# Package 'nhSDM'

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**Title** Tools for Natural Heritage SDMs

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**Version** 0.0.1-1

**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_best                    *Extract areas with best (highest value) as polygons from an SDM pre-
diction raster, with optional feature mask*

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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)
```

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| | |
|---|---|
| nh_burn | *Add areas represented by features ('burn-in') to a binary raster SDM output* |

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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

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

## 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 `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 min.cell are also set to 1. If a given `orig.thresh` is lower than the calculated min.cell value, `buffer` distance will have no impact on the output.

`return.thresh = TRUE` 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)
```

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nh_group                        *Group spatial features using a defined separation distance*

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#### 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_patchdrop | *Remove patches (contiguous cells representing habitat area) smaller than a given patch size from thresholded SDM output* |
|---|---|

### 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) 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 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) |
| `...` | Other arguments as to `raster::writeRaster` |

### 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 units of the input raster.

### Value

RasterLayer

### Author(s)

David Bucklin

### Examples

```
## Not run:
spf <- st_read("D:/SDM/Tobacco/inputs/species/ambymabe/polygon_data/ambymabe.shp")
rast <- raster("E:/projects/SDM_ancilliary/Hypergrid/VA_methods/raster/screen_lpsh/thumb/ambymabe.tif")

# use minimum patch size from presence features
rast_contig_minpres <- nh_patchdrop(spf, rast, filename = "bla.tif", datatype = "INT2U")

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

## End(Not run)
```

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nh_sample                  *Create points in features in reference raster cells*

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### 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 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), than [n * 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)
```

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