Package 'pgirmess'

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Title Spatial Analysis and Data Mining for Field Ecologists

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Imports boot (>= 1.3-4), sf (>= 1.0-4), sp (>= 0.9-97), spdep (>= 1.1-7)

Suggests MASS (>= 7.3-1), nlme (>= 3.1-120)

Description Set of tools for reading, writing and transforming spatial and seasonal data, model selection and specific statistical tests for ecologists. It includes functions to interpolate regular positions of points between landmarks, to discretize polylines into regular point positions, link distant observations to points and convert a bounding box in a spatial object. It also provides miscellaneous functions for field ecologists such as spatial statistics and inference on diversity indexes, writing data.frame with Chinese characters.

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URL https://github.com/pgiraudoux/pgirmess

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Contents

bbox2sf *Convert a bounding box into a sf object.*

Description

Convert a bounding box into a sf object.

Usage

```
bbox2sf(n,s,w,e,bbox=NA,crs=4326)
```

Arguments

n	the top north latitude
s	the bottom south latitude
w	the most western longitude
e	the most eastern longitude
bbox	a bounding box 2 x 2 matrix as produced e.g. by bbox, with first row = w, e and second row = s, n, or a numeric vector with xmin, ymin, xmax, ymax in this order as produced by st_bbox
crs	the ID number of a coordinate reference system as defined in the EPSG system https://epsg.io/ (default 4326, WGS84)

Details

This function converts a set of coordinates limiting a bounding box into a an object of class "sfc_POLYGON" (see st_sfc). It can be used for instance to clip a subset of a larger spatial object (e.g. using st_intersection)

Value

A simple feature geometry of class "sfc_POLYGON" with a coordinate reference system, see st_sfc.

Examples

```
n<-79
s<--54
w<--166
e<-178


myPoly1<-bbox2sf(n,s,e,w)
plot(myPoly1)

# bbox as a 2 x 2 matrix as produced by sp:bbox
mybbox<-matrix(c(w,e,s,n),nrow=2,byrow=TRUE)
```

```
myPoly2<-bbox2sf(bbox=mybbox)
plot(myPoly2,border="red")

# bbox as produced by sf:st_bbox
if (require(sf)) {
myPoly3<-bbox2sf(bbox=st_bbox(myPoly2))
plot(myPoly3,border="blue")
}
```

CI *Confidence interval of percentages*

Description

Computes the lower limit and upper limit of the 95 percent confidence interval of percentage estimates

Usage

```
CI(x, ...)
```

Arguments

x	a two-dimensional table, matrix or data.frame with 2 columns, giving the counts of successes and failures, respectively
...	other arguments to pass to prop.test, eg conf.level

Details

Simple wrapper of prop.test. The default confidence interval is 95 percent, but can be modified passing values to prop.test by the conf.level argument.

Value

A 3 column matrix.

- Column 1: percentage estimate
- Column 2: lower limit of the confidence interval
- column 3: upper limit of the confidence interval

See Also

prop.test

Examples

```
x<-c(2,10,7,8,7) # eg: number of positive cases
y<-c(56,22,7,20,5)# eg: number of negative cases
CI(cbind(x,y))
CI(cbind(x,y), conf.level=0.99)
```

`classnum` *Gives an index vector of the class category of each value of a numerical vector*

Description

Gives an index vector of the class category of each value of a numerical vector

Usage

```
classnum(x, breaks = "Sturges")
```

Arguments

`x`	a vector of values for which the indices are desired
`breaks`	one of: • a vector giving the breakpoints between bins, • a single number giving the number of bins, • a character string naming an algorithm to compute the number of cells (see Details).

Details

The default for 'breaks' is '"Sturges"': see 'nclass.Sturges'. Other names for which algorithms are supplied are '"Scott"' and '"FD"' for '"Friedman-Diaconis"' (with corresponding functions 'nclass.scott' and 'nclass.FD'). Case is ignored and partial matching is used. Breaks and labels are stored as attributes.

Value

A vector of the same length as x, with the index of the class which each value of x belongs to

See Also

`cut`, `classIntervals`

Examples

```
x<-rnorm(30)
classnum(x)
classnum(x,breaks="fd")
classnum(x, breaks=c(-1,0,1))
classnum(x,breaks=5)
```

`cormat` *Gives a correlation matrix and the probability of Ho for each correlation*

Description

Gives a correlation matrix and the probability of Ho for each correlation estimate

Usage

```
cormat(donnees, method = "spearman", sep = FALSE)
```

Arguments

`donnees`	a data frame of numerics
`method`	a string of characters among 'pearson', 'spearman' (default), 'kendall'
`sep`	If true, gives the results in two matrices (default = F)

Details

Wrapper for 'cor' and 'cor.test'. The results can be given in one or two matrices.

Value

If sep = F (default) a list including:

`method`	The method used
`prob.cor`	Upper triangle, the correlations; lower triangle, the probability of Ho

If sep = T a list including:

`method`	The method used
`coef.estimates`	The correlation matrix
`p.value`	The Ho probability matrix

See Also

`cor`, `cor.test`

Examples

```
cormat(longley)
cormat(longley,sep=TRUE)
```

correlog *Computes Moran's or Geary's coefficients on distance classes*

Description

Computes Moran's or Geary's coefficients on distance classes from a set of spatial coordinates and corresponding z values

Usage

```
correlog(coords, z, method="Moran", nbclass = NULL,...)
```

Arguments

coords	a two columns array, data.frame or matrix of spatial coordinates. Column 1 = X, Column 2 = Y.
z	a vector for the values at each location. Must have the same length as the row number of coords
method	the method used. Must be "Moran" (default) or "Geary"
nbclass	number of bins. If NULL Sturges method is used to compute an optimal number
...	further arguments to pass to e.g. moran.test or geary.test

Details

Uses the library spdep including moran.test or geary.test. Distances are euclidian and in the same unit as the spatial coordinates. Moran's Ho: I values larger than 0 due to chance; Geary's Ho: C values lesser than 1 due to chance. Correlog has print and plot methods; statistically significant values ($p<0.05$) are plotted in red.

Value

An object of class "correlog", a matrix including:

class	bin centers
I	the coefficient values
p.value	probability of Ho
n	the number of pairs

Warning

Computing can take a long time for large data sets

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References

see library spdep

See Also

geary.test, moran.test

Examples

```
library(spdep)
data(oldcol)
attach(COL.OLD)
coords<-cbind(X,Y)
res<-correlog(coords,CRIME)
plot(res)

res<-correlog(coords,CRIME,method="Geary")
plot(res)
```

---

date2winter *Convert a POSIXt date into categories corresponding to a autumn/winter/spring sequence*

Description

Convert a POSIXt date into categories corresponding to the time spanning from the late months of a year to the early months of the following year

Usage

```
date2winter(x, first = 10, last=4)
```

Arguments

x	a vector of POSIXt dates
first	number of the first month to include (default 10, October)
last	number of the last month to include (default 4, April)

Details

In ecology, time data must often be analysed on a time span category covering two successive years (e.g. the winter period). This function convert POSIXt dates into categories corresponding to the time span stretching from a user defined month of a given year (by default October) to a user-defined month of the following year (by default April). If date month is out of the user defined time span the value 'Excluded' is returned.

Value

A vector of the same length as x, with the time span category each value belongs to.

Examples

```
dates <- strptime(c("02/12/2002", "15/01/2003","15/10/2003","15/6/2003",NA),"%d/%m/%Y")
date2winter(dates)
```

---

diag2edge *Computes the edge of a square from its diagonal*

Description

Computes the edge of a square from its diagonal.

Usage

```
diag2edge(cordseg)
```

Arguments

cordseg	The diagonal coordinates. This can be a vector c(x1,y1,x2,y2), a 2 x 2 matrix or a data.frame (each line a coordinate)

Details

The first point coordinates are the left top of the diagonal. The other coordinates computed are the other top of the square edge. Can be used e.g. to pass a square edge to pave in order to compute a sampling grid.

Value

A 2x2 matrix of points coordinates

See Also

pave

Examples

```
# diagonal sloping up
coord<-matrix(c(20,20,90,90),nr=2,byrow=TRUE)
plot(coord,type="n",xlim=c(0,100),ylim=c(0,110),asp=1)
lines(coord,lty=2)
# square edge
lines(diag2edge(coord),col="red")

# diagonal sloping down
coord<-matrix(c(20,90,90,20),nr=2,byrow=TRUE)
```

```
plot(coord,type="n",xlim=c(0,100),ylim=c(0,110),asp=1)
lines(coord,lty=2)
# square edge
lines(diag2edge(coord),col="red")

# diagonal vertical
coord<-matrix(c(20,90,20,20),nr=2,byrow=TRUE)
plot(coord,type="n",xlim=c(0,100),ylim=c(0,110),asp=1)
lines(coord,lty=2)
# square edge
lines(diag2edge(coord),col="red")
```

`difshannonbio` *Empirical confidence interval of the bootstrap of the difference between two Shannon indices*

Description

Computes the empirical confidence interval of the bootstrap of the difference between two Shannon indices

Usage

```
difshannonbio(dat1, dat2, R = 1000, probs = c(0.025, 0.975))
```

Arguments

`dat1`	a data.frame of two columns; column = category, column 2 = biomass
`dat2`	a data.frame of two columns; column = category, column 2 = biomass
`R`	number of permutations
`probs`	the limits of the confidence interval

Details

Designated to compare the difference between two Shannon's indices computed from two data frames. In each data frame, the first column is the category of prey item, and the second column the estimated biomass.

Value

A list with the confidence interval of H' and J'

See Also

`shannonbio`

Examples

```
data(preybiom)
attach(preybiom)
jackal<-preybiom[site=="Y" & sp=="C",5:6]
genet<-preybiom[site=="Y" & sp=="G",5:6]

difshannonbio(jackal,genet,R=150)
```

---

dirProj *Computes new coordinates given bearings and distances.*

Description

Computes new coordinates from bearings (North = 0) and distances

Usage

```
dirProj(df,deg=TRUE)
```

Arguments

df	a matrix or data frame of 4 columns giving x, y coordinates, bearings and distances
deg	if TRUE (default) bearings are in degree, otherwise in radian

Details

Computings are based on euclidian distance. Therefore, the coordinates should be given in a projected (plan) system (e.g. UTM, Lambert, etc.) and the distance in the same units as the projection system (e.g. meters).

Value

a matrix of two columns with the projected coordinates

See Also

distSeg

Examples

```
df<-data.frame(x1=0,y1=0,alpha=runif(3,0,360),d=runif(3,0,1))
df
plot(-1:1,-1:1,type="n")
points(0,0,pch=19)
points(dirProj(df))
text(dirProj(df)[,1],dirProj(df)[,2],1:3,pos=4)
```

dirSeg *Computes segment directions.*

Description

Computes the direction of segments from the first top clockwise (North = 0)

Usage

```
dirSeg(x,deg=TRUE)
```

Arguments

x	a matrix or data frame of 4 columns giving the coordinates of each segment tops x1, y1, x2, y2
deg	if TRUE (default) the output is in degrees, otherwise in radians

Details

The first two colomns give the first top coordinates, x then y, and the next two the second top coordinates.

Value

A vector of directions

See Also

dirProj

Examples

```
x2<-rnorm(10)
y2<-rnorm(10)
mydata<-cbind(0,0,x2,y2)
dirs<-dirSeg(mydata)
dirs

plot(range(mydata[,c(1,3)]),range(mydata[,c(2,4)]),type="n")
Segments(mydata)
text(mydata[,3],mydata[,4],paste(round(dirs,0),"\u00b0"),cex=0.7)
```

distNNeigh *Computes distances to the nearest neighbour*

Description

Computes distances to the nearest neighbour

Usage

```
distNNeigh(db)
```

Arguments

db	A matrix or data.frame of points coordinates column 1 = x,column 2 = y.

Details

Computes distances to the nearest neighbour for each line of a matrix of points coordinates

Value

A vector of distances

See Also

knearneigh, knn2nb, nbdists

Examples

```
distNNeigh(cbind(rnorm(30),rnorm(30)))
```

distNode *Computes the distances between each nodes of a polyline.*

Description

Computes the distances between each nodes of a polyline.

Usage

```
distNode(pts,decdeg=FALSE)
```

Arguments

pts	A matrix or data.frame of the node coordinates column 1 = x,column 2 = y.
decdeg	TRUE if point coordinates are longitude-latitude decimal degrees, in which case distances are measured in meters

Details

If degdec is FALSE (default), distance computed is Euclidian. Units depends on the coordinate systems. If decdeg = TRUE, D = 1852 * 60 * (180/pi) * acos (sin(la1) * sin(la2) + cos(la1) * cos(la2) * cos(abs(lg1 - lg2)). This method calculates the great circle distance, is based on spherical trigonometry, and assumes that:

- 1 minute of arc is 1 nautical mile
- 1 nautical mile is 1.852 km

Value

A vector of distances

See Also

distTot, distSeg

Examples

```
x<-c(10,56,100)
y<-c(23,32,150)
distNode(cbind(x,y))
```

`distSeg` *Computes distances between the top coordinates of segments.*

Description

Computes the distances between the top coordinates of segments.

Usage

```
distSeg(mydata,decdeg=FALSE)
```

Arguments

`mydata`	A matrix or data frame of 4 columns giving the coordinates of each segment tops x1, y1, x2, y2
`decdeg`	TRUE if point coordinates are longitude-latitude decimal degrees, in which case distances are measured in meters

Details

If degdec is FALSE (default), distance computed is Euclidian. Units depends on the coordinate systems. If decdeg = TRUE, D = 1852 * 60 * (180/pi) * acos (sin(la1) * sin(la2) + cos(la1) * cos(la2) * cos(abs(lg1 - lg2)). This method calculates the great circle distance, is based on spherical trigonometry, and assumes that:

- 1 minute of arc is 1 nautical mile
- 1 nautical mile is 1.852 km

When computing with decdeg=TRUE duplicated coordinates strictly identical can lead to produce NaN. The corresponding distance is coerced to zero with warnings and if so, an attribute 'NaNcoerced2zero' with the row numbers of the distances that have been coerced to zero is created

Value

A vector of distances, possibly with the attribute 'NaNcoerced2zero' with the row numbers of the distances that have been coerced to zero if any.

See Also

distNode, distTot

Examples

```
x1<-rnorm(20)
y1<-rnorm(20)
x2<-rnorm(20)
y2<-rnorm(20)
mydata<-cbind(x1,y1,x2,y2)
distSeg(mydata)
```

---

distTot *Computes the total length of a polyline.*

Description

Computes the total length of a polyline.

Usage

```
distTot(pts,decdeg=FALSE)
```

Arguments

pts	A matrix or data.frame of the node coordinates column 1 = x,column 2 = y.
decdeg	TRUE if point coordinates are longitude-latitude decimal degrees, in which case distances are measured in meters

Details

If degdec is FALSE (default), distance computed is Euclidian. Units depends on the coordinate systems. If decdeg = TRUE, D = 1852 * 60 * (180/pi) * acos (sin(la1) * sin(la2) + cos(la1) * cos(la2) * cos(abs(lg1 - lg2)). This method calculates the great circle distance, is based on spherical trigonometry, and assumes that:

- 1 minute of arc is 1 nautical mile
- 1 nautical mile is 1.852 km

Value

A numeric distance.

See Also

, distNode, distSeg

Examples

```
x<-c(10,56,100)
y<-c(23,32,150)
distTot(cbind(x,y))
```

---

expandpoly *Homothetia (size expansion) of a polygon*

Description

Compute the new coordinates of polygon expanded by a factor.

Usage

```
expandpoly(mypol, fact)
```

Arguments

mypol	matrix or data.frame of polygon coordinates
fact	expansion factor

Details

The polygon area obtained after expansion is equal to $fact^2$ times the original polygon area

Value

A matrix of polygon coordinates

See Also

polygon

Examples

```
x<-c(-5,-4.5,0,10,5)
y<-c(-10,0,5,5,-8)
poly<-cbind(x,y)
plot(-10:20,-20:10,type="n")
polygon(poly)
polygon(expandpoly(poly,1.5),border="red")
polygon(expandpoly(poly,0.5),border="blue")
```

---

findR *Computes the distance between the centroid and the most distant coordinate of a geographical coordinate set*

Description

Computes the distance between the centroid and the most distant coordinate of a geographical coordinate set.

Usage

```
findR(coords)
```

Arguments

coords	A matrix or data frame of 2 columns of geographical coordinates

Value

The distance

See Also

polycirc

Examples

```
mydata<-cbind(x=rnorm(20),y=rnorm(20))
radius<-findR(mydata)
centroid<-matrix(colMeans(mydata),ncol=2)
plot(mydata,asp=1)
points(centroid,pch=19,col="red",cex=2)
polygon(polycirc(radius,centroid),border="red")
```

`friedmanmc` *Multiple comparisons after Friedman test*

Description

Test of multiple comparison after Friedman test

Usage

```
friedmanmc(y, groups, blocks,alpha=0.05)
```

Arguments

`y`	a numeric vector of data values, or a data matrix
`groups`	a vector giving the group for the corresponding elements of 'y' if this is a vector; ignored if 'y' is a matrix. If not a factor object, it is coerced to one.
`blocks`	a vector giving the block for the corresponding elements of 'y' if this is a vector; ignored if 'y' is a matrix. If not a factor object, it is coerced to one.
`alpha`	the significiance level

Details

Method for formula still not implemented. Formula 7.5a (Siegel & Castellan, 1988 p 180-181) can lead to p-values larger than 1 when differences between groups are small. Eventually, they are set to NA and a warning is generated.

Value

A list of class 'mc' with the following items:

`statistic`	statistics used
`alpha`	the significance level
`dif.com`	a data.frame with observed and critical differences, statistical significance at the alpha risk (true/false) and p-value

References

Siegel & Castellan (1988) Non parametric statistics for the behavioural sciences. Mc Graw Hill Int. Edt.

See Also

`friedman.test`; for other functions about median multiple comparison see package 'PMCMRplus'

Examples

```
data(siegelp179)
attach(siegelp179)

friedman.test(score,treatment,block)
friedmanmc(score,treatment,block)
friedmanmc(score,treatment,block,alpha=0.01)

mymatrix<-matrix(score,nc=3)
friedman.test(mymatrix)
friedmanmc(mymatrix)
detach(siegelp179)
```

---

kruskalmc *Multiple comparison test after Kruskal-Wallis*

Description

Multiple comparison test between treatments or treatments versus control after Kruskal-Wallis test

Usage

```
kruskalmc(resp,...)
## Default S3 method:
kruskalmc(resp, categ, alpha = 0.05, cont=NULL,...)
## S3 method for class 'formula'
kruskalmc(resp,data=NULL,...)
```

Arguments

resp	a numeric vector of data values or a formula of the type 'response~category'.
categ	a factor object giving the group for the corresponding elements of 'x'
alpha	the significance level
cont	NULL (default) for multiple comparison between treatments; 'one-tailed' or 'two-tailed' for corresponding multiple comparisons treatments versus control; partial matching allowed
data	a data.frame including the variables used in the formula
...	other parameters to be passed as arguments (not used here)

Details

When the value of a Kruskal-Wallis test is significant, it indicates that at least one of the groups is different from at least one of the others. This test helps determining which groups are different with pairwise comparisons adjusted appropriately for multiple comparisons. Those pairs of groups which have observed differences larger than a critical value are considered statistically different

at a given significance level. Three types of multiple comparisons are implemented: comparisons between treatments, 'one-tailed' and 'two-tailed' comparison treatments versus control. The first factor level is considered the control. NAs are omitted from data before processing.

For further details please consider the refence below where the method is fully described, or visit https://giraudoux.pagesperso-orange.fr/#pgirmess where a copy of the corresponding book section can be downloaded.

Value

A list of class 'mc' with the following items:

`statistic`	statistics used
`signif.level`	the significance level
`dif.com`	a data.frame with observed and critical differences

Note

Alternative methods are proposed in the section 'see also', on FranÃ§ois Gillet's suggestion. The three methods do not give necessarily the same results, and the why is still to investigate

References

Siegel and Castellan (1988) Non parametric statistics for the behavioural sciences. MacGraw Hill Int., New York. pp 213-214

See Also

`kruskal.test`; to reorder factor levels see `relevel`; for other functions about median multiple comparison see package 'PMCMRplus'; `kruskal`

Examples

```
resp<-c(0.44,0.44,0.54,0.32,0.21,0.28,0.7,0.77,0.48,0.64,0.71,0.75,0.8,0.76,0.34,0.80,0.73,0.8)
categ<-as.factor(rep(c("A","B","C"),times=1,each=6))
kruskalmc(resp, categ)
kruskalmc(resp, categ, alpha=0.01)
kruskalmc(resp, categ, cont="one-tailed")
kruskalmc(resp, categ, cont="two-tailed")

kruskalmc(resp~categ)
kruskalmc(resp~categ, alpha=0.01)
kruskalmc(resp~categ, cont="one-tailed")
kruskalmc(resp~categ, cont="two-tailed")
```

`ks.gof` *Kolmogorof-Smirnov goodness of fit test to normal distribution*

Description

Kolmogorof-Smirnov goodness of fit test to normal distribution

Usage

```
ks.gof(var)
```

Arguments

`var`	a numeric vector

Details

A wrapper of ks.test()

Value

A list with class '"htest"' containing the following components:

`statistic`	the value of the test statistic.
`p.value`	a character string indicating what type of test was performed.
`alternative`	a character string describing the alternative hypothesis.
`method`	a character string indicating what type of test was performed.
`data.name`	a character string giving the name(s) of the data.

References

see ks.test

See Also

`ks.test`

Examples

```
x<-rnorm(50)
ks.gof(x)
```

`mergeTrackObs` *Count the nearest observations to points corresponding to track intervals*

Description

Count the nearest observations to points corresponding to track intervals (e.g. observation counts along a road discretized into points).

Usage

```
mergeTrackObs(sppdfInt,sppdfObs,obscol=NULL)
```

Arguments

`sppdfInt`	`sfc` object containing points (POINT) (the track)
`sppdfObs`	`sfc` object containing points (POINT) (the observations)
`obscol`	The column number in which the number of observations at this point can be found in sppdfObs, if any (default=NULL, no such data)

Details

Road side counts and faeces collections are often carried out along tracks (paths, roads, transects, trails, etc.). Tracks can be discretized in regular intervals e.g. with `transLines2pix` or `st_thintrack`, each point being the center of a track interval. mergeTrackobs computes the number of observations that are the closest to each interval (compare to the other intervals) and give it in the column 'nObs'. if the argument 'obscol' is NULL, observations are considered presence/absence. If the number of observations is a true count (0 or any positive number) the argument 'obscol' can be used to identify the column of 'sppdfObs' where those counts must be found. Coordinate reference systems must be the identical.

Value

A `sfc` object, of POINT geometry, with the following columns:

- ID, ID number
- nObs, The number of observations in the interval
- geometry, POINT geometry

See Also

`transLines2pix`, `st_thintrack`

Examples

```
if(require(sf)){
# track

sl<-st_sfc(st_linestring(cbind(c(1,2,3),c(1,1.5,1))))
plot(sl, col = "blue")

    #observations
     obs <- structure(list(ID = 1:15, long = c(1.04609377280342, 1.0890625305741,
1.08125002916125, 1.24921880953755, 1.34687507719818, 1.50312510545521,
1.88984392539134, 2.37812526369453, 2.39375026652023, 2.36640651157525,
2.38593776510738, 2.62031280749291, 2.69843782162142, 2.85078159917202,
2.90546910906198), lat = c(1.04062476682306, 1.05624976964876,
1.03671851611663, 1.13828103448369, 1.16562478942867, 1.26718730779574,
1.43124983746561, 1.32968731909855, 1.32187481768569, 1.30624981485999,
1.28281231062144, 1.20468729649293, 1.13828103448369, 1.08749977530016,
1.03671851611663)), .Names = c("ID", "long", "lat"), row.names = c(NA,
-15L), class = "data.frame")
points(obs[,2:3],col="red")

obs<-st_as_sf(obs,coords=c(2:3))
# possibly a count (number of individuals observed) on each location
obs$n<-c(3,4,0,1,1,5,6,4,3,4,4,7,2,2,1)

# examples

# Presence/absence on each observation
track<-transLines2pix(sl,0.1)
trackObs<-mergeTrackObs(track,obs)

par(mfrow=c(1,2))
plot(sl,reset=FALSE)
plot(track,add=TRUE,col="blue")
plot(st_geometry(obs),add=TRUE,col="red",pch=1)

plot(sl,reset=FALSE)
plot(track,add=TRUE,col="blue")
plot(trackObs,cex=trackObs$nObs,pch=19, col="red",add=TRUE)


# 0 or more observations on each location
head(obs)
st_drop_geometry(obs) # the counts are in column "n" (column 2 in the data.frame)

trackObs<-mergeTrackObs(track,obs,obscol="n")

par(mfrow=c(1,2))
plot(sl,reset=TRUE)
plot(track,add=TRUE,col="blue")
plot(st_geometry(obs),add=TRUE,col="red",pch=1)
```

```
plot(sl)
plot(track,add=TRUE,col="blue")
plot(st_geometry(trackObs),cex=trackObs$nObs/3,pch=19, col="red",add=TRUE)


}
```

---

pairsrp *Produces a matrix of scatterplot, regression coefficient and p(Ho)*

Description

Produces a matrix with scatterplot, regression line and a loess smooth in the upper right panel; correlation coefficient (Pearson, Spearman or Kendall) and the probability of Ho in the lower left panel

Usage

```
pairsrp(dataframe, meth = "spearman", pansmo = FALSE, abv = FALSE, lwt.cex = NULL, ...)
```

Arguments

dataframe	a data.frame of numeric values
meth	a character string indicating which correlation coefficient is to be computed. One of 'pearson', 'kendall', or 'spearman'(default). Can be abbreviated.
pansmo	True if a loess smooth is to be plotted. Default to False.
abv	True if the variable names must be abbreviates. Default to False.
lwt.cex	character size expansion in the lower panel.
...	graphical parameters can be given as arguments to 'plot'.

Details

This function is a wrapper for pairs() and cor()

See Also

pairs

Examples

```
data(iris)
pairsrp(iris[,1:4],meth="pears",pansmo=TRUE,abv=TRUE)
```

pave *Provide square polygons or their node coordinates along a segment*

Description

Provide a user-defined cell grid of polygon squares (or square node points) along a segment. This can be used to define a sampling grid for spatial analysis.

Usage

```
pave(cordseg, yc, xc, fix.edge=NULL, ydown = TRUE, output = "list")
```

Arguments

cordseg	the segment coordinates. This can be a vector c(x1,y1,x2,y2), a 2 x 2 matrix or a data.frame (each line a coordinate)
yc	the number of segment divisions (y cells)
xc	the number of columns (x cells)
fix.edge	the edge length of a cell (user specified, default to NULL)
ydown	if TRUE (default) squares are computed decreasing y
output	a character string indicating which output is required. One of "list", "points" or "spdf". Partial match allowed

Details

The segment must have x1 < x2. If not, it is automatically reordered. When "spdf" is selected the output is an object of class SpatialPolygonsDataFrame. The value of the edge length of a cell can passed with the argument fix.edge. In this case, the coordinates of the segment right top are re-computed to adjust the cell edge to an user defined fixed value.

Value

According to the output selected, a list of polygon coordinates, a 2 column matrix with the nodes coordinates or a SpatialPolygonsDataFrame.

See Also

over, diag2edge

Examples

```
# segment sloping up
coord<-matrix(c(20,20,90,90),nr=2,byrow=TRUE)
plot(coord,type="n",xlim=c(0,100),ylim=c(0,110),asp=1)
lines(coord)
# point grids
gr<-pave(coord,20,4,output="points") # y decreasing
```

```
points(gr)
gr<-pave(coord,20,4,output="points",ydown=FALSE) # y increasing
points(gr,col="blue")
# square polygon grids
gr<-pave(coord,20,4) # y decreasing
for (i in 1:length(gr)) polygon(gr[[i]])
gr<-pave(coord,20,4,ydown=FALSE) # y increasing
for (i in 1:length(gr)) polygon(gr[[i]],border="blue")

# segment sloping down
coord<-matrix(c(20,90,90,20),nr=2,byrow=TRUE)
plot(coord,type="n",xlim=c(0,100),ylim=c(0,110),asp=1)
lines(coord)

# point grids
gr<-pave(coord,20,4,output="points")  # y decreasing
points(gr)
gr<-pave(coord,20,4,output="points",ydown=FALSE) # y increasing
points(gr,col="blue")

# fixed edge
plot(coord,type="n",xlim=c(0,100),ylim=c(0,110),asp=1)
lines(coord)
gr<-pave(coord,20,4,fix.edge=4,output="points")
points(gr,col="blue")

plot(coord,type="n",xlim=c(0,100),ylim=c(0,110),asp=1)
lines(coord)
gr<-pave(coord,20,4,fix.edge=5.5,output="points")
points(gr,col="red")

# square polygon grids
coord<-matrix(c(20,90,90,20),nr=2,byrow=TRUE)
plot(coord,type="n",xlim=c(0,100),ylim=c(0,110),asp=1)
lines(coord,lwd=2)
gr<-pave(coord,20,4)# y decreasing
for (i in 1:length(gr)) polygon(gr[[i]])
gr<-pave(coord,20,4,ydown=FALSE) # y increasing
for (i in 1:length(gr)) polygon(gr[[i]],border="blue")

# geting a SpatialPolygonsDataFrame
gr<-pave(coord,20,4,output="spdf") # y decreasing
```

---

permcont *Random permutation of a contingency table n row x 2 columns*

Description

Return a random permutation of a contingency table n rows x 2 columns keeping the marginal totals

Usage

```
permcont(Table)
```

Arguments

Table	a contingency table

Details

The contingency table is split in a two colums table of 0/1 categories, sampled and re-organised with the function table()

Value

A matrix with the permuted values

Examples

```
tab<-cbind(n1=c(10,12,8,7,5),n2=c(4,5,8,10,12))
tab
permcont(tab)
```

PermTest *Permutation test for lm, lme and glm (binomial and Poisson) objects*

Description

Permutation test for lm, lme and glm (binomial and Poisson) objects

Usage

```
    PermTest(obj, B=1000,...)

    ## S3 method for class 'lm'
PermTest(obj, B=1000,...)
    ## S3 method for class 'lme'
PermTest(obj, B=1000,...)
    ## S3 method for class 'glm'
PermTest(obj, B=1000,...)
```

Arguments

obj	an object of class lm, lme, or glm
B	number of permutations, default = 1000
...	used to pass other arguments

Details

For glm, when the response is a two-column matrix with the columns giving the numbers of successes and failures, PermTest.glm uses permcont(); PermTest.lme requires the library nlme.

Value

A list object of class PermTest including:

`p.value`	the p value obtained
`B`	the number of permutations
`call`	the call

Warning

This generic function is implemented in R language, thus can be quite slow.

Note

The implementation of PermTest.lme has been helped by Renaud Lancelot

Examples

```
if(require(MASS)){
mylm<-lm(Postwt~Prewt,data=anorexia)
PermTest(mylm,B=250)


## Dobson (1990) Page 93: Randomized Controlled Trial :
    counts <- c(18,17,15,20,10,20,25,13,12)
    outcome <- gl(3,1,9)
    treatment <- gl(3,3)
    glm.D93 <- glm(counts ~ outcome + treatment, family=poisson)
    PermTest(glm.D93,B=100)
    }

if(require(nlme)){
fm2 <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1)
PermTest(fm2,B=100)
}
```

piankabio *Computes the Pianka's index of niche overlap*

Description

Computes the Pianka's index of niche overlap

Usage

```
piankabio(dataframe1, dataframe2)
```

Arguments

dataframe1	a data frame of two columns: column 1 = dietary category, column 2 = biomass
dataframe2	a data frame of two columns: column 1 = dietary category, column 2 = biomass

Details

Computes the Pianka's index of niche overlap

Value

Return the Pianka's index

References

Pianka R.D. 1973 The scructure of lizard communities. Annual Review of Ecology and Systematics, 4: 53-74.

Amroun M., Giraudoux P., Delattre P. 2006 Comparative study of the diets of two sympatric carnivores - the Jackal (Canis aureus) and the Genet (Genetta genetta) - at two sites in Kabylia, Algeria. Mammalia, 70 (3): 247-254

See Also

piankabioboot

Examples

```
data(preybiom)
attach(preybiom)
jackal<-preybiom[site=="Y" & sp=="C",5:6]
genet<-preybiom[site=="Y" & sp=="G",5:6]

piankabio(jackal,genet)
```

piankabioboot *Bootstrap Pianka's index*

Description

Bootstrap Pianka's index and return the limits of the empirical confidence interval specified with probs

Usage

```
piankabioboot(dataframe1, dataframe2, B = 1000, probs = c(0.025, 0.975))
```

Arguments

dataframe1	a data frame of two columns: column 1 = dietary category, column 2 = biomass
dataframe2	a data frame of two columns: column 1 = dietary category, column 2 = biomass
B	number of permutations
probs	the limits of the confidence interval

Details

Bootstrap Pianka's index and return the limits of the empirical confidence interval sepcified with probs

Value

a vector of the two CI limits

See Also

piankabio

Examples

```
data(preybiom)
attach(preybiom)
jackal<-preybiom[site=="Y" & sp=="C",5:6]
genet<-preybiom[site=="Y" & sp=="G",5:6]

piankabioboot(jackal,genet,B=100)
```

polycirc *Computes the polygon coordinates of a circle*

Description

Computes the polygon coordinates of a circle

Usage

```
polycirc(radius, pts = c(0, 0), nbr = 50)
```

Arguments

radius	the length of the radius.
pts	the coordinates of the center.
nbr	the number of segments required to draw the perimeter

Details

The matrix of coordinates can then be used with the function polygon

Value

A matrix of coordinates.

See Also

polygon,findR

Examples

```
plot(1:10,1:10,type="n",asp=1)
polygon(polycirc(5),col="blue")
polygon(polycirc(2,c(5,5)), col="red")
```

polycirc2 *Computes the polygon coordinates of a circle sector*

Description

Computes the polygon coordinates of a circle sector

Usage

```
polycirc2(radius = 1, center = c(0, 0), edges = 50, init = pi/2, angle = pi/2)
```

Arguments

radius	the circle radius
center	the centre coordinates (defaut to x=0, y=0)
edges	the circular outline of the sector is approximated by a polygon with this many edges
init	number (in radian) specifying the starting angle
angle	number (in radian) specifying the sector angle

Details

The matrix of coordinates obtained is intended to be passed to the function polygon

Value

A matrix of coordinates

See Also

polygon,polycirc, floating.pie

Examples

```
plot(c(-1,+1),c(-1,+1),type="n",asp=1)
polygon(polycirc2(),col="red")
polygon(polycirc2(init=pi,angle=pi/4),col="green")
polygon(polycirc2(init=1.5*pi,angle=pi/4),col="violet")
polygon(polycirc2(radius=0.5,center=c(0.5,1)),col="blue")

polycirc2(init=pi,angle=pi/4)
```

preybiom *Jackal and Genet diet in Algeria*

Description

This data set gives the results of dietary analysis performed by Amroun Mansour in two sites of Kabylie, Algeria

Usage

```
data(preybiom)
```

Format

A data frame with 2196 observations on the following variables.

`faeces` a factor for faeces corresponding to faeces identification numbers

`site` a factor for study sites with levels `S` Sebaou `Y` Yacouren

`saison` a factor for seasons with levels `H` `HD` `HP` `S` `SD` `SP`

`sp` a factor for species with levels `C` Jackal `G` Genet

`category` a factor for dietary items with levels `dech` `ind` `ins` `mam` `mol` `oisauv` `oisdom` `rept` `vege` `vegn`

`biomasse` a numeric vector for the weight of each dietary item

References

M. Amroun, P. Giraudoux and P. Delattre 2006 Comparative study of the diets of two sympatric carnivores - the Jackal (Canis aureus) and the Genet (Genetta genetta) - at two sites in Kabylia, Algeria. Mammalia, 70 (3/4): 247-254.

print.mc *print method for objects of class 'mc'*

Description

print method for objects of class 'mc'

Usage

```
    ## S3 method for class 'mc'
print(x, ...)
```

Arguments

x	an object of class 'mc'
...	further arguments to be passed to or from other methods. They are ignored in this function

See Also

kruskalmc, friedmanmc

Examples

```
resp<-c(0.44,0.44,0.54,0.32,0.21,0.28,0.7,0.77,0.48,0.64,0.71,0.75,0.8,0.76,0.34,0.80,0.73,0.8)
categ<-as.factor(rep(c("A","B","C"),times=1,each=6))
kruskalmc(resp, categ)
```

Segments *Draw line segments between pairs of points.*

Description

Draw line segments between pairs of points from a vector, matrix or data frame of 4 points coordinates x0, y0, x1, y1

Usage

```
Segments(mydata, ...)
```

Arguments

mydata	a vector, matrix or data frame
...	further graphical parameters (from 'par')

Details

a wrapper to 'segments' to handle coordinates passed as vector, matrix or data frame. Any vector is turned into a matrix of four columns.

See Also

segments

Examples

```
mydata<-cbind(rnorm(20),rnorm(20),rnorm(20),rnorm(20))
plot(range(rbind(mydata[,1],mydata[,3])),range(rbind(mydata[,2],mydata[,4])),
type="n",xlab="",ylab="")
Segments(mydata,col=rainbow(20))

myvec<-rnorm(4)
plot(myvec[c(1,3)],myvec[c(2,4)],type="n",xlab="",ylab="")
Segments(myvec)

myvec<-rnorm(16)
plot(myvec,myvec,type="n",xlab="",ylab="")
Segments(myvec)
```

`selMod` *Model selection according to information theoretic methods*

Description

Handles lm, glm and list of e.g. lm, glm, nls, lme and nlme objects and provides parameters to compare models according to Anderson et al. (2001)

Usage

```
    selMod(aModel, Order = "AICc", ...)

    ## S3 method for class 'lm'
selMod(aModel, Order = "AICc", dropNull = FALSE, selconv=TRUE, ...)
    ## S3 method for class 'list'
selMod(aModel, Order = "AICc", ...)
```

Arguments

`aModel`	a lm or glm model or a list of relevant models (see details)
`dropNull`	if TRUE, drops the simplest model (e.g. y 1)
`Order`	if set to "AICc" (default) sort the models on this parameter, otherwise "AIC" is allowed
`selconv`	if TRUE (default) keep the models for which convergence is obtained (glm object only) and with no anova singularity (lm and glm)
`...`	other parameters to be passed as arguments (not used here)

Details

This function provides parameters used in the information theoretic methods for model comparisons.

- lm and glm objects can be passed directly as the upper scope of term addition (all terms added). Every model from y$\sim$1 is computed adding one term at a time until the upper scope model is derived. This is a stepwise analysis where the terms are added sequentially and this does NOT provide all combinations of terms and interactions. Offset terms cannot be proceeded here.
- A list of user specified lm, glm, nls, lme or nlme objects (actually any object for which AIC and logLik functions are applicable) to compare can alternately be passed.

Value

A dataframe including:

- LL, the maximized log-likelihood
- K, the number of estimated parameters
- N2K, the number of observations/K
- AIC, the Akaike index criterion
- deltAIC,the difference between AIC and the lowest AIC value
- w_i, the Akaike weights
- deltAICc, the difference between AICc and the lowest AICc value; advised to be used when n2K < 40
- w_ic, the AICc weights

The models examined from first to last are stored as attribute

Author(s)

Patrick Giraudoux and David Pleydell: pgiraudo@univ-fcomte.fr, david.pleydell@inra.fr

References

- Anderson, D.R., Link, W.A., Johnson, D.H. and Burnham, K.P. (2001). Suggestions for presenting the results of data analyses. Journal of Wildlife Management, 65, 373-378
- Burnham, K.P. and Anderson, D.R. (2002) Model Selection and Multimodel Inference: a Practical Information-Theoretic Approach, 2nd edn., Springer-Verlag, New York. 353 pp

See Also

AIC,logLik, aictab

Examples

```
if(require(MASS)){
anorex.1 <- lm(Postwt ~ Prewt*Treat, data = anorexia)
selMod(anorex.1)
anorex.2 <- glm(Postwt ~ Prewt*Treat, family=gaussian,data = anorexia)
selMod(anorex.2)
anorex.3<-lm(Postwt ~ Prewt+Treat, data = anorexia)
mycomp<-selMod(list(anorex.1,anorex.2,anorex.3))
mycomp
attributes(mycomp)$models
}
```

---

shannon *Computes Shannon's and equitability indices*

Description

Computes Shannon's and equitability indices

Usage

```
shannon(vect, base=2)
```

Arguments

vect	a probability vector whose sum = 1 or a frequency vector
base	logarithm base used (default=2)

Details

Computes Shannon's and equitability indices. The vector passed can be a probability vector whose sum equal 1 or a vector of frequencies (e.g. the number of food item of each category).

Value

A vector of two values: Shannon's and equitability indices. The base logarithm used is stored as attribute

See Also

shannonbio

Examples

```
x<-c(0.1,0.5,0.2,0.1,0.1)
sum(x)
shannon(x)

x<-rpois(10,6)
shannon(x, base=exp(1))
```

---

shannonbio *Computes Shannon's and equitability indices from a data frame of dietary analysis (n, biomass,...)*

Description

Computes Shannon's and equitability indices from a data frame of two columns: column 1, dietary category; column 2, abundance (n, biomass,...)

Usage

```
shannonbio(data1)
```

Arguments

data1	a data frame of two columns: column 1, dietary category; column 2, abundance (n, biomass,...)

Details

Computes Shannon's and equitability indices from a data frame of two columns: column 1, dietary category; column 2, abundance (n, biomass,...)

Value

A vector of two values: Shannon's and equitability indices

See Also

shannon, difshannonbio

Examples

```
data(preybiom)
shannonbio(preybiom[,5:6])
```

shannonbioboot *Boostrap Shannon's and equitability indices*

Description

Boostrap Shannon's and equitability indices and return an object of class boot. Confidence intervals can be computed with boot.ci().

Usage

```
shannonbioboot(data1, B = 1000)
```

Arguments

data1	a data frame of two columns: column 1, dietary category; column 2, abundance (n, biomass,...)
B	number of permutations

Details

Boostrap Shannon\'s and equitability indices and return an object of class boot. Confidence intervals can be computed with boot.ci(). Requires the boot library.

Value

An object of class boot including the bootstrap statistics for H' (t1*) and J' (t2*)

See Also

boot, boot.ci, shannonbio

Examples

```
data(preybiom)
myboot<-shannonbioboot(preybiom[,5:6],B=100)
library(boot)
boot.ci(myboot, index=1,type=c("norm","basic","perc")) # confidence intervals for H'
boot.ci(myboot, index=2,type=c("norm","basic","perc")) # confidence intervals for J'
```

siegelp179 *Data on rats training*

Description

Ranks of 18 matched groups of rats after training under three methods of reinforcement.

Usage

```
data(siegelp179)
```

Format

A data frame with 54 observations on the following 3 variables.

block Group (each of three litter mates)

treatment A factor for the type of reinforcement with levels RR RU UR

score Speed of transfer to another behaviour (the lower, the better the learning)

Details

18 blocks made of three rats of the same litter, each being given a different learning pattern (RR, RU or UR)

Source

Grosslight J.H. and Radlow R. (1956) Patterning effect of the nonreinforcement-reinforcement sequence in a discrimination situation. Journal of Comparative and Physiological Psychology, 49: 542-546 in Siegel & Castellan 1988. Non parametric statistics for the behavioural sciences. Mc Graw Hill Int. Edt.

Examples

```
data(siegelp179)
```

st_thintrack *Thin a track just keeping the points separated by a user defined minimal distance*

Description

Thin a track stored as a sf POINT object, just keeping the points separated by a user defined minimal distance.

Usage

```
st_thintrack(spdf,mindist=100)
```

Arguments

spdf	a sf of POINT tracks
mindist	minimal distance requested between two points (default = 100)

Details

Tracks downloaded from GPS often provide an unnecessary large density of points at irregular distances. This function starts reading from the first point of the track and removes all points within a user specified radius (USR), then reads the next point and removes all points within the USR, and so on...

Value

A sf POINT object of the track thinned.

See Also

mergeTrackObs

Examples

```
if(require(sf)){

mySPDF<-structure(list(x = c(748775, 748807, 748834, 748854, 748871,
748873, 748880, 748910, 748919, 748917, 748921, 748923, 748924,
748921, 748921, 748921, 748922, 748915, 748616, 748613, 748612,
748613, 748613, 748615, 748613, 748616, 748615, 748618, 748615,
748619, 748618, 748620, 748586, 748553, 748494, 748444, 748424,
748366, 748305, 748305), y = c(105716, 105761, 105808, 105856,
105911, 105964, 106019, 106065, 106114, 106167, 106219, 106274,
106329, 106385, 106441, 106494, 106550, 106571, 105835, 105779,
105723, 105665, 105600, 105537, 105473, 105412, 105350, 105293,
105234, 105180, 105123, 105070, 105023, 104960, 104956, 104947,
104906, 104905, 104901, 104904), ID = 1:40), .Names = c("x",
"y", "ID"), row.names = c("1", "2", "3", "4", "5", "6", "7",
"8", "9", "10", "11", "12", "13", "14", "15", "16", "17", "18",
"19", "20", "21", "22", "23", "24", "25", "26", "27", "28", "29",
"30", "31", "32", "33", "34", "35", "36", "37", "38", "39", "40"
), class = "data.frame")

mySPDF<-st_as_sf(mySPDF,coords=c("x","y"))

plot(st_geometry(mySPDF),pch=19,cex=0.5)
plot(st_thintrack(mySPDF),pch=19,cex=0.7,col="red",add=TRUE)

plot(mySPDF,pch=19,cex=0.5)
plot(st_thintrack(mySPDF,min=200),pch=19,cex=0.7,col="red",add=TRUE)

}
```

tabcont2categ *Convert a contingency table (data.frame) into a presence/absence table of categories*

Description

Convert a contingency table (data frame) into a data.frame of factors

Usage

```
tabcont2categ(tab)
```

Arguments

tab	A data.frame (contingency table)

Details

Convert a contingency table (data frame) into a data.frame of factors

Value

A data frame

Examples

```
mydata<-as.data.frame(matrix(rpois(9,5),nr=3,nc=3))
names(mydata)<-LETTERS[1:3]
row.names(mydata)<-letters[1:3]

tabcont2categ(mydata)
```

trans2pix *Convert a transect coordinate file with some waypoints separated by NA into a matrix with intermediate coordinates replacing NA.*

Description

Convert a transect coordinate file with some waypoints separated by NA into a matrix with intermediate coordinates replacing NA.

Usage

```
trans2pix(vect)
```

Arguments

vect	A two column matrix or data.frame

Details

If vect has more than two column the two first column only are read. This function computes the intermediate coordinates between two waypoints replacing NA values.

Value

A matrix with the intermediate coordinates computed.

See Also

trans2seg

Examples

```
x<-c(10,NA, NA, NA,56,NA,NA,100)
y<-c(23,NA, NA, NA,32,NA,NA,150)
cols=c("red","blue","blue","blue","red","blue","blue","red")
plot(x,y,col=cols,pch=19)
plot(trans2pix(cbind(x,y)),col=cols,pch=19)
```

---

trans2seg *Convert a transect coordinate file into a matrix with segment coordinates.*

Description

Convert a transect coordinate file (e.g.: waypoints) into a matrix with segment coordinates.

Usage

```
trans2seg(vect)
```

Arguments

vect	A two column matrix or data.frame

Details

The argument passed is a matrix or data.frame of two columns each row is a transect interval; each column must start (first row) and end (last row) with a landmark ; intermediate waypoints must have coordinates in the two columns of the row. Other rows must be NA values.

Value

A matrix of 4 columns to be passed e.g. to functions as "segments".

See Also

trans2pix

Examples

```
x<-c(10,NA, NA, NA,56,NA,NA,100)
y<-c(23,NA, NA, NA,32,NA,NA,150)
cols=c("red","blue","blue","blue","red","blue","blue","red")
plot(x,y,col=cols,pch=19)
mysegs<-trans2seg(cbind(x,y))
segments(mysegs[,1],mysegs[,2],mysegs[,3],mysegs[,4])
```

---

transLines2pix *Convert MULTILINESTRING and/or LINESTRING into POINT geometry with points at regular distance between nodes*

Description

Convert a simple feature geometry made of MULTILINESTRING and/or LINESTRING into a POINT geometry with points at regular distance between nodes

Usage

```
transLines2pix(spldf,mindist=100)
```

Arguments

spldf	A sfc object containing MULTILINESTRING or LINESTRING or both, exclusively
mindist	the distance between two points (default to 100)

Details

This function can be used e.g to discretize track lines (roads, paths, transects, etc.) into series of regular points. Each point is the centre of one interval. Beware that if mindist is larger than the distance between nodes, the output file will keep the nodes. Furthermore, mindist might not be fully respected in some spatial configurations. In such cases to filter points using st_thintrack complementarily is advised.

Value

A sf object with a POINT geometry type.

See Also

trans2pix, st_thintrack, mergeTrackObs

Examples

```
if (require(sf)) {
l1 = st_linestring(cbind(c(1,2,3),c(3,2,2)))
S1<-st_multilinestring(list(l1,cbind(l1[,1]+.05,l1[,2]+.05)))
S2<-st_linestring(cbind(c(1,2,3),c(1,1.5,1)))
sl<-st_sfc(list(S1,S2))
plot(sl, col = c("red", "blue"),reset=FALSE)

trpt<-transLines2pix(sl,mindist=0.1)

plot(st_geometry(trpt),add=TRUE)
}
```

TukeyHSDs *Simplify the list of a TukeyHSD object keeping the significant differences only.*

Description

Simplify the list of a TukeyHSD object keeping the significant differences only.

Usage

```
TukeyHSDs(TukeyHSD.object)
```

Arguments

TukeyHSD.object	An object of calls "TukeyHSD"

Details

When TukeyHSD is used on a fitted model with large numbers of categories, the number of pairwise comparisons is extremely large (n(n-1)/2). TukeyHSDs simplify the TukeyHSD object keeping the significant pairwise comparisons only. A plot method exists for TukeyHSD objects.

Value

An object of class "multicomp" and "TukeyHSD"

See Also

TukeyHSD

Examples

```
summary(fm1 <- aov(breaks ~ wool + tension, data = warpbreaks))
myobject<-TukeyHSD(fm1, "tension", ordered = TRUE)
myobject
TukeyHSDs(myobject)
```

`val4symb` *Center a numerical vector on a parameter position and provides absolute values and colors according to negative and positive values*

Description

Center a numerical vector on a parameter position and provides absolute values and colors according to negative and positive values

Usage

```
val4symb(x, FUN=mean, col = c("blue", "red"),...)
```

Arguments

`x`	a numerical vector
`FUN`	a function computing a position parameter, typically `mean` or `median`. Default to `mean`
`col`	a character vector of 2 values, default=c("blue","red"), blue for <0, red for >=0
`...`	optional arguments to 'FUN'

Value

A list with

`size`	the absolute values of the difference to the position parameter (eg mean, median)
`col`	a character vector with 2 colors, each corresponding to positive or negative values

See Also

`symbols`, `mean`, `median`, `scale`

Examples

```
x<-rnorm(30)
y<-rnorm(30)

z<-val4symb(rnorm(30))
symbols(x,y,circle=z$size,inches=0.2,bg=z$col)

z<-val4symb(scale(rnorm(30)))
symbols(x,y,circle=z$size,inches=0.2,bg=z$col)

z<-val4symb(rnorm(30),col=c("green","violet"))
symbols(x,y,circle=z$size,inches=0.2,bg=z$col)

z<-val4symb(rnorm(30),trim=0.025)
symbols(x,y,circle=z$size,inches=0.2,bg=z$col)

z<-val4symb(rnorm(30),median)
symbols(x,y,circle=z$size,inches=0.2,bg=z$col)

myfun<-function(x) 20 # passes an arbitrary constant
z<-val4symb(1:30,myfun)
symbols(x,y,circle=z$size,inches=0.2,bg=z$col)
```

`write.delim` *Write a data.frame*

Description

Write a simple data.frame into a text file with header, no row.names, fields separated by tab.

Usage

```
write.delim(x, file = "", row.names = FALSE, quote = FALSE, sep = "\t", ...)
```

Arguments

`x`	a data.frame
`file`	a character string for file name
`row.names`	either a logical value indicating whether the row names of 'x' are to be written along with 'x', or a character vector of row names to be written
`quote`	a logical value or a numeric vector. If 'TRUE', any character or factor columns will be surrounded by double quotes. If a numeric vector, its elements are taken as the indices of the columns to quote. In both cases, row and column names are quoted if they are written. If 'FALSE', nothing is quoted.
`sep`	the field separator string. Values within each row of 'x' are separated by this string.
`...`	additional arguments accepted by write.table

Details

Simple wrapper of write.table.

Value

A tab delimited text file.

See Also

write.table

Examples

```
 data(preybiom)
 write.delim(preybiom[1:10,]) # output to the console

## Not run:
 write.delim(preybiom[1:10,],file="Myfile.txt") # write a file in the working directory

## End(Not run)
```

---

writecn.delim *Write a data.frame that has Chinese characters*

Description

Handle a data.frame with Chinese characters and write it into a UTF-8 text file with header, no row.names, tab delimited fields.

Usage

```
writecn.delim(db, file = "",row.names = FALSE, quote = FALSE, sep = "\t", ...)
```

Arguments

db	a data.frame
file	file name (character string)
row.names	either a logical value indicating whether the row names of 'x' are to be written along with 'x', or a character vector of row names to be written
quote	a logical value or a numeric vector. If 'TRUE', any character or factor columns will be surrounded by double quotes. If a numeric vector, its elements are taken as the indices of the columns to quote. In both cases, row and column names are quoted if they are written. If 'FALSE', nothing is quoted.
sep	the field separator string. Values within each row of 'x' are separated by this string.
...	additional arguments to pass to write.table

Details

Writing a data.frame into text files can be quite cumbersome if the system locale is not Chinese. This function set up the locale to Chinese, write the data.frame using `write.table` with fileEncoding = "UTF-8", then restore the original locale.

Value

An ascii text file, tab delimited.

See Also

`write.table`, `Sys.setlocale`

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