

# Package ‘rflexscan’

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**Type** Package

**Title** The Flexible Spatial Scan Statistic

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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. 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)

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**LinkingTo** Rcpp

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rflexscan-package	<i>Analyze spatial count data using the flexible spatial scan statistic</i>
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## 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

- 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](#)

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choropleth	<i>Display choropleth map</i>
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---

## Description

Display choropleth map of detected clusters.

## Usage

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

## Arguments

<code>polygons</code>	A <code>SpatialPolygonsDataFrame</code> .
<code>fls</code>	An <code>rflexscan</code> object.
<code>col</code>	A vector of colors for each cluster.
<code>region_color</code>	Color of regions that are not included in any clusters.
<code>rank</code>	An integer vector which specifies ranks of clusters to be displayed.
<code>pval</code>	A threshold of P-value. Clusters with P-values of $<pval$ will be displayed.
<code>...</code>	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

```
# 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$coordinates[, 1]),
  xlab = colnames(x$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 <a href="#">plot.igraph</a> 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.  
`...`                  Ignored.

### **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](#)

---

```
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
)

```

### 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). <b>"ORIGINAL"</b> the likelihood ratio statistic by Kulldorff and Nagarwalla (1995) <b>"RESTRICTED"</b> the restricted likelihood ratio statistic by Tango (2008), with a preset parameter ralpha for restriction
scanmethod	Scanning method to be used (case-insensitive). <b>"FLEXIBLE"</b> flexible scan statistic by Tango and Takahashi (2005) <b>"CIRCULAR"</b> 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).



	<b>"MULTINOMIAL"</b> Total number of cases in whole area is fixed. It can be chosen in either Poisson or Binomial model.
	<b>"POISSON"</b> 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.

### 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.

---

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.

**See Also**

[rflexscan](#)

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