Package ‘rangemodelR’

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Type Package

Depends R (>= 3.5)

Title Mid-Domain Effect and Species Richness

Version 1.0.6

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

Description Used for generating randomized community matrices under strict range cohesion. The package can handle data where species occurrence are recorded across sites ordered along gradients such as elevation and latitude, as well as species occurrences recorded on spatial grids with known geographic coordinates.

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NeedsCompilation no

Imports sf, spdep

Author Aniruddha Marathe [aut, cre]

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Contents

`random.range` *random.range - supporting function for other rangemodel fucntions*

Description

It is used within other functions in this package to radomly place given number of species occurrences

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 occurrence 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 this package.

Value

a numeric vector specifying selected positions in 'uid'

`rangemod1d` *Range Cohesion Model for Ordered (and Non-spatial) Data*

Description

The function 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 range sizes to use for simulation, can be an integer vector of same length as number of species(columns) or either 'observed' or 'unif'. See details for explanations
`reps`	number of replicates

Details

Implements 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 neighbors for each site can also be used.It is important that each site must have at least one neighbor. 'rsize' provides a vector of range sizes.It can be 'unif' - ranges are drawn from a uniform distribution,between 1 to number of sites or 'observed' - range size 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 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])
```

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