Package 'spThin'

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Type Package

Title Functions for Spatial Thinning of Species Occurrence Records for Use in Ecological Models

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Description A set of functions that can be used to spatially thin species occurrence data. The resulting thinned data can be used in ecological modeling, such as ecological niche modeling.

BugReports https://github.com/mlammens/spThin/issues

Depends spam, grid, fields, knitr

Imports grDevices, graphics, utils

LazyData TRUE

License GPL-3

VignetteBuilder knitr

RoxygenNote 7.0.0

NeedsCompilation no

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Heteromys_anomalus_South_America

Occurrence record locations for Heteromys anomalus

Description

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A dataset containing compiled occurrence record locations for Heteromys anomalus in northern coastal South America. These records have been examined to check for accurate species identification

Format

A data frame with 201 rows and 4 variables

Details

- SPEC. species name assigned to occurrence record
- LAT. decimal degree latitude value
- LONG. decimal degree longitude value
- REGION. region, or island, of occurrence

plotThin

Plot diagnosis for results of thin function

Description

Three plots (selected by which) are currently available: a plot of the number of repetitions versus the number of maximum records retained at each repetition ([1] observed values; [2] log transformed) and a histogram of the maximum records retained [3].

Usage

```
plotThin(
  thinned,
  which = c(1:3),
  ask = prod(par("mfcol")) < length(which) && dev.interactive(),
  ...
)</pre>
```

summaryThin 3

Arguments

thinned A list of data.frames returned by thin function.

which if a subset of the plots is required, specify a subset of the numbers 1:3.

ask logical; if TRUE, the user is asked before each plot, see par(ask=.).

... other parameters to be passed through to plotting functions.

See Also

thin.algorithm thin

summaryThin

Summary method for results of thin function

Description

Summarize the results of thin function.

Usage

```
summaryThin(thinned, show = TRUE)
```

Arguments

thinned A list of data.frames returned by thin function.

show logical; if TRUE, the summary values are printed at the console.

Value

Returns a list with the (1) maximun number of records, (2) number of data frames with maximun number of records and (3) a table with the number of data frames per number of records.

See Also

```
thin.algorithm
thin
```

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thin

Spatially thin species occurence data

Description

thin returns spatially thinned species occurence data sets. A randomizaiton algorithm (thin.algorithm) is used to create data set in which all occurnece locations are at least thin.par distance apart. Spatial thinning helps to reduce the effect of uneven, or biased, species occurence collections on spatial model outcomes.

Usage

```
thin(
  loc.data,
 lat.col = "LAT",
 long.col = "LONG",
  spec.col = "SPEC",
  thin.par,
  reps,
  locs.thinned.list.return = FALSE,
 write.files = TRUE,
 max.files = 5,
 out.dir,
  out.base = "thinned_data",
 write.log.file = TRUE,
 log.file = "spatial_thin_log.txt",
  verbose = TRUE
)
```

Arguments

loc.data	A data frame of occurence locations. It can include several columns, but must include at minimum a column of latitude values, a column of longitude values, and a column of species names.	
lat.col	Name of column of latitude values. Caps sensitive.	
long.col	Name of column of longitude values. Caps sensitive.	
spec.col	Name of column of species name. Caps sensitive.	
thin.par	Thinning parameter - the distance (in kilometers) that you want records to be separated by.	
reps	The number of times to repete the thinning process. Given the random process of removing nearest-neighbors there should be 'rep' number of different sets of coordinates.	
locs.thinned.list.return		

TRUE/FALSE - If true, the 'list' of the data.frame of thinned locs resulting from each replication is returned (see Returns below).

thin.algorithm 5

write.files	TRUE/FALSE - If true, new *.csv files will be written with the thinned locs data
max.files	The maximum number of *csv files to be written based on the thinned data
out.dir	Directory to write new *csv files to
out.base	A file basename to give to the thinned datasets created
write.log.file	TRUE/FALSE create/append log file of thinning run
log.file	Text log file
verbose	TRUE/FALSE - If true, running details of the function are print at the console.

Value

locs.thinned.dfs A list of data.frames, each data.frame the spatially thinned locations of the algorithm for a single replication. This list will have 'reps' elements.

See Also

```
thin.algorithm
```

thin.algorithm Implements random spatial thinning algorithm	
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Description

thin.algorithm implements a randomization approach to spatially thinning species occurence data. This function is the algorithm underlying the thin function.

Usage

```
thin.algorithm(rec.df.orig, thin.par, reps)
```

Arguments

rec.df.orig	A data frame of long/lat points for each presence record. The data.frame should be a two-column data frame, one column of long and one of lat
thin.par	Thinning parameter - the distance (in kilometers) that you want records to be separated by.
reps	The number of times to repete the thinning process. Given the random process of removing nearest-neighbors there should be 'rep' number of different sets of coordinates.

Value

reduced.rec.dfs: A list object of length 'rep'. Each list element is a different data.frame of spatially thinned presence records.

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```
* datasets Heteromys_anomalus_South_America, \frac{2}{2} Heteromys_anomalus_South_America, \frac{2}{2} plotThin, \frac{2}{3} summaryThin, \frac{3}{3} thin, \frac{3}{3}, \frac{4}{5} thin.algorithm, \frac{3}{5}, \frac{5}{5}
```