Package ‘rangemodelR’

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Description Generates expected values of species richness, with continuous or scattered ranges, for data across one or two dimensions.
License GPL (>= 2)
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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).

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References

random.range - supporting function for other rangemodel functions

Description
random.range is used within other rangemodel functions to randomly 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 'rangemodelR'.

Value
a numeric vector specifying selected positions in 'uid'

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 (columns) or either `observed` or `unif`. See details for explanations
reps   number of replicates

details

rangemod1d 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 be 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

Examples

```r
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))})))
rownames(tempmat) <- letters[1:10]
temp <- rangemod2d(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

```r
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 `poly2nb` of `spdep` 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(columns) 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


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,rsize = "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**

*Polygon Grid Roughly Located on Central India*

**Description**

A grid with 100 cells, each 1° by 1° 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**

*Site by Species Matrix of Hypothetical Assemblage of 20 Species Across the Grid 'shp'*

**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
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