Package ‘rflexscan’

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Type Package

Title The Flexible Spatial Scan Statistic

Version 1.2.0

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Description Provides functions for detecting 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. For details, see Otani et al. (2021) <doi:10.18637/jss.v099.i13>.

URL `https://tkhrotn.github.io/rflexscan/`

License GPL-3

Depends R (>= 3.1.0)

Imports Rcpp, igraph, sf, grDevices

LinkingTo Rcpp

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Contents

`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.

Author(s)

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Authors:

- Kunihiko Takahashi

References

- Otani T. and Takahashi K. (2021). Flexible scan statistics for detecting spatial disease clusters: The rflexscan R package, Journal of Statistical Software 99:13.
- Tango T. and Takahashi K. (2005). A flexibly shaped spatial scan statistic for detecting clusters, International Journal of Health Geographics 4:11.
- Takahashi K, Yokoyama T and Tango T. (2010). FleXScan v3.1: Software for the Flexible Scan Statistic. National Institute of Public Health, Japan, `https://sites.google.com/site/flexscansoftware/home`.

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,
  ...
)
```

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.

Value

No return value, called for side effects. This function generates a choropleth map of cluster results.

See Also

rflexscan

Examples

```
# load sample data (North Carolina SIDS data)
library(sf)
library(spdep)
data("nc.sids")
sids.shp <- st_read(system.file("shapes/sids.gpkg", package="spData")[1], quiet=TRUE)

# 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$coordinates[, 1]),
  xlab = colnames(x$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.

Value

No return value, called for side effects. Displays the detected clusters on a graph.

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.
`...`	Ignored.

Value

No return value, called for side effects. Prints a concise summary of the detected clusters and model settings.

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.

Value

No return value, called for side effects. Prints details of a single detected cluster, including member regions and statistics.

`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.

Value

No return value, called for side effects. Prints the summarized results of the flexible spatial scan statistic, including the number of clusters and test statistics.

See Also

rflexscan, summary.rflexscan

`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,
  secondary = NULL,
  clustertype = "HOT",
  clusterradius = .Machine$double.xmax
)
```

Arguments

`x`	A vector of X-coordinates.
`y`	A vector of Y-coordinates.
`lat`	(DEPRECATED) A vector of latitude.
`lon`	(DEPRECATED) A vector of longitude.
`name`	A vector of names of each area.

`observed`	A vector with the observed number of disease cases.
`expected`	A vector with the expected number of disease cases under the null hypothesis. This is used on "Poisson" model.
`population`	A vector with the background population at risk in each area. This is used on "Binomial" model.
`nb`	A neighbors list or an adjacency matrix.
`clustersize`	The number of maximum spatial cluster size to scan, i.e., the maximum number of regions included in the detected cluster
`radius`	Radius of Earth to calculate a distance between two sets of latitude and longitude. It is approximately 6370 km in Japan. This parameter is used when `lat` and `lon` are specified. This is DEPRECATED. The distance calculated using this parameter is not accurate. This feature is implemented to maintain compatibility with FleXScan. It is recommended to transform latitude and longitude onto the Cartesian coordinate system beforehand and use the `x` and `y` parameters that are projected coordinates.
`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`	Threshold parameter of the middle p-value for the restricted likelihood ratio statistic.
`simcount`	The number of Monte Carlo replications to calculate a p-value for statistical test.
`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.
`secondary`	The number of secondary clusters to be enumerated. If `NULL` is specified (default), the search for secondary clusters is stopped when the Monte Carlo p-value reaches 1.
`clustertype`	Type of cluster to be scanned. **"HOT"** Hot-spot clusters with elevated risk. **"COLD"** Cold-spot clusters with reduced risk. **"BOTH"** Hot- and cold-spot clusters simultaneously.
`clusterradius`	The maximum radius of spatial cluster to scan.

Details

Centroid coordinates for each region should be specified EITHER by Cartesian coordinates using arguments `x` and `y` or by latitudes and longitudes using arguments `lat` and `lon`. Note that `lat` and `lon` are DEPRECATED due to accuracy issues. This feature is implemented to maintain compatibility with FleXScan software. We recommend to transform latitude and longitude onto the Cartesian coordinate system beforehand (using `spTransform` function in sp package, for example) and use the `x` and `y` parameters that are projected coordinates.

Value

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

References

Otani T. and Takahashi K. (2021). Flexible scan statistics for detecting spatial disease clusters: The rflexscan R package, Journal of Statistical Software 99:13.

Tango T. and Takahashi K. (2005). A flexibly shaped spatial scan statistic for detecting clusters, International Journal of Health Geographics 4:11.

Kulldorff M. and Nagarwalla N. (1995). Spatial disease clusters: Detection and Inference. Statistics in Medicine 14:799-810.

Kulldorff M. (1997). A spatial scan statistic. Communications in Statistics: Theory and Methods, 26:1481-1496.

Tango T. (2008). A spatial scan statistic with a restricted likelihood ratio. Japanese Journal of Biometrics 29(2):75-95.

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)
```

`runFleXScan` *Run main routine of FleXScan.*

Description

Run main routine of FleXScan.

Usage

```
runFleXScan(setting, case_mat, coord_mat, adj_mat)
```

Arguments

`setting`	A list of parameter setting.
`case_mat`	A matrix of case counts.
`coord_mat`	A matrix of coordinates.
`adj_mat`	A matrix of neighbourhood relationships.

Value

A list containing the detected clusters, test statistics, and Monte Carlo p-values.

`summary.rflexscan` *Summarizing rflexscan results*

Description

Summary method for rflexscan objects.

Usage

```
## S3 method for class 'rflexscan'
summary(object, ...)
```

Arguments

`object`	An rflexscan object to be summarized.
`...`	Ignored.

Value

An object of class `"summary.rflexscan"` including summary tables of detected clusters, test statistics, and p-values. This object can be printed with `print.summary.rflexscan`.

See Also

rflexscan

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