

Package ‘Strategy’

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addpiechartclustermarkers
<i>Change leaflet cluster markers to pie charts</i>

Description

Change leaflet cluster markers to pie charts

Usage

addpiechartclustermarkers(map, .data, .colors, group)

Arguments

- | | |
|---------|---|
| map | the map to add awesome pie chart cluster markers to |
| .data | data for the cluster markers |
| .colors | a vector of colors of at least the same size that nlevels(.data[[group]]) |
| group | the name of a factor variable of .data |

Examples

```
data("breweries91",package="leaflet")
breweries91$goodbear<-sample(as.factor(c("terrific","marvelous","culparterretaping")),nrow(breweries91),replace=TRUE)
library(leaflet)
library(dplyr)
leaflet(breweries91) %>%
  addTiles() %>%
  addAwesomeMarkers()
map<-leaflet(breweries91) %>%addTiles()
addpiechartclustermarkers(map,.data=breweries91,.colors=c("red","green","blue"),group="goodbear")
leaflet(breweries91) %>%
  addTiles() %>%
  addpiechartclustermarkers(.data=breweries91,.colors=c("red","green","blue"),group="goodbear")
```

distpointtoseg	<i>computes the distance between a point and a segment</i>
----------------	--

Description

computes the distance between a point and a segment

Usage

```
distpointtoseg(p, s)
```

Arguments

p	a numeric vector of length 2
s	a 2x2 numeric matrix, representing a segment. Each row of the matrix are the coordinates of a extreme point of the segment.

Examples

```
zz<-function(p){
  s=matrix(c(0,3,0,0),2,2)
  plot(s,type="l",xlim=c(-2,5),ylim=c(-2,2))
  points(x=p[1],y=p[2] ,col="red",cex=.5)
  points(projpointonseg(p,s)[1],projpointonseg(p,s)[2],col="red",cex=.5)
  segments(x0 = p[1],y0=p[2],x1=projpointonseg(p,s)[1],y1=projpointonseg(p,s)[2],col="red")
  text((projpointonseg(p,s)[1]+p[1])/2,(projpointonseg(p,s)[2]+p[2])/2,round(distpointtoseg(p,s),2))}
  par(mfrow=c(3,3))
  set.seed(1);replicate(9,zz(c(sample(-2:3,1),sample(-2:2,1))))
```

distpolytopoly	<i>Computes distance between two polygons</i>
----------------	---

Description

Computes distance between two polygons

Usage

```
distpolytopoly(poly1, poly2)
```

Arguments

poly1	a polygon (a n x 2 numerical matrix)
poly2	a polygon (a n x 2 numerical matrix)

Value

a positive number, the distance between the two polygons

Examples

```
polys=lapply(c(0:1),function(x){
  cbind(c(x,x,x+.5,x+.5,x),c(0,1,1,0,0))})
par(mfrow=c(1,1))
plot(do.call(rbind,polys),xlab="",yaxt="n")
for(.poly in polys){segments(x0 = .poly[-5,1],y0 = .poly[-5,2],.poly[-1,1],.poly[-1,2])}
distpolytopoly(polys[[1]],polys[[2]])
polys=lapply(c(1:2),function(x){
  cbind(c(-x,-x,x,x,-x),c(-x,x,x,-x,-x))})
par(mfrow=c(1,1))
plot(do.call(rbind,polys),xlab="",yaxt="n")
for(.poly in polys){segments(x0 = .poly[-5,1],y0 = .poly[-5,2],.poly[-1,1],.poly[-1,2])}
distpolytopoly(polys[[1]],polys[[2]])
polys=lapply(c(1:2),function(x){
  cbind(c(-2,-2,2,2,-2),c(-1,1,1,-1,-1)),c(x,(1:2)[-x]))})
par(mfrow=c(1,1))
plot(do.call(rbind,polys),xlab="",yaxt="n")
for(.poly in polys){segments(x0 = .poly[-5,1],y0 = .poly[-5,2],.poly[-1,1],.poly[-1,2])}
distpolytopoly(polys[[1]],polys[[2]])
```

distsegmenttopoly	<i>Distance between a segment and a polygon</i>
-------------------	---

Description

Distance between a segment and a polygon

Usage

```
distsegmenttopoly(s, .poly)
```

Arguments

<code>s</code>	a 2x2 numeric matrix, representing a segment. Each row of the matrix are the coordinates of a extreme point of the segment.
<code>.poly</code>	a polygon (a nx2 matrix, each line is a point)

Examples

```
data(Avo_fields,package="Strategy")
polygon1<-Avo_fields[1,]
A<-polygon1@polygons
B<-A[[1]]@Polygons[[1]]@coords
s<-cbind(runif(2,min = min(B[,1]),max=max(B[,1])),runif(2,min=min(B[,2]),max=max(B[,2])))
plot(B,type='l')
```

```

s1<-s
points(s,type="l",lwd=4,col="green")
x<-vector()
for(i in 1:(nrow(B)-1)){
  s2<-B[(i:(i+1)),]
  dd<-distsegmenttosegment(s1,s2)
  l<-which(c(distpointtoseg(s1[1,],s2),distpointtoseg(s1[2,],s2),distpointtoseg(s2[1,],s1),distpointtoseg(s2[2,],s1))
  min(as.matrix(dist(rbind(s1,s2),diag=T,upper = T))[3:4,1:2]);dd
  sk<-if(l<=2){s2}else{s1}
  p=rbind(s1,s2)[l,]
  points(x=p[1],y=p[2],col="red",cex=2)
  points(projpointonseg(p,sk)[1],projpointonseg(p,sk)[2],col="red",cex=2)
  segments(x0 = p[1],y0=p[2],x1=projpointonseg(p,sk)[1],y1=projpointonseg(p,sk)[2])
  x=c(x,dd)
}
min(x)
distsegmenttopoly(s,B)
distpolytopoly()

```

distsegmenttosegment *distance segment to segment*

Description

distance segment to segment

Usage

```
distsegmenttosegment(s1, s2)
```

Arguments

s1	a 2x2 numeric matrix, representing a segment. Each row of the matrix are the coordinates of a extreme point of the segment.
s2	a 2x2 numeric matrix, representing a segment. Each row of the matrix are the coordinates of a extreme point of the segment.

Value

a number

Examples

```

zz<-function(){
  s1=matrix(sample(0:4,4,rep=T),2,2)
  s2=matrix(sample(0:4,4,rep=T),2,2)
  s<-rbind(s1,s2)
  dd<-distsegmenttosegment(s1,s2)
  plot(s,cex=.5,main=paste0("Distance: ", signif(dd,3)),asp=1,xlim=range(s),ylim=range(s))
}

```

```
points(s1,type="l",lwd=4,col="green")
points(s2,type="l",lwd=4,col="blue")
if(dd>0){l<-which(c(distpointtoseg(s1[1,],s2),distpointtoseg(s1[2,],s2),distpointtoseg(s2[1,],s1),distpointtos
s<-if(l<=2){s2}else{s1}
p=rbind(s1,s2)[1,]
points(x=p[1],y=p[2] ,col="red",cex=2)
points(projpointonseg(p,s)[1],projpointonseg(p,s)[2],col="red",cex=2)
segments(x0 = p[1],y0=p[2],x1=projpointonseg(p,s)[1],y1=projpointonseg(p,s)[2],lty=3)}}

par(mfrow=c(3,3))
set.seed(3);replicate(9,zz())
```

dist_areas_f	<i>Distances between hexagonal bins</i>
--------------	---

Description

Distances between hexagonal bins

Usage

```
dist_areas_f(
  U,
  delta = (range(U$x)[2] - range(U$x)[1])/100,
  h = neighbourhoods(U, delta)
)
```

Arguments

- U : a dataframe containing the numerical variables x and y and preferable hexagon
- delta : needed if hexagon is not a variable of U: bins will be recomputed

Value

a named matrix

Examples

```
data(U)
dist_areas_f(U)
delta<-0.01
```

Generate_Discrete_Time_Epidemic
Generate epidemic

Description

Generate epidemic

Usage

```
Generate_Discrete_Time_Epidemic(
  U,
  TT,
  .distriskhalf = 5 * 10-4,
  jumprisk = 10-6,
  delta = 0.05
)
```

Arguments

U	a data.frame
TT	an integer
.distriskhalf	a positive number(default 5*10 ⁻⁴)
jumprisk	=10 ⁻⁶ a positive number
delta	=0.05 a positive number

Examples

```
.distriskhalf=5*10-4;jumprisk=10-6;delta=0.05; TT=10
UE<-Generate_Discrete_Time_Epidemic(U,3)
```

Generate_U *Generate spatial data that matches population counts*

Description

Generate spatial data that matches population counts

Usage

```
Generate_U(SpatialData, .id = NULL, .spatialobject, type = "random")
```

Arguments

SpatialData	: an object of class that includes
type	: argument to be passed to sp::spsample

Examples

```

data(parish110217popest,package="dataONS")
data("mtcty150217population",package="dataONS")
shapeData2<-dataONS::dataParishes_December_2011_Boundaries_EW_BFC()
yy<-unique(get(data(Output_Area_to_Parish_to_Local_Authority_District_December_2011_Lookup_in_England_and_Wale
names(yy)<-tolower(names(yy))
shapeData<-sp::merge(shapeData2,yy,by="par11cd",duplicateGeoms = TRUE)
parish110217popest2<-parish110217popest[
  is.element(parish110217popest$PAR11CD,
    shapeData$par11cd)&
    parish110217popest$year=="mid_2006",
    c("PAR11CD", "Population")]
  names(parish110217popest2)<-tolower(names(parish110217popest2))
shapeData=sp::merge(shapeData,parish110217popest2,by="par11cd",duplicateGeoms = TRUE)
shapeData$population[is.na(shapeData$population)]<-mean(shapeData$population,na.rm=TRUE)
shapeData<-subset(shapeData,is.element(lad11nm ,c("Allerdale", "Barrow-in-Furness", "Carlisle", "C

U<-Generate_U(shapeData,.id="par11cd",.spatialobject="st_areasha",type="random")
popbins<-quantile(shapeData$population,(seq_len(11)-1)/10)
poppal <- colorBin(heat.colors(5), bins=popbins, na.color = "#aaff56",reverse = T)
library(leaflet)

leaflet(U) %>%
  addPolygons(data=shapeData,
    stroke=TRUE,
    weight=1,
    color="black",
    fillOpacity=5,
    fillColor=~poppal(shapeData$population)) %>%
  addTiles() %>%
  addLegend(title = "Population count", pal=poppal,
    values=shapeData$population,
    opacity=1,
    na.label = "Not Available")

```

neighbourhoods

*hexagonal bins***Description**

hexagonal bins

Usage

```

neighbourhoods(
  U,
  delta = (range(U$x, na.rm = TRUE)[2] - range(U$x, na.rm = TRUE)[1])/100
)

```


Arguments

U : a dataframe containing the numerical variables x and y
 delta: controls the bin diameter

Value

a hexbin object hexagonal bins

Examples

```
# plot the hex bins of cumbria
data(U)
plot(neighbourhoods(U,.1))
plot(neighbourhoods(U,.01))
plot(neighbourhoods(U,.001))
```

newdist	<i>compute distances between new infected and exposed</i>
---------	---

Description

compute distances between new infected and exposed

Usage

```
newdist(
  closeddistances = NULL,
  U,
  sick,
  new.sicks = NULL,
  delta = 0.005,
  dist_areas = dist_areas_f(U, delta)
)
```

Arguments

closeddistances NULL, or a named list with 2 named elements: closeddistances\$ra, closeddistances\$id
 U a data.frame with the variables hexagon (can be any bin identifier), x, y : coordinates,
 sick a vector of integers
 new.sicks a vector of integers
 delta a positive number : a threshold
 dist_areas: a function between

Value

NULL, or a named list with 2 named elements: closeddistances\$ra, closeddistances\$sd

Examples

```
data(UE,package="Strategy")
delta<-.005
sicks<-(1:nrow(UE))[UE$I001=="sick"]
closedistance=newdist(NULL,UE,sicks)
do.call(cbind,closedistances)[1:3,]
```

polydistmat

Compute distance matrix for a list of polygons

Description

Compute distance matrix for a list of polygons

Usage

```
polydistmat(list.poly)
```

Arguments

list.poly a list of nx2 numeric matrices

Value

a $(n*(n-1)/2) \times 3$ matrix

Examples

```
polys=lapply(c(0:3,5:7),function(x){
  cbind(c(x,x,x+.5,x+.5,x),c(0,1,1,0,0))})
par(mfrow=c(1,1))
plot(do.call(rbind,polys),xlab="",yaxt="n")
for(.poly in polys){segments(x0 = .poly[-5,1],y0 = .poly[-5,2],.poly[-1,1],.poly[-1,2])}
polydistmat(polys)
#data(Avo_fields,package="Strategy")
#polygons<-Avo_fields
#MM<-polydistmat(extractpolygonsaslist(Avo_fields))
#parallel::detectCores()
#save(MM,file=file.path(Mydirectories::googledrive.directory(),"Travail/Recherche/Travaux/Epidemiologie/Strate
```

projpointonseg	<i>computes the position of a projected point in the basis formed by a segment</i>
----------------	--

Description

computes the position of a projected point in the basis formed by a segment

Usage

```
projpointonseg(p, s)
```

Arguments

p	a numeric vector of length 2
s	a 2x2 numeric matrix, representing a segment. Each row of the matrix are the coordinates of a extreme point of the segment.

Examples

```
zz<-function(p){
  s=matrix(c(0,1,0,0),2,2)
  plot(s,type="l",xlim=c(-.5,1.5))
  points(x=p[1],y=p[2] ,col="red",cex=.5)
  points(projpointonseg(p,s)[1],projpointonseg(p,s)[2],col="red",cex=.5)
  segments(x0 = p[1],y0=p[2],x1=projpointonseg(p,s)[1],y1=projpointonseg(p,s)[2],col="red")
  par(mfrow=c(3,3))
  set.seed(1);replicate(9,zz(c(runif(1,-.5,1.5),runif(1,-1,1))))
```

projpointonseg_a	<i>computes the position of a projected point in the basis formed by a segment</i>
------------------	--

Description

computes the position of a projected point in the basis formed by a segment

Usage

```
projpointonseg_a(p, s)
```

Arguments

p	a numeric vector of length 2
s	a 2x2 numeric matrix, representing a segment. Each row of the matrix are the coordinates of a extreme point of the segment.

Examples

```
data(Avo_fields,package="Strategy")
polygon1<-Avo_fields[1,]
A<-polygon1@polygons
B<-A[[1]]@Polygons[[1]]@coords
i=sample(nrow(B)-1,1)
s<-B[i:(i+1),]
p<-c(runif(1,min = 142.162,max=142.165),runif(1,min=-34.171,max=-34.167))
plot(B,type='l')
points(s,type="l",lwd=4,col="red")
points(x=p[1],y=p[2] ,col="red",cex=2)
points(projpointonseg(p,s)[1],projpointonseg(p,s)[2],col="red",cex=2)
segments(x0 = p[1],y0=p[2],x1=projpointonseg(p,s)[1],y1=projpointonseg(p,s)[2])
projpointonseg_a(p,s)
distpointtoseg(p,s)
dist(rbind(p,projpointonseg(p,s)))

zz<-function(p){
s=matrix(c(0,1,0,0),2,2)
plot(s,type="l",xlim=c(-.5,1.5))
points(x=p[1],y=p[2] ,col="red",cex=2)
points(projpointonseg(p,s)[1],projpointonseg(p,s)[2],col="red",cex=2)
segments(x0 = p[1],y0=p[2],x1=projpointonseg(p,s)[1],y1=projpointonseg(p,s)[2],col="red")
text(projpointonseg_a(p,s),-.8,paste0("a=",projpointonseg_a(p,s)))}
par(mfrow=c(2,2))
zz(c(-.5,1))
zz(0:1)
zz(c(.5,1))
zz(c(1.5,1))
```

risktobeinfected

Computes the risk to be infected

Description

Computes the risk to be infected

Usage

```
risktobeinfected(
  U,
  closeddistances = NULL,
  sick,
  new.sicks = NULL,
  .distriskhalf = 5 * 10^(-4),
  jumprisk = 10^-6,
  delta = 0.01,
  previouslyexposed = c(),
  previousrisk = numeric()
)
```

Examples

```
y=rep("Sane",nrow(U));y[sample(length(y),10)]<-"sick"
jumprisk=10^-6
.distriskhalf=10^-6
```

```
risktobeinfectedbydistancetoallinfectedunit
```

Risk to be infected by many neighbours a neighbour at a certain distance

Description

Risk to be infected by many neighbours a neighbour at a certain distance

Usage

```
risktobeinfectedbydistancetoallinfectedunit(
  .dist,
  nI,
  .distriskhalf = 5 * 10^(-4),
  jumprisk = 10^-6
)
```

Arguments

```
.dist          : a vector (distances)
.disthalfrisk  : distance for which the risk is one half
nI:            total number of infected
jumprisk:      probability to be infected by one person, no matter how far he(she) is
```

Value

$1 - (\text{prod}(1 - \text{risktobeinfectedbydistancetooneinfectedunit}(\text{.dist}, \text{distriskhalf})) * (1 - \text{jumprisk})^{\text{nI}})$

Examples

```
#Risk to be infected 2 m from the victim when the 50%risk distance is 1 m:
risktobeinfectedbydistancetooneinfectedunit(2,1)
```

```
risktobeinfectedbydistancetooneinfectedunit
```

Risk to be infected by a neighbour at a distance x

Description

Risk to be infected by a neighbour at a distance x

Usage

```
risktobeinfectedbydistancetooneinfectedunit(.dist, .distriskhalf = 5 * 10^(-4))
```

Arguments

`.dist` : a distance
`.disthalfrisk` : distance for which the risk is one half

Value

```
exp(-.dist/(log(2)*.distriskhalf))
```

Examples

```
#Risk to be infected 2 m from the victim when the 50%risk distance is 1 m:
risktobeinfectedbydistancetooneinfectedunit(2,1)
```

```
segment.intersect
```

test if two segments intersect

Description

test if two segments intersect

Usage

```
segment.intersect(s1, s2)
```

Arguments

`s1` a 2x2 numeric matrix, representing a segment. Each row of the matrix are the coordinates of an extreme point of the segment.
`s2` a 2x2 numeric matrix, representing a segment. Each row of the matrix are the coordinates of an extreme point of the segment.

Examples

```
zz<-function(s1=matrix(sample(0:3,4,rep=T),2,2),s2=matrix(sample(0:3,4,rep=T),2,2)){
  si<-segment.intersect(s1,s2)
  s<-rbind(s1,s2)
  plot(s,cex=.5,main=if(si){"Intersect"}else{"Disjoint"},xlab="",ylab="",xaxt='n', yaxt='n',xlim=range(s)+c(-1,1),
  points(s1,type="l")
  points(s2,type="l")
  text(s[,1],s[,2],toupper(letters[1:4]),cex=1,col="red")
}
par(mfrow=c(3,4),mar=c(5,3,2,2))
set.seed(12);replicate(4,zz())
zz(matrix(0,2,2),matrix(0,2,2))
zz(matrix(0,2,2),matrix(1,2,2))
zz(matrix(c(1,1,1,1),2,2),matrix(c(2,3,2,3),2,2))
zz(matrix(c(1,1,0,0),2,2),matrix(c(0,1,0,0),2,2))
zz(matrix(c(1,3,1,3),2,2),matrix(c(2,4,2,4),2,2))
zz(matrix(c(0,1,0,1),2,2),matrix(c(2,3,2,3),2,2))
zz(matrix(c(0,4,0,4),2,2),matrix(c(1,3,1,3),2,2))
zz(matrix(c(0,1,0,1),2,2),matrix(c(0,3,0,3),2,2))
```

test	<i>runCompare</i>
------	-------------------

Description

Shiny App to

Usage

test()

Examples

```
package1<-NULL
package2<-NULL
runCompare()
```

triangleorientation	<i>computes the orientation of a triangle</i>
---------------------	---

Description

computes the orientation of a triangle

Usage

triangleorientation(s)

Arguments

s a 3x2 numeric matrix, representing a triangle. Each row of the matrix are the coordinates of an extreme point of the triangle.

Examples

```
zz<-function(p){
s=matrix(sample(0:4,6,rep=T),3,2)
plot(s[c(1:3,1),],type="l",main=if(triangleorientation(s)==1){"+"}else{if(triangleorientation(s)==-1){"-"}else{
text(s[,1],s[,2],toupper(letters[1:3]),cex=1,col="red")
}
}
par(mfrow=c(2,2),mar=c(5,3,2,2))
set.seed(7);replicate(4,zz(c(sample(-2:3,1),sample(-2:2,1))))
```

updatedist	<i>update the list of the already nown distances between subjects with distances between new infected and exposed</i>
------------	---

Description

update the list of the already nown distances between subjects with distances between new infected and exposed

Usage

```
updatedist(
  closeddistances = NULL,
  U,
  sick,
  new.sicks = NULL,
  delta = 0.005,
  dist_areas = dist_areas_f(U, delta)
)
```

Arguments

closeddistances NULL, or a named list with 2 named elements: closeddistances\$ra, closeddistances\$id

U a data.frame with the variables hexagon (can be any bin identifier), x, y : coordinates,

delta a positive number : a threshold

dist_areas: a function between

Value

NULL, or a named list with 2 named elements: closeddistances\$ra, closeddistances\$id

Examples

```
data(UE,package="Strategy")
delta<-.005
sicks<-(1:nrow(UE))[UE$I001=="sick"]
closedistance=updatedist(NULL,UE,sicks)
do.call(cbind,closedistances)[1:3,]
```

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