

# Package ‘eSDM’

August 19, 2019

**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. (in press - contact author for paper).

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**URL** <https://github.com/smwoodman/eSDM>

**BugReports** <https://github.com/smwoodman/eSDM/issues>

**Depends** R (>= 3.5.0)

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**License** GPL-3

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eSDM-package	<i>eSDM: A tool for creating and exploring ensembles of predictions from Species Distribution Models</i>
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### Description

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](#)

### Details

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.

---

ensemble_create	<i>Create ensemble of SDM predictions</i>
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---

### Description

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

### Usage

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

## S3 method for class 'sf'
ensemble_create(x, x.idx, w = NULL, x.var.idx = NULL, ...)

## S3 method for class 'data.frame'
ensemble_create(x, x.idx, w = NULL,
  x.var.idx = NULL, ...)
```

### Arguments

x	object of class <code>sf</code> or class <code>data.frame</code>
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 <code>ncol(w) == length(x.idx)</code> . If w is a numeric vector, its values (i.e. the weights) must sum to 1. The default value is $1 / \text{length}(x.idx)$ , 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 <code>x.var.idx = NULL</code> (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 <code>na.rm</code> argument to <code>sum</code>

### 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)
```

---

ensemble_rescale	<i>Rescale SDM predictions</i>
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---

**Description**

Rescale SDM predictions and (if applicable) associated uncertainties

**Usage**

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

**Arguments**

<code>x</code>	object of class <code>sf</code>
<code>x.idx</code>	vector of column names or column indices; indicates columns in <code>x</code> with prediction values that will be rescaled
<code>y</code>	rescaling method; must be either <code>"abundance"</code> or <code>"sumto1"</code> . See <code>'Details'</code> section for descriptions of the rescaling methods
<code>y.abund</code>	numeric value; ignored if <code>y</code> is not <code>"abundance"</code>
<code>x.var.idx</code>	vector of column names or column indices; indicates columns in <code>x</code> with variance values that will be rescaled. If <code>x.var.idx</code> is specified, it must be the same length as <code>x.idx</code> . Use <code>x.var.idx = NULL</code> (the default) if none of the predictions have associated uncertainty values; see the <code>'Details'</code> 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  $\text{var}(c * x) = c^2 * \text{var}(x)$ , 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

```
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)
)
```

---

eSDM\_GUI

*Open the eSDM GUI*

---

## Description

Open the eSDM graphical user interface (GUI); an R Shiny app for creating ensemble predictions using SDM predictions. The GUI can also be accessed at <https://swoodman.shinyapps.io/eSDM/>

## Usage

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

## Arguments

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

---

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, 1, validation.data, "sight")
```

```
evaluation_metrics(preds.1, "Density", validation.data, "count", TRUE)
```

---

gshhg.1.L16

*Low resolution GSHHG world map*


---

**Description**

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

**Usage**

```
gshhg.1.L16
```

**Format**

An object of class `sfc`

**Source**

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

---

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**

<code>x</code>	object of class <code>sf</code> ; SDM with density predictions. Must have a valid crs code
<code>dens.idx</code>	name or index of column(s) in <code>x</code> with density predictions. Can be a character vector (column names) or numeric vector (column indices)
<code>sum.abund</code>	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**

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

---

 overlay\_sdm

*Overlay SDM predictions onto base geometry*


---

**Description**

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

**Usage**

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

**Arguments**

<code>base.geom</code>	object of class <code>sfc</code> ; base geometry
<code>sdm</code>	object of class <code>sf</code> ; original SDM predictions
<code>sdm.idx</code>	names or indices of column(s) with data to be overlaid
<code>overlap.perc</code>	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**

Goodchild, M.F. & Lam, N.S.-N. (1980) Areal interpolation: a variant of the traditional spatial problem. *Geo-Processing*, 1, 297-312.

**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)
```

---

preds	<i>Sample SDM density predictions</i>
-------	---------------------------------------

---

**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`)

**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 <a href="#">st_sf</a> or to <a href="#">st_sfc</a> , 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

```
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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