

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 | <i>Group spatial features using a defined separation distance</i> |
|----------|-------------------------------------------------------------------|

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 |

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("D:/SDM/Tobacco/inputs/species/ambymabe/polygon_data", "ambymabe")
spg <- nh_group(spf, 1000)

## End(Not run)
```

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. The points will inherit the raster's projection.

Usage

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

Arguments

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

Details

num.samps can be 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), then $[n * \text{num.samps}]$ 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 is reduced to 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.

Author(s)

David Bucklin

Examples

```
## Not run:
r<-raster::raster("D:/SDM/Tobacco/env_vars/Tobacco/AnnMnTemp.tif")
spf <- rgdal::readOGR("D:/SDM/Tobacco/inputs/species/ambymabe/polygon_data", "ambymabe")
spf <- sf::st_read("D:/SDM/Tobacco/inputs/species/ambymabe/polygon_data/ambymabe.shp")
spf.samps <- nh_sample(spf, r, num.samps)

## End(Not run)
```

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