabels(bb1$hclust, bb1$values, col="green", pos=3, offset=0.1)

Bclust(t(atmospheres), bootstrap=FALSE) # jacknife
```

`BestOverlap` *Calculates the best overlap*

Description

Uses multiple datasets, measures overlaps between class-related convex hulls and reports the best dataset, the best overlap table and summary with confidence intervals. Can be used to assess bootstrap or jackknife results, to compare different dimension reduction and/or clustering methods, and to average results of stochastic methods.

Usage

```
BestOverlap(xylabels, ci="95%", round=4)
```

Arguments

`xylabels`	List of data frames, each with at least 3 columns named exactly as: "x" for x coordinates, "y" for y coordinates and "labels" for class labels
`ci`	Confidence interval (character string with percent sign)
`round`	How to round numbers in summary table

Details

'BestOverlap()' requires object, typically created after bootstrapping or similar procedure (see below for examples). This 'xylabels' object must contain at least three columns named exactly as c("x", "y", "labels"), in any order.

Please note that label types must be the same between data frames inside 'xylabels' list. For consistency, first data frame is used a label standard. If any next data frame contain label types different from standard, it will be ignored.

Value

List with three components: 'best' data frame, 'best.overlap' table and 'summary' data frame.

Author(s)

Alexey Shipunov

Examples

```
## Bootstrap PCA
B <- 100
xylabels <- vector("list", length=0)
for (n in 1:B) {
ROWS <- sample(nrow(iris), replace=TRUE)
tmp <- prcomp(iris[ROWS, -5], scale=TRUE)$x[, 1:2]
```

```
xylabels[[n]] <- data.frame(x=tmp[, 1], y=tmp[, 2], labels=iris[ROWS, 5])
}
BestOverlap(xylabels)

## Jacknife PCA
B <- nrow(iris)
xylabels <- vector("list", length=0)
for (n in 1:B) {
ROWS <- (1:B)[-n]
tmp <- prcomp(iris[ROWS, -5], scale=TRUE)$x[, 1:2]
xylabels[[n]] <- data.frame(x=tmp[, 1], y=tmp[, 2], labels=iris[ROWS, 5])
}
BestOverlap(xylabels)

## Stochastic method: Stochastic Proximity Embedding
library(tapkee)
B <- 100
xylabels <- vector("list", length=0)
for (n in 1:B) {
tmp <- Tapkee(iris[, -5], method="spe")
xylabels[[n]] <- data.frame(x=tmp[, 1], y=tmp[, 2], labels=iris[, 5])
}
BestOverlap(xylabels)

## Diverse dimension reduction methods
library(tapkee)
B <- c("lle", "npe", "ltsa", "lltsa", "hlle", "la", "lpp", "dm", "isomap", "l-isomap")
xylabels <- vector("list", length=0)
for (n in B) {
tmp <- Tapkee(iris[, -5], method=n, add="-k 50")
xylabels[[n]] <- data.frame(x=tmp[, 1], y=tmp[, 2], labels=iris[, 5])
}
BestOverlap(xylabels)

## One dimension reduction but many clusterings
B <- 100
xylabels <- vector("list", length=0)
tmp1 <- prcomp(iris[, -5], scale=TRUE)$x[, 1:2]
for (n in 1:B) {
tmp2 <- kmeans(iris[, -5], centers=3)$cluster
xylabels[[n]] <- data.frame(x=tmp1[, 1], y=tmp1[, 2], labels=letters[tmp2])
}
BestOverlap(xylabels)
```

Biokey *Convert diagnostic keys and classification lists*

Description

Convert the oldest biological data structures: diagnostic keys ("keys") and classification lists ("classifs")

Usage

```
Biokey(data, from="", to="", recalculate=TRUE, internal=FALSE, force=FALSE)
Numranks(nums=NULL, ranks=NULL, add=NULL, empty="Species")
```

Arguments

data	Diagnostic keys ("keys"), classification lists ("classifs") and tables, or Newick phylogeny trees
from	Data type to convert from
to	Data type to convert to
recalculate	Recalculate the numeric ids?
internal	(For debugging) Output internal 4-column 'key' objects instead?
force	(For debugging) Ignore list of allowable conversion pairs?
nums	Numbers to convert into ranks
ranks	Ranks to convert into numbers
add	Rank-number conversion rule to add (overrides embedded rules)
empty	What rank to use for empty number?

Details

Biokey() is a way to convert classification lists ("classifs") or diagnostic keys into each other. In addition, it handles species classification tables ("table") and Newick trees ("newick").

To know which conversions are allowed, simply type Biokey() without arguments (this will also induce the harmless error message).

Numranks() converts biological rank names into numbers and numbers into rank names (Shipunov, 2017). To see the embedded conversion table, type Numranks() without arguments.

To know more about keys and classifs, read help for "classifs" and "keys".

Bracket keys (see help for "keys") could have more than two conditions, other keys not, so problems might arise during conversion (see examples).

Backreferenced keys (see help for "keys") is just a variety of bracket keys so the only possible way to make them is from bracket keys.

Branched key (see help for "keys") is an indented key with omitted "indent" column, therefore it does not require the separate conversion way. See examples about how to convert indent column into actual indents.

Classification "table" is the data frame where each column represent some particular rank (see examples to understand better). Similarly to "classif", "table" should use numerical ranks. In this case, numerical ranks should be column names (see examples).

When Biokey() converts "classif" to "newick", it keeps higher group names as node labels. It does not do that in all other cases.

It is an open question if phylogeny tree (Newick) should be converted into "classif" (see help for "classifs") with all intermediate ranks propagated (thus frequently become monotypic, i.e. with just one subgroup), or with only main ranks (whole numbers) propagated, or terminals (by default, they always have "species" rank = 1) could follow much bigger ranks (i.e., "species" = 1 might follow "family" = 3, not "genus" = 2). At the moment, the last variant is implemented.

Comparably, "newick" to "classif" conversion does _not_ remove names of monotypic intermediate taxa, this might result in "crowding" of node labels (see the example). Also, this conversion automatically propagates intermediate ranks to make all ranks concerted, this might result in empty labels.

Value

Typically, the data frame or just a character string (in case of Newick output). Output may contain column names but this is only to facilitate understanding of the format and could be stripped without consequences. If 'internal=TRUE', outputs a standardized 4-column data frame in a form of branched key (columns 'id', 'description', 'terminal'), plus 'goto' column which might be just NAs.

Author(s)

Alexey Shipunov

References

Shipunov A. 2017. "Numerical ranks" to improve biological nomenclature of higher groups. 2017. URL: 'https://arxiv.org/abs/1708.07260'

See Also

classifs, keys

Examples

```
## Biokey() # makes (harmless) error message but also shows which conversions are available
Numranks() # shows the conversion table

## ===

Numranks(nums=1:7)
Numranks(ranks="kingdom") # "kingdom", "order", "family" and "tribe" translate into Latin

## ===

## three branched keys
i1 <- c("1 A ", "2 B Name1", "2 BB Name2", "1 AA ", "3 C Name3", "3 CC Name4")
i2 <- c("1 A Name1", "2 B Name2", "2 BB ", "3 C Name3", "3 CC Name4")
i3 <- c("1 A Name1", "2 B Name2", "2 BB ", "3 C Name3",
 "3 CC Name4", "2 BBB ", "4 D Name5", "4 DD Name6", "4 DDD Name7")
k1 <- read.table(textConnection(i1), sep=" ", as.is=TRUE)
k2 <- read.table(textConnection(i2), sep=" ", as.is=TRUE)
k3 <- read.table(textConnection(i3), sep=" ", as.is=TRUE)
```

```
## convert them into phylogeny trees and plot
t1 <- Biokey(k1, from="branched", to="newick")
t2 <- Biokey(k2, from="branched", to="newick")
t3 <- Biokey(k3, from="branched", to="newick")
library(ape) # load 'ape' to plot Newick trees below
plot(read.tree(text=t1))
plot(read.tree(text=t2))
plot(read.tree(text=t3))

## ===

## Bracket keys
bracket1 <- keys[[1]]
bracket1
Biokey(bracket1, from="bracket", to="backreferenced")
(ii <- Biokey(bracket1, from="bracket", to="indented"))
## Remove third condition to avoid warnings:
Biokey(bracket1[bracket1[, 3] != "Horse", ], from="bracket", to="serial")
(nn <- Biokey(bracket1, from="bracket", to="newick"))
plot.phylo(read.tree(text=nn)) # plot newick as phylogeny trees

## Now convert indent column into actual indents:
for (i in 1:length(ii[, 1])) ii[i, 1] <- paste(rep(" ", ii[i, 1]), collapse="")
## and make also dot leaders
ifelse(!is.na(ii[, 3]), "...", "")
ii

## Branched keys
branched1 <- keys[[3]]
head(branched1)
Biokey(branched1, from="branched", to="bracket")[1:7, ]
Biokey(branched1, from="branched", to="indented")[1:7, ]
Biokey(branched1, from="branched", to="serial")[1:7, ]
(nn <- Biokey(branched1, from="branched", to="newick"))
plot.phylo(read.tree(text=nn))

## Indented keys (same as branched but with indent as first column)
indented0 <- c("0 1 Blue ", "1 2 Gas Sky", "1 2 Liquid ",
 "0 1 Yellow ", "2 3 Star Sun", "2 3 Buttecup Flower")
(indented1 <- read.table(textConnection(indented0), sep=" ", as.is=TRUE))
Biokey(indented1, from="indented", to="bracket")
Biokey(indented1, from="indented", to="serial")
(nn <- Biokey(indented1, from="indented", to="newick"))
plot.phylo(read.tree(text=nn))

## Serial keys
serial1 <- keys[[4]]
head(serial1)
Biokey(serial1, from="serial", to="bracket")[1:7, ]
Biokey(serial1, from="serial", to="indented")[1:7, ]
(nn <- Biokey(serial1, from="serial", to="newick"))
plot.phylo(read.tree(text=nn))
```

```
## Classifs
classif2 <- classifs[[2]]
classif2[, 1] <- Numranks(ranks=classif2[, 1], add=c(Series=1.1))
head(classif2)
Biokey(classif2, from="classif", to="table")[1:7, ]
(nn <- Biokey(classif2, from="classif", to="newick"))
tt <- read.tree(text=nn)
plot.phylo(tt, node.depth=2)
nodelabels(tt$node.label, frame="none", bg="transparent", adj=-0.05)

## Classification tables
table0 <- c("FAMILY SUBFAMILY TRIBE GENUS", "Hominidae Homininae Hominini Homo",
 "Hominidae Homininae Hominini Pan", "Hominidae Homininae Gorillini Gorilla",
 "Hominidae Ponginae Ponginini Pongo")
(table1 <- read.table(textConnection(table0), sep=" ", as.is=TRUE, h=TRUE))
names(table1) <- Numranks(ranks=names(table1))
table1
Biokey(table1, from="table", to="classif")

## Newick phylogeny trees
newick1 <- "((Coronopus,Plantago),(Bougueria,(Psyllium_s.str.,Albicans)),Littorella);"
plot.phylo(read.tree(text=newick1))
Biokey(newick1, from="newick", to="classif")
```

BootA *Bootstrap clustering*

Description

How to bootstrap clustering with 'ape'

Usage

```
BootA(dat, FUN=function(.x) ape::nj(dist(.x)), iter=1000, mc.cores=1, tresh=50,
 cons=TRUE, prop=0.5)
```

Arguments

dat	data
FUN	how to bootstrap (see examples)
iter	number of iterations, default 1000
mc.cores	how many cores to employ (system-dependent)
tresh	Threshold for printing bootstrap values
cons	Calculate consensus tree?
prop	0.5 is majority-rule consensus (default), 1 is strict consensus

Details

This is how to bootstrap clustering with 'ape::boot.phylo()'.

Author(s)

Alexey Shipunov

See Also

ape::boot.phylo

Examples

```
dat <- iris[, -5]
row.names(dat) <- abbreviate(make.names(iris[, 5], unique=TRUE))
iris.BA1 <- BootA(dat, iter=100)
plot(iris.BA1$boot.tree, show.node.label=TRUE)
plot(iris.BA1$cons.tree)
iris.BA2 <- BootA(dat, FUN=function(.x) ape::as.phylo(hclust(dist(.x))), iter=100)
## Not run:
## change (or remove) 'mc.cores=...' in accordance with your system features
iris.BA3 <- BootA(dat, FUN=function(.x) phangorn::NJ(dist(.x)), iter=100,
 mc.cores=4)

## End(Not run)
```

BootKNN *Bootstrap with kNN*

Description

How to bootstrap with kNN

Usage

```
BootKNN(data, classes, sub="none", nsam=4, nboot=1000, misclass=TRUE)
```

Arguments

data	Data frame to classify
classes	Character vector of class names
sub	Subsample to use (see example)
nsam	Number of training items from each level of grouping factor, default 4
nboot	Number of iterations
misclass	Calculate misclassification table?

Details

This is an example of how to bootstrap with 'class::knn1()'.

Samples equal numbers ('nsam') of training items from *each level* of grouping factor.

Allows to use *sub*set of data which will be used for sub-sampling of training data.

Value

Returns all predictions as character matrix, each boot is a column

Author(s)

Alexey Shipunov

See Also

`class::knn1`, `Dev`

Examples

```
iris.sub <- 1:nrow(iris) %in% seq(1, nrow(iris), 5)
iris.bootknn <- BootKNN(iris[, -5], iris[, 5], sub=iris.sub)
```

BootRF *Bootstrap with 'randomForest()'*

Description

How to bootstrap with 'randomForest()'

Usage

```
BootRF(data, classes, sub="none", nsam=4, nboot=1000, misclass=TRUE)
```

Arguments

`data`	Data frame to classify
`classes`	Character vector of class names
`sub`	Subsample to use (see example)
`nsam`	Number of training items from each level of grouping factor, default 4
`nboot`	Number of iterations
`misclass`	Calculate misclassification table?

Details

This an example of how to bootstrap with 'randomForest::randomForest()'.

Samples equal numbers ('nsam') of training items from *each level* of grouping factor.

Allows to use *sub*set of data which will be used for sub-sampling of training data.

Value

Returns all predictions as character matrix, each boot is a column

Author(s)

Alexey Shipunov

See Also

`randomForest::randomForest`, `Dev`

Examples

```
iris.sub <- 1:nrow(iris) %in% seq(1, nrow(iris), 5)

## could be slow
iris.bootrf <- BootRF(iris[, -5], iris[, 5], sub=iris.sub)
iris.bootrf <- BootRF(iris[, -5], iris[, 5])
## naturally, in the second case misclassification rate is lower
```

Boxplots *Grouped boxplots*

Description

Boxplots for every scaled variable grouped by factor

Usage

```
Boxplots(vars, groups, boxcols=Pastels, legpos="topleft", srt=45, adj=1,
 slty=3, yticks=FALSE, ymarks=FALSE, ...)
```

Arguments

`vars`	data frame consists of variables to plot
`groups`	grouping factor
`boxcols`	colors of character boxes, default is 'Pastels', i.e. c("white", "lightblue", "mistyrose", "lightcyan", "lavender", "cornsilk")
`legpos`	where to place automatic legend, default is 'topleft', for no legend use 'legpos=NA'

`slty`	line type to delimit groups of boxes
`srt, adj, yticks, ymarks`	regular 'plot()' arguments
`...`	additional arguments to 'boxplot()'

Details

There are many ways to represent groups in data. One is trellis plots. 'Boxplots()' make grouped plots which fit the plot box linearly and therefore easy to compare. So the main idea for grouped plots is to make comparison easier.

Please note that because characters within group are likely of different nature, they are scaled. Consequently, tick marks are removed as they have no sense.

Alternatives: trellis designs.

Value

For the efficiency reasons, the function does not return anything.

Author(s)

Alexey Shipunov

See Also

`boxplot`, `Linechart`, `Dotchart3`

Examples

```
Trees <- trees
Trees[, 4] <- sample(letters[1:3], nrow(Trees), replace=TRUE)
Boxplots(Trees[, 1:3], factor(Trees[, 4]), srt=0, adj=c(.5, 1)) # horizontal labels

sp <- Recode(eq_s$N.POP, eq_l$N.POP, as.character(eq_l$SPECIES))
eq <- cbind(sp, eq_s[-1])
eq3 <- eq[eq$sp %in% levels(eq$sp)[1:3], ]
Boxplots(eq3[, 2:9], eq3[, 1], boxcols=grey(1:3/3), slty=0) # no border lines
```

Cdate *System date, time plus easy save history*

Description

System date in 'yyyymmdd' format, system time in 'yyyymmdd_hhmmss' format plus easy save history

Usage

```
Cdate()
Ctime()
Save.history()
```

Details

System date / time in compact formats. These formats are by experience, the most appropriate formats both for file systems and for spreadsheets.

There is also easy 'savehistory' (does not work under macOS R GUI – but works under macOS 'Terminal.app' R).

Author(s)

Alexey Shipunov

See Also

savehistory

Examples

```
Cdate()
Ctime()
## Not run:
## does not work under macOS GUI
Save.history()

## End(Not run)
```

---

chaetocnema *Chaetocnema flea beetles*

Description

Lubischew data (1962, pp. 465–468, tables 4–6): 74 Chaetocnema flea beetles specimens which belong to three cryptic species.

Sources of specimens:

Chaetocnema concinna Marsh:

1-6 Environs of Uljianovsk; 7 Khvalynsk, the Volga; 8-9 Perm; 10-14 Environs of Leningrad; 15-17 The Ukraine; 18 Ashkhabad, Turkmenistan; 19-21 France.

Ch. heikertintgeri Lubis.:

1-8 Environs of Uljianovsk; 9 Khvalynsk; 10-14 Perm; 15-17 Environs of Leningrad; 18-20 The Ukraine; 21 Ustj-Zilma; 22 Gagra, Abkhazia; 23-27 Ussuri district; 28-29 Yakutsk district; 30 Khabarovsk; 31 Germany.

Ch. heptapotamnica Lubis.:

1-18 Environs of Lake Issyk-Kul, Kirghizia; 19 Alma-ata, Kazachstan; 20-22 Environs of Frunze, Kirghizia.

Usage

```
chaetocnema
```

Format

These data frame contains the following columns:

`Species` Species epithet

`No` Number of sample (see below)

`x10` Width of the first joint of the first tarsus (the sum of measurements for both tarsi), in microns

`x12` The same for the second joint

`x14` The maximal width of the aedeagus in the fore-part, in microns

`x18` The front angle of the aedeagus, 1 unit = 7.5 degrees

`x40` The maximal width of the head between the external edges of the eyes, in 0.01 mm

`x48` The aedeagus width from the side, in microns

Source

Lubischew A.A. 1962. On the use of discriminant functions in taxonomy. Biometrics. 18:455–477.

Cladd *Adds confidence bands to the simple linear model plots*

Description

Adds confidence bands to the simple linear model plots

Usage

```
Cladd(model, data, level=.95, lty=2, ab.lty=0, col="black", ab.col="black")
```

Arguments

`model`	Simple linear model name
`data`	Original data
`level`	Confidence level
`lty`	Confidence bands line type
`ab.lty`	Regression line type
`col`	Confidence bands line color
`ab.col`	Regression line color

Details

'Cladd()' adds confidence bands to the simple linear model plots. Works only for simple lm(y ~ x) objects!

Author(s)

Alexey Shipunov

See Also

lm

Examples

```
hg.lm <- lm(Height ~ Girth, data=trees)
plot(Height ~ Girth, data=trees)
Cladd(hg.lm, data=trees, ab.lty=1)
```

Class.sample *Samples along the class labels*

Description

Samples within each class separately

Usage

```
Class.sample(labels, nsam)
```

Arguments

labels	Vector of labels to convert into factor
nsam	Number of samples to take from each class

Details

'Class.sample()' splits labels into groups in accordance with classes, and samples each of them separately.

If 'nsam' is bigger then class size, the whole class will be sampled.

Value

Logical vector of length equal to 'vector'

Author(s)

Alexey Shipunov

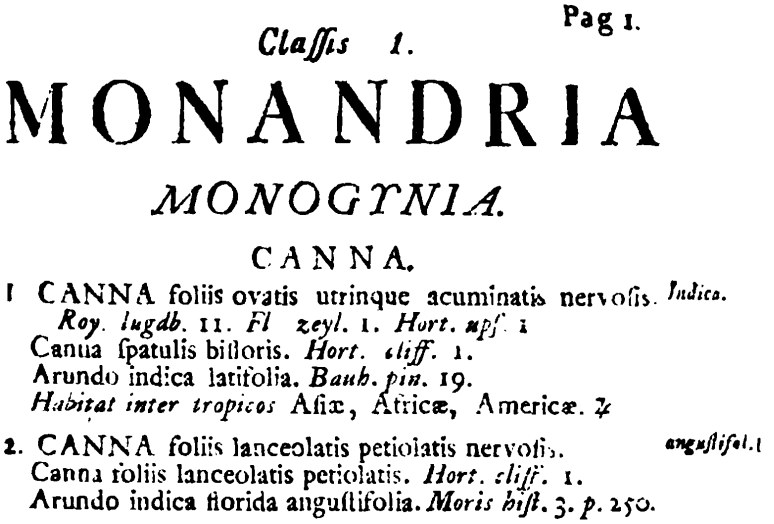
Examples

```
(sam <- Class.sample(iris$Species, 5))
iris.trn <- iris[sam, ]
iris.tst <- iris[-sam, ]
```

`classifs` *Classification lists*

Description

Classification lists ('classifs') are probably one of the most ancient attempts to represent biological diversity, the ordered heterogeneity of living things. In biological systematics, they dated from 1753 when Linnaeus published his "Species Plantarum":



Pag 1.

Claſſis 1.

MONANDRIA

MONOGYNIA.

CANNA.

1 CANNA foliis ovatis utrinque acuminatis nervoſis. *Indica.*
Roy. lugdb. 11. *Fl zeyl.* 1. *Hort. upſ.* 1
Canna ſpatulis biflоris. *Hort. cliff.* 1.
Arundo indica latifolia. *Bauh. pin.* 19.
Habitat inter tropicos Aſiæ, Africæ, Americæ. ♃

2. CANNA foliis lanceolatis petiolatis nervoſis. *anguſtifol.*
Canna foliis lanceolatis petiolatis. *Hort. cliff.* 1.
Arundo indica florida anguſtifolia. *Moris hiſt.* 3. *p.* 250.

(here on the first page of this book four ranks and five names are represented: class ("Monandria"), order ("Monogynia"), genus ("Canna") and species ("Canna indica" and "Canna angustilolia"))

In essence, classifs require only two columns: rank and name (in that order) so they are easy to standardize as two-column data frames. However, we need to know how to order the ranks. One way is to convert ranks into numbers (Shipunov, 2017). Numranks() implements this functionality.

It is possible to extend classifs with more columns: synonyms, name comments and taxonomic comments. Synonyms (the third column) are especially useful; each synonym will be then one row where second position is a valid name and third position is (one of) synonyms.

Please note that while 'classifs' as data frames are human-readable, they are not typographic. To make them better suited for publication, one might convert them into LaTeX where many packages could be used to typeset classifications (for example, my 'classif2' package).

Note also that in classif, species names must be given in full (in biology, species name consists of two words, (a) genus name and (b) species epithet). One of examples below shows how to replace abbreviations with full genus names.

Usage

```
classifs
```

Format

The list with two data frames representing 'classifs', classification lists. First is the classif with textual ranks, second with numerical ranks. Both based on some classifications of Plantago (ribworts, plantains), first (Shipunov, 2000) include species only from European Russia, the other is from the oldest Plantago monograph (Barneoud, 1845).

Source

Linnaeus C. 1753. Species Plantarum. Holmieae.

Barneoud F.M. 1845. Monographie generale de la familie des Plantaginaceae. Paris.

Shipunov A. classif2 – Biological classification tables. Version 2.2.
URL: "https://ctan.org/pkg/classif2'

Shipunov A. 2000. The genera Plantago L. and Psyllium Mill. (Plantaginaceae Juss.) in the flora of East Europe. T. Novosti Systematiki Vysshikh Rastenij. 32: 139–152. [In Russian]

Shipunov A. 2017. "Numerical ranks" to improve biological nomenclature of higher groups. 2017.
URL: 'https://arxiv.org/abs/1708.07260'

See Also

Biokey, Numranks

Examples

```
## European Russian species classif
plevru <- classifs$plevru
## convert rank names into numbers
plevru[, 1] <- Numranks(ranks=plevru[, 1], add=c(Series=1.1))

## now convert into Newick tree and plot it
plevru.n <- Biokey(plevru, from="classif", to="newick")
library(ape) # to plot, load the 'ape' package
plot(read.tree(text=plevru.n))

## Barneoud classif
brn.n <- Biokey(classifs$plbarn, from="classif", to="newick")
plot((read.tree(text=brn.n)), no.margin=TRUE)

## convert classif to taxonomic table
plevru.t <- Biokey(plevru, from="classif", to="table")
colnames(plevru.t) <- Numranks(nums=as.numeric(colnames(plevru.t)))
plevru.t

## two Newick trees
aa <- "(A,(B,C),(D,E));"
```

```
bb <- "((A,(B,C)),(D,E));"
## convert them to classif
aa.c <- Biokey(aa, from="newick", to="classif")
bb.c <- Biokey(bb, from="newick", to="classif")
## ... and back to Newick
aa.n <- Biokey(aa.c, from="classif", to="newick")
bb.n <- Biokey(bb.c, from="classif", to="newick")

## how to convert abbreviated species names
spp <- c ("Plantago afra", "P. arborescens", "P. arenaria")
stt <- do.call(rbind, strsplit(spp, " "))
stt[, 1] <- Fill(stt[, 1], "P.")
(res <- apply(stt, 1, paste, collapse=" "))
```

`Classproj` *Class projection*

Description

Class projection which preserves distances between class centers

Usage

```
Classproj(data, classes, method="DMS")
```

Arguments

`data`	Data: must be numeric and convertible into matrix
`classes`	Class labels (correspond to data rows), NAs are allowed (sic!)
`method`	Either "DMS" for Dhillon et al., 2002 or "QJ" for Qiu and Joe, 2006

Details

'Classproj' is the semi-supervised (leveraged or educated) manifold learning (dimension reduction). See examples for the variety of its uses.

It uses classes to determine centers and then tries to preserve distances between centers; two methods are possible: "DMS" which is slightly faster, and "QJ" which frequently finds a better projection.

The code is based on the functions from 'clusterGeneration' package from Weiliang Qiu.

Value

Returns list with 'proj' coordinates of projected data points and 'centers' coordinates of class centers.

Author(s)

Alexey Shipunov

References

Dhillon I.S., Modha D.S., Spangler W.S., 2002. Class visualization of high-dimensional data with applications. Computational Statistics and Data Analysis. 41: 59–90.

Qiu W.-L., Joe H. 2006. Separation Index and Partial Membership for Clustering. Computational Statistics and Data Analysis. 50: 585–603.

Examples

```
## Leveraged approach (all classes are known)
iris.dms <- Classproj(iris[, -5], iris$Species, method="DMS")
plot(iris.dms$proj, col=iris$Species)
text(iris.dms$centers, levels(iris$Species), col=1:3)

iris.qj <- Classproj(iris[, -5], iris$Species, method="QJ")
plot(iris.qj$proj, col=iris$Species)
text(iris.qj$centers, levels(iris$Species), col=1:3)

## Educated approach (classes are known only for 10 data points per class)
sam <- Class.sample(iris$Species, 10)
newclasses <- iris$Species
newclasses[!sam] <- NA

iris.dms <- Classproj(iris[, -5], newclasses)
plot(iris.dms$proj, col=iris$Species, pch=ifelse(sam, 19, 1))
text(iris.dms$centers, levels(iris$Species), col=1:3)

iris.qj <- Classproj(iris[, -5], newclasses, method="QJ")
plot(iris.qj$proj, col=iris$Species, pch=ifelse(sam, 19, 1))
text(iris.qj$centers, levels(iris$Species), col=1:3)

## Automated approach (classes calculated automatically)
## Good to visualize _any_ clustering or learning
iris.km <- kmeans(iris[, -5], 3)

iris.dms <- Classproj(iris[, -5], iris.km$cluster)
plot(iris.dms$proj, col=iris.km$cluster)
text(iris.dms$centers, labels=1:3, col=1:3, cex=2)

iris.qj <- Classproj(iris[, -5], iris.km$cluster, method="QJ")
plot(iris.qj$proj, col=iris.km$cluster)
text(iris.qj$centers, labels=1:3, col=1:3, cex=2)
```

`Co.test` *Correlation test between cophenetic and original distances*

Description

Correlation test between cophenetic and original distances

Usage

```
Co.test(hclust, dist, method="spearman")
```

Arguments

hclust	'hclust' object
dist	Distance matrix
method	How to calculate correlation

Details

Correlation between cophenetic distances and original distances.

Reveals the consistency of used methods.

Spearman correlation is default because cophenetic distances are frequently non-parametric.

Author(s)

Alexey Shipunov

Examples

```
iris.d <- dist(iris[, -5])
iris.h <- hclust(iris.d)
Co.test(iris.h, iris.d, method="kendall")
```

Coeff.det *Average coefficients of determination for each variable*

Description

Average coefficients of determination for each variable

Usage

```
Coeff.det(X, ...)
```

Arguments

X	Data frame or matrix with values
...	Arguments to 'cor()'

Details

Average coefficients of determination for each variable.

Allow to compare various correlation structures (Rostova, 1999).

Value

Numerical vector of coefficients of determination

Author(s)

Alexey Shipunov

References

Rostova N.S. 1999. The variability of correlations systems between the morphological characters. Part 1. Natural populations of Leucanthemum vulgare (Asteraceae). Botanicheskij Zhurnal. 84(11): 50–66.

Examples

```
Coeff.det(trees, use="pairwise")
```

Coml *Compare checklists*

Description

Compare species checklists

Usage

```
Coml(df1, df2)
## S3 method for class 'Coml'
summary(object, ..., n=10)
```

Arguments

df1	First data frame with species presence/absence data, species as row names
df2	Second data frame
object	Object of the class 'Coml'
n	Number of indicator species
...	Additional arguments

Details

Compare two (groups of) checklists (Abramova et al., 2003).

Calculates difference (in %) between checklists with *common base*, i.e., species occurrence/abundance columns of data frame with species names as row names.

Finds names of "indicators" most characteristic to each group

Value

Object of the class 'Coml', or nothing

Author(s)

Alexey Shipunov

References

Abramova L. A., Rimskaya-Korsakova N. N., Shipunov A. B. 2003. The comparative study of the flora of Kiv Gulf, Chupa Gulf and Keret' Archipelago islands (Kandalaksha Bay of White Sea). Proceedings of the Pertsov White Sea Biological Station. Vol. 9. Moscow. P. 22–33. in Russian (English abstract)

Examples

```
y.Coml <- Coml(dolbli[1:45], dolbli[46:79])
summary(y.Coml, n=5)
```

Cor *Correlation matrix with p-values*

Description

Correlation matrix with p-values

Usage

```
Cor(X, stars=TRUE, dec=4, p.level=0.05, ...)
Cor2(X, dec=4, p.level=0.05)
```

Arguments

X	Matrix or data frame with values
stars	Replaces p-values with stars if it not greater than 'p.level'
dec	Decimal point
p.level	P-level
...	Arguments to 'cor.test()'

Details

'Cor()' calculates correlation matrix with p-values.

'Cor2()' is another (faster) variant of correlation matrix with p-values based on F-statistic. Shows significances in the upper triagle. Uses Pearson correlation only but much faster than 'Cor()'.

Author(s)

Alexey Shipunov

Examples

```
Cor(longley, dec=2)
Cor2(longley, dec=2)
```

Cor.vec *Calculates correlation and converts results into the named long vector*

Description

Calculates correlation and converts results into the named long vector

Usage

```
Cor.vec(X, ...)
```

Arguments

X	Data frame or matrix with values
...	Arguments to 'cor()'

Details

Calculates correlation and converts results into the named long vector.

Value

Named numerical vector of correlations.

Author(s)

Alexey Shipunov

References

Rostova N.S. 1999. The variability of correlations systems between the morphological characters. Part 1. Natural populations of Leucanthemum vulgare (Asteraceae). Botanicheskij Zhurnal. 84(11): 50–66.

See Also

Rostova.tbl

Examples

```
Cor.vec(trees, method="spearman")
```

`Cosine.dist` *Cosine distance*

Description

Calculates cosine distance

Usage

```
Cosine.dist(data.x, data.y=data.x)
```

Arguments

`data.x`	A matrix containing variables that should be used in the computation of the distance.
`data.y`	A matrix compatible with 'data.x' (optional).

Details

Cosine.dist() does not work with data frames, convert them with e.g., as.matrix().

Value

Distance object with distances among rows of 'data.x' and optionally those of 'data.y'

Author(s)

Alexey Shipunov

See Also

`dist`

Examples

```
plot(hclust(Cosine.dist(as.matrix(iris[!c(rep(1, 9), 0), -5]))))
```

CVs *Coefficients of variation*

Description

Coefficients of variation

Usage

```
CVs(sample, na.rm=TRUE)
```

Arguments

sample	Numerical vector
na.rm	Remove NAs?

Details

Coefficients of variation: different variants of the standardized range

Value

Named numerical vector

Author(s)

Alexey Shipunov

Examples

```
sapply(trees, CVs)
```

Dev *Which object is predicted with less accuracy?*

Description

Allows to know which object is predicted with less accuracy

Usage

```
Dev(pred, useNA = "no", adj = FALSE)
```

Arguments

pred	Predictions as character matrix, each boot is a column
useNA	Use NAs?
adj	Adjust deviation coefficients? (see below)

Details

Allows to know which object is predicted with less accuracy.

It calculates deviation coefficient out of the table where rows are objects, and columns are (bootstrapped) predictions.

By default, does not use NA's (use useNA="always" on your risk).

Deviation coefficient is a minimal absolute deviation from one of the range ends (0 and number of predictions), divided by number of predictions, multiplied by number of deviations minus one, and (optionally) adjusted by division to number of prediction levels (to make different situations comparable).

Value

Numeric vector of deviation coefficients

Author(s)

Alexey Shipunov

See Also

BootRF, BootKNN

Examples

```
## could be slow
iris.bootrf <- BootRF(iris[, -5], iris[, 5])
data.frame(Iris=make.names(iris[, 5], unique=TRUE), Dev=Dev(iris.bootrf))
```

Ditto *Removes duplicated data values downstream*

Description

Replaces duplicated values with "ditto" string

Usage

```
Ditto(x, ditto="")
```

Arguments

x	Vector, possibly with missing values
ditto	String to replace with, typically empty string "" (default)

Value

Vector with replaced values

Author(s)

Alexey Shipunov

See Also

Fill

Examples

```
Ditto(c("a", "a", "", "b", "b"))
Ditto(c("a", "a", "", "b", NA, "b"))
Ditto(c("a", "a", "", "b", NA, "b"), ditto=NA)
```

DNN *Distance matrix based kNN classification*

Description

DNN uses pre-cooked distance matrix to replace missing values in class labels.

Usage

```
DNN(dst, cl, k, d, details=FALSE)
Dnn(trn, tst, classes, FUN=function(.x) dist(.x), ...)
```

Arguments

dst	Distance matrix (object of class 'dist').
cl	Factor of class labels, should contain NAs to designate testing sub-group.
k	How many neighbors to select, odd numbers preferable. If specified, do not use "d".
d	Distance to consider for neighborhood, in fractions of maximal distance. If specified, do not use "k".
details	If TRUE, function will return voting matrix. Default is FALSE.
trn	Data to train from, classes variable out.
tst	Data with unknown classes.

classes	Classes variable for training data.
FUN	Function to calculate distances, by default, just dist() (i.e., Euclidean distances).
...	Additional arguments from Dnn() to DNN(), note that either 'k' or 'd' must be specified.

Details

If classic kNN is a lazy classifier, DNN is super-lazy because it does not even calculate the distance matrix itself. Instead, you supply it with distance matrix (object of class 'dist') pre-computed with _any_ possible tool. This lifts many restrictions. For example, arbitrary distance could be used (like Gower distance which allows any type of variable). This is also much faster than typical kNN.

In addition to neighbor-based kNN classification, DNN implements _neighborhood_ classification when all neighbors within selected distance used for voting.

As usual in kNN, ties are broken at random. DNN also controls situations when no neighbors are within the given distance (and returns NA), and also when all neighbors are relevant (also returns NA).

By default, DNN() returns missing part of class labels, completely or partially filled with new (predicted) class labels. If 'cl' has no NAs, DNN() returns it back with warning. It allows for combined and stepwise extensions (see examples). If 'details=TRUE', DNN() will return matrix where each column represents the table used for voting.

Dnn() is based on DNN() but has more class::knn()-like interface (see examples).

Value

Character vector with predicted class labels; or matrix if 'details=TRUE'.

Author(s)

Alexey Shipunov

See Also

class::knn

Examples

```
iris.d <- dist(iris[, -5])

cl1 <- iris$Species
sam <- c(rep(0, 4), 1) > 0
cl1[!sam] <- NA
table(cl1, useNA="ifany")

## based on neighbor number
iris.pred <- DNN(dst=iris.d, cl=cl1, k=5)
Misclass(iris$Species[is.na(cl1)], iris.pred)

## based on neighborhood size
iris.pred <- DNN(dst=iris.d, cl=cl1, d=0.05)
```

```
table(iris.pred, useNA="ifany")
Misclass(iris$Species[is.na(cl1)], iris.pred)

## protection against "all points relevant"
DNN(dst=iris.d, cl=cl1, d=1)[1:5]
## and all are ties:
DNN(dst=iris.d, cl=cl1, d=1, details=TRUE)[, 1:5]

## any distance works
iris.d2 <- Gower.dist(iris[, -5])
iris.pred <- DNN(dst=iris.d2, cl=cl1, k=5)
Misclass(iris$Species[is.na(cl1)], iris.pred)

## combined
cl2 <- cl1
iris.pred <- DNN(dst=iris.d, cl=cl2, d=0.05)
cl2[is.na(cl2)] <- iris.pred
table(cl2, useNA="ifany")
iris.pred2 <- DNN(dst=iris.d, cl=cl2, k=5)
cl2[is.na(cl2)] <- iris.pred2
table(cl2, useNA="ifany")
Misclass(iris$Species, cl2)

## stepwise, note the warning when no NAs left
cl3 <- cl1
for (d in (5:14)/100) {
iris.pred <- DNN(dst=iris.d, cl=cl3, d=d)
cl3[is.na(cl3)] <- iris.pred
}
table(cl3, useNA="ifany")
Misclass(iris$Species, cl3)
## rushing to d=14% gives much worse results
iris.pred <- DNN(dst=iris.d, cl=cl1, d=0.14)
table(iris.pred, useNA="ifany")
Misclass(iris$Species[is.na(cl1)], iris.pred)

## Dnn() has more class::knn()-like interface
iris.trn <- iris[sam, ]
iris.tst <- iris[!sam, ]
Dnn(iris.trn[, -5], iris.tst[, -5], iris.trn[, 5], k=7)
```

`dolbli` *dolbli*

Description

Plants of two Arctic lakes.

Observations on the coastal flora of Arctic lakes. Flora was sampled on the 20 m coastline. 1999–2004.

Usage

```
dolbli
```

Format

`columns` Lake names with plot numbers, data is abundance of plant species, in 1543 scale (0 – absent; 1 – one individual plant; 2 – no more than 12 individual plants (rametes); 3 – number of individuals is more than 12 but no more than 5% of total number of plants on a plot; 4 – number of individuals is more than 5% but no more than 25% of total number of plants on a plot; 5 – number of individuals is more than 25% but no more than 50% of total number of plants on a plot; 6 – number of individuals is more than 50% but no more than 75% of total number of plants on a plot; 7 – number of individuals is more than 75% of total number of plants on a plot.)

`rows` Names of plant species, trees start with 0

Source

Shipunov, A. The creation of databases about flora of isles and lakes of North Karelia. Abstract. P. 97–98. Study of the flora of East Europe: Achievements and prospects. 23–28 May 2005, St.-Petersburg.

Shipunov A., Motyleva M. The comparative study of the flora of lakes in Tchupa gulf environs. III scientific session of Marine Biological Station of Saint-Petersburg State University. Abstracts. P. 27–29. Saint-Petersburg, 2002. [In Russian].

Dotchart *Improved dotcharts*

Description

Dotcharts, improved and extended

Usage

```
Dotchart1(x, labels=NULL, groups=NULL, gdata=NULL, cex=par("cex"), pt.cex=cex,
 pch=21, gpch=21, bg=par("bg"), color=par("fg"), gcolor=par("fg"), lcolor="gray",
 xlim=range(x[is.finite(x)]), main=NULL, xlab=NULL, ylab=NULL, ...)

Dotchart(...)

Dotchart3(values, left, right, pch=21, bg="white", pt.cex=1.2, lty=1, lwd=2,
 gridcol="grey", ...)
```

Arguments

x	Either a vector or matrix of numeric values. Inputs are coerced by 'as.numeric()', with a message.
labels	A vector of labels for each point.
groups	An optional factor indicating how the elements of 'x' are grouped.
gdata	Data values for the groups. This is typically a summary such as the median or mean of each group.
cex	The character size to be used.
pt.cex	The 'cex' to be applied to plotting symbols.
pch	The plotting character or symbol to be used.
gpch	The plotting character or symbol to be used for group values.
bg	The background color of plotting characters.
color	The color(s) to be used for points and labels.
gcolor	The single color to be used for group labels and values.
lcolor	The color(s) to be used for the horizontal lines.
xlim	Horizontal range for the plot.
main	Overall title for the plot, see 'title'.
xlab, ylab	Axis annotations as in 'title'.
values	Centers for 'Dotchart3()'
left	Left margins for 'Dotchart3()'
right	Right margins for 'Dotchart3()'
lty	Line type for 'Dotchart3()'
lwd	Line width for 'Dotchart3()'
gridcol	Grid color for 'Dotchart3()'
...	Additional arguments

Details

For better explanations of options, see 'help(dotchart)'.

'Dotchart1()' is a default 'dotchart()' corrected for use with 1-dimensional tables with 'ylab' and/or changed 'par("mar")[2]'. So comparing with the default 'dotchart()', it has a better left margin. It also outputs message instead of warning.

'Dotchart()' is a prettified 'Dotchart1()' with the following defaults: 'Dotchart1(lcolor="black", bg="white", pt.cex=1.2, ...)'. Use it as a shortcut.

'Dotchart3()' shows values together with ranges. It is an extension of 'Dotchart1()'; for each value, it shows ranges. Does not work with grouped data. A bit similar to 'Linechart()' but more general.

Author(s)

Alexey Shipunov

See Also

dotchart, Linechart

Examples

```
## Compare:
aa <- table(c(1, 1, 1, 2, 2, 3))
##
Dotchart1(aa, ylab="Ylab") # shows 'ylab'; outputs message instead of warning
dotchart(aa, ylab="Ylab") # does not show 'ylab'; produces warning
##
## changes all margins (note: Dotchart1() cannot forcedly _decrease_ left margin)
old.par <- par(mar=c(1, 10, 1, 1)) ; Dotchart1(aa, ylab="Ylab") ; par(old.par)
## does not change left margin
old.par <- par(mar=c(1, 10, 1, 1)) ; dotchart(aa, ylab="Ylab") ; par(old.par)

Dotchart(aa)

Dotchart3(structure(1:3, names=LETTERS[1:3]), 0:2, 2:4)
Dotchart3(structure(0:2, names=LETTERS[1:3]), 0:2, 2:4, pch="") # ranges only
```

---

drosera *drosera*

Description

Observations on the round-leaf sundew, Drosera rotundifolia, White Sea coast, August 2000.

Usage

```
drosera
```

Format

This data frame contains the following columns:

`POP` Code of the population

`YOUNG.L` Number of young, not opened leaves

`MATURE.L` Number of mature, catching leaves

`OLD.L` Number of old, degrading leaves

`INSECTS` Total number of insects per plant

`INFL.L` Inflorescence length (0 if absent), mm

`STALK.L` Length of stalk (without flowers), mm

`N.FLOW` Number of flowers

`LEAF.L` Length of maximal leaf, mm

`LEAF.W` Width of maximal leaf, mm

`PET.L` Length of maximal leaf petiole, mm

Ell *Plot ellipse*

Description

Plot ellipse

Usage

```
Ell(x, y, width, height=width, theta=2*pi, npoints=100, plot=TRUE, ...)
```

Arguments

x	x coordinate of center
y	y coordinate of center
width	length of major axis
height	length of minor axis
theta	rotation
npoints	number of points to send to polygon
plot	if TRUE, add to current device, if FALSE, returns list of components
...	arguments to 'polygon()'

Details

Plots ellipse based on 'polygon()'.

Value

If plot=FALSE, returns list of components.

Author(s)

Alexey Shipunov

Examples

```
plot(1:8, type="n")
Ell(4, 5, 6)
```

`Ellipses` *Groups' confidence ellipses*

Description

Groups' confidence ellipses

Usage

```
Ellipses(pts, groups, match.color=TRUE, usecolors=NULL, centers=FALSE, c.pch=0, c.cex=3,
 level=0.95, coords=NULL, plot=TRUE, ...)
```

Arguments

`pts`	Data points to plot
`groups`	Grouping variable
`level`	Confidence level
`match.color`	Match colors
`usecolors`	Use colors (palette)
`centers`	Show centers?
`c.pch`	Color of center points
`c.cex`	Scale of center points
`coords`	List of coordinates: two-column matrices named as groups, does not need by default
`plot`	Plot?
`...`	Arguments to 'Confelli()' and finally to 'lines()'

Details

Uses internal 'Confelli()' function which plots an ellipse with covariance matrix C, center b, and P-content level according to the F(2, df) distribution.

Value

Invisibly returns the list in form similar to Hulls(), to use as 'coords' or with Overlap()

Author(s)

Alexey Shipunov

See Also

`Hulls`

Examples

```
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
plot(iris.p, type="n", xlab="PC1", ylab="PC2")
text(iris.p, labels=abbreviate(iris[, 5], 1, method="both.sides"))
Ellipses(iris.p[, 1:2], iris[, 5], centers=TRUE)

library(MASS)
ch.lda <- lda(Species ~ ., data=chaetocnema[, -2])
ch.lda.pred <- predict(ch.lda, chaetocnema[, -(1:2)])
## ellipses here are by default bigger then plot so use workaround:
ee <- Ellipses(ch.lda.pred$x, chaetocnema$Species, plot=FALSE)
xx <- range(c(do.call(rbind, ee)[, 1], ch.lda.pred$x[, 1]))
yy <- range(c(do.call(rbind, ee)[, 2], ch.lda.pred$x[, 2]))
plot(ch.lda.pred$x, col=chaetocnema$Species, xlim=xx, ylim=yy)
Ellipses(ch.lda.pred$x, chaetocnema$Species, coords=ee)

## search for the maximal level which gives zero overlap
plot(x5 ~ x17, data=haltica, pch=as.numeric(haltica$Species))
for (i in (99:59)/100) {
cat(i, "\n")
ee <- Ellipses(haltica[, c("x17", "x5")], haltica$Species, level=i, plot=FALSE)
print(mean(Overlap(ee), na.rm=TRUE))
cat("\n")
}
Ellipses(haltica[, c("x17", "x5")], haltica$Species, level=.62)
```

---

eq *eq*

Description

Horsetails (*Equisetum*) are the old, pre-dinosaur plant lineage. Only several dozen species survived, but despite a long evolution the borders between these species are still unclear for researchers.

In 2005–2006, morphometric analysis was performed of more than 1,000 horsetail plants belong to most widespread Eurasian species growing in Middle Russia. For the analysis, we used 8 morphological characters and also tried to identify species.

'eq_l' contains population locations and species determinations.

'eq_s' and 'eq' are actual morphometric data, but 'eq' contains only 2 species out of 8.

Usage

```
eq
eq_l
eq_s
```

Format

This data frame contains the following columns:

`DL.R` plant height, mm

`DIA.ST` maximal diameter of stem, mm

`N.REB` number of ridges on a stem

`N.ZUB` number of teeth (reduced leaves)

`DL.OSN.Z` length of tooth base

`DL.TR.V` length of sheath

`DL.BAZ` length of basal segment of branch

`DL.PER` length of first (after the basal) segment of branch

`SPECIES` preliminary species determination

`N.POP` population number

`WHERE` population location (region)

`Ex.boxplot` *Boxplot explanation*

Description

Boxplot explanation

Usage

```
Ex.boxplot(...)
```

Arguments

`...`	Arguments to 'boxplot()'

Details

The scheme which explains typical boxplot.

Author(s)

Alexey Shipunov

See Also

`boxplot`

Examples

```
Ex.boxplot()
```

Ex.col *Examples of colors*

Description

Examples of standard colors (also shows all colors)

Usage

```
Ex.col(all=FALSE)
Ex.cols(all=FALSE)
```

Arguments

all	if TRUE, shows all 476 named colors

Details

Examples of standard colors (also shows all colors). For the palettes, run 'example(rainbow)'.

Note: large device is required to see all 476 named colors.

Author(s)

Alexey Shipunov

See Also

palette

Examples

```
Ex.cols()
Ex.cols(all=TRUE)
```

Ex.font *Examples of fonts*

Description

Examples of standard fonts

Usage

```
Ex.font()
```

Details

Examples of standard fonts

Author(s)

Alexey Shipunov

See Also

par

Examples

```
Ex.fonts()
```

Ex.lty *Examples of line types*

Description

Line type examples

Usage

```
Ex.lty(custom="431313")
Ex.lines(custom="431313")
```

Arguments

custom	character string to specify custom line type (see '?lines').

Details

Line type examples. To see other possible custom line types, try custom="F8" or similar.

Author(s)

Alexey Shipunov

See Also

lines

Examples

```
Ex.lines(custom="F8")
```

Ex.margins *Example of plot margins*

Description

Example of plot margins

Usage

```
Ex.margins()
```

Details

Example of plot margins. Modified from Paul Murrell (2006).

Author(s)

Alexey Shipunov

References

Murrell P. 2006. R Graphics.

See Also

par

Examples

```
Ex.margins()
```

Ex.pch *Point examples*

Description

Point ('pch') examples

Usage

```
Ex.pch(extras=c("*", ".", "+", "a"), cex=2, col="black", bg="gray",
 coltext="black", cextext=1.2, main="")
Ex.points(extras=c("*", ".", "+", "a"), cex=2, col="black", bg="gray",
 coltext="black", cextext=1.2, main="")
```

Arguments

extras	which extra symbols to show
cex	point scale, default 2
col	point color, default black
bg	point background (for symbols with a 'bg'-colored interior), default gray
coltext	text color, default black
cextext	text scale, default 1.2
main	plot title, no title by default

Details

Point ('pch') examples, modified from 'example(points)'.

Author(s)

Alexey Shipunov

See Also

points

Examples

```
Ex.points()
```

Ex.plots *Examples of plot types*

Description

Examples of plot types

Usage

```
Ex.plots()
Ex.types()
```

Details

Examples of nine standard plot types.

Author(s)

Alexey Shipunov

See Also

par

Examples

```
Ex.types()
```

`Files` *Textual file system browser*

Description

Textual file system browser

Usage

```
Files(root=getwd(), multiple=FALSE, hidden=FALSE)
```

Arguments

`root`	Root directory
`multiple`	Allows multiple files to be selected
`hidden`	Show hidden files?

Details

Interactive text-based file chooser dialog. Alternatives for Linux: 'tcltk::tk_choose.files()' and 'tcltk::tk_choose.dir()'

Value

Returns character vector of selected files, or directory name (useful for 'setwd()'), or new user-defined file name with full path.

Author(s)

Alexey Shipunov

See Also

setwd, getwd, dir

Examples

```
## Not run:
## interactive commands
setwd <- Files() # then select directory to work in
Files("~", hidden=TRUE) # explore home directory with hidden files (Linux, macOS)

## End(Not run)
```

`Fill` *Fill data values downstream, like in spreadsheets*

Description

Replaces "ditto" values with preceding values

Usage

```
Fill(x, ditto="")
```

Arguments

`x`	Vector, possibly with missing values
`ditto`	What to fill, typically empty string "" (default) or NA

Value

Vector with replaced values

Author(s)

Alexey Shipunov

See Also

`Ditto`

Examples

```
aa <- c("a", "a", "", "b", "", "c", "d", "")
Fill(aa)
bb <- c("a", "a", NA, "b", NA, "c", "d", NA)
Fill(bb, ditto=NA)
dd <- c("", "a", "a", "", "", "b", NA, "", "c", "d", "")
Fill(dd)
```

Gap.code *Gap coding*

Description

Gap coding of DNA nucleotide alignments

Usage

```
Gap.code(seqs)
```

Arguments

seqs	Character vector of aligned (and preferably flank trimmed) DNA sequences.

Details

FastGap-like gap code nucleotide alignments ('ATGCN-' are allowed).

Encodes gap presence as 'A' and absence as 'C'.

Likely too straightforward, and only weakly optimized (really slow).

Value

Outputs character matrix where each column is a gapcoded position.

Author(s)

Alexey Shipunov

References

Borchsenius F. 2009. FastGap 1.2. Department of Biosciences, Aarhus University, Denmark. Published online at "http://www.aubot.dk/FastGap_home.htm".

Examples

```
write(file=file.path(tempdir(), "tmp.fasta"),  c(
 ">1\nGAAC------ATGC",
 ">2\nGAAC------TTGC",
 ">3\nGAAC---CCTTTGC",
 ">4\nGAA---------GC"))
write(file=file.path(tempdir(), "tmp_expected.fasta"), c(
 ">1\nGAAC------ATGCCA-",
 ">2\nGAAC------TTGCCA-",
 ">3\nGAAC---CCTTTGCCCA",
 ">4\nGAA---------GCA--"))
tmp <- Read.fasta(file=file.path(tempdir(), "tmp.fasta"))
expected <- Read.fasta(file=file.path(tempdir(), "tmp_expected.fasta"))
```

```
seqs <- tmp$sequence
gc <- Gap.code(seqs)
tmp$sequence <- apply(cbind(seqs, gc), 1, paste, collapse="")
identical(tmp, expected) # TRUE, isn't it?
```

`Gen.cl.data` *Generates datasets for clustering*

Description

Imitation of the Python `sklearn.datasets` functions.

Usage

```
Gen.cl.data(type=c("blobs", "moons", "circles"), N=100, noise=NULL,
 shuffle=TRUE, bdim=2, bcenters=3, bnoise=1, bbox=c(-10, 10), cfactor=0.8)
```

Arguments

`type`	'blobs' are Gaussian blobs; 'moons' are two interleaving half-circles; 'circles' are two embedded circles
`N`	Number of data points
`shuffle`	Whether to randomize the output
`noise`	Standard deviation of Gaussian noise applied to point positions
`bdim`	Dimensionality of 'blobs' dataset
`bcenters`	Number of 'blobs' centers
`bnoise`	Standard deviation of 'blobs' Gaussian noise: vector of length one or length equal to the number of centers
`bbox`	The bounding box within which blobs centers will be created
`cfactor`	Scale factor between 'circles' (should be > 0 and < 1)

Details

Algorihms were taken partly from Python 'scikit-learn' and from Github 'elbamos/clusteringdatasets'.

Author(s)

Alexey Shipunov

Examples

```
scikit.palette <- c("#377EB8", "#FF7F00", "#4DAF4A", "#F781BF", "#A65628", "#984EA3",
"#999999", "#E41A1C", "#DEDE00", "#000000")
palette(scikit.palette)
n.samples <- 500

## data
set.seed(21)
no.structure <- list(samples=cbind(runif(n.samples), runif(n.samples)),
 labels=rep(1, n.samples))
noisy.circles <- Gen.cl.data(type="circles", N=n.samples, cfactor=0.5, noise=0.05)
noisy.moons <- Gen.cl.data(type="moons", N=n.samples, noise=0.05)
blobs <- Gen.cl.data(type="blobs", N=n.samples, noise=1)
## anisotropically distributed data
aniso <- Gen.cl.data(type="blobs", N=n.samples)
aniso$samples <- aniso$samples %*% rbind(c(0.6, -0.6), c(-0.4, 0.8))
## blobs with varied variances
varied <- Gen.cl.data(type="blobs", N=n.samples, bnoise=c(1, 2.5, 0.5))
set.seed(NULL)

## single example
plot(aniso$samples, col=aniso$labels, pch=19)

## all data objects example
## old.X11.options <- X11.options(width=6, height=6) # to make square cells
oldpar <- par(mfrow=c(2, 3), mar=c(1, 1, 3, 1))
for (n in c("noisy.circles", "noisy.moons", "no.structure",
 "blobs", "aniso", "varied")) {
 plot(get(n)$samples, col=get(n)$labels, pch=19, main=n, xlab="", ylab="",
 xaxt="n", yaxt="n")
}
par(oldpar)
## X11.options <- old.X11.options


## comparison of clustering techniques example
## old.X11.options <- X11.options(width=10, height=6)  # to make square cells
oldpar <- par(mfrow=c(6, 10), mar=c(0, 0, 0, 0))
COUNT <- 1
for (n in c("noisy.circles", "noisy.moons", "no.structure", "blobs", "aniso", "varied")) {
 K <- 3
 if (n %in% c("noisy.circles", "noisy.moons")) K <- 2
 TITLE <- function(x) if (COUNT==1) { legend("topleft", legend=x, cex=1.25, bty="n") }
##
 newlabels <- cutree(hclust(dist(get(n)$samples), method="ward.D2"), k=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("Ward")
##
 newlabels <- cutree(hclust(dist(get(n)$samples), method="average"), k=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("UPGMA")
##
```

```
 newlabels <- kmeans(get(n)$samples, centers=K)$cluster
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("K-means")
##
 newlabels <- cutree(as.hclust(cluster::diana(dist(get(n)$samples))), k=K) # slow
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("DIANA")
##
 nn <- cluster::fanny(get(n)$samples, k=K) # a bit slow
 dunn <- apply(nn$membership, 1, function(.x) (sum(.x^2) - 1/K) / (1 - 1/K))
 fuzzy <- dunn < 0.05
 plot(get(n)$samples[!fuzzy, ], col=nn$clustering[!fuzzy], pch=19, main="", xlab="",
  ylab="", xaxt="n", yaxt="n")
 points(get(n)$samples[fuzzy, ], col="black", pch=1)
 TITLE("FANNY")
##
 newlabels <- kernlab::specc(get(n)$samples, centers=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("spectral")
##
 nn <- apcluster::apclusterK(apcluster::negDistMat(), get(n)$samples, K=K) # very slow
 newlabes <- apply(sapply(nn@clusters,
  function(.y) 1:nrow(get(n)$samples) %in% .y), 1, which)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("AP") # affinity propagation
##
 ## eps values taken out of scikit and 'dbscan::kNNdistplot() "knee"', 'minPts' default
 EPS <- c(noisy.circles=0.3, noisy.moons=0.3, no.structure=0.3, blobs=1,
  aniso=0.5, varied=1)
 nn <- dbscan::dbscan(get(n)$samples, eps=EPS[n])
 outliers <- nn$cluster == 0
 plot(get(n)$samples[!outliers, ], col=nn$cluster[!outliers], pch=19, main="", xlab="",
  ylab="", xaxt="n", yaxt="n")
 points(get(n)$samples[outliers, ], col="black", pch=1)
 TITLE("DBSCAN")
##
 newlabels <- meanShiftR::meanShift(get(n)$samples, nNeighbors=10)$assignment
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("mean-shift")
##
 library(mclust)
 newlabels <- Mclust(get(n)$samples)$classification
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("Gaussian")
 COUNT <- COUNT + 1
}
par(oldpar)
## X11.options <- old.X11.options



## comparison of linkages example
## old.X11.options <- X11.options(width=8, height=6) # to make square cells
```

```
oldpar <- par(mfrow=c(6, 8), mar=c(0, 0, 0, 0))
COUNT <- 1
for (n in c("noisy.circles", "noisy.moons", "no.structure", "blobs", "aniso", "varied")) {
 K <- 3 ; if (n %in% c("noisy.circles", "noisy.moons")) K <- 2
 TITLE <- function(x) if (COUNT==1) { legend("topleft", legend=x, cex=1.25, bty="n") }
 newlabels <- cutree(hclust(dist(get(n)$samples), method="ward.D2"), k=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("Ward orig")
 newlabels <- cutree(hclust(dist(get(n)$samples), method="ward.D"), k=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("Ward")
 newlabels <- cutree(hclust(dist(get(n)$samples), method="average"), k=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("UPGMA")
 newlabels <- cutree(hclust(dist(get(n)$samples), method="single"), k=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("single")
 newlabels <- cutree(hclust(dist(get(n)$samples), method="complete"), k=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("complete")
 newlabels <- cutree(hclust(dist(get(n)$samples), method="mcquitty"), k=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("WPGMA")
 newlabels <- cutree(hclust(dist(get(n)$samples), method="median"), k=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("WPGMC")
 newlabels <- cutree(hclust(dist(get(n)$samples), method="centroid"), k=K)
 plot(get(n)$samples, col=newlabels, pch=19, main="", xlab="", ylab="", xaxt="n", yaxt="n")
 TITLE("UPGMC")
 COUNT <- COUNT + 1
}
par(oldpar)
## X11.options <- old.X11.options
```

`Gower.dist` *Gower distance*

Description

Calculates Gower distance

Usage

```
Gower.dist(data.x, data.y=data.x, rngs=NULL, KR.corr=TRUE)
```

Arguments

`data.x`	A matrix or a data frame containing variables that should be used in the computation of the distance.

data.y	A numeric matrix or data frame with the same variables, of the same type, as those in 'data.x'
rngs	A vector with the ranges to scale the variables. Its length must be equal to number of variables in 'data.x'
KR.corr	When TRUE (default) the extension of the Gower's dissimilarity measure proposed by Kaufman and Rousseeuw (1990) is used. Otherwise the original Gower's (1971) formula is considered.

Details

Gower.dist() code was taken (and amended to keep dimnames and return 'dist' object in case of one matrix) from 'StatMatch' package; please see this package for the original code and full documentation.

This function computes the Gower's distance (dissimilarity) among units in a dataset or among observations in two distinct datasets. Columns of mode numeric will be considered as interval scaled variables; columns of mode character or class factor will be considered as categorical nominal variables; columns of class ordered will be considered as categorical ordinal variables and, columns of mode logical will be considered as binary asymmetric variables. Missing values (NA) are allowed. If only data.x is supplied, the dissimilarities between _rows_ of data.x will be computed.

For 'rngs', in correspondence of non-numeric variables, just put 1 or NA. When rngs=NULL (default), the range of a numeric variable is estimated by jointly considering the values for the variable in 'data.x' and those in 'data.y'.

Value

A distance object with distances among rows of 'data.x' and those of 'data.y'.

Author(s)

Alexey Shipunov

References

Gower J.C. 1971. A general coefficient of similarity and some of its properties. Biometrics, 27, 623–637.

Kaufman L., Rousseeuw P.J. 1990. Finding Groups in Data: An Introduction to Cluster Analysis. Wiley, New York.

See Also

dist, cluster::daisy

Examples

```
x1 <- as.logical(rbinom(10, 1, 0.5))
x2 <- sample(letters, 10, replace=TRUE)
x3 <- rnorm(10)
x4 <- ordered(cut(x3, -4:4, include.lowest=TRUE))
xx <- data.frame(x1, x2, x3, x4, stringsAsFactors=FALSE)
```

```
## matrix of distances among first obs. in xx and the remaining ones
Gower.dist(data.x=xx[1:6, ], data.y=xx[7:10, ])

## matrix of distances among observations in xx
row.names(xx) <- LETTERS[1:nrow(xx)]
dx <- Gower.dist(xx)
plot(hclust(dx))
```

`Gradd` *Classification grid*

Description

Adds to the 2D ordination plot small semi-transparent points which make color classification grid

Usage

```
Gradd(model2var, data2var, spacing=75, trnsp=0.3, pch=20, cex=0.2,
 palette=NULL, type="ids", User.Predict=function(model2var, X) {}, ...)
```

Arguments

`model2var`	Model based on 'data2var' (see below).
`data2var`	Data with exactly 2 variables.
`spacing`	Space between points.
`trnsp`	Transparency.
`pch`	Type of point.
`cex`	Scale of points.
`palette`	Palette to use.
`type`	Type of the model: "ids", "lda", "neuralnet", "tree", or "user" (see examples).
`User.Predict`	Function to define in case of 'type="user"'.
`...`	Additional arguments to plot().

Details

'Gradd()' adds to the 2D ordination plot small semi-transparent points which make color classification grid.

Requires model with 'predict' method to be computed first.

Model should use ids (to make colors) and exactly 2 variables with names same as 'data2var' column names, e.g:

model2var <- somefunction(ids ~ ., data=cbind(ids, data2var))

If type="user", uses predefined 'User.Predict(model2var, X)' function which must return factor ids from testing X data.

Please see examples to understand all of these better.

Note that instead of dots, one can use contours, but they are harder to employ because they need membership values in order to calculate borders (places where memberships are equal).

Author(s)

Alexey Shipunov

Examples

```
## SVM:
library(e1071)
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
iris.svm.pca <- svm(Species ~ ., data=cbind(iris[5], iris.p))
plot(iris.p, type="n", main="SVM")
Gradd(iris.svm.pca, iris.p)
text(iris.p, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))

## LDA:
library(MASS)
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
iris.lda.pca <- lda(Species ~ . , data=cbind(iris[5], iris.p))
plot(iris.p, type="n", main="LDA")
Gradd(iris.lda.pca, iris.p, type="lda")
text(iris.p, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))

## 'tree::tree':
library(tree)
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
iris.tree.pca <- tree(Species ~ . , data=cbind(iris[5], iris.p))
plot(iris.p, type="n", main="tree")
Gradd(iris.tree.pca, iris.p, type="tree")
text(iris.p, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))

## randomForest:
library(randomForest)
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
iris.rf.pca <- randomForest(Species ~ ., data=cbind(iris[5], iris.p))
plot(iris.p, type="n", main="randomForest")
Gradd(iris.rf.pca, iris.p)
text(iris.p, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))

## naiveBayes:
library(e1071)
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
iris.nb.pca <- naiveBayes(Species ~ ., data=cbind(iris[5], iris.p))
plot(iris.p, type="n", main="naiveBayes")
Gradd(iris.nb.pca, iris.p)
```

```
text(iris.p, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))

## neuralnet:
library(neuralnet)
iris.p2 <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
iris.p2 <- cbind(iris.p2, Tobin(iris$Species, convert.names=FALSE))
iris.nn.pca <- neuralnet(setosa + versicolor + virginica ~ PC1 + PC2, data=iris.p2,
 hidden=3, lifesign="full")
plot(iris.p, type="n", main="neuralnet")
Gradd(iris.nn.pca, iris.p, type="neuralnet")
text(iris.p, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))

## rpart + MDS for the base plot:
iris.dist <- dist(iris[, 1:4], method="manhattan")
iris.dist[iris.dist == 0] <- abs(jitter(0))
library(MASS)
iris.m <- isoMDS(iris.dist)$points
colnames(iris.m) <- c("Dim1", "Dim2")
library(rpart)
iris.rpart.mds <- rpart(Species ~ . , data=cbind(iris[5], iris.m))
plot(iris.m, type="n", main="rpart + MDS")
Gradd(iris.rpart.mds, iris.m, type="tree")
text(iris.m, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))

## QDA:
library(MASS)
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
iris.qda.pca <- qda(Species ~ . , data=cbind(iris[5], iris.p))
plot(iris.p, type="n", main="QDA")
Gradd(iris.qda.pca, iris.p, type="lda")
text(iris.p, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))

## AdaBoost:

library(adabag)
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
iris.ada.pca <- boosting(Species ~ . , data=cbind(iris[5], iris.p)) # slow!
plot(iris.p, type="n", main="AdaBoost")
Gradd(iris.ada.pca, iris.p, type="lda")
text(iris.p, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))


## nnet:
library(nnet)
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
iris.nnet.pca <- nnet(Species ~ . , data=cbind(iris[5], iris.p), size=4)
plot(iris.p, type="n", main="nnet")
Gradd(iris.nnet.pca, iris.p, type="tree")
```

```
text(iris.p, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))

## kNN:
library(class)
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
plot(iris.p, type="n", main="kNN")
Gradd(cbind(iris[5], iris.p), iris.p, type="user",
 User.Predict=function(model2var, X) knn(model2var[, 2:3], X, model2var[, 1], k=5))
text(iris.p, col=as.numeric(iris[, 5]), labels=abbreviate(iris[, 5], 1,
 method="both.sides"))
```

`Gridmoon` *Draw with 'R'*

Description

Sraw with 'R'

Usage

```
Gridmoon(Skyres=50, Nightsky=TRUE, Daysky="deepskyblue", Moon=TRUE,
 Moonsize=0.05, Stars=TRUE, Hillcol="black", Text=c("Once upon a time..."),
 Textsize=22, Textpos=c(.15, .51), Textcol="white")
```

Arguments

`Skyres`	Sky resoluiton
`Nightsky`	If TRUE, ther eis a night
`Daysky`	Color of day sky
`Moon`	If TRUE, there is a moon
`Moonsize`	Moon size
`Stars`	If TRUE, there are stars
`Hillcol`	Hill color
`Text`	Text to print
`Textsize`	Text size
`Textpos`	Text position
`Textcol`	Text color

Details

'Gridmoon()' is an example how to paint (draw) with 'R'. Just for fun. From Murrell (2006) "R Graphics", with modifications.

Author's comments:

An example of a one-off image drawn using the grid system.

The code is somewhat modular and general, with functions for producing different shapes, but the sizes and locations used in this particular image assume a 2:1 aspect ratio.

The gradient-fill background (dark at the top to lighter at the bottom) is achieved by filling multiple overlapping polygons with slowly changing shades of grey.

Author(s)

Alexey Shipunov

References

Murrell P. 2006. R Graphics.

Examples

```
## Examples best viewed with 2:1 aspect ratio
Gridmoon(Skyres=75)
Gridmoon(Nightsky=FALSE, Moon=FALSE, Stars=FALSE, Hillcol="forestgreen",
 Text="Use R!", Textcol="yellow", Textpos=c(.25, .85), Textsize=96)
```

---

haltica *Haltica flea beetles*

Description

Lubischew data (1962, pp. 460–461, table 2): 39 Haltica flea beetles specimens which belong to two cryptic species.

Sources of specimens:

Haltica oleracea:

1, 2, 3, 4, 6: Western Europe (Germany, France, Italy); 5: Leningrad; 7, 8: Perm; 11, 12: Kiev; 15, 16: Middle Volga (Kuibyshev); 17: Orel district, Middle Russia; 9, 10: Northern Caucasus; 13, 14, 18, 19: Transcaucasia (Delizhan, Akstafa).

H. carduorum:

6: Northern Russia (Elabuga); 1, 5, 9, 10, 11, 12, 14, 16, 20: Middle Russia (Penza, Orel, Voronezh districts); 3, 4, 17; Northern Caucasus; 2, 15, 18, 19: Black Sea Coast of the Caucasus; 13: Transcaucasia (Armenia); 7, 8: Middle Asia (Schachriziabs).

Usage

```
haltica
```

Format

These data frame contains the following columns:

`Species` Species epithet

`No` Number of sample (see below)

`x5` The distance of the transverse groove from the posterior border of the prothorax, in microns

`x14` The length of the elytram, in 0.01 mm

`x17` The length of the second antennal joint, in microns

`x18` The length of the third antennal joint, in microns

Source

Lubischew A.A. 1962. On the use of discriminant functions in taxonomy. Biometrics. 18:455–477.

Examples

```
plot(prcomp(haltica[, -(1:2)])$x[, 1:2], col=haltica$Species)

haltica.qj <- Classproj(haltica[, -(1:2)], haltica$Species, method="QJ")
plot(haltica.qj$proj, col=haltica$Species)
text(haltica.qj$centers, levels(haltica$Species), col=1:2)
```

`Hcl2mat` *Clustering to matrix*

Description

Converts clustering to matrix

Usage

```
Hcl2mat(hcl)
```

Arguments

`hcl`	`hclust` object

Details

This function converts 'hclust' object into binary matrix in accordance with clusterings.

It has many uses: clustering bootstrap, clustering compare, and matrix representation of hierarchical clustering.

See Also

`Bclust`, `MRH`

Examples

```
head(Hcl2mat(hclust(dist(iris[, -5]))))
```

`Hclust.match` *Counts matches between two hierarchical clusterings*

Description

Counts matches between two hierarchical clusterings

Usage

```
Hclust.match(hc1, hc2, scale=FALSE)
```

Arguments

`hc1`	First hclust object
`hc2`	Second hclust object
`scale`	Scale by the sum size of trees?

Details

'Hclust.match()' counts matches between two hierarchical clusterings (based on 'cutree()').

Result is a sort of consensus distances. Useful, for example, for clustering heatmaps.

Author(s)

Alexey Shipunov

Examples

```
aa.d1 <- hclust(dist(t(atmospheres)))
aa.d2 <- hclust(as.dist(1 - abs(cor(atmospheres, method="spearman"))),
 method="ward.D")
aa12.match <- Hclust.match(aa.d1, aa.d2)
heatmap(aa12.match, scale="none")
```

Hcoords *Plot bootstrap values on 'hclust' plot*

Description

This function calculate coordinates for each 'hclust' node. Inspired by pvclust::hc2axes()

Usage

```
Hcoords(hcl)
```

Arguments

hcl	hclust object

See Also

Bclust

Examples

```
head(Hcoords(hclust(dist(iris[, -5]))))
```

Histr *Histogram with overlaid curve*

Description

Histogram with overlaid normal curve or density, optionally with rug

Usage

```
Histr(x, overlay="normal", rug=FALSE, col="gray80", ...)
```

Arguments

x	numerical vector
overlay	type of curve to overlay, accepted values are "normal" and "density"
rug	if TRUE, will add rug plot
col	curve color
...	arguments to 'hist()'

Details

Histr() plots histogram with overlaid normal curve or density, optionally with rug. Based on analogous function from Stephen Turner's 'Tmisc' package.

Author(s)

Alexey Shipunov

See Also

hist, density, rnorm

Examples

```
x <- rnorm(1000, mean=5, sd=2)
Histr(x)
Histr(x, overlay="density")
Histr(x^2, overlay="density", rug=TRUE, breaks=50, col="lightblue2")
```

Hulls *Groups' hulls*

Description

Groups' hulls with centroids calculation

Usage

```
Hulls(pts, groups, match.color=TRUE, usecolors=NULL, plot=TRUE, centers=FALSE,
 c.pch=0, c.cex=3, outliers=TRUE, coef=1.5, ...)
```

Arguments

pts	Data points to plot
groups	Grouping variable, any type
match.color	Match color
usecolors	Which colors to use (similar to plot(..., col=))
plot	Plot?
centers	Show centers?
c.pch	Color of center points
c.cex	Scale of center points
outliers	Include outliers?
coef	Determines how to detect outliers, see 'coef' from 'boxplot.stats()'
...	Arguments to 'lines()'

Details

Groups' hulls with optional centroids calculation (requires 'PBSmapping').

If 'outliers=FALSE', uses 'boxplot.stats()' to detect outliers (points which are most distant from centers). This option automatically switch 'centers=TRUE' so if you want to plot smoothed hulls but do not want to plot centers, use something like 'c.pch=""' or 'c.cex=0'. This could be used for cluster sharpening.

Value

Invisibly outputs list of hulls with coordinates, and possibly also with 'centers' and 'outliers' components

Author(s)

Alexey Shipunov

See Also

Ellipses

Examples

```
iris.p <- prcomp(iris[, -5], scale=TRUE)$x[, 1:2]
plot(iris.p, type="n", xlab="PC1", ylab="PC2")
pal <- rainbow(3)
text(iris.p, labels=abbreviate(iris[, 5], 1, method="both.sides"),
 col=pal[as.numeric(iris[, 5])])
Hulls(iris.p, iris[, 5], centers=TRUE, usecolors=pal)

## smoothed hulls
iris.p <- prcomp(iris[, 1:4], scale=TRUE)$x[, 1:2]
plot(iris.p, col=iris$Species, xlab="PC1", ylab="PC2")
ppts <- Hulls(iris.p, iris[, 5], centers=TRUE, outliers=FALSE, coef=2)
ppts$outliers
```

---

hwc *hwc*

Description

Artificial data for teaching purposes.

Usage

```
hwc
hwc2
hwc3
```

Format

This data frame contains the following columns:

`COLOR` hair color

`WEIGHT` weight, kg

`HEIGHT` height, cm

Examples

```
# 'hwc' was made like (commands repeated until sd was around 3):
sd(VES.BR <- round(rnorm(30, mean=mean(70:90), sd=3)))
sd(VES.BL <- round(rnorm(30, mean=mean(69:79), sd=3)))
sd(VES.SH <- round(rnorm(30, mean=mean(70:80), sd=3)))
sd(ROST.BR <- round(rnorm(30, mean=mean(160:180), sd=3)))
sd(ROST.BL <- round(rnorm(30, mean=mean(155:160), sd=3)))
sd(ROST.SH <- round(rnorm(30, mean=mean(160:170), sd=3)))
data.frame(COLOR=rep(c("black", "blond", "brown"), each=30),
 WEIGHT=c(VES.BR, VES.BL, VES.SH), HEIGHT=c(ROST.BR, ROST.BL, ROST.SH))

# 'hwc2' is similar but 'sd' was not controlled so it is usually not homogeneous

# 'hwc3' was made like:
set.seed(1683)
VES.BR <- sample(70:90, 30, replace=TRUE)
VES.BL <- sample(69:79, 30, replace=TRUE)
VES.SH <- sample(70:80, 30, replace=TRUE)
ROST.BR <- sample(160:180, 30, replace=TRUE)
ROST.BL <- sample(155:160, 30, replace=TRUE)
ROST.SH <- sample(160:170, 30, replace=TRUE)
data.frame(COLOR=rep(c("black", "blond", "brown"), each=30),
 WEIGHT=c(VES.BR, VES.BL, VES.SH), HEIGHT=c(ROST.BR, ROST.BL, ROST.SH))
```

`Infill` *Rarefaction curves*

Description

Rarefaction curves

Usage

```
Infill(x, n=10)
## S3 method for class 'Infill'
plot(x, ...)
## S3 method for class 'Infill'
summary(object, ...)
```

Arguments

`x`	Data frame where columns are species
`object`	Object of the class "Infill"
`n`	Number of permutations
`...`	Arguments to 'plot()' or 'summary()'

Details

'Infill()' returns matrix to draw accumulation curves (each column is one curve).

'Infill' uses checklists of biological organisms to build rarefaction curves. You can estimate how many taxa will appear in the next sample to plan your investigations (e.g. revealing flora or fauna of the certain area).

If cells contain taxa abundance it will be automatically replaced with 1 or 0. Permutation is a random shuffle of the samples to get more valid estimation of the taxa accumulation process. It does not matter which sample appeared first. The resulting plot gives information on the process of taxa revealing during the investigation. High number of permutations gives more precise results, but the calculations are more slow. Empirically, 100 permutations are enough. The plot indicates full taxa number which has been accumulated in this and all the previous samples.

Value

Object of the class "Infill", or nothing

Author(s)

Alexey Shipunov, Eugeny Altshuler

References

Diaz-Frances E., Soberon J. 2005. Statistical estimation and model selection of species accumulation curves. Conservation Biology. Vol. 19, N 2. P. 569-573.

Gotelli N.J., Colwell R.C. 2001. Quantifying biodiversity: procedures and pitfalls in the measurement and comparison of species richness. Ecology Letters. Vol. 4. P. 379-391.

Soberon J.M., Llorente J.B. 1993. The use of species accumulation functions for the prediction of species richness. Conservation Biology. Vol. 7. N 3. P. 480-488.

Examples

```
x <- t(dolbli)
data <- x[1:45, ] # one of two lakes selected
data.I <- Infill(data)
summary(data.I)
plot(data.I)
```

Is.tax.inform.char *Taxonomic informativeness*

Description

Is the character potentially taxonomically informative?

Usage

```
Is.tax.inform.char(vec)
```

Arguments

vec	Character vector from the column of DNA alignment

Details

Is the character potentially taxonomically informative?

If DNA encoding used, 'Nn?' should be converted into NA. Gaps ('-') counted, NAs not.

Value

Number of the potentially taxonomically informative characters.

Author(s)

Alexey Shipunov

Examples

```
Is.tax.inform.char(c("A", "C", "T", "T", "T", "T", "A"))
Is.tax.inform.char(c("A", "C", "T", "T", "T", "T", "G"))
Is.tax.inform.char(c("-", "T", "T", "T", "T", "T", "-", NA))
Is.tax.inform.char(c("A", "T", "T", "T", "T", "T", NA, NA))
Is.tax.inform.char(c(1, 0, 1, 1, 0, 0, 0, 0))
```

Jclust *Simple bootstrap and jackknife clustering*

Description

Simple bootstrap and jackknife clustering

Usage

```
Jclust(data, n.cl, iter=100, method.d="manhattan", method.c="ward.D", bootstrap=TRUE)
## S3 method for class 'Jclust'
print(x, ...)
## S3 method for class 'Jclust'
plot(x, main="", xlab="", sub=NULL, rect.lty=3, rect.col=1, ...)
```

Arguments

data	Data
n.cl	Number of desired clusters
iter	Number of iterations
method.d	Distance method
method.c	Hierarchical clustering method
bootstrap	Bootstrap or jackknife?
x	Object of the class 'Jclust'
rect.lty	Line type for the rectangles
rect.col	Color of rectangles
main	Plot title
xlab	Horizontal axis label
sub	Horizontal axis sub-label
...	Additional arguments to the 'print()' or 'plot.hclust()'

Details

Simple bootstrap and jackknife clustering, requires the desired number of clusters.

Alternative: 'pvc::pvc()'.

Author(s)

Alexey Shipunov

See Also

Bclust, link{BootA}

Examples

```
(mo.j <- Jclust(t(moldino), 3, iter=1000))
plot(mo.j)


## This is how one can bootstrap _all_ reliable cluster numbers:
for (i in 2:(nrow(t(moldino)) - 1)) print(Jclust(t(moldino), i, iter=1000, boot=TRUE))
```

K *Coefficient of divergence*

Description

Lubischew's coefficient of divergence (SSMD^2)

Usage

```
K(x, y=NULL, data=NULL, mad=FALSE, na.rm=TRUE)
## S3 method for class 'K'
print(x, ...)
## S3 method for class 'K'
summary(object, ..., num=2)
```

Arguments

x	Numeric vector, or formula, or object of the class 'K'
y	Second numeric vector, or nothing
data	Data with two columns (in case of formula)
mad	Non-parametric variant of K (not Lubischew's)
na.rm	Remove NAs?
object	Object of the class 'K'
num	Digits to round
...	Additional arguments

Details

One of the effect size measures, Lubischew's K, coefficient of divergence (Lubischew, 1959). Interestingly, the recently invented "striclty standardized mean difference" SSMD (see, for example, "https://en.wikipedia.org/wiki/Strictly_standardized_mean_difference") is just a square root of K.

Value

K() returns value of K, or nothing. summary.K() returns also magnitude and P, "probability of misclassification".

Author(s)

Alexey Shipunov

References

Lubischew A. A. 1959. How to apply biometry to systematics. Leningrad University Herald. N 9. P. 128–136. [In Russian, English abstract].

Examples

```
K(1:3, 2:100)
sapply(eq[, -1], function(.x) K(.x ~ eq[, 1]))
summary(K(x17 ~ Species, data=haltica), num=5)
```

---

keys *Diagnostic keys*

Description

Diagnostic keys are data structures which help to identify biological samples, i.e. give them (scientific) names. They are old but still very popular because they are simple and efficient, sometimes even for not very experienced user.

The second goal of these keys is the compact representation of biological diversity. Diagnostic keys are not very far from classification lists (see 'classifs'), phylogeny trees (like 'phylo' objects in 'ape' package), from core R 'dendrogram' and 'hclust' objects, and especially from recursive partitioning objects (e.g., from 'tree' or 'rpart' packages).

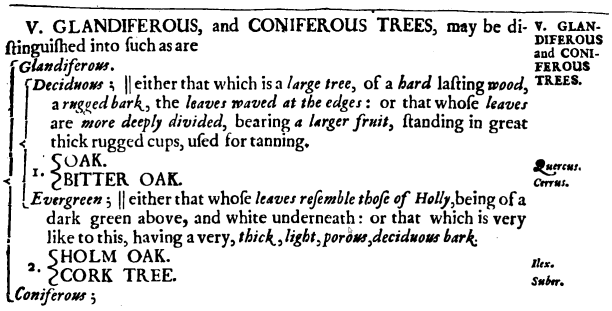
In biology, diagnostic keys exist in many flavors which are possible to reduce into two main types:

I. Branched keys, where alternatives are separated.

You compare your sample with the first description. Then, if the sample agrees with first description, you go to second description (these keys are usually fully dichotomous). If not, you find the alternative description of the _same level_ (same depth). The main difficulty here is how to find it.

To help user find descriptions of the same depths, branched keys are usually presented as _indented_ where each line starts with an indent. Bigger indent means bigger depth.

Branched or indented keys could be traced at least to 1668, to one of John Wilkins books:



V. GLANDIFEROUS, and CONIFEROUS TREES, may be distinguiſhed into ſuch as are

Glandiferous.

Deciduous; ‖ either that which is a *large tree*, of a *hard* laſting *wood*, a *rugged bark*, the *leaves waved at the edges*: or that whoſe *leaves* are *more deeply divided*, bearing *a larger fruit*, ſtanding in great thick rugged cups, uſed for tanning.

1. OAK. *Quercus.*
   BITTER OAK. *Cerrus.*

Evergreen; ‖ either that whoſe *leaves reſemble thoſe of Holly*, being of a dark green above, and white underneath: or that which is very like to this, having a very, *thick*, *light*, *porous*, *deciduous bark*.

2. HOLM OAK. *Ilex.*
   CORK TREE. *Subr.*

Coniferous;

V. GLANDIFEROUS and CONIFEROUS TREES.

(and maybe to much earlier scholastic works.)

Indented keys are widely used, especially in English-language publications.

Another modification could be traced to 1892 when A. Semenow-Tjan-Shanskij published his serial key:

1 (2). *Vertex tuberculo fere corniformi in utroque sexu praeditus. Mandibulae in utroque sexu simplices, i. e. absque appendicibus.*

sg. **Abrognathus** Jak.

2 (1). *Vertex absque tuberculo corniformi.*

3 (4). *Mandibularum appendices in ♂ saepius vix indicatae, dentiformes seu obtuse anguliformes, rarius magis evolutae, spiniformes, semper aequales. Corpus supra rude sculptum.*

sg. **Lethrulus** m.

4 (3). *Mandibularum appendices in ♂ plus minusve evolutae (saltem sinistra), modo aequales, modo inaequales.*

Serial keys are similar to all branched keys but numbering style is different. All steps are numbered sequentially but each has a back-reference to the alternative so user is not required to find the description of the same depth, they already found. Serial keys are strictly dichotomous. They are probably the most space-saving keys, and still in use, especially in entomology.

II. Bracket keys, where alternatives are together, and user required to use 'goto' references to take the next step.

They can be traced to the famous "Flora Francoise" (1778) where J.-B. Lamarck likely used them the first time:

9. *Fleurs libres & non réunies dans un calice commun*	Corolle monopétale	10
	Corolle polypétale	13
10. *Corolle monopétale*	Corolle régulière	11
	Corolle irrégulière	12
11. Corolle régulière. *Anagallis arvenſis.*		
12. Corolle irrégulière. *Salvia pratenſis.*		

You compare your sample with first description, and if it agrees, go to where 'goto' reference says. If not, go to second (alternative) description, and then again use its 'goto'. Sometimes, bracket keys have more than one alternative (e.g., not fully dichotomous).

Bracket keys pose another difficulty: it is not easy to go back (up) if you by mistake went into the wrong direction. Williamson (1922) proposed backreferenced keys where each step supplied with back-reference:

1.	Tarsi spurred	2.
1′.	Tarsi not spurred	5.
2 (1).		*a.*
2′.		3.
3 (2′).		
		4.
3′.		
		b.
4 (3).		*c.*
4′.		*d.*

Sometimes, back-references exist only in case where the referenced step is not immediately before the current.

Bracket keys (backreferenced or not) are probably most popular in biology, and most international as well.

Here bracket, branched and serial keys are standardized as rectangular tables (data frames). Each feature (id, backreference, description, terminal, 'goto') is just one column. Order of columns is important, column name is not. Please see examples to understand better.

Note that while this format is human-readable, it is not typographic. To make keys more typographic, user might want to convert them into LaTeX where several packages allow for typesetting diagnostic keys (for example, my 'biokey' package.)

Usage

```
keys
```

Format

The list which contains four data frames representing three different flavors of biological diagnostic keys: two simple bracket keys, one branched (indented without indent) and one serial key. Last two keys are real-world keys, first to determine Plantago (ribworts, plantains) from European Russia (Shipunov, 2000), second – from North America (Shipunov, 2019).

Source

Lamarck J.-B., de. 1778. Flore Francoise. Paris.

Semenow-Tjan-Shanskij A.P. 1892. Note sur la subdivision du genre Lethrus Scop. et description de deux nouvelles. Trudy Russkago Entomologicheskago Obschestva. 26: 232–244.

Shipunov A. 2000. The genera Plantago L. and Psyllium Mill. (Plantaginaceae Juss.) in the flora of East Europe. Novosti Systematiki Vysshikh Rastenij. 32: 139–152. [In Russian]

Shipunov A. 2019. Plantago. In: Freeman, C. and Rabeler R. (eds.) Flora of North America. 2019. 17: 280–293. Oxford University Press, New York and Oxford.

Shipunov A. biokey – Flexible identification key tables in LaTeX. Version 3.1.
URL: "https://ctan.org/pkg/biokey'

Sviridov A.V. 1994. Types of the biodiagnostic keys and their uses. Moscow. [In Russian]

Wilkins J. 1663. An essay towards the real character and philosophical language. London.

Williamson E. 1922. Keys in systematic work. Science. 55: 703.

See Also

Biokey

Examples

```
attach(keys)

head(bracket1)
head(bracket2)
head(branched)
head(serial)

## convert keys with Biokey()
sii <- Biokey(serial, from="serial", to="indented")
sbb <- Biokey(serial, from="serial", to="bracket")
bbr <- Biokey(branched, from="branched", to="bracket")

## convert keys and visualize them as trees
library(ape) # load 'ape' library to plot Newick trees
plot(read.tree(text=Biokey(bracket1, from="bracket", to="newick")))
plot(read.tree(text=Biokey(bracket2, from="bracket", to="newick")))
plot(read.tree(text=Biokey(branched, from="branched", to="newick")))
plot(read.tree(text=Biokey(serial, from="serial", to="newick")))

detach(keys)
```

Life *Game of Life*

Description

Conway's Game of Life

Usage

```
Life(n.rows=40, n.cols=40, n.cycles=100, sleep.time=0.05,
 cols=c("#f0f0f0", "#2f81c1"), rnd.threshold=0.3)
```

Arguments

n.rows	Number of rows
n.cols	Number of columns
n.cycles	Number of cycles
sleep.time	Time for pause after each cycle
cols	Main colors
rnd.threshold	0 empty board; 1 all squares are filled

Details

Please note that at the moment, this function is not interactive.

Author(s)

Alexey Shipunov

Examples

```
Life(10, 10, 10, .3)
```

`Linechart` *Dotchart-like plot sfor every scaled variable grouped by factor*

Description

Dotchart-like plot sfor every scaled variable grouped by factor

Usage

```
Linechart(vars, groups, xticks=TRUE, xmarks=TRUE, mad=FALSE, pch=19,
 se.lwd=1, se.col=1, ...)
```

Arguments

`vars`	Variables to draw (data frame)
`groups`	Grouing factor
`xticks`	Show xticks?
`xmarks`	Show xmarks?
`mad`	Show MAD instead of IQR?
`pch`	Points type
`se.lwd`	Lines width
`se.col`	Lines color
`...`	arguments to 'plot()'

Details

Dotchart-based plot showing medians and IQRs (or MADs) for every scaled variable grouped by 'groups' factor.

Alternatives: trellis designs.

Author(s)

Alexey Shipunov

See Also

Boxplots

Examples

```
Trees <- trees
Trees[, 4] <- sample(letters[1:3], nrow(Trees), replace=TRUE)
Linechart(Trees[, 1:3], factor(Trees[, 4]))
```

Ls *Ls*

Description

Advanced object browser

Usage

```
Ls (pos = 1, pattern, mode = "any", type = "any", exclude = "function", sort = "name")
```

Arguments

mode	which object mode to include, "any" to include all
type	which object type to include ("type" is typically, but not always an object's class attribute), "any" to include all
exclude	exclude functions (default), "none" to include all
sort	sort by name (default), "size" to sort by size
pos	specify environment, passed to ls()
pattern	optional regular expression, passed to ls()

Details

Based on 'ls()' but outputs data frame.

Value

Data frame with object features columns.

Author(s)

Alexey Shipunov

See Also

ls

Examples

```
data(trees)
Ls()
```

`Mag` *Interpreter for effect sizes*

Description

Interprets R^2-related effect sizes

Usage

```
Mag(x, squared=TRUE)
```

Arguments

`x`	Value
`squared`	Is value squared?

Details

Interpreter for R^2-related effect sizes (see example).

Author(s)

Alexey Shipunov

Examples

```
aa <- apply(cor(trees), 1:2, function(.x) Mag(.x, squared=FALSE))
aa[upper.tri(aa, diag=TRUE)] <- "-"
noquote(aa)
```

`MDSv` *MDS: explained variance (surrogate)*

Description

MDS: explained variance (surrogate)

Usage

```
MDSv(scores)
```

Arguments

scores	Data frame or matrix with values (e.g., result of 'isoMDS()'

Details

MDS explained variance (surrogate, regression-based)

Value

Numeric vector, one values per column of scores

Author(s)

Alexey Shipunov

Examples

```
iris.dist <- dist(iris[, 1:4], method="manhattan")
iris.dist[iris.dist == 0] <- abs(jitter(0))
library(MASS)
iris.m <- isoMDS(iris.dist)
cor(iris[, 1:4], iris.m$points) # MDS loadings surrogate
MDSv(iris.m$points) # MDS explained variance surrogate
```

Miney *Miney game*

Description

Miney minesweeper game

Usage

```
Miney(n, ucol="black", gcol="white", bcol="red")
```

Arguments

n	Indicates the size of the matrix to play, i.e. n=5 results in n x n = 5 x 5 matrix.
ucol	Color of unknown cells
gcol	Color of good cells
bcol	Color of bad cells

Details

Miney game, modified from 'miney' package of Roland Rau. See also the 'fun' package.

Author(s)

Alexey Shipunov

Examples

```
## Not run:
## interactive command:
Miney(3)

## End(Not run)
```

Misclass *Misclassification (confusion) table*

Description

Misclassification (confusion) table

Usage

```
Misclass(pred, obs, best=FALSE, ignore=NULL, quiet=FALSE, ...)
```

Arguments

pred	Predicted class labels
obs	Observed class labels
best	Perform a search for the classification table with minimal misclassification rate?
ignore	Vector of class labels to ignore
quiet	Output summary?
...	Arguments to 'table'

Details

'Misclass()' produces misclassification (confusion) 2D table based on two classifications.

The simple variant ('best=FALSE') assumes that class labels are concerted (same number of corresponding classes).

Advanced variant ('best=TRUE') can search for the best classification table (with minimal misclassification rate), this is especially useful in case of unsupervised classifications which typically return numeric labels. However, internally it generates all permutations of factor levels, thei could be very slow if there are many class labels.

Variant with 'best=TRUE' might also add empty rows (filled with zeros) to the table in case if numbers of classes are not equal.

Additional arguments could be passed for table(), for example, 'useNA="ifany"'. If supplied data contains NAs, there will be also note in the end.

It is possible to ignore some class labels with 'ignore=...', this is useful for methods like DBSCAN which output special label for outliers. In that case, note about missing data is also issued.

Alternatives: confusion matrix from 'caret::confusionMatrix()' which is more feature rich but much less flexible.

Note that partial "Misclassification errors" are reverse sensitivities, and "Mean misclassification error" is a reverse accuracy.

Association plot assocplot() is probably the best to plot misclassification table.

Value

Invisibly returns the table of class comparison

Author(s)

Alexey Shipunov

Examples

```
iris.dist <- dist(iris[, -5], method="manhattan")
iris.hclust <- hclust(iris.dist)
iris.3 <- cutree(iris.hclust, 3)
Misclass(iris.3, iris[, 5])

set.seed(1)
iris.k <- kmeans(iris[, -5], centers=3)
Misclass(iris.k$cluster, iris[, 5])
Misclass(iris.k$cluster, iris[, 5], best=TRUE)

res <- Misclass(iris.k$cluster, iris[, 5], best=TRUE, quiet=TRUE)
## statistics implemented in caret::confusionMatrix()
binom.test(sum(diag(res)), sum(res))$conf.int
mcnemar.test(res + 1e-9) # to avoid NaN's

library(dbscan)
iris.db <- dbscan(iris[, -5], eps=0.3)
Misclass(iris.db$cluster, iris$Species, ignore=0, best=TRUE)

set.seed(NULL)
```

Missing.map *Textual plot of missing data*

Description

Textual plot of missing data

Usage

```
Missing.map(df)
```

Arguments

df	Data frame with any data

Details

'Missing.map()' makes textual plot of missing data, inspired by 'DescTools::PlotMiss()'.

Author(s)

Alexey Shipunov

Examples

```
Missing.map(salix_leaves)
```

---

moldino *moldino*

Description

Observations on island floras. Islands are located in the freshwater Moldino lake, Middle Russia. Data collected in 2013.

'moldino_l' contains squares and GPS locations.

'moldino' contains the actual abundance data.

Usage

```
moldino
```

Format

`columns` Island names, data is abundance of plant species, in 1543 scale (0 – absent; 1 – one individual plant; 2 – no more than 12 individual plants (rametes); 3 – number of individuals is more than 12 but no more than 5% of total number of plants on a plot; 4 – number of individuals is more than 5% but no more than 25% of total number of plants on a plot; 5 – number of individuals is more than 25% but no more than 50% of total number of plants on a plot; 6 – number of individuals is more than 50% but no more than 75% of total number of plants on a plot; 7 – number of individuals is more than 75% of total number of plants on a plot.)

`rows` Names of plant species

`NAME` Island name

`SQUARE` Island square, m2

`LAT` Latitude

`LON` Longitude

Source

Abramova L., Volkova P., Eliseeva E., Troshina A., Shipunov A. The checklist of flora from environs of village Polukarpovo (Tver region). 2005–onward. "http://ashipunov.info/shipunov/moldino/nauka/molflora.pdf".

Shipunov A., Abramova L. Islands in lakes and the sea: how do they differ? European Journal of Environmental Sciences. 2014. 4: 112–115.

`MrBayes` *Calls MrBayes*

Description

A slight improvement of 'ips::mrbayes()'

Usage

```
MrBayes(x, file="", nst=6, rates="invgamma", ngammacat=4, nruns=2, ngen=1e+06,
 printfreq=100, samplefreq=10, nchains=4, savebrlens="yes", temp=0.2, burnin=10,
 contype="allcompat", run=FALSE, simple=TRUE, exec="mb-mpi", method="dna")
```

Arguments

`x`	The object to process (must be 'DNAbin' class)
`file`	A character string, giving the name of the MrBayes input file
`nst`	An integer giving the number of rates in the model of sequence evolution
`rates`	A character string; allowed are "equal", "gamma", "propinv", "invgamma", and "adgamma"; the default is "equal"
`ngammacat`	An integer; the number rate categories for the discretized Gamma distribution; the default is '4'
`nruns`	An integer; the number of runs
`ngen`	An integer; the number of states of the MCMC
`printfreq`	An integer; the interval between states of the MCMC to be printed on the screen
`samplefreq`	An integer; the interval between states of the MCMC to be sampled
`nchains`	An integer; number of Metropolis coupled MCMCs in each run
`savebrlens`	Logical; shall branch lengths be saved
`temp`	Heating parameter
`burnin`	An integer; the number of samples from the MCMC to be discarded prior to further analysis
`contype`	A character string; the type of consensus tree calculated from the posterior distribution of treeseither "halfcompat" (majority-rule consensus tree) or "allcombat" (strict consensus tree)
`run`	Logical; 'run = FALSE' will only print the NEXUS file, 'run = TRUE' will also start the MCMC runs, if the 'path' argument is correctly specified

simple	New option: if TRUE (default), then outputs tree in the format readable by functions from 'ape' package
exec	New option: name of UNIX executable (to allow multi-threaded version)
method	New option: either "dna", or "mixed" to handle mixed or purely morphologic data (see below)

Details

MrBayes() is an improvement of ips::mrbayes() and ips::mrbayes.mixed(). Please see its documentation for clarity and other options.

Comparing with 'ips' sources, MrBayes() has some code alterations and three more options. It also both views and saves output (works only on UNIX).

If 'method="mixed"', the function requires character matrix as input where missing data are labeled with "N", morphological columns encoded as 0/1 and placed after nucleotide columns (which might be absent).

Author(s)

Alexey Shipunov

See Also

ips::mrbayes

Examples

```
require(ips)
data(ips.cox1)
x <- ips.cox1[, 100:140]

## Not run:
## requires MrBayes program installation
MrBayes(x, file="cox1", ngen=100, run=TRUE)

str(plantago)
plantago[is.na(plantago)] <- "N"
row.names(plantago) <- gsub(" ", "_", row.names(plantago))
## requires MrBayes program installation
tr <- MrBayes(plantago, file="plantago", method="mixed", burnin=5000, run=TRUE) # makes many files
tr <- tr[[1]]
tr <- root(tr, outgroup="Plantago_maritima", resolve.root=TRUE)
tr$node.label <- suppressWarnings(round(as.numeric(tr$node.label)*100)) # warning is OK
tr$node.label[tr$node.label == "NA"] <- ""
plot(tr)
nodelabels(tr$node.label, frame="none", bg="transparent", adj=-0.1)
add.scale.bar()

## End(Not run)
```

MRH *Matrix Representation of Hierarchical Clustering*

Description

Matrix Representation of Hierarchical clustering (MRH)

Usage

```
MRH(hcl, dim=NULL, method="groups")
```

Arguments

hcl	'hclust' object
dim	Number of desired dimensions, if defaults are not suitable
method	Either "groups" (default), or "height", or "branches", or "cophenetic" (see below for explanations)

Details

This function calls cutree(), or Hcl2mat(), or cmdscale(cophenetic()) in order to output the Matrix Representation of Hierarchical clustering (MRH).

If method="groups" then clustering tree is cut by all possible numbers of clusters 'k' (excluding 'k=1' and 'k=n' which bring no information) so 'dim' is always 'n-2'.

If method="height" then clustering tree is cut by equally spaced agglomeration heights (excluding minimal and maximal heights which bring no information). Default 'dim' here is '2*n', but higher values might work even better.

If method="branches" then use Hcl2mat() to transform object into the binary matrix of memberships, always with 'n-1' dimensions (so user-specified 'dim' is not taken into account). Each column in this matrix represents the tree branch.

If method="cophenetic" then multidimensional scaling scores with maximum dimensionality on cophenetic distances are computed. Default 'dim' is 'n-1' but lesser numbers might work better.

The main feature of the resulted matrices is that they provide the "bridge" of conversion between original data, distance matrices and clustering (including phylogenetic trees) results. After conversion, many interesting applications become possible. For example, if converted trees represent the _same_ objects, it is possible to "hyper-bind", or "average" (Ashkenazy et al., 2018) them.

To work with 'phylo' objects, convert them first to 'hclust' with as.hclust(), and before that, possibly also apply compute.brlen(), multi2di() and collapse.singles().

Value

Matrix with default number of columns equal to number of objects (n) minus 1 (method="branches" or method="cophenetic") or 'n-2' (method="groups"), or '2*n' (method="height").

Rows are objects, values are either cluster numbers (method="groups" or method="height") so matrix consist of whole positive numbers, binary cluster memberships (method="branches") or decimal MDS scores (method="cophenetic").

References

Ashkenazy H., Sela I., Levy Karin E., Landan G., Pupko T. 2018. Multiple sequence alignment averaging improves phylogeny reconstruction. Systematic Biology. 68: 117–130.

See Also

cutree, link{cmdscale}, link{Hcl2mat}

Examples

```
aa.h <- hclust(dist(t(atmospheres)))
plot(aa.h)

(aa.mrh1 <- MRH(aa.h))
plot(hclust(dist(aa.mrh1)))

aa.mrh2 <- MRH(aa.h, method="height", dim=100) # here 'dim' should better be large
str(aa.mrh2)
plot(hclust(dist(aa.mrh2)))

plot(hclust(dist(cbind(aa.mrh1, aa.mrh2)))) # hyper-bind

(aa.mrh3 <- MRH(aa.h, method="branches"))
plot(hclust(dist(aa.mrh3)))

(aa.mrh4 <- MRH(aa.h, method="cophenetic"))
plot(hclust(dist(aa.mrh4)))

library(ape)
tree <- read.tree(text="((A:1,B:1):2,(C:3,D:4):2):3;")
(tree.mrh3 <- MRH(as.hclust(compute.brlen(tree)), method="branches"))
```

Normality *Check normality*

Description

Check normality through Shapiro-Wilks test

Usage

```
Normality(x, p=0.05)
```

Arguments

x	numerical vector
p	level of significance

Details

Normality via Shapiro-Wilks test. Kolmogorov-Smirnov is apparently too weak for small samples. The word of caution: this function only *helps* to decide if the data complains with parametric methods ("normal").

Value

Character vector of length one.

Author(s)

Alexey Shipunov

See Also

qqnorm, hist, rnorm

Examples

```
Normality(rnorm(100))
sapply(trees, Normality)
```

Overlap *Polygons' overlap*

Description

Measures polygons' overlap

Usage

```
Overlap(ppts, Hulls=TRUE)
## S3 method for class 'Overlap'
summary(object, ...)
```

Arguments

ppts	List with hulls information (e.g., output from Hulls())
Hulls	Did the information came from Hulls()?
object	Object of the class 'Overlap'
...	Additional arguments

Details

'Overlap()' calculates polygons (hulls) overlap (it requires 'PBSmapping' package).

If 'Hulls=FALSE', then list components with names 'centers' and 'outliers' will not be attempted to delete from 'ppts' list.

Value

Object of class 'Overlap', or nothing.

Author(s)

Alexey Shipunov

See Also

Hulls

Examples

```
iris.pca <- prcomp(iris[, 1:4], scale=TRUE)
iris.p <- iris.pca$x[, 1:2]
iris.h <- Hulls(iris.p[, 1:2], iris[, 5], plot=FALSE)
iris.o <- Overlap(iris.h)
summary(iris.o)
```

---

pairwise.Eff *Pairwise table of effects with magnitudes*

Description

Pairwise table of effects with magnitudes

Usage

```
pairwise.Eff(vec, fac, eff="K", dec=2, mad=FALSE)
```

Arguments

vec	Values
fac	Groups
eff	Effect, either 'K' or 'cohen.d', or 'cliff.delta'
dec	Decimals to round
mad	Use MAD-based nonparametric modification of K?

Details

Pairwise table of effect sizes.

At the moment, classic Lyubischev's K (a.k.a. SSSMD), effsize::cliff.delta() and effsize::cohen.d() are supported.

Value

List with test outputs.

Author(s)

Alexey Shipunov

Examples

```
pairwise.Eff(hwc$WEIGHT, hwc$COLOR)
pairwise.Eff(hwc$WEIGHT, hwc$COLOR, mad=TRUE)
pairwise.Eff(hwc$WEIGHT, hwc$COLOR, eff="cohen.d")
pairwise.Eff(hwc$WEIGHT, hwc$COLOR, eff="cliff.delta")
```

---

pairwise.Rro.test *Robust rank order test post hoc derivative*

Description

Robust rank order test post hoc derivative

Usage

```
pairwise.Rro.test(x, g, p.adjust.method="BH")
```

Arguments

x	Values
g	Groups
p.adjust.method	See '?p.adjust'

Details

'pairwise.Rro.test()' is the Robust rank order test post hoc derivative.

Value

List with test outputs

Author(s)

Alexey Shipunov

See Also

Rro.test

Examples

```
pairwise.Rro.test(airquality$Ozone, airquality$Month)
```

`pairwise.Table2.test` *Pairwise Chi-squared or Fisher test for 2-dimensional tables*

Description

Pairwise Chi-squared or Fisher test for 2-dimensional tables

Usage

```
pairwise.Table2.test(tbl, names=rownames(tbl), p.adjust.method="BH", exact=FALSE, ...)
```

Arguments

`tbl`	Contingency table
`names`	Level names
`p.adjust.method`	See '?p.adjust'
`exact`	Run exact test?
`...`	Arguments to test function

Details

Pairwise Chi-squared or Fisher test for 2-dimensional tables.

Possible alternatives: NCStats::chisqPostHoc(); fifer::chisq.post.hoc().

Value

List with test outputs.

Author(s)

Alexey Shipunov

Examples

```
titanic <- margin.table(Titanic, c(1, 4))
chisq.test(titanic)
pairwise.Table2.test(titanic)
```

Peaks *Find local maxima*

Description

Find local maxima

Usage

```
Peaks(series, span=3, do.pad=TRUE)
```

Arguments

series	Numerical vector
span	Window size
do.pad	Padding

Details

Finding peaks in a simple dataset.

Author(s)

Alexey Shipunov

Examples

```
## count peaks on joint histogram, this suggests number of clusters
histdata <- hist(apply(scale(iris[, -5]), 1, function(.x) sum(abs(.x))), breaks=10, plot=FALSE)
sum(Peaks(histdata$counts)) # 3 is the first value after 1 and does not change when 8 < breaks < 22
```

Phyllotaxis *Plant phyllotaxis*

Description

Outputs the plant phyllotaxis formula or angle of divergence

Usage

```
Phyllotaxis(n, angle=FALSE)
Fibonacci(x)
```

Arguments

n	non-negative integer
angle	if TRUE, output angle of divergence
x	non-negative integer

Details

'Fibonacci(x)' calculates the n's Fibonacci's number, it is the rare case that is not exercise but really used for work.

'Phyllotaxis(n)' uses 'Fibonacci(x)' to output the phyllotaxis formula (see examples) or (if 'angle=TRUE') the angle of divergence.

Value

Number or character vector of length one.

Author(s)

Alexey Shipunov

Examples

```
sapply(1:10, Fibonacci)
sapply(1:10, Phyllotaxis)
sapply(1:10, Phyllotaxis, angle=TRUE)
```

---

plantago *plantago*

Description

Plantago (ribworts, plantains) species from European Russia: morphological table (Shipunov, 1998).

Usage

```
plantago
```

Format

This data frame has species names as row names, and contains the following columns (all variables are binary):

`V01` 0 annuals or biennials, 1 perennials

`V02` 0 not taller than 20 cm, 1 taller than 20 cm

`V03` 0 aboveground stems herbaceous, 1 aboveground stems woody

`V04` 0 vegetative nodes shortened, 1 vegetative nodes elongated

V05 0 vegetative shoots do not branch, 1 vegetative shoots branch

V06 0 phyllotaxis opposite, 1 phyllotaxis alternate

V07 0 well developed green leaves <= 5, 1 more

V08 0 the base of main shoot covered with remains of withered leaves, 1 the base is not covered with remains of withered leaves

V09 0 rhizome > 1 cm diam, 1 rhizome thinner

V10 0 slanted or horizontal rhizome, 1 vertical rhizome

V11 0 main root fast degrading, 1 main root presents on adult plants

V12 0 adventitious and lateral roots >= 1 mm diam, 1 less than 1 mm diam

V13 0 heterophylly present, 1 leaves similar

V14 0 leaves thin, transparent, 1 leaves not transparent

V15 0 leaves darken when dry, 1 leaves do not darken, sometimes became yellow or brown

V16 0 leaves (almost) naked, 1 leaves pubescent

V17 0 leaves flat, 1 leaves section rounded or leaves with furrow

V18 0 leaves with large teeth or even lobes, 1 leaves margin whole or with small teeth

V19 0 leaves linear, 1 leaves more broad

V20 0 leaves lanceolate, 1 leaves more broad

V21 0 leaves obovate, 1 leaves elliptic or ovate

V22 0 leaf tip blunt, 1 leaf tip sharp

V23 0 leaf base broad, suddenly narrowing into petiole, 1 leaf base narrow, smoothly become a petiole

V24 0 leaf margin with teeth, 1 leaf margin whole

V25 0 leaf veins >=7, 1 < 7

V26 0 petioles present, 1 petioles absent

V27 0 petioles almost equal or a bit shorter than leaf blades, 1 petioles much shorter than blades

V28 0 petioles without wings at the lowest 1/3 of length, 1 petioles with wings at the lowest 1/3 of length

V29 0 stalks horizontal or arcuate, 1 stalks straight or curved

V30 0 stalks naked, 1 stalks pubescent

V31 0 stalks with ribs, 1 stalks without ribs

V32 0 spikes longer, equal or slightly shorter than stalks, 1 spikes much shorter than stalks

V33 0 spikes long cylindrical or tail-like, 1 spikes rounded or short cylindrical

V34 0 lower bracts are much much broader than others, 1 all bracts similar

V35 0 middle and upper bracts not longer than sepals, 1 longer than sepals

V36 0 bracts with sharp tip, 1 bracts with blunt tip

V37 0 bract width >= length, 1 bract length > width

V38 0 bracts pubescent, 1 bracts naked

V39 0 bracts awned, 1 bracts not awned

`V40` 0 flowers slanted, spike lax, 1 flowers appressed, spike dense

`V41` 0 outer and inner sepals significantly different, 1 all sepals more or less similar

`V42` 0 sepals narrow, 1 sepals broad

`V43` 0 sepals with sharp tip, 1 sepals with blunt tip

`V44` 0 sepals pubescent, 1 sepals naked

`V45` 0 outer sepals fused, 1 outer sepals separate

`V46` 0 corolla tube pubescent, 1 corolla tube naked

`V47` 0 corolla lobes broad, elliptic or rounded, 1 corolla lobes narrow, oblanceolate or lanceolate

`V48` 0 corolla lobes with sharp tip, 1 corolla lobes with blunt tip

`V49` 0 corolla lobes white or silver, 1 corolla lobes yellowish or brownish

`V50` 0 stamens not exserted, 1 stamens exserted

`V51` 0 filaments yellowish or brownish, 1 filaments white, pinkish or purplish

`V52` 0 pollen grains with thickened pore margin, 1 pollen grains without thickened pore margin

`V53` 0 pollen grains with >= 9 pores, 1 pollen grains with < 9 pores

`V54` 0 pyxidium ovate or broadly conical, 1 pyxidium narrowly conical or elongated

`V55` 0 one or two seeds are much smaller than others, 1 all seeds similar

`V56` 0 seeds =< 2, 1 seeds > 2

`V57` 0 seeds 3–5, 1 seeds >= 6

`V58` 0 seeds flattened, 1 seeds rounded or angled

`V59` 0 plane which passes through embryo cotyledons is perpendicular to placenta, 1 plane which passes through embryo cotyledons is parallel to placenta

`V60` 0 polyploids, 1 diploids

`V61` 0 x=5, 1 x=6

Source

Shipunov A. 1998. Plantains (genera Plantago L. and Psyllium Mill., Plantaginaceae) of European Russia and adjacent territories. Ph. D. Thesis. Moscow State University.

Examples

```
plot(hclust(dist(plantago, method="binary")))
```

`Pleiad` *Correlation circles (correlation pleiads)*

Description

Correlation circles (correlation pleiads)

Usage

```
Pleiad(tbl, abs=FALSE, corr=FALSE, dist=FALSE, treshold=FALSE,
 circ=list(1, 1, 1), breaks=5, auto=TRUE, gr=6, lwd=NULL, lty=NULL, lcol=NULL,
 abbr=-1, lbltext="internal", lblcex=1, off=1.09, hofft=0.07, hoff=1.02, legend=TRUE,
 legtext=1, legpos="topright", leghoriz=FALSE, show.int=FALSE, dig.lab=1, ...)
```

Arguments

`tbl`	Data: square matrix
`abs`	If TRUE, uses absolute values instead of real
`corr`	If TRUE, uses absolute values instead of real and cuts from 0 to 1, this is good for correlation matrices
`dist`	If TRUE, converts distance matrix to the data frame – good for "dist" objects
`treshold`	If this is (saying) =.5, selects for plotting (with lty=1) only those values which are >.5
`circ`	Line type, width and color for the cirle; if first or third =0, no cicrle
`breaks`	How to cut() values, if "cramer", then =c(0, .1, .3, .5, 1)
`auto`	If FALSE, specify 'lwd', 'lty' and 'lcol'
`gr`	Grayscale scheme starts from 6 breaks
`lwd`	If autolines=FALSE, change to vector concerted with breaks
`lty`	If autolines=FALSE, change to vector concerted with breaks
`lcol`	If autolines=FALSE, change to vector concerted with breaks; if length(lcol) == 1, all lines are of particular color
`abbr`	If =-1, no abbreviation; if =0, no labels; other values run abbreviate(..., abbr)
`lbltext`	If this is a vector starting from something else, will replace dimnames
`lblcex`	Magnification of labels
`off`	Radial offset of labels, be careful!
`hofft`	Treshold determining which labels are rigtmost/leftmost, 'hofft=0' put all labels into this group
`hoff`	Horizontal offset for rightmost/leftmost labels; 'hoff=1' removes offset
`legend`	If FALSE, no legend
`legtext`	If =1 then "weaker ... stronger"; if =2, shows cutting intervals; if =3, then 1:5; if >3, issues error

legpos	This is from 'legend()'
leghoriz	Equal to 'horiz=' from 'legend()'
show.int	Show intervals in (...] form
dig.lab	dig.lab for 'cut()'
...	Arguments to 'points()'

Details

Correlation circles (correlation pleiads). Based on the works of Petr Terentjev's (Saint Petersburg) school. Alternatives: those graph plotting packages which are able to plot "correlogram". It is probably a good idea to order data entries with hierarchical clustering results to optimize resulted graph. The plot has no margins so consider second 'legend()' to add any text to the plot (see examples).

Value

Data frame with position of points, helps in subsequent plot enhancing

Author(s)

Alexey Shipunov

Examples

```
l.c <- cor(datasets::longley, method="spearman", use="pairwise")
Pleiad(l.c, corr=TRUE, legtext=2, pch=21, cex=2, bg="white",
 breaks=3, gr=3, hoff=1, show.int=TRUE)
legend("topleft", legend="Title", text.font=2, bty="n")

dr.c <- cor(drosera[, -1], method="spearman", use="pairwise")
Pleiad(dr.c, corr=TRUE, legtext=2, pch=19, cex=1.2)
```

---

plot.nnet *Plots 'nnet' object*

Description

Plots 'nnet' object

Usage

```
## S3 method for class 'nnet'
plot(x, ..., nid=TRUE, all.out=TRUE, all.in=TRUE, wts.only=FALSE,
 rel.rsc=5, circle.cex=5, node.labs=TRUE, line.stag=NULL, cex.val=1, alpha.val=1,
 circle.col="lightgrey", pos.col="black", neg.col="grey")
```

Arguments

x	'nnet' model
...	arguments to 'plot()'
nid	TRUE
all.out	TRUE
all.in	TRUE
wts.only	FALSE
rel.rsc	5
circle.cex	5
node.labs	TRUE
line.stag	NULL
cex.val	1
alpha.val	1
circle.col	"lightgrey"
pos.col	"black"
neg.col	"grey"

Details

Plots 'nnet' object. Requires 'nnet' and 'scales' libraries. Based on the code from Marcus W Beck.

Author(s)

Alexey Shipunov

Examples

```
library(nnet)
iris.train <- iris[seq(1, nrow(iris), 5), ]
iris.unknown <- iris[-seq(1, nrow(iris), 5), ]
iris.nnet <- nnet(Species ~ . , data=iris.train, size=4)
iris.predicted <- predict(iris.nnet, iris.unknown[, -5], type="class")
Misclass(iris.predicted, iris.unknown[, 5])
##
oldpar <- par(mar=c(0, 0, 0, 0))
plot(iris.nnet)
par(oldpar)
```

`Plot.phylocl` *Plot phylogenetic tree with clades collapsed*

Description

Plot phylogenetic tree with clades collapsed into triangles or rectangles

Usage

```
Plot.phylocl(tree, cl, strict=TRUE, what="triangles", col.ed="black",
 col.td="black", col.etr="transparent", col.ttr="transparent", col.pfl="lightgrey",
 col.pbr="black", lty.p=1, lwd.p=1, col.ct="black", ct.off=0, ct.fnt=1,
 longer="0%", ...)
```

Arguments

`tree`	phylo object
`cl`	two columns classification table
`strict`	default TRUE: do not join all descendants
`what`	default "triangles", also possible to use "rectangles"
`col.ed`	default "black", default edge color
`col.td`	default black", default tips color
`col.etr`	default "transparent", color to suppress original edges
`col.ttr`	default "transparent", color to suppress original tips
`col.pfl`	default "lightgrey", fill color for polygons
`col.pbr`	default "black", border color of polygons
`lty.p`	default 1, line type of polygon borders
`lwd.p`	default 1, line width
`col.ct`	default "black", color of clade labels
`ct.off`	default 0, text offset of clade labels
`ct.fnt`	default 1, text font of clade labels
`longer`	default "0%", percent to increase xlim to fit longer clade labels
`...`	options to ape::plot.phylo()

Details

Plot.phylocl() plots phylogenetic tree with clades collapsed into triangles or rectangles.

Alternative is phytools::plot.backbonePhylo() which however requires more manual work.

Some tricks used (null plotting and transparent elements), the last one is actually useful in other ways.

Intersections and other deviated cases not controlled. However, they are really easy to spot.

All parameters of polygons should be either "scalars" or vectors of the same length as clade list (minus monotypic clades), clades are in alphabetical order. To help, list of clade names is invisibly returned in the end.

Value

Returns list of clade names.

Author(s)

Alexey Shipunov

See Also

phytools::plot.backbonePhylo()

Examples

```
aa.d <- hclust(dist(t(atmospheres)))
tree <- ape::unroot(ape::as.phylo(aa.d))
cl <- data.frame(planet=c("Mercury", "Venus", "Earth", "Mars", "Jupiter", "Saturn",
 "Uranus", "Neptune"),
clade=c("Earth group", "Earth group", "Earth group", "Earth group", "Close giants",
 "Close giants", "Distant giants", "Distant giants"), stringsAsFactors=FALSE)
Plot.phylocl(tree, cl, longer="5%")
```

PlotBest.dist *Plots dotchart with best base distance method*

Description

Plots dotchart with best base distance method

Usage

```
PlotBest.dist(data, distances=c("euclidean", "maximum", "manhattan",
 "canberra", "binary", "minkowski"), dim=2, plot=TRUE)
```

Arguments

data	Data frame with values
distances	Distances to use
dim	Number of dimensions
plot	Plot?

Details

Plots the "best" base distance method. Uses correlation between multidimensional scaling of distance object and PCA of data. Two dimensions are default, change it with "dim" option.

Value

Numeric vector with correlation values (equal to the number of distances involved)

Author(s)

Alexey Shipunov

Examples

```
PlotBest.dist(iris[, -5])
```

PlotBest.hclust *Plots dotchart with best clustering method*

Description

Plots dotchart with best clustering method

Usage

```
PlotBest.hclust(dist, clust=c("ward.D", "ward.D2", "single", "complete",
 "average", "mcquitty", "median", "centroid"), plot=TRUE)
```

Arguments

dist	Distance matrix
clust	Clustering method
plot	Plot?

Details

Plots the "best" hierarchical clustering method. Uses cophenetic correlation.

Value

Numeric vector with correlation values (equal to the number of clusterings involved)

Author(s)

Alexey Shipunov

Examples

```
PlotBest.hclust(dist(iris[, -5], method="manhattan"))
```

`PlotBest.mdist` *Plots dotchart with best distance method, use multiple non-base distances*

Description

Plots dotchart with best distance method, use multiple non-base distances

Usage

```
PlotBest.mdist(data, distances=c("manhattan", "euclidean", "canberra", "clark",
 "bray", "kulczynski", "jaccard", "gower", "altGower", "morisita", "horn", "binomial",
 "chao", "cao", "mahalanobis", "cor.pearson", "cor.spearman", "cor.kendall",
 "gower_dist", "daisy.gower", "smirnov"), dim=2, binary.only=FALSE, plot=TRUE, ...)
```

Arguments

`data`	Data frame with values
`distances`	Distances to use
`dim`	Number of dimensions
`binary.only`	Use binary only distances?
`plot`	Plot?
`...`	Arguments to 'vegdist()'

Details

Plots the "best" distance method, uses many non-base distances from diverse packages. Uses correlation between multidimensional scaling of distance object and PCA of data. Does not include "mountford" and "raup" from vegdist() as they are very special. Two dimensions are default, change it with "dim" option.

Value

Numeric vector with correlation values (equal to the number of distances involved)

Author(s)

Alexey Shipunov

See Also

`PlotBest.dist`

Examples

```
PlotBest.mdist(iris[, -5], scale.pca=TRUE)

m1 <- t((moldino > 0) * 1)
PlotBest.mdist(m1, binary.only=TRUE)
```

Ploth *Changes the appearance of cluster dendrogram*

Description

Changes the appearance of cluster dendrogram

Usage

```
Ploth(hclust, labels=hclust[["labels"]], lab.col=1, col=1, pch.cex=1, pch="",
 bg=0, col.edges=FALSE, ...)
```

Arguments

hclust	Hclust object
labels	Labels
lab.col	Label colors
col	Colors
pch.cex	Scale of points
pch	Point types
bg	Points backgrounds
col.edges	Colorize edges?
...	Arguments to 'plot()'

Details

Changes the appearance of cluster dendrogram. Be sure to check plot margins!

Author(s)

Alexey Shipunov

Examples

```
iris.dist <- dist(iris[, 1:4], method="manhattan")
iris.hclust <- hclust(iris.dist)
Ploth(iris.hclust, col=as.numeric(iris[, 5]), pch=16, col.edges=TRUE, horiz=TRUE,
 leaflab="none")
legend("topleft", fill=1:nlevels(iris[, 5]), legend=levels(iris[, 5]))
```

`Points` *Number of cases in each location reflected in the point size*

Description

Number of cases in each location reflected in the point size

Usage

```
Points(x, y, pch=1, centers=FALSE, scale=1, cex.min=1, col=1,
 na.omit=TRUE, plot=TRUE, ...)
PPoints(groups, x, y, cols=as.numeric(groups), pchs=as.numeric(groups),
 na.omit.all=TRUE, ...)
```

Arguments

`x, y`	Coordinates
`pch`	Point type
`pchs`	Types of point groups
`centers`	If TRUE, show centers of each location as a pixel-size dot (pch=".")
`cex.min`	Minimal point size
`col`	Color of points
`cols`	Color of point groups
`na.omit`	If TRUE (default), skip data points with NAs
`plot`	If FALSE, does not plot
`na.omit.all`	If TRUE (default), skip data points and corresponding factor values with NAs, then make 'na.omit' for internal Points() FALSE
`scale`	Scale factor for point size
`groups`	Factor defining groups
`...`	Points() passes other arguments to points(), PPoints() passes other arguments to Points()

Details

Frequently, more then one data point is located in one coordinate place (so called "overplotting"). How to show overplotting? One way is 'jitter()', these is also (really advanced) 'sunflowerplot()'. 'Points()' does it in its own way: number of cases in each point will be reflected in the point size. 'Points()' is a low-level graphic function, analogous to 'points()'.

'PPoints()' is the same as 'Points()' but for multiple subgroups.

To prettify plot, it is recommended to change 'scale' and optionally also 'cex.min'.

Alternative is the base R 'sunflowerplot()' but it is hard to read and there is no possibility to show multiple groups in data. Another alternative might be points with transparent color.

Value

Invisibly returns vector of "multiplication indexes", in case of PPoints() it is group-wise so overplotting between groups does not count. Please keep in mind that these indexes only indicate how many times the point is overplotted, but do not show groups of duplicates. Use Alldups() for groups.

Author(s)

Alexey Shipunov

See Also

jitter, sunflowerplot

Examples

```
## colors modified via palette()
plot(iris[, 1:2], type="n")
palette(rainbow(3))
PPoints(iris[, 5], iris[, 1], iris[, 2], pchs=0, scale=0.7)
palette("default")
## now with centers, colors default, pch by group, and one NA
iris[1, 1] <- NA
plot(iris[, 1:2], type="n")
PPoints(iris[, 5], iris[, 1], iris[, 2], scale=0.7, centers=TRUE)
data(iris) ## to restore default embedded object
```

R.logo *Imitation (!) of the modern 'R' logo*

Description

Imitation (!) of the modern 'R' logo

Usage

```
R.logo(x, y, col.e="#B8BABF", col.l="#1E63B5", cex=12)
```

Arguments

x	x coordinate of the letter
y	y coordinate of the letter
col.e	ellipse color
col.l	letter color
cex	scale, default 12

Details

Imitation (sic!) of the modern (flat) 'R' logo. Font and proportions are not exactly the same, also there is no gradient.

Author(s)

Alexey Shipunov

See Also

Ell

Examples

```
plot(1, type="n", axes=FALSE, xlab="", ylab="")
R.logo(1.1, 0.9, cex=25)
##
plot(1:20, type="n")
for (i in 1:20) R.logo(i, i, cex=2)
```

Read.fasta *Read 'FASTA' files*

Description

Simple reading of 'FASTA' files

Usage

```
Read.fasta(file)
```

Arguments

file	File name

Details

Simple reading of 'FASTA' files.

Value

Data frame with two columns: 'name' and 'sequence'.

Author(s)

Alexey Shipunov

Examples

```
write(file=file.path(tempdir(), "tmp.fasta"), ">some_id\nATGC")
Read.fasta(file=file.path(tempdir(), "tmp.fasta"))
```

`Read.tri.nts` *Read 'NTSYSpc' files*

Description

Read a lower triangular matrix

Usage

```
Read.tri.nts(file, ...)
```

Arguments

`file`	File to read
`...`	Arguments to 'scan()'

Details

Reads a lower triangular matrix which at least in my practice, typically come from 'NTSYSpc' program.

Author(s)

Alexey Shipunov

Examples

```
write(file=file.path(tempdir(), "tmp.nts"), x=c(
'" Procrustes distances between all pairs:
2 12 12 0
0.000E+000
4.058E-002 0.000E+000
5.753E-002 6.489E-002 0.000E+000
6.445E-002 8.124E-002 9.509E-002 0.000E+000
2.610E-001 2.395E-001 2.317E-001 3.051E-001 0.000E+000
2.719E-001 2.508E-001 2.461E-001 3.132E-001 4.531E-002 0.000E+000
2.563E-001 2.357E-001 2.278E-001 3.008E-001 4.414E-002 6.510E-002 0.000E+000
8.003E-002 6.611E-002 7.738E-002 9.885E-002 2.206E-001 2.270E-001 2.161E-001
0.000E+000
6.838E-002 8.893E-002 6.691E-002 1.018E-001 2.585E-001 2.704E-001 2.497E-001
1.019E-001 0.000E+000
6.233E-002 6.756E-002 4.079E-002 8.329E-002 2.396E-001 2.507E-001 2.338E-001
5.519E-002 5.932E-002 0.000E+000
2.504E-001 2.313E-001 2.230E-001 2.967E-001 8.714E-002 1.080E-001 6.522E-002
2.205E-001 2.323E-001 2.281E-001 0.000E+000
```

```
2.590E-001 2.688E-001 2.424E-001 2.757E-001 3.698E-001 3.926E-001 3.689E-001
3.051E-001 2.280E-001 2.603E-001 3.312E-001 0.000E+000 '
))

## interactive
file.show(file=file.path(tempdir(), "tmp.nts"))

Read.tri.nts(file=file.path(tempdir(), "tmp.nts"), skip=2)
```

`Recode` *Basic multiple recoding*

Description

Basic multiple recoding (similar to the 'SQL' left join)

Usage

```
Recode(var, from, to, char=TRUE, recycle=FALSE)
Recode4(var, from, to, missed="", ...)
RecodeR(var, from, to, char=TRUE, recycle=FALSE)
Recode4R(var, from, to, missed="", ...)
```

Arguments

`var`	Variable to recode
`from`	'from' column of the recoding "table"
`to`	'to' column
`char`	If TRUE (default), do not treat 'to' character vectors as factors
`recycle`	If TRUE (not default), recycle 'to' along 'from'
`missed`	Replace missed (not recoded) with something, default is "" (empty charactrer string)
`...`	Further options to Recode() and RecodeR()

Details

Basic multiple recoding is similar to 'SQL' left join.

Inspired from Paul Johnston (Univ. of Kansas) recode() function.

Alternatives are car::recode(), lessR::Recode(), admisc::recode() and 'mgsub' package. First three are much more complicated, last is much slower and less flexible.

To understand the idea better, please look on the examples.

There are four functions:

1. Recode() – base function. If starting points ("from") are the same, only the *last* rule ("from-to" pair) has an effect. If rules are chained, they still work independently (i.e., chaining has no effect).

2. Recode4() – considers not recoded (missing). By default, this will replace non-Recode()'d entries with empty string ("").

3. RecodeR() – running recode. If starting points ("from") are the same, only the *first* rule ("from-to" pair) has an effect. Chaining is possible.

4. Recode4R() – running plus considers missing. By default, this will replace non-RecodeR()'ed entries with empty string ("").

Value

Recoded vector (note that mode will not necessarily be the same, e.g., when recoding numbers with characters).

Author(s)

Alexey Shipunov

Examples

```
## recoding a phrase
phrase <- "The quick brown fox jumps over 123 lazy dogs"
var <- unlist(strsplit(phrase, split=""))
from <- letters[1:20]
to <- rev(from)
Recode.result <- paste(Recode(var, from, to), collapse="")
Recode4.result <- paste(Recode4(var, from, to, missed="-"), collapse="")
RecodeR.result <- paste(RecodeR(var, from, to), collapse="")
Recode4R.result <- paste(Recode4R(var, from, to, missed="-"), collapse="")
from.rule <- paste(from, collapse=" ")
to.rule <- paste(to, collapse=" ")
rbind(from.rule, to.rule, phrase, Recode.result, Recode4.result, RecodeR.result, Recode4R.result)

## reverse complement of DNA sequence
dna <- "GAATTC" # EcoR1 palindromic sequence
paste(Recode(rev(strsplit(dna, NULL)[[1]]),
 c("A", "T", "G", "C"), c("T", "A", "C", "G")), collapse="") # = 'dna', as expected
dna <- "ATTCGGC" # something random
paste(Recode(rev(strsplit(dna, NULL)[[1]]),
 c("A", "T", "G", "C"), c("T", "A", "C", "G")), collapse="")

## Recode4() when value recoded to itself
Recode4(1:5, 1:4, c(2, 1, 3, 3), NA)
Recode4(1:5, 1:4, c(2, 1, 3, 3))

## this is how "char" option works
Recode(1, 1, factor(2), char=FALSE)
Recode(1, 1, factor(2))

## this is how "recycle" option works
Recode(1:3, 1:3, 4)
Recode(1:3, 1:3, 4, recycle=TRUE)
```

Root1 *Roots phylogenetic trees even if outgroup is not monophyletic*

Description

Root1 non-interactively reroots a phylogenetic tree with respect to the specified outgroup even if it is not monophyletic.

Usage

```
Root1(phy, outgroup, select=1, ...)
```

Arguments

phy	An object of class "phylo".
outgroup	A vector of mode numeric or character specifying the new outgroup.
select	Which element of outgroup to select if it is not monophyletic.
...	Arguments passed to ape::root().

Details

This is a wrapper of ape::root() to use in non-interactive mode. If specified outgroup is not monophyletic, instead of error, it issues error _message_, and chooses the 'select' element as a new outgroup.

Value

An object of class "phylo"

Author(s)

Alexey Shipunov

See Also

ape::root

Examples

```
data(bird.orders, package="ape")
ape::root(bird.orders, 1:2)
## ape::root(bird.orders, 1:3) # gives error
Root1(bird.orders, 1:3) # only outputs error _message_
Root1(bird.orders, 1, resolve.root=TRUE)
```

`Rostova.tbl` *Calculates multiple correlation matrices (via 'factor1') and stacks them together*

Description

Calculates multiple correlation matrices (via 'factor1') and stacks them together

Usage

```
Rostova.tbl(X, GROUP, ...)
```

Arguments

`X`	Data frame or matrix with values
`GROUP`	Number of grouping variable
`...`	Arguments to 'Cor.vec()'

Details

Calculates multiple correlation matrices (via GROUP) and stacks them together.

Output is suitable for PCA, distance calculations and other multivariate methods (Rostova, 1999).

Value

Data frame with correlation structure

Author(s)

Alexey Shipunov

References

Rostova N.S. 1999. The variability of correlations systems between the morphological characters. Part 1. Natural populations of Leucanthemum vulgare (Asteraceae). Botanicheskij Zhurnal. 84(11): 50–66.

See Also

`Cor.vec`

Examples

```
Trees <- trees
Trees[, 4] <- sample(letters[1:3], nrow(Trees), replace=TRUE)
Rostova.tbl(Trees, 4)
```

Rows *Select rows from data frame*

Description

Selects rows from data frame basing on logical on the evaluation of the second argument

Usage

```
Rows(df, ...)
```

Arguments

df	Data frame to select from
...	Arguments to with(df, ...)

Details

If the first argument is not a data frame, function will stop with error.

Rows() is similar to dplyr::filter() function.

Please avoid using Rows() in non-ineractive mode.

Value

Data frame

Author(s)

Alexey Shipunov

Examples

```
`[`(trees, 3, 1) # ... so square bracket is a command
## arguments of `[` are independent; this is why square bracket does not "catch" the context:
trees[trees$Girth < 11 & trees$Height == 65, ] # boring and long
trees[trees$Girth < 11 & sample(0:1, nrow(trees), replace=TRUE), ] # yes, boring, long but flexible
trees[with(trees, Girth < 11 & Height == 65), ] # less boring but still long
## it would be nice to avoid typing "trees" twice:
Rows(trees, Girth < 11 & Height == 65) # shorter
Rows(trees, Girth < 11 & sample(0:1, nrow(trees), replace=TRUE)) # flexibility is still here
Rows(trees, Girth < 11 & sample(0:1, nrow(trees),
 replace=TRUE))$Height # if you want also select columns
Rows(trees, grep(81, Height)) # select not only by TRUE/FALSE but also by row index
```

Rpart2newick *Converts 'rpart' object into Newick tree*

Description

Converts 'rpart' object into Newick tree

Usage

```
Rpart2newick(rpart.object)
```

Arguments

rpart.object	'rpart' object, output of rpart::rpart()

Details

Inspired by 'shaunpwilkinson/rpart2dendro.R' gist.

Value

Newick tree (text string).

Examples

```
library(rpart)
(fit <- rpart(Kyphosis ~ Age + Number + Start, data=kyphosis))
plot(fit); text(fit, all=TRUE)
library(ape)
tree1 <- read.tree(text=Rpart2newick(fit))
plot(tree1)
nodelabels(tree1$node.label, frame="none", bg="transparent", adj=-0.1)

(fit2 <- rpart(Species ~ ., data=iris))
plot(fit2); text(fit2, all=TRUE)
tree2 <- read.tree(text=Rpart2newick(fit2))
plot(tree2)
nodelabels(tree2$node.label, frame="none", bg="transparent", adj=-0.1)
```

Rresults *Rresults shell script*

Description

Rresults shell script

Details

'Rresults' is a bash shell script which allows to gather all R input and R textual output in one text file, and (unnamed) R graphical output in another (PDF) file (only if the 'pdftk' utility is installed). If graphical output has name(s), it will be saved in its own file(s).

Very good for the debugging and other non-interactive activities with R scripts as everything is one place.

The script has one option "-d" which adds the timestamp to the file name of text results.

Author(s)

Alexey Shipunov

Examples

```
## works only if the script is properly installed
cat("\"Hello, world!\"\n", "plot(1:20)\n", file="hello.r")
system("Rresults hello.r")
system("Rresults -d hello.r")
## interactive command
file.show("hello_rresults.txt")
```

Rro.test *Robust rank order test*

Description

Robust rank order test

Usage

```
Rro.test(x1, y1)
```

Arguments

x1	Fist numerical variable
y1	Second numerical variable

Details

Robust rank order test (modification of Wilcoxon test for samples with contrasting variation)

It is a variant of Fligner-Policello test.

Possible alternatives: 'robustrank::mod.wmw.test()'; 'npsm::fp.test()'; 'NSM3::pFligPoli()'; 'RVAideMemoire::fp.test()'.

Value

Returns z statistic and p-value.

Author(s)

Alexey Shipunov

Examples

```
## data from help(wilcox.test)
x <- c(0.80, 0.83, 1.89, 1.04, 1.45, 1.38, 1.91, 1.64, 0.73, 1.46)
y <- c(1.15, 0.88, 0.90, 0.74, 1.21)
Rro.test(x, y)
```

S.value *S-value*

Description

`S.value` returns S-values, Shannon information transforms of p-values.

Usage

```
S.value(x)
```

Arguments

`x`	Either numerical vector of p-values, or list where at least one element has the name similar to "p.value".

Details

Greenland (2019) proposes that researchers "think of p-values as measuring the _compatibility_ between hypotheses and datas." S-values should help to understand this concept better.

From Wasserstein et al. (2019): S-values supplement a focal p-value p with its Shannon information transform (s-value or surprisal) s = -log2(p). This measures the amount of information supplied by the test against the tested hypothesis (or model): rounded off, the s-value shows the number of heads in a row one would need to see when tossing a coin to get the same amount of information against the tosses being "fair" (independent with "heads" probability of 1/2) instead of being loaded for heads. For example, if p = 0.03, this represents -log2(0.03) = 5 bits of information against the

hypothesis (like getting 5 heads in a trial of "fairness" with 5 coin tosses); and if p = 0.25, this represents only -log2(0.25) = 2 bits of information against the hypothesis (like getting 2 heads in a trial of "fairness" with only 2 coin tosses).

For the convenience, S.value() works directly with output of many statistical tests (see examples). If the output is a list which has more than one component with name similar to "pvalue", only first will be used.

Value

Numerical vector.

Author(s)

Alexey Shipunov

References

Wasserstein R.L., Schirm A.L., Lazar N.A. 2019. Moving to a World Beyond "p < 0.05". The American Statistician. 73(S1): 1–19.

Greenland S. 2019. Valid P-Values Behave Exactly as They Should: Some Misleading Criticisms of P-Values and Their Resolution With S-Values. The American Statistician. 73(S1): 106–114.

Examples

```
S.value(0.05)

S.value(0.01)
S.value(0.1)
S.value(0.00000000001)

S.value(t.test(extra ~ group, data = sleep))
S.value(list(pvalues=c(0.01, 0.002)))
```

`salix_leaves` *salix_leaves*

Description

Morphometry on willows (Salix).

Three files (datasets): 'salix_pop' localities, 'salix_plants' measures on whole plants, 'salix_leaves' measures on leaves from from these plants.

Usage

```
salix_leaves
```

Format

These data frames contain the following columns:

`POP` Location ID

`WHERE` Geography

`SPECIES` Species

`PLN` Plant ID

`HEIGHT` Height, m

`SEX` Plant sex (willows are dioeciuos)

`PID` Shoot ID

`N.CIRCLES` Number of circles of the imaginary spiral between two leaves (below)

`N.LEAVES` Number of leaves between the chosen one and the next in the same position

`INTERNODE` Internode length, average, mm

`DIAM` Stem diameter in the middle of shoot, mm

`NL` Leaf ID

`LL` Maximal length of the leaf, mm (along midvein from blade basement to blade top)

`LW` Maximal width of the leaf, mm

`PW` Position of maximal width, mm (along midvein)

`PTL` Length of the petiole, mm (from the place of attachment to blade base)

`STPL` Stipules present?

`SL` Maximal width of maximal stipule, mm (0 if no stipule present)

`SW` Maximal width of maximal stipule, mm (0 if no stipule present)

`TL` Length of maximal marginal tooth, mm (0 in no teeth)

`ADC` Color of the adaxial (upper) leaf surface: 1 glaucous, 2 other shades of green

`ABC` Color of the abaxial (lower) leaf surface: 1 glaucous, 2 other shades of green

`ADP` Pubescence of the adaxial (upper) leaf surface under magnification: 1 absent, 2 rare (epidermis surface visible), 3 dense (epidermis surface is not visible or barely visible)

`ABP` Pubescence of the abaxial (lower) leaf surface under magnification: 1 absent, 2 rare (epidermis surface visible), 3 dense (epidermis surface is not visible or barely visible)

`Saynodynamite` *Say "no" to dynamite plots!*

Description

Say "no" to dynamite plots!

Usage

```
Saynodynamite()
```

Details

'Poster' plot to emphasize the harmfulness of so called dynamite plots.

See, for example, thorough analysis at "http://emdbolker.wikidot.com/blog%3Adynamite".

Author(s)

Alexey Shipunov

See Also

boxplot

Examples

```
Saynodynamite()
```

Squares *Polygons' squares*

Description

Polygons' squares

Usage

```
Squares(ppts, relative=FALSE)
```

Arguments

ppts	Hulls information (e.g., output from 'Hulls()')
relative	Calculate relative squares?

Details

Calculates polygons' squares (requires 'PBSmapping' package).

Value

Numerical vector of squares

Author(s)

Alexey Shipunov

See Also

Hulls

Examples

```
iris.pca <- prcomp(iris[, 1:4], scale=TRUE)
iris.p <- iris.pca$x[, 1:2]
iris.h <- Hulls(iris.p[, 1:2], as.numeric(iris[, 5]), plot=FALSE)
iris.o <- Squares(iris.h, relative=TRUE)
```

`Str` *'str()' enchanced for data frames*

Description

Enhanced 'str()': with variable numbers, row names and missing data indication

Usage

```
Str(df)
```

Arguments

`df`	Data frame

Details

'Str()' is an enhanced 'str()'. If the object is a data frame with atomic columns, this function captures output of internal 'str()', changes it and outputs the new one.

If the object is not a data frame or is a data frame with non-atomic columns, then output is not changed.

'Str()' (1) shows data frame structure with column indexes, (2) indicates presence of NA(s) with star (*) and (3) lists first five row names, if they are not default.

'Str()' does not work (therefore, passes everything back to common 'str()') with data frames which have non-atomic columns (fortunately, rare case).

Alternative: DescTools::Str() which uses cycles (slower!), has less features, but works with non-atomic columns.

Author(s)

Alexey Shipunov

See Also

`str`, DescTools::`Str`

Examples

```
trees1 <- trees
row.names(trees1)[1] <- "a"
trees1[1, 1] <- NA
Str(trees)
Str(trees1)
## Not run:
trees.crazy <- trees
trees.crazy[[2]] <- trees[, 2, drop=FALSE]
Str(trees.crazy) # does not work with these crazy objects

## End(Not run)
```

Table2df *Convert table to data frame saving structure*

Description

Convert table to data frame saving structure

Usage

```
Table2df(table)
```

Arguments

table	'table' object

Details

Convert contingency table into data frame and keep structure.

Value

Data frame

Author(s)

Alexey Shipunov

Examples

```
Table2df(table(iris[, 5]))
```

Tobin *Binarize (make dummy variables)*

Description

Converts vector into matrix with binary columns

Usage

```
Tobin(var, convert.names=TRUE)
```

Arguments

var	character or numerical variable
convert.names	if TRUE (default), construct new variable names, otherwise, use unique variable values as variable names

Details

'Tobin()' transforms character or numeric vector into the matrix with 0/1 (absent/present) cells.

Two approaches are in use: through '==' operation and through the conversion into factor.

First approach also constructs new names of variables whereas the second ('convert.names=FALSE') makes variable names from names of factor levels (i.e., labels).

Alternatives: "*dumm*" packages (there are few in CRAN).

Value

Matrix with binary columns

Author(s)

Alexey Shipunov

Examples

```
(ee <- sample(letters[1:5], 10, replace=TRUE))
Tobin(ee, conv=FALSE)
Tobin(ee, conv=TRUE)
```

`Toclip` *Insert content to Linux X11 clipboard*

Description

Insert content to Linux X11 clipboard (uses 'xclip')

Usage

```
Toclip(x, sep="\t", row.names=FALSE, col.names=TRUE, ...)
```

Arguments

`x`	Data frame
`sep`	Separator, tab by default
`row.names`	FALSE by default
`col.names`	TRUE by default
`...`	Arguments to 'write.table()'

Details

Linux-specific. Inserts data frame to Linux X11 clipboard (not primary or secondary). Useful for interface with spreadsheets.

Works if 'xclip' utility is already installed.

Alternative with more flexibility: 'clipr' package.

Author(s)

Alexey Shipunov

Examples

```
## Not run:
aa <- data.frame(1:3) # Linux- (and X11-) specific
Toclip(aa) # then load the content into spreadsheet

## End(Not run)
```

Topm *Stacks correlation matrix*

Description

Stacks (correlation) matrix and selects values which are above the “level”

Usage

```
Topm(X, level=0.45, values=0, corr=TRUE, square=TRUE)
```

Arguments

X	Data frame or matrix with values
level	Threshold
values	If > 0, ignores "level" and outputs until reaches number, if "all", outputs all values
corr	If FALSE, does not show magnitude
square	If FALSE, does not use lower triangle, some rows could be redundant

Details

’Topm()’ stacks (correlation) matrix and selects (and sorts) values which are above the “level”.

Good for the analysis of correlation matrices.

Value

Data frame with correlation values

Author(s)

Alexey Shipunov

See Also

Cor

Examples

```
Topm(cor(trees), corr=TRUE)
```

Updist *Educated distances for semi-supervised clustering*

Description

Updates distance matrix to help link or unlink objects

Usage

```
Updist(dst, link=NULL, unlink=NULL, dmax=max(dst), dmin=min(dst))
```

Arguments

dst	dist object
link	1-level list with the arbitrary number of components, each component is a numeric vector of row numbers for objects which you prefer to be linked
unlink	1-level list with the arbitrary number of components, each component is a numeric vector of row numbers for objects which you prefer to be not linked
dmax	Distance to set for not linked objects
dmin	Distance to set for linked objects

Details

This function borrows the idea of MPCKM semi-supervised k-means (Bilenko et al., 2004) but instead of updating distances on the run, it simply updates the distances object beforehand in accordance with 'link' and 'unlink' constraints.

Amazingly, it works as expected :) Please see the examples below.

References

Bilenko M., Basu S., Mooney R.J. 2004. Integrating constraints and metric learning in semi-supervised clustering. In: Proceedings of the twenty-first international conference on Machine learning. P. 11. ACM.

See Also

dist

Examples

```
iris.d <- dist(iris[, -5])
iris.km <- kmeans(iris.d, 3)
iris.h <- cutree(hclust(iris.d, method="ward.D"), k=3)

Misclass(iris.km$cluster, iris$Species, best=TRUE)
Misclass(iris.h, iris$Species, best=TRUE)
```

```
i.vv <- cbind(which(iris$Species == "versicolor"), which(iris$Species == "virginica"))
i.link <- list(sample(i.vv[, 2], 25), sample(i.vv[, 1], 25))
i.unlink <- list(i.vv[1, ], i.vv[2, ])

iris.upd <- Updist(iris.d, link=i.link, unlink=i.unlink)

iris.ukm <- kmeans(iris.upd, 3)
iris.uh <- cutree(hclust(iris.upd, method="ward.D"), k=3)

Misclass(iris.ukm$cluster, iris$Species, best=TRUE)
Misclass(iris.uh, iris$Species, best=TRUE)

## ===

aad <- dist(t(atmospheres))
plot(hclust(aad))

aadu <- Updist(aad, unlink=list(c("Earth", "Mercury")))
plot(hclust(aadu))
```

`VTcoeffs` *Effect sizes of association between categorical variables*

Description

Effect sizes of association between categorical variables

Usage

```
VTcoeffs(table, correct=FALSE, ...)
```

Arguments

`table`	Contingency table
`correct`	Perform continuity correction in underlying chi-square test?
`...`	Additional arguments to underlying chisq.test()

Details

Association between categorical variables.

Calculates Cramer's V and Tschuprow's, original and corrected (Bergsma, 2013)

Alternative: vcd::assocstats()

Includes magnitude interpretation for original Cramer's V (for df < 6).

Value

Data frame with coefficients, values and tables.

Author(s)

Alexey Shipunov

Examples

```
x <- margin.table(Titanic, 1:2)
VTcoeffs(x)
VTcoeffs(x)[2, ] # most practical
```

Write.fasta *Write 'FASTA' files*

Description

Simple writing of 'FASTA' files

Usage

```
Write.fasta(df, file)
```

Arguments

df	Name of data frame
file	File name

Details

Simple writing of 'FASTA' files. If the data frame has more then two columns, only two first columns will be used (with warning).

Value

'FASTA' file on the disk.

Author(s)

Alexey Shipunov

Examples

```
ff <- data.frame(one="some_id", two="ATGC", three="something else")
Write.fasta(ff, file=file.path(tempdir(), "tmp.fasta")) # warning will be produced
file.show(file=file.path(tempdir(), "tmp.fasta")) # interactive
```

`Xpager` *Separate terminal pager for Linux*

Description

Separate terminal pager for Linux X11 (uses some terminal and 'less')

Usage

```
Xpager(pager="xterm")
```

Arguments

`pager`	name of the terminal application to use, or "old" for the default

Details

Linux pager in the new terminal window. 'xterm' is default, there is also setting for 'mate-terminal'; 'konsole' (KDE terminal) and 'gnome-terminal' are easy to add.

Run Xpager("old") to restore default behavior.

BTW, for some reason, 'editor()' does not work this way.

Author(s)

Alexey Shipunov

Examples

```
## Linux- (and X11-) specific
Xpager()
?help
Xpager("old")
?help
```

`%-%` *Minus names*

Description

Subtract names from names

Usage

```
x %-% y
```

Arguments

x	Character vector (likely named) to subtract from
y	Subtracting character vector

Details

Instead of 'x', the function uses 'names(x)'. If 'x' has no names, they will be assigned from values.

Value

Character vector

Author(s)

Alexey Shipunov

Examples

```
str(iris[, iris %-% "Species"])
str(iris[, !names(iris) %in% "Species"]) # this is how to make it without %-%
c("apples", "bananas") %-% c("apples") # simple character string also works
```

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