Package 'nhSDM'

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Title Tools for Natural Heritage SDMs

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Version 0.0.1

Description Miscellaneous tools for working with Natural Heritage data in
Species Distribution Modelling (SDM) workflows.

Depends R (>= 3.4.1)

Imports methods, sf, raster, sp

Suggests dplyr, lwgeom

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

R topics documented:

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nh_group   *Group spatial features using a defined separation distance*

Description

Input features are allocated into new groups depending on whether they lie within the separation
distance of another input feature.

Usage

```
nh_group(spf, sep.dist = 0, union = FALSE)
```

Arguments

spf	input spatial features (sp or sf spatial object)
sep.dist	separation distance with which to define groups (see description)
union	whether to union output groups into multi-features

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Details

The grouping is done by input ID, so multi-features are considered one input feature (they will not be be ungrouped).

The separation distance `sep.dist` is numeric and in the units of `spf`'s coordinate system, unless the coordinate system uses latitude/longitude as the unit (e.g. WGS 84). In these cases, geodesic distances will be used and `sep.dist` should be specified in meters.

A column 'group' will be added to the output features. Specifying `union = TRUE` will output one (multi)feature per group, meaning original attributes will be discarded - only 'group' and 'count' (the number of original features in the group) will be returned. This feature requires the package `dplyr` to be installed.

Author(s)

David Bucklin

Examples

```
## Not run:
spf <- rgdal::readOGR("ambymabe/polygon_data", "ambymabe")
spg <- nh_group(spf, 1000)

## End(Not run)
```

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nh_sample   *Create points in polygons in reference raster cells*

Description

For each spatial polygon, a given number (`num_samps`) of points are created in cells that the polygon intersects.

Usage

```
nh_sample(spf, rast, num.samps = NULL, replace = FALSE, force.min = FALSE)
```

Arguments

`spf`	input spatial features (sp or sf spatial object)
`rast`	raster dataset with extent overlapping spf
`num.samps`	number of samples to create in each polygon (see details)
`replace`	whether to sample with or without replacement
`force.min`	whether to force `num.samps` points in polygons, even if they are duplicates

Details

num.samps can be a a proportion (a decimal value < 1), single integer, or vector of integers equal to length of spf indicated the number of samples to take from each polygon. If left NULL, num.samps will be set to the number of cells [n] intersecting the polygon. If a proportion is given (e.g., 0.5), than [n * num.samps] will be returned. If a single integer is given, num.samps points will be sampled in each polygon.

When replace = FALSE and force.min = FALSE (defaults), each cell can only contain one point (across each polygon, and the entire returned set of points). In this case, when the number of samples points to create exceeds the number of unique cells intersected by a given polygon, the number of samples for that polygon equals the number of cells. If replace = TRUE, sampling is done with replacement and duplicates may be taken. The special case replace = FALSE and force.min = TRUE will always return num.samps per polygon. It only produces duplicates if num.samps exceeds the number of cells intersecting the polygon, in which case it will replicate the samples until num.samps is reached.

If CRS do not match, the SpatialPolygons will be transformed to the CRS of the raster.

A column 'poly.id' is added to the output point features to indicate the row number of the polygon that the point was generated within.

Author(s)

David Bucklin

Examples

```
## Not run:
r<-raster::raster("AnnMnTemp.tif")
spf <- rgdal::readOGR("ambymabe/polygon_data", "ambymabe")
# can also use sf: spf <- sf::st_read("ambymabe/polygon_data/ambymabe.shp")
spf.samps <- nh_sample(spf, r, num.samps)

## End(Not run)
```

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