Package ‘SDMtune’

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Type  Package
Title  Species Distribution Model Selection
Version  1.1.6
Description  User-friendly framework that enables the training and the evaluation of species distribution models (SDMs). The package implements functions for data driven variable selection and model tuning and includes numerous utilities to display the results. All the functions used to select variables or to tune model hyperparameters have an interactive real-time chart displayed in the 'RStudio' viewer pane during their execution.

License  GPL-3

BugReports  https://github.com/ConsBiol-unibern/SDMtune/issues

SystemRequirements  Java (>= 8) and maxent.jar >= 3.4.1 to use Maxent

Depends  R (>= 3.6.0)
Imports  dismo (>= 1.3-3), gbm (>= 2.1.5), ggplot2 (>= 3.3.1), jsonlite (>= 1.6), maxnet (>= 0.1.4), methods, nnet (>= 7.3-12), progress (>= 1.2.2), randomForest (>= 4.6-14), raster (>= 2.9-5), Rcpp (>= 1.0.1), rlang (>= 0.4.5), rstudioapi (>= 0.10), stringr (>= 1.4.0), whisker (>= 0.3-2)

Encoding  UTF-8
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VignetteBuilder knitr

Collate 'ANN-class.R' 'BRT-class.R' 'Maxent-class.R' 'Maxnet-class.R'
  'RF-class.R' 'RcppExports.R' 'SWD-class.R' 'SDMmodel-class.R'
  'SDMmodel2MaxEnt.R' 'SDMmodelCV-class.R' 'SDMtune-class.R'
  'SDMtune-package.R' 'addSamplesToBg.R' 'aicc.R' 'auc.R'
  'chart-utils.R' 'checkMaxentInstallation.R' 'confMatrix.R'
  'convertFolds.R' 'corVar.R' 'doJk.R' 'getTunableArgs.R'
  'gridSearch.R' 'maxentTh.R' 'maxentVarImp.R' 'mergeSWD.R'
  'modelReport.R' 'optimizeModel.R' 'plotCor.R' 'plotJk.R'
  'plotPA.R' 'plotPred.R' 'plotROC.R' 'plotResponse.R'
  'plotVarImp.R' 'predict-ANN.R' 'predict-BRT.R'
  'predict-Maxent.R' 'predict-RFR' 'predict-SDMmodel.R'
  'predict-SDMmodelCV.R' 'prepareSWD.R' 'randomFolds.R'
  'randomSearch.R' 'reduceVar.R' 'swd2csv.R' 'thinData.R'
  'thresholds.R' 'train.R' 'trainANN.R' 'trainBRT.R'
  'trainMaxent.R' 'trainMaxnet.R' 'trainRFR' 'trainValTest.R'
  'tss.R' 'utils.R' 'varImp.R' 'varSel.R' 'virtualSp.R' 'zzz.R'

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addSamplesToBg

Description

The function add the presence locations to the background. This is equivalent to the Maxent argument addsamplestobackground=true.

Usage

addSamplesToBg(x, all = FALSE)
Arguments

- **x**: SWD object.
- **all**: logical, if TRUE it adds all the presence locations even if already included in the background locations, default is FALSE. This is equivalent to the Maxent argument addallsamplestobackground=true.

Value

An object of class SWD.

Author(s)

Sergio Vignali

Examples

```r
# Acquire environmental variables
files <- list.files(pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bgs_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bgs_coords, env = predictors, categorical = "biome")

# Add presence locations with values not included in the background to the background locations
new_data <- addSamplesToBg(data)
new_data

# Add all the presence locations to the background locations, even if they have values already included in the background
new_data <- addSamplesToBg(data, all = TRUE)
new_data
```

Description

Compute the Akaike Information Criterion corrected for small samples size (Warren and Seifert, 2011).

Usage

```r
aicc(model, env)
```
Arguments

model  SDM model object.
env    stack containing the environmental variables.

Details

The function is available only for Maxent and Maxnet methods.

Value

The computed AICc

Author(s)

Sergio Vignali

References

Warren D.L., Seifert S.N., (2011). Ecological niche modeling in Maxent: the importance of
model complexity and the performance of model selection criteria. Ecological Applications, 21(2),
335–342.

See Also

auc and tss.

Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                     pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Train a model
model <- train(method = "Maxnet", data = data, fc = "1")

# Compute the AICc
aicc(model, predictors)
```
**ANN-class**  
*Artificial Neural Network*

**Description**

This Class represents an Artificial Neural Network model object and hosts all the information related to the model.

**Usage**

```r
## S4 method for signature 'ANN'
show(object)
```

**Arguments**

- `object`  
  ANN object

**Details**

See `nnet` for the meaning of the slots.

**Slots**

- `size`  
  integer. Number of the units in the hidden layer.
- `decay`  
  numeric. Weight decay.
- `rang`  
  numeric. Initial random weights.
- `maxit`  
  integer. Maximum number of iterations.
- `model`  
  `nnet`. The randomForest model object.

**Author(s)**

Sergio Vignali

---

**auc**  
*`AUC`*

**Description**

Compute the AUC using the Man-Whitney U Test formula.

**Usage**

```r
auc(model, test = NULL)
```
Arguments

model  An SDMmodel or SDMmodelCV object.
test   SWD object when model is an SDMmodel object; logical or SWD object when model is an SDMmodelCV object. If not provided it computes the training AUC, see details. Default is NULL.

Details

For SDMmodelCV objects, the function computes the mean of the training AUC values of the k-folds. If test = TRUE it computes the mean of the testing AUC values for the k-folds. If test is an SWD object, it computes the mean AUC values for the provided testing dataset.

Value

The value of the AUC.

Author(s)

Sergio Vignali

References


See Also

aicc and tss.

Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]
# Train a model
model <- train(method = "Maxnet", data = train, fc = "l")

# Compute the training AUC
auc(model)

# Compute the testing AUC
auc(model, test = test)

# Same example but using cross validation instead of training and testing datasets
# Create the folds
folds <- randomFolds(data, k = 4, only_presence = TRUE)
model <- train(method = "Maxnet", data = data, fc = "l", folds = folds)

# Compute the training AUC
auc(model)

# Compute the testing AUC
auc(model, test = TRUE)

# Compute the AUC for the held apart testing dataset
auc(model, test = test)

---

**BRT-class**

*Boosted Regression Tree*

**Description**

This Class represents a Boosted Regression Tree model objects and hosts all the information related to the model.

**Usage**

```r
## S4 method for signature 'BRT'
show(object)
```

**Arguments**

- `object` BRT object

**Details**

See `gbm` for the meaning of the slots.
checkMaxentInstallation

Slots

distribution character. Name of the used distribution.
n.trees integer. Maximum number of grown trees.
interaction.depth integer. Maximum depth of each tree.
brshrinkage numeric. The shrinkage parameter.
bag.fraction numeric. Random fraction of data used in the tree expansion.
model gbm. The Boosted Regression Tree model object.

Author(s)

Sergio Vignali

checkMaxentInstallation

Check Maxent Installation

Description

The function checks if Maxent is correctly installed.

Usage

checkMaxentInstallation(verbosr = TRUE)

Arguments

verbose logical, if TRUE the function provides useful messages to understand what is not correctly installed, default is TRUE.

Details

In order to have Maxent correctly configured is necessary that:

- Java is installed;
- the package "rJava" is installed;
- the file "maxent.jar" is in the correct folder.

Value

TRUE if Maxent is correctly installed, FALSE otherwise.

Author(s)

Sergio Vignali

Examples

checkMaxentInstallation()
Description

Computes Confusion Matrixes for threshold values varying from 0 to 1.

Usage

```r
confMatrix(model, test = NULL, th = NULL, type = NULL)
```

Arguments

- `model`: SDMmodel object.
- `test`: SWD testing locations, if not provided it uses the training dataset, default is `NULL`.
- `th`: numeric vector, if provided it computes the evaluation at the given thresholds, default is `NULL` and it computes the evaluation for the unique predicted values at presence and absence/background locations.
- `type`: character. The output type used for "Maxent" and "Maxnet" methods, possible values are "cloglog" and "logistic", default is `NULL`.

Details

- For models trained with the `Maxent` method the argument `type` can be: "raw", "logistic" and "cloglog".
- For models trained with the `Maxnet` method the argument `type` can be: "link", "exponential", "logistic" and "cloglog", see `maxnet` for more details.

Value

The Confusion Matrix for all the used thresholds.

Author(s)

Sergio Vignali

Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                     pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
b_p_coords <- virtualSp$background
```
# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                  env = predictors, categorical = "biome")

# Train a model
model <- train(method = "Maxnet", data = data, fc = "l")

# Get the confusion matrix for thresholds ranging from 0 to 1
cm <- confMatrix(model, type = "cloglog")
head(cm)
tail(cm)

# Get the confusion matrix for a specific threshold
confMatrix(model, type = "logistic", th = 0.6)

---

**corVar**  
*Print Correlated Variables*

**Description**

Utility that prints the name of correlated variables and the relative correlation coefficient value.

**Usage**

```r
corVar(
  bg,  
  method = "spearman",  
  cor_th = NULL,  
  order = TRUE,  
  remove_diagonal = TRUE
)
```

**Arguments**

- **bg**  
  SWD object with the locations used to compute the correlation between environmental variables.

- **method**  
  character. The method used to compute the correlation matrix, default is spearman.

- **cor_th**  
  numeric. If provided it prints only the variables whose correlation coefficient is higher or lower than the given threshold, default is NULL.

- **order**  
  logical, if TRUE the variable are ordered from the most to the less highly correlated, default is TRUE.

- **remove_diagonal**  
  logical, if TRUE the values in the diagonal are, removed, default is TRUE.

**Value**

The name of the correlated variables.
Author(s)
Sergio Vignali

Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare background locations
bg_coords <- dismo::randomPoints(predictors, 10000)

# Create SWD object
bg <- prepareSWD(species = "Virtual species", a = bg_coords,
                  env = predictors, categorical = "biome")

# Get the correlation among all the environmental variables
corVar(bg, method = "spearman")

# Get the environmental variables that have a correlation greater or equal to
# the given threshold
corVar(bg, method = "pearson", cor_th = 0.8)

---

**doJk**

*Jackknife Test*

Description

Run the Jackknife test for variable importance removing one variable at time.

**Usage**

```r
doJk(model = , metric = , variables = NULL, test = NULL, with_only = TRUE, env = NULL, return_models = FALSE)
```

**Arguments**

- **model**: SDMmodel or SDMmodelCV object.
- **metric**: character. The metric used to evaluate the models, possible values are: "auc", "tss" and "aicc".
doJk

variables vector. Variables used for the test, if not provided it takes all the variables used to train the model, default is NULL.

test SWD. If provided it reports the result also for the testing dataset. Not used for aicc and SDMmodelCV.

with_only logical. If TRUE it runs the test also for each variable in isolation, default is TRUE.

env stack containing the environmental variables, used only with "aicc", default is NULL.

return_models logical, if TRUE returns all the models together with the test result, default is FALSE.

Value

A data frame with the test results. If return_model = TRUE it returns a list containing the test results together with the models.

Author(s)

Sergio Vignali

Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                   pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "lq")

# Execute the Jackknife test only for the environmental variables "bio1" and # "bio12", using the metric AUC
doJk(model, metric = "auc", variables = c("bio1", "bio12"), test = test)

# Execute the Jackknife test only for the environmental variables "bio1" and # "bio12", using the metric TSS but without running the test for one single # variable
getTunableArgs

Get Tunable Arguments

Description

Returns the name of all function arguments that can be tuned for a given model.

Usage

getTunableArgs(model)

Arguments

model SDMmodel or SDMmodelCV object.

Value

character vector.

Author(s)

Sergio Vignali

Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                   pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background
# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                     env = predictors, categorical = "biome")

# Train a Maxnet model and get tunable hyperparameters
model <- train(method = "Maxnet", data = data, fc = "1")
getTunableArgs(model)

gridSearch | Grid Search

Description
Given a set of possible hyperparameter values, the function trains models with all the possible combinations of hyperparameters.

Usage
gridSearch(model, hypers, metric, test = NULL, env = NULL, save_models = TRUE)

Arguments
- **model**: SDMmodel or SDMmodelCV object.
- **hypers**: named list containing the values of the hyperparameters that should be tuned, see details.
- **metric**: character. The metric used to evaluate the models, possible values are: "auc", "tss" and "aicc".
- **test**: SWD object. Testing dataset used to evaluate the model, not used with aicc and SDMmodelCV objects, default is NULL.
- **env**: stack containing the environmental variables, used only with "aicc", default is NULL.
- **save_models**: logical, if FALSE the models are not saved and the output contains only a data frame with the metric values for each hyperparameter combination. Default is TRUE, set it to FALSE when there are many combinations to avoid R crashing for memory overload.

Details
- To know which hyperparameters can be tuned you can use the output of the function `getTunableArgs`. Hyperparameters not included in the `hypers` argument take the value that they have in the passed model.

Value
- SDMtune object.
gridSearch

Author(s)
Sergio Vignali

See Also
randomSearch and optimizeModel.

Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                  pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "l")

# Define the hyperparameters to test
h <- list(reg = 1:2, fc = c("lqp", "lqph"))

# Run the function using the AUC as metric
output <- gridSearch(model, hypers = h, metric = "auc", test = test)
output$results
output@models

# Order results by highest test AUC
head(output$results[order(-output$results$test_AUC), ])

# Run the function using the AICc as metric and without saving the trained models, helpful when numerous hyperparameters are tested to avoid memory problems
output <- gridSearch(model, hypers = h, metric = "aicc", env = predictors,
                     save_models = FALSE)
output$results
```
Maxent-class

Maxent-class

Description

This Class represents a MaxEnt model objects and hosts all the information related to the model.

Usage

## S4 method for signature 'Maxent'
show(object)

Arguments

object  Maxent object

Slots

results  matrix. The result that usually MaxEnt provide as a csv file.
reg  numeric. The value of the regularization multiplier used to train the model.
fc  character. The feature class combination used to train the model.
iter  numeric. The number of iterations used to train the model.
extra_args  character. Extra arguments used to run MaxEnt.
lambdas  vector. The lambdas parameters of the model.
coeff  data.frame. The lambda coefficients of the model.
formula  formula. The formula used to make prediction.
lpn  numeric. Linear Predictor Normalizer.
dn  numeric. Density Normalizer.
entropy  numeric. The entropy value.
min_max  data.frame. The minimum and maximum values of the continuous variables, used for clamping.

Author(s)

Sergio Vignali
maxentTh  

**MaxEnt Thresholds**

**Description**

Returns the value of the thresholds generated by the MaxEnt software.

**Usage**

```r
maxentTh(model)
```

**Arguments**

- `model`  
  SDMmodel object trained using the "Maxent" method.

**Value**

data.frame with the thresholds.

**Author(s)**

Sergio Vignali

**See Also**

maxentVarImp.

**Examples**

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Train a Maxent model
# The next line checks if Maxent is correctly configured but you don't need
# to run it in your script
if (dismo::maxent(silent = TRUE)) {
  model <- train(method = "Maxent", data = data, fc = "l")
  maxentTh(model)
}
```
maxentVarImp

Maxent Variable Importance

Description
Shows the percent contribution and permutation importance of the environmental variables used to train the model.

Usage
maxentVarImp(model)

Arguments
model SDMmodel or SDMmodelCV object trained using the "Maxent" method.

Details
When an SDMmodelCV object is passed to the function, the output is the average of the variable importance of each model trained during the cross validation.

Value
A data frame with the variable importance.

Author(s)
Sergio Vignali

See Also
maxentTh.

Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p.coords <- virtualSp$presence
bg.coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p.coords, a = bg.coords,
env = predictors, categorical = "biome")

# Train a Maxent model
# The next line checks if Maxent is correctly configured but you don't need
# to run it in your script
if (dismo::maxent(silent = TRUE)) {
  model <- train(method = "Maxent", data = data, fc = "1")
  maxentVarImp(model)
}

Maxnet-class

Description

This Class represents a Maxnet model objects and hosts all the information related to the model.

Usage

## S4 method for signature 'Maxnet'
show(object)

Arguments

| object | Maxnet object |

Slots

- reg  numeric. The value of the regularization multiplier used to train the model.
- fc  character. The feature class combination used to train the model.
- model  maxnet. The maxnet model object.

Author(s)

Sergio Vignali
mergeSWD

**Merge SWD Objects**

**Description**

Merge two SWD objects.

**Usage**

```r
mergeSWD(swd1, swd2, only_presence = FALSE)
```

**Arguments**

- `swd1`: SWD object.
- `swd2`: SWD object.
- `only_presence`: logical, if `TRUE` only for the presence locations are merged and the absence/background locations are taken only from the `swd1` object, default is `FALSE`.

**Details**

- In case the two SWD objects have different columns, only the common columns are used in the merged object.
- The SWD object is created in a way that the presence locations are always before than the absence/background locations.

**Value**

The merged SWD object.

**Author(s)**

Sergio Vignali

**Examples**

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
gc_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = gc_coords,
                   env = predictors, categorical = "biome")
```
# Split only presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Merge the training and the testing datasets together
merged <- mergeSWD(train, test, only_presence = TRUE)

# Split presence and absence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2)
train <- datasets[[1]]
test <- datasets[[2]]

# Merge the training and the testing datasets together
merged <- mergeSWD(train, test)

---

## modelReport

### Model Report

#### Description

Make a report that shows the main results.

#### Usage

```r
modelReport(
  model,
  folder,
  test = NULL,
  type = NULL,
  response_curves = FALSE,
  only_presence = FALSE,
  jk = FALSE,
  env = NULL,
  clamp = TRUE,
  permut = 10,
  factors = NULL
)
```

#### Arguments

- **model**: SDMmodel object.
- **folder**: character. The name of the folder in which to save the output. The folder is created in the working directory.
- **test**: SWD object with the test locations, default is NULL.
- **type**: character. The output type used for "Maxent" and "Maxnet" methods, possible values are "cloglog" and "logistic", default is NULL.
response_curves

logical, if TRUE it plots the response curves in the html output, default is FALSE.

only_presence

logical, if TRUE it uses only the range of the presence location for the marginal response, default is FALSE.

jk

logical, if TRUE it runs the jackknife test, default is FALSE.

env

stack. If provided it computes and adds a prediction map to the output, default is NULL.

clamp

logical for clumping during prediction, used for response curves and for the prediction map, default is TRUE.

permut

integer. Number of permutations, default is 10.

factors

list with levels for factor variables, see predict

Details

The function produces a report similar to the one created by MaxEnt software.

Author(s)

Sergio Vignali

Examples

# If you run the following examples with the function example(), you may want # to set the argument ask like following: example("modelReport", ask = FALSE)
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
  pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords, 
  env = predictors, categorical = "biome")

datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "lq")

# Create the report
# Not run:
modelReport(model, type = "cloglog", folder = "my_folder", test = test, 
  response_curves = TRUE, only_presence = TRUE, jk = TRUE,
The function uses a Genetic Algorithm implementation to optimize the model hyperparameter configuration according to the chosen metric.

**Usage**

```r
optimizeModel(
  model,
  hypers,
  metric,
  test = NULL,
  pop = 20,
  gen = 5,
  env = NULL,
  keep_best = 0.4,
  keep_random = 0.2,
  mutation_chance = 0.4,
  seed = NULL
)
```

**Arguments**

- `model` 
  SDMmodel or SDMmodelCV object.
- `hypers` 
  named list containing the values of the hyperparameters that should be tuned, see details.
- `metric` 
  character. The metric used to evaluate the models, possible values are: "auc", "tss" and "aicc".
- `test` 
  SWD object. Testing dataset used to evaluate the model, not used with aicc and SDMmodelCV objects, default is NULL.
- `pop` 
  numeric. Size of the population, default is 5.
- `gen` 
  numeric. Number of generations, default is 20.
- `env` 
  stack containing the environmental variables, used only with "aicc", default is NULL.
- `keep_best` 
  numeric. Percentage of the best models in the population to be retained during each iteration, expressed as decimal number. Default is 0.4.
keep_random  numeric. Probability of retaining the excluded models during each iteration, expressed as decimal number. Default is 0.2.

mutation_chance numeric. Probability of mutation of the child models, expressed as decimal number. Default is 0.4.

seed numeric. The value used to set the seed to have consistent results, default is NULL.

Details

To know which hyperparameters can be tuned you can use the output of the function getTunableArgs. Hyperparameters not included in the hypers argument take the value that they have in the passed model.

- Part of the code is inspired by this post.

Value

SDMtune object.

Author(s)

Sergio Vignali

See Also

gridSearch and randomSearch.

Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"), pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords, env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, val = 0.2, test = 0.2, only_presence = TRUE, seed = 61516)

train <- datasets[[1]]
val <- datasets[[2]]

# Train a model
model <- train("Maxnet", data = train)

# Define the hyperparameters to test
h <- list(reg = seq(0.2, 5, 0.2),
         fc = c("l", "lq", "lh", "lp", "lqp", "lqph"))

# Run the function using as metric the AUC
## Not run:
output <- optimizeModel(model, hypers = h, metric = "auc", test = val,
                        pop = 15, gen = 2, seed = 798)
output@results
output@models
output@models[[1]] # Best model
## End(Not run)

---

**plotCor**  
*Plot Correlation*

**Description**

Plot a correlation matrix heat map with the value of the correlation coefficients according with the given method. If cor_th is passed then it prints only the coefficients that are higher or lower than the given threshold.

**Usage**

```r
plotCor(bg, method = "spearman", cor_th = NULL)
```

**Arguments**

- `bg` *SWD object used to compute the correlation matrix.*
- `method` character. The method used to compute the correlation matrix, default is "spearman".
- `cor_th` numeric. If provided it prints only the coefficients that are higher or lower than the given threshold, default is NULL.

**Value**

A **ggplot** object.

**Author(s)**

Sergio Vignali
Examples

```r
# Acquire environmental variables
glob <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                   pattern = "grd", full.names = TRUE)
predictors <- raster::stack(glob)

# Prepare background locations
bg_coords <- dismo::randomPoints(predictors, 10000)

# Create SWD object
bg <- prepareSWD(species = "Virtual species", a = bg_coords,
                  env = predictors, categorical = "biome")

# Plot heat map
plotCor(bg, method = "spearman")

# Plot heat map showing only values higher than given threshold
plotCor(bg, method = "spearman", cor_th = 0.8)
```

---

**plotJk**

*Plot Jackknife Test*

**Description**

Plot the Jackknife Test for variable importance.

**Usage**

```r
plotJk(jk, type = c("train", "test"), ref = NULL)
```

**Arguments**

- **jk**
  - data.frame with the output of the `doJk` function.
- **type**
  - character, "train" or "test" to plot the result of the test on the train or testing dataset.
- **ref**
  - numeric. The value of the chosen metric for the model trained using all the variables. If provided it plots a vertical line showing the reference value. Default is `NULL`.

**Value**

A `ggplot` object.

**Author(s)**

Sergio Vignali
Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                   pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "lq")

# Execute the Jackknife test for all the environmental variables using the
# metric AUC
jk <- doJk(model, metric = "auc", test = test)

# Plot Jackknife test result for training
plotJk(jk, type = "train", ref = auc(model))

# Plot Jackknife test result for testing
plotJk(jk, type = "test", ref = auc(model, test = test))

plotPA

Plot Presence Absence Map

Description

Plot a presence absence map using the given threshold.

Usage

plotPA(
  map,
  th,
  colors = NULL,
  hr = FALSE,
  filename = NULL,
Arguments

- **map**: raster object with the prediction.
- **th**: numeric. The threshold used to convert the output in a presence/absence map.
- **colors**: vector. Colors to be used, default is NULL and uses red and blue.
- **hr**: logical, if TRUE produces an output with high resolution, default is FALSE.
- **filename**: character, if provided the raster map is saved in a file, default is NULL.
- **format**: character. The output format, see writeRaster for all the options, default is Geo-tiff.

... Additional arguments, see writeRaster for all the options.

Value

A ggplot object.

Author(s)

Sergio Vignali

See Also

plotPred.

Examples

```r
map <- raster::raster(matrix(runif(400, 0, 1), 20, 20))
plotPA(map, th = 0.8)
# Custom colors
plotPA(map, th = 0.5, colors = c("#d8b365", "#018571"))
# Save the file
## Not run:
# The following command will save the map in the working directory
plotPA(map, th = 0.7, filename = "my_map", format = "ascii")
## End(Not run)
```
plotPred

Plot Prediction

Description

Plot Prediction output.

Usage

plotPred(map, lt = "", colorramp = NULL, hr = FALSE)

Arguments

map 
  raster object with the prediction.
lt 
  character. Legend title, default is an empty string.
colorramp 
  vector. A custom color ramp given as a vector of colors (see example), default is NULL and uses a blue/red color ramp.
hr 
  logical, if TRUE produces an output with high resolution, default is FALSE.

Value

A ggplot object.

Author(s)

Sergio Vignali

See Also

plotPA.

Examples

map <- raster::raster(matrix(runif(400, 0, 1), 20, 20))
plotPred(map, lt = "Habitat suitability \n\ncloglog")
# Custom colors
plotPred(map, lt = "Habitat suitability",
  colorramp = c("#2c7bb6", "#ffffff", 
    "#d7191c"))
plotResponse

Plot Response Curve

Description
Plot the Response Curve of the given environmental variable.

Usage
plotResponse(
  model, 
  var, 
  type = NULL, 
  only_presence = FALSE, 
  marginal = FALSE, 
  fun = mean, 
  rug = FALSE, 
  color = "red"
)

Arguments
model 
SDMmodel or SDMmodelCV object.

var 
character. Name of the variable to be plotted.

type 
character. The output type used for "Maxent" and "Maxnet" methods, possible values are "cloglog" and "logistic", default is NULL.

only_presence 
logical, if TRUE it uses only the presence locations when applying the function for the marginal response, default is FALSE.

marginal 
logical, if TRUE it plots the marginal response curve, default is FALSE.

fun 
function used to compute the level of the other variables for marginal curves, default is mean.

rug 
logical, if TRUE it adds the rug plot for the presence and absence/background locations, available only for continuous variables, default is FALSE.

color 
The color of the curve, default is "red".

Details
Note that fun is not a character argument, you must use mean and not "mean".

Value
A ggplot object.

Author(s)
Sergio Vignali
Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                   pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Train a model
model <- train(method = "Maxnet", data = data, fc = "lq")

# Plot cloglog response curve for a continuous environmental variable (bio1)
plotResponse(model, var = "bio1", type = "cloglog")

# Plot marginal cloglog response curve for a continuous environmental variable (bio1)
plotResponse(model, var = "bio1", type = "cloglog", marginal = TRUE)

# Plot logistic response curve for a continuous environmental variable (bio12) adding the rugs and giving a custom color
plotResponse(model, var = "bio12", type = "logistic", rug = TRUE,
             color = "blue")

# Plot response curve for a categorical environmental variable (biome) giving a custom color
plotResponse(model, var = "biome", type = "logistic", color = "green")

# Train a model with cross validation
folds <- randomFolds(data, k = 4, only_presence = TRUE)
model <- train(method = "Maxnet", data = data, fc = "lq", folds = folds)

# Plot cloglog response curve for a continuous environmental variable (bio17)
plotResponse(model, var = "bio1", type = "cloglog")

# Plot logistic response curve for a categorical environmental variable (biome) giving a custom color
plotResponse(model, var = "biome", type = "logistic", color = "green")

---

plotROC

Plot ROC curve
Description

Plot the ROC curve of the given model and print the AUC value.

Usage

```r
plotROC(model, test = NULL)
```

Arguments

- `model` SDMmodel object.
- `test` SWD object. The testing dataset, default is NULL.

Value

A ggplot object.

Author(s)

Sergio Vignali

Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "1")

# Plot the training ROC curve
plotROC(model)

# Plot the training and testing ROC curves
plotROC(model, test = test)
```
plotVarImp

<table>
<thead>
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<td>Plot the variable importance as a bar plot.</td>
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<td>plotVarImp(df, color = &quot;grey&quot;)</td>
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<td>A ggplot object.</td>
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<tr>
<th>Author(s)</th>
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<tr>
<td>Sergio Vignali</td>
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<table>
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<tr>
<th>Examples</th>
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<tbody>
<tr>
<td># Acquire environmental variables</td>
</tr>
<tr>
<td>files &lt;- list.files(path = file.path(system.file(package = &quot;dismo&quot;), &quot;ex&quot;), pattern = &quot;grd&quot;, full.names = TRUE)</td>
</tr>
<tr>
<td>predictors &lt;- raster::stack(files)</td>
</tr>
</tbody>
</table>

| # Prepare presence and background locations |
| p.coords <- virtualSp$presence |
| bg.coords <- virtualSp$background |

| # Create SWD object |
| data <- prepareSWD(species = "Virtual species", p = p.coords, a = bg.coords, env = predictors, categorical = "biome") |

| # Train a model |
| model <- train(method = "Maxnet", data = data, fc = "l") |

| # Compute variable importance |
| vi <- varImp(model, permut = 1) |

| # Plot variable importance |
| plotVarImp(vi) |
# Predict ANN

## Description

Predict the output for a new dataset from a trained ANN model.

## Usage

```r
## S4 method for signature 'ANN'
predict(object, data, type, clamp)
```

## Arguments

- `object`: ANN object.
- `data`: data.frame with the data for the prediction.
- `type`: Not used.
- `clamp`: Not used.

## Details

Used by the `predict.SDMmodel-method`, not exported.

## Value

A vector with the predicted values.

## Author(s)

Sergio Vignali
**predict,BRT-method  Predict BRT**

**Description**

Predict the output for a new dataset from a trained BRT model.

**Usage**

```r
## S4 method for signature 'BRT'
predict(object, data, type, clamp)
```

**Arguments**

- `object`: BRT object.
- `data`: data.frame with the data for the prediction.
- `type`: Not used.
- `clamp`: Not used.

**Details**

Used by the `predict.SDMmodel-method`, not exported.

The function uses the number of tree defined to train the model and the "response" type output.

**Value**

A vector with the predicted values.

**Author(s)**

Sergio Vignali

---

**predict,Maxent-method  Predict Maxent**

**Description**

Predict the output for a new dataset from a trained Maxent model.

**Usage**

```r
## S4 method for signature 'Maxent'
predict(object, data, type = c("cloglog", "logistic", "raw"), clamp = TRUE)
```
Arguments

object: Maxent object.
data: data.frame with the data for the prediction.
type: character MaxEnt output type, possible values are "cloglog", "logistic" and "raw", default is "cloglog".
clamp: logical for clumping during prediction, default is TRUE.

Details

Used by the predict.SDMmodel-method, not exported.
The function performs the prediction in R without calling the MaxEnt Java software. This results in a faster computation for large datasets and might result in a slightly different output compared to the Java software.

Value

A vector with the prediction

Author(s)

Sergio Vignali

References


Description

Predict the output for a new dataset from a trained RF model.

Usage

```r
## S4 method for signature 'RF'
predict(object, data, type, clamp)
```

Arguments

object: RF object.
data: data.frame with the data for the prediction.
type: Not used.
clamp: Not used.
predict,SDMmodel-method

Details
Used by the predict,SDMmodel-method, not exported.

Value
A vector with the predicted probabilities of class 1.

Author(s)
Sergio Vignali

Description
Predict the output for a new dataset given a trained SDMmodel model.

Usage
```r
## S4 method for signature 'SDMmodel'
predict(
  object,
  data,
  type = NULL,
  clamp = TRUE,
  filename = "",
  format = "GTiff",
  extent = NULL,
  progress = "",
  ...)
```

Arguments
- `object`  SDMmodel object.
- `data`  data.frame, SWD or stack with the data for the prediction.
- `type`  character. Output type, see details, used only for Maxent and Maxnet methods, default is NULL.
- `clamp`  logical for clumping during prediction, used only for Maxent and Maxnet methods, default is TRUE.
- `filename`  character. Output file name for the prediction map, used only when data is a stack object. If provided the output is saved in a file.
- `format`  character. The output format, see writeRaster for all the options, default is "GTiff".
extent object, if provided it restricts the prediction to the given extent, default is NULL.

progress character to display a progress bar: "text", "window" or "" (default) for no progress bar.

... Additional arguments to pass to the writeRaster function.

Details

- filename, format, extent, progress, and ... are arguments used only when the prediction is done for a stack object.
- For models trained with the Maxent method the argument type can be: "raw", "logistic" and "cloglog". The function performs the prediction in R without calling the MaxEnt Java software. This results in a faster computation for large datasets and might result in a slightly different output compared to the Java software.
- For models trained with the Maxnet method the argument type can be: "link", "exponential", "logistic" and "cloglog", see maxnet for more details.
- For models trained with the ANN method the function uses the "raw" output type.
- For models trained with the RF method the output is the probability of class 1.
- For models trained with the BRT method the function uses the number of trees defined to train the model and the "response" output type.

Value

A vector with the prediction or a raster object if data is a raster stack.

Author(s)

Sergio Vignali

References


Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                    env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
```
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "l")

# Make cloglog prediction for the test dataset
predict(model, data = test, type = "cloglog")

# Make logistic prediction for the all study area
predict(model, data = predictors, type = "logistic")

## Not run:
# Make logistic prediction for the all study area and save it in a file
# The function saves the file in your working directory
predict(model, data = predictors, type = "logistic", filename = "my_map")

## End(Not run)

predict,SDMmodelCV-method

Predict for Cross Validation

Description

Predict the output for a new dataset given a trained SDMmodelCV model. The output is given as the provided function applied to the prediction of the k models.

Usage

## S4 method for signature 'SDMmodelCV'
predict(
  object, 
  data, 
  fun = "mean", 
  type = NULL, 
  clamp = TRUE, 
  filename = "", 
  format = "GTiff", 
  extent = NULL, 
  ... 
)

Arguments

object SDMmodelCV object.
data data.frame, SWD or raster stack with the data for the prediction.
fun  character. function used to combine the output of the k models, default is "mean". Note that fun is a character argument, you must use "mean" and not mean. You can also pass a vector of character containing multiple function names, see details.

type  character. Output type, see details, used only for Maxent and Maxnet methods, default is NULL.

clamp  logical for clumping during prediction, used only for Maxent and Maxnet methods, default is TRUE.

filename  character. Output file name for the prediction map, used only when data is a stack object. If provided the output is saved in a file, see details.

format  character. The output format, see writeRaster for all the options, default is "GTiff".

extent  extent object, if provided it restricts the prediction to the given extent, default is NULL.

...  Additional arguments to pass to the writeRaster function.

Details

- filename, format, extent, and ... arguments are used only when the prediction is done for a stack object.
- When a character vector is passed to the fun argument, than all the given functions are applied and a named list is returned, see examples.
- When filename is provided and the fun argument contains more than one function name, the saved files are named as filename_fun, see example.
- For models trained with the Maxent method the argument type can be: "raw", "logistic" and "cloglog". The function performs the prediction in R without calling the MaxEnt Java software. This results in a faster computation for large datasets and might result in a slightly different output compared to the Java software.
- For models trained with the Maxnet method the argument type can be: "link", "exponential", "logistic" and "cloglog", see maxnet for more details.
- For models trained with the ANN method the function uses the "raw" output type.
- For models trained with the RF method the output is the probability of class 1.
- For models trained with the BRT method the function uses the number of trees defined to train the model and the "response" output type.

Value

A vector with the prediction or a raster object if data is a raster stack or a list in the case of multiple functions.

Author(s)

Sergio Vignali
Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                  pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                  env = predictors, categorical = "biome")

# Create 4 random folds splitting only the presence data
folds <- randomFolds(data, k = 4, only_presence = TRUE)
model <- train(method = "Maxnet", data = data, fc = "l", folds = folds)

# Make cloglog prediction for the all study area and get the result as
# average of the k models
predict(model, data = predictors, fun = "mean", type = "cloglog")

# Make cloglog prediction for the all study area, get the average, standard
# deviation, and maximum values of the k models, and save the output in three
# files
## Not run:
# The following commands save the output in the working directory
maps <- predict(model, data = predictors, fun = c("mean", "sd", "max"),
                 type = "cloglog", filename = "prediction")
# In this case three files are created: prediction_mean.tif,
# prediction_sd.tif and prediction_max.tif
plotPred(maps$mean)
plotPred(maps$sd)
plotPred(maps$max)

# Make logistic prediction for the all study area, given as standard
# deviation of the k models, and save it in a file
predict(model, data = predictors, fun = "sd", type = "logistic",
         filename = "my_map")
## End(Not run)
```

References

prepareSWD

Prepare an SWD object

Description
Given the coordinates, the species' name and the environmental variables, the function creates an SWD object (sample with data).

Usage
prepareSWD(species, env, p = NULL, a = NULL, categorical = NULL)

Arguments
- `species` character. The name of the species.
- `env` stack containing the environmental variables used to extract the values at coordinate locations.
- `p` data.frame. The coordinates of the presence locations.
- `a` data.frame. The coordinates of the absence/background locations.
- `categorical` vector indicating which of the environmental variable are categorical, default is NULL.

Details
The SWD object is created in a way that the presence locations are always before than the absence/background locations.

Value
An SWD object.

Author(s)
Sergio Vignali

Examples
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                   pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create the SWD object
randomFolds <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords, env = predictors, categorical = "biome")
data

randomFolds

Create Random Folds

Description
Create random folds for cross validation.

Usage
randomFolds(data, k, only_presence = FALSE, seed = NULL)

Arguments
- data: SWD object that will be used to train the model.
- k: integer. Number of fold used to create the partition.
- only_presence: logical. If TRUE the random folds are created only for the presence locations and all the background locations are included in each fold, used mainly for presence-only methods, default is FALSE.
- seed: integer. The value used to set the seed for the fold partition, default is NULL.

Details
When only_presence = FALSE, the proportion of presence and absence is preserved.

Value
list with two matrices, the first for the training and the second for the testing dataset. Each column of one matrix represents a fold with TRUE for the locations included in and FALSE excluded from the partition.

Author(s)
Sergio Vignali

Examples
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"), pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords, 
eenv = predictors, categorical = "biome")

# Create 4 random folds splitting presence and absence locations
folds <- randomFolds(data, k = 4)

# Create 4 random folds splitting only the presence locations
folds <- randomFolds(data, k = 4, only_presence = TRUE)

randomSearch

**Random Search**

**Description**

The function performs a random search in the hyperparameters space, creating a population of random models each one with a random combination of the provided hyperparameters values.

**Usage**

```r
randomSearch(
  model, 
  hypers, 
  metric, 
  test = NULL, 
  pop = 20, 
  env = NULL, 
  seed = NULL
)
```

**Arguments**

- **model**: `SDMmodel` or `SDMmodelCV` object.
- **hypers**: named list containing the values of the hyperparameters that should be tuned, see details.
- **metric**: character. The metric used to evaluate the models, possible values are: "auc", "tss" and "aicc".
- **test**: `SWD` object. Test dataset used to evaluate the model, not used with aicc and `SDMmodelCV` objects, default is NULL.
- **pop**: numeric. Size of the population, default is 20.
- **env**: stack containing the environmental variables, used only with "aicc", default is NULL.
- **seed**: numeric. The value used to set the seed to have consistent results, default is NULL.
Details

- To know which hyperparameters can be tuned you can use the output of the function getTunableArgs. Hyperparameters not included in the hypers argument take the value that they have in the passed model.

Value

SDMtune object.

Author(s)

Sergio Vignali

Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                   pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                    env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
data <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- data[[1]]
test <- data[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "l")

# Define the hyperparameters to test
h <- list(reg = seq(0.2, 3, 0.2), fc = c("lqp", "1qph", "1h"))

# Run the function using as metric the AUC
output <- randomSearch(model, hypers = h, metric = "auc", test = test,
                        pop = 10, seed = 25)

# Order results by highest test AUC
output@results[order(-output@results@test_AUC),]
```
Reduce Variables

Description

Remove variables whose importance is less than the given threshold. The function removes one variable at time and after trains a new model to get the new variable contribution rank. If use_jk is TRUE the function checks if after removing the variable the model performance decreases (according to the given metric and based on the starting model). In this case the function stops removing the variable even if the contribution is lower than the given threshold.

Usage

```r
reduceVar(
  model, 
  th, 
  metric, 
  test = NULL, 
  env = NULL, 
  use_jk = FALSE, 
  permut = 10, 
  use_pc = FALSE
)
```

Arguments

- **model**: SDMmodel or SDMmodelCV object.
- **th**: numeric. The contribution threshold used to remove variables.
- **metric**: character. The metric used to evaluate the models, possible values are: "auc", "tss" and "aicc", used only if use_jk is TRUE.
- **test**: SWD object containing the test dataset used to evaluate the model, not used with aicc, and if use_jk = FALSE, default is NULL.
- **env**: stack containing the environmental variables, used only with "aicc", default is NULL.
- **use_jk**: Flag to use the Jackknife AUC test during the variable selection, if FALSE the function uses the percent variable contribution, default is FALSE.
- **permut**: integer. Number of permutations, used if use_pc = FALSE, default is 10.
- **use_pc**: logical, use percent contribution. If TRUE and the model is trained using the Maxent method, the algorithm uses the percent contribution computed by Maxent software to score the variable importance, default is FALSE.

Value

The model trained using the selected variables.
reduceVar

Author(s)
Sergio Vignali

Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                   pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a Maxnet model
model <- train(method = "Maxnet", data = train, fc = "lq")

# Remove all variables with permutation importance lower than 2%
output <- reduceVar(model, th = 2, metric = "auc", test = test, permut = 1)

# Remove variables with permutation importance lower than 2% only if testing
# TSS doesn’t decrease
## Not run:
output <- reduceVar(model, th = 2, metric = "tss", test = test, permut = 1,
                    use_jk = TRUE)

# Remove variables with permutation importance lower than 2% only if AICc
# doesn’t increase
output <- reduceVar(model, th = 2, metric = "aicc", permut = 1,
                    use_jk = TRUE, env = predictors)

# Train a Maxent model
# The next line checks if Maxent is correctly configured but you don’t need
# to run it in your script
if (dismo::maxent(silent = TRUE)) {
  model <- train(method = "Maxent", data = train, fc = "lq")
}

# Remove all variables with percent contribution lower than 2%
output <- reduceVar(model, th = 2, metric = "auc", test = test,
                    use_pc = TRUE)
Description

This Class represents a Random Forest model objects and hosts all the information related to the model.

Usage

```r
## S4 method for signature 'RF'
show(object)
```

Arguments

- `object` RF object

Details

See `randomForest` for the meaning of the slots.

Slots

- `mtry` integer. Number of variable randomly sampled.
- `ntree` integer. Number of grown trees.
- `nodesize` integer. Minimum size of terminal nodes.
- `model` `randomForest`. The randomForest model object.

Author(s)

Sergio Vignali
SDMmodel-class  

**Description**

This Class represents an SDMmodel object and hosts all the information related to the model.

**Usage**

```r
## S4 method for signature 'SDMmodel'
show(object)
```

**Arguments**

- `object`  
  SDMmodel object

**Slots**

- `data`  
  SWD object. The data used to train the model.
- `model`  
  An object of class ANN, BRT, RF, Maxent or Maxnet.

**Author(s)**

Sergio Vignali

---

SDMmodel2MaxEnt  

**Description**

Converts an SDMmodel object containing a Maxent model into a dismo MaxEnt object.

**Usage**

```r
SDMmodel2MaxEnt(model)
```

**Arguments**

- `model`  
  SDMmodel object to be converted.

**Value**

The converted dismo MaxEnt object.

**Author(s)**

Sergio Vignali
Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                   pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Train a Maxent model
# The next line checks if Maxent is correctly configured but you don’t need
# to run it in your script
if (dismo::maxent(silent = TRUE)) {
  model <- train(method = "Maxent", data = data, fc = "l")
  dismo_model <- SDMmodel2MaxEnt(model)
  dismo_model
}

SDMmodelCV-class

SDMmodelCV

Description

This Class represents an SDMmodel model object with replicates and hosts all the models trained
during the cross validation.

Usage

## S4 method for signature 'SDMmodelCV'
show(object)

Arguments

object SDMmodelCV object

Slots

models list. A list containing all the models trained during the cross validation.
data SWD object. Full dataset used to make the partitions.
folds list with two matrices, the first for the training and the second for the testing dataset. Each column of one matrix represents a fold with TRUE for the locations included in and FALSE excluded from the partition.

Author(s)
Sergio Vignali

---

SDMtune-class  SDMtune class

Description
Class used to save the results of one of the following functions: gridSearch, randomSearch or optimizeModel.
Plot an SDMtune object. Use the interactive argument to create an interactive chart.

Usage
```r
## S4 method for signature 'SDMtune'
show(object)

## S4 method for signature 'SDMtune,missing'
plot(x, title = "", interactive = FALSE)
```

Arguments
- `object`: SDMtune object
- `x`: SDMtune object.
- `title`: character. The title of the plot, by default is an empty string.
- `interactive`: logical, if TRUE plot an interactive chart, default is FALSE.

Value
If `interactive = FALSE` the function returns a `ggplot` object otherwise it returns an SDMtuneChart object that contains the path of the temporary folder where the necessary files to create the chart are saved. In both cases the objects are returned as invisible.

Slots
- `results`: data.frame. Results with the evaluation of the models.
- `models`: list. List of SDMmodel or SDMmodelCV objects.

Author(s)
Sergio Vignali
Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                  pattern = "grd", full.names = TRUE)
names <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "l")

# Define the hyperparameters to test
h <- list(reg = 1:5, fc = c("lq", "lqph"))

# Run the gridSearch function using as metric the AUC
output <- gridSearch(model, hypers = h, metric = "auc", test = test)

# Plot the output
plot(output, title = "My experiment")

# Plot the interactive chart
p <- plot(output, title = "My experiment", interactive = TRUE)

# Print the temporary folder that stores the files used to create the chart
str(p)

---

**SWD-class**

**Sample With Data**

**Description**

Object similar to the MaxEnt SWD format that hosts the species name, the coordinates of the locations and the value of the environmental variables at the location places.

**Usage**

```r
## S4 method for signature 'SWD'
show(object)
```
Arguments

object  SWD object

Details

The object can contain presence/absence, presence/background, presence only or absence/background only data. Use the `prepareSWD` function to create the object.

Slots

- species  character. Name of the species.
- coords  data.frame. Coordinates of the locations.
- data  data.frame. Value of the environmental variables at location sites.
- pa  numeric. Vector with 1 for presence and 0 for absence/background locations.

Author(s)

Sergio Vignali

---

**swd2csv**

*SWD to csv*

Description

Save an SWD object as csv file.

Usage

`swd2csv(swd, file_name)`

Arguments

- `swd`  SWD object.
- `file_name`  character. The name of the file in which to save the object, see details.

Details

- The `file_name` argument should include the extension (i.e. my_file.csv).
- If `file_name` is a single name the function saves the presence absence/background locations in a single file, adding the column `pa` with 1s for presence and 0s for absence/background locations. If `file_name` is a vector with two names, it saves the object in two files: the first name is used for the presence locations and the second for the absence/background locations.

Author(s)

Sergio Vignali
Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p.coords <- virtualSp$presence
bg.coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p.coords, a = bg.coords,
                  env = predictors, categorical = "biome")

## Not run:
# The following commands save the output in the working directory
# Save the SWD object as a single csv file
swd2csv(data, "train_data.csv")

# Save the SWD object in two separate csv files
swd2csv(data, c("presence.csv", "absence.csv"))

## End(Not run)

---

**thinData**

**Thin Data**

Description

Remove all but one location per raster cell. The function removes NAs and if more than one location falls within the same raster cell it selects randomly one.

Usage

```
thinData(coords, env, x = "x", y = "y")
```

Arguments

- **coords**: data.frame or matrix with the coordinates, see details.
- **env**: stack containing the environmental variables, or a single raster layer.
- **x**: character. Name of the column containing the x coordinates, default is "x".
- **y**: character. Name of the column containing the y coordinates, default is "y".
Details

- `coords` and `env` must have the same coordinate reference system.
- The `coords` argument can contain several columns. This is useful if the user has information related to the coordinates that doesn't want to loose with the thinning procedure. The function expects to have the x coordinates in a column named "x", and the y coordinates in a column named "y". If this is not the case, the name of the columns containing the coordinates can be specified using the arguments `x` and `y`.

Value

A matrix or a data frame with the thinned locations.

Author(s)

Sergio Vignali

Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                  pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare background locations
bg_coords <- dismo::randomPoints(predictors, 9000)
nrow(bg_coords)

# Thin the locations
# There are probably few coordinates that have NAs for some predictors, the
# function will remove these coordinates. Note that the function expects to
# the coordinates in two column named "x" and "y"
colnames(bg_coords)
thinned_bg <- thinData(bg_coords, env = predictors)
nrow(thinned_bg)

# Here we double the coordinates and run the function again
thinned_bg <- thinData(rbind(bg_coords, bg_coords), env = predictors)
nrow(thinned_bg)

# In case of a dataframe containing more than two columns (e.g. a dataframe
# with the coordinates plus an additional column with the age of the species)
# and custom column names, use the function in this way
age <- sample(c(1, 2), size = nrow(bg_coords), replace = TRUE)
data <- cbind(age, bg_coords)
colnames(data) <- c("age", "X", "Y")
thinned_bg <- thinData(data, env = predictors, x = "X", y = "Y")
head(data)
```
**thresholds**  

**Thresholds**

**Description**

Compute three threshold values: minimum training presence, equal training sensitivity and specificity and maximum training sensitivity plus specificity together with fractional predicted area and the omission rate. If a test dataset is provided it returns also the equal test sensitivity and specificity and maximum test sensitivity plus specificity thresholds and the p-values of the one-tailed binomial exact test.

**Usage**

thresholds(model, type = NULL, test = NULL)

**Arguments**

- **model**: `SDMmodel` object.
- **type**: character. The output type used for "Maxent" and "Maxnet" methods, possible values are "cloglog" and "logistic", default is `NULL`.
- **test**: `SWD` testing locations, if not provided it returns the training and test thresholds, default is `NULL`.

**Details**

The equal training sensitivity and specificity minimizes the difference between sensitivity and specificity. The one-tailed binomial test checks that test points are predicted no better than by a random prediction with the same fractional predicted area.

**Value**

data.frame with the thresholds.

**Author(s)**

Sergio Vignali

**Examples**

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background
# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,  
env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "l")

# Get the cloglog thresholds
thresholds(model, type = "cloglog")

# Get the logistic thresholds passing the test dataset
thresholds(model, type = "logistic", test = test)

---

### train

**Description**

Train a model using one of the following methods: Artificial Neural Networks, Boosted Regression Trees, Maxent, Maxnet or Random Forest.

**Usage**

train(method, data, folds = NULL, verbose = TRUE, ...)

**Arguments**

- **method**: character or character vector. Method used to train the model, possible values are "ANN", "BRT", "Maxent", "Maxnet" or "RF", see details.
- **data**: SWD object with presence and absence/background locations.
- **folds**: list. Output of the function randomFolds or folds object created with other packages, see details, default is NULL.
- **verbose**: logical, if TRUE shows a progress bar during cross validation, default is TRUE.
- **...**: Arguments passed to the relative method, see details.

**Details**

- For the ANN method possible arguments are (for more details see nnet):
  - **size**: integer. Number of the units in the hidden layer.
  - **decay**: numeric. Weight decay, default is 0.
  - **rang**: numeric. Initial random weights, default is 0.7.
  - **maxit**: integer. Maximum number of iterations, default is 100.
• For the BRT method possible arguments are (for more details see gbm):
  – distribution: character. Name of the distribution to use, default is "bernoulli".
  – n.trees: integer. Maximum number of tree to grow, default is 100.
  – interaction.depth: integer. Maximum depth of each tree, default is 1.
  – shrinkage: numeric. The shrinkage parameter, default is 0.1.
  – bag.fraction: numeric. Random fraction of data used in the tree expansion, default is 0.5.
• For the RF method the model is trained as classification. Possible arguments are (for more details see randomForest):
  – mtry: integer. Number of variable randomly sampled at each split, default is floor(sqrt(number of variables)).
  – ntree: integer. Number of tree to grow, default is 500.
  – nodesize: integer. Minimum size of terminal nodes, default is 1.
• Maxent models are trained using the arguments "removeduplicates=false" and "addsamplesstobackground=false". Use the function thinData to remove duplicates and the function addSamplesToBg to add presence locations to background locations. For the Maxent method, possible arguments are:
  – reg: numeric. The value of the regularization multiplier, default is 1.
  – fc: character. The value of the feature classes, possible values are combinations of "l", "q", "p", "h" and "t", default is "lqph".
  – iter: numeric. Number of iterations used by the MaxEnt algorithm, default is 500.
• Maxnet models are trained using the argument "addsamplesstobackground = FALSE", use the function addSamplesToBg to add presence locations to background locations. For the Maxnet method, possible arguments are (for more details see maxnet):
  – reg: numeric. The value of the regularization intensity, default is 1.
  – fc: character. The value of the feature classes, possible values are combinations of "l", "q", "p", "h" and "t", default is "lqph".

The folds argument accepts also objects created with other packages: ENMeval or blockCV. In this case the function converts internally the folds into a format valid for SDMtune. When multiple methods are given as method argument, the function returns a named list of model object, with the name corresponding to the used method, see examples.

Value

An SDMmodel or SDMmodelCV or a list of model objects.

Author(s)

Sergio Vignali

References


See Also

randomFolds.

Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
env = predictors, categorical = "biome")

## Train a Maxent model
# The next line checks if Maxent is correctly configured but you don't need
# to run it in your script
if (dismo::maxent(silent = TRUE)) {
  model <- train(method = "Maxent", data = data, fc = "l", reg = 1.5,
  iter = 700)
}

## Train a Maxnet model
model <- train(method = "Maxnet", data = data, fc = "lq", reg = 1.5)

## Cross Validation
# Create 4 random folds splitting only the presence data
folds <- randomFolds(data, k = 4, only_presence = TRUE)
```


model <- train(method = "Maxnet", data = data, fc = "l", reg = 0.8,
folds = folds)

## Not run:
# Run only if you have the package ENMeval installed
## Block partition using the ENMeval package
require(ENMeval)
block_folds <- get.block(occ = data@coords[data@pa == 1, ],
bg.coords = data@coords[data@pa == 0, ])
model <- train(method = "Maxnet", data = data, fc = "l", reg = 0.8,
folds = block_folds)

## Checkerboard1 partition using the ENMeval package
cb_folds <- get.checkerboard1(occ = data@coords[data@pa == 1, ],
env = predictors,
bg.coords = data@coords[data@pa == 0, ],
aggregation.factor = 4)
model <- train(method = "Maxnet", data = data, fc = "l", reg = 0.8,
folds = cb_folds)

## Environmental block using the blockCV package
# Run only if you have the package blockCV
require(blockCV)
# Create spatial points data frame
library(raster)
sp_df <- SpatialPointsDataFrame(data@coords, data = as.data.frame(data@pa),
proj4string = crs(predictors))
e_folds <- envBlock(rasterLayer = predictors,
speciesData = sp_df,
species = "data@pa",
k = 4,
standardization = "standard",
rasterBlock = FALSE)
model <- train(method = "Maxnet", data = data, fc = "l", reg = 0.8,
folds = e_folds)

## End(Not run)

## Train presence absence models
# Prepare presence and absence locations
p_coords <- virtualSp$presence
a_coords <- virtualSp$absence
# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = a_coords,
env = predictors[[1:5]])

## Train an Artificial Neural Network model
model <- train("ANN", data = data, size = 10)

## Train a Random Forest model
model <- train("RF", data = data, ntree = 300)

## Train a Boosted Regression Tree model
model <- train("BRT", data = data, n.trees = 300, shrinkage = 0.001)

## Multiple methods trained together with default arguments
output <- train(method = c("ANN", "BRT", "RF"), data = data, size = 10)
output$ANN
output$BRT
output$RF

## Multiple methods trained together passing extra arguments
output <- train(method = c("ANN", "BRT", "RF"), data = data, size = 10,
              ntree = 300, n.trees = 300, shrinkage = 0.001)
output

---

### trainValTest

**Train, Validation and Test datasets**

**Description**

Split a dataset randomly in training and testing datasets or training, validation and testing datasets.

**Usage**

```r
trainValTest(x, test, val = 0, only_presence = FALSE, seed = NULL)
```

**Arguments**

- **x**
  - SWD object containing the data that have to be split in training, validation and testing datasets.
- **test**
  - numeric. The percentage of data withhold for testing.
- **val**
  - numeric. The percentage of data withhold for validation, default is 0.
- **only_presence**
  - logical, if TRUE the split is done only for the presence locations and all the background locations are included in each partition, used mainly for presence-only methods, default is FALSE.
- **seed**
  - numeric. The value used to set the seed in order to have consistent results, default is NULL.

**Details**

When `only_presence = FALSE`, the proportion of presence and absence is preserved.

**Value**

A list with the training, validation and testing or training and testing SWD objects accordingly.

**Author(s)**

Sergio Vignali
Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p.coords <- virtualSp$presence
bg.coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p.coords, a = bg.coords,
                   env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
# and splitting only the presence locations
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Split presence locations in training (60%), validation (20%) and testing
# (20%) datasets and splitting the presence and the absence locations
datasets <- trainValTest(data, val = 0.2, test = 0.2)
train <- datasets[[1]]
val <- datasets[[2]]
test <- datasets[[3]]
```

---

### tss

**True Skill Statistics**

**Description**

Compute the max TSS of a given model.

**Usage**

```r
tss(model, test = NULL)
```

**Arguments**

- `model` : SDMmodel or SDMmodelCV object.
- `test` : SWD object when `model` is an SDMmodel object; logical or SWD object when `model` is an SDMmodelCV object. If not provided it computes the training TSS, see details. Default is NULL.

**Details**

For SDMmodelCV objects, the function computes the mean of the training TSS values of the k-folds. If `test = TRUE` it computes the mean of the testing TSS values for the k-folds. If `test` is an SWD object, it computes the mean TSS values for the provided testing dataset.
Value

The value of the TSS of the given model.

Author(s)

Sergio Vignali

References


See Also

aicc and auc.

Examples

# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                   env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "l")

# Compute the training TSS
tss(model)

# Compute the testing TSS
tss(model, test)

# Same example but using cross validation instead of training and testing
# datasets
# Create 4 random folds splitting only the presence locations
folds = randomFolds(train, k = 4, only_presence = TRUE)
model <- train(method = "Maxnet", data = train, fc = "l", folds = folds)
# Compute the training TSS
tss(model)

# Compute the testing TSS
tss(model, test = TRUE)

# Compute the TSS for the held apart testing dataset
tss(model, test = test)

---

### varImp

<table>
<thead>
<tr>
<th>Variable Importance</th>
</tr>
</thead>
</table>

**Description**

The function randomly permutes one variable at a time (using training and absence/background datasets) and computes the decrease in training AUC. The result is normalized to percentages. Same implementation of MaxEnt java software but with the additional possibility of running several permutations to obtain a better estimate of the permutation importance. In case of more than one permutation (default is 10) the average of the decrease in training AUC is computed.

**Usage**

```r
varImp(model, permut = 10)
```

**Arguments**

- `model`: SDMmodel or SDMmodelCV object.
- `permut`: integer. Number of permutations, default is 10.

**Details**

Note that it could return values slightly different from MaxEnt Java software due to a different random permutation.

For SDMmodelCV objects the function returns the average and the standard deviation of the permutation importances of the single models.

**Value**

- data.frame with the ordered permutation importance.

**Author(s)**

- Sergio Vignali
Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
                    pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
                    env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "l")

# Compute variable importance
vi <- varImp(model, permut = 5)
vi
```

# Same example but using cross validation instead of training and testing datasets
# Create 4 random folds splitting only the presence locations
folds = randomFolds(data, k = 4, only_presence = TRUE)
model <- train(method = "Maxnet", data = data, fc = "l", folds = folds)

# Compute variable importance
vi <- varImp(model, permut = 5)
vi
```

varSel  

Variable Selection

Description

The function performs a data-driven variable selection. Starting from the provided model it iterates through all the variables starting from the one with the highest contribution (permutation importance or maxent percent contribution). If the variable is correlated with other variables (according to the given method and threshold) it performs a Jackknife test and among the correlated variables it removes the one that results in the best performing model when removed (according to the given metric for the training dataset). The process is repeated until the remaining variables are not highly correlated anymore.
Usage

```r
varSel(
  model,
  metric,
  bg4cor,
  test = NULL,
  env = NULL,
  method = "spearman",
  cor_th = 0.7,
  permut = 10,
  use_pc = FALSE
)
```

Arguments

- **model**: SDMmodel or SDMmodelCV object.
- **metric**: character. The metric used to evaluate the models, possible values are: "auc", "tss" and "aicc".
- **bg4cor**: SWD object. Background locations used to test the correlation between environmental variables.
- **test**: SWD. Test dataset used to evaluate the model, not used with aicc and SDMmodelCV objects, default is NULL.
- **env**: stack containing the environmental variables, used only with "aice", default is NULL.
- **method**: character. The method used to compute the correlation matrix, default "spearman".
- **cor_th**: numeric. The correlation threshold used to select highly correlated variables, default is 0.7.
- **permut**: integer. Number of permutations, default is 10.
- **use_pc**: logical, use percent contribution. If TRUE and the model is trained using the Maxent method, the algorithm uses the percent contribution computed by Maxent software to score the variable importance, default is FALSE.

Details

- To find highly correlated variables the following formula is used:

  \[
  |coeff| \leq cor_{th}
  \]

Value

The SDMmodel or SDMmodelCV object trained using the selected variables.

Author(s)

Sergio Vignali
Examples

```r
# Acquire environmental variables
files <- list.files(path = file.path(system.file(package = "dismo"), "ex"),
  pattern = "grd", full.names = TRUE)
predictors <- raster::stack(files)

# Prepare presence and background locations
p_coords <- virtualSp$presence
bg_coords <- virtualSp$background

# Create SWD object
data <- prepareSWD(species = "Virtual species", p = p_coords, a = bg_coords,
  env = predictors, categorical = "biome")

# Split presence locations in training (80%) and testing (20%) datasets
datasets <- trainValTest(data, test = 0.2, only_presence = TRUE)
train <- datasets[[1]]
test <- datasets[[2]]

# Train a model
model <- train(method = "Maxnet", data = train, fc = "l")

# Prepare background locations to test autocorrelation, this usually gives a
# warning message given that less than 10000 points can be randomly sampled
bg_coords <- dismo::randomPoints(predictors, 10000)
bg <- prepareSWD(species = "Virtual species", a = bg_coords,
  env = predictors, categorical = "biome")

## Not run:
# Remove variables with correlation higher than 0.7 accounting for the AUC,
# in the following example the variable importance is computed as permutation
# importance
vs <- varSel(model, metric = "auc", bg4cor = bg, test = test, cor_th = 0.7, 
  permut = 1)

vs

# Remove variables with correlation higher than 0.7 accounting for the TSS,
# in the following example the variable importance is the MaxEnt percent
# contribution
# Train a model
# The next line checks if Maxent is correctly configured but you don’t need
# to run it in your script
if (dismo::maxent(silent = TRUE)) {
  model <- train(method = "Maxent", data = train, fc = "l")
  vs <- varSel(model, metric = "tss", bg4cor = bg, test = test, cor_th = 0.7, 
    use_pc = TRUE)
}

vs

# Remove variables with correlation higher than 0.7 accounting for the aicc,
# in the following example the variable importance is the MaxEnt percent
# contribution
```
virtualSp

vs <- varSel(model, metric = "aicc", bg4cor = bg, cor_th = 0.7,
             use_pc = TRUE, env = predictors)
vs
}
## End(Not run)

---

**virtualSp**  
*Virtual Species*

---

**Description**

Dataset containing a random generated virtual species. The purpose of this dataset is to demonstrate the use of the functions included in the package.

**Usage**

```r
virtualSp
```

**Format**

A list with five elements:

- **presence** 400 random generated coordinates for the presence locations.
- **absence** 300 random generated coordinates for the absence locations.
- **background** 5000 random generated coordinates for the background locations.
- **pa_map** Presence absence map used to extract the presence and absence locations.
- **prob_map** Probability map of the random generated virtual species.

**Details**

The random species has been generated using the package `virtualspecies`.

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