

Package ‘OasisR’

August 30, 2017

Type Package

Version 3.0.0

Date 2017-08-30

Title Outright Tool for the Analysis of Spatial Inequalities and Segregation

Author Mihai Tivadar <mihai.tivadar@irstea.fr>

Maintainer Mihai Tivadar <mihai.tivadar@irstea.fr>

Description A set of indexes and tests for the analysis of social segregation.

Depends R (>= 3.4.1)

Imports rgdal (>= 1.2-8), rgeos (>= 0.3-23), spdep (>= 0.6-13),
measurements (>= 1.1.0), methods (>= 3.3.1), seg (>= 0.5-1),
outliers (>= 0.14)

License GPL-2 | GPL-3

LazyData true

Suggests testthat, knitr

VignetteBuilder knitr

RoxygenNote 6.0.1

NeedsCompilation no

Repository CRAN

Date/Publication 2017-08-30 15:09:22 UTC

R topics documented:

ACE	3
ACEDuncan	4
ACEDuncanPoly	6
ACEDuncanPolyK	7
ACEPoly	9
ACL	10
ACO	12

area	13
Atkinson	14
boundaries	15
CMulti	16
contig	17
Delta	18
DIDuncan	19
DIMorrill	20
DIMorrillK	21
distance	22
distcenter	23
DIWong	24
DMulti	26
DPxx	27
DPxy	28
Eta2	29
Gini	30
Gini2	31
GiniMulti	32
Gorard	33
GreHSize	34
HLoc	34
HMulti	35
HShannon	36
HTheil	37
ISDuncan	38
ISimpson	39
ISMorrill	40
ISMorrillK	41
ISWong	42
LQ	44
LShannon	45
LSimpson	46
NShannon	47
ordinalseg	48
perimeter	49
PMulti	50
Poo	51
Pxx	52
Pxy	54
rankorderseg	55
RCE	57
RCEPoly	58
RCEPolyK	59
RCL	61
RCO	62
RelDivers	63
ResamplePlot	64

<i>ACE</i>	3
ResampleTest	65
segdata	68
segdataclean	69
SP	71
spatinteract	72
spatmultiseg	74
xPx	75
xPy	76
Index	77

ACE *A function to compute Massey Absolute Centralisation Index (ACE)*

Description

The absolute centralization index measures a group spatial distribution compared to the distribution of land area around the city center. The function can be used in two ways: to provide an area vector and a vector containing the distances between spatial units centroids and the central spatial unit or a external geographic information source (spatial object or shape file).

Usage

```
ACE(x, a = NULL, dc = NULL, center = 1,
    spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

- x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
- a - a numeric vector containing spatial unit areas
- dc - a numeric vector containing the distances between spatial units centroids and the central spatial unit
- center - a numeric value giving the number of the spatial unit that represents the center in the table
- spatobj - a spatial object (SpatialPolygonsDataFrame) with geographic information
- folder - a character vector with the folder (directory) name indicating where the shapefile is located on the drive
- shape - a character vector with the name of the shapefile (without the .shp extension).

Value

a numeric vector containing asolute centralisation index value for each group

References

Massey D. S. and Denton N. A. (1988) *The dimensions of residential segregation*. Social Forces 67(2), pp. 281-315.

See Also

[ACEPoly](#),
[RCE](#), [RCEPoly](#), [RCEPolyK](#),
[ACEDuncan](#), [ACEDuncanPoly](#),
[ACEDuncanPolyK](#)

Examples

```
x <- segdata@data[ ,1:2]
ar<-area(segdata)
distc<- distcenter(segdata, center = 28)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

ACE(x, a = ar, dc=distc)

ACE(x, spatobj = segdata, center = 28)

ACE(x, folder = foldername, shape = shapename, center = 28)
```

ACEDuncan

A function to compute Duncan's Absolute Centralisation Index (ACE-Duncan)

Description

Duncan's absolute centralization index measures the proportion of a group that should change its localization to achieve the same level of centralization as the rest of the population. The function can be used in two ways: to provide a vector containing the distances between spatial/organizational unit centroids or a external geographic information source (spatial object or shape file).

Usage

```
ACEDuncan(x, dc = NULL, center = 1,
  spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
dc	- a numeric vector containing the distances between spatial units centroids and the central spatial unit
center	- a numeric value giving the number of the spatial unit that represents the center in the table
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a numeric vector containing Duncan's asolute centralisation index value for each group

References

Duncan O. D. and Duncan B. (1955) *A Methodological Analysis of Segregation Indexes*. American Sociological Review 41, pp. 210-217

See Also

[ACEDuncanPoly](#), [ACEDuncanPolyK](#),

[RCE](#), [RCEPoly](#), [RCEPolyK](#)

[ACE](#), [ACEPoly](#)

Examples

```
x <- segdata@data[ ,1:2]
distc<- distcenter(segdata, center = 28)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

ACEDuncan(x, dc=distc)

ACEDuncan(x, spatobj = segdata, center = 28)

ACEDuncan(x, folder = foldername, shape = shapename, center = 28)
```

ACEDuncanPoly	<i>A function to compute Duncan's Polycentric Absolute Centralisation Index</i>
---------------	---

Description

Polycentric version of Duncan's absolute centralization index. The function can be used in two ways: to provide a vector containing the distances between spatial/organizational unit centroids or a external geographic information source (spatial object or shape file).

Usage

```
ACEDuncanPoly(x, dc = NULL, center = 1,
              spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
dc	- a numeric matrix/vector containing the distances between spatial units centroids and the central spatial unit(s).
center	- a numeric vector giving the number of the spatial/organizational units that represents the centers in the table
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a numeric vector containing Duncan's absolute centralisation index value for each group

References

Duncan O. D. and Duncan B. (1955) *A Methodological Analysis of Segregation Indexes*. American Sociological Review 41, pp. 210-217

See Also

[ACEDuncan](#), [ACEDuncanPolyK](#),
[RCE](#), [RCEPoly](#), [RCEPolyK](#)
[ACE](#), [ACEPoly](#)

Examples

```
x <- segdata@data[ ,1:2]
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

ACEDuncanPoly(x, spatobj = segdata, center = c(28, 83) )

ACEDuncanPoly(x, folder = foldername, shape = shapename, center = c(28, 83))

center <- c(28, 83)
polydist <- matrix(data = NA, nrow = nrow(x), ncol = length(center))
for (i in 1:ncol(polydist))
  polydist[,i] <- distcenter(spatobj = segdata, center = center[i])
ACEDuncanPoly(x, dc = polydist)

distmin <- vector(length = nrow(x))
for (i in 1:nrow(polydist)) distmin[i] <- min(polydist[i,])
ACEDuncan(x, dc = distmin)
```

ACEDuncanPolyK	<i>A function to compute Duncan's Constrained Absolute Centralisation Index</i>
----------------	---

Description

Constrained (local) version of Duncan's centralization index. The function can be used in two ways: to provide a matrix containing the distances between spatial/organizational unit centroids or a external geographic information source (spatial object or shape file).

Usage

```
ACEDuncanPolyK(x, dc = NULL, K = NULL, kdist = NULL, center = 1,
               spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
dc	- a numeric matrix/vector containing the distances between spatial units centroids and the central spatial unit(s).
K	- the number of neighbourhoods under the influence of a center
kdist	- the maximal distance that defines the neighbourhoods influenced by a center

center	- a numeric vector giving the number of the spatial units that represent the centers in the table
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a matrix containing relative centralisation index values

References

Duncan O. D. and Duncan B. (1955) *A Methodological Analysis of Segregation Indexes*. American Sociological Review 41, pp. 210-217

Folch D.C and Rey S. J (2016) *The centralization index: A measure of local spatial segregation*. Papers in Regional Science 95 (3), pp. 555-576

See Also

[ACEDuncan](#), [ACEDuncanPoly](#),

[RCE](#), [RCEPoly](#), [RCEPolyK](#)

[ACE](#), [ACEPoly](#)

Examples

```
x <- segdata@data[,1:2]
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

ACEDuncanPolyK(x, spatobj = segdata, center = c(28, 83))

ACEDuncanPolyK(x, folder = foldername, shape = shapename, center = c(28, 83), K = 3)

center <- c(28, 83)
polydist <- matrix(data = NA, nrow = nrow(x), ncol = length(center))
for (i in 1:ncol(polydist))
  polydist[,i] <- distcenter(spatobj = segdata, center = center[i])
ACEDuncanPolyK(x, dc = polydist, kdist = 2)
```

ACEPoly

A function to compute Massey's Polycentric Absolute Centralisation Index

Description

The absolute centralization index measures a group spatial distribution compared to the distribution of land area around the city center. The function can be used in two ways: to provide an area vector and a vector containing the distances between spatial units centroids and the central spatial unit or a external geographic information source (spatial object or shape file).

Usage

```
ACEPoly(x, a = NULL, dc = NULL, center = 1,  
        spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

- | | |
|---------|--|
| x | - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group. |
| a | - a numeric vector containing spatial unit areas |
| dc | - a numeric matrix containing the distances between spatial units centroids and the central spatial units |
| center | - a numeric vector giving the number of the spatial units that represent the centers in the table |
| spatobj | - a spatial object (SpatialPolygonsDataFrame) with geographic information |
| folder | - a character vector with the folder (directory) name indicating where the shapefile is located on the drive |
| shape | - a character vector with the name of the shapefile (without the .shp extension). |

Value

a numeric vector containing absolute centralisation index value for each group

References

Massey D. S. and Denton N. A. (1988) *The dimensions of residential segregation*. Social Forces 67(2), pp. 281-315.

See Also

[ACE](#), [RCE](#),
[RCEPoly](#), [RCEPolyK](#),
[ACEDuncan](#), [ACEDuncanPoly](#),
[ACEDuncanPolyK](#)

Examples

```

x <- segdata@data[ ,1:2]
ar<-area(segdata)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

ACEPoly(x, spatobj = segdata, center = c(28, 83) )

ACEPoly(x, folder = foldername, shape = shapename, center = c(28, 83))

center <- c(28, 83)
polydist <- matrix(data = NA, nrow = nrow(x), ncol = length(center))
for (i in 1:ncol(polydist))
  polydist[,i] <- distcenter(spatobj = segdata, center = center[i])
ACEPoly(x, a = ar, dc = polydist)

distmin <- vector(length = nrow(x))
for (i in 1:nrow(polydist)) distmin[i] <- min(polydist[i,])
ACE(x, a = ar, dc = distmin)

```

 ACL

A function to compute Absolute Clustering Index (ACL)

Description

The absolute clustering index, ACL, expresses the average number of a group's members in nearby spatial units, as a proportion of the total population in those spatial units. The spatial interactions can be expressed as a contiguity matrix (with diagonal equal to 1), as an inverse exponential function of the distance between spatial units centers (with diagonal equal to 0.6 of the square root of each spatial units area) or other user specified interaction matrix. The function can be used in two ways: to provide a spatial interactions matrix (a contiguity matrix or a distance matrix) or a external geographic information source (spatial object or shape file).

Usage

```

ACL(x, spatmat = 'c', c = NULL, queen = FALSE, d = NULL, distin = 'm',
distout = 'm', diagval = '0', beta = 1, spatobj = NULL, folder = NULL, shape = NULL)

```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
spatmat	- the method used for spatial calculations: 'c' for the contiguity matrix (by default) or any other user spatial interaction matrix and 'd' for the inverse exponential function of the distance.
c	- a modified binary contiguity (adjacency) symmetric matrix where each element C_{ij} equals 1 if i -th and j -th spatial units are adjacent or identical, and 0 otherwise.
queen	- logical parameter defining criteria used for contiguity matrix computation, TRUE for queen, FALSE (by default) for rook
d	- a matrix of the distances between spatial unit centroids
distin	- input metric conversion, based on bink package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
distout	- output metric conversion, based on bink package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
diagval	- when providing a spatial object or a shape file, the user has the choice of the spatial matrix diagonal definition: diagval = '0' (by default) for a null diagonal and diagval = 'a' to compute the diagonal as $0.6 * \text{square root}$ (spatial/organizational unitsarea) (White, 1983)
beta	- distance decay parameter
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a numeric vector containing Absolute Clustering index value for each group

References

Massey D. S. and Denton N. A. (1988) *The dimensions of residential segregation*. Social Forces 67(2), pp. 281-315.

See Also

Proximity measures: [Pxx](#), [Pxy](#), [Poo](#), [SP](#)

Relative Clustering Index: [RCL](#)

Examples

```

x <- segdata@data[,1:2]
contiguity <- contig(segdata)
diag(contiguity) <- 1
ar<-area(segdata)
dist <- distance(segdata)
diag(dist)<-sqrt(ar) * 0.6
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

ACL(x, c = contiguity)

ACL(x, spatobj = segdata)

ACL(x, spatmat = 'd', folder = foldername, shape = shapename)

ACL(x, spatmat = 'd', diagval = 'a', spatobj = segdata)

ACL(x, d = dist, spatmat = 'd')
```

ACO

A function to compute Absolute Concentration index (ACO)

Description

The absolute concentration index, ACO, computes the total area inhabited by a group, and compares the result to the minimum and maximum possible areas that could be inhabited by that group in the study area. The function can be used in two ways: to provide an area vector or a external geographic information source (spatial object or shape file).

Usage

```
ACO(x, a = NULL, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
a	- a numeric vector containing spatial unit areas
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a numeric vector containing Absolute Concentration index value for each group

References

Massey D. S. and Denton N. A. (1988) *The dimensions of residential segregation*. Social Forces 67(2), pp. 281-315.

See Also

Delta Index: [Delta](#)

Relative Concentration Index: [RCO](#)

Examples

```
x <- GreHSize@data[,3:5]
ar <- area(GreHSize)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'GreHSize'

ACO(x, a = ar)

ACO(x, spatobj = GreHSize)

ACO(x, folder = foldername, shape = shapename)
```

area

A function to compute the spatial units' areas

Description

The function is based on **rgdal** package and can be used with a shape file or an R spatial object (SpatialPolygonsDataFrame).

Usage

```
area(spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

spatobj	- a spatial object (SpatialPolygonsDataFrame) containing geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile with the geographic information is located.
shape	- a character vector with the name of the shapefile (without the .shp extension) which contains the geographic information

Value

A area vector

See Also

Other spatial functions used for segregation indices computation: [contig](#), [perimeter](#), [distance](#), [distcenter](#), [boundaries](#)

Examples

```
area(segdata)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'
area(folder = foldername, shape = shapename)
```

Atkinson

A function to compute Atkinson segregation index

Description

The spatial version of Atkinson inequality index is based on Lorenz curves. The user can decide which part of the curve contributes more to the index, by choosing the value of the shape parameter, delta.

Usage

```
Atkinson (x, delta = 0.5)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
delta	- an inequality aversion parameter

Value

a numeric vector containing the Atkinson's segregation index value for each group

References

James, D. and K. E. Taeuber (1985) *Measures of Segregation*. Sociological Methodology 15, pp. 1-32

See Also

One-group evenness indices: [ISDuncan](#), [Gini](#), [Gorard](#), [HTheil](#), [ISWong](#), [ISMorrill](#), [ISMorrillK](#)
Between groups dissimilarity indices: [DIDuncan](#), [Gini2](#), [DIMorrill](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[,7:8]
Atkinson(x)
Atkinson(x, 0.1)
Atkinson(x, delta = 0.9)
```

boundaries

A function to compute the matrix of common boundaries

Description

The function is based on **rgdal** and **rgeos** packages and it can be used with a shape file or an R spatial object (`SpatialPolygonsDataFrame`).

Usage

```
boundaries(spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

spatobj	- a spatial object (<code>SpatialPolygonsDataFrame</code>) containing geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile with the geographic information is located.
shape	- a character vector with the name of the shapefile (without the <code>.shp</code> extension) which contains the geographic information

Value

A common boundaries matrix

See Also

Other spatial functions used for segregation indices computation: [area](#), [contig](#), [perimeter](#), [distance](#), [distcenter](#)

Examples

```
boundaries(segdata)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'
boundaries(folder = foldername, shape = shapename)
```

CMulti	<i>A function to compute multi-group squared coefficient of variation index</i>
--------	---

Description

The index can be interpreted as a measure of the variance of the spatial representation of the groups across spatial units, or as a normalized chi-squared measure of association between groups and units.

Usage

```
CMulti(x)
```

Arguments

`x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

multi-group entropy segregation index

References

Reardon S. F. and Firebaugh G. (2002) *Measures of multi-group segregation*. *Sociological Methodology*, 32, pp. 33-67.

See Also

Multi-group indices: [PMulti](#), [GiniMulti](#), [DMulti](#), [HMulti](#), [RelDivers](#)

Social diversity indices: [HShannon](#), [NShannon](#), [ISimpson](#),

Examples

```
x <- segdata@data[,1:2]
CMulti(x)
```

contig *A function to compute the contiguity matrix*

Description

The function is based on **rgdal** and **spdep** packages and can be used with a shape file or an R spatial object (SpatialPolygonsDataFrame).

Usage

```
contig(spatobj = NULL, folder = NULL, shape = NULL, queen = FALSE)
```

Arguments

spatobj	- a spatial object (SpatialPolygonsDataFrame) containing geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile with the geographic information is located.
shape	- a character vector with the name of the shapefile (without the .shp extension) which contains the geographic information
queen	= TRUE for queen criteria, FALSE (by default) for rook criteria

Value

A first order contiguity (adjacency) matrix, where each element $[i,j]$ equals 1 if i -th and j -th spatial units are adjacent, 0 otherwise (queen or rook criteria)

See Also

Other spatial functions used for segregation indices computation: [area](#), [perimeter](#), [distance](#), [distcenter](#), [boundaries](#)

Examples

```
contig(segdata)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'
contig(folder = foldername, shape = shapename)
```

Delta

A function to compute Delta index

Description

The Delta index is a specific application of dissimilarity index [DIDuncan](#) which simply measures the dissimilarity between the spatial distribution of a group and the spatial distribution of available land. It can be interpreted as the share of group that would have to move to achieve uniform density over all spatial units. The function can be used in two ways: to provide an area vector or a external geographic information source (spatial object or shape file).

Usage

```
Delta(x, a = NULL, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

- | | |
|---------|--|
| x | - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group. |
| a | - a numeric vector containing spatial unit areas |
| spatobj | - a spatial object (SpatialPolygonsDataFrame) with geographic information |
| folder | - a character vector with the folder (directory) name indicating where the shapefile is located on the drive |
| shape | - a character vector with the name of the shapefile (without the .shp extension). |

Value

a numeric vector containing Delta index value for each group

References

Duncan O. D., Cuzzoert and Duncan B. (1961) *Problems in analyzing areal data*. Statistical geography, Glencoe, Illinois: The free press of Glencoe

See Also

Absolute Concentration Index: [ACO](#)

Relative Concentration Index: [RCO](#)

Examples

```
x <- segdata@data[ ,1:2]
ar <- area(segdata)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

Delta(x, a = ar)

Delta(x, spatobj = segdata)

Delta(x, folder = foldername, shape = shapename)
```

DIDuncan

A function to compute Duncan dissimilarity segregation index

Description

Duncan's dissimilarity index is the segregation index most commonly used in the literature. It is derived from Lorenz curves as the maximum difference between the segregation curve and the diagonal. The index measures the unevenness of a group's spatial distribution compared to another group. It can be interpreted as the share of the group that would have to move to achieve an even distribution compared to another group.

Usage

```
DIDuncan(x)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

a matrix containing dissimilarity index values

References

Duncan O. D. and Duncan B. (1955) *A Methodological Analysis of Segregation Indexes*. American Sociological Review 41, pp. 210-217

See Also

Other one-group evenness indices: [ISDuncan](#), [Gini](#), [Gorard](#), [Atkinson](#), [HTheil](#), [ISWong](#), [ISMorrill](#), [ISMorrillK](#)

Between groups dissimilarity indices: [DIMorrill](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[,1:2]
DIDuncan(x)
```

 DIMorrill

A function to compute Morrill's dissimilarity index

Description

Morrill's dissimilarity index is a development of [DIDuncan](#)'s index which takes into account the interactions between spatial units(contiguity). The function can be used in two ways: to provide a contiguity matrix or a external geographic information source (spatial object or shape file).

Usage

```
DIMorrill(x, c = NULL, queen = FALSE, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

- | | |
|---------|--|
| x | - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group. |
| c | - a standard binary contiguity (adjacency) symmetric matrix where each element C_{ij} equals 1 if i -th and j -th spatial units are adjacent, and 0 otherwise. |
| queen | - a logical parameter defining criteria used for contiguity matrix computation, TRUE for queen, FALSE (by default) for rook |
| spatobj | - a spatial object (SpatialPolygonsDataFrame) with geographic information |
| folder | - a character vector with the folder (directory) name indicating where the shapefile is located on the drive |
| shape | - a character vector with the name of the shapefile (without the .shp extension) . |

Value

a matrix with Morrill's dissimilarity index values

References

Morrill B. (1991) *On the measure of geographic segregation*. Geography research forum, 11, pp. 25-36.

See Also

Other one-group evenness indices: [ISDuncan](#), [Gini](#), [Gorard](#), [Atkinson](#), [HTheil](#), [ISWong](#), [ISMorrill](#), [ISMorrillK](#)

Between groups dissimilarity indices: [DIDuncan](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[ ,1:2]
contiguity <- contig(segdata)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

DIMorrill(x, c = contiguity)

DIMorrill(x, spatobj = segdata, queen = FALSE)

DIMorrill(x, folder = foldername, shape = shapename)
```

 DIMorrillK

A function to compute K-th order Morrill's dissimilarity index

Description

This function compute an adaptation of Morrill's dissimilarity index which takes into account the interactions between spatial units defined by K order contiguity matrix. The function can be used in two ways: to provide a contiguity matrix or a external geographic information source (spatial object or shape file).

Usage

```
DIMorrillK(x, ck = NULL, queen = FALSE, spatobj = NULL,
  folder = NULL, shape = NULL, K = 2, f = 'exp', beta = 1, prec = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
ck	- a list with contiguity matrix for each order (from 1 to K)
queen	- logical parameter difining criteria used for contiguity matrix computation, TRUE for queen, FALSE (by default) for rook
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension) .
K	- contiguity matrix order
f	- the distance function, f = 'exp' (by default) for negative exponential function and f = 'rec' for reciprocal function
beta	- distance decay parameter
prec	- precision parameter. If not NULL, the function stop computing the spatial interaction when the impact on the indice is bellow 10^{-prec}

Value

a matrix with Generalized Morrill's dissimilarity index values

References

Morrill B. (1991) *On the measure of geographic segregation*. Geography research forum, 11, pp. 25-36.

See Also

Other one-group evenness indices: [ISDuncan](#), [Gini](#), [Gorard](#), [Atkinson](#), [HTheil](#), [ISWong](#), [ISMorrill](#), [ISMorrillK](#)

Between groups dissimilarity indices: [DIDuncan](#), [DIMorrill](#), [DIWong](#)

Examples

```
x <- segdata@data[ ,1:2]
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

DIMorrillK(x, spatobj = segdata, queen = FALSE, K = 3)

DIMorrillK(x, folder = foldername, shape = shapename, K = 4, f = 'rec')
```

distance	<i>A function to compute the distance matrix between centroids of spatial units</i>
----------	---

Description

The function is based on **rgdal** and **rgeos** packages and can be used with a shape file or an R spatial object (`SpatialPolygonsDataFrame`).

Usage

```
distance(spatobj = NULL, folder = NULL, shape = NULL,
  distin = 'm', distout = 'm', diagval = '0')
```

Arguments

spatobj	- a spatial object (<code>SpatialPolygonsDataFrame</code>) containing geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile with the geographic information is located.
shape	- a character vector with the name of the shapefile (without the <code>.shp</code> extension) which contains the geographic information

- distin - input metric conversion, based on **measurements** package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
- distout - output metric conversion, based on **measurements** package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
- diagval - the user has the choice of the definition of the diagonal: diagval = '0' (by default) for an 'empty' diagonal and diagval = 'a' to compute the diagonal as $0.6 * \text{square root}(\text{spatial units area})$ (White, 1983)

Value

A matrix with the distance between centroids

See Also

Other spatial functions used for segregation indices computation: [area](#), [contig](#), [perimeter](#), [distcenter](#), [boundaries](#)

Examples

```
distance(segdata)

foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'
distance(folder = foldername, shape = shapename)
```

distcenter	<i>A function to compute the distance from spatial units centroids to the center</i>
------------	--

Description

The function is based on **rgdal** and **rgeos** packages and it can be used with a shape file or an R spatial object (SpatialPolygonsDataFrame).

Usage

```
distcenter(spatobj = NULL, folder = NULL, shape = NULL,
center = 1, distin = 'm', distout = 'm')
```

Arguments

- spatobj - a spatial object (SpatialPolygonsDataFrame) containing geographic information
- folder - a character vector with the folder (directory) name indicating where the shapefile with the geographic information is located.
- shape - a character vector with the name of the shapefile (without the .shp extension) which contains the geographic information

center	- the row number of the center
distin	- input metric conversion, based on measurements package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
distout	- output metric conversion, based on measurements package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.

Value

A vector with the distance to the center's centroid

See Also

Other spatial functions used for segregation indices computation: [area](#), [contig](#), [perimeter](#), [distance](#), [boundaries](#)

Examples

```
distcenter(segdata, center = 46)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'
distcenter(folder = foldername, shape = shapename, center = 19)
```

 DIWong

A function to compute Wongs's dissimilarity index

Description

Wong's dissimilarity index is a development of [DIDuncan](#)'s which takes into account the interactions between spatial units (common boundaries and perimeter/area ratios). The function can be used in two ways: to provide spatial data (boundaries matrix, a perimeter vector and an area vector) or a external geographic information source (spatial object or shape file).

Usage

```
DIWong(x, b = NULL, a = NULL, p = NULL, ptype = 'int', variant = 's',
       spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total totals because this will be interpreted as a group
b	- a common boundaries matrix where each element B_{ij} equals the shared boundary of i -th and j -th spatial units.
a	- a numeric vector containing spatial unit areas
p	- a numeric vector containing spatial units perimeters.

ptype	- a string variable giving two options for perimeter calculation when a spatial object or shapefile is provided: 'int' to use only interior borders of spatial units, and 'all' to use entire borders, including to the exterior of the area
variant	- a character variable that allows to choose the index version: variant = 's' for the dissimilarity index adjusted for contiguous spatial units boundary lengths and perimeter/area ratio (by default) and variant = 'w' for the version without perimeter/area ratio
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a matrix containing Wong's dissimilarity index values

References

Wong D. W. S. (1993) *Spatial Indices of Segregation*. Urban Studies, 30 (3), pp. 559-572.

See Also

Other one-group evenness indices: [ISDuncan](#), [Gini](#), [Gorard](#), [Atkinson](#), [HTheil](#), ['ISWong](#), [ISMorrill](#), [ISMorrillK](#)

Between groups dissimilarity indices: [DIDuncan](#), [DIMorrill](#), [DIMorrillK](#)

Examples

```
x <- segdata@data[ ,1:2]
bound <- boundaries(segdata)
per <- perimeter(segdata)
ar <- area(segdata)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

DIWong(x, b = bound, p = per, a = ar)

DIWong(x, spatobj = segdata, variant = 'w')

DIWong(x, folder = foldername, shape = shapename, ptype = 'all')
```

DMulti*A function to compute multi-group dissimilarity index*

Description

Multi-group dissimilarity index, is a multi-group version of Duncan's dissimilarity index ([DIDuncan](#))

Usage

```
DMulti(x)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

multi-group dissimilarity index

References

Sakoda J. N. (1981) *A generalized Index of dissimilarity*. Demography,18, 245-250

See Also

Multi-group indices: [PMulti](#), [GiniMulti](#), [HMulti](#), [CMulti](#), [RelDivers](#)

Social diversity indices: [HShannon](#), [NShannon](#), [ISimpson](#),

Examples

```
x <- segdata@data[ ,1:2]
DMulti(x)
```

DPxx

*A function to compute the distance-decay isolation index (DPxx)***Description**

The distance decay isolation index, DPxx, is a spatial adaptation of isolation index xPx. The function can be used in two ways: to provide a distance matrix or a external geographic information source (spatial object or shape file).

Usage

```
DPxx(x, d = NULL, distin = 'm', distout = 'm', diagval = '0', beta = 1,
     spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

- | | |
|---------|--|
| x | - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group. |
| d | - a matrix of the distances between spatial unit centroids |
| distin | - input metric conversion, based on bink package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc. |
| distout | - output metric conversion, based on bink package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc. |
| diagval | - when providing a spatial object or a shape file, the user has the choice of the spatial matrix diagonal definition: diagval = '0' (by default) for an null diagonal and diagval = 'a' to compute the diagonal as 0.6 * square root (spatial/organizational unitsarea) (White, 1983) |
| beta | - distance decay parameter |
| spatobj | - a spatial object (SpatialPolygonsDataFrame) with geographic information |
| folder | - a character vector with the folder (directory) name indicating where the shapefile is located on the drive |
| shape | - a character vector with the name of the shapefile (without the .shp extension). |

Value

a numeric vector containing the distance-decay isolation index value for each group

References

Morgan, B. S. (1983) *A Distance-Decay Based Interaction Index to Measure Residential Segregation*. Area 15(3), pp. 211-217.

See Also

Isolation indices: [xPx](#), [Eta2](#)

Interaction indices: [xPy](#), [DPxy](#)

Examples

```
x <- segdata@data[,1:2]
ar <- area(segdata)
dist <- distance(segdata)
diag(dist)<-sqrt(ar) * 0.6
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

DPxx(x, d = dist)

DPxx(x, spatobj = segdata, diagval = 'a')

DPxx(x, folder = foldername, shape = shapename, diagval = '0')
```

 DPxy

A function to compute the distance-decay interaction index (DPxy)

Description

The distance decay interaction index, DPxy, is a spatial adaptation of interaction index [xPy](#). The function can be used in two ways: to provide a distance matrix or a external geographic information source (spatial object or shape file).

Usage

```
DPxy(x, d = NULL, distin = 'm', distout = 'm', diagval = '0',
     beta = 1, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
d	- a matrix of the distances between spatial unit centroids
distin	- input metric conversion, based on bin k package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
distout	- output metric conversion, based on bin k package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.

diagval	- when providing a spatial object or a shape file, the user has the choice of the spatial matrix diagonal definition: diagval = '0' (by default) for an null diagonal and diagval = 'a' to compute the diagonal as 0.6 * square root (spatial/organizational unitsarea) (White, 1983)
beta	- distance decay parameter
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a numeric matrix containing the distance-decay isolation index values

References

Morgan, B. S. (1983) *An Alternate Approach to the Development of a Distance-Based Measure of Racial Segregation*. American Journal of Sociology 88, pp. 1237-1249.

See Also

Isolation indices: [xPx](#), [Eta2](#), [DPxx](#)

Interaction index: [xPy](#)

Examples

```
x <- segdata@data[,1:2]
ar <- area(segdata)
dist <- distance(segdata)
diag(dist)<-sqrt(ar) * 0.6
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

DPxy(x, d = dist)

DPxy(x, spatobj = segdata, diagval = 'a')

DPxy(x, folder = foldername, shape = shapename, diagval = '0')
```

Eta2

A function to compute adjusted isolation index (Eta2)

Description

The adjusted isolation index is the standardized version of the isolation index, [xPx](#), which controls for the effect of total population structure. Using the approximate version of [xPx](#), the adjusted index is equal to Eta2 (the square of the correlation ratio) which, in the case of the binomial variable, is identical to the square of the mean square contingency coefficient phi. It can be used as a segregation score and varies from 0 (minimum segregation) to 1 (maximum segregation).

Usage`Eta2(x)`**Arguments**

`x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

a numeric vector containing the adjusted isolation index value for each group

References

Bell W. (1954) *A probability model for the measurement of ecological segregation*. Social Forces 32(4), pp. 357-364

Duncan O. D. and Duncan B. (1955) *Residential Distribution and Occupational Stratification..* American Journal of Sociology 60 (5), pp. 493-503

See Also

Isolation indices: [xPx](#), [DPxx](#)

Interaction indices: [xPy](#), [DPxy](#)

Examples

```
x <- segdata@data[ ,1:2]
Eta2(x)
```

Gini

A function to compute Spatial Gini's segregation index

Description

The spatial version of the Gini index can be derived from the Lorenz curve as the area between the segregation curve and the diagonal.

Usage`Gini(x)`

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

a numeric vector containing the Gini's segregation index value for each group

References

Duncan O. D. and Duncan B. (1955) *A Methodological Analysis of Segregation Indexes*. American Sociological Review 41, pp. 210-217

See Also

Other one-group evenness indices: [ISDuncan](#), [Atkinson](#), [Gorard](#), [HTheil](#), ['ISWong](#), [ISMorrill](#), [ISMorrillK](#)

Between groups dissimilarity indices: [DIDuncan](#), [Gini2](#), [DIMorrill](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[,1:2]
Gini(x)
```

Gini2

A function to compute Spatial Gini's between group index

Description

The between group version of Gini index is obtained by computing the index for a subpopulation formed by each pair of groups

Usage

```
Gini2(x)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

a matrix with between group Gini index

References

Duncan O. D. and Duncan B. (1955) *A Methodological Analysis of Segregation Indexes*. American Sociological Review 41, pp. 210-217

See Also

Other one-group evenness indices: [ISDuncan](#), [Gini](#), [Gorard](#), [Atkinson](#), [HTheil](#), [ISWong](#), [ISMorrill](#), [ISMorrillK](#)

Between groups dissimilarity indices: [DIDuncan](#), [DIMorrill](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[ ,1:2]
Gini2(x)
```

GiniMulti

A function to compute multi-group Gini index

Description

Multi-group Gini is a multi-group version of the [Gini](#) index

Usage

```
GiniMulti(x)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

References

Reardon S. F. (1998) *Measures of racial diversity and segregation in multi-group and hierarchical structured Populations*. Annual meeting of the Eastern Sociological Society, Philadelphia

See Also

Multi-group indices: [PMulti](#), [GiniMulti](#), [HMulti](#), [CMulti](#), [RelDivers](#)

Social diversity indices: [HShannon](#), [NShannon](#), [ISimpson](#),

Examples

```
x <- segdata@data[ ,1:2]
GiniMulti(x)
```

Gorard

A function to compute Gorard's segregation index

Description

Gorard's index is an alternative to [ISDuncan](#)'s index, which measures the dissimilarity between the distribution of a group and the total population.

Usage

```
Gorard(x)
```

Arguments

`x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total totals because this will be interpreted as a group

Value

a numeric vector containing the Gorard's segregation index value for each group

References

Gorard S. (2000) *Education and Social Justice*. Cardiff, University of Wales Press

See Also

One-group evenness indices: [ISDuncan](#), [Gini](#), [Atkinson](#), [HTheil](#), [ISWong](#), [ISMorrill](#), [ISMorrillK](#)

Between groups dissimilarity indices: [DIDuncan](#), [Gini2](#), [DIMorrill](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[ ,1:2]
Gorard(x)
```

GreHSize	<i>Households distribution by size in Grenoble urban area in 2011</i>
----------	---

Description

This data set gives the households distribution by size in Grenoble urban area in 2011, including the area vectorial map at municipality level.

Usage

```
data(GreHSize)
```

Format

A Spatial object including 52 polygons corresponding to each municipality of Grenoble Urban Area (Insee definition) and following data attributes:

Details

- code: Municipality code
- name: Municipality name
- small: (1-2 persons household)
- medium: (3-4 persons household)
- big: (more then 5 persons household)

Source

Insee: Resultats du recensement de la population 2011, [Insee](#)

HLoc	<i>A function to compute local diversity index</i>
------	--

Description

Local diversity index, HLoc, is a local adaptation of Pielou's normalized diversity index [NShannon](#).

Usage

```
HLoc(x)
```

Arguments

- x
- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

a numeric vector containing diversity index value for each group

References

Theil H. (1972) *Statistical Decomposition Analysis*. North-Holland, Amsterdam

See Also

Other local indices [LQ](#) [LShannon](#), [LSimpson](#)

Examples

```
x <- segdata@data[,1:2]
HLoc(x)
```

HMulti

A function to compute multi-group entropy segregation index

Description

The multi-group version of Theil's entropy index [HTheil](#)

Usage

```
HMulti(x)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

multi-group entropy segregation index

References

Theil H. (1972) *Statistical decomposition analysis: with applications in the social and administrative*. Amsterdam, North-Holland, 337 p.

See Also

Multi-group indices: [PMulti](#), [GiniMulti](#), [DMulti](#), [CMulti](#), [RelDivers](#)
 Social diversity indices: [HShannon](#), [NShannon](#), [ISimpson](#),

Examples

```
x <- segdata@data[ ,1:2]
HMulti(x)
```

HShannon*A function to compute Shannon-Wiener diversity (entropy) index*

Description

The Shannon-Wiener diversity index is based on the notion of entropy and measures population heterogeneity.

Usage

```
HShannon(x)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

Shannon-Wiener diversity index

References

Shannon C. E. (1948) *A mathematical theory of communication*. Bell System Technical Journal (27)

See Also

Social diversity indices: [NShannon](#), [ISimpson](#),
Multi-group indices: [PMulti](#), [GiniMulti](#), [DMulti](#), [HMulti](#), [CMulti](#), [RelDivers](#)

Examples

```
x <- segdata@data[ ,1:2]
HShannon(x)
```

`HTheil`*A function to compute Theil's entropy segregation index*

Description

The entropy index (also called information index) measures departure from evenness by assessing each spatial unit deviation from the entropy in the area.

Usage

```
HTheil (x)
```

Arguments

`x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

a numeric vector containing Theil's entropy index value for each group

References

Theil H. (1972) *Statistical decomposition analysis: with applications in the social and administrative*. Amsterdam, North-Holland, 337 p.

See Also

One-group evenness indices: [ISDuncan](#), [Gini](#), [Gorard](#), [Atkinson](#), [ISWong](#), [ISMorrill](#), [ISMorrillK](#)

Between groups dissimilarity indices: [DIDuncan](#), [Gini2](#), [DIMorrill](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[ ,1:2]
HTheil(x)
```

`ISDuncan`*A function to compute Duncan & Duncan segregation index*

Description

Duncan's segregation index is one-group form of dissimilarity index [DIDuncan](#) and measures the unevenness of a group distribution compared to the rest of the population. It can be interpreted as the share of the group that would have to move to achieve an even distribution compared to the rest of the population.

Usage

```
ISDuncan (x)
```

Arguments

`x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

a numeric vector with values of the Duncan's segregation index for each group

References

Duncan O. D. and Duncan B. (1955) *Residential Distribution and Occupational Stratification*. American Journal of Sociology 60 (5), pp. 493-503

See Also

One-group evenness indices: [Gini](#), [Atkinson](#), [Gorard](#), [HTheil](#), [ISWong](#), [ISMorrill](#), [ISMorrillK](#)
Between groups dissimilarity indices: [DIDuncan](#), [Gini2](#), [DIMorrill](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[ ,1:2]  
ISDuncan(x)
```

`ISimpson`*A function to compute Simpson's interaction index*

Description

Simpson's interaction index measures the probability that randomly selected individuals are not in the same group.

Usage

```
ISimpson(x)
```

Arguments

`x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

Simpson's interaction index

References

Simpson E. H. (1949) *Measurement of diversity*. Nature 163:688

See Also

Social diversity indices: [HShannon](#), [NShannon](#),

Multi-group indices: [PMulti](#), [GiniMulti](#), [DMulti](#), [HMulti](#), [CMulti](#), [RelDivers](#)

Examples

```
x <- segdata@data[,1:2]
ISimpson(x)
```

 ISMorrill

A function to compute Morrill's segregation index

Description

Morrill's segregation index is a development of [ISDuncan](#)'s index which takes into account the interactions between spatial units(contiguity). The function can be used in two ways: to provide a contiguity matrix or a external geographic information source (spatial object or shape file).

Usage

```
ISMorrill(x, c = NULL, queen = FALSE,
          spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

- | | |
|---------|--|
| x | - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group. |
| c | - a standard binary contiguity (adjacency) symmetric matrix where each element C_{ij} equals 1 if i -th and j -th spatial units are adjacent, and 0 otherwise. |
| queen | - a logical parameter defining criteria used for the contiguity matrix computation, TRUE for queen, FALSE (by default) for rook |
| spatobj | - a spatial object (SpatialPolygonsDataFrame) with geographic information |
| folder | - a character vector with the folder (directory) name indicating where the shapefile is located on the drive |
| shape | - a character vector with the name of the shapefile (without the .shp extension) . |

Value

a numeric vector containing the Morrill's segregation index value for each group

References

Morrill B. (1991) *On the measure of geographic segregation*. Geography research forum, 11, pp. 25-36.

See Also

One-group evenness indices: [ISDuncan](#), [Gini](#), [Gorard](#), [HTheil](#), [Atkinson](#), [ISWong](#), [ISMorrillK](#)
 Between groups dissimilarity indices: [DIDuncan](#), [Gini2](#), [DIMorrill](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[ ,1:2]
contiguity <- contig(segdata)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

ISMorrill(x, c = contiguity)

ISMorrill(x, spatobj = segdata)

ISMorrill(x, folder = foldername, shape = shapename)
```

ISMorrillK

*A function to compute K-th order Morrill's segregation index***Description**

This function computes an adaptation of Morrill's segregation index which takes into account the interactions between spatial units defined by K-th ordered contiguity matrix. The index can be used in two ways: to provide a contiguity units defined by K order contiguity matrix. The function can be used in two matrix or a external geographic information source (spatial object or shape file).

Usage

```
ISMorrillK(x, ck = NULL, queen = FALSE, spatobj = NULL, folder = NULL,
  shape = NULL, K = 2, f = 'exp', beta = 1, prec = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
ck	- a list containing contiguity matrices corresponding to each order (from 1 to K)
queen	- logical parameter defining criteria used for contiguity matrix computation, TRUE for queen, FALSE (by default) for rook
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive is located.
shape	- a character vector with the name of the shapefile (without the .shp extension).
K	- the order of the contiguity matrix
f	- the distance function, f = 'exp' (by default) for negative exponential function and f = 'rec' for reciprocal function

beta - distance decay parameter
 prec - precision parameter. If not NULL, the function stop computing the spatial interaction when the impact on the indice is bellow 10^{-prec}

Value

a matrix with Generalized Morrill's dissimilarity index values

References

Morrill B. (1991) *On the measure of geographic segregation*. Geography research forum, 11, pp. 25-36.

See Also

One-group evenness indices: [ISDuncan](#), [Gini](#), [Gorard](#), [HTheil](#), [Atkinson](#), [ISWong](#), [ISMorrill](#)

Between groups dissimilarity indices: [DIDuncan](#), [Gini2](#), [DIMorrill](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[ ,1:2]
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

ISMorrillK(x, spatobj = segdata, queen = FALSE, K = 3)

ISMorrillK(x, folder = foldername, shape = shapename, K = 4, f = 'rec')
```

 ISWong

A function to compute Wong's segregation index

Description

Wong's segregation index is a development of [ISDuncan](#)'s which takes into account the interactions between spatial units (common boundaries and perimeter/area ratio). The function can be used in two ways: to provide spatial data (boundaries matrix, a perimeter vector and an area vector) or a external geographic information source (spatial object or shape file).

Usage

```
ISWong(x, b = NULL, a = NULL, p = NULL, ptype = 'int', variant = 's',
  spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total totals because this will be interpreted as a group
b	- a common boundaries matrix where each element B_{ij} equals the shared boundary of i -th and j -th spatial units.
a	- a numeric vector containing spatial unit areas
p	- a numeric vector containing spatial units perimeters.
ptype	- a string variable giving two options for perimeter calculation when a spatial object or shapefile is provided: 'int' to use only interior boundaries of spatial units, and 'all' to use entire boundaries, including the boundaries to the exterior
variant	- a character variable that allows to choose the index version: variant = 's' for the index adjusted for contiguous spatial/organizational units boundary lengths and perimeter/area ratio (by default) and variant = 'w' for the version based only on shared boundaries length
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a numeric vector containing the Wong's segregation index value for each group

References

Wong D. W. S. (1998) *Measuring multiethnic spatial segregation*. Urban Geography, 19 (1), pp. 77-87.

See Also

One-group evenness indices: [ISDuncan](#), [Gini](#), [Gorard](#), [HTheil](#), [Atkinson](#), [ISMorrill](#), [ISMorrillK](#)
 Between groups dissimilarity indices: [DIDuncan](#), [Gini2](#), [DIMorrill](#), [DIMorrillK](#), [DIWong](#)

Examples

```
x <- segdata@data[,1:2]
bound <- boundaries(segdata)
per <- perimeter(segdata)
ar <- area(segdata)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

ISWong(x, b = bound, p = per, a = ar)

ISWong(x, spatobj = segdata, variant = 's', ptype = 'int')
```

```
ISWong(x, folder = foldername, shape = shapename, variant = 'w')
```

LQ

A function to compute location quotients (LQs)

Description

Location quotients compare the relative part of a group in a particular spatial unit, to the relative part of that same group in the area.

Usage

```
LQ(x)
```

Arguments

`x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

a matrix of location quotients

References

Isard W. (1960) *Methods of regional analysis: an introduction to regional science*. The MIT Press, Cambridge

See Also

Other local indices [LShannon](#) [HLoc](#), [LSimpson](#)

Examples

```
x <- segdata@data[ ,1:2]
LQ(x)
```

LShannon	<i>A function to compute Shannon-Wiener local diversity (entropy) index</i>
----------	---

Description

The Shannon-Wiener diversity index is based on the notion of entropy and measures population heterogeneity.

Usage

```
LShannon(x)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

Local Shannon-Wiener diversity index

References

Shannon C. E. (1948) *A mathematical theory of communication*. Bell System Technical Journal (27)

See Also

Other local indices: [LQ](#), [HLoc](#), [LSimpson](#)

Examples

```
x <- segdata@data[ ,1:2]
LShannon(x)
```

`LSimpson`*A function to compute local Simpson's index*

Description

Local Simpson's interaction index measures the probability that randomly selected individuals are not in the same group in each spatial unit.

Usage

```
LSimpson (x)
```

Arguments

`x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

Local Simpson's interaction index

References

Simpson E. H. (1949) *Measurement of diversity*. Nature 163:688

See Also

Other local indices: [LQ](#), [HLoc](#), [LShannon](#)

Examples

```
x <- segdata@data[ ,1:2]
LSimpson (x)
```

NShannon

A function to compute Shannon-Wiener diversity normalized index

Description

The Shannon-Wiener diversity index is based on the notion of entropy and measures population heterogeneity.

Usage

```
NShannon(x)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

Shannon-Wiener normalized diversity index

References

Shannon C. E. (1948) *A mathematical theory of communication*. Bell System Technical Journal (27)

See Also

Other multi-group evenness indices: [HShannon](#), [ISimpson](#), [GiniMulti](#), [DMulti](#), [HMulti](#), [CMulti](#)

Other multi-group indices: [PMulti](#), [RelDivers](#)

Examples

```
x <- segdata@data[,1:2]
NShannon(x)
```

ordinalseg	<i>A function to compute Reardon multi-group ordinal segregation indices</i>
------------	--

Description

A function to compute Reardon (2009) ordinal indices

Usage

```
ordinalseg(x)
```

Arguments

`x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group. The rows represent the nominal categories (spatial units) and the columns the ordinal categories.

Value

A vector with Reardon multi-group ordinal segregation indices: Lambda1 - ordinal generalization of the information theory index Lambda2 - ordinal generalization of the variation ratio index Lambda3 - ordinal square root index Lambda4 - ordinal absolute difference index

References

Reardon S. F. (2009) *Measures of ordinal segregation*. Research on Economic Inequality, 17, pp. 129-155.

See Also

[rankorderseg](#)

Examples

```
x <- GreHSize@data[,3:5]
ordinalseg(x)

x1 <- matrix(nrow = 4, ncol = 3)
x1[1,] <- c(0, 0, 30)
x1[2,] <- c(0, 20, 10)
x1[3,] <- c(10, 20, 0)
x1[4,] <- c(30, 0, 0)

x2 <- matrix(nrow = 4, ncol = 3)
x2[1,] <- c(0, 30, 0)
```



```
x2[2,] <- c(0, 10, 20)
x2[3,] <- c(10, 0, 20)
x2[4,] <- c(30, 0, 0)

ordinalgseg(x1)
ordinalgseg(x2)
```

perimeter

A function to compute the spatial units' perimeters

Description

The function is based on **rgdal** and **rgeos** packages and can be used with a shape file or an R spatial object (`SpatialPolygonsDataFrame`).

Usage

```
perimeter(spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

spatobj	- a spatial object (<code>SpatialPolygonsDataFrame</code>) containing geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile with the geographic information is located.
shape	- a character vector with the name of the shapefile (without the <code>.shp</code> extension) which contains the geographic information

Value

A perimeter vector

See Also

Other spatial functions used for segregation indices computation: [area](#), [contig](#), [distance](#), [distcenter](#), [boundaries](#)

Examples

```
perimeter(segdata)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'
perimeter(folder = foldername, shape = shapename)
```

PMulti

A function to compute multi-group normalised exposure (PMulti)

Description

The multi-group normalised isolation index is a multi-group version of the isolation index ([xPx](#))

Usage

```
PMulti(x)
```

Arguments

`x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

multi-group normalised isolation index

References

James, F. J. (1986) *A New Generalized 'Exposure-Based' Segregation Index*. Sociological Methods and Research, 14, pp. 301-316

Reardon S. F. and G. Firebaugh (2002) *Measures of multi-group Segregation*. Sociological Methodology, 32(1), pp 33-67

See Also

Multi-group indices: [GiniMulti](#), [DMulti](#), [HMulti](#), [CMulti](#), [RelDivers](#)

Social diversity indices: [HShannon](#), [NShannon](#), [ISimpson](#),

Examples

```
x <- segdata@data[ ,1:2]
PMulti(x)
```

Poo *A function to compute the mean proximity between persons without regard to group (Poo)*

Description

Mean proximity, Poo, computes the mean distance between the individuals in the area with no regard for group. The function can be used in two ways: to provide a distance matrix or a external geographic information source (spatial object or shape file)

Usage

```
Poo(x, d = NULL, fdist = 'e', distin = 'm', distout = 'm', diagval = '0',
    itype = 'multi', beta = 1, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
d	- a matrix of the distances between spatial unit centroids
fdist	- the method used for distance interaction matrix: 'e' for inverse exponential function (by default) and 'l' for linear.
distin	- input metric conversion, based on bink package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
distout	- output metric conversion, based on bink package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
diagval	- when providing a spatial object or a shape file, the user has the choice of the spatial matrix diagonal definition: diagval = '0' (by default) for a null diagonal and diagval = 'a' to compute the diagonal as 0.6 * square root (spatial/organizational unitsarea) (White, 1983)
itype	- a character string defining the index type: itype = 'multi' (by default) for the multi-group index (White, 1986) or itype = 'between' for the between groups version (White, 1983)
beta	- distance decay parameter
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

Poo index value(s)

References

- White M. J. (1983) *The Measurement of Spatial Segregation*. American Journal of Sociology, 88, p. 1008-1019
- White, M. J. (1986) *Segregation and Diversity Measures in Population Distribution*. Population Index 52(2): 198-221.

See Also

Proximity measures: [Pxx](#), [Pxy](#), [SP](#)

Clustering Indices: [ACL](#), [RCL](#)

Examples

```
x <- segdata@data[ ,1:2]
ar<-area(segdata)
dist <- distance(segdata)
diag(dist)<-sqrt(ar) * 0.6
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

Poo(x, spatobj = segdata)

Poo(x, folder = foldername, shape = shapename, fdist = 'l')

Poo(x, spatobj = segdata, diagval = 'a')

Poo(x, d = dist, fdist = 'e')
```

Pxx

A function to compute the mean proximity between members of a group (Pxx)

Description

Mean proximity, Pxx, computes the mean distance between the members of a group. The distance matrix can be expressed as a linear or as an inverse exponential function of the distance between spatial unit centroids. The function can be used in two ways: to provide a distance matrix or a external geographic information source (spatial object or shape file).

Usage

```
Pxx(x, d = NULL, fdist = 'e', distin = 'm', distout = 'm', diagval = '0',
beta = 1, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
d	- a matrix of the distances between spatial unit centroids
fdist	- the method used for distance interaction matrix: 'e' for inverse exponential function (by default) and 'l' for linear.
distin	- input metric conversion, based on bink package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
distout	- output metric conversion, based on bink package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
diagval	- when providing a spatial object or a shape file, the user has the choice of the spatial matrix diagonal definition: diagval = '0' (by default) for a null diagonal and diagval = 'a' to compute the diagonal as 0.6 * square root (spatial/organizational unitsarea) (White, 1983)
beta	- distance decay parameter
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a numeric vector containing Pxx index value for each group

References

White M. J. (1983) *The Measurement of Spatial Segregation*. American Journal of Sociology, 88, p. 1008-1019

See Also

Proximity measures: [Pxy](#), [Poo](#), [SP](#)

Clustering Indices: [ACL](#), [RCL](#)

Examples

```
x <- segdata@data[,1:2]
ar<-area(segdata)
dist <- distance(segdata)
diag(dist)<-sqrt(ar) * 0.6
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'
```

```

Pxx(x, spatobj = segdata)

Pxx(x, folder = foldername, shape = shapename, fdist = 'l')

Pxx(x, spatobj = segdata, diagval = 'a')

Pxx(x, d = dist, fdist = 'e')

```

Pxy	<i>A function to compute the mean proximity between persons of different groups (Pxy)</i>
-----	---

Description

Mean proximity, Pxy, computes the mean distance between the members of different groups. The function can be used in two ways: to provide a distance matrix or a external geographic information source (spatial object or shape file).

Usage

```

Pxy(x, d = NULL, fdist = 'e', distin = 'm', distout = 'm', diagval = '0',
    beta = 1, spatobj = NULL, folder = NULL, shape = NULL)

```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
d	- a matrix of the distances between spatial unit centroids
fdist	- the method used for distance interaction matrix: 'e' for inverse exponential function (by default) and 'l' for linear.
distin	- input metric conversion, based on bink package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
distout	- output metric conversion, based on bink package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
diagval	- when providing a spatial object or a shape file, the user has the choice of the spatial matrix diagonal definition: diagval = '0' (by default) for a null diagonal and diagval = 'a' to compute the diagonal as 0.6 * square root (spatial/organizational unitsarea) (White, 1983)
beta	- distance decay parameter
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a matrix containing Pxy index values for each pair of groups

References

White M. J. (1983) *The Measurement of Spatial Segregation*. American Journal of Sociology, 88, p. 1008-1019

See Also

Proximity measures: [Pxx](#), [Poo](#), [SP](#)

Clustering Indices: [ACL](#), [RCL](#)

Examples

```
x <- segdata@data[ ,1:2]
ar<-area(segdata)
dist <- distance(segdata)
diag(dist)<-sqrt(ar) * 0.6
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

Pxy(x, spatobj = segdata)

Pxy(x, folder = foldername, shape = shapename, fdist = 'l')

Pxy(x, spatobj = segdata, diagval = 'a')

Pxy(x, d = dist, fdist = 'e')
```

rankorderseg

A function to compute rank-ordered segregation indices

Description

A function computing Reardon (2011) rank-ordered segregation indices

Usage

```
rankorderseg(x, polorder = 4, pred = NULL)
```

Arguments

- `x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group. The rows represent the nominal categories (spatial units) and the columns the population distribution as ordered groups divided by thresholds
- `polorder` - order of the polynomial approximation (4 by default)
- `pred` - a numerical vector with percentiles to be predicted. If NULL, the predictions are made at threshold levels

Value

A list containing the results for three rank-ordered indices: rank-order information theory index (Hr), rank-order variation ratio index (Rr) and rank-order square root index (Sr). For each index, a sublist is provided, containing: Index - the rank-ordered index value Hp/Rp/Sp - a vector with ordinal information theory/variance ratio/square root segregation index values at thresholds Coefficients - Coefficients extracted from the polynomial estimation model, including basic statistics Predict - a list containing predicted values of the corresponding ordinal index (fit); standard error of predicted means (se.fit); degrees of freedom for residual (df); and residual standard deviations (residuale.scale). If pred is NULL, the function will return the the statistics at thresholds

References

Reardon S. F. (2011) *Measures of Income Segregation* . The Stanford Center on Poverty and Inequality

See Also

[ordinalgseg](#)

Examples

```
x1 <- matrix(nrow = 4, ncol = 7)
x1[1,] <- c( 10, 10, 10, 20, 30, 40, 50)
x1[2,] <- c( 0, 20, 10, 10, 10, 20, 20)
x1[3,] <- c(10, 20, 10, 10, 10, 0, 0 )
x1[4,] <- c(30, 30, 20, 10, 10, 0, 0 )
x2 <- x1
x2[,c(3,4,6,7)] <- x1[,c(6,7,3,4)]

rankorderseg(x1)
rankorderseg(x2, pred = seq(0, 1, 0.1))
```

RCE*A function to compute Relative Centralisation Index (RCE)*

Description

The relative centralisation index measures the proportion of a group that should change its localization to achieve the same level of centralization as another group. The function can be used in two ways: to provide a vector containing the distances between spatial unit centroids or a external geographic information source (spatial object or shape file).

Usage

```
RCE(x, dc = NULL, center = 1, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

- | | |
|---------|--|
| x | - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group. |
| dc | - a numeric vector containing the distances between spatial units centroids and the central spatial unit |
| center | - a numeric value giving the number of the spatial unit that represents the center in the table |
| spatobj | - a spatial object (SpatialPolygonsDataFrame) with geographic information |
| folder | - a character vector with the folder (directory) name indicating where the shapefile is located on the drive |
| shape | - a character vector with the name of the shapefile (without the .shp extension). |

Value

a matrix containing relative centralisation index values

References

Duncan O. D. and Duncan B. (1955) *A Methodological Analysis of Segregation Indexes*. American Sociological Review 41, pp. 210-217

See Also

[RCEPoly](#), [RCEPolyK](#),
[ACEDuncan](#), [ACEDuncanPoly](#),
[ACEDuncanPolyK](#), [ACE](#), [ACEPoly](#)

Examples

```
x <- segdata@data[ ,1:2]
distc<- distcenter(segdata, center = 28)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

RCE(x, dc=distc)

RCE(x, spatobj = segdata, center = 28)

RCE(x, folder = foldername, shape = shapename, center = 28)
```

RCEPoly

A function to compute Polycentric Relative Centralisation Index

Description

The polycentric version of the relative centralisation index. The function can be used in two ways: to provide a matrix containing the distances between spatial/organizational unit centroids or a external geographic information source (spatial object or shape file).

Usage

```
RCEPoly(x, dc = NULL, center = 1, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
dc	- a numeric matrix/vector containing the distances between spatial units centroids and the central spatial unit(s).
center	- a numeric vector giving the number of the spatial units that represent the centers in the table
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a matrix containing relative centralisation index values

References

Duncan O. D. and Duncan B. (1955) *A Methodological Analysis of Segregation Indexes*. American Sociological Review 41, pp. 210-217

See Also

[RCE](#), [RCEPolyK](#),
[ACEDuncan](#), [ACEDuncanPoly](#),
[ACEDuncanPolyK](#), [ACE](#), [ACEPoly](#)

Examples

```
x <- segdata@data[ ,1:2]
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

RCEPoly(x, spatobj = segdata, center = c(28, 83) )

RCEPoly(x, folder = foldername, shape = shapename, center = c(28, 83))

center <- c(28, 83)
polydist <- matrix(data = NA, nrow = nrow(x), ncol = length(center))
for (i in 1:ncol(polydist))
  polydist[,i] <- distcenter(spatobj = segdata, center = center[i])
RCEPoly(x, dc = polydist)

distmin <- vector(length = nrow(x))
for (i in 1:nrow(polydist)) distmin[i] <- min(polydist[i,])
RCE(x, dc = distmin)
```

RCEPolyK

A function to compute Constrained Relative Centralisation Index

Description

The constrained (local) version of relative centralization index. The function can be used in two ways: to provide a matrix containing the distances between spatial unit centroids or a external geographic information source (spatial object or shape file).

Usage

```
RCEPolyK(x, dc = NULL, K = NULL, kdist = NULL, center = 1,
          spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
dc	- a numeric matrix/vector containing the distances between spatial units centroids and the central spatial unit(s).
K	- the number of neighbourhoods under the influence of a center
kdist	- the maximal distance that defines the neighbourhoods influenced by a center
center	- a numeric vector giving the number of the spatial units that represent the centers in the table
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a matrix containing relative centralisation index values

References

Duncan O. D. and Duncan B. (1955) *A Methodological Analysis of Segregation Indexes*. American Sociological Review 41, pp. 210-217

Folch D.C and Rey S. J (2016) *The centralization index: A measure of local spatial segregation*. Papers in Regional Science 95 (3), pp. 555-576

See Also

[RCE](#), [RCEPoly](#),
[ACEDuncan](#), [ACEDuncanPoly](#),
[ACEDuncanPolyK](#), [ACE](#), [ACEPoly](#)

Examples

```
x <- segdata@data[,1:2]
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

RCEPolyK(x, spatobj = segdata, center = c(28, 83))

RCEPolyK(x, folder = foldername, shape = shapename, center = c(28, 83), K = 3)

center <- c(28, 83)
polydist <- matrix(data = NA, nrow = nrow(x), ncol = length(center))
for (i in 1:ncol(polydist))
```

```
polydist[,i] <- distcenter(spatobj = segdata, center = center[i])
RCEPolyK(x, dc = polydist, kdist = 2)
```

RCL

A function to compute the relative clustering index (RCL)

Description

The relative clustering index, RCL, compares the mean proximity of a group to the mean proximity of another group. The function can be used in two ways: to provide a distance matrix or a external geographic information source (spatial object or shape file).

Usage

```
RCL(x, d = NULL, fdist = 'e', distin = 'm', distout = 'm', diagval = '0',
beta = 1, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
d	- a matrix of the distances between spatial unit centroids
fdist	- the method used for distance interaction matrix: 'e' for inverse exponential function (by default) and 'l' for linear.
distin	- input metric conversion, based on bink package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
distout	- output metric conversion, based on bink package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
diagval	- when providing a spatial object or a shape file, the user has the choice of the spatial matrix diagonal definition: diagval = '0' (by default) for a null diagonal and diagval = 'a' to compute the diagonal as 0.6 * square root (spatial/organizational unitsarea) (White, 1983)
beta	- distance decay parameter
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

a matrix containing relative clustering index values for each pair of groups

References

Massey D. S. and Denton N. A. (1988) *The dimensions of residential segregation*. Social Forces 67(2), pp. 281-315.

See Also

Proximity measures: [Pxx](#), [Pxy](#), [Poo](#), [SP](#)

Clustering Indices: [ACL](#)

Examples

```
x <- segdata@data[ ,1:2]
ar<-area(segdata)
dist <- distance(segdata)
diag(dist)<-sqrt(ar) * 0.6
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

RCL(x, spatobj = segdata)

RCL(x, folder = foldername, shape = shapename, fdist = 'l')

RCL(x, spatobj = segdata, diagval ='a')

RCL(x, d = dist, fdist = 'e')
```

RCO

A function to compute Relative Concentration index (RCO)

Description

The relative concentration index, measures the share of space occupied by a group compared to another group. The function can be used in two ways: to provide an area vector or a external geographic information source (spatial object or shape file).

Usage

```
RCO(x, a = NULL, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
a	- a numeric vector containing spatial unit areas

spatobj - a spatial object (SpatialPolygonsDataFrame) with geographic information
 folder - a character vector with the folder (directory) name indicating where the shapefile is located on the drive
 shape - a character vector with the name of the shapefile (without the .shp extension).

Value

a matrix containing relative concentration index values

References

Massey D. S. and Denton N. A. (1988) *The dimensions of residential segregation*. Social Forces 67(2), pp. 281-315.

See Also

one-group concentration indices: [Delta](#), [ACO](#)

Examples

```

x <- GreHSize@data[,3:5]
ar <- area(GreHSize)
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'GreHSize'

RCO(x, a = ar)

RCO(x, spatobj = GreHSize)

RCO(x, folder = foldername, shape = shapename)

```

 RelDivers

A function to compute multi-group relative diversity index

Description

The relative diversity index is a multi-group index based on Simpson's interaction index [ISimpson](#)

Usage

```
RelDivers(x)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

Value

multi-group relative diversity index

References

Carlson S. M. (1992) *Trends in race/sex occupational inequality: conceptual and measurement issues*. *Social Problems*, 39, p. 269-290

See Also

Multi-group indices: [PMulti](#), [GiniMulti](#), [DMulti](#), [HMulti](#), [CMulti](#)

Social diversity indices: [HShannon](#), [NShannon](#), [ISimpson](#),

Examples

```
x <- segdata@data[ ,1:2]
RelDivers(x)
```

ResamplePlot

A function to plot the results of resampling methods

Description

Plot of Monte Carlo simulations results. The function can be used in two ways: by providing a `ResampleTest` object, using [ResampleTest](#) or a simulated distribution vector, a value and a name of the index

Usage

```
ResamplePlot(ResampleTest, var = 1, coldist = 'red', colind = 'blue',
  legend = TRUE, legendpos = 'top', cex.legend = 1, bty = 'o')
```

Arguments

<code>ResampleTest</code>	- a <code>ResampleTest</code> object produced with ResampleTest function
<code>var</code>	- the number of the variable to be plot
<code>coldist</code>	- color used to plot the simulated distribution
<code>colind</code>	- color used to plot the index
<code>legend</code>	- logical parameter, to control the legend's plots
<code>legendpos</code>	- a character string giving the legend's position: 'bottomright', 'bottom', 'bottomleft', 'left', 'topleft', 'top', 'topright', 'right' and 'center'.
<code>cex.legend</code>	- a numerical value giving the amount by which plotting text and symbols in legend should be magnified relative to the default.
<code>bty</code>	- a character string which determines the type of box of the legend. If <code>bty</code> is one of 'o' (the default), 'l', '7', 'c', 'u', or 'j' the resulting box resembles the corresponding upper case letter. A value of 'n' suppresses the box.

Value

A plot with resampling distribution

References

Tivadar M., Schaeffer Y, Torre A. and Bray F. (2014) *OASIS - un Outil d'Analyse de la Segregation et des Inegalites Spatiales*. Cybergeog : European Journal of Geography, GeOpenMod, document 699

See Also

[ResampleTest](#)

Examples

```
x <- segdata@data[ ,1:2]

xtest <- ResampleTest(x, fun = 'ISMorrill', simtype = 'MonteCarlo',
                     sampleunit = 'unit', spatobj = segdata)

ResamplePlot(xtest, var = 1)
```

ResampleTest

A function to test segregation indices by resampling

Description

Resampling tests for segregation indexes.

Usage

```
ResampleTest(x, fun, var = NULL, simtype = "MonteCarlo",
             sampleunit = "unit", samplesize = NULL, perc = c(0.05, 0.95),
             outl = FALSE, outmeth = "bp", sdtimes = 2, IQRrange = 1.5,
             proba = NULL, nsim = NULL, setseed = FALSE, spatobj = NULL,
             folder = NULL, shape = NULL, delta = 0.5, exact = FALSE, d = NULL,
             c = NULL, a = NULL, ck = NULL, f = "exp", b = NULL, p = NULL,
             spatmat = "c", queen = FALSE, distin = "m", distout = "m",
             diagval = "0", fdist = "e", itype = "multi", dc = NULL, center = 1,
             polorder = 4, pred = NULL, K = 2, ptype = "int", variant = "s", ...)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
fun	- a character vector with the segregation function to be tested
var	- vector with the variables to be tested
simtype	- a character vector with the type of simulation. If simtype = 'Boot', the function generates bootstrap replications. If simtype = 'Jack', the function generates jackknife replications. If simtype = 'MonteCarlo', the function produces a randomization test using Monte Carlo simulations.
sampleunit	= 'unit' (by default) when the sampling unit is the spatial/organisational unit and sampleunit = 'ind' for individual sampling
samplesize	- the size of the sample used for bootstrapping. If null, the samplesize equals the number of spatial/organizational units (sampleunit = 'unit') or the total population (sampleunit = 'ind')
perc	- the percentiles for the bootstrap replications
outl	- logical parameter for jackknife simulations, if TRUE the function provides the outliers obtained by jackknife iterations
outmeth	- a character vector designating the outliers detection method: outmeth = 'bp' (by default) for boxplot method outmeth = 'sd' for standard deviation method outmeth = 'z' for normal scores method outmeth = 't' for t Student scores method outmeth = 'chisq' for chi-squared scores method outmeth = 'mad' for median absolute deviation method. The estimations based on scoring methods are obtained using outliers package
sdtimes	- multiplication factor of the standard deviation used for outliers detection with jackknife simulations (2 by default)
IQRrange	- determines the boxplot thresholds (1.5 by default) as multiplication of IQR (Inter Quartile Range)
proba	- for Monte Carlo simulations, proba is a vector with location probabilities. If proba = NULL, the vector is equiprobable. If outliers are determined with jackknife technique, proba indicates the probability (confidence interval) for scoring tests.
nsim	- the number of simulations
setseed	- if TRUE, specify zero seed for repeated simulation
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).
delta	- an inequality aversion parameter
exact	- a logical variable to specify the index version: exact = FALSE (by default) for the approximate version of the index, and exact = TRUE for the exact version

d	- a matrix of the distances between spatial unit centroids
c	- a standard binary contiguity (adjacency) symmetric matrix where each element C_{ij} equals 1 if i -th and j -th spatial units are adjacent, and 0 otherwise.
a	- a numeric vector containing spatial unit areas
ck	- a list containing contiguity matrices corresponding to each order (from 1 to K)
f	- the distance function, $f = 'exp'$ (by default) for negative exponential function and $f = 'rec'$ for reciprocal function
b	- a common boundaries matrix where each element B_{ij}
p	- a numeric vector containing spatial units perimeters.
spatmat	- the method used for spatial calculations: 'c' for the contiguity matrix (by default) or any other user spatial interaction matrix and 'd' for the inverse exponential function of the distance.
queen	- logical parameter defining criteria used for contiguity matrix computation, TRUE for queen, FALSE (by default) for rook
distin	- input metric conversion, based on bin package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
distout	- output metric conversion, based on bin package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
diagval	- when providing a spatial object or a shape file, the user has the choice of the spatial matrix diagonal definition: $diagval = '0'$ (by default) for a null diagonal and $diagval = 'a'$ to compute the diagonal as $0.6 * \text{square root (spatial/organizational unitsarea)}$ (White, 1983)
fdist	- the method used for distance interaction matrix: 'e' for inverse exponential function (by default) and 'l' for linear.
itype	- a character string defining the index type: $itype = 'multi'$ (by default) for the multi-group index (White, 1986) or $itype = 'between'$ for the between groups version (White, 1983)
dc	- a numeric vector containing the distances between spatial units centroids and the central spatial unit
center	- a numeric value giving the number of the spatial unit that represents the center in the table
polorder	- order of the polynomial approximation (4 by default)
pred	- a numerical vector with percentiles to be predicted.
K	- the order of the contiguity matrix
pctype	- a string variable giving two options for perimeter calculation when a spatial object or shapefile is provided: 'int' to use only interior boundaries of spatial units, and 'all' to use entire boundaries, including the boundaries to the exterior
variant	- a character variable that allows to choose the index version: $variant = 's'$ for the dissimilarity index adjusted for contiguous spatial units boundary lengths and perimeter/area ratio (by default) and $variant = 'w'$ for the version without perimeter/area ratio
...	- other specific parameters

Value

A list with: - index's name - simulation type - statistics summary of the simulations - simulated index distribution - simulated population distribution - matrix with outliers (jackknife) - list with outliers values (jackknife)

References

Efron, B., and Tibshirani, R. J. (1993). *An Introduction to the Bootstrap*. New York, Chapman and Hall

Tivadar M., Schaeffer Y, Torre A. and Bray F. (2014) *OASIS - un Outil d'Analyse de la Segregation et des Inegalites Spatiales*. Cybergeog : European Journal of Geography, GeOpenMod, document 699

See Also

[ResamplePlot](#)

Examples

```
x <- segdata@data[ ,1:2]

xtest <- ResampleTest (x, fun = 'ISMorrill', simtype = 'MonteCarlo',
                      sampleunit = 'ind', spatobj = segdata)
xtest$Summary

xtest <- ResampleTest (x, fun = 'ISMorrill', simtype = 'Boot',
                      sampleunit = 'unit', spatobj = segdata)
xtest$Summary

xtest <- ResampleTest (GreHSize@data[,3:5], fun='ISDuncan', simtype = 'Jack',
                      sampleunit = 'unit', spatobj = GreHSize,
                      outl = TRUE, outmeth = 'sd', sdtimes = 3)
xtest$Summary
xtest$OutliersVal
```

segdata

Theoretical two groups distribution on a 10x10 grid map.

Description

The theoretical examples (Morrill 1991, Wong 1993) adapted from Hong and O'Sullivan (2015). The space is represented by a 10x10 checkboard, with different distributions of two social groups in the area.

Usage

```
data(segdata)
```

Format

A 10x10 grid Spatial object and following data attributes:

Details

- : spatial ID;
- : municipality name;
- : pattern A: minority distribution;
- : pattern A: majority distribution;
- : pattern B: minority distribution;
- : pattern B: majority distribution;
- : pattern C: minority distribution;
- : pattern C: majority distribution;
- : pattern D: minority distribution;
- : pattern D: majority distribution;
- : pattern E: minority distribution;
- : pattern E: majority distribution;
- : pattern F: minority distribution;
- : pattern F: majority distribution;
- : pattern G: minority distribution;
- : pattern G: majority distribution;
- : pattern H: minority distribution;
- : pattern H: majority distribution;
- : pattern I: minority distribution;
- : pattern I: majority distribution;

Source

Hong S-Y (2014): R package 'seg', [Hong's page](#)

segdataclean

A function to clean and prepare the data for segregation analysis

Description

The function cleans and prepares the data for segregation analysis

Usage

```
segdataclean (x, c = NULL, b = NULL, a = NULL, p = NULL,  
ck = NULL, d = NULL, dc = NULL, spatobj = NULL, folder = NULL, shape = NULL,  
warnings = T)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
c	- a standard binary contiguity (adjacency) symmetric matrix where each element C_{ij} equals 1 if i -th and j -th spatial units are adjacent, and 0 otherwise.
b	- a common boundaries matrix where each element B_{ij}
a	- a numeric vector containing spatial unit areas
p	- a numeric vector containing spatial units perimeters.
ck	- a list containing contiguity matrices corresponding to each order (from 1 to K)
d	- a matrix of the distances between spatial unit centroids
dc	- a numeric vector containing the distances between spatial units centroids and the central spatial unit
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).
warnings	- warning alert (by default TRUE)
...	- specific geographic vectors or matrices to be cleaned

Value

The objects (data matrix, geographical vectors/matrices, spatial objects) cleaned from null rows or columns

See Also

Other local indices: [LQ](#), [HLoc](#), [LShannon](#)

Examples

```
x <- segdata@data[ ,1:2]
x[ ,3] <- rep (0 ,100)
x[1:3, ] <- rep (c(0, 0, 0), 3)
x1 <- x
spatobj <- segdata
cldata <- segdataclean(x1, segdata)
x1 <- cldata$x
spatobj <- cldata$spatobj

c <- contig (segdata)
c <- segdataclean(x, c = c)$c
```

SP *A function to compute the spatial proximity index (SP)*

Description

The spatial proximity index, SP, compares the clustering level (mean proximity) of a group compared to another group. The function can be used in two ways: to provide a distance matrix or a external geographic information source (spatial object or shape file).

Usage

```
SP(x, d = NULL, fdist = 'e', distin = 'm', distout = 'm', diagval = '0',
  itype = 'multi', beta = 1, spatobj = NULL, folder = NULL, shape = NULL)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
d	- a matrix of the distances between spatial unit centroids
fdist	- the method used for distance interaction matrix: 'e' for inverse exponential function (by default) and 'l' for linear.
distin	- input metric conversion, based on bink package and includes conversions from 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
distout	- output metric conversion, based on bink package and includes conversions to 'm', 'km', 'inch', 'ft', 'yd', 'mi', 'naut_mi', etc.
diagval	- when providing a spatial object or a shape file, the user has the choice of the spatial matrix diagonal definition: diagval = '0' (by default) for a null diagonal and diagval = 'a' to compute the diagonal as 0.6 * square root (spatial/organizational unitsarea) (White, 1983)
itype	- a character string defining the index type: itype = 'multi' (by default) for the multi-group index (White, 1986), itype = 'between' for the between groups version (White, 1983), or itype = 'one' for the one-group version (Apparicio et al, 2008)
beta	- distance decay parameter
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension).

Value

spatial proximity index value(s)

References

- White M. J. (1983) *The Measurement of Spatial Segregation*. American Journal of Sociology, 88, p. 1008-1019.
- White, M. J. (1986) *Segregation and Diversity Measures in Population Distribution*. Population Index 52(2): 198-221.
- Apparicio, P., V. Petkevitch and M. Charron (2008): *Segregation Analyzer: A C#.Net application for calculating residential segregation indices*, Cybergeog: European Journal of Geography, 414, 1-27.

See Also

- Proximity measures: [Pxx](#), [Pxy](#), [Poo](#)
- Clustering Indices: [ACL](#), [RCL](#)

Examples

```
x <- segdata@data[ ,1:2]
ar<-area(segdata)
dist <- distance(segdata)
diag(dist)<-sqrt(ar) * 0.6
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

SP(x, spatobj = segdata)

SP(x, folder = foldername, shape = shapename, fdist = 'l', itype = 'between')

SP(x, spatobj = segdata, diagval = 'a', itype = 'one')

SP(x, d = dist, fdist = 'e')
```

spatinteract	<i>A function adapted from seg package to compute spatial exposure/isolation indices</i>
--------------	--

Description

A function adapted from seg package (Hong et al. 2014) to compute spatial exposure/isolation indices developed by Reardon and O’Sullivan (2004)

Usage

```
spatinteract(x, spatobj = NULL, folder = NULL, shape = NULL, ...)
```


Arguments

- `x` - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
- `spatobj` - a spatial object (`SpatialPolygonsDataFrame`) with geographic information
- `folder` - a character vector with the folder (directory) name indicating where the shapefile is located on the drive
- `shape` - a character vector with the name of the shapefile (without the `.shp` extension) .
- `...` - other parameters of `spseg` function from `seg` package.

Value

A matrix with Reardon's spatial exposure/isolation indices

References

- Reardon, S. F. and O'Sullivan, D. (2004) *Measures of spatial segregation*. *Sociological Methodology*, 34, 121-162.
- Hong S.Y., O'Sullivan D., Sadahiro Y. (2014) *Implementing Spatial Segregation Measures in R*. *PLoS ONE*, 9(11)

See Also

Multi-group indices: [PMulti](#), [GiniMulti](#), [DMulti](#), [HMulti](#), [RelDivers](#)

Social diversity indices: [HShannon](#), [NShannon](#), [ISimpson](#),

Examples

```
x <- segdata@data[,1:2]
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

spatinteract(x, spatobj = segdata)

spatinteract(x, folder = foldername, shape = shapename)
```

spatmultiseg	<i>A function from seg package to compute spatial multi-group segregation indices</i>
--------------	---

Description

A function adapted from seg package (Hong et al. 2014) to compute spatial multi-group segregation indices developed by Reardon and O’Sullivan (2004)

Usage

```
spatmultiseg(x, spatobj = NULL, folder = NULL, shape = NULL, ...)
```

Arguments

x	- an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.
spatobj	- a spatial object (SpatialPolygonsDataFrame) with geographic information
folder	- a character vector with the folder (directory) name indicating where the shapefile is located on the drive
shape	- a character vector with the name of the shapefile (without the .shp extension) .
...	- other parameters of spseg function from seg package.

Value

A vector with Reardon’s spatial multi-group segregation indices: D* - spatial multi-group dissimilarity index R* - spatial multi-group relative diversity index H* - spatial multi-group information theory index

References

Reardon, S. F. and O’Sullivan, D. (2004) *Measures of spatial segregation*. Sociological Methodology, 34, 121-162.

Hong S.Y., O’Sullivan D., Sadahiro Y. (2014) *Implementing Spatial Segregation Measures in R’*. PLoS ONE, 9(11)

See Also

Multi-group indices: [PMulti](#), [GiniMulti](#), [DMulti](#), [HMulti](#), [RelDivers](#)
 Social diversity indices: [HShannon](#), [NShannon](#), [ISimpson](#),

Examples

```
x <- segdata@data[ ,1:2]
foldername <- system.file('extdata', package = 'OasisR')
shapename <- 'segdata'

spatmultiseg(x, spatobj = segdata)

spatmultiseg(x, folder = foldername, shape = shapename)
```

xPx

*A function to compute Bell's isolation index (xPx)***Description**

The isolation index, xPx, is an exposure index that measures the probability that two members of a group share the same spatial unit. This index can be calculated using the approximate or the exact method (see Bell, 1954).

Usage

```
xPx(x, exact = FALSE)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

exact - a logical variable to specify the index version: exact = FALSE (by default) for the approximate version of the index, and exact = TRUE for the exact version

Value

a numeric vector containing the isolation index value for each group

References

Bell W. (1954) *A probability model for the measurement of ecological segregation*. Social Forces 32(4), pp. 357-364

See Also

Isolation indices: [Eta2](#), [DPxx](#)

Interaction indices: [xPy](#), [DPxy](#)

Examples

```
x <- segdata@data[ ,7:8]
xPx(x)
xPx(x, exact = TRUE)
```

xPy

A function to compute interaction index (xPy)

Description

The interaction index, xPy, is an exposure between groups index which measures the probability that a member of a group shares the same spatial unit with a member of another group. The index can be calculated with the approximate or exact method (see Bell, 1954).

Usage

```
xPy(x, exact = FALSE)
```

Arguments

x - an object of class matrix (or which can be coerced to that class), where each column represents the distribution of a group within spatial units. The number of columns should be greater than 1 (at least 2 groups are required). You should not include a column with total population, because this will be interpreted as a group.

exact - a logical variable to specify the index version: exact = FALSE (by default) for the approximate version of the index, and exact = TRUE for the exact version

Value

a matrix with interaction index values

References

Bell W. (1954) *A probability model for the measurement of ecological segregation*. Social Forces 32(4), pp. 357-364

See Also

Isolation indices: [xPx](#), [Eta2](#), [DPxx](#)

Distance decay interaction index: [DPxy](#)

Examples

```
x <- segdata@data[ ,1:2]
xPy(x)
```

Index

*Topic **datasets**

- GreHSize, 34
- segdata, 68

- ACE, 3, 5, 6, 8, 10, 57, 59, 60
- ACEDuncan, 4, 4, 6, 8, 10, 57, 59, 60
- ACEDuncanPoly, 4, 5, 6, 8, 10, 57, 59, 60
- ACEDuncanPolyK, 4–6, 7, 10, 57, 59, 60
- ACEPoly, 4–6, 8, 9, 57, 59, 60
- ACL, 10, 52, 53, 55, 62, 72
- ACO, 12, 18, 63
- area, 13, 15, 17, 23, 24, 49
- Atkinson, 14, 19, 20, 22, 25, 31–33, 37, 38, 40, 42, 43

- boundaries, 14, 15, 17, 23, 24, 49

- CMulti, 16, 26, 32, 35, 36, 39, 47, 50, 64
- contig, 14, 15, 17, 23, 24, 49

- Delta, 13, 18, 63
- DIDuncan, 15, 18, 19, 20, 22, 24–26, 31–33, 37, 38, 40, 42, 43
- DIMorrill, 15, 19, 20, 22, 25, 31–33, 37, 38, 40, 42, 43
- DIMorrillK, 15, 19, 20, 21, 25, 31–33, 37, 38, 40, 42, 43
- distance, 14, 15, 17, 22, 24, 49
- distcenter, 14, 15, 17, 23, 23, 49
- DIWong, 15, 19, 20, 22, 24, 31–33, 37, 38, 40, 42, 43
- DMulti, 16, 26, 35, 36, 39, 47, 50, 64, 73, 74
- DPxx, 27, 29, 30, 75, 76
- DPxy, 28, 28, 30, 75, 76

- Eta2, 28, 29, 29, 75, 76

- Gini, 15, 19, 20, 22, 25, 30, 32, 33, 37, 38, 40, 42, 43
- Gini2, 15, 31, 31, 33, 37, 38, 40, 42, 43

- GiniMulti, 16, 26, 32, 32, 35, 36, 39, 47, 50, 64, 73, 74
- Gorard, 15, 19, 20, 22, 25, 31, 32, 33, 37, 38, 40, 42, 43
- GreHSize, 34

- HLoc, 34, 44–46, 70
- HMulti, 16, 26, 32, 35, 36, 39, 47, 50, 64, 73, 74
- HShannon, 16, 26, 32, 35, 36, 39, 47, 50, 64, 73, 74
- HTheil, 15, 19, 20, 22, 25, 31–33, 35, 37, 38, 40, 42, 43

- ISDuncan, 15, 19, 20, 22, 25, 31–33, 37, 38, 40, 42, 43
- ISimpson, 16, 26, 32, 35, 36, 39, 47, 50, 63, 64, 73, 74
- ISMorrill, 15, 19, 20, 22, 25, 31–33, 37, 38, 40, 42, 43
- ISMorrillK, 15, 19, 20, 22, 25, 31–33, 37, 38, 40, 41, 43
- ISWong, 15, 19, 20, 22, 25, 31–33, 37, 38, 40, 42, 42

- LQ, 35, 44, 45, 46, 70
- LShannon, 35, 44, 45, 46, 70
- LSimpson, 35, 44, 45, 46

- NShannon, 16, 26, 32, 34–36, 39, 47, 50, 64, 73, 74

- ordinalgseg, 48, 56

- perimeter, 14, 15, 17, 23, 24, 49
- PMulti, 16, 26, 32, 35, 36, 39, 47, 50, 64, 73, 74
- Poo, 11, 51, 53, 55, 62, 72
- Pxx, 11, 52, 52, 55, 62, 72
- Pxy, 11, 52, 53, 54, 62, 72

rankorderseg, [48](#), [55](#)
RCE, [4–6](#), [8](#), [10](#), [57](#), [59](#), [60](#)
RCEPoly, [4–6](#), [8](#), [10](#), [57](#), [58](#), [60](#)
RCEPolyK, [4–6](#), [8](#), [10](#), [57](#), [59](#), [59](#)
RCL, [11](#), [52](#), [53](#), [55](#), [61](#), [72](#)
RCO, [13](#), [18](#), [62](#)
RelDivers, [16](#), [26](#), [32](#), [35](#), [36](#), [39](#), [47](#), [50](#), [63](#),
[73](#), [74](#)
ResamplePlot, [64](#), [68](#)
ResampleTest, [64](#), [65](#), [65](#)

segdata, [68](#)
segdataclean, [69](#)
SP, [11](#), [52](#), [53](#), [55](#), [62](#), [71](#)
spatinteract, [72](#)
spatmultiseg, [74](#)

xPx, [27–30](#), [50](#), [75](#), [76](#)
xPy, [28–30](#), [75](#), [76](#)