Package ‘sirus’

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Type Package

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Description A regression and classification algorithm based on random forests, which takes the form of a short list of rules. SIRUS combines the simplicity of decision trees with a predictivity close to random forests. The core aggregation principle of random forests is kept, but instead of aggregating predictions, SIRUS aggregates the forest structure: the most frequent nodes of the forest are selected to form a stable rule ensemble model. The algorithm is fully described in the following articles: Benard C., Biau G., da Veiga S., Scornet E. (2021), Electron. J. Statist., 15:427-505 <DOI:10.1214/20-EJS1792> for classification, and Benard C., Biau G., da Veiga S., Scornet E. (2020) <arXiv:2004.14841> for regression. This R package is a fork from the project ranger (<https://github.com/imbs-hl/ranger>).

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Imports Rcpp (>= 0.11.2), Matrix, ROCR, ggplot2, glmnet

LinkingTo Rcpp, RcppEigen

Depends R (>= 3.1)

Suggests survival, testthat

RoxygenNote 7.1.1

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BugReports https://gitlab.com/drti/sirus/-/issues

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\begin{tabular}{ll}
\texttt{sirus.cv} & \textit{Estimate p0.} \\
\end{tabular}

\section*{Description}

Estimate the optimal hyperparameter $p_0$ used to select rules in \texttt{sirus.fit} using cross-validation (Benard et al. 2020, 2021).

\section*{Usage}

\begin{verbatim}
sirus.cv(  data,  y,  type = "auto",  nfold = 10,  ncv = 10,  num.rule.max = 25,  q = 10,  discrete.limit = 10,  num.trees.step = 1000,  alpha = 0.05,  mtry = NULL,  max.depth = 2,  num.trees = NULL,  num.threads = NULL,  replace = TRUE,  sample.fraction = NULL,  verbose = TRUE,  seed = NULL)
\end{verbatim}

\section*{Arguments}

\begin{itemize}
  \item \texttt{data} \hspace{1cm} Input dataframe, each row is an observation vector. Each column is an input variable and is numeric or factor.
  \item \texttt{y} \hspace{1cm} Numeric response variable. For classification, \texttt{y} takes only 0 and 1 values.
  \item \texttt{type} \hspace{1cm} 'reg' for regression, 'classif' for classification and 'auto' for automatic detection (classification if \texttt{y} takes only 0 and 1 values).
\end{itemize}
sirus.cv

nfold  Number of folds in the cross-validation. Default is 10.
ncv   Number of repetitions of the cross-validation. Default is 10 for a robust estimation of $p_0$.
num.rule.max  Maximum number of rules of SIRUS model in the cross-validation grid. Default is 25.
q  Number of quantiles used for node splitting in the forest construction. Default and recommended value is 10.
discrete.limit  Maximum number of distinct values for a variable to be considered discrete. If higher, variable is continuous.
num.trees.step  Number of trees grown between two evaluations of the stopping criterion. Ignored if num.trees is provided.
alpha  Parameter of the stopping criterion for the number of trees: stability has to reach $1 - \alpha$ to stop the growing of the forest. Ignored if num.trees is provided. Default value is 0.05.
mtry  Number of variables to possibly split at each node. Default is the number of variables divided by 3.
max.depth  Maximal tree depth. Default and recommended value is 2.
num.trees  Number of trees grown in the forest. If NULL (recommended), the number of trees is automatically set using a stability stopping criterion.
num.threads  Number of threads used to grow the forest. Default is number of CPUs available.
replace  Boolean. If true (default), sample with replacement.
sample.fraction  Fraction of observations to sample. Default is 1 for sampling with replacement and 0.632 for sampling without replacement.
verbose  Boolean. If true, information messages are printed.
seed  Random seed. Default is NULL, which generates the seed from R. Set to 0 to ignore the R seed.

Details
For a robust estimation of $p_0$, it is recommended to run multiple cross-validations (typically $ncv = 10$). Two optimal values of $p_0$ are provided: $p_0$\_pred (Benard et al. 2021) and $p_0$\_stab (Benard et al. 2020), defined such that $p_0$\_pred minimizes the error, and $p_0$\_stab finds a tradeoff between error and stability. Error is 1-AUC for classification and the unexplained variance for regression. Stability is the average proportion of rules shared by two SIRUS models fit on two distinct folds of the cross-validation.

Value
Optimal value of $p_0$ with the elements

$p0$\_pred  Optimal $p_0$ value to minimize model error (recommended for classification).
$p0$\_stab  Optimal $p_0$ value for a tradeoff between error and stability (recommended for regression).
error.grid.p0  Table with the full cross-validation results for a fine grid of p0: number of rules, stability, and error. The last three columns of the table are the standard deviations of the metrics across the ncv repetitions of the cross-validation. See details for the definitions of the error and stability metrics.

type  'reg' for regression, 'classif' for classification.

References


Examples

```r
## load SIRUS
require(sirus)

## prepare data
data <- iris
y <- rep(0, nrow(data))
y[data$Species == "setosa"] = 1
data$Species <- NULL

## run cv
cv.grid <- sirus.cv(data, y, nfold = 3, ncv = 2, num.trees = 100)
```

sirus.fit  

**Fit SIRUS.**

Description

Fit SIRUS for a given number of rules (10 by default) or a given p0. SIRUS is a regression and classification algorithm, based on random forests (Breiman, 2001), that takes the form of a short list of rules. SIRUS combines the simplicity of rule algorithms or decision trees with an accuracy close to random forests. More importantly, the rule selection is stable with respect to data perturbation. SIRUS for classification is defined in (Benard et al. 2021), and the extension to regression is provided in (Benard et al. 2020).

Usage

```r
sirus.fit(
  data, 
  y, 
  type = "auto", 
  num.rule = 10, 
  p0 = NULL, 
)```
num.rule.max = 25,
q = 10,
discrete.limit = 10,
num.trees.step = 1000,
alpha = 0.05,
mtry = NULL,
max.depth = 2,
num.trees = NULL,
num.threads = NULL,
replace = TRUE,
sample.fraction = ifelse(replace, 1, 0.632),
verbose = TRUE,
seed = NULL
)

Arguments

data
Input dataframe, each row is an observation vector. Each column is an input variable and is numeric or factor.

y
Numeric response variable. For classification, y takes only 0 and 1 values.

type
‘reg’ for regression, ‘classif’ for classification and ‘auto’ for automatic detection (classification if y takes only 0 and 1 values).

num.rule
Number of rules in SIRUS model. Default is 10. Ignored if a \( p_0 \) value is provided. For regression, the effective number of rules can be smaller than num.rule because of null coefficients in the final linear aggregation of the rules.

\( p_0 \)
Selection threshold on the frequency of appearance of a path in the forest to set the number of rules. Default is NULL and num.rule is used to select rules. sirus.cv provides the optimal \( p_0 \) by cross-validation.

num.rule.max
Maximum number of rules in SIRUS model. Ignored if num.rule is provided.

q
Number of quantiles used for node splitting in the forest construction. Default and recommended value is 10.

discrete.limit
Maximum number of distinct values for a variable to be considered discrete. If higher, variable is continuous.

num.trees.step
Number of trees grown between two evaluations of the stopping criterion. Ignored if num.trees is provided.

alpha
Parameter of the stopping criterion for the number of trees: stability has to reach 1-alpha to stop the growing of the forest. Ignored if num.trees is provided. Default value is 0.05.

mtry
Number of variables to possibly split at each node. Default is the number of variables divided by 3.

max.depth
Maximal tree depth. Default and recommended value is 2.

num.trees
Number of trees grown in the forest. Default is NULL. If NULL (recommended), the number of trees is automatically set using a stability based stopping criterion.

num.threads
Number of threads used to grow the forest. Default is number of CPUs available.
replace

Boolean. If true (default), sample with replacement.

sample.fraction

Fraction of observations to sample. Default is 1 for sampling with replacement and 0.632 for sampling without replacement.

verbose

Boolean. If true, information messages are printed.

seed

Random seed. Default is NULL, which generates the seed from R. Set to 0 to ignore the R seed.

Details

If the output \( y \) takes only 0 and 1 values, a classification model is fit, otherwise a regression model is fit. SIRUS algorithm proceeds the following steps:

1. Discretize data
2. Fit a random forest
3. Extract rules from tree nodes
4. Select the most frequent rules (which occur in at least a fraction \( p_0 \) of the trees)
5. Filter rules to remove linear dependence between them
6. Aggregate the selected rules
   - Classification: rules are averaged
   - Regression: rules are linearly combined via a ridge regression (constrained to have all coefficients positive)

The hyperparameter \( p_0 \) can be tuned using \texttt{sirus.cv} to set the optimal number of rules.

The number of trees is automatically set with a stopping criterion based on stability: the forest growing is stopped when the number of trees is high enough to ensure that 95\% of the rules in average are identical over two runs of SIRUS on the provided dataset.

Data is discretized depending on variable types: numerical variables are binned using \( q \)-quantiles, categorical variables are transformed in ordered variables as in \texttt{ranger} (standard method to handle categorical variables in trees), while discrete variables (numerical variables with less than \texttt{discrete.limit} distinct values) are left untouched. Notice that categorical variables with a high number of categories should be discarded or transformed, as SIRUS is likely to identify associated irrelevant rules.

Value

SIRUS model with elements

\begin{itemize}
\item \texttt{rules} \hspace{1cm} List of rules in SIRUS model.
\item \texttt{rules.out} \hspace{1cm} List of rule outputs. \texttt{rule.out}: the output mean whether the rule is satisfied or not. \texttt{supp.size}: the number of points inside and outside the rule.
\item \texttt{proba} \hspace{1cm} Frequency of occurrence of paths in the forest.
\item \texttt{paths} \hspace{1cm} List of selected paths (symbolic representation with quantile order for continuous variables).
\item \texttt{rule.weights} \hspace{1cm} Vector of positive or null coefficients assigned to each rule for the linear aggregation (1/number of rules for classification).
\end{itemize}
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rule.glm Fitted glmnet object for regression (linear rule aggregation with ridge penalty).
type Type of SIRUS model: ‘reg’ for regression, ‘classif’ for classification.
num.trees Number of trees used to build SIRUS.
data.names Names of input variables.
mean Mean output over the full training data. Default model output if no rule is selected.
bins List of type and possible split values for all input variables.

References


Examples

```r
## load SIRUS
require(sirus)

## prepare data
data <- iris
y <- rep(0, nrow(data))
y[data$Species == 'setosa'] = 1
data$Species <- NULL

## fit SIRUS
sirus.m <- sirus.fit(data, y)
```

sirus.plot.cv  Plot SIRUS cross-validation path.

Description

Plot SIRUS cross-validation path: error and stability versus the number of rules when $p_0$ varies.

Usage

```r
sirus.plot.cv(sirus.cv.grid, p0.criterion = NULL, num.rule.max = 25)
```
Arguments

sirus.cv.grid  Cross-validation results returned by sirus.cv.

p0.criterion  Criterion to pick the optimal p0 displayed in the plots: if 'pred' then p0.pred is used for a minimal error, if 'stab' then p0.stab is used for a tradeoff error/stability. Default is 'pred' for classification and 'stab' for regression.

num.rule.max  Upper limit on the number of rules for the x-axis. Default is 25.

Details

Error is 1-AUC for classification and the unexplained variance for regression. Stability is the average proportion of rules shared by two SIRUS models fit on two distinct folds of the cross-validation.

Value

Plots of cross-validation results.

error  plot of error vs number of rules (ggplot2 object).

stability  plot of stability vs number of rules (ggplot2 object).

Examples

```r
## load SIRUS
require(sirus)

## prepare data
data <- iris
y <- rep(0, nrow(data))
y[data$Species == 'setosa'] = 1
data$Species <- NULL

## run cv
cv.grid <- sirus.cv(data, y, nfold = 3, ncv = 2, num.trees = 100)

## plot cv result
plot.error <- sirus.plot.cv(cv.grid)$error
plot(plot.error)
```

sirus.predict  Predict.

Description

Compute SIRUS predictions for new observations.

Usage

sirus.predict(sirus.m, data.test)
sirus.print

Arguments

sirus.m A SIRUS model generated by sirus.fit.
data.test Testing data (dataframe of new observations).

Value

Predictions. For classification, vector of the predicted probability of each new observation to be of class 1.

Examples

```r
## load SIRUS
require(sirus)

## prepare data
data <- iris
y <- rep(0, nrow(data))
y[iris$Species == "setosa"] = 1
data$Species <- NULL

## fit SIRUS
sirus.m <- sirus.fit(data, y)

## predict
predictions <- sirus.predict(sirus.m, data)
```

---

sirus.print  

Print SIRUS.

Description

Print the list of rules output by SIRUS.

Usage

sirus.print(sirus.m, digits = 3)

Arguments

sirus.m A SIRUS model generated by sirus.fit.
digits Number of significant digits for numerical values. Default value is 3.

Value

Formatted list of rules.
Examples

```r
## load SIRUS
require(sirus)

## prepare data
data <- iris
y <- rep(0, nrow(data))
y[data$Species == 'setosa'] = 1
data$Species <- NULL

## fit SIRUS
sirus.m <- sirus.fit(data, y)

## print sirus model
sirus.print(sirus.m)
```
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