Package ‘mldr’

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Title Exploratory Data Analysis and Manipulation of Multi-Label Data Sets

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Description Exploratory data analysis and manipulation functions for multi-label data sets along with an interactive Shiny application to ease their use.

URL https://github.com/fcharte/mldr

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Imports shiny (>= 0.11), XML, circlize, graphics, grDevices, stats, methods

Suggests pROC, knitr, mldr.datasets, testthat

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Generates a new mldr object joining the rows in the two mldrs given as input

Usage

```r
## S3 method for class 'mldr'
mldr1 + mldr2
```

Arguments

- `mldr1` First mldr object to join
- `mldr2` Second mldr object to join

Value

A new mldr object with all rows in the two parameters
==.mldr

Checks if two mldr objects have the same structure

Description
Checks if two mldr objects have the same structure

Usage
## S3 method for class 'mldr'
mldr1 == mldr2

Arguments
mldr1 First mldr object to compare
mldr2 Second mldr object to compare

Value
TRUE if the two mldr objects have the same structure, FALSE otherwise

Averaged metrics Multi-label averaged evaluation metrics

Description
Evaluation metrics based on simple metrics for the confusion matrix, averaged through several criteria.

Usage
accuracy(true_labels, predicted_labels, undefined_value = "diagnose")

precision(true_labels, predicted_labels, undefined_value = "diagnose")

micro_precision(true_labels, predicted_labels, ...)

macro_precision(true_labels, predicted_labels, undefined_value = "diagnose")

recall(true_labels, predicted_labels, undefined_value = "diagnose")

micro_recall(true_labels, predicted_labels, ...)

macro_recall(true_labels, predicted_labels, undefined_value = "diagnose")
fmeasure(true_labels, predicted_labels, undefined_value = "diagnose")

micro_fmeasure(true_labels, predicted_labels, ...)

macro_fmeasure(true_labels, predicted_labels, undefined_value = "diagnose")

Arguments

true_labels Matrix of true labels, columns corresponding to labels and rows to instances.
predicted_labels Matrix of predicted labels, columns corresponding to labels and rows to instances.
undefined_value The value to be returned when a computation results in an undefined value due to a division by zero. See details.
...

Details

Available metrics in this category

- accuracy: Bipartition based accuracy
- fmeasure: Example and binary partition F_1 measure (harmonic mean between precision and recall, averaged by instance)
- macro_fmeasure: Label and bipartition based F_1 measure (harmonic mean between precision and recall, macro-averaged by label)
- macro_precision: Label and bipartition based precision (macro-averaged by label)
- macro_recall: Label and bipartition based recall (macro-averaged by label)
- micro_fmeasure: Label and bipartition based F_1 measure (micro-averaged)
- micro_precision: Label and bipartition based precision (micro-averaged)
- micro_recall: Label and bipartition based recall (micro-averaged)
- precision: Example and bipartition based precision (averaged by instance)
- recall: Example and bipartition based recall (averaged by instance)

Deciding a value when denominators are zero

Parameter undefined_value: The value to be returned when a computation results in an undefined value due to a division by zero. Can be a single value (e.g. NA, 0), a function with the following signature:

function(tp, fp, tn, fn)

or a string corresponding to one of the predefined strategies. These are:

- "diagnose": This strategy performs the following decision:
  - Returns 1 if there are no true labels and none were predicted
Averaged metrics

- Returns 0 otherwise

This is the default strategy, and the one followed by MULAN.

• "ignore": Occurrences of undefined values will be ignored when averaging (averages will be computed with potentially less values than instances/labels). Undefined values in micro-averaged metrics cannot be ignored (will return NA).

• "na": Will return NA (with class numeric) and it will be propagated when averaging (averaged metrics will potentially return NA).

Value

Atomical numeric vector containing the resulting value in the range [0, 1].

See Also

mldr_evaluate, mldr_to_labels

Other evaluation metrics: Basic metrics, Ranking-based metrics

Examples

ture_labels <- matrix(c(
  1,1,1,
  0,0,0,
  1,0,0,
  1,1,1,
  0,0,0,
  1,0,0
), ncol = 3, byrow = TRUE)
predicted_labels <- matrix(c(
  1,1,1,
  0,0,0,
  1,0,0,
  1,1,0,
  1,0,0,
  0,1,0
), ncol = 3, byrow = TRUE)

precision(true_labels, predicted_labels, undefined_value = "diagnose")
macro_recall(true_labels, predicted_labels, undefined_value = 0)
macro_fmeasure(
  true_labels, predicted_labels,
  undefined_value = function(tp, fp, tn, fn) as.numeric(fp == 0 && fn == 0)
)
Basic metrics

Multi-label evaluation metrics

Description

Several evaluation metrics designed for multi-label problems.

Usage

hamming_loss(true_labels, predicted_labels)

subset_accuracy(true_labels, predicted_labels)

Arguments

t_true_labels: Matrix of true labels, columns corresponding to labels and rows to instances.
predicted_labels: Matrix of predicted labels, columns corresponding to labels and rows to instances.

Details

Available metrics in this category

- hamming_loss: describes the average absolute distance between a predicted label and its true value.
- subset_accuracy: the ratio of correctly predicted labelsets.

Value

Resulting value in the range \([0, 1]\)

See Also

mldr_evaluate, mldr_to_labels

Other evaluation metrics: Averaged metrics, Ranking-based metrics

Examples

t_true_labels <- matrix(c(
  1,1,1,
  0,0,0,
  1,0,0,
  1,1,1,
  0,0,0,
  1,0,0
), ncol = 3, byrow = TRUE)
predicted_labels <- matrix(c(
  1,0,0,
  0,1,1,
  1,0,0,
  0,0,0,
  1,1,1,
  0,0,0
), ncol = 3, byrow = TRUE)

Description

birds dataset.

Usage

birds

Format

An mldr object with 645 instances, 279 attributes and 19 labels

Source


Examples

summary(birds)
birds$labels
concurrenceReport  Generates a label concurrence report

Description

This function produces a label concurrence report, providing the average SCUMBLE, SCUMBLE by label, a list with the minority labels most affected by this problem indicating which majority labels they appear with, and a concurrence plot. The report output is written in the standard output by default, but it could be redirected to a PDF file.

Usage

concurrenceReport(mld, pdfOutput = FALSE, file = "Rconcurrence.pdf")

Arguments

mld  mldr object to analyze
pdfOutput  Boolean value indicating if the output has to be sent to a PDF file. Defaults to true, so the output is shown in the console.
file  If the pdfOutput parameter is true the output will be written in the file specified by this parameter. The default file name is Rconcurrence.pdf.

Value

None

See Also

remedial, labelInteractions

Examples

library(mldr)
### Not run:
concurrenceReport(birds)

### End(Not run)
emotions

Description
emotions dataset.

Usage
data(emotions)

Format
An mldr object with 593 instances, 78 attributes and 6 labels

Source

Examples
summary(emotions)
emotions$labels

genbase

Description
genbase dataset.

Usage
data(genbase)

Format
An mldr object with 662 instances, 1213 attributes and 27 labels

Source
**labelInteractions**

*Provides data about interactions between labels*

**Examples**

```r
summary(genbase)
genbase$labels
```

**Description**

This function facilitates a list with the minority labels most affected by the problem of concurrence with majority labels, providing the indexes of the majority labels interacting with each minority and also the number of instances in which they appear together.

**Usage**

```r
labelInteractions(mld, labelProportion)
```

**Arguments**

- **mld** — mldr object to analyze
- **labelProportion**
  
  A value in the (0,1] range establishing the proportion of minority labels to be included as result. By default at least 3 or 10% of minority labels are included, or all of them if there are fewer than 3.

**Value**

A list with two slots, indexes and interactions. The former contains the indexes of the minority labels, sorted from higher to lower SCUMBLE metric. The latter will provide an element for each of the previous labels, communicating the indexes of the majority labels it interacts with and the number of samples in which they appear together.

**See Also**

`remedial, concurrenceReport`

**Examples**

```r
library(mldr)
labelInteractions(birds)
```
mldr

*mldr*  
*Creates an object representing a multilabel dataset*

**Description**
Reads a multilabel dataset from a file and returns an mldr object containing the data and additional measures. The file has to be in ARFF format. The label information could be in a separate XML file (MULAN style) or in the the arff header (MEKA style).

**Usage**
```
mldr(filename, use_xml = TRUE, auto_extension = TRUE, xml_file, 
    label_indices, label_names, label_amount, 
    force_read_from_file = !all(c(missing(xml_file), 
    missing(label_indices), missing(label_names), missing(label_amount), 
    use_xml, auto_extension)), ...
```

**Arguments**
- **filename**: Name of the dataset
- **use_xml**: Specifies whether to use an associated XML file to identify the labels. Defaults to TRUE
- **auto_extension**: Specifies whether to add the `.arff` and `.xml` extensions to the filename where appropriate. Defaults to TRUE
- **xml_file**: Path to the XML file. If not provided, the filename ending in ".xml" will be assumed
- **label_indices**: Optional vector containing the indices of the attributes that should be read as labels
- **label_names**: Optional vector containing the names of the attributes that should be read as labels
- **label_amount**: Optional parameter indicating the number of labels in the dataset, which will be taken from the last attributes of the dataset
- **force_read_from_file**: Set this parameter to TRUE to always read from a local file, or set it to FALSE to look for the dataset within the `mldr.datasets` package
- **...**: Extra parameters to be passed to `read_arff`

**Value**
An mldr object containing the multilabel dataset

**See Also**
`mldr_from_dataframe`, `read.arff`, `summary.mldr`
Examples

library(mldr)
## Not run:
# Read "yeast.arff" and labels from "yeast.xml"
mymld <- mldr("yeast")

# Read "yeast.arff" and labels from "yeast.xml", converting categorical
# attributes to factors
mymld <- mldr("yeast", stringsAsFactors = TRUE)

# Read "yeast-tra.arff" and labels from "yeast.xml"
mymld <- mldr("yeast-tra", xml_file = "yeast.xml")

# Read "yeast.arff" specifying the amount of attributes to be used as labels
mymld <- mldr("yeast", label_amount = 14)

# Read MEKA style dataset, without XML file and giving extension
mymld <- mldr("IMDB.arff", use_xml = FALSE, auto_extension = FALSE)

## End(Not run)

mldrGUI

Launches the web-based GUI for mldr

Description

Loads an interactive user interface in the web browser, built using R shiny.

Usage

mldrGUI()

Details

The mldr package provides a basic, Shiny-based GUI to work with multilabel datasets. You have to install the shiny package to be able to use this GUI.

The user interface allows working with any of the previous loaded datasets, as well as loading new ones. The GUI is structured into the following pages:

- **Main:** This page is divided into two sections. The one at the left can be used to choose a previously loaded dataset, as well as to load datasets from files. The right part shows some basic statistics about the selected multilabel dataset.
- **Labels:** This page shows a table containing for each label its name, index, count, relative frequency and imbalance ratio (IRLbl). The page also includes a bar plot of the label frequency. The range of labels in the plot can be customized.
- **Labelsets:** This page shows a table containing for each labelset its representation and a counter.
- **Attributes**: This page shows a table containing for each attribute its name, type and a summary of its values.

- **Concurrence**: This page shows for each label the number of instances in which it appears and its mean SCUMBLE measure, along with a plot that shows the level of concurrence among the selected labels. Clicking the labels in the table makes it possible to add/remove them from the plot.

The tables shown in these pages can be sorted by any of its fields, as well as filtered. The content of the tables can be copied to clipboard, printed and saved in CSV and Microsoft Excel format.

**Value**

Nothing

**Examples**

```r
## Not run:
library(mldr)
mldrGUI()
## End(Not run)
```

---

**mldr_evaluate**

*Evaluate predictions made by a multilabel classifier*

**Description**

Taking as input an `mldr` object and a matrix with the predictions given by a classifier, this function evaluates the classifier performance through several multilabel metrics.

**Usage**

`mldr_evaluate(mldr, predictions, threshold = 0.5)`

**Arguments**

- `mldr` Object of "mldr" class containing the instances to evaluate
- `predictions` Matrix with the labels predicted for each instance in the `mldr` parameter. Each element should be a value into [0,1] range
- `threshold` Threshold to use to generate bipartition of labels. By default the value 0.5 is used
Value

A list with multilabel predictive performance measures. The items in the list will be

- accuracy
- example_auc
- average_precision
- coverage
- fmeasure
- hamming_loss
- macro_auc
- macro_fmeasure
- macro_precision
- macro_recall
- micro_auc
- micro_fmeasure
- micro_precision
- micro_recall
- one_error
- precision
- ranking_loss
- recall
- subset_accuracy
- roc

The roc element corresponds to a roc object associated to the MicroAUC value. This object can be given as input to plot for plotting the ROC curve. The example_auc, macro_auc, micro_auc and roc members will be NULL if the pROC package is not installed.

See Also

mldr, Basic metrics, Averaged metrics, Ranking-based metrics, roc.mldr

Examples

```r
## Not run:
library(mldr)

# Get the true labels in emotions
predictions <- as.matrix(emotions$dataset[, emotions$labels$index])
# and introduce some noise (alternatively get the predictions from some classifier)
noised_labels <- cbind(sample(1:593, 200, replace = TRUE), sample(1:6, 200, replace = TRUE))
predictions[noised_labels] <- sample(0:1, 100, replace = TRUE)
# then evaluate predictive performance
res <- mldr_evaluate(emotions, predictions)
```
str(res)
plot(res$roc, main = "ROC curve for emotions")
## End(Not run)

**mldr_from_dataframe**

Generates an mldr object from a data.frame and a vector with label indices

**Description**

This function creates a new mldr object from the data stored in a data.frame, taking as labels the columns pointed by the indexes given in a vector.

**Usage**

mldr_from_dataframe(dataframe, labelIndices, attributes, name)

**Arguments**

* dataframe
  The data.frame containing the dataset attributes and labels.
* labelIndices
  Vector containing the indices of attributes acting as labels. Usually the labels will be at the end (right-most columns) or the beginning (left-most columns) of the data.frame
* attributes
  Vector with the attributes type, as returned by the attributes member of an mldr object. By default the type of the data.frame columns will be used.
* name
  Name of the dataset. The name of the dataset given as first parameter will be used by default

**Value**

An mldr object containing the multilabel dataset

**See Also**

* mldr
* summary.mldr

**Examples**

```r
library(mldr)

df <- data.frame(matrix(rnorm(1000), ncol = 10))
df$Label1 <- c(sample(c(0,1), 100, replace = TRUE))
df$Label2 <- c(sample(c(0,1), 100, replace = TRUE))
mymldr <- mldr_from_dataframe(df, labelIndices = c(11, 12), name = "testMLDR")

summary(mymldr)
```
mldr_to_labels  
*Label matrix of an MLD*

**Description**

Extracts a matrix with the true 0-1 assignment of labels of an "mldr" object.

**Usage**

```r
mldr_to_labels(mldr)
```

**Arguments**

- `mldr`  
  "mldr" object.

**Value**

Numeric matrix of labels.

**See Also**

Basic metrics, Averaged metrics, Ranking-based metrics.

---

mldr_transform  
*Transforms an MLDR into binary or multiclass datasets*

**Description**

Transforms an `mldr` object into one or serveral binary or multiclass datasets, returning them as `data.frame` objects.

**Usage**

```r
mldr_transform(mldr, type = "BR", labels)
```

**Arguments**

- `mldr`  
  The `mldr` object to transform

- `type`  
  Indicates the type of transformation to apply. Possible types are:
  - "BR" Produces one or more binary datasets, each one with one label
  - "LP" Produces a multiclass dataset using each labelset as class label

- `labels`  
  Vector with the label indexes to include in the transformation. All labels will be used if not specified.
plot.mldr

Value

A list of data.frames containing the resulting datasets (for BR) or a data.frame with the dataset (for LP). The result is no longer an mldr object, but a plain data.frame

Examples

```r
library(mldr)
emotionsbr <- mldr_transform(emotions, type = "BR")
emotionslp <- mldr_transform(emotions, type = "LP")
```

---

plot.mldr  
*Generates graphic representations of an mldr object*

---

Description

Generates graphic representations of an mldr object

Usage

```r
## S3 method for class 'mldr'
plot(x, type = "LC", labelCount, labelIndices, title, ask = length(type) > prod(par("mfcol")), ...)
```

Arguments

- `x` The mldr object whose features are to be drawn
- `type` Indicates the type(s) of plot to be produced. Possible types are:
  - "LC" Draws a circular plot with sectors representing each label and links between them depicting label co-occurrences
  - "LH" for label histogram
  - "LB" for label bar plot
  - "CH" for cardinality histogram
  - "AT" for attributes by type pie chart
  - "LSH" for labelset histogram
  - "LSB" for labelset bar plot
- `labelCount` Samples the labels in the dataset to show information of only labelCount of them
- `labelIndices` Establishes the labels to be shown in the plot
- `title` A title to be shown above the plot. Defaults to the name of the dataset passed as first argument
- `ask` Specifies whether to pause the generation of plots after each one
- `...` Additional parameters to be given to barplot, hist, etc.
Examples

library(mldr)
## Not run:
# Label concurrence plot
plot(genbase, type = "LC") # Plots all labels
plot(genbase) # Same as above
plot(genbase, title = "genbase dataset", color.function = heat.colors) # Changes the title and color
plot(genbase, labelCount = 10) # Randomly selects 10 labels to plot
plot(genbase, labelIndices = genbase$labels$index[1:10]) # Plots info of first 10 labels

# Label bar plot
plot(emotions, type = "LB", col = terrain.colors(emotions$measures$num.labels))

# Label histogram plot
plot(emotions, type = "LH")

# Cardinality histogram plot
plot(emotions, type = "CH")

# Attributes by type
plot(emotions, type = "AT", cex = 0.85)

# Labelset histogram
plot(emotions, type = "LSH")
## End(Not run)

print.mldr

Prints the mldr content

Description

Prints the mldr object data, including input attributes and output labels

Usage

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

Arguments

x Object whose data are to be printed
...

Additional parameters to be given to print

See Also

mldr, summary.mldr
Examples

```
library(mldr)

emotions
print(emotions) # Same as above
```

Description

Functions that compute ranking-based metrics, given a matrix of true labels and a matrix of predicted probabilities.

Usage

```
average_precision(true_labels, predictions, ...)

one_error(true_labels, predictions)

coverage(true_labels, predictions, ...)

ranking_loss(true_labels, predictions)

macro_auc(true_labels, predictions, undefined_value = 0.5,
           na.rm = FALSE)

micro_auc(true_labels, predictions)

eexample_auc(true_labels, predictions, undefined_value = 0.5,
             na.rm = FALSE)
```

Arguments

```
true_labels    Matrix of true labels, columns corresponding to labels and rows to instances.
predictions    Matrix of probabilities predicted by a classifier.
...            Additional parameters to be passed to the ranking function.
undefined_value A default value for the cases when macro-averaged and example-averaged AUC
                 encounter undefined (not computable) values, e.g. 0, 0.5, or NA.
na.rm          Logical specifying whether to ignore undefined values when undefined_value
               is set to NA.
```
Details

Available metrics in this category

- `average_precision`: Example and ranking based average precision (how many steps have to be made in the ranking to reach a certain relevant label, averaged by instance)
- `coverage`: Example and ranking based coverage (how many steps have to be made in the ranking to cover all the relevant labels, averaged by instance)
- `example_auc`: Example based Area Under the Curve ROC (averaged by instance)
- `macro_auc`: Label and ranking based Area Under the Curve ROC (macro-averaged by label)
- `micro_auc`: Label and ranking based Area Under the Curve ROC (micro-averaged)
- `one_error`: Example and ranking based one-error (how many times the top-ranked label is not a relevant label, averaged by instance)
- `ranking_loss`: Example and ranking based ranking-loss (how many times a non-relevant label is ranked above a relevant one, evaluated for all label pairs and averaged by instance)

Breaking ties in rankings

The additional `ties_method` parameter for the ranking function is passed to R’s own `rank`. It accepts the following values:

- "average"
- "first"
- "last"
- "random"
- "max"
- "min"

See `rank` for information on the effect of each parameter. The default behavior in `mldr` corresponds to value "last", since this is the behavior of the ranking method in MULAN, in order to facilitate fair comparisons among classifiers over both platforms.

Value

Atomical numeric vector specifying the resulting performance metric value.

See Also

`mldr_evaluate, mldr_to_labels`

Other evaluation metrics: `Averaged metrics, Basic metrics`

Examples

```r
true_labels <- matrix(c(1,1,1,
0,0,0,
1,0,0,
1,1,1,)
```

\begin{verbatim}
0,0,0,
1,0,0
), ncol = 3, byrow = TRUE)
predicted_probs <- matrix(c(
  .6,.5,.9,
  .0,.1,.2,
  .8,.3,.2,
  .7,.9,.1,
  .7,.3,.2,
  .1,.8,.3
), ncol = 3, byrow = TRUE)

# by default, labels with same ranking are assigned ascending rankings
# in the order they are encountered
coverage(true_labels, predicted_probs)
# in the following, labels with same ranking will receive the same,
# averaged ranking
average_precision(true_labels, predicted_probs, ties_method = "average")

# the following will treat all undefined values as 0 (counting them
# for the average)
example_auc(true_labels, predicted_probs, undefined_value = 0)
# the following will ignore undefined values (not counting them for
# the average)
example_auc(true_labels, predicted_probs, undefined_value = NA, na.rm = TRUE)
\end{verbatim}

---

**read.arff**

*Read an ARFF file*

**Description**

Reads a multilabel dataset from an ARFF file in Mulan or MEKA and retrieves instances distinguishing attributes corresponding to labels.

**Usage**

```r
read.arff(filename, use_xml = TRUE, auto_extension = TRUE, xml_file, label_indices, label_names, label_amount, ...)
```

**Arguments**

- `filename` Name of the dataset
- `use_xml` Specifies whether to use an associated XML file to identify the labels. Default to \texttt{TRUE}
- `auto_extension` Specifies whether to add the `.arff` and `.xml` extensions to the filename where appropriate. Default to \texttt{TRUE}
- `xml_file` Path to the XML file. If not provided, the filename ending in ".xml" will be assumed
remedial

Description

This function implements the REMEDIAL algorithm. It is a preprocessing algorithm for imbalanced multilabel datasets, whose aim is to decouple frequent and rare classes appearing in the same instance. For doing so, it aggregates new instances to the dataset and edit the labels present in them.

Usage

remedial(mld)

Arguments

mld mldr object with the multilabel dataset to preprocess
**Value**

An mldr object containing the preprocessed multilabel dataset

**Source**


**See Also**

concurrenceReport, labelInteractions

**Examples**

```r
library(mldr)
## Not run:
summary(birds)
summary(remedial(birds))
## End(Not run)
```

---

**roc**

**ROC curve**

**Description**

Calculates the ROC (Receiver Operating Characteristic) curve for given true labels and predicted ones. The pROC package is needed for this functionality.

**Usage**

```r
roc(...)```

**Arguments**

- `...`: Additional parameters to be passed to the pROC::roc function. See `roc` for more information.
- `mldr`: An "mldr" object. Its labels will be extracted via `mldr_to_labels`.
- `predictions`: Matrix of predicted labels or probabilities, columns corresponding to labels and rows to instances.
### summary.mldr

ROC object from pROC package.

#### See Also

- `mldr_evaluate.roc`

---

#### Description

Prints a summary of the measures obtained from the mldr object.

#### Usage

```r
## S3 method for class 'mldr'
summary(object, ...)
```

#### Arguments

- `object` Object whose measures are to be printed
- `...` Additional parameters to be given to print

#### See Also

- `mldr`, `print.mldr`

#### Examples

```r
library(mldr)
summary(emotions)
```
write_arff

Write an "mldr" object to a file

Description

Save the mldr content to an ARFF file and the label data to an XML file. If you need faster write, more options and support for other formats, please refer to the write.mldr function in package mldr.datasets.

Usage

write_arff(obj, filename, write.xml = FALSE)

Arguments

obj The "mldr" object whose content is going to be written
filename Base name for the files (without extension)
write.xml TRUE or FALSE, stating if the XML file has to be written

See Also

mldr_from_dataframe, mldr

In mldr.datasets: write.mldr

Examples

dir <- tempdir()
write_arff(emotions, file.path(dir, "myemotions"))
file.remove(file.path(dir, "myemotions.arff"))

.

Description

Filter rows in a mldr returning a new mldr

Usage

## S3 method for class 'mldr'
mldrObject[rowFilter = T]

Description

Generates a new mldr object containing the selected rows from an existent mldr

Usage

## S3 method for class 'mldr'
mldrObject[rowFilter = T]
Arguments

- **mldrObject**  
  Original mldr object from which some rows are going to be selected
- **rowFilter**  
  Expression to filter the rows

Value

A new mldr object with the selected rows

See Also

- `mldr_from_dataframe`, `==.mldr`, `+.mldr`

Examples

```r
library(mldr)

highlycoupled <- genbase[, .SCUMBLE > 0.05]  # Select instances with highly imbalanced coupled labels
summary(highlycoupled)  # Compare the selected instances
summary(genbase)        # with the traits of the original MLD
```
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