Package ‘eSDM’

April 26, 2020

Title Ensemble Tool for Predictions from Species Distribution Models

Description A tool which allows users to create and evaluate ensembles of species distribution model (SDM) predictions. Functionality is offered through R functions or a GUI (R Shiny app). This tool can assist users in identifying spatial uncertainties and making informed conservation and management decisions. The package is further described in Woodman et al (2019) <doi:10.1111/2041-210X.13283>.

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**Description**

eSDM: A tool for creating and exploring ensembles of predictions from Species Distribution Models

**Details**

eSDM provides functionality for overlaying SDM predictions onto a single base geometry and creating and evaluating ensemble predictions. This can be done manually in R, or using the eSDM GUI (an R Shiny app) opened through **eSDM_GUI**

eSDM allows users to overlay SDM predictions onto a single base geometry, create ensembles of these predictions via weighted or unweighted averages, calculate performance metrics for each set of predictions and for resulting ensembles, and visually compare ensemble predictions with original predictions. The information provided by this tool can assist users in understanding spatial uncertainties and making informed conservation decisions.

The GUI ensures that the tool is accessible to non-R users, while also providing a user-friendly environment for functionality such as loading other polygons to use and visualizing predictions. However, user choices are restricted to the workflow provided by the GUI.

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**See Also**

https://smwoodman.github.io/eSDM/
**ensemble_create**  
Create ensemble of SDM predictions

**Description**
Create a weighted or unweighted ensemble of SDM predictions, including associated uncertainty values

**Usage**

```r
ensemble_create(x, x.idx, w = NULL, x.var.idx = NULL, ...)
```

**Arguments**
- `x`: object of class `sf` or class `data.frame`
- `x.idx`: vector of column names or numerical indices; indicates which columns in `x` will be used to create the ensemble
- `w`: weights for the ensemble; either a numeric vector the same length as `x` or a data frame (or tibble) with the same number of rows as `x` and `ncol(w) == length(x.idx)`. If `w` is a numeric vector, its values (i.e., the weights) must sum to 1. The default value is `1 / length(x.idx)`, i.e., an unweighted ensemble
- `x.var.idx`: vector of column names or column indices; indicates columns in `x` with variance values with which to calculate uncertainty values for the ensemble. If `x.var.idx` is specified, it must be the same length as `x.idx`. Use `x.var.idx = NULL` (the default) if none of the predictions have associated uncertainty values; in this case the uncertainty values for the ensemble will be calculated using the among-model uncertainty. See the 'Details' section for more information
- `...`: Arguments to be passed to methods; specifically designed for passing `na.rm` argument to `sum`

**Details**

`ensemble_create` is designed to be used after overlaying predictions with `overlay_sdm` and (if desired) rescaling the overlaid predictions with `ensemble_rescale`.

This function implements ensemble methods provided in eSDM_GUI. Note that it does not implement regional exclusion, which must be done manually if not using the GUI.

Ensemble uncertainty is calculated using either the within-model uncertainty (if `x.var.idx` is specified) or the among-model uncertainty (if `x.var.idx` is `NULL`). See the eSDM GUI manual for applicable formulas.
Value

An object of the same class as x with two columns appended to the data frame:

• ‘Pred_ens’ - The ensemble predictions
• ‘Var_ens’ - The variance of the ensemble predictions, calculated using either the within-model uncertainty (if x.var.idx is specified) or the among-model uncertainty (if x.var.idx is NULL)

Note that all other columns of x will be included in the returned object. Also, if x is of class sf then 1) the geometry list-column will be the last column of the returned object and 2) the agr attribute will be set as 'constant' for 'Pred_ens' and 'Var_ens'

Examples

ensemble_create(preds.1, c("Density", "Density2"), c(0.2, 0.8))
ensemble_create(preds.1, 1:2, c(0.2, 0.8), c("Var1", "Var2"))
ensemble_create(data.frame(a = 1:5, b = 3:7), c(1, 2))

weights.df <- data.frame(runif(325), c(rep(NA, 100), runif(225)))
ensemble_create(preds.1, c("Density", "Density2"), weights.df, na.rm = TRUE)

Description

Rescale SDM predictions and (if applicable) associated uncertainties

Usage

ensemble_rescale(x, x.idx, y, y.abund = NULL, x.var.idx = NULL)

Arguments

x          object of class sf
x.idx      vector of column names or column indices; indicates columns in x with prediction values that will be rescaled
y          rescaling method; must be either "abundance" or "sumto1". See 'Details' section for descriptions of the rescaling methods
y.abund    numeric value; ignored if y is not "abundance"

x.var.idx  vector of column names or column indices; indicates columns in x with variance values that will be rescaled. If x.var.idx is specified, it must be the same length as x.idx. Use x.var.idx = NULL (the default) if none of the predictions have associated uncertainty values; see the 'Details' section for more information
Details

`ensemble_rescale` is intended to be used after overlaying predictions with `overlay_sdm` and before creating ensembles with `ensemble_create`. The provided rescaling methods are:

- 'abundance' - Rescale the density values so that the predicted abundance is y.abund
- 'sumto1' - Rescale the density values so their sum is 1

SDM uncertainty values must be rescaled differently than the prediction values. Columns specified in `x.var.idx` must contain variance values. These values will be rescaled using the formula $\text{var}(c \times x) = c^2 \times \text{var}(x)$, where $c$ is the rescaling factor for the associated predictions.

If `x.var.idx` is not `NULL`, then the function assumes `x.var.idx[1]` contains the variance values associated with the predictions in `x.idx[1]`. `x.var.idx[2]` contains the variance values associated with the predictions in `x.idx[2]`, etc. Use `NA` in `x.var.idx` to indicate a set of predictions that does not have associated uncertainty values (e.g., `x.var.idx = c(4,NA,5)`)

Value

The `sf` object `x` with the columns specified by `x.idx` and `x.var.idx` rescaled. The `agr` attributes of `x` will be conserved

Examples

```r
ensemble_rescale(preds.1, c("Density", "Density2"), "abundance", 50)
ensemble_rescale(preds.1, c(1, 2), "sumto1")
ensemble_rescale(
  preds.1, c("Density", "Density2"), "abundance", 100, c(3,4)
)
```

Description

Open the eSDM graphical user interface (GUI); an R Shiny app for creating ensemble predictions using SDM predictions.

Usage

```r
eSDM_GUI(launch.browser = TRUE)
```

Arguments

- `launch.browser` Logical with default of `TRUE`; passed to `launch.browser` argument of `runApp`
See Also

https://smwoodman.github.io/eSDM/

evaluation_metrics   Calculate SDM evaluation metrics

Description

Calculate AUC, TSS, and RMSE for given density predictions and validation data

Usage

evaluation_metrics(x, x.idx, y, y.idx, count.flag = FALSE)

Arguments

x          object of class sf; SDM predictions
x.idx      name or index of column in x with prediction values
y          object of class sf; validation data
y.idx      name or index of column in y with validation data. This validation data column
            must have at least two unique values, e.g. 0 and 1
count.flag logical: TRUE indicates that the data in column y.idx is count data, while FALSE
            indicates that the data is presence/absence. See details for differences in data
            processing based on this flag.

Details

If count.flag == TRUE, then eSDM::model_abundance(x, x.idx, FALSE) will be run to calculate
predicted abundance and thus calculate RMSE. Note that this assumes the data in column x.idx of
x are density values.

If count.flag == FALSE, then all of the values in column y.idx of y must be 0 or 1.
All rows of x with a value of NA in column x.idx and all rows of y with a value of NA in column
y.idx are removed before calculating metrics

Value

A numeric vector with AUC, TSS and RMSE values, respectively. If count.flag == FALSE, the
RMSE value will be NA

Examples

evaluation_metrics(preds.1, 2, validation.data, "sight")

evaluation_metrics(preds.1, "Density2", validation.data, "count", TRUE)
**gshhg.l.L16**

*Low resolution GSHHG world map*

**Description**

Low resolution GSHHG world map, includes hierarchical levels L1 and L6. Processed using `st_make_valid`

**Usage**

`gshhg.l.L16`

**Format**

An object of class `sfc`

**Source**

http://www.soest.hawaii.edu/pwessel/gshhg/

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**model_abundance**

*Calculate predicted abundance*

**Description**

Calculates the predicted abundance by multiplying the density prediction values by prediction polygon areas

**Usage**

`model_abundance(x, dens.idx, sum.abund = TRUE)`

**Arguments**

- `x` object of class `sf`; SDM with density predictions. Must have a valid crs code
- `dens.idx` name or index of column(s) in `x` with density predictions. Can be a character vector (column names) or numeric vector (column indices)
- `sum.abund` logical; whether or not to sum all of the predicted abundances

**Details**

Multiplies the values in the specified column(s) (i.e. the density predictions) by the area in square kilometers of their corresponding prediction polygon. The area of each prediction polygon is calculated using `st_area` from `geos_measures`. `x` must have a valid crs code to calculate area for these abundance calculations.
Value

If `sum.abund == TRUE`, then a vector of the same length as `dens.idx` representing the predicted abundance for the density values in each column.

If `sum.abund == FALSE` and the length of `dens.idx` is 1, then a numeric vector with the predicted abundance of each prediction polygon of `x`.

If `sum.abund == FALSE` and the length of `dens.idx` is greater than 1, then a data frame with `length(dens.idx)` columns of the predicted abundance of prediction polygons

Examples

```r
data = model_abundance(preds.1, "Density")
data = model_abundance(preds.1, c(1, 1))
data = model_abundance(preds.1, c(1, 1), FALSE)
```

Overlay SDM predictions onto base geometry

Description

Overlay specified SDM predictions that meet the percent overlap threshold requirement onto base geometry

Usage

```r
overlay_sdm(base.geom, sdm, sdm.idx, overlap.perc)
```

Arguments

- `base.geom`: object of class `sfc`; base geometry
- `sdm`: object of class `sf`; original SDM predictions
- `sdm.idx`: names or indices of column(s) with data to be overlaid
- `overlap.perc`: numeric; percent overlap threshold, i.e. percentage of each base geometry polygon must overlap with SDM prediction polygons for overlaid density value to be calculated and not set as NA

Details

See the eSDM GUI manual for specifics about the overlay process. This process is equivalent to areal interpolation (Goodchild and Lam 1980), where `base.geom` is the target, `sdm` is the source, and the data specified by `sdm.idx` are spatially intensive.

Note that `overlay_sdm` removes rows in `sdm` that have NA values in the first column specified in `sdm.idx` (i.e. `sdm.idx[1]`), before the overlay. Thus, for valid overlay results, all columns of `sdm` specified in `sdm.idx` must either have NA values in the same rows or contain only NAs.
Value

Object of class sf with the geometry of base.geom and the data in the sdm.idx columns of sdm overlaid onto that geometry. Note that this means all columns of sdm not in sdm.idx will not be in the returned object. Because the data are considered spatially intensive, the agr attribute will be set as 'constant' for all columns in the returned object.

References


Examples

overlay_sdm(sf::st_geometry(preds.1), preds.2, 1, 50)
overlay_sdm(sf::st_geometry(preds.2), preds.1, c("Density", "Density2"), 50)

Description

preds.1, preds.2, and preds.3 are objects of class sf that serve as sample sets of SDM density predictions for the eSDM package.

Usage

preds.1
preds.2
preds.3

Format

Objects of class sf with a column of density predictions (name: Density) and a simple feature list column (name: geometry). preds.1 also has a second column of sample density predictions (name: Density2), as well as Var1 and Var2, representing the variance.

preds1: An object of class sf (inherits from data.frame) with 325 rows and 5 columns.
preds2: An object of class sf (inherits from data.frame) with 1891 rows and 2 columns.
preds3: An object of class sf (inherits from data.frame) with 1445 rows and 2 columns.
pts2poly_centroids

Details

preds.1 sample SDM density predictions created by importing Sample_predictions_2.csv into the eSDM GUI, exporting predictions, and then clipping them to the SoCal_bite.csv region. Also manually added two variance columns (numbers are randomly generated with a max of 0.01)
preds.2 sample SDM density predictions created by importing Sample_predictions_1.csv into the eSDM GUI, exporting predictions, and then clipping them to the SoCal_bite.csv region
preds.3 is a set of sample SDM density predictions created by importing Sample_predictions_4_gdb into the eSDM GUI, exporting predictions, and then clipping them to the SoCal_bite.csv region

pts2poly_centroids Create polygons from centroid coordinates

Description

Create polygon(s) from a data frame with coordinates of the polygon centroid(s)

Usage

pts2poly_centroids(x, y, ...)

Arguments

x data frame with at least two columns; the first two columns must contain longitude and latitude coordinates, respectively. See 'Details' section for how additional columns are handled
y numeric; the perpendicular distance from the polygon centroid (center) to its edge (i.e. half the length of one side of a polygon)
... passed to st_sf or to st_sfc, e.g. for passing named arguments crs and agr

Details

This function was designed for someone who reads in a .csv file with a grid of coordinates representing SDM prediction points and needs to create prediction polygons with the .csv file coordinates as the polygon centroids. However, the function can be used to create square polygons of any size around the provided points, regardless of if those polygons touch or overlap. The created polygons are oriented so that, in a 2D plane, their edges are parallel to either the x or the y axis.

If x contains more than two column, then additional columns will be treated as simple feature attributes, i.e. passed along as the first argument to st_sf
If a crs is not specified in ..., then the crs attribute of the polygon(s) will be NULL.

Value

Object of class sfc (if x has exactly two columns) or class sf (if x has exactly more than two columns). The object will have a geometry type of POLYGON. If the object is of class sf, the name of the geometry list-column will be "geometry"
Examples

# Create an sfc object from a data frame of two columns
x <- data.frame(
  lon = c(5, 10, 15, 20, 5, 10, 15, 20),
  lat = c(5, 5, 5, 5, 10, 10, 10, 10)
)
pts2poly_centroids(x, 2.5, crs = 4326)

# Create an sf object from a data frame of more than two columns
x <- data.frame(
  lon = c(5, 10, 15, 20, 5, 10, 15, 20),
  lat = c(5, 5, 5, 5, 10, 10, 10, 10),
  sdm.pred = runif(8),
  sdm.pred2 = runif(8)
)
pts2poly_centroids(x, 2.5, crs = 4326, agr = "constant")

pts2poly_vertices

Create polygons from vertex coordinates

Description

Create polygon(s) from a data frame with the coordinates of the polygon vertices

Usage

pts2poly_vertices(x, ...)

Arguments

x
data frame with at least two columns; the first two columns must contain longitude and latitude coordinates, respectively. See 'Details' section for how additional columns are handled

...passed to st_sfc, e.g. for passing named argument crs

Details

Vertices of different polygons must be demarcated by rows with values of NA in both the first and second columns (i.e. the longitude and latitude columns).

All columns in x besides the first two columns are ignored.

If a crs is not specified in ..., then the crs attribute of the polygon(s) will be NULL.

Value

Object of class sfc with the geometry type POLYGON
Examples

```r
x <- data.frame(
  lon = c(40, 40, 50, 50, 40),
  lat = c(0, 10, 10, 0, 0)
)
pts2poly_vertices(x, crs = 4326)

# Create an sf object
x <- data.frame(
  lon = c(40, 40, 50, 50, 40, NA, 20, 20, 30, 30, 20),
  lat = c(0, 10, 10, 0, 0, NA, 0, 10, 10, 0, 0)
)
sf::st_sf(Pred = 1:2, geometry = pts2poly_vertices(x, crs = 4326))
```

validation.data  
Sample validation data

Description

Sample validation data created by cropping Validation_data.csv to the SoCal_bite.csv region (.csv files from ...)

Usage

validation.data

Format

An object of class `sf` with 8 rows and 3 variables

`sight` 1’s and 0’s indicating species presence/absence

`count` number of individuals observed at each point

`geometry` simple feature list column representing validation data points
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