Package: autoEnsemble (via r-universe)

August 29, 2024

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Type Package
Title Automated Stacked Ensemble Classifier for Severe Class Imbalance
Version 0.3
Depends R ($>= 3.5.0$),
Description An AutoML algorithm is developed to construct homogeneous or heterogeneous stacked ensemble models using specified base-learners. Various criteria are employed to identify optimal models, enhancing diversity among them and resulting in more robust stacked ensembles. The algorithm optimizes the model by incorporating an increasing number of top-performing models to create a diverse combination. Presently, only models from 'h2o.ai' are supported. License MIT + file LICENSE
Encoding UTF-8 Imports b2c (5 = 2.24.0.0) b2ctsels (5 = 0.2) and (5 = 4.2.0)
Imports h2o (>= 3.34.0.0), h2otools (>= 0.3), curl (>= 4.3.0) RoxygenNote 7.2.1
<pre>URL https://github.com/haghish/autoEnsemble,</pre>
https://www.sv.uio.no/psi/english/people/academic/haghish/
<pre>BugReports https://github.com/haghish/autoEnsemble/issues</pre>
Repository https://haghish.r-universe.dev
RemoteUrl https://github.com/haghish/autoensemble
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autoEnsemble

Automatically Trains H2O Models and Builds a Stacked Ensemble Model

Description

Automatically trains various algorithms to build base-learners and then automatically creates a stacked ensemble model

Usage

```
autoEnsemble(
  х,
 у,
  training_frame,
  validation_frame = NULL,
 nfolds = 10,
 balance_classes = TRUE,
 max_runtime_secs = NULL,
 max_runtime_secs_per_model = NULL,
 max\_models = NULL,
  sort_metric = "AUCPR",
  include_algos = c("GLM", "DeepLearning", "DRF", "XGBoost", "GBM"),
  save_models = FALSE,
  directory = paste("autoEnsemble", format(Sys.time(), "%d-%m-%y-%H:%M")),
  zip = FALSE,
  verbosity = NULL,
  newdata = NULL,
  family = "binary",
  strategy = c("search"),
 model_selection_criteria = c("auc", "aucpr", "mcc", "f2"),
 min_improvement = 1e-05,
 max = NULL,
  top\_rank = seq(0.01, 0.99, 0.01),
  stop\_rounds = 3,
  reset_stop_rounds = TRUE,
  stop_metric = "auc",
  seed = -1,
  verbatim = FALSE,
  startH20 = FALSE,
  nthreads = NULL,
 max_mem_size = NULL,
 min_mem_size = NULL,
  ignore_config = FALSE,
  bind_to_localhost = FALSE,
  insecure = TRUE
)
```

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Arguments

training_frame h2o training frame (data.frame) for model training

newdata h2o frame (data.frame). the data.frame must be already uploaded on h2o server

(cloud). when specified, this dataset will be used for evaluating the models. if not specified, model performance on the training dataset will be reported.

family model family. currently only "binary" classification models are supported.

strategy character, the current available strategies are "search" (default) and "top". The

"search" strategy searches for the best combination of top-performing diverse models whereas the "top" strategy is more simplified and just combines the specified of top-performing diverse models without examining the possibility of improving the model by searching for larger number of models that can further improve the model. generally, the "search" strategy is preferable, unless the

computation runtime is too large and optimization is not possible.

model_selection_criteria

character, specifying the performance metrics that should be taken into consideration for model selection. the default are "c('auc', 'aucpr', 'mcc', 'f2')".

other possible criteria are "'f1point5', 'f3', 'f4', 'f5', 'kappa', 'mean_per_class_error',

'gini', 'accuracy'", which are also provided by the "evaluate" function.

min_improvement

numeric. specifies the minimum improvement in model evaluation metric to

qualify further optimization search.

max integer. specifies maximum number of models for each criteria to be extracted.

the default value is the "top_rank" percentage for each model selection criteria.

top_rank numeric vector. specifies percentage of the top models taht should be selected.

if the strategy is "search", the algorithm searches for the best best combination of the models from top ranked models to the bottom. however, if the strategy is

"top", only the first value of the vector is used (default value is top 1%).

stop_rounds integer. number of stoping rounds, in case the model stops improving

reset_stop_rounds

logical. if TRUE, everytime the model improves the stopping rounds penalty is

resets to 0.

stop_metric character. model stopping metric. the default is "auc", but "aucpr" and "mcc"

are also available.

seed random seed (recommended)

verbatim logical. if TRUE, it reports additional information about the progress of the

model training, particularly used for debugging.

models H2O search grid or AutoML grid or a character vector of H2O model IDs. the

"h2o.get_ids" function from "h2otools" can retrieve the IDs from grids.

Value

a list including the ensemble model and the top-rank models that were used in the model

Author(s)

E. F. Haghish

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Examples

```
# load the required libraries for building the base-learners and the ensemble models
library(h2o)
library(autoEnsemble)
# initiate the h2o server
h2o.init(ignore_config = TRUE, nthreads = 2, bind_to_localhost = FALSE, insecure = TRUE)
# upload data to h2o cloud
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")</pre>
prostate <- h2o.importFile(path = prostate_path, header = TRUE)</pre>
### H2O provides 2 types of grid search for tuning the models, which are
### AutoML and Grid. Below, I tune 2 set of model grids and use them both
### for building the ensemble, just to set an example ...
### PREPARE AutoML Grid (takes a couple of minutes)
# run AutoML to tune various models (GLM, GBM, XGBoost, DRF, DeepLearning) for 120 seconds
v <- "CAPSULE"
prostate[,y] <- as.factor(prostate[,y]) #convert to factor for classification</pre>
aml <- h2o.automl(y = y, training_frame = prostate, max_runtime_secs = 120,</pre>
              include_algos=c("DRF","GLM", "XGBoost", "GBM", "DeepLearning"),
            # this setting ensures the models are comparable for building a meta learner
              seed = 2023, nfolds = 10,
              keep_cross_validation_predictions = TRUE)
### PREPARE H20 Grid (takes a couple of minutes)
# make sure equal number of "nfolds" is specified for different grids
grid <- h2o.grid(algorithm = "gbm", y = y, training_frame = prostate,</pre>
              hyper_params = list(ntrees = seq(1,50,1)),
              grid_id = "ensemble_grid",
            # this setting ensures the models are comparable for building a meta learner
              seed = 2023, fold_assignment = "Modulo", nfolds = 10,
              keep_cross_validation_predictions = TRUE)
### PREPARE ENSEMBLE MODEL
### get the models' IDs from the AutoML and grid searches.
### this is all that is needed before building the ensemble,
### i.e., to specify the model IDs that should be evaluated.
ids
      <- c(h2o.get_ids(aml), h2o.get_ids(grid))
top
      <- ensemble(models = ids, training_frame = prostate, strategy = "top")</pre>
```

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ensemble

Builds Stacked Ensemble Model from H2O Models

Description

Multiple trained H2O models are stacked to create an ensemble

Usage

```
ensemble(
 models,
  training_frame,
  newdata = NULL,
  family = "binary",
  strategy = c("search"),
 model_selection_criteria = c("auc", "aucpr", "mcc", "f2"),
 min_improvement = 1e-05,
 max = NULL,
  top_rank = seq(0.01, 0.99, 0.01),
  stop\_rounds = 3,
  reset_stop_rounds = TRUE,
  stop_metric = "auc",
  seed = -1,
  verbatim = FALSE
)
```

Arguments

newdata

models H2O search grid or AutoML grid or a character vector of H2O model IDs. the

"h2o.get_ids" function from "h2otools" can retrieve the IDs from grids.

training_frame h2o training frame (data.frame) for model training

or drifting_ir differ in20 training frame (datastraine) for incder training

h2o frame (data.frame). the data.frame must be already uploaded on h2o server (cloud). when specified, this dataset will be used for evaluating the models. if not specified, model performance on the training dataset will be reported.

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family model family. currently only "binary" classification models are supported.

strategy character. the current available strategies are "search" (default) and "top". The

"search" strategy searches for the best combination of top-performing diverse models whereas the "top" strategy is more simplified and just combines the specified of top-performing diverse models without examining the possibility of improving the model by searching for larger number of models that can further improve the model. generally, the "search" strategy is preferable, unless the

computation runtime is too large and optimization is not possible.

model_selection_criteria

character, specifying the performance metrics that should be taken into consideration for model selection. the default are "c('auc', 'aucpr', 'mcc', 'f2')".

other possible criteria are "'f1point5', 'f3', 'f4', 'f5', 'kappa', 'mean_per_class_error',

'gini', 'accuracy'", which are also provided by the "evaluate" function.

min_improvement

numeric. specifies the minimum improvement in model evaluation metric to

qualify further optimization search.

max integer. specifies maximum number of models for each criteria to be extracted.

the default value is the "top_rank" percentage for each model selection criteria.

top_rank numeric vector. specifies percentage of the top models taht should be selected.

if the strategy is "search", the algorithm searches for the best best combination of the models from top ranked models to the bottom. however, if the strategy is

"top", only the first value of the vector is used (default value is top 1%).

stop_rounds integer. number of stoping rounds, in case the model stops improving

reset_stop_rounds

logical. if TRUE, every time the model improves the stopping rounds penalty is

resets to 0.

stop_metric character. model stopping metric. the default is "auc", but "aucpr" and "mcc"

are also available.

seed random seed (recommended)

verbatim logical. if TRUE, it reports additional information about the progress of the

model training, particularly used for debugging.

Value

a list including the ensemble model and the top-rank models that were used in the model

Author(s)

E. F. Haghish

Examples

```
## Not run:
```

load the required libraries for building the base-learners and the ensemble models library(h2o)

library(autoEnsemble)

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initiate the h2o server

```
h2o.init(ignore_config = TRUE, nthreads = 2, bind_to_localhost = FALSE, insecure = TRUE)
# upload data to h2o cloud
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")</pre>
prostate <- h2o.importFile(path = prostate_path, header = TRUE)</pre>
### H2O provides 2 types of grid search for tuning the models, which are
### AutoML and Grid. Below, I tune 2 set of model grids and use them both
### for building the ensemble, just to set an example ...
### PREPARE AutoML Grid (takes a couple of minutes)
# run AutoML to tune various models (GLM, GBM, XGBoost, DRF, DeepLearning) for 120 seconds
v <- "CAPSULE"
prostate[,y] \leftarrow as.factor(prostate[,y]) #convert to factor for classification
aml <- h2o.automl(y = y, training_frame = prostate, max_runtime_secs = 120,</pre>
              include_algos=c("DRF","GLM", "XGBoost", "GBM", "DeepLearning"),
           # this setting ensures the models are comparable for building a meta learner
              seed = 2023, nfolds = 10,
              keep_cross_validation_predictions = TRUE)
### PREPARE H20 Grid (takes a couple of minutes)
# make sure equal number of "nfolds" is specified for different grids
grid <- h2o.grid(algorithm = "gbm", y = y, training_frame = prostate,</pre>
              hyper_params = list(ntrees = seq(1,50,1)),
              grid_id = "ensemble_grid",
           # this setting ensures the models are comparable for building a meta learner
              seed = 2023, fold_assignment = "Modulo", nfolds = 10,
              keep_cross_validation_predictions = TRUE)
### PREPARE ENSEMBLE MODEL
### get the models' IDs from the AutoML and grid searches.
### this is all that is needed before building the ensemble,
### i.e., to specify the model IDs that should be evaluated.
ids
     <- c(h2o.get_ids(aml), h2o.get_ids(grid))
     <- ensemble(models = ids, training_frame = prostate, strategy = "top")</pre>
search <- ensemble(models = ids, training_frame = prostate, strategy = "search")</pre>
### EVALUATE THE MODELS
# best model identified by h2o.automl
h2o.auc(aml@leader)
h2o.auc(h2o.getModel(grid@model_ids[[1]])) # best model identified by grid search
```

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```
h2o.auc(top$model). # ensemble model with 'top' search strategy
h2o.auc(search$model). # ensemble model with 'search' search strategy

## End(Not run)
```

evaluate

Evaluate H2O Model(s) Performance

Description

Multiple model performance metrics are computed for each model

Usage

```
evaluate(id, newdata = NULL, ...)
```

Arguments

id a character vector of H2O model IDs retrieved from H2O Grid search or Au-

toML random search. the "h2o.get_ids" function from "h2otools" can re-

trieve the IDs from grids.

newdata h2o frame (data.frame). the data.frame must be already uploaded on h2o server

(cloud). when specified, this dataset will be used for evaluating the models. if

not specified, model performance on the training dataset will be reported.

... arguments to be passed to "h2o.performance" from H2O package

Value

a data.frame of various model performance metrics for each model

Author(s)

E. F. Haghish

Examples

```
## Not run:
library(h2o)
library(h2otools) #for h2o.get_ids() function
library(autoEnsemble)

# initiate the H2O server to train a grid of models
h2o.init(ignore_config = TRUE, nthreads = 2, bind_to_localhost = FALSE, insecure = TRUE)

# Run a grid search or AutoML search
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(path = prostate_path, header = TRUE)</pre>
```

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h2o.get_ids

h2o.get_ids

Description

extracts the model IDs from H2O AutoML object or H2O grid

Usage

```
h2o.get_ids(automl)
```

Arguments

automl

a h2o "AutoML" grid object

Value

a character vector of trained models' names (IDs)

Author(s)

E. F. Haghish

Examples

```
## Not run:
library(h2o)
library(autoEnsemble)
h2o.init(ignore_config = TRUE, nthreads = 2, bind_to_localhost = FALSE, insecure = TRUE)
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")
prostate <- h2o.importFile(path = prostate_path, header = TRUE)
y <- "CAPSULE"
prostate[,y] <- as.factor(prostate[,y]) #convert to factor for classification
aml <- h2o.automl(y = y, training_frame = prostate, max_runtime_secs = 30)
# get the model IDs
ids <- h2o.get_ids(aml)</pre>
```

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```
## End(Not run)
```

modelSelection Selects Diverse Top-Performing Models for Stacking an Ensemble Model

Description

Multiple model performance metrics are computed

Usage

```
modelSelection(
  eval,
  family = "binary",
  top_rank = 0.01,
  max = NULL,
  model_selection_criteria = c("auc", "aucpr", "mcc", "f2")
)
```

Arguments

eval an object of class "ensemble.eval" which is provided by 'evaluate' function. this object is a data.frame, including several performance metrics for the evaluated models. model family. currently only "binary" classification models are supported. family top_rank numeric. what percentage of the top model should be selected? the default value is top 1% models. max integer. specifies maximum number of models for each criteria to be extracted. the default value is the "top_rank" percentage for each model selection criteria. model_selection_criteria character, specifying the performance metrics that should be taken into consideration for model selection. the default are "c('auc', 'aucpr', 'mcc', 'f2')". other possible criteria are "'f1point5', 'f3', 'f4', 'f5', 'kappa', 'mean_per_class_error', 'gini', 'accuracy'", which are also provided by the "evaluate" function.

Value

a matrix of F-Measures for different thresholds or the highest F-Measure value

Author(s)

E. F. Haghish

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Examples

```
## Not run:
library(h2o)
library(h2otools) #for h2o.get_ids() function
library(h2oEnsemble)
# initiate the H2O server to train a grid of models
h2o.init(ignore_config = TRUE, nthreads = 2, bind_to_localhost = FALSE, insecure = TRUE)
# Run a grid search or AutoML search
prostate_path <- system.file("extdata", "prostate.csv", package = "h2o")</pre>
prostate <- h2o.importFile(path = prostate_path, header = TRUE)</pre>
y <- "CAPSULE"
prostate[,y] <- as.factor(prostate[,y]) #convert to factor for classification</pre>
aml <- h2o.automl(y = y, training_frame = prostate, max_runtime_secs = 30,</pre>
                   seed = 2023, nfolds = 10, keep_cross_validation_predictions = TRUE)
# get the model IDs from the H2O Grid search or H2O AutoML Grid
ids <- h2otools::h2o.get_ids(aml)</pre>
# evaluate all the models and return a dataframe
evals <- evaluate(id = ids)</pre>
# perform model selection (up to top 10% of each criteria)
select <- modelSelection(eval = evals, top_rank = 0.1))</pre>
## End(Not run)
```

stopping_criteria

Stopping Criteria for Ending the Search

Description

Defines criteria for ending the optimization search

Usage

```
stopping_criteria(
   df,
   round,
   stop,
   min_improvement,
   stop_rounds = 3,
   reset_stop_rounds = TRUE,
   stop_metric = "auc"
)
```

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Arguments

df data.frame. includes the metrics of ensemblem model performance

round integer. the current round of optimization stop integer. current round of stopping penalty

min_improvement

numeric. specifies the minimum improvement in model evaluation metric to

qualify further optimization search.

stop_rounds integer. number of stoping rounds, in case the model stops improving

reset_stop_rounds

logical. if TRUE, everytime the model improves the stopping rounds penalty is

resets to 0.

stop_metric character. model stopping metric. the default is "auc", but "aucpr" and "mcc"

are also available.

Value

a matrix of F-Measures for different thresholds or the highest F-Measure value

Author(s)

E. F. Haghish

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