

Package ‘rangemodelR’

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Type Package

Depends R (>= 3.2.0)

Title Mid-Domain Effect and Species Richness

Version 1.0.4

Author Aniruddha Marathe <aniruddha.pravin.marathe@gmail.com>

Maintainer Aniruddha Marathe <aniruddha.pravin.marathe@gmail.com>

Description Generates expected values of species richness, with continuous or scattered ranges, for data across one or two dimensions.

License GPL (>= 2)

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Suggests ggplot2,maptools,rgdal,rgeos

NeedsCompilation no

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R topics documented:

rangemodelR-package	2
neigh_ob	2
random.range	3
rangedata	3
rangemod1d	4
rangemod2d	5
range_shuffle	7
shp	9
spmat	9

Index	10
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rangemodelR-package *Mid-Domain Effect and Species Richness Patterns*

Description

Range Cohesion and Range Scatter Models in R

Details

Package: rangemodelR
 Type: Package
 Version: 1.0.4
 Date: 2015-08-09
 License: GPL (>= 2)
 LazyLoad: No

The package is useful for generating randomized community matrices under strict range cohesion. The package can handle data where species occurrence are recorded across one or two dimensions. One dimensional data are typically for sites ordered along a variable of interest such as elevation or latitude. `rangemod1d` is used for such data. Two dimensional data have species occurrences recorded on grids with known geographic coordinates and are handled with function `rangemod2d`. Range cohesion is enforced using an 'nb' object (generated by `poly2nb` of the `spdep` package).

Author(s)

Aniruddha Marathe <aniruddha.pravin.marathe@gmail.com>

References

Rahbek, C., Gotelli, N., Colwell, R., Entsminger, G., Rangel, T. & Graves, G. (2007) Predicting continental-scale patterns of bird species richness with spatially explicit models. *Proceedings of the Royal Society B: Biological Sciences*, 274, 165.

neigh_ob *Spatial Adjacency Data for the Polygon Grid 'shp'*

Description

A spatial adjacency object of class 'nb' for the polygon shapefile 'shp'. See documentation for `card` for details on structure of the object. The neighbours are according to 'queen's move' i.e sharing atleast one corner. So each cell can have upto eight neighbours.

Format

an object of class 'nb'

random.range	<i>random.range - supporting function for other rangemodel functions</i>
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Description

random.range is used within other rangemodel functions to radomly place given number of species occurences

Usage

```
random.range(uid, nb, range.size, var, first)
```

Arguments

uid	a vector of unique ids for selection
nb	a neighbour object similar to generated from 'shp2nb'
range.size	a vector of number of sites occupied by each species
var	an optional vector of variables for constraining the randomization
first	If true, var is used while choosing the first occurence as well. if var is null, first is always set FALSE

Details

this function is not intended for any direct use but is called within other functions of 'rangemodelR'.

Value

a numeric vector specifying selected possitions in 'uid'

rangedata	<i>Randomely generated elevational extents data for twenty species</i>
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Description

An example data that can be used with the function [range_shuffle](#). The data contains randomly generated elevational extents between 600m and 2400m. The function will expect same column names as in the example data.

Format

a dataframe with 20 rows and five columns

Details

It is a data.frame contains five columns with following names:

- "min" minimum elevation of range extent
- "max" maximum elevation of range extent
- "range" max - min
- "mid" mid points of the range extents
- "num_zones" number of elevation zone across which the species was recorded

rangemod1d

Range Cohesion Model for Ordered (and Non-spatial) Data

Description

rangemod1d takes observed site by species matrix and returns expected species richness values of each site

Usage

```
rangemod1d(spmat, var = NULL, cohesion = T, first = FALSE,
            degen = FALSE, rsize = c("observed", "unif"), reps)
```

Arguments

spmat	a site by species matrix or data frame with species in columns
var	an optional vector containing explanatory variable for constraining the randomization. It should be NULL when absent
cohesion	If true, species distributions are without gaps i.e. result is range cohesion, otherwise it is range scatter
first	If TRUE, 'var' is used while choosing the first occurrence as well. if 'var' is null, first is always set 'FALSE'
degen	If true, each randomized site by species matrix is saved and provided in output
rsize	which rangesizes to use for simulation, can be an integer vector of same length as number of species(collumns) or either 'observed' or 'unif'. See details for explanations
reps	number of replicates

Details

rangemod1d impliments simulations used by Rahbeck et.al (2007) to data which are only in form of a site by species matrix and without any spatial information. A list similar to an nb object of spdep can prepared according to order in which the rows (sites) are arranged. A manually prepared list of neighbours for each site can also be used. It is important that each site must have at least one neighbour. 'rsize' provides a vector of rangesizes. It can be 'unif' - ranges are drawn from a uniform distribution, between 1 to number of sites or 'observed' - rangesize of each species is exactly the same as in the observed matrix. Alternatively it can also be a user specified integer vector, of same length as number of species.

Value

If `degen` is `FALSE`, a data frame with four columns for mean, SD and confidence intervals of expected richness

- "mod.rich" mean richness of each site
- "mod.sd" standard deviation of species richness
- "q2.5" lower limit of the confidence interval
- "q97.5" upper limit of the confidence interval

If `degen` is `TRUE`, then a list containing above data frame and a list of all the randomized matrices

References

Rahbek, C., Gotelli, N., Colwell, R., Entsminger, G., Rangel, T. & Graves, G. (2007) Predicting continental-scale patterns of bird species richness with spatially explicit models. *Proceedings of the Royal Society B: Biological Sciences*, 274, 165.

Gotelli, N.J., Anderson, M.J., Arita, H.T., Chao, A., Colwell, R.K., Connolly, S.R., Currie, D.J., Dunn, R.R., Graves, G.R. & Green, J.L. (2009) Patterns and causes of species richness: a general simulation model for macroecology. *Ecology Letters*, 12, 873-886.

Examples

```
tempmat <- matrix(0,nrow=10,ncol=200,dimnames=list(letters[1:10],1:200))
tempmat <- as.matrix(apply(tempmat,2,function(x){rbinom(nrow(tempmat),1,
               runif(1,0.1,1))}))
rownames(tempmat) <- letters[1:10]
temp <- rangemod1d(tempmat,cohesion = TRUE,var = NULL,rsize = "observed",reps = 5)
plot(temp[,1],ylim= c(min(temp[,1] -2),max(temp[,1]+2)),pch = 16,ylab = 'Species Richness')
segments(1:10,y0=temp[,1]-temp[,2],y1= temp[,1]+temp[,2])
```

rangemod2d

Range Cohesion Models for Spatial Polygon Grids

Description

`rangemod2d` takes observed site by species matrix and returns expected species richness values of each site based on user defined neighbour relationships.

Usage

```
rangemod2d(spmat, shp, field, nb, rsize = c("observed", "unif"), var = NULL,
           reps, degen = FALSE, first = FALSE)
```

Arguments

spmat	a site by species matrix or data frame with species in columns
shp	shapefile of sites where species occurrences are recorded
field	a number or character vector indicating which column in the dbf of shapefile is the unique id
nb	a neighbour object similar to one generated from <code>poly2nb</code> of <code>spdep</code> . If 'nb' is NA then result is range scatter
rsize	which rangesizes to use for simulation, can be an integer vector of same length as number of species(collumns) or either 'observed' or'unif'. See details for explanations
var	an optional vector containing explanatory variable for constraining the randomization
reps	number of replicates
degen	If true, each randomized site by species matrix is saved and provided in output
first	If true, 'var' is used while choosing the first occurrence as well.if 'var' is null, first is always set 'FALSE'

Details

`rangemod2d` impliments simulations used by Rahbeck et.al. (2007) to species distribution data on a continuous grid. In 'spmat' the sites (rows) represent each cell in the grid.The species occurrences across sites are randomly spread maintaining strict range cohesion. A neighbour object is used to limit the choice of cells during random selctions to immidiate neighbours. Options for creating four cell (rook) or eight cell (queen) neighbours can be accessed while creating the 'nb' object, (typically from package `spdep`). The randomisation proceeds by selecting a single site,(weighted by 'var' if provided, and first is TRUE), and then continues selecting one site at a time from a vector of available neighbours taken from 'nb' and weighted by 'var' if provided. The vector of available sites is updated after each site is selected.

Value

A list containing following elements:

- "out.df" a data frame with four columns for mean, standard deviation, lower and upper limits of confidence intervals of predicted species richness
- "out.shp" same as the input shapefile with additional the four colums of 'out.df' in attribute table
- "degenerate.matrices" a list of all the randomized matrices(only present if 'degen' is TRUE)

References

- Rahbek, C., Gotelli, N., Colwell, R., Entsminger, G., Rangel, T. & Graves, G. (2007) Predicting continental-scale patterns of bird species richness with spatially explicit models. *Proceedings of the Royal Society B: Biological Sciences*, 274, 165.
- Gotelli, N.J., Anderson, M.J., Arita, H.T., Chao, A., Colwell, R.K., Connolly, S.R., Currie, D.J., Dunn, R.R., Graves, G.R. & Green, J.L. (2009) Patterns and causes of species richness: a general simulation model for macroecology. *Ecology Letters*, 12, 873-886.

Examples

```

if(require(rgdal)&&require(maptools)&&require(rgeos)&&require(ggplot2)){
  data(shp)
  data(neigh_ob)
  data(spmat)
  mod.out <- rangemod2d(spmat,shp,"ID",nb = neigh_ob,rsiz = "observed",
                      var = NULL, reps = 5)
  shp.out <- mod.out$out.shp
  shp.out.df <- shp.out@data
  shp.out.fort <- fortify(shp.out,region = "ID")
  seq <- match(shp.out.fort$id,shp.out.df$ID)
  shp.out.gg <- data.frame(shp.out.fort,shp.out.df[seq,])
  ggplot(shp.out.gg)+
    geom_map(map=shp.out.gg,aes_string(map_id="id",
                                       fill = "mod.rich"))+
    geom_path(aes(x = long,y = lat,group = group),colour = "white")+
    coord_equal() + theme_bw()+
    scale_fill_continuous(low = "white",high = "black")
}

```

range_shuffle

*Range shuffle models for for range extents recorded along gradients***Description**

This function was used by Wang et. al.(2012) to test geometric constraints, on elevational gradients. The function randomizes the range extents and range location for each species and returns expected pattern in species richness under geometric constraints.

Usage

```

range_shuffle(x, boundary, var, interval, sites, reps, degen, lowest = NA,
             highest = NA)

```

Arguments

x	Input data for elevational extents of species.data.dataframe with names 'genus_species','min','max','range','num_zones'. See Wang et.al (2012) for details. Species names column is optional.
boundary	nature of boundaries at the extremes of the gradient ie. either 'hard boundaries' that species cannot cross, or 'soft boundaries' that species can move across. Can be one of the following choices "hh", "sh", "hs", or "ss"
var	Predictor variable for constraining randomizations. dataframe with columns 'mid' and 'weights'. Where 'weights' provide relative chance of selecting a range location, typically based on environmental predictors
interval	Numeric. Interval between
sites	Numeric. Locations on domain for calculating species richness

reps	number of iterations
degen	logical. If TRUE save each randomized distribution.
lowest	Numeric. If analysis is only for a subset of the sampled gradient then the minimum point within the subset
highest	Numeric. If analysis is only for a subset of the sampled gradient then the maximum point within the subset

Details

range_shuffle implements simulations described by Wang et.al (2012) to estimate effect of geometric and environmental constraints on pattern in species richness across spatial gradients. It calculates a vector of all possible range locations for each given range extent based on the conditions for geometric constraints given by 'boundary'. Range locations are randomized by sampling from this vector.

Value

If degen is FALSE, a data frame with four columns for mean, SD and confidence intervals of expected richness

- "mod.rich" mean richness of each site
- "mod.sd" standard deviation of species richness
- "q2.5" lower limit of the confidence interval
- "q97.5" upper limit of the confidence interval

If degen is TRUE, then a list containing above data frame and a list of all the randomized matrices

References

Wang, X., and J. Fang. 2012. Constraining null models with environmental gradients: a new method for evaluating the effects of environmental factors and geometric constraints on geographic diversity patterns. *Ecography* 35:1147-1159.

Examples

```
data(rangedata)
range_shuffle_rnd <- range_shuffle(x=rangedata,boundary = 'hh',
                                  interval = 200, var = NULL,
                                  sites = seq(600,2400,200),
                                  reps =10,degen = FALSE)

range_shuffle_rnd
plot(range_shuffle_rnd$mean,ylab = "Species Richness",pch = 19)
```

shp	<i>Polygon Grid Roughly Located on Central India</i>
-----	--

Description

A grid with 100 cells, each 1⁰ by 1⁰ in size roughly located on central India. Each cell is assigned a hypothetical assemblage of varying species richness from a hypothetical regional pool of 20 species. The attribute table of the shape file has one unique id field observed species richness of each cell and one explanatory variable. Observed species richness is generated by assigning a randomly selected number of species among the 20 species in the regional pool.

- ID a unique id field
- obs_rich observed species richness
- trend a variable with spatial trend obtained using a linear function of coordinates

Format

an ESRI shapefile imported with [readShapeSpatial](#) with four columns in attribute table

spmat	<i>Site by Species Matrix of Hypothetical Assemblage of 20 Species Across the Grid 'shp'</i>
-------	--

Description

A site by species matrix with cells of the grid in shapefile [shp](#) in rows and 20 species in columns. Presence of species is denoted by '1' and absence by '0'.

Format

a dataframe with 100 rows and 20 columns

Index

*Topic **package**

rangemod1R-package, 2

card, 2

neigh_ob, 2

poly2nb, 2, 6

random.range, 3

range_shuffle, 3, 7

rangedata, 3

rangemod1d, 2, 4

rangemod2d, 2, 5

rangemod1R (rangemod1R-package), 2

rangemod1R-package, 2

readShapeSpatial, 9

shp, 9, 9

spdep, 2, 6

spmat, 9