

# Package ‘FSelectorRcpp’

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**Type** Package

**Title** 'Rcpp' Implementation of 'FSelector' Entropy-Based Feature Selection Algorithms with a Sparse Matrix Support

**Version** 0.3.1

**Description** 'Rcpp' (free of 'Java'/'Weka') implementation of 'FSelector' entropy-based feature selection algorithms based on an MDL discretization (Fayyad U. M., Irani K. B.: Multi-Interval Discretization of Continuous-Valued Attributes for Classification Learning. In 13'th International Joint Conference on Uncertainty in Artificial Intelligence (IJ-CAI93), pages 1022-1029, Chambery, France, 1993.) <<https://www.ijcai.org/Proceedings/93-2/Papers/022.pdf>> with a sparse matrix support. It is also equipped with a parallel backend.

**Depends** R (>= 3.4)

**License** GPL-2

**LazyData** TRUE

**SystemRequirements** C++11

**Imports** Rcpp (>= 0.12.12), foreach, iterators

**LinkingTo** Rcpp, BH, RcppArmadillo, testthat

**Suggests** testthat, Matrix, RcppArmadillo, dplyr, RWeka, entropy, FSelector, randomForest, doParallel, rpart, MASS, covr, parallel, htmltools, magrittr, knitr, RTCGA.rnaseq, ggplot2, microbenchmark, pbapply, tibble, rmarkdown, lintr, pkgdown

**RoxygenNote** 6.1.0

**Encoding** UTF-8

**BugReports** <https://github.com/mi2-warsaw/FSelectorRcpp/issues>

**URL** <http://mi2-warsaw.github.io/FSelectorRcpp/>

**VignetteBuilder** knitr

**NeedsCompilation** yes

**Author** Zygmunt Zawadzki [aut, cre],  
Marcin Kosinski [aut],  
Krzysztof Slomczynski [ctb],  
Damian Skrzypiec [ctb]

**Maintainer** Zygmunt Zawadzki <zygmunt@zstat.pl>

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cut_attrs	<i>Select Attributes by Score Depending on the Cutoff</i>
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### Description

Select attributes by their score/rank/weights, depending on the cutoff that may be specified by the percentage of the highest ranked attributes or by the number of the highest ranked attributes.

### Usage

```
cut_attrs(attrs, k = 0.5)
```

### Arguments

attrs	A <a href="#">data.frame</a> with attributes' importance.
k	A numeric. For $k \geq 1$ it takes $\text{floor}(k)$ and then it indicates how many attributes to take with the highest attribute rank (chooses $k$ best attributes). For $0 < k < 1$ it stands for the percent of top attributes to take (chooses best $k * 100\%$ of attributes).

### Author(s)

Damian Skrzypiec <damian.j.skrzypiec@gmail.com> and Zygmunt Zawadzki <zygmunt@zstat.pl>

### Examples

```
x <- information_gain(Species ~ ., iris)
cut_attrs(attrs = x)
to_formula(cut_attrs(attrs = x), "Species")
cut_attrs(attrs = x, k = 1)
```

---

`discretize`*Discretization*

---

**Description**

Discretize a range of numeric attributes in the dataset into nominal attributes. Minimum Description Length (MDL) method is set as the default control. There is also available `equalsizeControl` method.

**Usage**

```
discretize(x, y, control = list(mdlControl(), equalsizeControl()),  
  all = TRUE, discIntegers = TRUE, call = NULL)
```

```
mdlControl()
```

```
equalsizeControl(k = 10)
```

```
customBreaksControl(breaks)
```

**Arguments**

<code>x</code>	Explanatory continuous variables to be discretized or a <a href="#">formula</a> .
<code>y</code>	Dependent variable for supervised discretization or a <a href="#">data.frame</a> when <code>x</code> is a <a href="#">formula</a> .
<code>control</code>	<code>discretizationControl</code> object containing the parameters for discretization algorithm. Possible inputs are <code>mdlControl</code> or <code>equalsizeControl</code> , so far. If passed as a list, the first element is used.
<code>all</code>	Logical indicating if a returned <a href="#">data.frame</a> should contain other features that were not discretized. (Example: should <code>Sepal.Width</code> be returned, when you pass <code>iris</code> and discretize <code>Sepal.Length</code> , <code>Petal.Length</code> , <code>Petal.Width</code> .)
<code>discIntegers</code>	logical value. If true (default), then integers are treated as numeric vectors and they are discretized. If false integers are treated as factors and they are left as is.
<code>call</code>	Keep as NULL. Inner method parameter for consistency.
<code>k</code>	Number of partitions.
<code>breaks</code>	custom breaks used for partitioning.

**Author(s)**

Zygmunt Zawadzki <[zygmunt@zstat.pl](mailto:zygmunt@zstat.pl)>

**References**

U. M. Fayyad and K. B. Irani. Multi-Interval Discretization of Continuous-Valued Attributes for Classification Learning. In 13th International Joint Conference on Uncertainty in Artificial Intelligence (IJCAI93), pages 1022-1029, 1993.

**Examples**

```

# vectors
discretize(x = iris[[1]], y = iris[[5]])

# list and vector
head(discretize(x = list(iris[[1]], iris$Sepal.Width), y = iris$Species))

# formula input
head(discretize(x = Species ~ ., y = iris))
head(discretize(Species ~ ., iris))

# use different methods for specific columns
ir1 <- discretize(Species ~ Sepal.Length, iris)
ir2 <- discretize(Species ~ Sepal.Width, ir1, control = equalsizeControl(3))
ir3 <- discretize(Species ~ Petal.Length, ir2, control = equalsizeControl(5))
head(ir3)

# custom breaks
ir <- discretize(Species ~ Sepal.Length, iris,
  control = customBreaksControl(breaks = c(0, 2, 5, 7.5, 10)))
head(ir)

## Not run:
# Same results
library(RWeka)
Rweka_disc_out <- RWeka::Discretize(Species ~ Sepal.Length, iris)[, 1]
FSelectorRcpp_disc_out <- FSelectorRcpp::discretize(Species ~ Sepal.Length,
  iris)[, 1]
table(Rweka_disc_out, FSelectorRcpp_disc_out)
# But faster method
library(microbenchmark)
microbenchmark(FSelectorRcpp::discretize(Species ~ Sepal.Length, iris),
  RWeka::Discretize(Species ~ Sepal.Length, iris))

## End(Not run)

```

---

discretize\_transform *Transform a data.frame using split points returned by discretize function.*

---

**Description**

Transform a data.frame using split points returned by discretize function.

**Usage**

```
discretize_transform(disc, data, dropColumns = NA)

extract_discretize_transformer(disc)
```

**Arguments**

disc	a result of the <a href="#">discretize</a> function.
data	a data.frame to transform using cutpoints from disc.
dropColumns	determine

**Value**

A new data.frame with discretized columns using cutpoints from the result of discretize function.

**Examples**

```
set.seed(123)
idx <- sort(sample.int(150, 100))
iris1 <- iris[idx, ]
iris2 <- iris[-idx, ]
disc <- discretize(Species ~ ., iris)
head(discretize_transform(disc, iris2))

# Chain discretization:
ir1 <- discretize(Species ~ Sepal.Length, iris1)
ir2 <- discretize(Species ~ Sepal.Width, ir1, control = equalsizeControl(3))
ir3 <- discretize(Species ~ Petal.Length, ir2, control = equalsizeControl(5))

## note that Petal.Width is untouched:
head(discretize_transform(ir3, iris2))

## extract_discretize_transformer
discObj <- extract_discretize_transformer(ir3)
head(discretize_transform(discObj, iris2))
```

**Description**

A convenience wrapper for greedy and exhaustive feature selection algorithms that extract valuable attributes depending on the evaluation method (called evaluator). This function is a reimplementation of **FSelector**'s [exhaustive.search](#) and [greedy.search](#).

**Usage**

```
feature_search(attributes, fun, data, mode = c("greedy", "exhaustive"),
  type = c("forward", "backward"), sizes = 1:length(attributes),
  parallel = TRUE, ...)
```

**Arguments**

attributes	A character vector with attributes' names to be used to extract the most valuable features.
fun	A function (evaluator) to be used to score features' sets at each iteration of the algorithm passed via mode. See Examples.
data	A data set for fun function (evaluator).
mode	A character that determines which search algorithm to perform. Default is "greedy".
type	Used when mode = "greedy" - whether to use the backward or the forward multiple-way search. Default is "forward".
sizes	Used when mode = "exhaustive" - a vector of sizes of attributes subsets.
parallel	Allow parallelization.
...	Other arguments passed to <a href="#">foreach</a> function.

**Details**

The evaluator function passed with fun is used to determine the importance score of current features' subset. The score is used in a multiple-way (backward or forward) greedy algorithm as a stopping moment or as a selection criterion in the exhaustive search that checks all possible attributes' subset combinations (of sizes passed in sizes).

**Value**

A list with following components

- best - a [data.frame](#) with the best subset and it's score (1 - feature used, 0 - feature not used),
- all - a [data.frame](#) with all checked features' subsets and their score (1 - feature used, 0 - feature not used),
- data - the data used in the feature selection,
- fun - the evaluator used to compute the score of importance for features' subsets,
- call - an origin call of the feature\_search,
- mode - the mode used in the call.

**Note**

Note that score depends on the evaluator you provide in the fun parameter.

**Author(s)**

Zygmunt Zawadzki <zygmunt@zstat.pl>

Krzysztof Slomczynski <krzysztofslomczynski@gmail.com>

**Examples**

```
# Enable parallelization in examples
## Not run:
library(doParallel)
cl <- makeCluster(2)
registerDoParallel(cl)

## End(Not run)
# Close at the end
# stopCluster(cl) #nolint
# registerDoSEQ() #nolint

# 1) Evaluator from FSelector package.
evaluator <- function(subset, data, dependent = names(iris)[5]) {
  library(rpart)
  k <- 5
  splits <- runif(nrow(data))
  results <- sapply(1:k, function(i) {
    test.idx <- (splits >= (i - 1) / k) & (splits < i / k)
    train.idx <- !test.idx
    test <- data[test.idx, , drop = FALSE]
    train <- data[train.idx, , drop = FALSE]
    tree <- rpart(to_formula(subset, dependent), train)
    error.rate <- sum(test[[dependent]] != predict(tree, test, type = "c")) /
      nrow(test)
    return(1 - error.rate)
  })
  return(mean(results))
}

set.seed(123)
# Default greedy search.
system.time(
  feature_search(attributes = names(iris)[-5],
                 fun = evaluator,
                 data = iris)
)
system.time(
  feature_search(attributes = names(iris)[-5],
                 fun = evaluator,
                 data = iris,
                 parallel = FALSE)
)

# Optional exhaustive search.
system.time(
```

```

feature_search(attributes = names(iris)[-5],
              fun = evaluator,
              data = iris,
              mode = "exhaustive")
)
system.time(
  feature_search(attributes = names(iris)[-5],
                fun = evaluator,
                data = iris,
                mode = "exhaustive",
                parallel = FALSE)
)

# 2) Maximize R^2 statistics in the linear regression model/problem.

evaluator_R2_lm <- function(attributes, data, dependent = names(iris)[1]) {
  summary(
    lm(to_formula(attributes, dependent), data = data)
  )$r.squared
}

feature_search(attributes = names(iris)[-1],
              fun = evaluator_R2_lm, data = iris,
              mode = "exhaustive")

# 3) Optimize BIC criterion in generalized linear model.
# Aim of Bayesian approach it to identify the model with the highest
# probability of being the true model. - Kuha 2004

utils::data(anorexia, package = "MASS")

evaluator_BIC_glm <- function(attributes, data, dependent = "Postwt") {
  extractAIC(
    fit = glm(to_formula(attributes, dependent), family = gaussian,
              data = data),
    k = log(nrow(data))
  )[2]
}

feature_search(attributes = c("Prewt", "Treat", "offset(Prewt)"),
              fun = evaluator_BIC_glm,
              data = anorexia,
              mode = "exhaustive")

# Close parallelization
## Not run:
stopCluster(c1)
registerDoSEQ()

## End(Not run)

```



---

information_gain	<i>Entropy-based Filters</i>
------------------	------------------------------

---

### Description

Algorithms that find ranks of importance of discrete attributes, basing on their entropy with a continuous class attribute. This function is a reimplementation of **FSelector**'s [information\\_gain](#), [gain\\_ratio](#) and [symmetrical\\_uncertainty](#).

### Usage

```
information_gain(formula, data, x, y, type = c("infogain", "gainratio",
      "symuncert"), equal = FALSE, discIntegers = TRUE, threads = 1)
```

### Arguments

formula	An object of class <a href="#">formula</a> with model description.
data	A <a href="#">data.frame</a> accompanying formula.
x	A <a href="#">data.frame</a> or sparse matrix with attributes.
y	A vector with response variable.
type	Method name.
equal	A logical. Whether to discretize dependent variable with the equal frequency binning discretization or not.
discIntegers	logical value. If true (default), then integers are treated as numeric vectors and they are discretized. If false integers are treated as factors and they are left as is.
threads	Number of threads for parallel backend.

### Details

type = "infogain" is

$$H(Class) + H(Attribute) - H(Class, Attribute)$$

type = "gainratio" is

$$\frac{H(Class) + H(Attribute) - H(Class, Attribute)}{H(Attribute)}$$

type = "symuncert" is

$$2 \frac{H(Class) + H(Attribute) - H(Class, Attribute)}{H(Attribute) + H(Class)}$$

where  $H(X)$  is Shannon's Entropy for a variable  $X$  and  $H(X, Y)$  is a conditional Shannon's Entropy for a variable  $X$  with a condition to  $Y$ .

**Value**

data.frame with the following columns:

- attributes - variables names.
- importance - worth of the attributes.

**Author(s)**

Zygmunt Zawadzki <zygmunt@zstat.pl>

**Examples**

```
irisX <- iris[-5]
y <- iris$Species

## data.frame interface
information_gain(x = irisX, y = y)

# formula interface
information_gain(formula = Species ~ ., data = iris)
information_gain(formula = Species ~ ., data = iris, type = "gainratio")
information_gain(formula = Species ~ ., data = iris, type = "symuncert")

# sparse matrix interface
library(Matrix)
i <- c(1, 3:8); j <- c(2, 9, 6:10); x <- 7 * (1:7)
x <- sparseMatrix(i, j, x = x)
y <- c(1, 1, 1, 1, 2, 2, 2, 2)

information_gain(x = x, y = y)
information_gain(x = x, y = y, type = "gainratio")
information_gain(x = x, y = y, type = "symuncert")
```

---

to\_formula

*Create a formula Object*

---

**Description**

Utility function to create a [formula](#) object. Note that it may be very useful when you use pipes.

**Usage**

```
to_formula(attrs, class)
```

**Arguments**

**attrs** Character vector with names of independent variables.  
**class** Single string with a dependent variable's name.

**Examples**

```
# evaluator from FSelector package
evaluator <- function(subset, data, dependent = names(iris)[5]) {
  library(rpart)
  k <- 5
  splits <- runif(nrow(data))
  results <- sapply(1:k, function(i) {
    test.idx <- (splits >= (i - 1) / k) & (splits < i / k)
    train.idx <- !test.idx
    test <- data[test.idx, , drop = FALSE]
    train <- data[train.idx, , drop = FALSE]
    tree <- rpart(to_formula(subset, dependent), train)
    error.rate <- sum(test[[dependent]] != predict(tree, test, type = "c")) /
      nrow(test)
    return(1 - error.rate)
  })
  return(mean(results))
}

set.seed(123)
fit <- feature_search(attributes = names(iris)[-5], fun = evaluator, data = iris,
  mode = "exhaustive", parallel = FALSE)

fit$best
names(fit$best)[fit$best == 1]
# with to_formula
to_formula(names(fit$best)[fit$best == 1], "Species")
```

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