Package 'FSelectorRcpp'

April 28, 2023

Type Package

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

Version 0.3.11

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 Uncertainly in Artificial Intelligence (IJ-
CAI93), pages 1022-1029, Cham-
bery, France, 1993.) <https://www.ijcai.org/Proceedings/93-2/Papers/022.pdf>
with a sparse matrix support.

Depends R (>= 3.4)

License GPL-2

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,
withr

RoxygenNote 7.2.3

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

URL https://github.com/mi2-warsaw/FSelectorRcpp

VignetteBuilder knitr

NeedsCompilation yes

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R **topics documented:**

.information_gain   *Direct Interface to Information Gain.*

Description

Direct Interface to Information Gain.

Usage

```
.information_gain(
  x,
  y,
  type = c("infogain", "gainratio", "symuncert"),
  equal = FALSE,
  discIntegers = TRUE,
  nbins = 5,
  threads = 1
)
```

Arguments

x	A [data.frame](), sparse matrix or formula with attributes.
y	A vector with response variable or data.frame if formula is used.
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.

nbins	Number of bins used for discretization. Only used if 'equal = TRUE' and the response is numeric.
threads	defunct. Number of threads for parallel backend - now turned off because of safety reasons.

Details

In principle using [information_gain](#) is safer.

data.frame with the following columns:

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

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cut_attrs	*Select Attributes by Score Depending on the Cutoff*

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 [data.frame](#) with attributes' importance.
k	A numeric. For k >= 1 it takes 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

x	Explanatory continuous variables to be discretized or a [formula.](#)
y	Dependent variable for supervised discretization or a [data.frame](#) when x ia a [formula.](#)
control	`discretizationControl` object containing the parameters for discretization algorithm. Possible inputs are `mdlControl` or `equalsizeControl`, so far. If passed as a list, the first element is used.
all	Logical indicating if a returned [data.frame](#) should contain other features that were not discretized. (Example: should `Sepal.Width` be returned, when you pass `iris` and discretize `Sepal.Length`, `Petal.Length`, `Petal.Width`.)
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.
call	Keep as `NULL`. Inner method parameter for consistency.
k	Number of partitions.
breaks	custom breaks used for partitioning.

Author(s)

Zygmunt Zawadzki <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 Uncertainly 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 discretize 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))
```

---

feature_search	*General Feature Searching Engine*

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. Defualt 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 foreach 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 crietion 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(cl)
registerDoSEQ()

## End(Not run)
```

---

information_gain   *Entropy-based Filters*

Description

Algorithms that find ranks of importance of discrete attributes, basing on their entropy with a conti-
nous 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,
  nbins = 5,
  threads = 1
)
```

Arguments

formula	An object of class formula with model description.
data	A data.frame accompanying formula.
x	A data.frame 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.
nbins	Number of bins used for discretization. Only used if 'equal = TRUE' and the response is numeric.
threads	defunct. Number of threads for parallel backend - now turned off because of safety reasons.

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 joint 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")
```

---

relief   *RReliefF filter*

Description

The algorithm finds weights of continuous and discrete attributes basing on a distance between instances.

Usage

```
relief(formula, data, x, y, neighboursCount = 5, sampleSize = 10)
```

Arguments

formula	An object of class [formula](#) with model description.
data	A [data.frame](#) accompanying formula.
x	A [data.frame](#) with attributes.
y	A vector with response variable.
neighboursCount	
	number of neighbours to find for every sampled instance
sampleSize	number of instances to sample

Details

The function and it's manual page taken directly from **FSelector**: Piotr Romanski and Lars Kotthoff (2018). FSelector: Selecting Attributes. R package version 0.31. https://CRAN.R-project.org/package=FSelector

Value

a data.frame containing the worth of attributes in the first column and their names as row names

References

Igor Kononenko: Estimating Attributes: Analysis and Extensions of RELIEF. In: European Conference on Machine Learning, 171-182, 1994.

Marko Robnik-Sikonja, Igor Kononenko: An adaptation of Relief for attribute estimation in regression. In: Fourteenth International Conference on Machine Learning, 296-304, 1997.

Examples

```
data(iris)

weights <- relief(Species~., iris, neighboursCount = 5, sampleSize = 20)
print(weights)
subset <- cut_attrs(weights, 2)
f <- to_formula(subset, "Species")
print(f)
```

---

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")
```

Index