

# Package ‘sbrl’

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**Type** Package

**Title** Scalable Bayesian Rule Lists Model

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**Description** An efficient implementation of Scalable Bayesian Rule Lists Algorithm, a competitor algorithm for decision tree algorithms; see Hongyu Yang, Cynthia Rudin, Margo Seltzer (2017) <<https://proceedings.mlr.press/v70/yang17h.html>>. It builds from pre-mined association rules and have a logical structure identical to a decision list or one-sided decision tree. Fully optimized over rule lists, this algorithm strikes practical balance between accuracy, interpretability, and computational speed.

**License** GPL (>= 2)

**Imports** Rcpp (>= 0.12.4), arules, methods

**RcppModules** sbrl

**LinkingTo** Rcpp

**NeedsCompilation** yes

**LazyData** yes

**SystemRequirements** gmp (>= 4.2.0), gsl

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## R topics documented:

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sbrl-package

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*SCALABLE BAYESIAN RULE LISTS*


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## Description

Fit a sbrl model. Learn from the data and create a decision rule list in the format of:

```
if (condition1) then positive probability = ...
else if (condition2) then positive probability = ...
else if (condition3) ...
...
else (default rule) then positive probability = ...
( See the examples below )
```

## Details

This package contains three functions: [sbrl](#), [print.sbrl](#), [show.sbrl](#), and [predict.sbrl](#)

## Author(s)

Hongyu Yang, Cynthia Rudin, Margo Seltzer

## References

Hongyu Yang, Morris Chen, Cynthia Rudin, Margo Seltzer (2016) *Scalable Bayesian Rule Lists*. Working paper on arXiv 2016.

Benjamin Letham, Cynthia Rudin, Tyler McCormick and David Madigan (2015) *Building Interpretable Classifiers with Rules using Bayesian Analysis*. Annals of Applied Statistics, 2015.

## See Also

[sbrl](#), [print.sbrl](#), [show.sbrl](#) and [predict.sbrl](#)

**Examples**

```

# Let us use the tictactoe dataset
data(tictactoe)
for (name in names(tictactoe)) {tictactoe[name] <- as.factor(tictactoe[,name])}

# Train on two-thirds of the data
b = round(2*nrow(tictactoe)/3, digit=0)
data_train <- tictactoe[1:b, ]
# Test on the remaining one third of the data
data_test <- tictactoe[(b+1):nrow(tictactoe), ]
# data_train, data_test are dataframes with factor columns
# The class column is "label"

# Run the sbrl algorithm on the training set
sbrl_model <- sbrl(data_train, iters=20000, pos_sign="1",
  neg_sign="0", rule_minlen=1, rule_maxlen=3,
  minsupport_pos=0.10, minsupport_neg=0.10,
  lambda=10.0, eta=1.0, nchain=25)
print(sbrl_model)

# Make predictions on the test set
yhat <- predict(sbrl_model, data_test)
# yhat will be a list of predicted negative and positive probabilities for the test data.

#clean up
rm(list = ls())
gc()

```

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get\_data\_feature\_mat    *GET BINARY MATRIX REPRESENTATION OF THE DATA-FEATURE RELATIONSHIP*

---

**Description**

Given some features in the form "feature1=x1", "feature2=x2" ..., this function will generate a matrix representation of which data are captured by which features.

**Usage**

```
get_data_feature_mat(data, featurenames)
```

**Arguments**

data	a data.frame representing the observations.
featurenames	a character vector representing the features in the form: "feature1=x1", "feature2=x2"...

**Value**

a binary matrix of size #observations-by-#featurenames

**Author(s)**

Hongyu Yang, Morris Chen, Cynthia Rudin, Margo Seltzer

**Examples**

```
data(tictactoe)
featurenames <- c("c1=b", "c1=o", "c1=x")
get_data_feature_mat(tictactoe, featurenames)
#it will generate a binary matrix representing which observations are captured by which features.

#clean up
rm(list = ls())
gc()
```

---

predict.sbrl	<i>PREDICT THE POSITIVE PROBABILITY FOR THE OBSERVATIONS</i>
--------------	--

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**Description**

Returns a list of probabilities.

**Usage**

```
## S3 method for class 'sbrl'
predict(object, tdata, ...)
```

**Arguments**

object	sbrl model returned from the <a href="#">sbrl</a> function.
tdata	test data
...	further arguments passed to or from other methods.

**Value**

return a list containing 2 lists of probabilities for the rule list, corresponding to probability being 0 and 1 for each observation. The two probabilities for each rule add up to 1,  $P(y=0 \mid \text{rule } r) + p(y=1 \mid \text{rule } r) = 1$

**Examples**

```
# Let us use the tictactoe dataset
data(tictactoe)
for (name in names(tictactoe)) {tictactoe[name] <- as.factor(tictactoe[,name])}

# Train on two-thirds of the data
b = round(2*nrow(tictactoe)/3, digit=0)
data_train <- tictactoe[1:b, ]
```

```

# Test on the remaining one third of the data
data_test <- tictactoe[(b+1):nrow(tictactoe), ]
# data_train, data_test are dataframes with factor columns
# The class column is "label"

# Run the sbrl algorithm on the training set
sbrl_model <- sbrl(data_train, iters=20000, pos_sign="1",
  neg_sign="0", rule_minlen=1, rule_maxlen=3,
  minsupport_pos=0.10, minsupport_neg=0.10,
  lambda=10.0, eta=1.0, nchain=25)
print(sbrl_model)

# Make predictions on the test set
yhat <- predict(sbrl_model, data_test)
# yhat will be a list of predicted negative and positive probabilities for the test data.

#clean up
rm(list = ls())
gc()

```

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print.sbrl

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*INTERPRETABLE VERSION OF A SBRL MODEL*


---

## Description

This function prints an sbrl object. It is a method for the generic function print of class "sbrl".

## Usage

```

# S3 method for class 'sbrl'
# This complies with the form of the standard generic method print
## S3 method for class 'sbrl'
print(x, useS4=FALSE, ...)
## S3 method for class 'sbrl'
show(x, useS4=FALSE, ...)

```

## Arguments

x	A sbrl model returned from <a href="#">sbrl</a> function
useS4	An argument used to match showDefault function. Fixed as FALSE.
...	further arguments passed to or from other methods.

## Details

This function is a method for the generic function print for class "sbrl". It can be invoked by calling print for an object of the appropriate class, or directly by calling print.sbrl regardless of the class of the object.

**Value**

No return value. This function prints out the logical structure of the sbrl model as a sequence of IF-THEN rules, identical to a decision list or one-sided decision tree.

**Examples**

```
# Let us use the tictactoe dataset
data(tictactoe)
for (name in names(tictactoe)) {tictactoe[name] <- as.factor(tictactoe[,name])}

# Train on two-thirds of the data
b = round(2*nrow(tictactoe)/3, digit=0)
data_train <- tictactoe[1:b, ]
# Test on the remaining one third of the data
data_test <- tictactoe[(b+1):nrow(tictactoe), ]
# data_train, data_test are dataframes with factor columns
# The class column is "label"

# Run the sbrl algorithm on the training set
sbrl_model <- sbrl(data_train, iters=20000, pos_sign="1",
  neg_sign="0", rule_minlen=1, rule_maxlen=3,
  minsupport_pos=0.10, minsupport_neg=0.10,
  lambda=10.0, eta=1.0, nchain=25)
print(sbrl_model)

#clean up
rm(list = ls())
gc()
```

---

sbrl

*fit the scalable bayesian rule lists model*


---

**Description**

Fit the scalable bayesian rule lists model with given data and parameters. It generates a model that is a probabilistic classifier that optimizes the posterior of a Bayesian hierarchical model over pre-mined association rules.

**Usage**

```
sbrl(tdata, iters=30000, pos_sign="1",
  neg_sign="0", rule_minlen=1, rule_maxlen=1,
  minsupport_pos=0.10, minsupport_neg=0.10,
  lambda=10.0, eta=1.0, alpha=c(1,1), nchain=10)
```

**Arguments**

<code>tdata</code>	a dataframe, with a "label" column specifying the correct labels for each observation.
<code>iters</code>	the number of iterations for each MCMC chain.
<code>pos_sign</code>	the sign for the positive labels in the "label" column.
<code>neg_sign</code>	the sign for the negative labels in the "label" column.
<code>rule_minlen</code>	the minimum number of cardinality for rules to be mined from the dataframe.
<code>rule_maxlen</code>	the maximum number of cardinality for rules to be mined from the dataframe.
<code>minsupport_pos</code>	a number between 0 and 1, for the minimum percentage support for the positive observations.
<code>minsupport_neg</code>	a number between 0 and 1, for the minimum percentage support for the negative observations.
<code>lambda</code>	a hyperparameter for the expected length of the rule list.
<code>eta</code>	a hyperparameter for the expected cardinality of the rules in the optimal rule list.
<code>alpha</code>	a prior pseudo-count for the positive and negative classes. fixed at 1's
<code>nchain</code>	an integer for the number of the chains that MCMC will be running.

**Value**

Return a list of :

<code>rs</code>	a ruleset which contains the rule indices and their positive probabilities for the best rule list by training sbri with the given data and parameters.
<code>rulenames</code>	a list of all the rule names mined with arules.
<code>featurenames</code>	a list of all the feature names.
<code>mat_feature_rule</code>	a binary matrix representing which features are included in which rules.

**Author(s)**

Hongyu Yang, Morris Chen, Cynthia Rudin, Margo Seltzer

**References**

- Hongyu Yang, Cynthia Rudin, Margo Seltzer (2017) *Scalable Bayesian Rule Lists*. Proceedings of the 34th International Conference on Machine Learning, PMLR 70:3921-3930, 2017.
- Benjamin Letham, Cynthia Rudin, Tyler McCormick and David Madigan (2015) *Building Interpretable Classifiers with Rules using Bayesian Analysis*. Annals of Applied Statistics, 2015.

**Examples**

```

# Let us use the tictactoe dataset
data(tictactoe)
for (name in names(tictactoe)) {tictactoe[name] <- as.factor(tictactoe[,name])}

# Train on two-thirds of the data
b = round(2*nrow(tictactoe)/3, digit=0)
data_train <- tictactoe[1:b, ]
# Test on the remaining one third of the data
data_test <- tictactoe[(b+1):nrow(tictactoe), ]
# data_train, data_test are dataframes with factor columns
# The class column is "label"

# Run the sbrl algorithm on the training set
sbrl_model <- sbrl(data_train, iters=20000, pos_sign="1",
  neg_sign="0", rule_minlen=1, rule_maxlen=3,
  minsupport_pos=0.10, minsupport_neg=0.10,
  lambda=10.0, eta=1.0, nchain=25)
print(sbrl_model)

# Make predictions on the test set
yhat <- predict(sbrl_model, data_test)
# yhat will be a list of predicted negative and positive probabilities for the test data.

#clean up
rm(list = ls())
gc()

```

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tictactoe

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*SHUFFLED TIC-TAC-TOE-ENDGAME DATASET*


---

**Description**

This is a shuffled version of the Tic-Tac-Toe Endgame Data Set on UCI Machine Learning Repository.

**Usage**

```
data("tictactoe")
```

**Format**

A data frame with 958 observations on the following 10 variables.

- c1 a factor with levels b, o, x
- c2 a factor with levels b, o, x
- c3 a factor with levels b, o, x
- c4 a factor with levels b, o, x



c5 a factor with levels b, o, x  
c6 a factor with levels b, o, x  
c7 a factor with levels b, o, x  
c8 a factor with levels b, o, x  
c9 a factor with levels b, o, x  
label an integer with values 0, 1

### Details

This database encodes the complete set of possible board configurations at the end of tic-tac-toe games, where "x" is assumed to have played first. The target concept is "win for x" (i.e., true when "x" has one of 8 possible ways to create a "three-in-a-row").

### Source

<https://archive.ics.uci.edu/ml/datasets/Tic-Tac-Toe+Endgame>

### Examples

```
data(tictactoe)
## maybe str(tictactoe) ; plot(tictactoe) ...

#clean up
rm(list = ls())
gc()
```

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