

# Package ‘rangemodelR’

August 19, 2018

**Type** Package

**Depends** R (>= 3.2.0)

**Title** Mid-Domain Effect and Species Richness

**Version** 1.0.3

**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

**Repository** CRAN

**Date/Publication** 2018-08-19 00:00:03 UTC

## R topics documented:

rangemodelR-package . . . . .	2
neigh_ob . . . . .	2
random.range . . . . .	3
rangemod1d . . . . .	3
rangemod2d . . . . .	5
shp . . . . .	7
spmat . . . . .	7
<b>Index</b>	<b>8</b>

---

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

---

## Description

Range Cohesion and Range Scatter Models in R

## Details

Package: rangemodelR  
 Type: Package  
 Version: 1.0.1  
 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 fuctions</i>
--------------	---

---

**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'

---

rangemod1d	<i>Range Cohesion Model for Ordered (and Non-spatial) Data</i>
------------	--

---

**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 a 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 colums 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 <a href="#">poly2nb</a> of <a href="#">spdep</a> . 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 implements 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 selections to immediate 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 columns 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")
}
```

---

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

---

### Description

A grid with 100 cells, each 1<sup>0</sup> by 1<sup>0</sup> 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, 5

random.range, 3

rangemod1d, 2, 3

rangemod2d, 2, 5

rangemod1R (rangemod1R-package), 2

rangemod1R-package, 2

readShapeSpatial, 7

shp, 7, 7

spdep, 2, 5, 6

spmat, 7