

# Package ‘bsnsing’

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**Type** Package

**Title** Build Decision Trees with Optimal Multivariate Splits

**Version** 1.0.1

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**Description** Functions for training an optimal decision tree classifier, making predictions and generating latex code for plotting. Works for two-class and multi-class classification problems. The algorithm seeks the optimal Boolean rule consisting of multiple variables to split a node, resulting in shorter trees. Use `bsnsing()` to build a tree, `predict()` to make predictions and `plot()` to plot the tree into latex and PDF. See Yanchao Liu (2022) <[arXiv:2205.15263](https://arxiv.org/abs/2205.15263)> for technical details. Source code and more data sets are at <<https://github.com/profyliu/bsnsing/>>.

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 bsnsing-package

*bsnsing: Build Decision Trees with Optimal Multivariate Splits*


---

## Description

The bsnsing package provides functions for building a decision tree classifier and making predictions. It solves a mixed-integer programming (MIP) model to maximize the Gini reduction at each node split, and each node split rule can utilize multiple input variables. Benchmarking experiments on 75 open data sets suggest that bsnsing trees are the most capable of discriminating new cases compared to trees trained by other decision tree codes including the rpart, C50, party and tree packages in R. Compared to other optimal decision tree packages, including DL8.5, OSDT, GOSDT and indirectly more, bsnsing stands out in its training speed, ease of use and broader applicability without losing in prediction accuracy. For more information, please check out the paper <https://arxiv.org/abs/2205.15263>, to be published in INFORMS Journal on Computing.

## The ENUM algorithm

In this package, the MIP model is solved using the implicit enumeration (ENUM) algorithm. The experimental version at <https://github.com/profyliu/bsnsing/> is able to use external solvers such as GUROBI, CPLEX and lpSolve (via specifying the opt.solver option in the bsnsing function). All benchmarking experiments were run using the C implementation of the ENUM algorithm, i.e., opt.solver = 'enum\_c', which is the default setting.

**More data sets**

Several data frames (i.e., `auto`, `iris`, `GlaucomaMVF` and `BreastCancer`) used in the example code are included in this package. More two-class and multi-class classification data sets can be found at <https://github.com/profyliu/bsnsing/>.

**Learn functions**

The learn (train) functions include `bsnsing`, `bsnsing.formula` and `bsnsing.default`.

**Predict functions**

The predict functions include: `predict.bsnsing` and `predict.mbsnsing`.

**Plot functions**

A `bsnsing` object (tree) can be plotted into a PDF file, or in the form of latex code, by the function `plot.bsnsing`. The ROC curve can be plotted using the function `ROC_func`.

**Auxilliary functions**

Here is a list of internal functions of the package that are open for end users. `summary.bsnsing`, `summary.mbsnsing`, `binarize`, `binarize.numeric`, `binarize.factor`, `binarize.y`, `bslearn`, `bscontrol`

**Author(s)**

Yanchao Liu

---

auto

*auto*

---

**Description**

A test data set.

**Usage**

auto

**Format**

A data frame with 392 rows and 8 variables

**Source**

<https://github.com/profyliu/bsnsing/>

binarize

*Create Binary Variables by the Classification Target***Description**

Create a set of variables (columns) with binary values for each column in the input data. For a variable with values of 0 and 1, the column is retained and no new column is created. For a numeric variable, the function `binarize.numeric` is called. For a factor column, the function `binarize.factor` is called.

**Usage**

```
binarize(
  x,
  y,
  target = stop("'target' (0 or 1) must be provided"),
  control = bscontrol()
)
```

**Arguments**

<code>x</code>	a data frame or matrix to be binarized.
<code>y</code>	a vector with two unique values (0 and 1). It is the response variable that guides the optimal discretization of variables in <code>x</code> .
<code>target</code>	the level of <code>y</code> (0 or 1) which indicates the boolean rule target
<code>control</code>	a list or a <code>bscontrol()</code> object. The list should contain the following three attributes: <i>nseg.numeric</i> , a positive integer indicating the maximum number of segments used in discretizing a numeric variable, <i>nseg.factor</i> , a positive integer indicating the maximum number of levels allowed for a factor variable, and <i>bin.size</i> , a positive integer indicating the minimum number of observations to fall in a segment.

**Value**

a data frame containing binary variables, or a character string describing the rule that perfectly split the target.

**Examples**

```
# Load and prepare data
x <- auto[, c('mpg', 'cylinders', 'displacement')]
x$cylinders <- as.factor(x$cylinders)
y <- ifelse(auto$origin == 'USA', 1L, 0L)
# binarize x by y = 1
bx1 <- binarize(x, y, target = 1)
head(bx1)
# binarize x by y = 0
```

```
bx0 <- binarize(x, y, target = 0)
head(bx0)
# when selecting only one column from a data frame, use drop = FALSE to maintain structure
binarize(auto[, 'mpg', drop = FALSE], y, target = 1)
```

---

binarize.factor      *Create Binary Features based on a Factor Vector*

---

### Description

Create binary dummy variables based on a factor variable. This function is used internally by [binarize](#).

### Usage

```
binarize.factor(x, name, y, segments = 10, bin.size = 5)
```

### Arguments

x	a numeric vector.
name	a character string, the variable name of x.
y	a numeric or integer vector of the same length as x, consisting of two unique values: 0 and 1.
segments	a positive integer indicating the maximum number of levels allowed in the factor variable.
bin.size	a positive integer. It is the minimum number of observations required to fall into each bin.

### Value

a data frame with binary (0 and 1) entries. The column names are indicative of the conditions used to form the corresponding columns.

---

binarize.numeric      *Create Binary Features based on a Numeric Vector*

---

### Description

Discretize a continuous variable x by splitting its range at a sequence of cutpoints. The cutpoints are determined so as to effectively split the binary target y. This function is used internally by [binarize](#).

**Usage**

```
binarize.numeric(
  x,
  name,
  y,
  target = stop("Must provide a target, 0 or 1"),
  segments = 10,
  bin.size = 5,
  node.size = 10
)
```

**Arguments**

x	a numeric vector.
name	a character string, the variable name of x.
y	a numeric or integer vector of the same length as x, consisting of two unique values: 0 and 1.
target	a scalar, valued 0 or 1, indicating the target level of y.
segments	a positive integer, any value below 3 is set to 3. It is the maximum number of segments the range of x is divided into.
bin.size	a positive integer. It is the minimum number of observations required to fall into each bin.
node.size	a positive integer. If either child node is smaller than the node.size, do not return the perfect rule.

**Value**

a data frame with binary (0 and 1) entries, or a character string describing the rule that perfectly splits y. If a data frame is returned, the column names are indicative of the conditions used to form the corresponding columns.

---

binarize.y

*Recode a Variable with Two Unique Values into an 0/1 Vector*


---

**Description**

Recode a Variable with Two Unique Values into an 0/1 Vector

**Usage**

```
binarize.y(y, verbose = FALSE)
```

**Arguments**

y	a vector, must contain two unique values.
verbose	a logical value, TRUE or FALSE, indicating whether details are to be printed on the screen.

**Value**

a list with three elements: `y`, a vector of the same length as `y`, whose entries are coded to 0 and 1, `coding.scheme`, a character string describing the map from the original coding to 0/1 coding, and `ycode`, a character vector containing the original level names of `y`.

**Examples**

```
y <- factor(c('good', 'bad', 'good', 'good', 'bad'))
(yb <- binarize.y(y))
y <- c(TRUE, FALSE, FALSE, FALSE, TRUE)
(yb <- binarize.y(y))
y <- c(1, 2, 2, 1, 2)
(yb <- binarize.y(y))
```

---

BreastCancer

*BreastCancer*

---

**Description**

A test data set.

**Usage**

BreastCancer

**Format**

A data frame with 699 rows and 10 variables.

**Source**

<https://github.com/profyliu/bsnsing/>

---

bscontrol

*Define Parameters for the `bsnsing` Fit*

---

**Description**

Define Parameters for the `bsnsing` Fit

**Usage**

```
bscontrol(
  bin.size = 5,
  nseg.numeric = 20,
  nseg.factor = 20,
  num2factor = 10,
  node.size = 0,
  stop.prob = 0.9999,
  opt.solver = c("enum_c", "enum"),
  solver.timelimit = 180,
  max.rules = 2,
  opt.model = c("gini", "error"),
  greedy.level = 0.9,
  import.external = TRUE,
  suppress.internal = FALSE,
  no.same.gender.children = FALSE,
  n0n1.cap = 40000,
  verbose = FALSE
)
```

**Arguments**

<code>bin.size</code>	the minimum number of observations required in a binarization bucket.
<code>nseg.numeric</code>	the maximum number of segments the range of a numeric variable is divided into for each inequality direction.
<code>nseg.factor</code>	the maximum number of unique levels allowed in a factor variable.
<code>num2factor</code>	an equality binarization rule will be created for each unique value of a numeric variable (in addition to the inequality binarization attempt), if the number of unique values of the numeric variable is less than <code>num2factor</code> .
<code>node.size</code>	if the number of training cases falling into a tree node is fewer than <code>node.size</code> , the node will become a leaf and no further split will be attempted on it; in addition, do not split a node if either child node that would result from the split contains fewer than <code>node.size</code> observation. Default is 0, which indicates that the <code>node.size</code> will be set automatically according to this formula: $\text{floor}(\text{sqrt}(\text{Number of training cases}))$ .
<code>stop.prob</code>	if the proportion of the majority class in a tree node is greater than <code>stop.prob</code> , the node will become a leaf and no further split will be attempted on it.
<code>opt.solver</code>	a character string in the set 'enum', 'enum_c', 'gurobi', 'cplex', 'lpSolve', 'greedy' indicating the optimization solver to be used in the program. The choice of 'cplex' requires the package <code>cplexAPI</code> , 'gurobi' requires the package <code>gurobi</code> , and 'lpSolve' requires the package <code>lpSolve</code> . These solver options are only available in the full version at <a href="https://github.com/profyliu/bsnsing/">https://github.com/profyliu/bsnsing/</a> . The default (and the best) is 'enum_c'.
<code>solver.timelimit</code>	the solver time limit in seconds. Note that this limits the time it takes to optimize each node split.



<code>max.rules</code>	the maximum number of features allowed to enter an OR-clause split rule. A small <code>max.rules</code> reduces the search space and regulates model complexity. Default is 2.
<code>opt.model</code>	a character string in the set 'gini','error' indicating the optimization model to solve in the program. The default is 'gini'. The 'error' option is not available in the current version.
<code>greedy.level</code>	a proportion value between 0 and 1, applicable only when <code>opt.solver</code> is 'greedy'. In the greedy forward selection process of split rules, a candidate rule is added to the OR-clause only if the split performance (gini reduction or accuracy) after the addition multiplied by <code>greedy.level</code> would still be greater than the split performance before the addition. A higher value of <code>greedy.level</code> tend to more aggressively produce multi-variable splits. Only available in the full version.
<code>import.external</code>	logical value indicating whether or not to try importing candidate split rules from other decision tree packages. Default is True.
<code>suppress.internal</code>	logical value indicating whether or not to suppress the feature binarization process that creates the pool of binary features. If it is set to True, then only the features imported from external methods (if <code>import.external</code> is True) will be used in the optimal rule selection model. Default is FALSE.
<code>no.same.gender.children</code>	logical value indicating whether or not to suppress splits that would result in both children having the same majority class. Default is FALSE.
<code>n0n1.cap</code>	a positive integer. It is applicable only when the <code>opt.solver</code> is 'hybrid' and the <code>opt.model</code> is 'gini'. When the <code>bslearn</code> function is called, if the product of the number of negative cases ( <code>n0</code> ) and the number of positive cases ( <code>n1</code> ) is greater than this number, 'enum' solver will be used; otherwise, gurobi solver will be used. Only available in the full version.
<code>verbose</code>	a logical value (TRUE or FALSE) indicating whether the solution details are to be printed on the screen.

## Value

An object of class `bscontrol`.

## Examples

```
bscontrol() # display the default parameters
bsc <- bscontrol(stop.prob = 0.8, nseg.numeric = 10, verbose = TRUE)
bsc
```

---

 bslearn

*Find the Optimal Boolean Rule for Binary Classification*


---

### Description

The function solves a mixed integer program (MIP) to maximize the Gini reduction (`opt.model = 'gini'`) or minimize the number of misclassified cases (`opt.model = 'error'`).

### Usage

```
bslearn(bx, y, control = bscontrol())
```

### Arguments

`bx` a data frame with binary (0 and 1) entries.  
`y` an integer vector with binary entries.  
`control` an object of class `bscontrol()`, specifying the algorithmic parameters. The list should contain the following attributes: `opt.model`, a character string in `'gini'`, `'error'` indicating the optimization model to solve, `opt.solver`, a character string in `'enum_c'`, `'enum'` indicating the algorithm to be used.

### Value

a list containing the splitting solution.

### Examples

```
x <- auto[, c('mpg', 'cylinders', 'displacement')]
y <- ifelse(auto$origin == 'USA', 1L, 0L)
# binarize x by y = 1
bx <- binarize(x, y, target = 1)
# learn the optimal Boolean rule
bssol <- bslearn(bx, y, bscontrol(opt.solver = 'enum'))
cat(paste("Optimal rule:" , bssol$rules, "\n"))
```

---

 bsnsing

*Learn a Classification Tree using Boolean Sensing*


---

### Description

Depending on the arguments provided, either `bsnsing.default` or `bsnsing.formula` will be called.

### Usage

```
bsnsing(x, ...)
```

**Arguments**

`x` a data frame or a [formula](#) object.  
`...` arguments passed on to [bsnsing.default](#) or [bsnsing.formula](#).

**Value**

an object of class `bsnsing` for a two-class problem or an object of class `mbsnsing` for a multi-class problem.

**Examples**

```
# Use the formula format
bs <- bsnsing(Class~., data = BreastCancer)
summary(bs)
# For multi-class classification
bs <- bsnsing(Species ~ ., data = iris)
summary(bs)
summary(bs[[1]]) # display the tree for the first class
summary(bs[[2]]) # display the tree for the second class
summary(bs[[3]]) # display the tree for the third class
predict(bs, type = 'class') # the fitted class membership
predict(bs, type = 'prob') # the fitted probabilities

# Use the (x, y) format, y must have two levels
y <- ifelse(iris$Species == 'setosa', 1L, 0L)
x <- iris[, c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')]
bs <- bsnsing(x, y, verbose = TRUE)
summary(bs)
```

---

 bsnsing.default

*Learn a Classification Tree with Boolean Sensing*


---

**Description**

This is the default method for `bsnsing` and handles binary classification only. [bsnsing.formula](#), which calls `bsnsing.default` as the basic tree builder, can handle multiclass classification problems. Missing values in numeric variables are imputed as the median of the non-missing ones, and missing values in factor variables are treated as a separate level named 'NA'.

**Usage**

```
## Default S3 method:
bsnsing(x, y, controls = bscontrol(), ...)
```

**Arguments**

x	a data frame containing independent variables. Columns can be of numeric, integer, factor and logical types. The column names must be proper identifiers (e.g., must start with a letter, cannot contain special characters and spaces, etc.).
y	a vector of the response variable. The response variable can be of an integer, numeric, logical or factor type, but must have only two unique values. Typical coding of a binary response variable is 0 (for negative case) and 1 (for positive cases).
controls	an object of class <code>bscontrol</code> .
...	further argument to be passed to <code>bsnsing.default</code> .

**Value**

an object of class `bsnsing`.

**Examples**

```
y <- ifelse(iris$Species == 'setosa', 1L, 0L)
x <- iris[, c('Sepal.Length', 'Sepal.Width', 'Petal.Length', 'Petal.Width')]
bs <- bsnsing(x, y, verbose = TRUE)
summary(bs)
```

---

bsnsing.formula

*Learn a Classification Tree using Boolean Sensing*

---

**Description**

The program builds a binary classification tree for each unique value in the response variable. Each tree classifies a target value against all the other values (internally coded as 'all.other') in the response variable. If the response variable is a numeric type, the number of unique values must not exceed 30. There is no programmatic restriction on the number of unique levels for a factor response.

**Usage**

```
## S3 method for class 'formula'
bsnsing(formula, data, subset, na.action = stats::na.pass, ...)
```

**Arguments**

formula	an object of class " <code>formula</code> ": a symbolic description of the model to be fitted.
data	an optional data frame, list or environment (or object coercible by <code>as.data.frame</code> to a data frame) containing the variables in the model. If not found in data, the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>bsnsing.formula</code> is called.

subset	an optional vector specifying a subset (in terms of index numbers, not actual data) of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain NAs. If <code>na.pass</code> is used, <code>bsnsing</code> will still apply an internal NA treatment logic, as follows: missing values in numeric variables will be replaced by the median of the non-missing values of the variable; missing values in factor variables will be treated as a separate level named 'NA'.
...	additional arguments to be passed to the low level fitting functions, e.g., elements in the <code>bscontrol</code> object.

**Value**

an object of `bsnsing` for a two-class problem or an object of `mbsnsing` for a multi-class problem.

**Examples**

```
# Multi-class classification
bs <- bsnsing(Species ~ ., data = iris)
summary(bs)
summary(bs[[1]]) # display the tree for the first class
summary(bs[[2]]) # display the tree for the second class
summary(bs[[3]]) # display the tree for the third class

# Two-class classification
bs <- bsnsing(origin ~ mpg + displacement + horsepower + weight, data = auto, verbose = TRUE)
summary(bs)
```

---

 GlaucomaMVF

*GlaucomaMVF*


---

**Description**

A test dataset

**Usage**

```
GlaucomaMVF
```

**Format**

A data frame with 170 rows and 67 variables:

**Source**

<https://github.com/profyliu/bsnsing/>

---

`import_external_rules` *Import split rules from other packages*

---

**Description**

Run other decision tree functions available in the system and collect the node split rules for optimal selection in bsnsing.

**Usage**

```
import_external_rules(x, y, verbose)
```

**Arguments**

<code>x</code>	a data frame.
<code>y</code>	a binary vector.
<code>verbose</code>	a logical value.

**Value**

a vector of character strings.

---

<code>iris</code>	<i>iris</i>
-------------------	-------------

---

**Description**

A test data set.

**Usage**

```
iris
```

**Format**

A data frame with 150 rows and 5 variables.

**Source**

<https://github.com/profyliu/bsnsing/>

---

mbsnsing-class	<i>A class that contains multi-class classification model built by bsnsing. Can be used in summary and predict functions.</i>
----------------	---

---

### Description

A class that contains multi-class classification model built by bsnsing. Can be used in summary and predict functions.

---

plot.bsnsing	<i>Generate latex code for plotting a bsnsing tree</i>
--------------	--

---

### Description

If the file argument is supplied, this function will invoke the external programs latex, dvips and ps2pdf. If these programs are not available, only the latex code will be generated. If the file argument is left empty, the latex code will be written to the console screen. The latex code utilizes the following packages: pstricks, pst-node, pst-tree.

### Usage

```
## S3 method for class 'bsnsing'
plot(
  x,
  file = "",
  class_labels = c(),
  class_colors = c("red", "green"),
  rule_font = c("footnotesize", "scriptsize", "tiny", "normalsize", "small"),
  rule_color = "blue",
  footnote = FALSE,
  landscape = FALSE,
  papersize = c("a0paper", "a1paper", "a2paper", "a3paper", "a4paper", "a5paper",
    "a6paper", "b0paper", "b1paper", "b2paper", "b3paper", "b4paper", "b5paper",
    "b6paper", "c0paper", "c1paper", "c2paper", "c3paper", "c4paper", "c5paper",
    "c6paper", "b0j", "b1j", "b2j", "b3j", "b4j", "b5j", "b6j", "ansiapaper",
    "ansibpaper", "ansicpaper", "ansidpaper", "ansiepaper", "letterpaper",
    "executivepaper", "legalpaper"),
  verbose = FALSE,
  ...
)
```

**Arguments**

x	an object of class <code>bsnsing</code> .
file	a writable connection or a character string naming the file to write to. If not supplied, the output will be written to the console.
class_labels	a character vector of two elements for leaf node label (for 0 and 1). If empty, the labels will be read from the <code>bsnsing</code> object.
class_colors	a character vector of two elements for leaf node color (for 0 and 1)
rule_font	a string specifying the font size of the split rule at each non-leaf node
rule_color	a string specifying the color of the split rule and node, e.g., blue, gray, black, etc. For a list of all usable colors, see <a href="https://en.wikibooks.org/wiki/LaTeX/Colors">https://en.wikibooks.org/wiki/LaTeX/Colors</a>
footnote	a boolean value indicating whether to add annotation text to the PDF page. The default is FALSE.
landscape	a boolean value indicating if the PDF page should be in landscape layout. The default is FALSE.
papersize	a string specifying the PDF paper size. The default is 'a0paper'.
verbose	a logical value, default is FALSE.
...	further parameters to the plot function.

**Value**

No return value.

**Examples**

```
bs <- bsnsing(Class ~ ., data = GlaucomaMVF)
plot(bs)
## Not run:
plot(bs, file = 'GlaucomaMVF_tree.pdf')
plot(bs, file = 'GlaucomaMVF_tree_letterpaper.pdf', paper='letterpaper')

## End(Not run)
```

---

plot.mbsnsing

*Generate latex code for plotting an mbsnsing tree*


---

**Description**

Users are advised to plot each `bsnsing` tree separately.

**Usage**

```
## S3 method for class 'mbsnsing'
plot(x, ...)
```



**Arguments**

x                    an object of class `mbsnsing`.  
 ...                  further arguments to the plot function.

**Value**

No return value.

---

predict.bsnsing            *Make Predictions with a Fitted `bsnsing` Model*

---

**Description**

Implements the generic predict function to make predictions on new data using a trained `bsnsing` model.

**Usage**

```
## S3 method for class 'bsnsing'
predict(object, newdata = NULL, type = c("prob", "class"), ...)
```

**Arguments**

object                a `bsnsing` model object.  
 newdata              a optional data frame in which to look for variables for prediction. If omitted, the fitted class or probability will be returned.  
 type                  a character string indicating the type of prediction. `'prob'` predicts the probability of being a positive case (i.e.,  $y = 1$ ), and `'class'` predicts the class membership.  
 ...                   further arguments to predict.bsnsing.

**Value**

a vector containing the predicted values.

**Examples**

```
# Load data
n <- nrow(GlaucomaMVF)
train_index = sample(1:n, round(0.5*n))
test_index = setdiff(1:n, train_index)
# Fit a model using training set
bs <- bsnsing(Class ~ ., data = GlaucomaMVF, subset = train_index)
# Make predictions on the test set
pred <- predict(bs, GlaucomaMVF[test_index, ], type = 'class')
# Display the confusion matrix
table(pred, actual = GlaucomaMVF[test_index, 'Class'])
```

---

predict.mbsnsing      *Make Predictions with a [bsnsing](#) Model*

---

## Description

Make Predictions with a [bsnsing](#) Model

## Usage

```
## S3 method for class 'mbsnsing'  
predict(object, newdata = NULL, type = c("prob", "class"), ...)
```

## Arguments

object	an object of class <a href="#">mbsnsing</a> .
newdata	an optional data frame in which to look for variables for prediction. If omitted, the fitted class or probability will be returned.
type	a character string indicating the type of prediction. <i>'prob'</i> predicts the probability of being in each class, and <i>'class'</i> predicts the class membership.
...	further arguments to predict.mbsnsing.

## Value

a data frame containing the predicted values.

## Examples

```
n <- nrow(iris)  
train_index <- sample(1:n, round(0.5*n))  
test_index <- setdiff(1:n, train_index)  
# Fit a model on the training set  
bs <- bsnsing(Species ~ ., data = iris, subset = train_index)  
# Make predictions on the test set  
pred <- predict(bs, iris[test_index, ], type = 'class')  
# Display the confusion matrix  
table(pred, actual = iris[test_index, 'Species'])  
# Predict the probabilities  
predprob <- predict(bs, iris[test_index, ], type = 'prob')  
head(predprob)
```

---

print.bscontrol      *Print the Object of Class [bscontrol](#)*

---

**Description**

Print the Object of Class [bscontrol](#)

**Usage**

```
## S3 method for class 'bscontrol'  
print(x = bscontrol(), ...)
```

**Arguments**

x                    an object of class [bscontrol](#).  
...                   further arguments to the print function.

**Value**

No return value.

---

print.bsnsing      *Print the Object of Class [bsnsing](#)*

---

**Description**

Print the Object of Class [bsnsing](#)

**Usage**

```
## S3 method for class 'bsnsing'  
print(x, print.call = TRUE, ...)
```

**Arguments**

x                    an object of class [bsnsing](#).  
print.call          print out the function called, default TRUE.  
...                   further arguments.

**Value**

No return value.

print.mbsnsing      *Print the Object of Class [mbsnsing](#)*

---

**Description**

Print the Object of Class [mbsnsing](#)

**Usage**

```
## S3 method for class 'mbsnsing'  
print(x, ...)
```

**Arguments**

x                    an object of class [mbsnsing](#).  
...                   further arguments.

**Value**

No return value.

---

print.summary.bsnsing      *Print the Summary of [bsnsing](#) Model*

---

**Description**

Print the Summary of [bsnsing](#) Model

**Usage**

```
## S3 method for class 'summary.bsnsing'  
print(x, print.call = TRUE, ...)
```

**Arguments**

x                    an object of class [summary.bsnsing](#).  
print.call           a logical value, print out the function called if TRUE.  
...                   further arguments.

**Value**

No return value.

---

```
print.summary.mbsnsing
```

*Print the summary of [mbsnsing](#) model fits*

---

**Description**

Print the summary of [mbsnsing](#) model fits

**Usage**

```
## S3 method for class 'summary.mbsnsing'  
print(x, ...)
```

**Arguments**

x	an object of class <a href="#">summary.mbsnsing</a> .
...	further arguments.

**Value**

No return value.

---

```
rcpp_bslearn
```

*C implementation of the bslearn function*

---

**Description**

C implementation of the bslearn function

**Usage**

```
rcpp_bslearn(  
  nrows,  
  ncols,  
  input_y,  
  input_x,  
  grp,  
  max_rules,  
  max_time,  
  node_size,  
  no_same_gender_children,  
  verbose  
)
```

**Arguments**

nrows	number of rows
ncols	number of columns
input_y	Integer vector
input_x	Integer matrix
grp	group membership indices
max_rules	max number of rules
max_time	max running time in seconds
node_size	minimum node size
no_same_gender_children	if TRUE child nodes must be of different predicted classes
verbose	verbose level

**Value**

a list containing four elements

---

ROC_func	<i>Plot the ROC curve and calculate the AUC</i>
----------	---

---

**Description**

This is a general utility function, not part of the bsnsing functionality.

**Usage**

```
ROC_func(
  df,
  label_colnum,
  score_colnum,
  pos.label = "1",
  plot.ROC = FALSE,
  add_on = FALSE,
  color = "black",
  lty = 1
)
```

**Arguments**

df	a data frame which must contain at least these two columns: the prediction scores (numeric values, not necessarily be between 0 and 1) and the true class labels.
label_colnum	the column index of the scores column in df.
score_colnum	the column index of the true class labels column in df.

pos.label	a character string matching the positive class label used in the class labels column.
plot.ROC	a logical value indicating whether the ROC curve should be plotted.
add_on	a logical value indicating whether the ROC curve should be added to an existing plot.
color	a character string specifying the color of the ROC curve in the plot.
lty	line type used in the plot, 1 solid, 2 dashed, etc.

**Value**

a numeric value representing the area under the ROC curve (AUC).

**Examples**

```
n <- nrow(BreastCancer)
trainset <- sample(1:n, 0.7*n) # randomly sample 70% for training
testset <- setdiff(1:n, trainset) # the remaining is for testing
# Build a tree to predict Class, using all default options
bs <- bsnsing(Class~., data = BreastCancer[trainset,])
summary(bs) # display the tree structure
pred <- predict(bs, BreastCancer[testset,], type='class')
actual <- BreastCancer[testset, 'Class']
table(pred, actual) # display the confusion matrix
# Plot the ROC curve and display the AUC
ROC_func(data.frame(predict(bs, BreastCancer[testset,]),
                    BreastCancer[testset, 'Class']),
          2, 1, pos.label = 'malignant', plot.ROC=TRUE)
```

summary.bsnsing

*Summarize the bsnsing Model Fits***Description**

Summarize the bsnsing Model Fits

**Usage**

```
## S3 method for class 'bsnsing'
summary(object = stop("no 'object' arg"), ...)
```

**Arguments**

object	an object of class <code>bsnsing</code> .
...	further arguments.

**Value**

a list of detailed information in the given object.

---

summary.mbsnsing      *Summarize mbsnsing Model Fits*

---

**Description**

Summarize mbsnsing Model Fits

**Usage**

```
## S3 method for class 'mbsnsing'  
summary(object = stop("no 'object' arg"), ...)
```

**Arguments**

object            an object of class [mbsnsing](#).  
...                further arguments.

**Value**

a list of detailed information in the given object.



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