

# Package ‘rgeoda’

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**Type** Package

**Title** R Library for Spatial Data Analysis

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**Description** Provides spatial data analysis functionalities including Exploratory Spatial Data Analysis, Spatial Cluster Detection and Clustering Analysis, Regionalization, etc. based on the C++ source code of 'GeoDa', which is an open-source software tool that serves as an introduction to spatial data analysis. The 'GeoDa' software and its documentation are available at <<https://geodacenter.github.io>>.

**URL** <https://github.com/geodacenter/rgeoda/>,  
<https://geodacenter.github.io/rgeoda/>

**BugReports** <https://github.com/geodacenter/rgeoda/issues/>

**Depends** R (>= 4.0.0), methods, digest

**License** GPL (>= 2)

**Collate** init.R rgeoda.R sf\_geoda.R RcppExports.R read\_geoda.R  
weights.R utils.R lisa.R clustering.R

**Imports** sf, Rcpp (>= 1.0.1)

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---

as.data.frame.geoda     *convert rgeoda instance to data.frame*

---

### Description

Override the as.data.frame function for rgeoda instance

### Usage

```
## S3 method for class 'geoda'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

### Arguments

x	A rgeoda object
row.names	NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
optional	optional parameters
...	other arguments passed to methods

### Value

A data.frame object

---

as.geoda     *Create an instance of geoda-class from either an 'sf' or 'sp' object*

---

### Description

Create an instance of geoda-class from an 'sf' object returned from 'st\_read()' function, or a 'sp' object returned from 'readOGR()' function. NOTE: The table content is NOT used to create an instance of geoda-class.

### Usage

```
as.geoda(obj, with_table = TRUE)
```

### Arguments

obj	An instance of 'sf' or 'sp' object
with_table	A boolean flag indicates if table is copied from sf object to create geoda object. Default is TRUE

### Value

An instance of geoda-class

---

as.matrix.Weight	<i>spatial weights to matrix</i>
------------------	----------------------------------

---

### Description

Convert a GeoDa spatial weights object to a Matrix object

### Usage

```
## S3 method for class 'Weight'
as.matrix(x, rownames = NULL, rownames.value = NULL, ...)
```

### Arguments

x	A weights object
rownames	optional, a single column name or column number to use as the rownames in the returned matrix. If TRUE the key of the data.table will be used if it is a single column, otherwise the first column in the data.table will be used.
rownames.value	optional, a vector of values to be used as the rownames in the returned matrix. It must be the same length as nrow(x).
...	Required to be present because the generic 'as.matrix' generic has it. Arguments here are not currently used or passed on by this method.

### Value

A matrix object

---

azp_greedy	<i>A greedy algorithm to solve the AZP problem</i>
------------	--

---

### Description

The automatic zoning procedure (AZP) was initially outlined in Openshaw (1977) as a way to address some of the consequences of the modifiable areal unit problem (MAUP). In essence, it consists of a heuristic to find the best set of combinations of contiguous spatial units into  $p$  regions, minimizing the within sum of squares as a criterion of homogeneity. The number of regions needs to be specified beforehand.

**Usage**

```
azp_greedy(
  p,
  w,
  df,
  bound_variable = data.frame(),
  min_bound = 0,
  inits = 0,
  initial_regions = vector("numeric"),
  scale_method = "standardize",
  distance_method = "euclidean",
  random_seed = 123456789,
  rdist = numeric()
)
```

**Arguments**

<code>p</code>	The number of spatially constrained clusters
<code>w</code>	An instance of Weight class
<code>df</code>	A data frame with selected variables only. E.g. <code>guerry[c("Crm_prs", "Crm_prp", "Litercy")]</code>
<code>bound_variable</code>	(optional) A data frame with selected bound variable
<code>min_bound</code>	(optional) A minimum bound value that applies to all clusters
<code>inits</code>	(optional) The number of construction re-runs, which is for ARiSeL "automatic regionalization with initial seed location"
<code>initial_regions</code>	(optional) The initial regions that the local search starts with. Default is empty. means the local search starts with a random process to "grow" clusters
<code>scale_method</code>	(optional) One of the scaling methods 'raw', 'standardize', 'demean', 'mad', 'range_standardize', 'range_adjust' to apply on input data. Default is 'standardize' (Z-score normalization).
<code>distance_method</code>	(optional) The distance method used to compute the distance between observation <i>i</i> and <i>j</i> . Defaults to "euclidean". Options are "euclidean" and "manhattan"
<code>random_seed</code>	(optional) The seed for random number generator. Defaults to 123456789.
<code>rdist</code>	(optional) The distance matrix (lower triangular matrix, column wise storage)

**Value**

A names list with names "Clusters", "Total sum of squares", "Within-cluster sum of squares", "Total within-cluster sum of squares", and "The ratio of between to total sum of squares".

**Examples**

```
## Not run:
library(sf)
```

```

guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
azp_clusters <- azp_greedy(5, queen_w, data)
azp_clusters

## End(Not run)

```

---

azp\_sa

*A simulated annealing algorithm to solve the AZP problem*


---

## Description

The automatic zoning procedure (AZP) was initially outlined in Openshaw (1977) as a way to address some of the consequences of the modifiable areal unit problem (MAUP). In essence, it consists of a heuristic to find the best set of combinations of contiguous spatial units into  $p$  regions, minimizing the within sum of squares as a criterion of homogeneity. The number of regions needs to be specified beforehand.

## Usage

```

azp_sa(
  p,
  w,
  df,
  cooling_rate,
  sa_maxit = 1,
  bound_variable = data.frame(),
  min_bound = 0,
  inits = 0,
  initial_regions = vector("numeric"),
  scale_method = "standardize",
  distance_method = "euclidean",
  random_seed = 123456789,
  rdist = numeric()
)

```

## Arguments

<code>p</code>	The number of spatially constrained clusters
<code>w</code>	An instance of Weight class
<code>df</code>	A data frame with selected variables only. E.g. <code>guerry[c("Crm_prs", "Crm_prp", "Litercy")]</code>
<code>cooling_rate</code>	The cooling rate of a simulated annealing algorithm. Defaults to 0.85
<code>sa_maxit</code>	(optional): The number of iterations of simulated annealing. Defaults to 1

bound_variable	(optional) A data frame with selected bound variabl
min_bound	(optional) A minimum bound value that applies to all clusters
inits	(optional) The number of construction re-runs, which is for ARiSeL "automatic regionalization with initial seed location"
initial_regions	(optional) The initial regions that the local search starts with. Default is empty. means the local search starts with a random process to "grow" clusters
scale_method	(optional) One of the scaling methods 'raw', 'standardize', 'demean', 'mad', 'range_standardize', 'range_adjust' to apply on input data. Default is 'standardize' (Z-score normalization).
distance_method	(optional) The distance method used to compute the distance between observation i and j. Defaults to "euclidean". Options are "euclidean" and "manhattan"
random_seed	(optional) The seed for random number generator. Defaults to 123456789.
rdist	(optional) The distance matrix (lower triangular matrix, column wise storage)

### Value

A names list with names "Clusters", "Total sum of squares", "Within-cluster sum of squares", "Total within-cluster sum of squares", and "The ratio of between to total sum of squares".

### Examples

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
azp_clusters <- azp_sa(5, queen_w, data, cooling_rate = 0.85)
azp_clusters

## End(Not run)
```

---

azp\_tabu

*A tabu algorithm to solve the AZP problem*

---

### Description

The automatic zoning procedure (AZP) was initially outlined in Openshaw (1977) as a way to address some of the consequences of the modifiable areal unit problem (MAUP). In essence, it consists of a heuristic to find the best set of combinations of contiguous spatial units into  $p$  regions, minimizing the within sum of squares as a criterion of homogeneity. The number of regions needs to be specified beforehand.



**Usage**

```
azp_tabu(
  p,
  w,
  df,
  tabu_length = 10,
  conv_tabu = 10,
  bound_variable = data.frame(),
  min_bound = 0,
  inits = 0,
  initial_regions = vector("numeric"),
  scale_method = "standardize",
  distance_method = "euclidean",
  random_seed = 123456789,
  rdist = numeric()
)
```

**Arguments**

p	The number of spatially constrained clusters
w	An instance of Weight class
df	A data frame with selected variables only. E.g. <code>guerry[c("Crm_prs", "Crm_prp", "Litercy")]</code>
tabu_length	The length of a tabu search heuristic of tabu algorithm. e.g. 10.
conv_tabu	(optional): The number of non-improving moves. Defaults to 10.
bound_variable	(optional) A data frame with selected bound variabl
min_bound	(optional) A minimum bound value that applies to all clusters
inits	(optional) The number of construction re-runs, which is for ARiSeL "automatic regionalization with initial seed location"
initial_regions	(optional) The initial regions that the local search starts with. Default is empty. means the local search starts with a random process to "grow" clusters
scale_method	(optional) One of the scaling methods 'raw', 'standardize', 'demean', 'mad', 'range_standardize', 'range_adjust' to apply on input data. Default is 'standardize' (Z-score normalization).
distance_method	(optional) The distance method used to compute the distance between observation i and j. Defaults to "euclidean". Options are "euclidean" and "manhattan"
random_seed	(optional) The seed for random number generator. Defaults to 123456789.
rdist	(optional) The distance matrix (lower triangular matrix, column wise storage)

**Value**

A names list with names "Clusters", "Total sum of squares", "Within-cluster sum of squares", "Total within-cluster sum of squares", and "The ratio of between to total sum of squares".

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
azp_clusters <- azp_tabu(5, queen_w, data, tabu_length=10, conv_tabu=10)
azp_clusters

## End(Not run)
```

---

create_weights	<i>Create an empty weights</i>
----------------	--------------------------------

---

**Description**

Create an empty weights

**Usage**

```
create_weights(num_obs)
```

**Arguments**

num\_obs            The number of observations for this empty weights

**Value**

An instance of Weight-class

---

distance_weights	<i>Distance-based Spatial Weights</i>
------------------	---------------------------------------

---

**Description**

Create a distance-based weights

**Usage**

```
distance_weights(
  sf_obj,
  dist_thres,
  power = 1,
  is_inverse = FALSE,
  is_arc = FALSE,
  is_mile = TRUE
)
```

**Arguments**

sf_obj	An sf (simple feature) object
dist_thres	A positive numeric value of distance threshold
power	(optional) The power (or exponent) of a number indicates how many times to use the number in a multiplication.
is_inverse	(optional) FALSE (default) or TRUE, apply inverse on distance value
is_arc	(optional) FALSE (default) or TRUE, compute arc distance between two observations
is_mile	(optional) TRUE (default) or FALSE, convert distance unit from mile to km.

**Value**

An instance of Weight-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
dist_thres <- min_distthreshold(guerry)
dist_w <- distance_weights(guerry, dist_thres)
summary(dist_w)
```

---

 eb\_rates

*Empirical Bayes(EB) Rate*


---

**Description**

The function to compute EB Rate from an event variable and a base variable.

**Usage**

```
eb_rates(df)
```

**Arguments**

df	A data frame with two selected variable: one is "event", another is "base" variable. E.g. guerry[c("hr60", "po60")]
----	---

**Value**

A data.frame with two columns "EB Rate" and "IsNull".

**Examples**

```
## Not run:
library(sf)
nat <- st_read("natregimes.shp")
ebr <- eb_rates(nat[c("HR60", "P060")])
ebr

## End(Not run)
```

---

`gda_distance_weights` *(For internally use and test only) Distance-based Spatial Weights*

---

**Description**

Create a distance-based weights

**Usage**

```
gda_distance_weights(
  geoda_obj,
  dist_thres,
  power = 1,
  is_inverse = FALSE,
  is_arc = FALSE,
  is_mile = TRUE
)
```

**Arguments**

<code>geoda_obj</code>	An instance of geoda-class
<code>dist_thres</code>	A positive numeric value of distance threshold
<code>power</code>	(optional) The power (or exponent) of a number indicates how many times to use the number in a multiplication.
<code>is_inverse</code>	(optional) FALSE (default) or TRUE, apply inverse on distance value
<code>is_arc</code>	(optional) FALSE (default) or TRUE, compute arc distance between two observations
<code>is_mile</code>	(optional) TRUE (default) or FALSE, convert distance unit from mile to km.

**Value**

An instance of Weight-class

**Examples**

```
## Not run:
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- geoda_open(guerry_path)
dist_thres <- gda_min_distthreshold(guerry)
dist_w <- gda_distance_weights(guerry, dist_thres)
summary(dist_w)

## End(Not run)
```

---

gda\_kernel\_knn\_weights

*(For internally use and test only) K-NN Kernel Spatial Weights*

---

**Description**

Create a kernel weights by specifying k-nearest neighbors and a kernel method

**Usage**

```
gda_kernel_knn_weights(
  geoda_obj,
  k,
  kernel_method,
  adaptive_bandwidth = TRUE,
  use_kernel_diagonals = FALSE,
  power = 1,
  is_inverse = FALSE,
  is_arc = FALSE,
  is_mile = TRUE
)
```

**Arguments**

geoda_obj	An instance of geoda
k	a positive integer number for k-nearest neighbors
kernel_method	a string value, which has to be one of 'triangular', 'uniform', 'epanechnikov', 'quartic', 'gaussian'
adaptive_bandwidth	(optional) TRUE (default) or FALSE: TRUE use adaptive bandwidth calculated using distance of k-nearest neighbors, FALSE use max distance of all observation to their k-nearest neighbors
use_kernel_diagonals	(optional) FALSE (default) or TRUE, apply kernel on the diagonal of weights matrix

power	(optional) The power (or exponent) of a number says how many times to use the number in a multiplication.
is_inverse	(optional) FALSE (default) or TRUE, apply inverse on distance value
is_arc	(optional) FALSE (default) or TRUE, compute arc distance between two observations
is_mile	(optional) TRUE (default) or FALSE, convert distance unit from mile to km.

**Value**

An instance of Weight-class

**Examples**

```
## Not run:
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- geoda_open(guerry_path)
adptkernel_w = gda_kernel_knn_weights(guerry, 6, "uniform")
summary(adptkernel_w)

## End(Not run)
```

---

`gda_kernel_weights` *(For internally use and test only) Distance-based Kernel Spatial Weights*

---

**Description**

Create a kernel weights by specifying a bandwidth and a kernel method

**Usage**

```
gda_kernel_weights(
  geoda_obj,
  bandwidth,
  kernel_method,
  use_kernel_diagonals = FALSE,
  power = 1,
  is_inverse = FALSE,
  is_arc = FALSE,
  is_mile = TRUE
)
```

**Arguments**

geoda_obj	An instance of geoda-class
bandwidth	A positive numeric value of bandwidth
kernel_method	a string value, which has to be one of 'triangular', 'uniform', 'epanechnikov', 'quartic', 'gaussian'
use_kernel_diagonals	(optional) FALSE (default) or TRUE, apply kernel on the diagonal of weights matrix
power	(optional) The power (or exponent) of a number says how many times to use the number in a multiplication.
is_inverse	(optional) FALSE (default) or TRUE, apply inverse on distance value
is_arc	(optional) FALSE (default) or TRUE, compute arc distance between two observations
is_mile	(optional) TRUE (default) or FALSE, convert distance unit from mile to km.

**Value**

An instance of Weight-class

**Examples**

```
## Not run:
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- geoda_open(guerry_path)
bandwidth <- gda_min_distthreshold(guerry)
kernel_w <- gda_kernel_weights(guerry, bandwidth, kernel_method = "uniform")
summary(kernel_w)

## End(Not run)
```

---

gda_knn_weights	<i>(For internally use and test only) K-Nearest Neighbors-based Spatial Weights</i>
-----------------	---

---

**Description**

Create a k-nearest neighbors based spatial weights

**Usage**

```
gda_knn_weights(
  geoda_obj,
  k,
  power = 1,
  is_inverse = FALSE,
  is_arc = FALSE,
  is_mile = TRUE
)
```

**Arguments**

geoda_obj	An instance of geoda
k	a positive integer number for k-nearest neighbors
power	(optional) The power (or exponent) of a number says how many times to use the number in a multiplication.
is_inverse	(optional) FALSE (default) or TRUE, apply inverse on distance value
is_arc	(optional) FALSE (default) or TRUE, compute arc distance between two observations
is_mile	(optional) TRUE (default) or FALSE, convert distance unit from mile to km.

**Value**

An instance of Weight-class

**Examples**

```
## Not run:
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- geoda_open(guerry_path)
knn6_w <- gda_knn_weights(guerry, 6)
summary(knn6_w)

## End(Not run)
```

---

`gda_min_distthreshold` *(For internally use and test only) Minimum Distance Threshold for Distance-based Weights*

---

**Description**

Get minimum threshold of distance that makes sure each observation has at least one neighbor

**Usage**

```
gda_min_distthreshold(geoda_obj, is_arc = FALSE, is_mile = TRUE)
```

**Arguments**

geoda_obj	An instance of geoda-class
is_arc	(optional) FALSE (default) or TRUE, compute arc distance between two observations
is_mile	(optional) TRUE (default) or FALSE, if 'is_arc' option is TRUE, then 'is_mile' will set distance unit to 'mile' or 'km'.

**Value**

A numeric value of minimum threshold of distance



---

`gda_queen_weights`      *(For internally use and test only) Queen Contiguity Spatial Weights*

---

## Description

Create a Queen contiguity weights with options of "order", "include lower order" and "precision threshold"

## Usage

```
gda_queen_weights(  
  geoda_obj,  
  order = 1,  
  include_lower_order = FALSE,  
  precision_threshold = 0  
)
```

## Arguments

<code>geoda_obj</code>	An object of [geoda] class
<code>order</code>	(Optional) Order of contiguity
<code>include_lower_order</code>	(Optional) Whether or not the lower order neighbors should be included in the weights structure
<code>precision_threshold</code>	(Optional) The precision of the underlying shape file is insufficient to allow for an exact match of coordinates to determine which polygons are neighbors

## Value

An instance of Weight-class

## Examples

```
## Not run:  
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")  
guerry <- geoda_open(guerry_path)  
queen_w <- gda_queen_weights(guerry)  
summary(queen_w)  
  
## End(Not run)
```

---

`gda_rook_weights`      *(For internally use and test only) Rook Contiguity Spatial Weights*

---

### Description

Create a Rook contiguity weights with options of "order", "include lower order" and "precision threshold"

### Usage

```
gda_rook_weights(  
  geoda_obj,  
  order = 1,  
  include_lower_order = FALSE,  
  precision_threshold = 0  
)
```

### Arguments

<code>geoda_obj</code>	An object of [geoda] class
<code>order</code>	(Optional) Order of contiguity
<code>include_lower_order</code>	(Optional) Whether or not the lower order neighbors should be included in the weights structure
<code>precision_threshold</code>	(Optional) The precision of the underlying shape file is insufficient to allow for an exact match of coordinates to determine which polygons are neighbors

### Value

An instance of Weight-class

### Examples

```
## Not run:  
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")  
guerry <- geoda_open(guerry_path)  
rook_w <- gda_rook_weights(guerry)  
summary(rook_w)  
  
## End(Not run)
```

---

geoda-class	<i>'geoda' class</i>
-------------	----------------------

---

### Description

'geoda' is a RefClass that wraps the C++ GeoDa class (via p\_GeoDa defines in rgeoda.R)

### Fields

gda The pointer to the instance of p\_GeoDa-class  
 map\_type The map type, could be either Point or Polygon  
 n\_cols The number of columns  
 n\_obs The number of observations  
 field\_names A string vector of field names  
 field\_types A string vector of field types (integer, real, string)

### Methods

GetFieldNames(...) Get the field names of all columns  
 GetFieldTypes(...) Get the field types (integer, real, string) of all columns  
 GetIntegerCol(col\_name) Get the integer values from a column  
 GetMapType(...) Get the map type  
 GetNumCols(...) Get the number of columns  
 GetNumObs(...) Get the number of observations  
 GetPointer() Get the C++ object pointer (internally used)  
 GetRealCol(col\_name) Get the real values from a column  
 GetUndefinedVals(col\_name) Get the undefined flags from a column  
 initialize(o\_gda) Constructor with a geoda object (internally used)

---

geoda_open	<i>Create an instance of geoda-class by reading from an ESRI Shapefile dataset</i>
------------	--

---

### Description

Create an instance of geoda-class by reading from an ESRI Shapefile dataset.

### Usage

geoda\_open(ds\_path)

**Arguments**

ds\_path (character) The path of the spatial dataset

**Value**

An instance of geoda-class

**Examples**

```
## Not run:
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- geoda_open(guerry_path)
guerry_df <- as.data.frame(guerry) # access as a data.frame
head(guerry_df)

## End(Not run)
```

---

get_neighbors	<i>Neighbors of one observation</i>
---------------	-------------------------------------

---

**Description**

Get neighbors for idx-th observation, idx starts from 1

**Usage**

```
get_neighbors(gda_w, idx)
```

**Arguments**

gda\_w A Weight object  
 idx A value indicates idx-th observation, idx start from 1

**Value**

A numeric vector of the neighbor indices, which start from 1

**Examples**

```
## Not run:
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
nbrs <- get_neighbors(queen_w, idx = 1)
cat("\nNeighbors of the 1-st observation are:", nbrs)

## End(Not run)
```

---

get\_neighbors\_weights *Weights values of the neighbors of one observation*

---

**Description**

Get the associated weights values of neighbors for idx-th observation

**Usage**

```
get_neighbors_weights(gda_w, idx)
```

**Arguments**

gda_w	A Weight object
idx	A value indicates idx-th observation, idx start from 1

**Value**

A numeric vector of the neighbor indices, which start from 1

**Examples**

```
## Not run:
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
nbrs <- get_neighbors_weights(queen_w, idx = 1)
cat("\nNeighbors of the 1-st observation are:", nbrs)

## End(Not run)
```

---

has\_isolates *Isolation/Island in Spatial Weights*

---

**Description**

Check if weights matrix has isolates, or if any observation has no neighbors

**Usage**

```
has_isolates(gda_w)
```

**Arguments**

gda_w	A Weight object
-------	-----------------

**Value**

A boolean value indicates if weights matrix is symmetric

**Examples**

```
## Not run:
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
has_isolates(queen_w)

## End(Not run)
```

---

hinge15_breaks	<i>(Box) Hinge15 Breaks</i>
----------------	-----------------------------

---

**Description**

Hinge15 breaks data into 6 groups like box plot groups (Lower outlier, < 25

**Usage**

```
hinge15_breaks(df)
```

**Arguments**

df                    A data frame with selected variable. E.g. guerry["Crm\_prs"]

**Value**

A vector of numeric values of computed breaks

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
hinge15_breaks(guerry['Crm_prs'])
```

---

hinge30\_breaks            *(Box) Hinge30 Breaks*

---

**Description**

Hinge30 breaks data into 6 groups like box plot groups (Lower outlier, < 25

**Usage**

```
hinge30_breaks(df)
```

**Arguments**

df                      A data frame with selected variable. E.g. guerry["Crm\_prs"]

**Value**

A vector of numeric values of computed breaks

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
hinge30_breaks(guerry['Crm_prs'])
```

---

is\_symmetric            *Symmetry of Weights Matrix*

---

**Description**

Check if weights matrix is symmetric

**Usage**

```
is_symmetric(gda_w)
```

**Arguments**

gda\_w                   A Weight object

**Value**

A boolean value indicates if weights matrix is symmetric

**Examples**

```
## Not run:
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
is_symmetric(queen_w)

## End(Not run)
```

---

join_count_ratio	<i>Join Count Ratio</i>
------------------	-------------------------

---

**Description**

Join count ratio is the join counts, the number of times a category is surrounded by neighbors of the same category, over the total number of neighbors after converting each category to a dummy variable.

**Usage**

```
join_count_ratio(clusters, w)
```

**Arguments**

clusters	A cluster classification variable (categorical values from a dataframe or values returned from cluster functions)
w	An instance of Weight class

**Value**

A data.frame with names "Cluster", "N", "Neighbors", "Join Count", "Ratio"

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
clusters <- skater(5, queen_w, data)
results <- join_count_ratio(clusters, queen_w)
results

## End(Not run)
```



---

kernel\_knn\_weights      *K-NN Kernel Spatial Weights*


---

**Description**

Create a kernel weights by specifying k-nearest neighbors and a kernel method

**Usage**

```
kernel_knn_weights(
  sf_obj,
  k,
  kernel_method,
  adaptive_bandwidth = TRUE,
  use_kernel_diagonals = FALSE,
  power = 1,
  is_inverse = FALSE,
  is_arc = FALSE,
  is_mile = TRUE
)
```

**Arguments**

sf_obj	An sf (simple feature) object
k	a positive integer number for k-nearest neighbors
kernel_method	a string value, which has to be one of 'triangular', 'uniform', 'epanechnikov', 'quartic', 'gaussian'
adaptive_bandwidth	(optional) TRUE (default) or FALSE: TRUE use adaptive bandwidth calculated using distance of k-nearest neighbors, FALSE use max distance of all observation to their k-nearest neighbors
use_kernel_diagonals	(optional) FALSE (default) or TRUE, apply kernel on the diagonal of weights matrix
power	(optional) The power (or exponent) of a number says how many times to use the number in a multiplication.
is_inverse	(optional) FALSE (default) or TRUE, apply inverse on distance value
is_arc	(optional) FALSE (default) or TRUE, compute arc distance between two observations
is_mile	(optional) TRUE (default) or FALSE, convert distance unit from mile to km.

**Value**

An instance of Weight-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
adptkernel_w = kernel_knn_weights(guerry, 6, "uniform")
summary(adptkernel_w)
```

---

kernel_weights	<i>Distance-based Kernel Spatial Weights</i>
----------------	--

---

**Description**

Create a kernel weights by specifying a bandwidth and a kernel method

**Usage**

```
kernel_weights(
  sf_obj,
  bandwidth,
  kernel_method,
  use_kernel_diagonals = FALSE,
  power = 1,
  is_inverse = FALSE,
  is_arc = FALSE,
  is_mile = TRUE
)
```

**Arguments**

sf_obj	An sf (simple feature) object
bandwidth	A positive numeric value of bandwidth
kernel_method	a string value, which has to be one of 'triangular', 'uniform', 'epanechnikov', 'quartic', 'gaussian'
use_kernel_diagonals	(optional) FALSE (default) or TRUE, apply kernel on the diagonal of weights matrix
power	(optional) The power (or exponent) of a number says how many times to use the number in a multiplication.
is_inverse	(optional) FALSE (default) or TRUE, apply inverse on distance value
is_arc	(optional) FALSE (default) or TRUE, compute arc distance between two observations
is_mile	(optional) TRUE (default) or FALSE, convert distance unit from mile to km.

**Value**

An instance of Weight-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
bandwidth <- min_distthreshold(guerry)
kernel_w <- kernel_weights(guerry, bandwidth, kernel_method = "uniform")
summary(kernel_w)
```

knn\_weights

*K-Nearest Neighbors-based Spatial Weights***Description**

Create a k-nearest neighbors based spatial weights

**Usage**

```
knn_weights(
  sf_obj,
  k,
  power = 1,
  is_inverse = FALSE,
  is_arc = FALSE,
  is_mile = TRUE
)
```

**Arguments**

sf_obj	An sf (simple feature) object
k	a positive integer number for k-nearest neighbors
power	(optional) The power (or exponent) of a number says how many times to use the number in a multiplication.
is_inverse	(optional) FALSE (default) or TRUE, apply inverse on distance value
is_arc	(optional) FALSE (default) or TRUE, compute arc distance between two observations
is_mile	(optional) TRUE (default) or FALSE, convert distance unit from mile to km.

**Value**

An instance of Weight-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
knn6_w <- knn_weights(guerry, 6)
summary(knn6_w)
```

---

LISA-class

*LISA class (Internally Used)*


---

### Description

A LISA-class that wrappers the statistics of LISA computation

### Fields

`gda_lisa` An object of GeoDaLISA

`p_vals` The pseudo-p values of significance of LISA computation

`c_vals` The cluster indicators of LISA computation

`lisa_vals` The local spatial autocorrelation values of LISA computation

`nn_vals` The number of neighbors of every observations in LISA computation

`labels` The cluster labels of LISA

`colors` The cluster colors (HEX format) of LISA

### Methods

`GetB0(current_p)` Get the Bonferroni bound value

`GetClusterIndicators()` Get the local cluster indicators returned from LISA computation.

`GetColors()` Get the cluster colors of LISA computation.

`GetFDR(current_p)` Get the False Discovery Rate value

`GetLISAValues()` Get the local spatial autocorrelation values returned from LISA computation.

`GetLabels()` Get the cluster labels of LISA computation.

`GetLocalSignificanceValues()` Get the local pseudo-p values of significance returned from LISA computation.

`GetNumNeighbors()` Get the number of neighbors of every observations in LISA computation.

`Run()` Call to run LISA computation

`SetPermutations(num_perm)` Set the number of permutations for the LISA computation

`SetSignificanceCutoff(cutoff)` Set the cutoff value of significance values

`SetThreads(num_threads)` Set the number of CPU threads for the LISA computation

`initialize(lisa_obj)` Constructor with a LISA object (internally used)

---

lisa_bo	<i>Bonferroni bound value of local spatial autocorrelation</i>
---------	--

---

**Description**

Get Bonferroni bound value based on current LISA computation and current significant p-value

**Usage**

```
lisa_bo(gda_lisa, current_p)
```

**Arguments**

gda_lisa	An instance of LISA object
current_p	A value of current significant p-value

**Value**

A numeric value of Bonferroni bound

**Examples**

```
## Not run:  
library(sf)  
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")  
guerry <- st_read(guerry_path)  
queen_w <- queen_weights(guerry)  
lisa <- local_moran(queen_w, guerry["Crm_prs"])  
bo <- lisa_bo(lisa, 0.05)  
bo  
  
## End(Not run)
```

---

lisa_clusters	<i>Get local cluster indicators</i>
---------------	-------------------------------------

---

**Description**

Get the local cluster indicators returned from LISA computation.

**Usage**

```
lisa_clusters(gda_lisa, cutoff = 0)
```

**Arguments**

gda_lisa	An instance of LISA object
cutoff	A value of cutoff for significance p-values to filter not-significant clusters, default=0.0, means not used

**Value**

A numeric vector of LISA cluster indicator

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_moran(queen_w, guerry["Crm_prs"])
clsts <- lisa_clusters(lisa)
clsts

## End(Not run)
```

---

lisa_colors	<i>Get cluster colors</i>
-------------	---------------------------

---

**Description**

Get the cluster colors of LISA computation.

**Usage**

```
lisa_colors(gda_lisa)
```

**Arguments**

gda_lisa	An instance of LISA object
----------	----------------------------

**Value**

A string vector of cluster colors

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_moran(queen_w, guerry["Crm_prs"])
clrs <- lisa_colors(lisa)
clrs

## End(Not run)
```

---

lisa_fdr	<i>False Discovery Rate value of local spatial autocorrelation</i>
----------	--

---

**Description**

Get False Discovery Rate value based on current LISA computation and current significant p-value

**Usage**

```
lisa_fdr(gda_lisa, current_p)
```

**Arguments**

gda_lisa	An instance of LISA object
current_p	A value of current significant p-value

**Value**

A numeric vector of False Discovery Rate

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_moran(queen_w, guerry["Crm_prs"])
fdr <- lisa_fdr(lisa, 0.05)
fdr

## End(Not run)
```

---

lisa_labels	<i>Get cluster labels</i>
-------------	---------------------------

---

**Description**

Get cluster labels of LISA computation.

**Usage**

```
lisa_labels(gda_lisa)
```

**Arguments**

gda\_lisa      An instance of LISA object

**Value**

A string vector of cluster labels

**Examples**

```
## Not run:  
library(sf)  
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")  
guerry <- st_read(guerry_path)  
queen_w <- queen_weights(guerry)  
lisa <- local_moran(queen_w, guerry["Crm_prs"])  
lbls <- lisa_labels(lisa)  
lbls  
  
## End(Not run)
```

---

lisa_num_nbrs	<i>Get numbers of neighbors for all observations</i>
---------------	--

---

**Description**

Get numbers of neighbors for all observations

**Usage**

```
lisa_num_nbrs(gda_lisa)
```

**Arguments**

gda\_lisa      An instance of LISA object



**Value**

A numeric vector of the number of neighbors

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_moran(queen_w, guerry["Crm_prs"])
nn <- lisa_num_nbrs(lisa)
nn

## End(Not run)
```

---

lisa\_pvalues

*Get pseudo-p values of LISA*

---

**Description**

Get the local pseudo-p values of significance returned from LISA computation.

**Usage**

```
lisa_pvalues(gda_lisa)
```

**Arguments**

gda\_lisa            An instance of LISA object

**Value**

A numeric vector of pseudo-p values of local spatial autocorrelation

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_moran(queen_w, guerry["Crm_prs"])
pvals <- lisa_pvalues(lisa)
pvals

## End(Not run)
```

---

lisa_values	<i>Get LISA values</i>
-------------	------------------------

---

**Description**

Get the local spatial autocorrelation values returned from LISA computation

**Usage**

```
lisa_values(gda_lisa)
```

**Arguments**

gda\_lisa            An instance of LISA object

**Value**

A numeric vector of local spatial autocorrelation

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_moran(queen_w, guerry["Crm_prs"])
lms <- lisa_values(lisa)
lms

## End(Not run)
```

---

local_bijoincount	<i>Bivariate Local Join Count Statistics</i>
-------------------	--

---

**Description**

The function to apply local Bivariate Join Count statistics

**Usage**

```
local_bijoincount(
  w,
  df,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
```

```

    cpu_threads = 6,
    seed = 123456789
  )

```

### Arguments

`w` An instance of Weight object

`df` A data frame with two selected variable. E.g. `guerry[c("TopCrm", "InvCrm")]`

`permutations` (optional) The number of permutations for the LISA computation

`permutation_method` (optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.

`significance_cutoff` (optional) A cutoff value for significance p-values to filter not-significant clusters

`cpu_threads` (optional) The number of cpu threads used for parallel LISA computation

`seed` (optional) The seed for random number generator

### Value

An instance of LISA-class

### Examples

```

library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
guerry["InvCrm"] <- 1 - guerry[["TopCrm"]]
lisa <- local_bijoincount(queen_w, guerry[c("TopCrm", "InvCrm")])
clsts <- lisa_clusters(lisa)
clsts

```

---

local\_bimoran

*Bivariate Local Moran Statistics*

---

### Description

The function to apply bivariate local Moran statistics

### Usage

```

local_bimoran(
  w,
  df,
  permutations = 999,
  permutation_method = "complete",

```

```

    significance_cutoff = 0.05,
    cpu_threads = 6,
    seed = 123456789
  )

```

### Arguments

**w** An instance of Weight object

**df** A data frame with two selected variable. E.g. `guerry[c('Crm_prs','Litercy')]`

**permutations** (optional) The number of permutations for the LISA computation

**permutation\_method** (optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.

**significance\_cutoff** (optional) A cutoff value for significance p-values to filter not-significant clusters

**cpu\_threads** (optional) The number of cpu threads used for parallel LISA computation

**seed** (optional) The seed for random number generator

### Value

An instance of LISA-class

### Examples

```

library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_bimoran(queen_w, guerry[c('Crm_prs','Litercy')])
lms <- lisa_values(lisa)
lms

```

---

local\_g

*Local Getis-Ord's G Statistics*

---

### Description

The function to apply Getis-Ord's local G statistics

**Usage**

```
local_g(
  w,
  df,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
  cpu_threads = 6,
  seed = 123456789
)
```

**Arguments**

w	An instance of Weight object
df	A data frame with selected variable only. E.g. <code>guerry["Crm_prs"]</code>
permutations	(optional) The number of permutations for the LISA computation
permutation_method	(optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.
significance_cutoff	(optional) A cutoff value for significance p-values to filter not-significant clusters
cpu_threads	(optional) The number of cpu threads used for parallel LISA computation
seed	(optional) The seed for random number generator

**Value**

An instance of LISA-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_g(queen_w, guerry["Crm_prs"])
lms <- lisa_values(lisa)
lms
```

---

local\_geary

*Local Geary Statistics*

---

**Description**

The function to apply local Geary statistics

**Usage**

```
local_geary(
  w,
  df,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
  cpu_threads = 6,
  seed = 123456789
)
```

**Arguments**

**w** An instance of Weight object

**df** A data frame with selected variable only. E.g. `guerry["Crm_prs"]`

**permutations** (optional) The number of permutations for the LISA computation

**permutation\_method** (optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.

**significance\_cutoff** (optional) A cutoff value for significance p-values to filter not-significant clusters

**cpu\_threads** (optional) The number of cpu threads used for parallel LISA computation

**seed** (optional) The seed for random number generator

**Value**

An instance of LISA-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_geary(queen_w, guerry["Crm_prs"])
lms <- lisa_values(lisa)
lms
```

---

local\_gstar

*Local Getis-Ord's G\* Statistics*

---

**Description**

The function to apply Getis-Ord's local G\* statistics

**Usage**

```
local_gstar(
  w,
  df,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
  cpu_threads = 6,
  seed = 123456789
)
```

**Arguments**

**w** An instance of Weight object

**df** A data frame with selected variable only. E.g. `guerry["Crm_prs"]`

**permutations** (optional) The number of permutations for the LISA computation

**permutation\_method** (optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.

**significance\_cutoff** (optional) A cutoff value for significance p-values to filter not-significant clusters

**cpu\_threads** (optional) The number of cpu threads used for parallel LISA computation

**seed** (optional) The seed for random number generator

**Value**

An instance of LISA-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_gstar(queen_w, guerry["Crm_prs"])
lms <- lisa_values(lisa)
lms
```

---

local\_joincount      *Local Join Count Statistics*

---

**Description**

The function to apply local Join Count statistics

**Usage**

```
local_joincount(
  w,
  df,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
  cpu_threads = 6,
  seed = 123456789
)
```

**Arguments**

**w** An instance of Weight object

**df** A data frame with selected variable only. E.g. `guerry["Crm_prs"]`

**permutations** (optional) The number of permutations for the LISA computation

**permutation\_method** (optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.

**significance\_cutoff** (optional) A cutoff value for significance p-values to filter not-significant clusters

**cpu\_threads** (optional) The number of cpu threads used for parallel LISA computation

**seed** (optional) The seed for random number generator

**Value**

An instance of LISA-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_joincount(queen_w, guerry['TopCrm'])
clsts <- lisa_clusters(lisa)
clsts
```

---

local\_moran

*Local Moran Statistics*

---

**Description**

The function to apply local Moran statistics



**Usage**

```
local_moran(
  w,
  df,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
  cpu_threads = 6,
  seed = 123456789
)
```

**Arguments**

w	An instance of Weight object
df	A data frame with only selected variable. E.g. guerry["Crm_prs"]
permutations	(optional) The number of permutations for the LISA computation
permutation_method	(optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.
significance_cutoff	(optional) A cutoff value for significance p-values to filter not-significant clusters
cpu_threads	(optional) The number of cpu threads used for parallel LISA computation
seed	(optional) The seed for random number generator

**Value**

An instance of LISA-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_moran(queen_w, guerry["Crm_prs"])
lms <- lisa_values(lisa)
lms
```

---

local\_moran\_eb

*Local Moran with Empirical Bayes(EB) Rate*


---

**Description**

The function to apply local Moran with EB Rate statistics. The EB rate is first computed from "event" and "base" variables, and then used in local moran statistics.

**Usage**

```
local_moran_eb(
  w,
  df,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
  cpu_threads = 6,
  seed = 123456789
)
```

**Arguments**

w	An instance of Weight object
df	A data frame with two selected variable: one is "event", another is "base" variable. E.g. <code>guerry[c("hr60", "po60")]</code>
permutations	(optional) The number of permutations for the LISA computation
permutation_method	(optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.
significance_cutoff	(optional) A cutoff value for significance p-values to filter not-significant clusters
cpu_threads	(optional) The number of cpu threads used for parallel LISA computation
seed	(optional) The seed for random number generator

**Value**

An instance of LISA-class

**Examples**

```
## Not run:
library(sf)
nat <- st_read("natregimes.shp")
nat_w <- queen_weights(nat)
lisa <- local_moran_eb(queen_w, guerry[c("hr60", "po60")])
lms <- lisa_values(lisa)
lms

## End(Not run)
```

---

local\_multigeary      *Local Multivariate Geary Statistics*

---

### Description

The function to apply local Multivariate Geary statistics

### Usage

```
local_multigeary(
  w,
  df,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
  cpu_threads = 6,
  seed = 123456789
)
```

### Arguments

w	An instance of Weight object
df	A data frame with selected variables only. E.g. guerry["Crm_prs"]
permutations	(optional) The number of permutations for the LISA computation
permutation_method	(optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.
significance_cutoff	(optional) A cutoff value for significance p-values to filter not-significant clusters
cpu_threads	(optional) The number of cpu threads used for parallel LISA computation
seed	(optional) The seed for random number generator

### Value

An instance of LISA-class

### Examples

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants',
  'Suicids')]
lisa <- local_multigeary(queen_w, data)
lms <- lisa_clusters(lisa)
lms
```

---

local\_multijoincount *(Multivariate) Colocation Local Join Count Statistics*

---

### Description

The function to apply (multivariate) colocation local Join Count statistics

### Usage

```
local_multijoincount(
  w,
  df,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
  cpu_threads = 6,
  seed = 123456789
)
```

### Arguments

w	An instance of Weight object
df	A data frame with selected variables only. E.g. <code>guerry[c("TopCrm", "TopWealth", "TopLit")]</code>
permutations	(optional) The number of permutations for the LISA computation
permutation_method	(optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.
significance_cutoff	(optional) A cutoff value for significance p-values to filter not-significant clusters
cpu_threads	(optional) The number of cpu threads used for parallel LISA computation
seed	(optional) The seed for random number generator

### Value

An instance of LISA-class

### Examples

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_multijoincount(queen_w,
  guerry[c('TopWealth', 'TopWealth', 'TopLit')])
clsts <- lisa_clusters(lisa)
clsts
```

---

 local\_multiquantilelisa

*Multivariate Quantile LISA Statistics*


---

## Description

The function to apply multivariate quantile LISA statistics

## Usage

```
local_multiquantilelisa(
  w,
  df,
  k,
  q,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
  cpu_threads = 6,
  seed = 123456789
)
```

## Arguments

w	An instance of Weight object
df	A data frame with selected variables only. E.g. <code>guerry[c("TopCrm", "TopWealth", "TopLit")]</code>
k	A vector of "k" values indicate the number of quantiles for each variable. Value range e.g. [1, 10]
q	A vector of "q" values indicate which quantile or interval for each variable used in local join count statistics. Value starts from 1.
permutations	(optional) The number of permutations for the LISA computation
permutation_method	(optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.
significance_cutoff	(optional) A cutoff value for significance p-values to filter not-significant clusters
cpu_threads	(optional) The number of cpu threads used for parallel LISA computation
seed	(optional) The seed for random number generator

## Value

An instance of LISA-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_multiquantilelisa(queen_w, guerry[c("Crm_prp", "Litercy")],
k=c(4,4), q=c(1,1))
clsts <- lisa_clusters(lisa)
clsts
```

---

local\_quantilelisa      *Quantile LISA Statistics*

---

**Description**

The function to apply quantile LISA statistics

**Usage**

```
local_quantilelisa(
  w,
  df,
  k,
  q,
  permutations = 999,
  permutation_method = "complete",
  significance_cutoff = 0.05,
  cpu_threads = 6,
  seed = 123456789
)
```

**Arguments**

w	An instance of Weight object
df	A data frame with selected variable only. E.g. guerry["Crm_prs"]
k	A value indicates the number of quantiles. Value range e.g. [1, 10]
q	A value indicates which quantile or interval used in local join count statistics. Value stars from 1.
permutations	(optional) The number of permutations for the LISA computation
permutation_method	(optional) The permutation method used for the LISA computation. Options are 'complete', 'lookup'. Default is 'complete'.
significance_cutoff	(optional) A cutoff value for significance p-values to filter not-significant clusters
cpu_threads	(optional) The number of cpu threads used for parallel LISA computation
seed	(optional) The seed for random number generator

**Value**

An instance of LISA-class

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
lisa <- local_quantilelisa(queen_w, guerry["Crm_prs"], k=4, q=1)
clsts <- lisa_clusters(lisa)
clsts
```

---

make\_spatial

*Make Spatial*

---

**Description**

Make spatially constrained clusters from spatially non-constrained clusters using the contiguity information from the input weights

**Usage**

```
make_spatial(clusters, w)
```

**Arguments**

clusters	A cluster classification variable (categorical values from a dataframe or values returned from cluster functions)
w	An instance of Weight class

**Value**

A vector of categorical values (cluster classification)

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
clusters <- kmeans(5, data)
queen_w <- queen_weights(guerry)
results <- make_spatial(clusters, queen_w)
results

## End(Not run)
```

---

maxp\_greedy

*A greedy algorithm to solve the max-p-region problem*


---

### Description

The max-p-region problem is a special case of constrained clustering where a finite number of geographical areas are aggregated into the maximum number of regions (max-p-regions), such that each region is geographically connected and the clusters could maximize internal homogeneity.

### Usage

```
maxp_greedy(
  w,
  df,
  bound_variable,
  min_bound,
  iterations = 99,
  initial_regions = vector("numeric"),
  scale_method = "standardize",
  distance_method = "euclidean",
  random_seed = 123456789,
  cpu_threads = 6,
  rdist = numeric()
)
```

### Arguments

w	An instance of Weight class
df	A data frame with selected variables only. E.g. <code>guerry[c("Crm_prs", "Crm_prp", "Litercy")]</code>
bound_variable	A numeric vector of selected bounding variable
min_bound	A minimum value that the sum value of bounding variable int each cluster should be greater than
iterations	(optional): The number of iterations of greedy algorithm. Defaults to 99.
initial_regions	(optional): The initial regions that the local search starts with. Default is empty. means the local search starts with a random process to "grow" clusters
scale_method	(optional) One of the scaling methods 'raw', 'standardize', 'demean', 'mad', 'range_standardize', 'range_adjust' to apply on input data. Default is 'standardize' (Z-score normalization).
distance_method	(optional) The distance method used to compute the distance between observation i and j. Defaults to "euclidean". Options are "euclidean" and "manhattan"
random_seed	(optional) The seed for random number generator. Defaults to 123456789.
cpu_threads	(optional) The number of cpu threads used for parallel computation
rdist	(optional) The distance matrix (lower triangular matrix, column wise storage)



**Value**

A names list with names "Clusters", "Total sum of squares", "Within-cluster sum of squares", "Total within-cluster sum of squares", and "The ratio of between to total sum of squares".

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
bound_variable <- guerry['Pop1831']
min_bound <- 3236.67 # 10% of Pop1831
maxp_clusters <- maxp_greedy(queen_w, data, bound_variable, min_bound, iterations=99)
maxp_clusters

## End(Not run)
```

---

maxp\_sa

*A simulated annealing algorithm to solve the max-p-region problem*


---

**Description**

The max-p-region problem is a special case of constrained clustering where a finite number of geographical areas are aggregated into the maximum number of regions (max-p-regions), such that each region is geographically connected and the clusters could maximize internal homogeneity.

**Usage**

```
maxp_sa(
  w,
  df,
  bound_variable,
  min_bound,
  cooling_rate,
  sa_maxit = 1,
  iterations = 99,
  initial_regions = vector("numeric"),
  scale_method = "standardize",
  distance_method = "euclidean",
  random_seed = 123456789,
  cpu_threads = 6,
  rdist = numeric()
)
```

**Arguments**

w	An instance of Weight class
df	A data frame with selected variables only. E.g. <code>guerry[c("Crm_prs", "Crm_prp", "Litercy")]</code>
bound_variable	A numeric vector of selected bounding variable
min_bound	A minimum value that the sum value of bounding variable int each cluster should be greater than
cooling_rate	The cooling rate of a simulated annealing algorithm. Defaults to 0.85
sa_maxit	(optional): The number of iterations of simulated annealing. Defaults to 1
iterations	(optional): The number of iterations of SA algorithm. Defaults to 99.
initial_regions	(optional): The initial regions that the local search starts with. Default is empty. means the local search starts with a random process to "grow" clusters
scale_method	(optional) One of the scaling methods 'raw', 'standardize', 'demean', 'mad', 'range_standardize', 'range_adjust' to apply on input data. Default is 'standardize' (Z-score normalization).
distance_method	(optional) The distance method used to compute the distance between observation i and j. Defaults to "euclidean". Options are "euclidean" and "manhattan"
random_seed	(optional) The seed for random number generator. Defaults to 123456789.
cpu_threads	(optional) The number of cpu threads used for parallel computation
rdist	(optional) The distance matrix (lower triangular matrix, column wise storage)

**Value**

A names list with names "Clusters", "Total sum of squares", "Within-cluster sum of squares", "Total within-cluster sum of squares", and "The ratio of between to total sum of squares".

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
bound_variable <- guerry['Pop1831']
min_bound <- 3236.67 # 10% of Pop1831
maxp_clusters <- maxp_sa(queen_w, data, bound_variable, min_bound, cooling_rate=0.85, sa_maxit=1)
maxp_clusters

## End(Not run)
```

---

maxp\_tabu

*A tabu-search algorithm to solve the max-p-region problem*


---

### Description

The max-p-region problem is a special case of constrained clustering where a finite number of geographical areas are aggregated into the maximum number of regions (max-p-regions), such that each region is geographically connected and the clusters could maximize internal homogeneity.

### Usage

```
maxp_tabu(
  w,
  df,
  bound_variable,
  min_bound,
  tabu_length = 10,
  conv_tabu = 10,
  iterations = 99,
  initial_regions = vector("numeric"),
  scale_method = "standardize",
  distance_method = "euclidean",
  random_seed = 123456789,
  cpu_threads = 6,
  rdist = numeric()
)
```

### Arguments

w	An instance of Weight class
df	A data frame with selected variables only. E.g. <code>guerry[c("Crm_prs", "Crm_prp", "Litercy")]</code>
bound_variable	A numeric vector of selected bounding variable
min_bound	A minimum value that the sum value of bounding variable in each cluster should be greater than
tabu_length	(optional): The length of a tabu search heuristic of tabu algorithm. Defaults to 10.
conv_tabu	(optional): The number of non-improving moves. Defaults to 10.
iterations	(optional): The number of iterations of Tabu algorithm. Defaults to 99.
initial_regions	(optional): The initial regions that the local search starts with. Default is empty. means the local search starts with a random process to "grow" clusters
scale_method	(optional) One of the scaling methods 'raw', 'standardize', 'demean', 'mad', 'range_standardize', 'range_adjust' to apply on input data. Default is 'standardize' (Z-score normalization).

distance\_method (optional) The distance method used to compute the distance between observation *i* and *j*. Defaults to "euclidean". Options are "euclidean" and "manhattan"

random\_seed (optional) The seed for random number generator. Defaults to 123456789.

cpu\_threads (optional) The number of cpu threads used for parallel computation

rdist (optional) The distance matrix (lower triangular matrix, column wise storage)

**Value**

A names list with names "Clusters", "Total sum of squares", "Within-cluster sum of squares", "Total within-cluster sum of squares", and "The ratio of between to total sum of squares".

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
bound_variable <- guerry['Pop1831']
min_bound <- 3236.67 # 10% of Pop1831
maxp_clusters <- maxp_tabu(queen_w, data, bound_variable, min_bound, tabu_length=10, conv_tabu=10)
maxp_clusters

## End(Not run)
```

---

max_neighbors	<i>Maximum Neighbors of Spatial Weights</i>
---------------	---

---

**Description**

Get the number of maximum neighbors of spatial weights

**Usage**

```
max_neighbors(gda_w)
```

**Arguments**

gda\_w            A Weight object

**Value**

The number of maximum neighbors of spatial weights

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
max_neighbors(queen_w)

## End(Not run)
```

---

mean_neighbors	<i>Mean Neighbors of Spatial Weights</i>
----------------	--

---

**Description**

Get the number of mean neighbors of spatial weights

**Usage**

```
mean_neighbors(gda_w)
```

**Arguments**

gda\_w            A Weight object

**Value**

The number of mean neighbors of spatial weights

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
mean_neighbors(queen_w)

## End(Not run)
```

---

median_neighbors	<i>Median Neighbors of Spatial Weights</i>
------------------	--

---

**Description**

Get the number of median neighbors of spatial weights

**Usage**

```
median_neighbors(gda_w)
```

**Arguments**

gda_w	A Weight object
-------	-----------------

**Value**

The number of median neighbors of spatial weights

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
median_neighbors(queen_w)

## End(Not run)
```

---

min_distthreshold	<i>Minimum Distance Threshold for Distance-based Weights</i>
-------------------	--

---

**Description**

Get minimum threshold of distance that makes sure each observation has at least one neighbor

**Usage**

```
min_distthreshold(sf_obj, is_arc = FALSE, is_mile = TRUE)
```

**Arguments**

sf_obj	An sf (simple feature) object
is_arc	(optional) FALSE (default) or TRUE, compute arc distance between two observations
is_mile	(optional) TRUE (default) or FALSE, if 'is_arc' option is TRUE, then 'is_mile' will set distance unit to 'mile' or 'km'.

**Value**

A numeric value of minimum threshold of distance

**Examples**

```
## Not run:  
library(sf)  
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")  
guerry <- st_read(guerry_path)  
dist_thres <- min_distthreshold(guerry)  
dist_thres  
  
## End(Not run)
```

---

min\_neighbors

*Minimum Neighbors of Spatial Weights*

---

**Description**

Get the number of minimum neighbors of spatial weights

**Usage**

```
min_neighbors(gda_w)
```

**Arguments**

gda\_w            A Weight object

**Value**

The number of minimum neighbors of spatial weights

**Examples**

```
## Not run:  
library(sf)  
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")  
guerry <- st_read(guerry_path)  
queen_w <- queen_weights(guerry)  
min_neighbors(queen_w)  
  
## End(Not run)
```

---

natural_breaks	<i>Natural Breaks (Jenks)</i>
----------------	-------------------------------

---

**Description**

Natural Breaks group data whose boundaries are set where there are relatively big differences.

**Usage**

```
natural_breaks(k, df)
```

**Arguments**

k	A numeric value indicates how many breaks
df	A data frame with selected variable. E.g. guerry["Crm_prs"]

**Value**

A vector of numeric values of computed breaks

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
natural_breaks(k=5, guerry['Crm_prs'])
```

---

neighbor_match_test	<i>Local Neighbor Match Test</i>
---------------------	----------------------------------

---

**Description**

The local neighbor match test is to assess the extent of overlap between k-nearest neighbors in geographical space and k-nearest neighbors in multi-attribute space.

**Usage**

```
neighbor_match_test(
  df,
  k,
  scale_method = "standardize",
  distance_method = "euclidean",
  power = 1,
  is_inverse = FALSE,
  is_arc = FALSE,
  is_mile = TRUE
)
```



**Arguments**

df	A subset of sf object with selected variables. E.g. <code>guerry[c("Crm_prs", "Crm_prp", "Litercy")]</code>
k	a positive integer number for k-nearest neighbors searching.
scale_method	(optional) One of the scaling methods 'raw', 'standardize', 'demean', 'mad', 'range_standardize', 'range_adjust' to apply on input data. Default is 'standardize' (Z-score normalization).
distance_method	(optional) The type of distance metrics used to measure the distance between input data. Options are 'euclidean', 'manhattan'. Default is 'euclidean'.
power	(optional) The power (or exponent) of a number says how many times to use the number in a multiplication.
is_inverse	(optional) FALSE (default) or TRUE, apply inverse on distance value.
is_arc	(optional) FALSE (default) or TRUE, compute arc distance between two observations.
is_mile	(optional) TRUE (default) or FALSE, convert distance unit from mile to km.

**Value**

A data.frame with two columns "Cardinality" and "Probability".

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
nbr_test <- neighbor_match_test(data, 6)
nbr_test
```

---

percentile\_breaks      *Percentile Breaks*

---

**Description**

Percentile breaks data into 6 groups: the lowest 1 10-50

**Usage**

```
percentile_breaks(df)
```

**Arguments**

df	A data frame with selected variable. E.g. <code>guerry["Crm_prs"]</code>
----	--

**Value**

A vector of numeric values of computed breaks

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
percentile_breaks(guerry['Crm_prs'])
```

---

*p\_GeoDa-class*                      *p\_GeoDa*

---

**Description**

*p\_GeoDa* class is a RefClass that wraps the C++ 'GeoDa' class. See C++ functions in `rcpp_rgeoda.cpp`

---

*p\_GeoDaTable-class*                      *p\_GeoDaTable*

---

**Description**

*p\_GeoDaTable* class is a RefClass that wraps the C++ 'GeoDaTable' class. See C++ functions in `rcpp_rgeoda.cpp`

---

*p\_GeoDaWeight-class*                      *p\_GeoDaWeight*

---

**Description**

*p\_GeoDaWeight* class is a RefClass that wraps the C++ GeoDaWeight class. See C++ functions in `rcpp_weights.cpp`

---

*p\_LISA-class*                              *p\_LISA*

---

**Description**

*p\_LISA* class is a RefClass that wraps the C++ LISA class. See C++ functions in `rcpp_lisa.cpp`

---

quantile_breaks	<i>Quantile Breaks</i>
-----------------	------------------------

---

**Description**

Quantile breaks data into groups that each have the same number of observations

**Usage**

```
quantile_breaks(k, df)
```

**Arguments**

k	A numeric value indicates how many breaks
df	A data frame with selected variable. E.g. guerry["Crm_prs"]

**Value**

A vector of numeric values of computed breaks

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
quantile_breaks(k=5, guerry['Crm_prs'])
```

---

queen_weights	<i>Queen Contiguity Spatial Weights</i>
---------------	---

---

**Description**

Create a Queen contiguity weights with options of "order", "include lower order" and "precision threshold"

**Usage**

```
queen_weights(  
  sf_obj,  
  order = 1,  
  include_lower_order = FALSE,  
  precision_threshold = 0  
)
```

**Arguments**

**sf\_obj**            An sf (simple feature) object  
**order**            (Optional) Order of contiguity  
**include\_lower\_order**  
                     (Optional) Whether or not the lower order neighbors should be included in the weights structure  
**precision\_threshold**  
                     (Optional) The precision of the underlying shape file is insufficient to allow for an exact match of coordinates to determine which polygons are neighbors

**Value**

An instance of Weight-class

**Examples**

```

library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
summary(queen_w)

```

---

read\_gal

*Read a .GAL file*

---

**Description**

Create a spatial weights object from a .GAL file

**Usage**

```
read_gal(file_path, id_vec = c())
```

**Arguments**

**file\_path**        The file path of the .GAL file  
**id\_vec**            The id\_vec is the id values used in the .GAL file. Default is empty.

**Value**

A weights object

---

read_gwt	<i>Read a .GWT file</i>
----------	-------------------------

---

**Description**

Create a spatial weights object from a .GWT file

**Usage**

```
read_gwt(file_path, id_vec = c())
```

**Arguments**

file_path	The file path of the .GWT file
id_vec	The id_vec is the id values used in the .GWT file. Default is empty.

**Value**

A weights object

---

read_swm	<i>Read a .SWM file</i>
----------	-------------------------

---

**Description**

Create a spatial weights object from a .SWM file

**Usage**

```
read_swm(file_path, id_vec = numeric())
```

**Arguments**

file_path	The file path of the .SWM file
id_vec	The id_vec is the id values used in the .SWM file. e.g. c(0,1,2,3,...)

**Value**

A weights object

---

redcap	<i>Regionalization with dynamically constrained agglomerative clustering and partitioning</i>
--------	---

---

## Description

REDCAP (Regionalization with dynamically constrained agglomerative clustering and partitioning) is developed by D. Guo (2008). Like SKATER, REDCAP starts from building a spanning tree with 4 different ways (single-linkage, average-linkage, ward-linkage and the complete-linkage). The single-linkage way leads to build a minimum spanning tree. Then, REDCAP provides 2 different ways (first-order and full-order constraining) to prune the tree to find clusters. The first-order approach with a minimum spanning tree is exactly the same with SKATER. In GeoDa and pygeoda, the following methods are provided: \\* First-order and Single-linkage \\* Full-order and Complete-linkage \\* Full-order and Average-linkage \\* Full-order and Single-linkage \\* Full-order and Ward-linkage

## Usage

```
redcap(
  k,
  w,
  df,
  method = "fullorder-averagelinkage",
  bound_variable = data.frame(),
  min_bound = 0,
  scale_method = "standardize",
  distance_method = "euclidean",
  random_seed = 123456789,
  cpu_threads = 6,
  rdist = numeric()
)
```

## Arguments

k	The number of clusters
w	An instance of Weight class
df	A data frame with selected variables only. E.g. <code>guerry[c("Crm_prs", "Crm_prp", "Litercy")]</code>
method	"firstorder-singlelinkage", "fullorder-completelinkage", "fullorder-averagelinkage", "fullorder-singlelinkage", "fullorder-wardlinkage"
bound_variable	(optional) A data frame with selected bound variabl
min_bound	(optional) A minimum bound value that applies to all clusters
scale_method	(optional) One of the scaling methods 'raw', 'standardize', 'demean', 'mad', 'range_standardize', 'range_adjust' to apply on input data. Default is 'standardize' (Z-score normalization).

distance\_method (optional) The distance method used to compute the distance between observation i and j. Defaults to "euclidean". Options are "euclidean" and "manhattan"

random\_seed (int,optional) The seed for random number generator. Defaults to 123456789.

cpu\_threads (optional) The number of cpu threads used for parallel computation

rdist (optional) The distance matrix (lower triangular matrix, column wise storage)

**Value**

A names list with names "Clusters", "Total sum of squares", "Within-cluster sum of squares", "Total within-cluster sum of squares", and "The ratio of between to total sum of squares".

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
guerry_clusters <- redcap(4, queen_w, data, "fullorder-completelinkage")
guerry_clusters

## End(Not run)
```

---

rook\_weights

*Rook Contiguity Spatial Weights*


---

**Description**

Create a Rook contiguity weights with options of "order", "include lower order" and "precision threshold"

**Usage**

```
rook_weights(
  sf_obj,
  order = 1,
  include_lower_order = FALSE,
  precision_threshold = 0
)
```

**Arguments**

sf\_obj An sf (simple feature) object

order (Optional) Order of contiguity

include\_lower\_order

(Optional) Whether or not the lower order neighbors should be included in the weights structure

precision\_threshold

(Optional) The precision of the underlying shape file is insufficient to allow for an exact match of coordinates to determine which polygons are neighbors

### Value

An instance of Weight-class

### Examples

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
rook_w <- rook_weights(guerry)
summary(rook_w)
```

---

save\_weights

*Save Spatial Weights*

---

### Description

Save spatial weights to a file

### Usage

```
save_weights(gda_w, id_variable, out_path, layer_name = "")
```

### Arguments

gda_w	A Weight object
id_variable	The id variable (a data.frame) that defines the unique value of each observation when saving a weights file
out_path	The path of an output weights file
layer_name	(optional) The name of the layer of input dataset

### Value

A boolean value indicates if save successfully or failed



## Examples

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
save_weights(queen_w, guerry_df['CODE_DE'], out_path = '/path/Guerry_r.gal')

## End(Not run)
```

---

schc

*Spatially Constrained Hierarchical Clustering (SCHC)*


---

## Description

Spatially constrained hierarchical clustering is a special form of constrained clustering, where the constraint is based on contiguity (common borders). The method builds up the clusters using agglomerative hierarchical clustering methods: single linkage, complete linkage, average linkage and Ward's method (a special form of centroid linkage). Meanwhile, it also maintains the spatial contiguity when merging two clusters.

## Usage

```
schc(
  k,
  w,
  df,
  method = "average",
  bound_variable = data.frame(),
  min_bound = 0,
  scale_method = "standardize",
  distance_method = "euclidean",
  rdist = numeric()
)
```

## Arguments

k	The number of clusters
w	An instance of Weight class
df	A data frame with selected variables only. E.g. <code>guerry[c("Crm_prs", "Crm_prp", "Litercy")]</code>
method	"single", "complete", "average", "ward"
bound_variable	(optional) A data frame with selected bound variabl
min_bound	(optional) A minimum bound value that applies to all clusters

scale\_method One of the scaling methods 'raw', 'standardize', 'demean', 'mad', 'range\_standardize', 'range\_adjust' to apply on input data. Default is 'standardize' (Z-score normalization).

distance\_method (optional) The distance method used to compute the distance between observation i and j. Defaults to "euclidean". Options are "euclidean" and "manhattan"

rdist (optional) The distance matrix (lower triangular matrix, column wise storage)

### Value

A names list with names "Clusters", "Total sum of squares", "Within-cluster sum of squares", "Total within-cluster sum of squares", and "The ratio of between to total sum of squares".

### Examples

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
guerry_clusters <- schc(4, queen_w, data, "complete")
guerry_clusters
```

---

set_neighbors	<i>Set neighbors of an observation</i>
---------------	--

---

### Description

Set neighbors for idx-th observation, idx starts from 1

### Usage

```
set_neighbors(gda_w, idx, nbrs)
```

### Arguments

gda\_w A Weight object

idx A value indicates idx-th observation, idx start from 1

nbrs A list indicates the neighbors of idx-th observation (id start from 1)

### Examples

```
## Not run:
new_w <- create_weights(10)
set_neighbors(new_w, 1, c(2,3))
update_weights(new_w)

## End(Not run)
```

---

 set\_neighbors\_with\_weights

*Set neighbors and weights values of an observation*


---

### Description

Set neighbors and the associated weights values for idx-th observation, idx starts from 1

### Usage

```
set_neighbors_with_weights(gda_w, idx, nbrs, wvals)
```

### Arguments

gda_w	A Weight object
idx	A value indicates idx-th observation, idx start from 1
nbrs	A list indicates the neighbors of idx-th observation (id start from 1)
wvals	A list indicates the associated weights values of the neighbors

### Examples

```
## Not run:
new_w <- create_weights(10)
set_neighbors(new_w, 1, c(2,3))
update_weights(new_w)

## End(Not run)
```

---

 sf\_to\_geoda

*Create an instance of geoda-class from a 'sf' object*


---

### Description

Create an instance of geoda-class from a 'sf' object returned from 'st\_read()' function. NOTE: The table content is NOT used to create an instance of geoda-class.

### Usage

```
sf_to_geoda(sf_obj, with_table = TRUE)
```

### Arguments

sf_obj	An instance of 'sf' object
with_table	A boolean flag indicates if table is copied from sf object to create geoda object. Default is TRUE.

**Value**

An instance of geoda-class

---

 skater

*Spatial C(K)luster Analysis by Tree Edge Removal*


---

**Description**

SKATER forms clusters by spatially partitioning data that has similar values for features of interest.

**Usage**

```
skater(
  k,
  w,
  df,
  bound_variable = data.frame(),
  min_bound = 0,
  scale_method = "standardize",
  distance_method = "euclidean",
  random_seed = 123456789,
  cpu_threads = 6,
  rdist = numeric()
)
```

**Arguments**

k	The number of clusters
w	An instance of Weight class
df	A data frame with selected variables only. E.g. <code>guerry[c("Crm_prs", "Crm_prp", "Litercy")]</code>
bound_variable	(optional) A data frame with selected bound variable
min_bound	(optional) A minimum bound value that applies to all clusters
scale_method	One of the scaling methods 'raw', 'standardize', 'demean', 'mad', 'range_standardize', 'range_adjust' to apply on input data. Default is 'standardize' (Z-score normalization).
distance_method	(optional) The distance method used to compute the distance between observation i and j. Defaults to "euclidean". Options are "euclidean" and "manhattan"
random_seed	(int,optional) The seed for random number generator. Defaults to 123456789.
cpu_threads	(optional) The number of cpu threads used for parallel computation
rdist	(optional) The distance matrix (lower triangular matrix, column wise storage)

**Value**

A names list with names "Clusters", "Total sum of squares", "Within-cluster sum of squares", "Total within-cluster sum of squares", and "The ratio of between to total sum of squares".

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
guerry_clusters <- skater(4, queen_w, data)
guerry_clusters
```

---

spatial\_lag

*Spatial Lag*


---

**Description**

Compute the spatial lag for idx-th observation using selected variable and current weights matrix

**Usage**

```
spatial_lag(gda_w, df)
```

**Arguments**

gda_w	A Weight object
df	A data frame with selected variable only. E.g. guerry["Crm_prs"]

**Value**

A data.frame with one column "Spatial Lag"

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
crm_lag <- spatial_lag(queen_w, guerry["Crm_prs"])
crm_lag

## End(Not run)
```

---

spatial\_validation      *Spatial Validation*

---

### Description

Spatial validation provides a collection of validation measures including 1. fragmentations (entropy, simpson), 2. join count ratio, 3. compactness (isoperimeter quotient) and 4. diameter.

### Usage

```
spatial_validation(sf_obj, clusters, w)
```

### Arguments

sf_obj	An sf (simple feature) object
clusters	A cluster classification variable (categorical values from a dataframe or values returned from cluster functions)
w	An instance of Weight class

### Value

A list with names "Is Spatially Constrained", "Fragmentation", "Join Count Ratio", "Compactness", and "Diameter".

### Examples

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
data <- guerry[c('Crm_prs', 'Crm_prp', 'Litercy', 'Donatns', 'Infants', 'Suicids')]
clusters <- skater(5, queen_w, data)
results <- spatial_validation(guerry, clusters, queen_w)
results

## End(Not run)
```

---

sp_to_geoda	<i>Create an instance of geoda-class from a 'sp' object</i>
-------------	---

---

**Description**

Create an instance of geoda-class from a 'sp' object. NOTE: The table content is NOT used to create an instance of geoda-class.

**Usage**

```
sp_to_geoda(sp_obj, with_table = TRUE)
```

**Arguments**

sp_obj	An instance of 'sp' object
with_table	A boolean flag indicates if table is copied from sf object to create geoda object. Default is TRUE

**Value**

An instance of geoda-class

---

stddev_breaks	<i>Standard Deviation Breaks</i>
---------------	----------------------------------

---

**Description**

Standard deviation breaks first transforms data to standard deviation units (mean=0, stddev=1), and then divide the range of values into 6 groups.

**Usage**

```
stddev_breaks(df)
```

**Arguments**

df	A data frame with selected variable. E.g. guerry["Crm_prs"]
----	---

**Value**

A vector of numeric values of computed breaks

**Examples**

```
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
stddev_breaks(guerry['Crm_prs'])
```

---

summary.Weight	<i>Summary of Spatial Weights</i>
----------------	-----------------------------------

---

**Description**

Override the summary() function for spatial weights

**Usage**

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

**Arguments**

object	A Weight object
...	summary optional parameters

**Value**

A summary description of an instance of Weight-class

**Examples**

```
## Not run:
library(sf)
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
summary(queen_w)

## End(Not run)
```

---

update_weights	<i>Update meta data of a spatial weights</i>
----------------	--

---

**Description**

Update meta data of a spatial weights. This function can be used after calling ‘set\_neighbor()’ function .

**Usage**

```
update_weights(gda_w)
```

**Arguments**

gda_w	A Weight object
-------	-----------------



**Examples**

```
## Not run:
new_w <- create_weights(10)
set_neighbors(new_w, 1, c(2,3))
update_weights(new_w)

## End(Not run)
```

---

 Weight-class

*Weight class (Internally Used)*


---

**Description**

A wrapper class for p\_GeoDaWeight class

**Fields**

gda\_w An object of p\_GeoDaWeight-class  
 is\_symmetric If weights matrix is symmetric  
 sparsity Sparsity of weights matrix  
 min\_neighbors Minimum number of neighbors  
 max\_neighbors Maximum number of neighbors  
 num\_obs Number of observations  
 mean\_neighbors Mean number of neighbors  
 median\_neighbors Median number of neighbors  
 has\_isolates If the weights matrix has any isolates

**Methods**

GetNeighborWeights(idx) Get weights values of neighbors for idx-th observation, idx starts from 0  
 GetNeighbors(idx) Get neighbors for idx-th observation, idx starts from 0  
 GetPointer() Get the C++ object pointer (internally used)  
 GetSparsity() Get sparsity computed from weights matrix  
 HasIsolates() Check if weights matrix has isolates, or if any observation has no neighbors  
 IsSymmetric() Check if weights matrix is symmetric  
 SaveToFile(out\_path, layer\_name, id\_name, id\_values) Save current spatial weights to a file.

out\_path: The path of an output weights file  
 layer\_name : The name of the layer of input dataset  
 id\_name : The id name (or field name), which is an associated column contains unique values, that makes sure that the weights are connected to the correct observations in the data table.  
 id\_values : The tuple of values of selected id\_name (column/field)

SetNeighbors(idx, nbrs) Set neighbors for one observation  
 SetNeighborsAndWeights(idx, nbrs, nbr\_w) Set neighbors with weights values for one observation  
 SpatialLag(values) Compute spatial lag values for values of selected variable  
 Update(updateStats = TRUE) Update the weights meta data  
 initialize(o\_gda\_w) Constructor with a GeoDaWeight object (internally used)

---

weights\_sparsity      *Sparsity of Spatial Weights*

---

### Description

Get sparsity (

### Usage

```
weights_sparsity(gda_w)
```

### Arguments

gda\_w                  A Weight object

### Value

A numeric value of spatial weights sparsity

### Examples

```
## Not run:
guerry_path <- system.file("extdata", "Guerry.shp", package = "rgeoda")
guerry <- st_read(guerry_path)
queen_w <- queen_weights(guerry)
weights_sparsity(queen_w)

## End(Not run)
```

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