Package ‘seg’

Version 0.5-7
Date 2019-12-18
Title Measuring Spatial Segregation
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Depends R (>= 3.4.0), methods, stats, sp
Imports splancs
Suggests spdep, spgrass6, rgdal
Description Measuring spatial segregation. The methods implemented in this
       package include White's P index (1983) <doi:10.1086/227768>,
       Morrill's D(adj) (1991), Wong's D(w) and D(s) (1993)
       <doi:10.1080/00420989320080551>, and Reardon and O'Sullivan's set of
       spatial segregation measures (2004)
License GPL (>= 3)
URL https://github.com/syunhong/seg
NeedsCompilation yes
Repository CRAN
Date/Publication 2019-12-18 15:20:02 UTC

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Description

Draws a graph that shows the pattern of residential concentration for a population group and calculates its summary statistic as suggested by Hong and Sadahiro (2013).

Usage

`conprof(data, grpID = 1, n = 999, graph = TRUE, add = FALSE, ...)`

Arguments

data an object of class `matrix`, or one that can be coerced to that class. Each column represents a population group. The number of columns should be greater than one (i.e., at least two population groups are required).

grpID a numeric value specifying the population group (i.e., column in `data`) to be analysed. Multiple values are not allowed.

n a numeric value indicating the number of thresholds to be used. A large value of `n` creates a smoother-looking graph but slows down the calculation speed.

graph logical. If TRUE, draw the concentration profile for the specified population group.

add logical. If TRUE, add the graph to the current plot.

... optional arguments to be passed to `plot` when `add` is FALSE, or to `lines` otherwise. Ignored when `graph` is FALSE.

Details

For ‘n’ equally-spaced thresholds between 0 and 1, `conprof` identifies the areas where the selected population group comprises at least the given threshold proportions; computes how many of the group members live in these areas; and plots them on a 2D plane with the threshold values in the horizontal axis and the proportions of the people in the vertical axis.

The summary statistic is calculated by estimating the area between the concentration profile and a hypothetical line that represents a uniform distribution (see the examples).
Value

A list object with the following three elements:

- `x` the threshold values.
- `y` the proportions of the people who live in the areas where they comprise at least the corresponding threshold percentages in the local population composition.
- `d` the summary statistic for the concentration profile.

Author(s)

Seong-Yun Hong

References


Examples

```r
xx <- runif(100) # random distribution
xx <- xx * (4000 / sum(xx))
yy <- rep(c(40, 60), 100) # no segregation
zz <- rep(c(100, 0), c(40, 60)) # complete segregation

set1 <- cbind(xx, 100 - xx)
set2 <- matrix(yy, ncol = 2, byrow = TRUE)
set3 <- cbind(zz, 100 - zz)

par(mar = c(5.1, 4.1, 2.1, 2.1))
out1 <- conprof(set1, grpID = 1,
                xlab = "Threshold level (%)",
                ylab = "Population proportion (%)",
                cex.lab = 0.9, cex.axis = 0.9, lty = "dotted")
out2 <- conprof(set2, grpID = 1, add = TRUE,
                lty = "longdash")
out3 <- conprof(set3, grpID = 1, add = TRUE)

title(main = paste("R =", round(out1$d, 2)))

# shaded areas represent the summary statistic value
if (require(graphics)) {
  polygon(c(out1$x[1:400], 0.4, 0),
          c(out1$y[1:400], 1, 1),
          density = 10, angle = 60,
          border = "transparent")
  polygon(c(out1$x[400:999], 1, 0.4),
          c(out1$y[400:999], 0, 0),
          density = 10, angle = 60,
```
Deseg

Calculates the decomposable segregation measure developed by Sadahiro and Hong (2013).

Usage

deseg(x, data, smoothing = "kernel", nrow = 100, ncol = 100,
       window, sigma, verbose = FALSE)

Arguments

- **x**: a numeric matrix or data frame with coordinates (each row is a point), or an object of class Spatial or ppp.
- **data**: an object of class matrix, or one that can be coerced to that class. The number of rows in 'data' should equal the number of points in 'x', and the number of columns should be greater than one (i.e., at least two population groups are required). This can be missing if 'x' has a data frame attached to it.
- **smoothing**: a character string indicating how to perform spatial smoothing of the population data. Currently only “kernel” is supported.
- **nrow**: a numeric value indicating the number of row cells in the rasterised data surface.
- **ncol**: a numeric value indicating the number of column cells.
- **window**: an optional object of class matrix to be passed to kernel2d. See ‘Details’.
- **sigma**: an optional numeric value specifying the kernel bandwidth to be passed to kernel2d. See also ‘Details’.
- **verbose**: logical. If TRUE, print the current stage of the computation and time spent on each job to the screen.

Details

The decomposable segregation measure is a surface-based, non-spatial method. The index calculation does not take into account the spatial arrangement of the population. It is the spatial smoothing process that deals with the spatial aspect of segregation. If the spatial smoothing is not performed properly, this measure may suffer from the same checkerboard problem as the traditional index of dissimilarity.

Currently deseg uses the function kernel2d in splancs, which employs a quartic kernel estimator. The points outside ‘window’ are not considered when computing the kernel estimates. The argument ‘window’ must be a polygon represented in a matrix form such that each row corresponds to a vertex. This is passed to kernel2d as ‘poly’. If ‘window’ is missing, a square that covers all points in ‘x’ will be used.

If ‘sigma’ is not given, bw.nrd in stats is used to find the optimal bandwidth.
Value

An object of SegDecomp-class.

Author(s)

Seong-Yun Hong

References


See Also

SegDecomp-class, kernel2d

Examples

# uses the idealised landscapes in 'segdata'
data(segdata)
grd <- GridTopology(cellcentre.offset=c(0.5,0.5),
                      cellsize=c(1,1), cells.dim=c(10,10))
grd.sp <- as.SpatialPolygons.GridTopology(grd)

# displays the test data
plot(grd.sp)
plot(grd.sp[segdata[,9] == 100,], col = "Black", add = TRUE)
plot(grd.sp[segdata[,9] == 50,], col = "Grey", add = TRUE)

# tries different bandwidths for the same data
bw1 <- deseg(grd.sp, segdata[,9:10], sigma = 1, nrow = 20, ncol = 20)
print(bw1, digits = 3)
bw1.val <- sum(as.vector(bw1))
spplot(bw1, col.regions=rev(heat.colors(20)),
       main = paste("Bandwidth = 1, S =", round(bw1.val, 2)))

bw2 <- deseg(grd.sp, segdata[,9:10], sigma = 2, nrow = 20, ncol = 20)
print(bw2, digits = 3)
bw2.val <- sum(as(vector(bw2, "vector"))
spplot(bw2, col.regions=rev(heat.colors(20)),
       main = paste("Bandwidth = 2, S =", round(bw2.val, 2)))

## Not run:
# let's see how the index value changes with different bandwidths
h0 <- seq(1, 5, length.out = 10); vals <- numeric()
for (i in 1:10) {
  d <- deseg(grd.sp, segdata[,9:10], sigma = h0[i], verbose = TRUE)
  vals <- append(vals, sum(as(d, "vector")))
}
plot(h0, vals, type = "b", xlab = "Bandwidth", ylab = "S")
title(main = "segdata[,9:10]")
# calculates the index for all data sets in 'segdata'

d.segdata <- matrix(NA, nrow = 3, ncol = 8)
for (i in 1:8) {
    idx <- 2 * i
    tmp <- deseg(grd.sp, segdata[, (idx-1):idx])
    d.segdata[,i] <- as(tmp, "vector")
}

# presents the results as a bar chart
barplot(d.segdata, names.arg = LETTERS[1:8], main = "segdata",
        legend.text = c(expression(italic(paste("S"[L]))),
                         expression(italic(paste("S"[C]))),
                         expression(italic(paste("S"[Q])))),
        args.legend = list(x = "topright", horiz = TRUE))

## End(Not run)

dissim

**Index of Dissimilarity**

**Description**

Calculates the index of dissimilarity proposed by Duncan and Duncan (1955). If 'x' or 'nb' is given, the index is adjusted to reflect the spatial distribution of population.

**Usage**

```r
dissim(x, data, nb, adjust = FALSE, p2n.args, n2m.args, wVECT.args, v2n.args, verbose = FALSE)
seg(data, nb)
```

**Arguments**

- **x**: an optional object of class SpatialPolygons or SpatialPolygonsDataFrame.
- **data**: a numeric matrix or data frame with two columns that represent mutually exclusive population groups (e.g., Asians and non-Asians). If more than two columns are given, only the first two will be used for computing the index.
- **nb**: an optional matrix object describing the intensity of interaction between geographic units.
- **adjust**: logical. If TRUE, and if 'x' is given, the index of dissimilarity is adjusted according to the suggestions of Morrill (1991) and Wong (1993), depending on packages installed on the system. See 'Details' for more information. Ignore if 'x' is not given.
- **p2n.args**: an optional list of arguments to be passed to poly2nb. To avoid confusion, it is best to name all objects in the list in a way that they exactly match the argument names in poly2nb.
- **n2m.args**: an optional list of arguments to be passed to nb2mat.
- **wVECT.args**: an optional list of arguments to be passed to writeVECT6.
dissim

v2n.args
verbose

Details
dissim calculates the index of dissimilarity for ‘data’. If ‘data’ is missing, it attempts to extract the data from ‘x’. If ‘x’ is not given, or if it is not a valid SpatialPolygonsDataFrame object, the function stops with an error.

When ‘x’ is given and ‘adjust’ is set to TRUE, the index is adjusted according to the suggestions of Morrill (1991) and Wong (1993). However, this automatic adjustment requires a number of packages to be installed on the user’s system: spdep for Morrill’s D(adj) and spgrass6 and rgdal for Morrill’s D(w) and D(s). Note that, for D(w) and D(s), GRASS commands should be accessible from within R.

Alternatively, the index value can be adjusted using a user-specified weighting matrix ‘nb’. ‘nb’ must be a square matrix (i.e., one that has the same number of rows and columns) but does not have to be symmetric. If ‘nb’ is not specified, the function calculates the traditional index of dissimilarity proposed by Duncan and Duncan (1955).

If ‘nb’ is a rook-based contiguity matrix standardised by the total number of neighbours, the index is adjusted as described in Morrill (1991). See the example code below and nb2mat in spdep for more information regarding how to construct such a matrix. For Wong’s D(w) and D(s), see https://sites.google.com/site/hongseongyun/seg. Note that the sum of all elements in ‘nb’ should equal one.

seg is a simplified version of dissim and will be deprecated later.

Value
dissim returns a list containing the following elements:

d
index of dissimilarity.
dm
index of dissimilarity adjusted according to Morrill (1991). NA if not calculated.
dw
index of dissimilarity adjusted according to Wong (1991). NA if not calculated.
ds
index of dissimilarity adjusted according to Wong (1991). NA if not calculated.
user
index of dissimilarity adjusted using the user-specified weighting matrix ‘nb’. NA if ‘nb’ is missing.

seg returns a single numeric value between 0 and 1, indicating the degree of segregation; 0 for no segregation, and 1 for complete segregation.

Author(s)

Seong-Yun Hong
References


See Also

`spseg`, `nb2mat`

Examples

```r
if (require(spdep)) { # package 'spdep' is required

  # uses the idealised landscapes in 'segdata'
  data(segdata)
  grd <- GridTopology(cellcentre.offset=c(0.5,0.5),
                       cellsize=c(1,1), cells.dim=c(10,10))
  grd.sp <- as.SpatialPolygons.GridTopology(grd)
  grd.nb <- nb2mat(poly2nb(grd.sp, queen = FALSE), style = "B")
  grd.nb <- grd.nb / sum(grd.nb)

  d <- rep(NA, 8); m <- rep(NA, 8)
  for (i in 1:8) {
    id <- 2 * i
    d[i] <- seg(segdata[,((id-1):id)])
    m[i] <- seg(segdata[,((id-1):id)], grd.nb)
    full <- segdata[,((id-1))] == 100
    half <- segdata[,((id-1))] == 50
    plot(grd.sp)
    plot(grd.sp[full,], col = "Black", add = TRUE)
    if (any(half))
      plot(grd.sp[half,], col = "Grey", add = TRUE)
    text(5, 11.5, labels = paste("D = ", round(d[i], 2),
                                ", D(adj) = ", round(m[i], 2), sep = "")
  }
}
```

---

**isp**

*Index of Spatial Proximity*

**Description**

Computes the index of spatial proximity developed by White (1983). This measure estimates the level of clustering by comparing the average distance between members of the same group with that between all individuals (regardless of the groups to which they belong). The results may change drastically depending on the definition of distance.
Usage

isp(x, data, nb, fun, verbose = FALSE, ...)
whiteseg(x, data, nb, fun, verbose = FALSE, ...)

Arguments

x
a numeric matrix or data frame with coordinates (each row is a point), or an object of class Spatial.
data
an object of class matrix, or one that can be coerced to that class. The number of rows in ‘data’ should equal the number of geographic units in ‘x’, and the number of columns should be greater than one (i.e., at least two population groups are required). This can be missing if ‘x’ has a data frame attached to it.

nb
an optional matrix object indicating the distances between the geographic units.
fun
a function for the calculation of proximity. The function should take a numeric vector as an argument (distance) and return a vector of the same length (proximity). If this is not specified, a negative exponential function is used by default.

verbose
logical. If TRUE, print the current stage of the computation and time spent on each job to the screen.

... optional arguments to be passed to dist when calculating the distances between the geographic units in ‘x’. Ignored if ‘nb’ is given. See help(dist) for available options.

Details

‘nb’ must be a square matrix (i.e., one that has the same number of rows and columns) but does not have to be symmetric. If ‘nb’ is not given, whiteseg attempts to create a distance matrix of ‘x’ using the function dist in stats and use it as ‘nb’. The optional arguments in ‘...’ will be passed to dist.

Value

A single numeric value indicating the degree of segregation; a value of 1 indicates absence of segregation, and values greater than 1.0 indicate clustering. If the index value is less than one, it indicates an unusual form of segregation (i.e., people live closer to other population groups).

Note

The function name whiteseg() was changed in version 0.4-3 to isp(). The old function name will be deprecated from 0.6-1.

Author(s)

Seong-Yun Hong

References

localenv

Local Population Composition

Description

localenv calculates the local population composition at each data point from a matrix of coordinates, or an object of class Spatial or ppp.

Usage

localenv(x, data, power = 2, useExp = TRUE, scale = FALSE, maxdist, sprel, tol = .Machine$double.eps)

Arguments

x  
a numeric matrix or data frame with coordinates (each row is a point), or an object of class Spatial or ppp.

data  
an object of class matrix, or one that can be coerced to that class. The number of rows in 'data' should equal the number of points in 'x', and the number of columns should be greater than one (at least two population groups are required). This can be missing if 'x' has a data frame attached to it.

Examples

# uses the idealised landscapes in 'segdata'
data(segdata)
grd <- GridTopology(cellcentre.offset=c(0.5,0.5),
cells=c(1,1), cells.dim=c(10,10))
grd.sp <- as.SpatialPolygons.GridTopology(grd)

d <- rep(NA, 8)  # index of dissimilarity
p <- rep(NA, 8)  # index of spatial proximity
for (i in 1:8) {
  idx <- 2 * i
  d[i] <- seg(segdata[, (idx-1):idx])
  p[i] <- whiteseg(grd.sp, data = segdata[, (idx-1):idx])
  full <- segdata[, (idx-1)] == 100
  half <- segdata[, (idx-1)] == 50
  plot(grd.sp)
  plot(grd.sp[full,], col = "Black", add = TRUE)
  if (any(half))
    plot(grd.sp[half,], col = "Grey", add = TRUE)
  text(5, 11.5, labels =
       paste("D = ", round(d[i], 2), ", P = ", round(p[i], 2), sep = ")
}

See Also

seg, dist
power a numeric value that determines the change rate of a distance weight function. If zero, all data points have the same weight regardless of the distance. Typically 1-5.

useExp logical. If FALSE, use a simple inverse distance function instead of a negative exponential function. See ‘Details’.

scale logical. If TRUE, the distances between points in ‘x’ are scaled so the weights are not affected by the measurement unit. The default is FALSE for consistency with the previous version.

maxdist an optional numeric value specifying a search radius for the construction of each local environment. Must be a positive value, or zero.

sprel an optional object of class dist or nb. See ‘Details’.

tol a small, positive non-zero value. If ‘useExp’ is FALSE, this value will be added to the denominator to avoid the divide-by-zero error.

Details

At each data point in ‘x’, localenv calculates the weighted average of the populations of all points that are within a search radius ‘maxdist’. The output from this function is an essential component to compute the spatial segregation measures.

By default, the weight of each point is calculated from a negative exponential function, which is defined as:

$$w(d) = e^{-d \times \text{power}}$$

where $d$ is the Euclidean distance between two points.

If ‘useExp’ is FALSE, a simple inverse distance function is used to calculate the weight of each point:

$$w(d) = \frac{1}{(d + \text{error})^{\text{power}}}$$

If ‘maxdist’ is not provided (default), all data points in the study area are used for the construction of each local environment. It is recommended to specify this parameter to speed up the calculation process.

If a distance measure other than the Euclidean distance is required to represent spatial proximity between the points, users can provide an object of class dist, which contains the distances between all pairs of the points, through an optional argument ‘sprel’. One convenient way of obtaining such information may be the use of the function dist, which offers a variety of distance measures, such as Manhattan, Canberra, and Minkowski.

Or alternatively, one can supply an object of class nb to use a k-nearest neighbour averaging or polygon contiguity.

Value

An object of SegLocal-class.
Note

Note that this function is not to interpolate between data points. The calculation of each local environment involves the point itself, so the simple inverse distance function with a power of 2 or more should be used with care.

Author(s)

Seong-Yun Hong

See Also

SegLocal-class, spatseg, dist

Examples

# uses the idealised landscapes in 'segdata'
data(segdata)
grd <- GridTopology(cellcentre.offset=c(0.5,0.5),
  cellsize=c(1,1), cells.dim=c(10,10))
grd.sp <- as.SpatialPolygons.GridTopology(grd)

# complete segregation:
# negative exponential function of distance
xx1 <- localenv(grd.sp, data = segdata[,1:2])
spplot(xx1, main = "Negative exponential")

# inverse distance
xx2 <- localenv(grd.sp, data = segdata[,1:2], useExp = FALSE)
spplot(xx2, main = "Inverse distance")

# inverse distance with p = 0, i.e., weight all points equally
xx3 <- localenv(grd.sp, data = segdata[,1:2], useExp = FALSE, power = 0)
spplot(xx3, main = "Inverse distance with p = 0")

## Not run:
# checkerboard pattern:
# negative exponential function with different p values
vv1 <- localenv(grd.sp, data = segdata[,5:6], power = 1)
spplot(vv1, main = "Negative exponential with p = 1")

vv2 <- localenv(grd.sp, data = segdata[,5:6])
spplot(vv2, main = "Negative exponential with p = 2")

vv3 <- localenv(grd.sp, data = segdata[,5:6], power = 3)
spplot(vv3, main = "Negative exponential with p = 3")
## End(Not run)
Description

This data set contains eight different spatial configurations that were used by Morrill (1991) and Wong (1993) to test their segregation measures.

Usage

data(segdata)

Format

An object of class `data.frame`. The data set contains 16 columns, representing eight idealised spatial patterns. Each column indicates the following information:

<table>
<thead>
<tr>
<th>Column</th>
<th>Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>[.1]</td>
<td>A1 Pattern A, Group 1</td>
</tr>
<tr>
<td>[.2]</td>
<td>A2 Pattern A, Group 2</td>
</tr>
<tr>
<td>[.3]</td>
<td>B1 Pattern B, Group 1</td>
</tr>
<tr>
<td>[.4]</td>
<td>B2 Pattern B, Group 2</td>
</tr>
<tr>
<td>[.5]</td>
<td>C1 Pattern C, Group 1</td>
</tr>
<tr>
<td>[.6]</td>
<td>C2 Pattern C, Group 2</td>
</tr>
<tr>
<td>[.7]</td>
<td>D1 Pattern D, Group 1</td>
</tr>
<tr>
<td>[.8]</td>
<td>D2 Pattern D, Group 2</td>
</tr>
<tr>
<td>[.9]</td>
<td>E1 Pattern E, Group 1</td>
</tr>
<tr>
<td>[.10]</td>
<td>E2 Pattern E, Group 2</td>
</tr>
<tr>
<td>[.11]</td>
<td>F1 Pattern F, Group 1</td>
</tr>
<tr>
<td>[.12]</td>
<td>F2 Pattern F, Group 2</td>
</tr>
<tr>
<td>[.13]</td>
<td>G1 Pattern G, Group 1</td>
</tr>
<tr>
<td>[.14]</td>
<td>G2 Pattern G, Group 2</td>
</tr>
<tr>
<td>[.15]</td>
<td>H1 Pattern H, Group 1</td>
</tr>
<tr>
<td>[.16]</td>
<td>H2 Pattern H, Group 2</td>
</tr>
</tbody>
</table>

Source


Examples

data(segdata)
grd <- GridTopology(cellcentre.offset=c(0.5,0.5),
                     cellsize=c(1,1), cells.dim=c(10,10))
grd.sp <- as.SpatialPolygons.GridTopology(grd)
pd <- par()
par(mfrow = c(2, 4), mar = c(0, 1, 0, 1))
for (i in 1:8) {
  full <- segdata[, (2*i)-1] == 100
  half <- segdata[, (2*i)-1] == 50
  plot(grd.sp)
  plot(grd.sp[full,], col = "Black", add = TRUE)
  if (any(half))
    plot(grd.sp[half,], col = "Grey", add = TRUE)
  text(5, 11.5, labels = paste("Pattern", LETTERS[i]))
}
par(mfrow = pd$mfrow, mar = pd$mar)

---

**SegDecomp**

Create an Object of Class SegDecomp

### Description

Creates a new object of SegDecomp-class.

### Usage

SegDecomp(d, coords, data, proj4string = CRS(as.character(NA)))

### Arguments

- **d**
  a numeric vector of length three, representing the locational, compositional, and qualitative segregation, respectively.
- **coords**
  a numeric matrix or data frame with coordinates (each row is a point).
- **data**
  an object of class matrix containing the population data at each data point. The number of rows in 'data' should equal the number of points in 'coords', and the number of columns should be greater than one (i.e., at least two population groups are required).
- **proj4string**
  an optional projection string of class CRS.

### Value

An object of SegDecomp-class.

### Author(s)

Seong-Yun Hong

### See Also

SegDecomp-class, deseg
SegDecomp-class

Examples

# creates a random data set with 50 data points and 3 population groups
xy <- matrix(runif(100), ncol = 2)
colnames(xy) <- c("x", "y")
pop <- matrix(runif(150), ncol = 3)
colnames(pop) <- LETTERS[1:3]

# constructs an object of class 'SegDecomp'
v <- SegDecomp(d = numeric(3), coords = xy, data = pop)
is(v)

SegDecomp-class  Class Decomp

Description

A class to hold results from deseg.

Objects from the Class

Objects can be created by calls to deseg, or the constructor SegDecomp.

Slots

d  a numeric vector of length three, representing the locational, compositional, and qualitative segregation, respectively.
coords  a numeric matrix or data frame with coordinates (each row is a point).
data  an object of class matrix containing the population data at each data point. The number of rows in 'data' should equal the number of points in 'coords', and the number of columns should be greater than one (i.e., at least two population groups are required).
proj4string  an optional projection string of class CRS.

Methods

coerce  signature(from = "SegDecomp", to = "SpatialPoints"): coerce an object of class SegDecomp to an object of class SpatialPoints. The points have no attribute data.

coerce  signature(from = "SegDecomp", to = "SpatialPointsDataFrame"): coerce an object of class SegDecomp to an object of class SpatialPointsDataFrame. The values in the slot 'data' will be used as the attribute data.

coerce  signature(from = "SegDecomp", to = "SpatialPixelsDataFrame"): coerce an object of class SegDecomp to an object of class SpatialPixelsDataFrame. This method is to retrieve the kernel density estimates and save it as a SpatialPixelsDataFrame object, with a proj4string.

coerce  signature(from = "SegDecomp", to = "vector"): coerce an object of class SegDecomp to an object of class vector. Use this to extract the segregation index values from the specified object.
SegLocal

Create an Object of Class SegLocal

Description

Create a new object of SegLocal-class from a matrix of coordinates and population data.

Usage

SegLocal(coords, data, env, proj4string = CRS(as.character(NA)))
Arguments

coords  a numeric matrix or data frame with coordinates (each row is a point).

data    an object of class matrix containing the population data at each data point. The number of rows in `data` should equal the number of points in `coords`, and the number of columns should be greater than one (i.e., at least two population groups are required).

env     an object of class matrix containing the local environment parameters. Must be the same dimensions as `data`.

proj4string  an optional projection string of class CRS.

Value

An object of SegLocal-class.

Author(s)

Seong-Yun Hong

See Also

SegLocal-class, localenv

Examples

# creates a random data set with 50 data points and 3 population groups
xy <- matrix(runif(100), ncol = 2)
colnames(xy) <- c("x", "y")

pop <- matrix(runif(150), ncol = 3)
colnames(pop) <- LETTERS[1:3]

# constructs an object of class 'SegLocal'
v <- SegLocal(coords = xy, data = pop, env = pop)
is(v)

---

SegLocal-class  Class SegLocal

Description

A class to hold the local population composition data.

Objects from the Class

Objects can be created by calls to localenv, or the constructor SegLocal.
Slots

**coords** a numeric matrix or data frame with coordinates (each row is a point).

**data** an object of class matrix containing the population data at each data point. The number of rows in ‘data’ should equal the number of points in ‘coords’, and the number of columns should be greater than one (i.e., at least two population groups are required).

**env** an object of class matrix containing the local environment parameters. Must be the same dimensions as ‘data’.

**proj4string** an optional projection string of class CRS.

Methods

**coerce** signature(from = "SegLocal", to = "SpatialPoints"): coerce an object of class SegLocal to an object of class SpatialPoints. The points have no attribute data.

**coerce** signature(from = "SegLocal", to = "SpatialPointsDataFrame"): coerce an object of class SegLocal to an object of class SpatialPointsDataFrame. The values in the slot ‘env’ will be used as the attribute data.

**coerce** signature(from = "SegLocal", to = "SpatialPixelsDataFrame"): coerce an object of class SegLocal to an object of class SpatialPixelsDataFrame. The values in the slot ‘env’ will be used as the attribute data. May not work when the points are irregularly spaced.

**coerce** signature(from = "SpatialPointsDataFrame", to = "SegLocal"): coerce an object of class SpatialPointsDataFrame to an object of class SegLocal.

**coerce** signature(from = "SpatialPolygonsDataFrame", to = "SegLocal"): coerce an object of class SpatialPolygonsDataFrame to an object of class SegLocal.

**show** signature(object = "SegLocal"): show the number of points and data columns in an object of class SegLocal.

**print** signature(x = "SegLocal"): same as show.

**plot** signature(x = "SegLocal"): draw a plot, or plots, of points in an object of class SegLocal. Use an optional argument ‘which.col’ to specify a column of the data that determines the points’ sizes. See the examples below for demonstration.

**points** signature(x = "SegLocal"): draw points in an object of class SegLocal on an active graphic device.

**spplot** signature(obj = "SegLocal"): coerce an object of class SegLocal to an object of class SpatialPixelsDataFrame or SpatialPointsDataFrame and display it. See help(spplot) for more details about the graphical parameter arguments.

**summary** signature(object = "SegLocal"): summarise the population compositions of points and local environments in an object of class SegLocal.

**update** signature(object = "SegLocal"): update an existing object of class SegLocal.

Author(s)

Seong-Yun Hong

See Also

SegLocal, localenv
### SegSpatial

**Create an Object of Class SegSpatial**

**Description**

Creates a new object of SegSpatial-class.

**Usage**

SegSpatial(d, r, h, p, coords, data, env, proj4string = CRS(as.character(NA)))

**Arguments**

- **d**: an object of class numeric containing the spatial dissimilarity index value.
- **r**: an object of class numeric containing the spatial diversity index value.
- **h**: an object of class numeric containing the spatial information theory index value.
- **p**: an object of class matrix that has the spatial exposure/isolation of all population groups.
- **coords, data, env, proj4string**: see SegLocal-class.
Value

An object of `SegSpatial-class`.

Author(s)

Seong-Yun Hong

See Also

`SegSpatial-class`, `spseg`

Examples

```r
# creates a random data set with 50 data points and 3 population groups
xy <- matrix(runif(100), ncol = 2)
colnames(xy) <- c("x", "y")
pop <- matrix(runif(150), ncol = 3)
colnames(pop) <- LETTERS[1:3]

# constructs an object of class 'SegSpatial'
v <- SegSpatial(d = numeric(), r = numeric(), h = numeric(),
                 p = matrix(0, 0, 0), coords = xy, data = pop, env = pop)

is(v)
```

---

### SegSpatial-class  
**Class SegSpatial**

**Description**

A class to hold results from `spatseg`.

**Objects from the Class**

Objects can be created by calls to `spseg`, or the constructor `SegSpatial`.

**Slots**

- `d` an object of class `numeric` containing the spatial dissimilarity index value.
- `r` an object of class `numeric` containing the spatial diversity index value.
- `h` an object of class `numeric` containing the spatial information theory index value.
- `p` an object of class `matrix` that has the spatial exposure/isolation of all population groups.

`coords, data, env, proj4string` see `SegLocal-class`.  

---
Methods

coerce signature(from = "SegSpatial", to = "SpatialPoints"): coerce an object of class SegSpatial to an object of class SpatialPoints. The points have no attribute data.

coerce signature(from = "SegSpatial", to = "SpatialPointsDataFrame"): coerce an object of class SegSpatial to an object of class SpatialPointsDataFrame. The values in the slot 'data' will be used as the attribute data.

coerce signature(from = "SegSpatial", to = "SpatialPixelsDataFrame"): coerce an object of class SegSpatial to an object of class SpatialPixelsDataFrame. The values in the slot 'data' will be used as the attribute data. May not work when the points are irregularly spaced.

coerce signature(from = "SegSpatial", to = "list"): retrieve the segregation index values and return it as a list object.

as.list signature(x = "SegSpatial"): same as the above.

show signature(object = "SegSpatial"): show the segregation index values.

print signature(x = "SegSpatial"): same as show.

spplot signature(obj = "SegSpatial"): coerce an object of class SegSpatial to an object of class SpatialPixelsDataFrame or SpatialPointsDataFrame and display it. See help(spplot) for more details about the graphical parameter arguments.

Extends
    SegLocal-class.

Author(s)
    Seong-Yun Hong

See Also
    SegSpatial, spseg

Examples

# creates 100 regularly-spaced data points and 3 population groups
xy <- expand.grid(1:10, 1:10)
co.names(xy) <- c("x", "y")
pop <- matrix(runif(300), ncol = 3)
env <- matrix(runif(300), ncol = 3)
co.names(pop) <- LETTERS[1:3]
co.names(env) <- LETTERS[4:6]

# constructs an object of class 'SegSpatial'
V <- SegSpatial(d = numeric(), r = numeric(), h = numeric(),
                    p = matrix(0, 0, 0),
                    coords = as.matrix(xy), data = pop, env = env)
print(V)

# changes the spatial dissimilarity index value
slot(V, "d") <- runif(1)
# retrieves the index values
as.list(v)

# displays the values in the slot 'data'
spplot(v, col.regions = heat.colors(20))

# displays the values in the slot 'env'
w <- as(v, "SegLocal")
spplot(w, col.regions = heat.colors(20))

---

spseg  

**Spatial Segregation Measures**

**Description**

Calculates the set of spatial segregation measures developed by Reardon and O’Sullivan (2004).

**Usage**

```r
spseg(x, data, method = "all", smoothing = "none", nrow = 100, ncol = 100,
      window, sigma, useC = TRUE, negative.rm = FALSE,
      tol = .Machine$double.eps, verbose = FALSE, ...)
spatseg(env, method = "all", useC = TRUE, negative.rm = FALSE,
        tol = .Machine$double.eps)
```

**Arguments**

- `x` a numeric matrix or data frame with coordinates (each row is a point), or an object of class `Spatial` or `ppp`.
- `env` an object of `SegLocal-class`.
- `data` an object of class `matrix`, or one that can be coerced to that class. The number of rows in ‘data’ should equal the number of points in ‘x’, and the number of columns should be greater than one (i.e., at least two population groups are required). This can be missing if ‘x’ has a data frame attached to it.
- `method` a vector of character strings indicating an measure or measures to be computed. This must be one or more of the strings “all” (default), “exposure”, “information”, “diversity”, and “dissimilarity”. Abbreviations are accepted, as long as it is clear which method is meant.
- `smoothing` a character string indicating how to perform spatial smoothing of the population data. This must be (an abbreviation of) one of the strings “none” (default), “kernel”, or “equal”.
- `nrow` a numeric value indicating the number of row cells in the rasterised data surface. Ignored if ‘smoothing’ is “none”.
- `ncol` a numeric value indicating the number of column cells.
window  an optional object of class matrix to be passed to kernel2d. See ‘Details’ in deseg.
sigma  an optional numeric value specifying the kernel bandwidth to be passed to kernel2d. See also ‘Details’ in deseg.
useC  logical. If TRUE, calculate the segregation values in C.
negative.rm  logical. If TRUE, all geographic units where at least one group (i.e., column) has a population of zero or less will be removed to prevent -Inf or NaN in the information theory index. If FALSE, the non-positive values will be replaced with ‘tol’.
tol  a small, positive non-zero value. See ‘Details’.
verbose  logical. If TRUE, print the current stage of the computation and time spent on each job to the screen.
...  optional arguments to be passed to localenv to compute the population composition of each local environment.

Details

spatseg computes the set of spatial segregation measures proposed by Reardon and O’Sullivan. spatseg is a wrapper function, which calls spatseg after constructing a population density surface and its local environment parameters with user-specified options. Currently the population density surface is constructed by assuming that the population density is uniform in each census tract, or by using kernel2d in the package splancs. In the previous version (< 0.4.1), the function rasterize in raster was used in the case of the former, and density.ppp in spatstat for the latter.

In R, \( \log(0) \) is defined as -Inf, and \( 0 \times \log(0) \) is NaN (not-a-number), in compliance with the IEEE Standard for Floating-Point Arithmetic. When computing the spatial information theory index, which is a spatial version of the entropy index, this is annoying because \( 0 \times \log(0) \) occurs quite often, especially when one or more groups are small, and/or when the grid size is very small. To work around this problem, the argument ‘tol’ is added, so instead of \( v \times \log(v) \), it calculates \( (v + tol) \times \log(v + tol) \), where \( v = 0 \). This makes the entropy practically zero, as ‘tol’ goes towards 0.

Value

An object of SegSpatial-class.

Note

The exposure/isolation index, P, is presented in a matrix form. The spatial exposure of group ‘m’ to group ‘n’ is located in the row ‘m’ and column ‘n’ of the matrix. The matrix is rarely symmetric in practice so the spatial exposure index should be interpreted with care.

The spatial isolation index values are given in the diagonal cells of the matrix; cell value at (m, m) indicates the degree of spatial isolation for group ‘m’ for example.

Author(s)

Seong-Yun Hong
References


See Also

SegSpatial-class, localenv, kernel2d

Examples

```r
# uses the idealised landscapes in 'segdata'
data(segdata)

grd <- GridTopology(cellcentre.offset = c(0.5, 0.5),
                     cellsize = c(1, 1), cells.dim = c(10, 10))
grd.sp <- as.SpatialPolygons.GridTopology(grd)
test.df <- segdata[, 1:2]

# no spatial smoothing
xx1 <- spseg(grd.sp, data = test.df)
print(xx1, digits = 3)
spplot(xx1, main = "No spatial smoothing")

# plots the values in the slot 'data'
spplot(xx1, main = "No spatial smoothing")

# smoothes the data points
xx2 <- spseg(grd.sp, data = test.df, smoothing = "equal")
print(xx2, digits = 3)
spplot(xx2, main = "Equal")

# uses the kernel smoothing of the data points
xx3 <- spseg(grd.sp, data = test.df, smoothing = "kernel",
            nrow = 20, ncol = 20)
print(xx3, digits = 3)
spplot(xx3, main = "Kernel")

## Not run:
# same as the above but with a boundary polygon
w <- matrix(c(1.5, 1.5,
              1.5, 8.5,
              8.5, 8.5,
              8.5, 4.5,
              5.5, 4.5,
              5.5, 1.5), ncol = 2, byrow = TRUE)
xx4 <- spseg(grd.sp, data = segdata[, 1:2], smoothing = "kernel",
            window = w, nrow = 20, ncol = 20)
print(xx4, digits = 3)
spplot(xx4, main = "Kernel with a boundary polygon")
```
# retrieves the index values
as.list(xx4)

# shows the values in the slot 'env'
spplot(as(xx4, "SegLocal"), main = "Local population composition")
## End(Not run)
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