

# Package ‘rflexscan’

September 13, 2019

**Type** Package

**Title** The Flexible Spatial Scan Statistic

**Version** 0.2.0

**Date** 2019-09-10

**Author** Takahiro Otani,  
Kunihiko Takahashi

**Maintainer** Takahiro Otani <otani@med.nagoya-u.ac.jp>

**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.

**URL** <https://tkhrotn.github.io/rflexscan/>

**License** GPL-3

**Depends** R (>= 3.1.0)

**Imports** Rcpp, igraph, rgdal, grDevices, sp

**LinkingTo** Rcpp

**Suggests** knitr, rmarkdown, spdep, spData

**RoxygenNote** 6.1.1

**Encoding** UTF-8

**NeedsCompilation** yes

**Repository** CRAN

**Date/Publication** 2019-09-12 22:50:03 UTC

## R topics documented:

rflexscan-package . . . . .	2
choropleth . . . . .	2
plot.rflexscan . . . . .	4
print.rflexscan . . . . .	5

print.rflexscanCluster . . . . .	6
print.summary.rflexscan . . . . .	6
rflexscan . . . . .	7
summary.rflexscan . . . . .	9

<b>Index</b>	<b>10</b>
--------------	-----------

---

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

---

### 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

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

---

### Description

Display choropleth map of detected clusters.

### Usage

```
choropleth(polygons, fls, col = palette(), region_color = "#F0F0F0",
           rank = 1:length(fls$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 $\leq pval$ 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	<i>Print rflexscan object</i>
-----------------	-------------------------------

---

**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	<i>Detect spatial disease clusters using the flexible/circular scan statistic</i>
-----------	---

---

## 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, statype = "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.
statype	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	Parameter 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.

### Value

An rflexscan object which contains analysis results and specified parameters.

### References

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)
```

---

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](#)

# Index

choropleth, [2](#), [8](#)

palette, [3](#), [4](#)

plot.igraph, [4](#)

plot.rflexscan, [4](#), [8](#)

print.rflexscan, [5](#)

print.rflexscanCluster, [6](#)

print.summary.rflexscan, [6](#)

rflexscan, [2-6](#), [7](#), [9](#)

rflexscan-package, [2](#)

summary.rflexscan, [6](#), [8](#), [9](#)