

Package ‘nhSDM’

July 17, 2018

Title Tools for Natural Heritage SDMs

Date 2018-06-13

Version 0.0.3

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, gdalUtils, stringi

Suggests dplyr, lwgeom

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

R topics documented:

nh_best	1
nh_burn	3
nh_group	4
nh_newproj	5
nh_patchdrop	5
nh_sample	6
nh_stack	8
Index	9

nh_best	<i>Extract areas with best (highest value) as polygons from an SDM prediction raster, with optional feature mask</i>
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Description

If `spf` is given, areas of cells intersecting these features will not be included in the returned polygons.

Usage

```
nh_best(spf = NULL, rast, top.percent = NULL, min.size = NULL,
        num.patches = NULL, rank.by = "area")
```

Arguments

spf	input spatial features (sp or sf spatial object); will be erased from output
rast	input raster model output with continuous values
top.percent	numeric; percent (e.g.; 0.01 = 0.01%) of highest cell values in raster to extract
min.size	numeric; optional minimal area of an extracted polygon
num.patches	numeric; optional number of patches to return, using rank.by criteria
rank.by	character; used for ranking patches when num.patches is not null; either 'area' (default) or 'value'

Details

top.percent and min.size will both be derived from spf if they are null and spf is given. In this case, top.percent will be set to be equal to spf's cell coverage (prevalence relative to non-NA areas in raster). min.size will be set to the area of the smallest feature in spf. If spf are line or point features, this will be zero.

rank.by only subsets the outputs if num.patches is set. rank.by must be set to "value" to return the mean prediction value of the patch.

For better performance, crop the raster prior to running, and/or use a very low top.percent value, to return a smaller proportion of the cells as polygons.

Value

sp or sf object (polygons)

Author(s)

David Bucklin

Examples

```
## Not run:
spf <- st_read("ambymabe/polygon_data/ambymabe.shp")
rast <- raster("ambymabe/grids/ambymabe_20171018_130837.tif")
best_polys <- nh_burn(spf, rast)

## End(Not run)
```

nh_burn	<i>Add areas represented by features ('burn-in') to a binary raster SDM output</i>
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Description

Takes spatial features, a continuous raster (values between 0 and 1), and returns a classified binary (0/1) raster. Areas greater than `orig.thresh` are set to 1, all others 0. Areas intersecting `spf` features are assigned a value of 1 in the returned classified raster. See details for default calculation of `orig.thresh` and usage of `buffer`.

Usage

```
nh_burn(spf, rast, orig.thresh = NULL, buffer = 0, return.thresh = FALSE,
...)
```

Arguments

<code>spf</code>	input spatial features (sp or sf spatial object)
<code>rast</code>	input raster model output (values between 0 and 1)
<code>orig.thresh</code>	numeric between 0 and 1; 'global' threshold value to apply to raster
<code>buffer</code>	numeric; spatial buffer around <code>spf</code> to include in burn-in
<code>return.thresh</code>	logical; whether to return thresholds along with raster in a list
<code>...</code>	Other arguments as to <code>raster::writeRaster</code>

Details

When `buffer` is used or `orig.thresh` is not provided, a minimum cell value (`min.cell`) across all `spf` is calculated. The `min.cell` value will be used as a threshold for the full raster, or just areas within buffer distance of `spf`, if `buffer` is greater than 0.

If `buffer` is greater than 0 and `orig.thresh` is not `NULL`, `orig.thresh` is used as the threshold for the full raster. Additionally, cells within buffer distance of `spf` which are greater than the calculated `min.cell` value are also set to 1. If a given `orig.thresh` is lower than the calculated `min.cell` value, `buffer` will have no impact on the output.

The default is to return the raster only. If `return.thresh = TRUE`, the function will return a list with 3 named objects: `rast`, the output raster; `orig.thresh`, the global threshold (if used); `min.cell`, the minimum cell value threshold (if used).

Value

RasterLayer

Author(s)

David Bucklin

Examples

```
## Not run:
spf <- st_read("ambymabe/polygon_data/ambymabe.shp")
rast <- raster("ambymabe/grids/ambymabe_20171018_130837.tif")
class_burn <- nh_burn(spf, rast, 0.75, 250, filename = "model_classified.tif", datatype = "INT2U")

## End(Not run)
```

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

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.

Value

sp or sf object (same as input)

Author(s)

David Bucklin

Examples

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

## End(Not run)
```

nh_newproj	<i>Initiate new SDM project</i>
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Description

Creates directory structure (if it doesn't exist) for SDMs and new SDM project SQLite database. Folder structure is initiated in current working directory, unless folder is specified.

Usage

```
nh_newproj(proj.name, folder = "nhSDM")
```

Arguments

proj.name	The name of the project. Appended to a new project database file.
folder	The SDM folder in which to initiate the project. Defaults to 'getwd()'.

Details

More details

Value

TRUE on succesful project creation

Author(s)

David Bucklin

Examples

```
## Not run:
setwd("D:/")
nh_newproj("invert")

## End(Not run)
```

nh_patchdrop	<i>Remove contiguous patches smaller than a given patch size from binary output</i>
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Description

Takes a binary/thresholded raster (values either NA, 0, or 1), and returns a binary raster. Clumps of contiguous cells with the value (1) that are smaller than the min.patch size are given a value of 0 (if 0 values are present in the input 'rast'); otherwise, they are given an NA value.

Usage

```
nh_patchdrop(spf = NULL, rast, min.patch = NULL, directions = 8, ...)
```

Arguments

spf	input spatial features (sp or sf spatial object)
rast	input binary raster output (values either NA/0 or 1)
min.patch	area of minimum patch size, in area units used in rast
directions	Integer. Which cells are considered adjacent? Should be 8 (default; Queen's case) or 4 (Rook's case). From <code>raster::clump</code>
...	Other arguments as to <code>raster::writeRaster</code>

Details

If 'spf' is given, the smallest feature's area will be used to derive a min.patch value, and any given 'min.patch' is ignored. If 'spf' is not given, a 'min.patch' value must be given, in area units of the input raster.

Value

RasterLayer

Author(s)

David Bucklin

Examples

```
## Not run:
spf <- st_read("ambymabe/polygon_data/ambymabe.shp")
rast <- raster("screen_lpsh/thumb/ambymabe.tif")

# use minimum patch size from presence features
rast_contig_minpres <- nh_patchdrop(spf, rast)

# use a minimum patch size of 10000 (in units from 'rast')
rast_contig_10km <- nh_patchdrop(rast = rast, min.patch = 10000,
  filename = "rast_contig_10km.tif", datatype = "INT2U")

## End(Not run)
```

nh_sample

Create points in features in reference raster cells

Description

For each spatial feature, a given number (num_samps) of points are created in cells that the feature 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 feature (see details)
replace	whether to sample with or without replacement
force.min	whether to force num.samps points in features, 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 feature. If left NULL, num.samps will be set to the number of cells [n] intersecting the feature. 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 feature.

When replace = FALSE and force.min = FALSE (defaults), each cell can only contain one point (across each feature, 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 feature, the number of samples for that feature 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 feature. It only produces duplicates if num.samps exceeds the number of cells intersecting the feature, in which case it will replicate the samples until num.samps is reached.

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

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

Value

sp or sf object (points)

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)
```

nh_stack

*Stack multiple binary SDMs into one raster layer.***Description**

Takes a list of binary raster's filenames, a template raster covering the extent desired for the stack, and optionally the codes (names) to use for the rasters, and returns a single raster layer (factor type with an attribute table) which indicates the number and identity of rasters overlapping in a given cell.

Usage

```
nh_stack(listr, rast, codes = NULL)
```

Arguments

<code>rast</code>	raster template dataset
<code>codes</code>	character vector; if given, must match length of <code>list</code>
<code>list</code>	input spatial features (sp or sf spatial object)

Details

All rasters must be of the same projection and resolution, though they can have different extents. To summarize all rasters across their entire extents, `template` should essentially be union (mosaic) of all raster extents.

If `codes` is not given, the raster layer name will be used as the unique identifier.

Value

RasterLayer

Author(s)

David Bucklin

Examples

```
## Not run:
rast<-raster::raster("project_mask.tif")
list <- sort(list.files(paste0(rastout, t, "/thumb"), full.names = T, pattern = "^[:lower:]{5,12}\\\\.tif$"))

stack <- nh_stack(list, rast)

## End(Not run)
```


Index

nh_best, [1](#)
nh_burn, [3](#)
nh_group, [4](#)
nh_newproj, [5](#)
nh_patchdrop, [5](#)
nh_sample, [6](#)
nh_stack, [8](#)