

# Package ‘SSDM’

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**Type** Package

**Title** Stacked Species Distribution Modelling

**Version** 0.2.9

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**URL** <https://github.com/sylvainschmitt/SSDM>

**BugReports** <https://github.com/sylvainschmitt/SSDM/issues>

**Description** Allows to map species richness and endemism based on stacked species distribution models (SSDM). Individuals SDMs can be created using a single or multiple algorithms (ensemble SDMs). For each species, an SDM can yield a habitat suitability map, a binary map, a between-algorithm variance map, and can assess variable importance, algorithm accuracy, and between-algorithm correlation. Methods to stack individual SDMs include summing individual probabilities and thresholding then summing. Thresholding can be based on a specific evaluation metric or by drawing repeatedly from a Bernoulli distribution. The SSDM package also provides a user-friendly interface.

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**LazyData** TRUE

**Imports** sf (>= 1.0-14), raster (>= 2.9-5), methods (>= 3.2.2), mgcv (>= 1.8.7), earth (>= 4.4.3), rpart (>= 4.1.10), gbm (>= 2.1.1), randomForest (>= 4.6.10), dismo (>= 1.0.12), nnet (>= 7.3.10), e1071 (>= 1.6.7), ggplot2 (>= 3.1.1), reshape2 (>= 1.4.3), scales (>= 1.0.0), shiny (>= 0.12.2), shinydashboard (>= 0.5.1), spThin (>= 0.1.0), poibin (>= 1.3.0), foreach (>= 1.4.4), doParallel (>= 1.0.14), iterators (>= 1.0.10), itertools (>= 0.1-3), parallel (>= 3.5.2), leaflet (>= 2.2.0), magrittr (>= 2.0.3), sdm (>= 1.1.8)

**Depends** R (>= 3.2.2)

**Collate** 'SDM.R' 'Algorithm.SDM.R' 'Ensemble.SDM.R' 'Env.R' 'Occurrences.R' 'PA.select.R' 'SSDM.R' 'Stacked.SDM.R' 'accuracy.R' 'checkargs.R' 'data.values.R' 'ensemble.R'

'optim.thresh.R' 'evaluate.R' 'modelling.R'  
 'ensemble\_modelling.R' 'evaluate.axes.R' 'get\_PA.R'  
 'get\_model.R' 'gui.R' 'load\_model.R' 'load\_occ.R' 'load\_var.R'  
 'mapDiversity.R' 'plot.model.R' 'project.R' 'save.model.R'  
 'stack\_modelling.R' 'stacking.R' 'update.stack.R'  
 'utils-pipe.R' 'zzz.R'

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## R topics documented:

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Algorithm.SDM-class     *An S4 class to represent an SDM based on a single algorithm*

---

### Description

This is an S4 class to represent an SDM based on a single algorithm (including generalized linear model, general additive model, multivariate adaptive splines, generalized boosted regression model, classification tree analysis, random forest, maximum entropy, artificial neural network, and support vector machines). This S4 class is obtained with [modelling](#).

### Slots

`name` character. Name of the SDM (by default Species.SDM).

`projection` raster. Habitat suitability map produced by the SDM.

`binary` raster. Presence/Absence binary map produced by the SDM.

`evaluation` data frame. Evaluation of the SDM (available metrics include AUC, Kappa, sensitivity, specificity and proportion of correctly predicted occurrences) and identification of the optimal threshold to convert the habitat suitability map into a binary presence/absence map.

`variable.importance` data frame. Relative importance of each variable in the SDM.

`data` data frame. Data used to build the SDM.

`parameters` data frame. Parameters used to build the SDM.

### See Also

[Ensemble.SDM](#) an S4 class for ensemble SDMs, and [Stacked.SDM](#) an S4 class for SSDMs.

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`ensemble`     *Methods to assemble multiple algorithms in an ensemble SDM*

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### Description

This is a method to assemble several algorithms in an ensemble SDM. The function takes as inputs several S4 [Algorithm.SDM](#) class objects returned by the [modelling](#) function. The function returns an S4 [Ensemble.SDM](#) class object containing the habitat suitability map, the binary map, and the uncertainty map (based on the between-algorithm variance) and the associated evaluation tables (model evaluation, algorithm evaluation, algorithm correlation matrix and variable importance).

**Usage**

```
ensemble(  
  x,  
  ...,  
  name = NULL,  
  ensemble.metric = c("AUC"),  
  ensemble.thresh = c(0.75),  
  weight = TRUE,  
  thresh = 1001,  
  uncertainty = TRUE,  
  SDM.projections = FALSE,  
  cores = 0,  
  verbose = TRUE,  
  GUI = FALSE  
)  
  
## S4 method for signature 'Algorithm.SDM'  
ensemble(  
  x,  
  ...,  
  name = NULL,  
  ensemble.metric = c("AUC"),  
  ensemble.thresh = c(0.75),  
  weight = TRUE,  
  thresh = 1001,  
  uncertainty = TRUE,  
  SDM.projections = FALSE,  
  cores = 0,  
  verbose = TRUE,  
  GUI = FALSE  
)  
  
## S4 method for signature 'Algorithm.SDM'  
sum(  
  x,  
  ...,  
  name = NULL,  
  ensemble.metric = c("AUC"),  
  ensemble.thresh = c(0.75),  
  weight = TRUE,  
  thresh = 1001,  
  format = TRUE,  
  verbose = TRUE,  
  na.rm = TRUE  
)
```

**Arguments**

|                                 |   |
|---------------------------------|---|
| <code>x, ...</code>             | SDMs. SDMs to be assembled.   |
| <code>name</code>               | character. Optional name given to the final Ensemble.SDM produced (by default 'Ensemble.SDM').                                    |
| <code>ensemble.metric</code>    | character. Metric(s) used to select the best SDMs that will be included in the ensemble SDM (see details below).                  |
| <code>ensemble.thresh</code>    | numeric. Threshold(s) associated with the metric(s) used to compute the selection.  |
| <code>weight</code>             | logical. If TRUE, SDMs are weighted using the ensemble metric or, alternatively, the mean of the selection metrics.               |
| <code>thresh</code>             | numeric. A integer value specifying the number of equal interval threshold values between 0 and 1.                                |
| <code>uncertainty</code>        | logical. If TRUE, generates an uncertainty map and an algorithm correlation matrix.   |
| <code>SDM.projections</code>    | logical. If FALSE (default), the Algorithm.SDMs inside the 'sdms' slot will not contain projections (for memory saving purposes). |
| <code>cores</code>              | integer. Specify the number of CPU cores used to do the computing. You can use <a href="#">detectCores</a> ) to automatically     |
| <code>verbose</code>            | logical. If set to true, allows the function to print text in the console.  |
| <code>GUI, format, na.rm</code> | logical. Do not take those arguments into account (parameters for the user interface and sum function).                           |

**Details**

`ensemble.metric` (metric(s) used to select the best SDMs that will be included in the ensemble SDM) can be chosen from among:

**AUC** Area under the receiver operating characteristic (ROC) curve

**Kappa** Kappa from the confusion matrix

**sensitivity** Sensitivity from the confusion matrix

**specificity** Specificity from the confusion matrix

**prop.correct** Proportion of correctly predicted occurrences from the confusion matrix

**calibration** Calibration metric (Naimi & Araujo 2016)

**Value**

an S4 [Ensemble.SDM](#) class object viewable with the [plot.model](#) function.

**See Also**

[ensemble\\_modelling](#) to build an ensemble SDM from multiple algorithms.

**Examples**

```
## Not run:
# Loading data
data(Env)
data(Occurrences)
Occurrences <- subset(Occurrences, Occurrences$SPECIES == 'elliptica')

# ensemble SDM building
CTA <- modelling('CTA', Occurrences, Env, Xcol = 'LONGITUDE', Ycol = 'LATITUDE')
SVM <- modelling('SVM', Occurrences, Env, Xcol = 'LONGITUDE', Ycol = 'LATITUDE')
ESDM <- ensemble(CTA, SVM, ensemble.thresh = c(0.6))

# Results plotting
plot(ESDM)

## End(Not run)
```

---

Ensemble.SDM-class      *An S4 class to represent an ensemble SDM*

---

**Description**

This is an S4 class to represent an ensemble SDM from multiple algorithms (including generalized linear model, general additive model, multivariate adaptive splines, generalized boosted regression model, classification tree analysis, random forest, maximum entropy, artificial neural network, and support vector machines). This S4 class is returned by [ensemble\\_modelling](#) or [ensemble](#).

**Slots**

`uncertainty_raster` raster. Between-algorithm variance map.

`algorithm_correlation` data frame. Between-algorithm correlation matrix.

`algorithm_evaluation` data frame. Evaluation of the ensemble SDM (available)

`sdms` list. Individual SDMs used to create the ESDM. metrics include AUC, Kappa, sensitivity, specificity and proportion of correctly predicted occurrences) and identification of the optimal threshold to convert the habitat suitability map into a binary presence/absence map.

**See Also**

[Algorithm.SDM](#) an S4 class to represent an SDM based on a single algorithm, and [Stacked.SDM](#) an S4 class for SSDMs.

---

ensemble\_modelling      *Build an ensemble SDM that assembles multiple algorithms*

---

## Description

Build an ensemble SDM that assembles multiple algorithms for a single species. The function takes as inputs an occurrence data frame made of presence/absence or presence-only records and a raster object for data extraction and projection. The function returns an S4 [Ensemble.SDM](#) class object containing the habitat suitability map, the binary map, the between-algorithm variance map and the associated evaluation tables (model evaluation, algorithm evaluation, algorithm correlation matrix and variable importance).

## Usage

```
ensemble_modelling(  
  algorithms,  
  Occurrences,  
  Env,  
  Xcol = "Longitude",  
  Ycol = "Latitude",  
  Pcol = NULL,  
  rep = 10,  
  name = NULL,  
  save = FALSE,  
  path = getwd(),  
  cores = 0,  
  parmode = "replicates",  
  PA = NULL,  
  cv = "holdout",  
  cv.param = c(0.7, 1),  
  final.fit.data = "all",  
  bin.thresh = "SES",  
  metric = NULL,  
  thresh = 1001,  
  axes.metric = "Pearson",  
  uncertainty = TRUE,  
  tmp = FALSE,  
  SDM.projections = FALSE,  
  ensemble.metric = c("AUC"),  
  ensemble.thresh = c(0.75),  
  weight = TRUE,  
  verbose = TRUE,  
  GUI = FALSE,  
  ...  
)
```

**Arguments**

|                |   |
|----------------|---|
| algorithms     | character. A character vector specifying the algorithm name(s) to be run (see details below).   |
| Occurrences    | data frame. Occurrences table (can be processed first by <code>load_occ</code> ).   |
| Env            | raster object. RasterStack object of environmental variables (can be processed first by <code>load_var</code> ).  |
| Xcol           | character. Name of the column in the occurrence table containing Latitude or X coordinates.   |
| Ycol           | character. Name of the column in the occurrence table containing Longitude or Y coordinates.  |
| Pcol           | character. Name of the column in the occurrence table specifying whether a line is a presence or an absence. A value of 1 is presence and value of 0 is absence. If NULL presence-only dataset is assumed.  |
| rep            | integer. Number of repetitions for each algorithm.  |
| name           | character. Optional name given to the final Ensemble.SDM produced (by default 'Ensemble.SDM').  |
| save           | logical. If TRUE, the ensemble SDM is automatically saved.  |
| path           | character. If save is If TRUE, the path to the directory in which the ensemble SDM will be saved.   |
| cores          | integer. Specify the number of CPU cores used to do the computing. You can use <code>detectCores</code> ) to automatically  |
| parmode        | character. Parallelization mode: along 'algorithms' or 'replicates'. Defaults to 'replicates'.  |
| PA             | list(nb, strat) defining the pseudo-absence selection strategy used in case of presence-only dataset. If PA is NULL, recommended PA selection strategy is used depending on the algorithm (see details below).  |
| cv             | character. Method of cross-validation used to evaluate the ensemble SDM (see details below).  |
| cv.param       | numeric. Parameters associated to the method of cross-validation used to evaluate the ensemble SDM (see details below).   |
| final.fit.data | strategy used for fitting the final/evaluated Algorithm.SDMs: 'holdout'= use same train and test data as in (last) evaluation, 'all'= train model with all data (i.e. no test data) or numeric (0-1)= sample a custom training fraction (left out fraction is set aside as test data)                                   |
| bin.thresh     | character. Classification threshold ( <code>threshold</code> ) used to binarize model predictions into presence/absence and compute the confusion matrix (see details below).   |
| metric         | (deprecated) character. Classification threshold ( <code>SDMTools::optim.thresh</code> ) used to binarize model predictions into presence/absence and compute the confusion matrix (see details below). This argument is only kept for backwards compatibility, if possible please use <code>bin.thresh</code> instead. |
| thresh         | (deprecated) integer. Number of equally spaced thresholds in the interval 0-1 ( <code>SDMTools::optim.thresh</code> ). Only needed when <code>metric</code> is set.   |



|                              |  |
|------------------------------|--|
| <code>axes.metric</code>     | Metric used to evaluate variable relative importance (see details below).  |
| <code>uncertainty</code>     | logical. If TRUE, generates an uncertainty map and an algorithm correlation matrix.  |
| <code>tmp</code>             | logical or character. If FALSE, no temporary rasters are written (this could quickly fill up your working memory, if many replicates are modelled). If TRUE, temporary rasters are written to the „tmp“ directory of your R environment. If character, temporary rasters are written to a custom path. But beware: if you close R, temporary files will be deleted. To avoid any loss you can save your ensemble SDM with <code>save.model</code> . Depending on number, resolution and extent of models, temporary files can take a lot of disk space. Temporary files are written to the R environment temporary folder. |
| <code>SDM.projections</code> | logical. If FALSE (default), the Algorithm.SDMs inside the 'sdms' slot will not contain projections (for memory saving purposes).  |
| <code>ensemble.metric</code> | character. Metric(s) used to select the best SDMs that will be included in the ensemble SDM (see details below).   |
| <code>ensemble.thresh</code> | numeric. Threshold(s) associated with the metric(s) used to compute the selection.   |
| <code>weight</code>          | logical. If TRUE, SDMs are weighted using the ensemble metric or, alternatively, the mean of the selection metrics.  |
| <code>verbose</code>         | logical. If TRUE, allows the function to print text in the console.  |
| <code>GUI</code>             | logical. Do not take this argument into account (parameter for the user interface).  |
| <code>...</code>             | additional parameters for the algorithm modelling function (see details below).  |

## Details

**algorithms** 'all' calls all the following algorithms. Algorithms include Generalized linear model (**GLM**), Generalized additive model (**GAM**), Multivariate adaptive regression splines (**MARS**), Generalized boosted regressions model (**GBM**), Classification tree analysis (**CTA**), Random forest (**RF**), Maximum entropy (**MAXENT**), Artificial neural network (**ANN**), and Support vector machines (**SVM**). Each algorithm has its own parameters settable with the ... (see each algorithm section below to set their parameters).

**"PA"** list with two values: **nb** number of pseudo-absences selected, and **strat** strategy used to select pseudo-absences: either random selection or disk selection. We set default recommendation from Barbet-Massin et al. (2012) (see reference).

**cv** **Cross-validation** method used to split the occurrence dataset used for evaluation: **holdout** data are partitioned into a training set and an evaluation set using a fraction (`cv.param[1]`) and the operation can be repeated (`cv.param[2]`) times, **k-fold** data are partitioned into k (`cv.param[1]`) folds being k-1 times in the training set and once the evaluation set and the operation can be repeated (`cv.param[2]`) times, **LOO** (Leave One Out) each point is successively taken as evaluation data.

**metric** Choice of the metric used to compute the binary map threshold and the confusion matrix (by default SES as recommended by Liu et al. (2005), see reference below): **Kappa** maximizes the Kappa, **CCR** maximizes the proportion of correctly predicted observations, **TSS** (True Skill Statistic) maximizes the sum of sensitivity and specificity, **SES** uses the sensitivity-specificity equality, **LW** uses the lowest occurrence prediction probability, **ROC** minimizes the distance between the ROC plot (receiving operating characteristic curve) and the upper left corner (1,1).

**axes.metric** Metric used to evaluate the variable relative importance (difference between a full model and one with each variable successively omitted): **Pearson** (computes a simple Pearson's correlation  $r$  between predictions of the full model and the one without a variable, and returns the score  $1-r$ : the highest the value, the more influence the variable has on the model), **AUC**, **Kappa**, **sensitivity**, **specificity**, and **prop.correct** (proportion of correctly predicted occurrences).

**ensemble.metric** Ensemble metric(s) used to select SDMs: **AUC**, **Kappa**, **sensitivity**, **specificity**, and **prop.correct** (proportion of correctly predicted occurrences).

"..." See algorithm in detail section

## Value

an S4 [Ensemble.SDM](#) class object viewable with the [plot.model](#) function.

## Generalized linear model (GLM)

Uses the `glm` function from the package 'stats'. You can set parameters by supplying `glm.args=list(arg1=val1, arg2=val2)` (see [glm](#) for all settable arguments). The following parameters have defaults:

**test** character. Test used to evaluate the SDM, default 'AIC'.

**control** list (created with [glm.control](#)). Contains parameters for controlling the fitting process. Default is `glm.control(epsilon = 1e-08, maxit = 500)`. 'epsilon' is a numeric and defines the positive convergence tolerance (eps). The iterations converge when  $|dev - dev\_old|/(|dev| + 0.1) < eps$ . 'maxit' is an integer giving the maximal number of IWLS (Iterative Weighted Last Squares) iterations.

## Generalized additive model (GAM)

Uses the `gam` function from the package 'mgcv'. You can set parameters by supplying `gam.args=list(arg1=val1, arg2=val2)` (see [gam](#) for all settable arguments). The following parameters have defaults:

**test** character. Test used to evaluate the model, default 'AIC'.

**control** list (created with [gam.control](#)). Contains parameters for controlling the fitting process. Default is `gam.control(epsilon = 1e-08, maxit = 500)`. 'epsilon' is a numeric used for judging the conversion of the GLM IRLS (Iteratively Reweighted Least Squares) loop. 'maxit' is an integer giving the maximum number of IRLS iterations to perform.

## Multivariate adaptive regression splines (MARS)

Uses the `earth` function from the package 'earth'. You can set parameters by supplying `mars.args=list(arg1=val1, arg2=val2)` (see [earth](#) for all settable arguments). The following parameters have defaults:

**degree** integer. Maximum degree of interaction (Friedman's  $m_i$ ) ; 1 meaning build an additive model (i.e., no interaction terms). By default, set to 2.

### Generalized boosted regressions model (GBM)

Uses the `gbm` function from the package 'gbm'. You can set parameters by supplying `gbm.args=list(arg1=val1, arg2=val2)` (see [gbm](#) for all settable arguments). The following parameters have defaults:

**distribution** character. Automatically detected from the format of the presence column in the occurrence dataset.

**n.trees** integer. The total number of trees to fit. This is equivalent to the number of iterations and the number of basis functions in the additive expansion. By default, set to 2500.

**n.minobsinnode** integer. minimum number of observations in the trees terminal nodes. Note that this is the actual number of observations, not the total weight. By default, set to 1.

**cv.folds** integer. Number of cross-validation folds to perform. If `cv.folds>1` then `gbm` - in addition to the usual fit - will perform a cross-validation. By default, set to 3.

**shrinkage** numeric. A shrinkage parameter applied to each tree in the expansion (also known as learning rate or step-size reduction). By default, set to 0.001.

**bag.fraction** numeric. Fraction of the training set observations randomly selected to propose the next tree in the expansion.

**train.fraction** numeric. Training fraction used to fit the first `gbm`. The remainder is used to compute out-of-sample estimates of the loss function. By default, set to 1 (since evaluation/holdout is done with `SSDM::evaluate`).

**n.cores** integer. Number of cores to use for parallel computation of the CV folds. By default, set to 1. If you intend to use this, please set `ncores=0` to avoid conflicts.

### Classification tree analysis (CTA)

Uses the `rpart` function from the package 'rpart'. You can set parameters by supplying `cta.args=list(arg1=val1, arg2=val2)` (see [rpart](#) for all settable arguments). The following parameters have defaults:

**control** list (created with [rpart.control](#)). Contains parameters for controlling the `rpart` fit. The default is `rpart.control(minbucket=1, xval=3)`. 'minbucket' is an integer giving the minimum number of observations in any terminal node. 'xval' is an integer defining the number of cross-validations.

### Random Forest (RF)

Uses the `randomForest` function from the package 'randomForest'. You can set parameters by supplying `cta.args=list(arg1=val1, arg2=val2)` (see [randomForest](#) all settable arguments). The following parameters have defaults:

**ntree** integer. Number of trees to grow. This should not be set to a too small number, to ensure that every input row gets predicted at least a few times. By default, set to 2500.

**nodesize** integer. Minimum size of terminal nodes. Setting this number larger causes smaller trees to be grown (and thus take less time). By default, set to 1.

### Maximum Entropy (MAXENT)

Uses the `maxent` function from the package 'dismo'. Make sure that you have correctly installed the `maxent.jar` file in the folder `~\R\library\version\dismo\java` available at [https://biodiversityinformatics.amnh.org/open\\_source/maxent/](https://biodiversityinformatics.amnh.org/open_source/maxent/). As with the other algorithms, you can set parameters by supplying `maxent.args=list(arg1=val1, arg2=val2)`. Mind that arguments are passed from `dismo` to the MAXENT software again as an argument list (see `maxent` for more details). No specific defaults are set with this method.

### Artificial Neural Network (ANN)

Uses the `nnet` function from the package 'nnet'. You can set parameters by supplying `ann.args=list(arg1=val1, arg2=val2)` (see `nnet` for all settable arguments). The following parameters have defaults:

**size** integer. Number of units in the hidden layer. By default, set to 6.

**maxit** integer. Maximum number of iterations, default 500.

### Support vector machines (SVM)

Uses the `svm` function from the package 'e1071'. You can set parameters by supplying `svm.args=list(arg1=val1, arg2=val2)` (see `svm` for all settable arguments). The following parameters have defaults:

**type** character. Regression/classification type SVM should be used with. By default, set to "eps-regression".

**epsilon** float. Epsilon parameter in the insensitive loss function, default 1e-08.

**cross** integer. If an integer value  $k > 0$  is specified, a  $k$ -fold cross-validation on the training data is performed to assess the quality of the model: the accuracy rate for classification and the Mean Squared Error for regression. By default, set to 3.

**kernel** character. The kernel used in training and predicting. By default, set to "radial".

**gamma** numeric. Parameter needed for all kernels, default  $1/(\text{length}(\text{data}) - 1)$ .

### Warning

Depending on the raster object resolution the process can be more or less time and memory consuming.

### References

M. Barbet-Massin, F. Jiguet, C. H. Albert, & W. Thuiller (2012) "Selecting pseudo-absences for species distribution models: how, where and how many?" *Methods Ecology and Evolution* 3:327-338 <http://onlinelibrary.wiley.com/doi/10.1111/j.2041-210X.2011.00172.x/full>

C. Liu, P. M. Berry, T. P. Dawson, R. & G. Pearson (2005) "Selecting thresholds of occurrence in the prediction of species distributions." *Ecography* 28:85-393 [http://www.researchgate.net/publication/230246974\\_Selecting\\_Thresholds\\_of\\_Occurrence\\_in\\_the\\_Prediction\\_of\\_Species\\_Distributions](http://www.researchgate.net/publication/230246974_Selecting_Thresholds_of_Occurrence_in_the_Prediction_of_Species_Distributions)

### See Also

`modelling` to build SDMs with a single algorithm, `stack_modelling` to build SSDMs.

## Examples

```
## Not run:
# Loading data
data(Env)
data(Occurrences)
Occurrences <- subset(Occurrences, Occurrences$SPECIES == 'elliptica')

# ensemble SDM building
ESDM <- ensemble_modelling(c('CTA', 'MARS'), Occurrences, Env, rep = 1,
                           Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
                           ensemble.thresh = c(0.6))

# Results plotting
plot(ESDM)

## End(Not run)
```

---

 Env

*A stack of three environmental variables*


---

## Description

A stack of three 30 arcsec-resolution rasters covering the north part of the main island of New Caledonia 'Grande Terre'. CRAINFALL and TEMPERATURE rasters are climatic variables from the WorldClim database, and SUBSTRATE raster is from the IRD Atlas of New Caledonia (2012) (see reference below).

## Usage

Env

## Format

A stack of three rasters:

**RAINFALL** Annual mean rainfall (mm)

**TEMPERATURE** Annual mean temperature (x10 degree Celsius)

**SUBSTRATE** Substrate type (categorical variable)

## References

R.J. Hijmans, C.H. & Graham (2006) "The ability of climate envelope models to predict the effect of climate change on species distributions." *Global Change Biology* 12:2272-2281 <http://onlinelibrary.wiley.com/doi/10.1111/j.1365-2486.2006.01256.x/full>

E. Fritsch (2012) "Les sols. Atlas de la Nouvelle-Caledonie (ed. by J. Bonvallot, J.-C. Gay and E. Habert)" *IRD-Congres de la Nouvelle-Caledonie, Marseille*. 73-76

---

 evaluate

*Evaluate*


---

### Description

Evaluation of SDM or ESDM habitat suitability predictions or evaluation of SSDM floristic composition with Pottier et al, 2013 method (see reference below)

### Usage

```

evaluate(obj, ...)

## S4 method for signature 'Algorithm.SDM'
evaluate(
  obj,
  cv,
  cv.param,
  final.fit.data = "all",
  bin.thresh = "SES",
  metric = NULL,
  thresh = 1001,
  Env,
  ...
)

## S4 method for signature 'MAXENT.SDM'
evaluate(
  obj,
  cv,
  cv.param,
  final.fit.data = "all",
  bin.thresh = "SES",
  metric = NULL,
  thresh = 1001,
  Env,
  ...
)

## S4 method for signature 'Stacked.SDM'
evaluate(obj, ...)

```

### Arguments

|     |  |
|-----|--|
| obj | Stacked.SDM. SSDM to evaluate  |
| ... | arguments for internal use (get_model), such as argument lists to be passed to the source functions (e.g. glm.args=list(test="AIC",singular.ok=FALSE)) |

|                             |   |
|-----------------------------|---|
| <code>cv</code>             | character. Method of cross-validation used to evaluate the SDM (see details below).   |
| <code>cv.param</code>       | numeric. Parameters associated to the method of cross-validation used to evaluate the SDM (see details below).  |
| <code>final.fit.data</code> | strategy used for fitting the final model to be returned: 'holdout'= use same train and test data as in (last) evaluation, 'all'= train model with all data (i.e. no test data) or numeric (0-1)= sample a custom training fraction (left out fraction is set aside as test data) |
| <code>bin.thresh</code>     | character. Classification threshold ( <a href="#">threshold</a> ) used to binarize model predictions into presence/absence and compute the confusion matrix (including related scores such as TPR, TNR, omission rate, Kappa, etc.).  |
| <code>metric</code>         | (deprecated) character. Classification threshold ( <code>SDMTools::optim.thresh</code> ) used to binarize model predictions into presence/absence and compute the confusion matrix (including related scores such as TPR, TNR, omission rate, Kappa, etc.).                       |
| <code>thresh</code>         | (deprecated) integer. Number of equally spaced thresholds in the interval 0-1 ( <code>SDMTools::optim.thresh</code> ).  |
| <code>Env</code>            | raster object. Stacked raster object of environmental variables (can be processed first by <a href="#">load_var</a> ).  |

### Value

SDM/ESDM/SSDM evaluation in a data.frame

### References

Pottier, J., Dubuis, A., Pellissier, L., Maiorano, L., Rossier, L., Randin, C. F., Guisan, A. (2013). The .accuracy of plant assemblage prediction from species distribution models varies along environmental gradients. *Global Ecology and Biogeography*, 22(1), 52-63. <https://doi.org/10.1111/j.1466-8238.2012.00790.x>

### Examples

```
## Not run:
# Loading data
data(Env)
data(Occurrences)
# SSDM building
SSDM <- stack_modelling(c('CTA', 'SVM'), Occurrences, Env, rep = 1,
                        Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
                        Spcol = 'SPECIES')

# Evaluation
evaluate(SSDM)

## End(Not run)
```

---

`gui`*SSDM package Graphic User Interface*

---

## Description

User interface of the SSDM package.

## Usage

```
gui(  
  port = getOption("shiny.port"),  
  host = getOption("shiny.host", "127.0.0.1"),  
  working.directory = getwd()  
)
```

## Arguments

|                                |   |
|--------------------------------|---|
| <code>port</code>              | char. The TCP port that the application should listen on (see <a href="#">runApp</a> for more details).     |
| <code>host</code>              | char. The IPv4 address that the application should listen on (see <a href="#">runApp</a> for more details). |
| <code>working.directory</code> | char. Directory in which the application will run.  |

## Details

If your environmental variables have an important size, you should give enough memory to the interface with the (`maxmem` parameter). Note that only one instance of `gui` can be run at a time.

## Value

Open a window with a shiny app to use the SSDM package with an user-friendly interface.

## Examples

```
## Not run:  
gui()  
  
## End(Not run)
```



---

|            |                                      |
|------------|--------------------------------------|
| load.model | <i>Load ensemble SDMs and SSDMs.</i> |
|------------|--------------------------------------|

---

**Description**

Load S4 [Ensemble.SDM](#) and [Stacked.SDM](#) objects saved with their respective save function.

**Usage**

```
load_esdm(name, path = getwd())
```

```
load_stack(name = "Stack", path = getwd(), GUI = FALSE)
```

**Arguments**

|      |   |
|------|---|
| name | character. Name of the folder containing the model to be loaded.  |
| path | character. Path to the directory containing the model to be loaded, by default the path to the current directory. |
| GUI  | logical. Do not take this argument into account (parameter for the user interface).                               |

**Value**

The corresponding SDM object.

**See Also**

[save.model](#)

---

|          |                             |
|----------|-----------------------------|
| load_occ | <i>Load occurrence data</i> |
|----------|-----------------------------|

---

**Description**

Load occurrence data from CSV file to perform [modelling](#), [ensemble\\_modelling](#) or [stack\\_modelling](#).

**Usage**

```
load_occ(  
  path = getwd(),  
  Env,  
  file = NULL,  
  ...,  
  Xcol = "Longitude",  
  Ycol = "Latitude",
```

```

    Spcol = NULL,
    GeoRes = TRUE,
    reso = max(res(Env@layers[[1]])),
    verbose = TRUE,
    GUI = FALSE
  )

```

### Arguments

|         |  |
|---------|--|
| path    | character. Path to the directory that contains the occurrence table.   |
| Env     | raster stack. Environmental variables in the form of a raster stack used to perform spatial thinning (can be the result of the <a href="#">load_var</a> function). |
| file    | character. File containing the occurrence table, if NULL (default) the .csv file located in the path will be loaded.   |
| ...     | additional parameters given to <a href="#">read.csv</a> .  |
| Xcol    | character. Name of the Latitude or X coordinate variable.  |
| Ycol    | character. Name of the Longitude or Y coordinate variable.   |
| Spcol   | character. Name of the column containing species names or IDs.   |
| GeoRes  | logical. If TRUE, performs geographical thinning on occurrences to limit geographical biases in the SDMs.  |
| reso    | numeric. Resolution used to perform the geographical thinning, default is the resolution of Env.   |
| verbose | logical. If TRUE, allows the function to print text in the console.  |
| GUI     | logical. Parameter reserved for graphical interface.   |

### Value

A data frame containing the occurrence dataset (spatially thinned or not).

### See Also

[load\\_var](#) to load environmental variables.

### Examples

```

## Not run:
load_occ(path = system.file('extdata', package = 'SSDM'), Env,
         Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
         file = 'Occurrences.csv', sep = ',')

## End(Not run)

```

---

|          |                                     |
|----------|-------------------------------------|
| load_var | <i>Load environmental variables</i> |
|----------|-------------------------------------|

---

### Description

Function to load environmental variables in the form of rasters to perform [modelling](#), [ensemble\\_modelling](#) or [stack\\_modelling](#).

### Usage

```
load_var(  
  path = getwd(),  
  files = NULL,  
  format = c(".grd", ".tif", ".asc", ".sdatt", ".rst", ".nc", ".envi", ".bil", ".img"),  
  categorical = NULL,  
  Norm = FALSE,  
  tmp = TRUE,  
  verbose = TRUE,  
  GUI = FALSE  
)
```

### Arguments

|             |   |
|-------------|---|
| path        | character. Path to the directory that contains the environmental variables files.   |
| files       | character. Files containing the environmental variables. If NULL (default) all files present in the path in the selected format will be loaded.                         |
| format      | character. Format of environmental variables files (including .grd, .tif, .asc, .sdatt, .rst, .nc, .tif, .envi, .bil, .img).  |
| categorical | character. Specify environmental variables that are categorical.  |
| Norm        | logical. Default FALSE. If set to TRUE, normalizes environmental variables into a range between 0 and 1.  |
| tmp         | logical. If set to TRUE, rasters are read in temporary file avoiding to overload the random access memory. But beware: if you close R, temporary files will be deleted. |
| verbose     | logical. If set to TRUE, allows the function to print text in the console.  |
| GUI         | logical. Do not take that argument into account (parameter for the user interface).   |

### Value

A stack containing the environmental rasters (normalized or not).

### See Also

[load\\_occ](#) to load occurrences.

**Examples**

```
## Not run:
load_var(system.file('extdata', package = 'SSDM'))

## End(Not run)
```

---

mapDiversity

*Map Diversity*


---

**Description**

Methods for Stacked.SDM or SSDM to map diversity and communities composition.

**Usage**

```
mapDiversity(obj, ...)

## S4 method for signature 'Stacked.SDM'
mapDiversity(obj, method, rep.B = 1000, verbose = TRUE, Env = NULL, ...)
```

**Arguments**

|         |  |
|---------|--|
| obj     | Stacked.SDM. SSDM to map diversity with.   |
| ...     | other arguments pass to the method.  |
| method  | character. Define the method used to create the local species richness map (see details below).  |
| rep.B   | integer. If the method used to create the local species richness is the random Bernoulli ( <b>Bernoulli</b> ), rep.B parameter defines the number of repetitions used to create binary maps for each species.  |
| verbose | logical. If set to true, allows the function to print text in the console.   |
| Env     | raster object. Stacked raster object of environmental variables (can be processed first by <a href="#">load_var</a> ). Needed only for stacking method using probability ranking from richness ( <b>PRR</b> ). |

**Details**

**Methods:** Choice of the method used to compute the local species richness map (see Calabrese et al. (2014) and D'Amen et al (2015) for more informations, see reference below):

**pSSDM** sum probabilities of habitat suitability maps

**Bernoulli** draw repeatedly from a Bernoulli distribution

**bSSDM** sum the binary map obtained with the thresholding (depending on the metric of the ESDM).

**MaximumLikelihood** adjust species richness of the model by linear regression

**PRR.MEM** model richness with a macroecological model (MEM) and adjust each ESDM binary map by ranking habitat suitability and keeping as much as predicted richness of the MEM

**PRR.pSSDM** model richness with a pSSDM and adjust each ESDM binary map by ranking habitat suitability and keeping as much as predicted richness of the pSSDM

### Value

a list with a diversity map and eventually ESDMs for stacking method using probability ranking from richness (**PPR**).

### References

M. D'Amen, A. Dubuis, R. F. Fernandes, J. Pottier, L. Pelissier, & A. Guisan (2015) "Using species richness and functional traits prediction to constrain assemblage predictions from stacked species distribution models" *Journal of Biogeography* 42(7):1255-1266 [http://doc.rero.ch/record/235561/files/pel\\_usr.pdf](http://doc.rero.ch/record/235561/files/pel_usr.pdf)

J.M. Calabrese, G. Certain, C. Kraan, & C.F. Dormann (2014) "Stacking species distribution models and adjusting bias by linking them to macroecological models." *Global Ecology and Biogeography* 23:99-112 <https://onlinelibrary.wiley.com/doi/full/10.1111/geb.12102>

### See Also

[stacking](#) to build SSDMs.

### Examples

```
## Not run:
# Loading data
data(Env)
data(Occurrences)
# SSDM building
SSDM <- stack_modelling(c('CTA', 'SVM'), Occurrences, Env, rep = 1,
                        Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
                        Spcol = 'SPECIES')

# Diversity mapping
mapDiversity(SSDM, method = 'pSSDM')

## End(Not run)
```

**Description**

This is a function to build an SDM with one algorithm for a single species. The function takes as inputs an occurrence data frame made of presence/absence or presence-only records and a raster object for data extraction and projection. The function returns an S4 [Algorithm.SDM](#) class object containing the habitat suitability map, the binary map and the evaluation table.

**Usage**

```
modelling(
  algorithm,
  Occurrences,
  Env,
  Xcol = "Longitude",
  Ycol = "Latitude",
  Pcol = NULL,
  name = NULL,
  PA = NULL,
  cv = "holdout",
  cv.param = c(0.7, 2),
  final.fit.data = "all",
  bin.thresh = "SES",
  metric = NULL,
  thresh = 1001,
  axes.metric = "Pearson",
  select = FALSE,
  select.metric = c("AUC"),
  select.thresh = c(0.75),
  verbose = TRUE,
  GUI = FALSE,
  ...
)
```

**Arguments**

|                          |   |
|--------------------------|---|
| <code>algorithm</code>   | character. Choice of the algorithm to be run (see details below).   |
| <code>Occurrences</code> | data frame. Occurrence table (can be processed first by <a href="#">load_occ</a> ).                           |
| <code>Env</code>         | raster object. Raster object of environmental variable (can be processed first by <a href="#">load_var</a> ). |
| <code>Xcol</code>        | character. Name of the column in the occurrence table containing Latitude or X coordinates.                   |
| <code>Ycol</code>        | character. Name of the column in the occurrence table containing Longitude or Y coordinates.                  |

|                             |   |
|-----------------------------|---|
| <code>Pcol</code>           | character. Name of the column in the occurrence table specifying whether a line is a presence or an absence. A value of 1 is presence and value of 0 is absence. If NULL presence-only dataset is assumed.  |
| <code>name</code>           | character. Optional name given to the final SDM produced (by default 'Algorithm.SDM').  |
| <code>PA</code>             | list(nb, strat) defining the pseudo-absence selection strategy used in case of presence-only dataset. If PA is NULL, recommended PA selection strategy is used depending on the algorithms (see details below).   |
| <code>cv</code>             | character. Method of cross-validation used to evaluate the SDM (see details below).   |
| <code>cv.param</code>       | numeric. Parameters associated to the method of cross-validation used to evaluate the SDM (see details below).  |
| <code>final.fit.data</code> | strategy used for fitting the final model to be returned: 'holdout'= use same train and test data as in (last) evaluation, 'all'= train model with all data (i.e. no test data) or numeric (0-1)= sample a custom training fraction (left out fraction is set aside as test data)                                       |
| <code>bin.thresh</code>     | character. Classification threshold ( <a href="#">threshold</a> ) used to binarize model predictions into presence/absence and compute the confusion matrix (see details below).  |
| <code>metric</code>         | (deprecated) character. Classification threshold ( <code>SDMTools::optim.thresh</code> ) used to binarize model predictions into presence/absence and compute the confusion matrix (see details below). This argument is only kept for backwards compatibility, if possible please use <code>bin.thresh</code> instead. |
| <code>thresh</code>         | (deprecated) integer. Number of equally spaced thresholds in the interval 0-1 ( <code>SDMTools::optim.thresh</code> ). Only needed when <code>metric</code> is set.   |
| <code>axes.metric</code>    | Metric used to evaluate variable relative importance (see details below).   |
| <code>select</code>         | logical. If set to true, models are evaluated before being projected, and not kept if they don't meet selection criteria (see details below).   |
| <code>select.metric</code>  | character. Metric(s) used to pre-select SDMs that reach a sufficient quality (see details below).   |
| <code>select.thresh</code>  | numeric. Threshold(s) associated with the metric(s) used to compute the selection.  |
| <code>verbose</code>        | logical. If set to true, allows the function to print text in the console.  |
| <code>GUI</code>            | logical. Don't take that argument into account (parameter for the user interface).  |
| <code>...</code>            | additional parameters, e.g. argument lists for the source algorithm modelling functions (see details below).  |

## Details

**algorithm** 'all' allows to call directly all available algorithms. Currently, available algorithms include Generalized linear model (**GLM**), Generalized additive model (**GAM**), Multivariate adaptive regression splines (**MARS**), Generalized boosted regressions model (**GBM**), Classification tree analysis (**CTA**), Random forest (**RF**), Maximum entropy (**MAXENT**), Artificial neural network (**ANN**), and Support vector machines (**SVM**). Each algorithm has its own parameters settable with the ... by supplying argument lists (see each algorithm section below to set their parameters).

- 'PA'** list with two values: **nb** number of pseudo-absences selected, and **strat** strategy used to select pseudo-absences: either random selection or disk selection. We set default recommendation from Barbet-Massin et al. (2012) (see reference).
- cv** **Cross-validation** method used to split the occurrence dataset used for evaluation: **holdout** data are partitioned into a training set and an evaluation set using a fraction (*cv.param[1]*) and the operation can be repeated (*cv.param[2]*) times, **k-fold** data are partitioned into k (*cv.param[1]*) folds being k-1 times in the training set and once the evaluation set and the operation can be repeated (*cv.param[2]*) times, **LOO** (Leave One Out) each point is successively taken as evaluation data.
- bin.thresh** Choice of the metric used to binarize model predictions and compute the confusion matrix (by default SES as recommended by Liu et al. (2005), see reference below): **Kappa** maximizes the Kappa, **NOM** highest threshold without omission, **TSS** (True Skill Statistic) maximizes the sum of sensitivity and specificity, **SES** uses the sensitivity-specificity equality, **EP** threshold where modeled prevalence is closest to observed prevalence.
- metric (deprecated)** Choice of the metric used to compute the binary map threshold and the confusion matrix (by default SES as recommended by Liu et al. (2005), see reference below): **Kappa** maximizes the Kappa, **CCR** maximizes the proportion of correctly predicted observations, **TSS** (True Skill Statistic) maximizes the sum of sensitivity and specificity, **SES** uses the sensitivity-specificity equality, **LW** uses the lowest occurrence prediction probability, **ROC** minimizes the distance between the ROC plot (receiving operating curve) and the upper left corner (1,1).
- axes.metric** Choice of the metric used to evaluate the variable relative importance (difference between a full model and one with each variable successively omitted): **Pearson** (computes a simple Pearson's correlation  $r$  between predictions of the full model and the one without a variable, and returns the score  $1-r$ : the highest the value, the more influence the variable has on the model), **AUC**, **Kappa**, **sensitivity**, **specificity**, and **prop.correct** (proportion of correctly predicted occurrences).
- select.metric** Selection metric(s) used to select SDMs: **AUC**, **Kappa**, **sensitivity**, **specificity**, and **prop.correct** (proportion of correctly predicted occurrences), **calibration** (calibration statistic as used by Naimi & Araujo 2016).
- '...'** See algorithm in detail section

## Value

an S4 [Algorithm.SDM](#) Class object viewable with the `plot.model` method.

## Generalized linear model (GLM)

Uses the `glm` function from the package 'stats'. You can set parameters by supplying `glm.args=list(arg1=val1, arg2=val2)` (see [glm](#) for all settable arguments). The following parameters have defaults:

**test** character. Test used to evaluate the SDM, default 'AIC'.

**control** list (created with `glm.control`). Contains parameters for controlling the fitting process. Default is `glm.control(epsilon = 1e-08, maxit = 500)`. 'epsilon' is a numeric and defines the positive convergence tolerance (eps). 'maxit' is an integer giving the maximal number of IWLS (Iterative Weighted Least Squares) iterations.



**Generalized additive model (GAM)**

Uses the `gam` function from the package `'mgcv'`. You can set parameters by supplying `gam.args=list(arg1=val1, arg2=val2)` (see `gam` for all settable arguments). The following parameters have defaults:

**test** character. Test used to evaluate the model, default `'AIC'`.

**control** list (created with `gam.control`). Contains parameters for controlling the fitting process. Default is `gam.control(epsilon = 1e-08, maxit = 500)`. `'epsilon'` is a numeric used for judging the convergence of the GLM IRLS (Iteratively Reweighted Least Squares) loop. `'maxit'` is an integer giving the maximum number of IRLS iterations to perform.

**Multivariate adaptive regression splines (MARS)**

Uses the `earth` function from the package `'earth'`. You can set parameters by supplying `mars.args=list(arg1=val1, arg2=val2)` (see `earth` for all settable arguments). The following parameters have defaults:

**degree** integer. Maximum degree of interaction (Friedman's `mi`) ; 1 meaning build an additive model (i.e., no interaction terms). By default, set to 2.

**Generalized boosted regressions model (GBM)**

Uses the `gbm` function from the package `'gbm'`. You can set parameters by supplying `gbm.args=list(arg1=val1, arg2=val2)` (see `gbm` for all settable arguments). The following parameters have defaults:

**distribution** character. Automatically detected from the format of the presence column in the occurrence dataset.

**n.trees** integer. The total number of trees to fit. This is equivalent to the number of iterations and the number of basis functions in the additive expansion. By default, set to 2500.

**n.minobsinnode** integer. minimum number of observations in the trees terminal nodes. Note that this is the actual number of observations, not the total weight. By default, set to 1.

**cv.folds** integer. Number of cross-validation folds to perform. If `cv.folds>1` then `gbm` - in addition to the usual fit - will perform a cross-validation. By default, set to 3.

**shrinkage** numeric. A shrinkage parameter applied to each tree in the expansion (also known as learning rate or step-size reduction). By default, set to 0.001.

**bag.fraction** numeric. Fraction of the training set observations randomly selected to propose the next tree in the expansion.

**train.fraction** numeric. Training fraction used to fit the first `gbm`. The remainder is used to compute out-of-sample estimates of the loss function. By default, set to 1 (since evaluation/holdout is done with `SSDM::evaluate`).

**n.cores** integer. Number of cores to use for parallel computation of the CV folds. By default, set to 1. If you intend to use this, please set `ncores=0` to avoid conflicts.

**Classification tree analysis (CTA)**

Uses the `rpart` function from the package `'rpart'`. You can set parameters by supplying `cta.args=list(arg1=val1, arg2=val2)` (see `rpart` for all settable arguments). The following parameters have defaults:

**control** list (created with `rpart.control`). Contains parameters for controlling the `rpart` fit. The default is `rpart.control(minbucket=1, xval=3)`. 'mibucket' is an integer giving the minimum number of observations in any terminal node. 'xval' is an integer defining the number of cross-validations.

### Random Forest (RF)

Uses the `randomForest` function from the package 'randomForest'. You can set parameters by supplying `cta.args=list(arg1=val1, arg2=val2)` (see `randomForest` all settable arguments). The following parameters have defaults:

**ntree** integer. Number of trees to grow. This should not be set to a too small number, to ensure that every input row gets predicted at least a few times. By default, set to 2500.

**nodesize** integer. Minimum size of terminal nodes. Setting this number larger causes smaller trees to be grown (and thus take less time). By default, set to 1.

### Maximum Entropy (MAXENT)

Uses the `maxent` function from the package 'dismo'. Make sure that you have correctly installed the `maxent.jar` file in the folder `~\R\library\version\dismo\java` available at [https://biodiversityinformatics.amnh.org/open\\_source/maxent/](https://biodiversityinformatics.amnh.org/open_source/maxent/). As with the other algorithms, you can set parameters by supplying `maxent.args=list(arg1=val1, arg2=val2)`. Mind that arguments are passed from `dismo` to the MAXENT software again as an argument list (see `maxent` for more details). No specific defaults are set with this method.

### Artificial Neural Network (ANN)

Uses the `nnet` function from the package 'nnet'. You can set parameters by supplying `ann.args=list(arg1=val1, arg2=val2)` (see `nnet` for all settable arguments). The following parameters have defaults:

**size** integer. Number of units in the hidden layer. By default, set to 6.

**maxit** integer. Maximum number of iterations, default 500.

### Support vector machines (SVM)

Uses the `svm` function from the package 'e1071'. You can set parameters by supplying `svm.args=list(arg1=val1, arg2=val2)` (see `svm` for all settable arguments). The following parameters have defaults:

**type** character. Regression/classification type SVM should be used with. By default, set to "eps-regression".

**epsilon** float. Epsilon parameter in the insensitive loss function, default 1e-08.

**cross** integer. If an integer value  $k > 0$  is specified, a  $k$ -fold cross-validation on the training data is performed to assess the quality of the model: the accuracy rate for classification and the Mean Squared Error for regression. By default, set to 3.

**kernel** character. The kernel used in training and predicting. By default, set to "radial".

**gamma** numeric. Parameter needed for all kernels, default  $1/(\text{length}(\text{data}) - 1)$ .

**Warning**

Depending on the raster object resolution the process can be more or less time and memory consuming.

**References**

- M. Barbet-Massin, F. Jiguet, C. H. Albert, & W. Thuiller (2012) 'Selecting pseudo-absences for species distribution models: how, where and how many?' *Methods Ecology and Evolution* 3:327-338 <http://onlinelibrary.wiley.com/doi/10.1111/j.2041-210X.2011.00172.x/full>
- C. Liu, P. M. Berry, T. P. Dawson, R. & G. Pearson (2005) 'Selecting thresholds of occurrence in the prediction of species distributions.' *Ecography* 28:85-393 [http://www.researchgate.net/publication/230246974\\_Selecting\\_Thresholds\\_of\\_Occurrence\\_in\\_the\\_Prediction\\_of\\_Species\\_Distributions](http://www.researchgate.net/publication/230246974_Selecting_Thresholds_of_Occurrence_in_the_Prediction_of_Species_Distributions)

**See Also**

[ensemble\\_modelling](#) to build ensemble SDMs, [stack\\_modelling](#) to build SSDMs.

**Examples**

```
# Loading data
data(Env)
data(Occurrences)
Occurrences <- subset(Occurrences, Occurrences$SPECIES == 'elliptica')

# SDM building
SDM <- modelling('GLM', Occurrences, Env, Xcol = 'LONGITUDE', Ycol = 'LATITUDE')

# Results plotting
## Not run:
plot(SDM)

## End(Not run)
```

---

Occurrences

*Plant occurrences data frame*

---

**Description**

A dataset containing plant occurrences of five *Cryptocarya* species native to New Caledonia. Occurrence data come from the Noumea Herbarium (NOU) and NC-PIPPN network (see Ibanez et al (2014) in reference below).

**Usage**

Occurrences

**Format**

A data frame with 57 rows and 3 variables:

**SPECIES** Species of the occurrence

**LONGITUDE** Longitude of the occurrence

**LATITUDE** Latitude of the occurrence

**References**

T. Ibanez, J. Munzinger, G. Dagostini, V. Hequet, F. Rigault, T. Jaffre, & P. Birnbaum (2014) "Structural and floristic characteristics of mixed rainforest in New Caledonia: new data from the New Caledonian Plant Inventory and Permanent Plot Network (NC-PIPPN)." *Applied Vegetation Science* 17:386-397

[http://www.researchgate.net/profile/Jerome\\_Munzinger/publication/258499017\\_Structural\\_and\\_floristic\\_diversity\\_of\\_mixed\\_tropical\\_rain\\_forest\\_in\\_New\\_Caledonia\\_new\\_data\\_from\\_the\\_New\\_Caledonian\\_Plant\\_Inventory\\_and\\_Permanent\\_Plot\\_Network\\_%28NC-PIPPN%29/links/0deec52b8b1996488e000000.pdf](http://www.researchgate.net/profile/Jerome_Munzinger/publication/258499017_Structural_and_floristic_diversity_of_mixed_tropical_rain_forest_in_New_Caledonia_new_data_from_the_New_Caledonian_Plant_Inventory_and_Permanent_Plot_Network_%28NC-PIPPN%29/links/0deec52b8b1996488e000000.pdf)

---

plot.model

*Plot SDMs, ensemble SDMs, and SSDMs*

---

**Description**

Allows to plot S4 [Algorithm.SDM](#), [Ensemble.SDM](#) and [Stacked.SDM](#) class objects.

**Usage**

```
## S4 method for signature 'Stacked.SDM,ANY'
plot(x, y, ...)

## S4 method for signature 'SDM,ANY'
plot(x, y, ...)
```

**Arguments**

|        |   |
|--------|---|
| x      | Object to be plotted (S4 <a href="#">Algorithm.SDM</a> , <a href="#">Ensemble.SDM</a> or <a href="#">Stacked.SDM</a> object). |
| y, ... | Plot-based parameter not used.  |

**Value**

Open a window with a shiny app rendering all the results (habitat suitability map, binary map, evaluation table, variable importance and/or between-algorithm variance map, and/or algorithm evaluation, and/or algorithm correlation matrix and/or local species richness map) in a user-friendly interface.

---

project

*Project model into environment*

---

## Description

This is a collection of methods to project SDMs, ESDMs or SSDMs into the supplied environment. The function is used internally to calculate the input for the projection slot of .SDM classes but can also be used to project existing .SDM objects (see Details).

## Usage

```
project(obj, Env, ...)  
  
## S4 method for signature 'Algorithm.SDM'  
project(obj, Env, output.format = "model", ...)  
  
## S4 method for signature 'MAXENT.SDM'  
project(obj, Env, output.format = "model", ...)  
  
## S4 method for signature 'Ensemble.SDM'  
project(  
  obj,  
  Env,  
  uncertainty = TRUE,  
  output.format = "model",  
  SDM.projections = FALSE,  
  cores = 0,  
  minimal.memory = FALSE,  
  tmp = FALSE,  
  ...  
)  
  
## S4 method for signature 'Stacked.SDM'  
project(  
  obj,  
  Env,  
  method = NULL,  
  uncertainty = TRUE,  
  output.format = "model",  
  SDM.projections = FALSE,  
  cores = 0,  
  minimal.memory = FALSE,  
  tmp = FALSE,  
  ...  
)
```

**Arguments**

|                              |  |
|------------------------------|--|
| <code>obj</code>             | Object of class <code>Algorithm.SDM</code> , <code>Ensemble.SDM</code> or <code>Stacked.SDM</code> . Model(s) to be projected.   |
| <code>Env</code>             | Raster stack. Updated environmental rasters to be used for projection.   |
| <code>...</code>             | arguments for internal use ( <code>get_model</code> ), such as argument lists to be passed to the source functions (e.g. <code>glm.args=list(test="AIC",singular.ok=FALSE)</code> ). See <a href="#">modelling</a> , algorithm section for more details.   |
| <code>output.format</code>   | character. If 'model' (default), the original <code>.SDM</code> object will be returned with updated projection slots. If 'rasters', the projected rasters will be returned as a list of rasters.  |
| <code>uncertainty</code>     | logical. If set to <code>TRUE</code> , generates an uncertainty map. If <code>output.format</code> is 'model' an algorithm correlation matrix is additionally returned.  |
| <code>SDM.projections</code> | logical. If <code>FALSE</code> (default), the projections of the <code>Algorithm.SDMs</code> will not be returned (only applies to <code>Ensemble.SDMs</code> and <code>Stack.SDMs</code> ).   |
| <code>cores</code>           | integer. Specify the number of CPU cores used to do the computing. You can use <a href="#">detectCores</a> to automatically use all the available CPU cores.   |
| <code>minimal.memory</code>  | logical. Only relevant if <code>cores &gt; 1</code> . If <code>TRUE</code> , only one model will be sent to each worker at a time, reducing used working memory.   |
| <code>tmp</code>             | logical or character. If <code>FALSE</code> , no temporary rasters are written. If <code>TRUE</code> , temporary rasters are written to the „tmp“ directory of your R environment. If character, temporary rasters are written to a custom path. Very useful to reduce working memory consumption (use together with <code>minimal.memory=TRUE</code> for maximal effect). But beware: Depending on number, resolution and extent of models, temporary files can take a lot of disk space. |
| <code>method</code>          | character. Define the method used to create the local species richness map (for details see <a href="#">stack_modelling</a> ). If <code>NULL</code> (default), the method used for building the <code>SSDM</code> is used.   |

**Details**

The function uses any `S4 .SDM` class object and a raster stack of environmental layers of the variables the model was trained with.

**Value**

Either returns the original `.SDM` object with updated projection slots (default) or if `output.format = 'rasters'` only returns the projections as `Raster*` objects or a list thereof.

---

|            |                                     |
|------------|-------------------------------------|
| save.model | <i>Save ensemble SDMs and SSDMs</i> |
|------------|-------------------------------------|

---

## Description

Allows to save S4 [Ensemble.SDM](#) and [Stacked.SDM](#) class objects.

## Usage

```
save.esdm(
  esdm,
  name = strsplit(esdm@name, ".", fixed = TRUE)[[1]][1],
  path = getwd(),
  verbose = TRUE,
  GUI = FALSE
)

## S4 method for signature 'Ensemble.SDM'
save.esdm(
  esdm,
  name = strsplit(esdm@name, ".Ensemble.SDM", fixed = TRUE)[[1]][1],
  path = getwd(),
  verbose = TRUE,
  GUI = FALSE
)

save.stack(stack, name = "Stack", path = getwd(), verbose = TRUE, GUI = FALSE)

## S4 method for signature 'Stacked.SDM'
save.stack(stack, name = "Stack", path = getwd(), verbose = TRUE, GUI = FALSE)
```

## Arguments

|         |  |
|---------|--|
| esdm    | Ensemble.SDM. Ensemble SDM to be saved.  |
| name    | character. Folder name of the model to save.   |
| path    | character. Path to the directory chosen to save the SDM, by default the path to the current directory. |
| verbose | logical. If set to true, allows the function to print text in the console.                             |
| GUI     | logical. Don't take that argument into account (parameter for the user interface).                     |
| stack   | Stacked.SDM. SSDM to be saved.   |

## Value

Nothing in R environment. Creates folders, tables and rasters associated to the SDM. Tables are in .csv and rasters in .grd/.gri.

**See Also**[load.model](#)

---

**SSDM***SSDM: Stacked species distribution modelling*

---

**Description**

SSDM is a package to map species richness and endemism based on Stacked Species Distribution Models (SSDM). It provides tools to build SDM, i.e. a single species fitted with a single algorithm, Ensemble SDM (ESDM), i.e. a single species fitted with multiple algorithms, SSDM several species with one or more algorithms. The package includes numerous modelling algorithms, and specifiable ensemble aggregating and stacking methods. This package also provides tools to evaluate and explore models such as variable importance, algorithm accuracy, and between-algorithm correlation, and tools to map results such as habitat suitability maps, binary maps, between-algorithm variance maps. For ease of use, the SSDM package provides a user-friendly graphical interface ([gui](#)).

**Details**

The SSDM package provides five categories of functions (that you can find in details below): Data preparation, Modelling main functions, Model main methods, Model classes, and Miscellaneous.

**Data preparation**[load\\_occ](#) Load occurrence data[load\\_var](#) Load environmental variables**Modelling main functions**[modelling](#) Build an SDM using a single algorithm[ensemble\\_modelling](#) Build an SDM that assembles multiple algorithms[stack\\_modelling](#) Build an SSDMs that assembles multiple algorithms and species**Model main methods**[ensemble,Algorithm.SDM-method](#) Build an ensemble SDM[stacking,Ensemble.SDM-method](#) Build an SSDM[update,Stacked.SDM-method](#) Update a previous SSDM with new occurrence data**Model classes**[Algorithm.SDM](#) S4 class to represent SDMs[Ensemble.SDM](#) S4 class to represent ensemble SDMs[Stacked.SDM](#) S4 class to represent SSDMs



**Miscellaneous**

[gui](#) User-friendly interface for SSDM package  
[plot.model](#) Plot SDMs  
[save.model](#) Save SDMs  
[load.model](#) Load SDMs

---

Stacked.SDM-class      *An S4 class to represent SSDMs*

---

**Description**

This is an S4 class to represent SSDMs that assembles multiple algorithms (including generalized linear model, general additive model, multivariate adaptive splines, generalized boosted regression model, classification tree analysis, random forest, maximum entropy, artificial neural network, and support vector machines) built for multiple species. It is obtained with [stack\\_modelling](#) or [stacking](#).

**Slots**

`name` character. Name of the SSDM (by default 'Species.SSDM').  
`diversity.map` raster. Local species richness map produced by the SSDM.  
`endemism.map` raster. Endemism map produced by the SSDM (see Crisp et al (2011) in references).  
`uncertainty` raster. Between-algorithm variance map.  
`evaluation` data frame. Evaluation of the SSDM (AUC, Kappa, omission rate, sensitivity, specificity, proportion of correctly predicted occurrences).  
`variable.importance` data frame. Relative importance of each variable in the SSDM.  
`algorithm.correlation` data frame. Between-algorithm correlation matrix.  
`esdms` list. List of ensemble SDMs used in the SSDM.  
`parameters` data frame. Parameters used to build the SSDM.  
`algorithm.evaluation` data frame. Evaluation of the algorithm averaging the metrics of all SDMs (AUC, Kappa, omission rate, sensitivity, specificity, proportion of correctly predicted occurrences).

**References**

M. D. Crisp, S. Laffan, H. P. Linder & A. Monro (2001) "Endemism in the Australian flora" *Journal of Biogeography* 28:183-198 [http://biology-assets.anu.edu.au/hosted\\_sites/Crisp/pdfs/Crisp2001\\_endemism.pdf](http://biology-assets.anu.edu.au/hosted_sites/Crisp/pdfs/Crisp2001_endemism.pdf)

**See Also**

[Ensemble.SDM](#) an S4 class to represent ensemble SDMs, and [Algorithm.SDM](#) an S4 class to represent SDMs.

stacking

*Stack different ensemble SDMs in an SSDM***Description**

This is a function to stack several ensemble SDMs in an SSDM. The function takes as inputs several S4 [Ensemble.SDM](#) class objects produced with [ensemble\\_modelling](#) or [ensemble](#) functions. The function returns an S4 [Stacked.SDM](#) class object containing the local species richness map, the between-algorithm variance map, and all evaluation tables coming with (model evaluation, algorithm evaluation, algorithm correlation matrix and variable importance), and a list of ensemble SDMs for each species (see [ensemble\\_modelling](#)).

**Usage**

```
stacking(
  esdm,
  ...,
  name = NULL,
  method = "pSSDM",
  rep.B = 1000,
  Env = NULL,
  range = NULL,
  endemism = c("WEI", "Binary"),
  eval = TRUE,
  uncertainty = TRUE,
  verbose = TRUE,
  GUI = FALSE
)

## S4 method for signature 'Ensemble.SDM'
stacking(
  esdm,
  ...,
  name = NULL,
  method = "pSSDM",
  rep.B = 1000,
  Env = NULL,
  range = NULL,
  endemism = c("WEI", "Binary"),
  eval = TRUE,
  uncertainty = TRUE,
  verbose = TRUE,
  GUI = FALSE
)
```

**Arguments**

`esdm, ...` character. Ensemble SDMs to be stacked.

|             |  |
|-------------|--|
| name        | character. Optional name given to the final SSDM produced (by default 'Species.SDM').  |
| method      | character. Define the method used to create the local species richness map (see details below).  |
| rep.B       | integer. If the method used to create the local species richness is the random bernoulli ( <b>Bernoulli</b> ), rep.B parameter defines the number of repetitions used to create binary maps for each species.  |
| Env         | raster object. Stacked raster object of environmental variables (can be processed first by <code>load_var</code> ). Needed only for stacking method using probability ranking from richness ( <b>PRR</b> ).  |
| range       | integer. Set a value of range restriction (in pixels) around presences occurrences on habitat suitability maps (all further points will have a null probability, see Crisp et al (2011) in references). If NULL, no range restriction will be applied. |
| endemism    | character. Define the method used to create an endemism map (see details below).   |
| eval        | logical. If set to FALSE, disable stack evaluation.  |
| uncertainty | logical. If set to TRUE, generates an uncertainty map and an algorithm correlation matrix.   |
| verbose     | logical. If set to TRUE, allows the function to print text in the console.   |
| GUI         | logical. Don't take that argument into account (parameter for the user interface).   |

## Details

**Methods:** Choice of the method used to compute the local species richness map (see Calabrese et al. (2014) and D'Amen et al (2015) for more informations, see reference below):

**pSSDM** sum probabilities of habitat suitability maps

**Bernoulli** draw repeatedly from a Bernoulli distribution

**bSSDM** sum the binary map obtained with the thresholding (depending on the metric of the ESDM).

**MaximumLikelihood** adjust species richness of the model by linear regression

**PRR.MEM** model richness with a macroecological model (MEM) and adjust each ESDM binary map by ranking habitat suitability and keeping as much as predicted richness of the MEM

**PRR.pSSDM** model richness with a pSSDM and adjust each ESDM binary map by ranking habitat suitability and keeping as much as predicted richness of the pSSDM

**Endemism:** Choice of the method used to compute the endemism map (see Crisp et al. (2001) for more information, see reference below):

**NULL** No endemism map

**WEI** (Weighted Endemism Index) Endemism map built by counting all species in each cell and weighting each by the inverse of its range

**CWEI** (Corrected Weighted Endemism Index) Endemism map built by dividing the weighted endemism index by the total count of species in the cell.

First string of the character is the method either WEI or CWEI, and in those cases second string of the vector is used to precise range calculation, whether the total number of occurrences '**NbOcc**' whether the surface of the binary map species distribution '**Binary**'.

**Value**

an S4 `Stacked.SDM` class object viewable with the `plot.model` function.

**References**

M. D'Amen, A. Dubuis, R. F. Fernandes, J. Pottier, L. Pelissier, & A. Guisan (2015) "Using species richness and functional traits prediction to constrain assemblage predictions from stacked species distribution models" *Journal of Biogeography* 42(7):1255-1266 [http://doc.rero.ch/record/235561/files/pel\\_usr.pdf](http://doc.rero.ch/record/235561/files/pel_usr.pdf)

J.M. Calabrese, G. Certain, C. Kraan, & C.F. Dormann (2014) "Stacking species distribution models and adjusting bias by linking them to macroecological models." *Global Ecology and Biogeography* 23:99-112 <https://onlinelibrary.wiley.com/doi/full/10.1111/geb.12102>

M. D. Crisp, S. Laffan, H. P. Linder & A. Monro (2001) "Endemism in the Australian flora" *Journal of Biogeography* 28:183-198 [http://biology-assets.anu.edu.au/hosted\\_sites/Crisp/pdfs/Crisp2001\\_endemism.pdf](http://biology-assets.anu.edu.au/hosted_sites/Crisp/pdfs/Crisp2001_endemism.pdf)

C. Liu, P. M. Berry, T. P. Dawson, R. & G. Pearson (2005) "Selecting thresholds of occurrence in the prediction of species distributions." *Ecography* 28:85-393 [http://www.researchgate.net/publication/230246974\\_Selecting\\_Thresholds\\_of\\_Occurrence\\_in\\_the\\_Prediction\\_of\\_Species\\_Distributions](http://www.researchgate.net/publication/230246974_Selecting_Thresholds_of_Occurrence_in_the_Prediction_of_Species_Distributions)

**See Also**

[stack\\_modelling](#) to build SSDMs.

**Examples**

```
## Not run:
# Loading data
data(Env)
data(Occurrences)
Occ1 <- subset(Occurrences, Occurrences$SPECIES == 'elliptica')
Occ2 <- subset(Occurrences, Occurrences$SPECIES == 'gracilis')

# SSDM building
ESDM1 <- ensemble_modelling(c('CTA', 'SVM'), Occ1, Env, rep = 1,
                             Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
                             name = 'elliptica', ensemble.thresh = c(0.6))
ESDM2 <- ensemble_modelling(c('CTA', 'SVM'), Occ2, Env, rep = 1,
                             Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
                             name = 'gracilis', ensemble.thresh = c(0.6))
SSDM <- stacking(ESDM1, ESDM2)

# Results plotting
plot(SSDM)

## End(Not run)
```

---

stack\_modelling      *Build an SSDM that assembles multiple algorithms and species.*

---

## Description

This is a function to build an SSDM that assembles multiple algorithm and species. The function takes as inputs an occurrence data frame made of presence/absence or presence-only records and a raster object for data extraction and projection. The function returns an S4 [Stacked.SDM](#) class object containing the local species richness map, the between-algorithm variance map, and all evaluation tables coming with (model evaluation, algorithm evaluation, algorithm correlation matrix and variable importance), and a list of ensemble SDMs for each species (see [ensemble\\_modelling](#)).

## Usage

```
stack_modelling(  
  algorithms,  
  Occurrences,  
  Env,  
  Xcol = "Longitude",  
  Ycol = "Latitude",  
  Pcol = NULL,  
  Spcol = "SpeciesID",  
  rep = 10,  
  name = NULL,  
  save = FALSE,  
  path = getwd(),  
  PA = NULL,  
  cv = "holdout",  
  cv.param = c(0.7, 1),  
  final.fit.data = "all",  
  bin.thresh = "SES",  
  metric = NULL,  
  thresh = 1001,  
  axes.metric = "Pearson",  
  uncertainty = TRUE,  
  tmp = FALSE,  
  SDM.projections = FALSE,  
  ensemble.metric = c("AUC"),  
  ensemble.thresh = c(0.75),  
  weight = TRUE,  
  method = "pSSDM",  
  rep.B = 1000,  
  range = NULL,  
  endemism = c("WEI", "Binary"),  
  verbose = TRUE,  
  GUI = FALSE,  
  cores = 0,  
)
```

```

    parmode = "species",
    ...
)

```

### Arguments

|                |   |
|----------------|---|
| algorithms     | character. Choice of the algorithm(s) to be run (see details below).  |
| Occurrences    | data frame. Occurrence table (can be processed first by <a href="#">load_occ</a> ).   |
| Env            | raster object. Raster object of environmental variables (can be processed first by <a href="#">load_var</a> ).  |
| Xcol           | character. Name of the column in the occurrence table containing Latitude or X coordinates.   |
| Ycol           | character. Name of the column in the occurrence table containing Longitude or Y coordinates.  |
| Pcol           | character. Name of the column in the occurrence table specifying whether a line is a presence or an absence. A value of 1 is presence and value of 0 is absence. If NULL presence-only dataset is assumed.  |
| Spcol          | character. Name of the column containing species names or IDs.  |
| rep            | integer. Number of repetitions for each algorithm.  |
| name           | character. Optional name given to the final Ensemble.SDM produced.  |
| save           | logical. If set to true, the SSDM is automatically saved.   |
| path           | character. If save is true, the path to the directory in which the ensemble SDM will be saved.  |
| PA             | list(nb, strat) defining the pseudo-absence selection strategy used in case of presence-only dataset. If PA is NULL, recommended PA selection strategy is used depending on the algorithm (see details below).  |
| cv             | character. Method of cross-validation used to evaluate the ensemble SDM (see details below).  |
| cv.param       | numeric. Parameters associated with the method of cross-validation used to evaluate the ensemble SDM (see details below).   |
| final.fit.data | strategy used for fitting the final/evaluated Algorithm.SDMs: 'holdout'= use same train and test data as in (last) evaluation, 'all'= train model with all data (i.e. no test data) or numeric (0-1)= sample a custom training fraction (left out fraction is set aside as test data)                                   |
| bin.thresh     | character. Classification threshold ( <a href="#">threshold</a> ) used to binarize model predictions into presence/absence and compute the confusion matrix (see details below).  |
| metric         | (deprecated) character. Classification threshold ( <code>SDMTools::optim.thresh</code> ) used to binarize model predictions into presence/absence and compute the confusion matrix (see details below). This argument is only kept for backwards compatibility, if possible please use <code>bin.thresh</code> instead. |
| thresh         | (deprecated) integer. Number of equally spaced thresholds in the interval 0-1 ( <code>SDMTools::optim.thresh</code> ). Only needed when <code>metric</code> is set.   |

|                              |  |
|------------------------------|--|
| <code>axes.metric</code>     | Metric used to evaluate variable relative importance (see details below).  |
| <code>uncertainty</code>     | logical. If set to true, generates an uncertainty map and an algorithm correlation matrix.   |
| <code>tmp</code>             | logical. If set to true, the habitat suitability map of each algorithms is saved in a temporary file to release memory. But beware: if you close R, temporary files will be deleted. To avoid any loss you can save your SSDM with <a href="#">save.model</a> . Depending on number, resolution and extent of models, temporary files can take a lot of disk space. Temporary files are written in R environment temporary folder. |
| <code>SDM.projections</code> | logical. If FALSE (default), the Algorithm.SDMs inside the 'sdms' slot will not contain projections (for memory saving purposes).  |
| <code>ensemble.metric</code> | character. Metric(s) used to select the best SDMs that will be included in the ensemble SDM (see details below).   |
| <code>ensemble.thresh</code> | numeric. Threshold(s) associated with the metric(s) used to compute the selection.   |
| <code>weight</code>          | logical. Choose whether or not you want the SDMs to be weighted using the selection metric or, alternatively, the mean of the selection metrics.   |
| <code>method</code>          | character. Define the method used to create the local species richness map (see details below).  |
| <code>rep.B</code>           | integer. If the method used to create the local species richness is the random bernoulli ( <b>Bernoulli</b> ), <code>rep.B</code> parameter defines the number of repetitions used to create binary maps for each species.   |
| <code>range</code>           | integer. Set a value of range restriction (in pixels) around presences occurrences on habitat suitability maps (all further points will have a null probability, see Crisp et al (2011) in references). If NULL, no range restriction will be applied.   |
| <code>endemism</code>        | character. Define the method used to create an endemism map (see details below).   |
| <code>verbose</code>         | logical. If set to true, allows the function to print text in the console.   |
| <code>GUI</code>             | logical. Don't take that argument into account (parameter for the user interface).   |
| <code>cores</code>           | integer. Specify the number of CPU cores used to do the computing. You can use <a href="#">detectCores</a> to automatically use all the available CPU cores.   |
| <code>parmode</code>         | character. Parallelization mode: along 'species', 'algorithms' or 'replicates'. Defaults to 'species'.   |
| <code>...</code>             | additional parameters for the algorithm modelling function (see details below).  |

## Details

**algorithms** 'all' allows you to call directly all available algorithms. Currently, available algorithms include Generalized linear model (**GLM**), Generalized additive model (**GAM**), Multivariate adaptive regression splines (**MARS**), Generalized boosted regressions model (**GBM**), Classification tree analysis (**CTA**), Random forest (**RF**), Maximum entropy (**MAXENT**), Artificial neural network (**ANN**), and Support vector machines (**SVM**). Each algorithm has its own parameters settable with the ... (see each algorithm section below to set their parameters).

**"PA"** list with two values: **nb** number of pseudo-absences selected, and **strat** strategy used to select pseudo-absences: either random selection or disk selection. We set default recommendation from Barbet-Massin et al. (2012) (see reference).

**cv** **Cross-validation** method used to split the occurrence dataset used for evaluation: **holdout** data are partitioned into a training set and an evaluation set using a fraction (*cv.param[1]*) and the operation can be repeated (*cv.param[2]*) times, **k-fold** data are partitioned into k (*cv.param[1]*) folds being k-1 times in the training set and once the evaluation set and the operation can be repeated (*cv.param[2]*) times, **LOO** (Leave One Out) each point is successively taken as evaluation data.

**metric** Choice of the metric used to compute the binary map threshold and the confusion matrix (by default SES as recommended by Liu et al. (2005), see reference below): **Kappa** maximizes the Kappa, **CCR** maximizes the proportion of correctly predicted observations, **TSS** (True Skill Statistic) maximizes the sum of sensitivity and specificity, **SES** uses the sensitivity-specificity equality, **LW** uses the lowest occurrence prediction probability, **ROC** minimizes the distance between the ROC plot (receiving operating curve) and the upper left corner (1,1).

**axes.metric** Choice of the metric used to evaluate the variable relative importance (difference between a full model and one with each variable successively omitted): **Pearson** (computes a simple Pearson's correlation  $r$  between predictions of the full model and the one without a variable, and returns the score  $1-r$ : the highest the value, the more influence the variable has on the model), **AUC**, **Kappa**, **sensitivity**, **specificity**, and **prop.correct** (proportion of correctly predicted occurrences).

**ensemble.metric** Ensemble metric(s) used to select SDMs: **AUC**, **Kappa**, **sensitivity**, **specificity**, and **prop.correct** (proportion of correctly predicted occurrences).

**method** Choice of the method used to compute the local species richness map (see Calabrese et al. (2014) and D'Amen et al (2015) for more informations, see reference below): **pSSDM** sum probabilities of habitat suitability maps, **Bernoulli** drawing repeatedly from a Bernoulli distribution, **bSSDM** sum the binary map obtained with the thresholding (depending on the metric, see metric parameter), **MaximumLikelihood** adjust species richness using maximum likelihood parameter estimates on the logit-transformed occurrence probabilities (see Calabrese et al. (2014)), **PRR.MEM** model richness with a macroecological model (MEM) and adjust each ESDM binary map by ranking habitat suitability and keeping as much as predicted richness of the MEM, **PRR.pSSDM** model richness with a pSSDM and adjust each ESDM binary map by ranking habitat suitability and keeping as much as predicted richness of the pSSDM

**endemism** Choice of the method used to compute the endemism map (see Crisp et al. (2001) for more information, see reference below): **NULL** No endemism map, **WEI** (Weighted Endemism Index) Endemism map built by counting all species in each cell and weighting each by the inverse of its range, **CWEI** (Corrected Weighted Endemism Index) Endemism map built by dividing the weighted endemism index by the total count of species in the cell. First string of the character is the method either WEI or CWEI, and in those cases second string of the vector is used to precise range calculation, whether the total number of occurrences 'NbOcc' whether the surface of the binary map species distribution 'Binary'.

... See algorithm in detail section

## Value

an S4 `Stacked.SDM` class object viewable with the `plot.model` function.



### Generalized linear model (GLM)

Uses the `glm` function from the package 'stats'. You can set parameters by supplying `glm.args=list(arg1=val1, arg2=val2)` (see [glm](#) for all settable arguments). The following parameters have defaults:

**test** character. Test used to evaluate the SDM, default 'AIC'.

**control** list (created with [glm.control](#)). Contains parameters for controlling the fitting process. Default is `glm.control(epsilon = 1e-08, maxit = 500)`. 'epsilon' is a numeric and defines the positive convergence tolerance (eps). 'maxit' is an integer giving the maximal number of IWLS (Iterative Weighted Last Squares) iterations.

### Generalized additive model (GAM)

Uses the `gam` function from the package 'mgcv'. You can set parameters by supplying `gam.args=list(arg1=val1, arg2=val2)` (see [gam](#) for all settable arguments). The following parameters have defaults:

**test** character. Test used to evaluate the model, default 'AIC'.

**control** list (created with [gam.control](#)). Contains parameters for controlling the fitting process. Default is `gam.control(epsilon = 1e-08, maxit = 500)`. 'epsilon' is a numeric used for judging the convergence of the GLM IRLS (Iteratively Reweighted Least Squares) loop. 'maxit' is an integer giving the maximum number of IRLS iterations to perform.

### Multivariate adaptive regression splines (MARS)

Uses the `earth` function from the package 'earth'. You can set parameters by supplying `mars.args=list(arg1=val1, arg2=val2)` (see [earth](#) for all settable arguments). The following parameters have defaults:

**degree** integer. Maximum degree of interaction (Friedman's  $m_i$ ) ; 1 meaning build an additive model (i.e., no interaction terms). By default, set to 2.

### Generalized boosted regressions model (GBM)

Uses the `gbm` function from the package 'gbm'. You can set parameters by supplying `gbm.args=list(arg1=val1, arg2=val2)` (see [gbm](#) for all settable arguments). The following parameters have defaults:

**distribution** character. Automatically detected from the format of the presence column in the occurrence dataset.

**n.trees** integer. The total number of trees to fit. This is equivalent to the number of iterations and the number of basis functions in the additive expansion. By default, set to 2500.

**n.minobsinnode** integer. minimum number of observations in the trees terminal nodes. Note that this is the actual number of observations, not the total weight. By default, set to 1.

**cv.folds** integer. Number of cross-validation folds to perform. If `cv.folds>1` then `gbm` - in addition to the usual fit - will perform a cross-validation. By default, set to 3.

**shrinkage** numeric. A shrinkage parameter applied to each tree in the expansion (also known as learning rate or step-size reduction). By default, set to 0.001.

**bag.fraction** numeric. Fraction of the training set observations randomly selected to propose the next tree in the expansion.

**train.fraction** numeric. Training fraction used to fit the first gbm. The remainder is used to compute out-of-sample estimates of the loss function. By default, set to 1 (since evaluation/holdout is done with `SSDM::evaluate`).

**n.cores** integer. Number of cores to use for parallel computation of the CV folds. By default, set to 1. If you intend to use this, please set `ncores=0` to avoid conflicts.

### Classification tree analysis (CTA)

Uses the `rpart` function from the package 'rpart'. You can set parameters by supplying `cta.args=list(arg1=val1, arg2=val2)` (see [rpart](#) for all settable arguments). The following parameters have defaults:

**control** list (created with `rpart.control`). Contains parameters for controlling the rpart fit. The default is `rpart.control(minbucket=1, xval=3)`. 'mibucket' is an integer giving the minimum number of observations in any terminal node. 'xval' is an integer defining the number of cross-validations.

### Random Forest (RF)

Uses the `randomForest` function from the package 'randomForest'. You can set parameters by supplying `cta.args=list(arg1=val1, arg2=val2)` (see [randomForest](#) all settable arguments). The following parameters have defaults:

**ntree** integer. Number of trees to grow. This should not be set to a too small number, to ensure that every input row gets predicted at least a few times. By default, set to 2500.

**nodesize** integer. Minimum size of terminal nodes. Setting this number larger causes smaller trees to be grown (and thus take less time). By default, set to 1.

### Maximum Entropy (MAXENT)

Uses the `maxent` function from the package 'dismo'. Make sure that you have correctly installed the `maxent.jar` file in the folder `~\R\library\version\dismo\java` available at [https://biodiversityinformatics.amnh.org/open\\_source/maxent/](https://biodiversityinformatics.amnh.org/open_source/maxent/). As with the other algorithms, you can set parameters by supplying `maxent.args=list(arg1=val1, arg2=val2)`. Mind that arguments are passed from `dismo` to the MAXENT software again as an argument list (see [maxent](#) for more details). No specific defaults are set with this method.

### Artificial Neural Network (ANN)

Uses the `nnet` function from the package 'nnet'. You can set parameters by supplying `ann.args=list(arg1=val1, arg2=val2)` (see [nnet](#) for all settable arguments). The following parameters have defaults:

**size** integer. Number of units in the hidden layer. By default, set to 6.

**maxit** integer. Maximum number of iterations, default 500.

### Support vector machines (SVM)

Uses the `svm` function from the package 'e1071'. You can set parameters by supplying `svm.args=list(arg1=val1, arg2=val2)` (see [svm](#) for all settable arguments). The following parameters have defaults:

**type** character. Regression/classification type SVM should be used with. By default, set to "epsilon-regression".

**epsilon** float. Epsilon parameter in the insensitive loss function, default 1e-08.

**cross** integer. If an integer value  $k > 0$  is specified, a  $k$ -fold cross-validation on the training data is performed to assess the quality of the model: the accuracy rate for classification and the Mean Squared Error for regression. By default, set to 3.

**kernel** character. The kernel used in training and predicting. By default, set to "radial".

**gamma** numeric. Parameter needed for all kernels, default  $1/(\text{length}(\text{data}) - 1)$ .

### Warning

Depending on the raster object resolution the process can be more or less time and memory consuming.

### References

M. D'Amen, A. Dubuis, R. F. Fernandes, J. Pottier, L. Pelissier, & A. Guisan (2015) "Using species richness and functional traits prediction to constrain assemblage predictions from stacked species distribution models" *Journal of Biogeography* 42(7):1255-1266 [http://doc.rero.ch/record/235561/files/pel\\_usr.pdf](http://doc.rero.ch/record/235561/files/pel_usr.pdf)

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J.M. Calabrese, G. Certain, C. Kraan, & C.F. Dormann (2014) "Stacking species distribution models and adjusting bias by linking them to macroecological models." *Global Ecology and Biogeography* 23:99-112 <https://onlinelibrary.wiley.com/doi/full/10.1111/geb.12102>

M. D. Crisp, S. Laffan, H. P. Linder & A. Monro (2001) "Endemism in the Australian flora" *Journal of Biogeography* 28:183-198 [http://biology-assets.anu.edu.au/hosted\\_sites/Crisp/pdfs/Crisp2001\\_endemism.pdf](http://biology-assets.anu.edu.au/hosted_sites/Crisp/pdfs/Crisp2001_endemism.pdf)

C. Liu, P. M. Berry, T. P. Dawson, R. & G. Pearson (2005) "Selecting thresholds of occurrence in the prediction of species distributions." *Ecography* 28:85-393 [http://www.researchgate.net/publication/230246974\\_Selecting\\_Thresholds\\_of\\_Occurrence\\_in\\_the\\_Prediction\\_of\\_Species\\_Distributions](http://www.researchgate.net/publication/230246974_Selecting_Thresholds_of_Occurrence_in_the_Prediction_of_Species_Distributions)

### See Also

[modelling](#) to build simple SDMs.

### Examples

```
## Not run:
# Loading data
data(Env)
data(Occurrences)

# SSDM building
SSDM <- stack_modelling(c('CTA', 'SVM'), Occurrences, Env, rep = 1,
```

```

Xcol = 'LONGITUDE', Ycol = 'LATITUDE',
Spcol = 'SPECIES')

# Results plotting
plot(SSDM)

## End(Not run)

```

---

update, Stacked.SDM-method

*Update a previous SSDM*

---

## Description

Update a previous SSDM with new occurrence data. The function takes as inputs updated or new occurrence data from one species, previous environmental variables, and an S4 [Stacked.SDM](#) class object containing a previously built SSDM.

## Usage

```

## S4 method for signature 'Stacked.SDM'
update(
  object,
  Occurrences,
  Env,
  Xcol = "Longitude",
  Ycol = "Latitude",
  Pcol = NULL,
  Spname = NULL,
  name = stack@name,
  save = FALSE,
  path = getwd(),
  thresh = 1001,
  tmp = FALSE,
  verbose = TRUE,
  GUI = FALSE,
  ...
)

```

## Arguments

|             |  |
|-------------|--|
| object      | Stacked.SDM. The previously built SSDM.  |
| Occurrences | data frame. New or updated occurrence table (can be processed first by <a href="#">load_occ</a> ). |
| Env         | raster object. Environment raster object (can be processed first by <a href="#">load_var</a> ).    |
| Xcol        | character. Name of the column in the occurrence table containing Latitude or X coordinates.        |

|         |  |
|---------|--|
| Ycol    | character. Name of the column in the occurrence table containing Longitude or Y coordinates.   |
| Pcol    | character. Name of the column in the occurrence table specifying whether a line is a presence or an absence. A value of 1 is presence and value of 0 is absence. If NULL presence-only dataset is assumed.   |
| Spname  | character. Name of the new or updated species.   |
| name    | character. Optional name given to the final SSDM produced, by default it's the name of the previous SSDM.  |
| save    | logical. If set to true, the model is automatically saved.   |
| path    | character. Name of the path to the directory to contain the saved SSDM.  |
| thresh  | numeric. A single integer value representing the number of equal interval threshold values between 0 and 1.  |
| tmp     | logical. If set to true, the habitat suitability map of each algorithm is saved in a temporary file to release memory. But beware: if you close R, temporary files will be deleted To avoid any loss you can save your model with <a href="#">save.model</a> . |
| verbose | logical. If set to true, allows the function to print text in the console.   |
| GUI     | logical. Don't take that argument into account (parameter for the user interface).   |
| ...     | additional parameters for the algorithm modelling function (see details below).  |

**Value**

an S4 [Stacked.SDM](#) class object viewable with the [plot.model](#) function.

**See Also**

[stack\\_modelling](#) to build SSDMs.

**Examples**

```
## Not run:
update(stack, Occurrences, Env, Spname = 'NewSpecie')

## End(Not run)
```

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