

Package ‘pgirmess’

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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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bbox2sf	<i>Convert a bounding box into a sf object.</i>
---------	---

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	<i>Confidence interval of percentages</i>
----	---

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 <code>conf.level</code>

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	<i>Gives an index vector of the class category of each value of a numerical vector</i>
----------	--

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	<i>Gives a correlation matrix and the probability of Ho for each correlation</i>
--------	--

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	<i>Computes Moran's or Geary's coefficients on distance classes</i>
----------	---

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	<i>Convert a POSIXt date into categories corresponding to a autumn/winter/spring sequence</i>
-------------	---

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(preymbiom)
attach(preymbiom)
jackal<-preymbiom[site=="Y" & sp=="C",5:6]
genet<-preymbiom[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	<i>Computes segment directions.</i>
--------	-------------------------------------

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 columns 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	<i>Computes distances to the nearest neighbour</i>
------------	--

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	<i>Computes the distances between each nodes of a polyline.</i>
----------	---

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, $D = 1852 * 60 * (180/\pi) * \arccos(\sin(la1) * \sin(la2) + \cos(la1) * \cos(la2) * \cos(abs(lg1 - lg2)))$. 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 degdeg = TRUE, $D = 1852 * 60 * (180/\pi) * \cos(\sin(la1) * \sin(la2) + \cos(la1) * \cos(la2) * \cos(abs(lg1 - lg2)))$. 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 degdeg=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	<i>Computes the total length of a polyline.</i>
---------	---

Description

Computes the total length of a polyline.

Usage

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

Arguments

- | | |
|--------|--|
| pts | A matrix or data.frame of the node coordinates column 1 = x,column 2 = y. |
| degdeg | 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, $D = 1852 * 60 * (180/\pi) * \arccos(\sin(la1) * \sin(la2) + \cos(la1) * \cos(la2) * \cos(abs(lg1 - lg2)))$. 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 significance 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 reference 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 François 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 `"hstest"` containing the following components:

<code>statistic</code>	the value of the test statistic.
<code>p.value</code>	a character string indicating what type of test was performed.
<code>alternative</code>	a character string describing the alternative hypothesis.
<code>method</code>	a character string indicating what type of test was performed.
<code>data.name</code>	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	<i>Count the nearest observations to points corresponding to track intervals</i>
---------------	--

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 $p(H_0)$

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 H_0 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	<i>Provide square polygons or their node coordinates along a segment</i>
------	--

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 be 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")

# getting 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 columns 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	<i>Permutation test for lm, lme and glm (binomial and Poisson) objects</i>
----------	--

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

<code>dataframe1</code>	a data frame of two columns: column 1 = dietary category, column 2 = biomass
<code>dataframe2</code>	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 structure 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(preymbiom)
attach(preymbiom)
jackal<-preymbiom[site=="Y" & sp=="C",5:6]
genet<-preymbiom[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 specified with probs

Value

a vector of the two CI limits

See Also

[piankabio](#)

Examples

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

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

polycirc	<i>Computes the polygon coordinates of a circle</i>
----------	---

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 (default 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(preymiom)
```

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: pgiraud@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	<i>Computes Shannon's and equitability indices from a data frame of dietary analysis (n, biomass,...)</i>
------------	---

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(prebybiom)
shannonbio(prebybiom[,5:6])
```

shannonbioboot	<i>Bootstrap Shannon's and equitability indices</i>
----------------	---

Description

Bootstrap 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

Bootstrap 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(preymbiom)
myboot<-shannonbioboot(preymbiom[,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*. McGraw 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, 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	<i>Convert a contingency table (data.frame) into a presence/absence table of categories</i>
---------------	---

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	<i>Convert a transect coordinate file with some waypoints separated by NA into a matrix with intermediate coordinates replacing NA.</i>
-----------	---

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	<i>Convert a transect coordinate file into a matrix with segment coordinates.</i>
-----------	---

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	<i>Convert MULTILINESTRING and/or LINESTRING into POINT geometry with points at regular distance between nodes</i>
----------------	--

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

## Not run:
write.delim(preymiom[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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