Package ‘rflexscan’

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Description Functions for the detection of spatial clusters using the flexible spatial scan statistic developed by Tango and Takahashi (2005) <doi:10.1186/1476-072X-4-11>. This package implements a wrapper for the C routine used in the FleXScan 3.1.2 <https://sites.google.com/site/flexscansoftware/home> developed by Takahashi, Yokoyama, and Tango.

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rflexscan-package

Analyze spatial count data using the flexible spatial scan statistic

Description

The rflexscan package provides functions and classes to analyze spatial count data using the flexible spatial scan statistic developed by Tango and Takahashi (2005). This package designed for any of the following interrelated purposes:

1. To evaluate reported spatial disease clusters, to see if they are statistically significant.
2. To test whether a disease is randomly distributed over space.
3. To perform geographical surveillance of disease, to detect areas of significantly high rates.

This package implements a wrapper for the C routine used in the FleXScan 3.1.2 developed by Takahashi, Yokoyama, and Tango.

References


See Also

rflexscan

choropleth

Display choropleth map

Description

Display choropleth map of detected clusters.

Usage

choropleth(polygons, fls, col = palette(), region_color = "#F0F0F0", rank = 1:length(fls$cluster), pval = 1, ...)
 choropleth

Arguments

- **polygons**: A SpatialPolygonsDataFrame.
- **fls**: An rflexscan object.
- **col**: A vector of colors for each cluster.
- **region_color**: Color of regions that are not included in any clusters.
- **rank**: An integer vector which specifies ranks of clusters to be displayed.
- **pval**: A threshold of P-value. Clusters with P-values of <pval will be displayed.
- ... Other parameters to be passed to plot function.

Details

Clusters are colored using the current palette. Please use `palette` function to specify colors of each cluster. Note that clusters with ranks larger than the number of colors in the palette are not highlighted.

See Also

rflexscan

Examples

```r
# load sample data (North Carolina SIDS data)
library(rgdal)
library(spdep)
data("nc.sids")
sids.shp <- readOGR(system.file("shapes/sids.shp", package="spData")[1])

# calculate the expected numbers of cases
expected <- nc.sids$BIR74 * sum(nc.sids$SID74) / sum(nc.sids$BIR74)

# run FleXScan
fls <- rflexscan(x = nc.sids$x, y = nc.sids$y,
                  observed = nc.sids$SID74,
                  expected = expected,
                  name = rownames(nc.sids),
                  clustersize = 10,
                  nb = ncCR85.nb)

# display all clusters
choropleth(sids.shp, fls)

# display clusters with rank 1, 2 and 3
choropleth(sids.shp, fls, rank = c(1, 2, 3))

# display clusters of P-value <= 0.05
choropleth(sids.shp, fls, pval = 0.05)
```
plot.rflexscan

Graph plotting of flexscan results

Description

Display detected clusters by a graph representation.

Usage

## S3 method for class 'rflexscan'
plot(x, rank = 1:length(x$cluster), pval = 1,
vertexsize = max(x$input$coordinates[, 1]) - min(x$input$coordinates[, 1]),
blab = colnames(x$input$coordinates)[1],
ylab = colnames(x$input$coordinates)[2],
xlim = c(min(x$input$coordinates[, 1]), max(x$input$coordinates[, 1])),
ylim = c(min(x$input$coordinates[, 2]), max(x$input$coordinates[, 2])),
col = palette(), frame_color = "gray40", vertex_color = "white",
...)

Arguments

x An rflexscan object.
rank An integer vector which specifies ranks of clusters to be displayed.
pval A threshold of P-value. Clusters with P-values of <pval will be displayed.
vertexsize Size of vertex of the graph.
xlab A label of the x axis.
ylab A label of the y axis.
xlim The x limits of the plot.
ylim The y limits of the plot.
col A vector of colors for each cluster.
frame_color Color of frames in the graph.
vertex_color Fill color of vertices that are not included in any clusters.
... Other parameters to be passed to plot.igraph function.

Details

Clusters are colored using the current palette. Please use palette function to specify colors of each cluster. Note that clusters with ranks larger than the number of colors in the palette are not highlighted.

See Also

rflexscan
Examples

# load sample data (North Carolina SIDS data)
library(spdep)
data("nc.sids")

# calculate the expected numbers of cases
expected <- nc.sids$BIR74 * sum(nc.sids$SID74) / sum(nc.sids$BIR74)

# run FleXScan
fls <- rflexscan(x = nc.sids$x, y = nc.sids$y,
                 observed = nc.sids$SID74,
                 expected = expected,
                 name = rownames(nc.sids),
                 clustersize = 10,
                 nb = ncCR85.nb)

# display all clusters
plot(fls)

# display clusters with rank 1, 2 and 3
plot(fls, rank = c(1, 2, 3))

# display clusters of P-value <= 0.05
plot(fls, pval = 0.05)

print.rflexscan  Print rflexscan object

Description

Print method for the rflexscan object.

Usage

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

Arguments

x  An rflexscan object to be printed.
...

See Also

rflexscan
print.rflexscanCluster

Print rflexscanCluster object

Description

Print method for the rflexscanCluster object.

Usage

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

Arguments

x An rflexscanCluster object to be printed.
...
Ignored.

print.summary.rflexscan

Print summary of flexscan results

Description

Print summary of flexscan results to the terminal.

Usage

## S3 method for class 'summary.rflexscan'
print(x, ...)

Arguments

x An summary.rflexscan object to be printed.
...
Ignored.

See Also

rflexscan, summary.rflexscan
Detect spatial disease clusters using the flexible/circular scan statistic

Description

This function analyzes spatial count data using the flexible spatial scan statistic developed by Tango and Takahashi (2005) or Kulldorff’s circular spatial scan statistic (1997), and detect spatial disease clusters.

Usage

rflexscan(x, y, lat, lon, name, observed, expected, population, nb, clustersize = 15, radius = 6370, stattype = "ORIGINAL", scanmethod = "FLEXIBLE", ralpha = 0.2, simcount = 999, rantype = "MULTINOMIAL", comments = ",", verbose = FALSE)

Arguments

x
An array of X-coordinates.
y
An array of Y-coordinates.
lat
An array of latitude.
lon
An array of longitude.
name
The name of each area.
observed
An array of observed number of diseases.
expected
An array of expected number of diseases under the null hypothesis. This is used on "Poisson" model.
population
An array of background population at risk in each area. This is used on "Binomial" model.
nb
A neighbours list or an adjacency matrix.
clustersize
The number of maximum spatial cluster size to scan.
radius
Radius of Earth to calculate a distance between two sets of latitude and longitude. It is approximately 6370 km in Japan.
stattype
Statistic type to be used (case-insensitive).
"ORIGINAL"  the likelihood ratio statistic by Kulldorff and Nagarwalla (1995)
"RESTRICTED"  the restricted likelihood ratio statistic by Tango (2008), with a preset parameter ralpha for restriction
scanmethod
Scanning method to be used (case-insensitive).
"FLEXIBLE"  flexible scan statistic by Tango and Takahashi (2005)
"CIRCULAR"  circular scan statistic by Kulldorff (1997)
ralpha
Parameter for the restricted likelihood ratio statistic.
simcount
The number of Monte Carlo replications to calculate a p-value for statistical test.
rflexscan

rantype  The type of random number for Monte Carlo simulation (case-insensitive).
"MULTINOMIAL" Total number of cases in whole area is fixed. It can be chosen in either Poisson or Binomial model.
"POISSON" Total number of cases is not fixed. It can be chosen in Poisson model.

comments  Comments for the analysis which will be written in summary.

verbose  Print progress messages.

Value  An rflexscan object which contains analysis results and specified parameters.

References


See Also

summary.rflexscan, plot.rflexscan, choropleth

Examples

# load sample data (North Carolina SIDS data)
library(spdep)
data("nc.sids")

# calculate the expected numbers of cases
expected <- nc.sids$BIR74 * sum(nc.sids$SID74) / sum(nc.sids$BIR74)

# run FleXScan
fls <- rflexscan(x = nc.sids$x, y = nc.sids$y,
                   observed = nc.sids$SID74,
                   expected = expected,
                   name = rownames(nc.sids),
                   clustersize = 10,
                   nb = ncCR85.nb)

# print rflexscan object
print(fls)

# print properties of the most likely cluster
print(fls$cluster[[1]])
# print summary to the terminal
summary(fls)

# plot graph
plot(fls, col = palette())
labs <- 1:length(fls$cluster)
legend("bottomleft", legend = labs, col = palette(), lty = 1)

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**summary.rflexscan**            **Summarizing rf lexscan results**

### Description

Summary method for rf lexscan objects.

### Usage

```r
## S3 method for class 'rf lexscan'
summary(object, ...)
```

### Arguments

- `object`  
  An rf lexscan object to be summarized.
- `...`     
  Ignored.

### See Also

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