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### Description

Join two multi-label confusion matrix

### Usage

```r
## S3 method for class 'mlconfmat'
mlcm1 + mlcm2
```

### Arguments

- `mlcm1`: A `mlconfmat`
- `mlcm2`: Other `mlconfmat`

### Value

- `mlconfmat`
as.bipartition

Convert a mlresult to a bipartition matrix

Description

Convert a mlresult to a bipartition matrix

Usage

as.bipartition(mlresult)

Arguments

mlresult The mlresult object

Value

matrix with bipartition values

as.matrix.mlconfmat

Convert a multi-label Confusion Matrix to matrix

Description

Convert a multi-label Confusion Matrix to matrix

Usage

## S3 method for class 'mlconfmat'

as.matrix(x, ...)

Arguments

x The mlconfmat

... passed to as.matrix

Value

A confusion matrix with TP, TN, FP and FN columns
### as.matrix.mlresult

Convert a mlresult to matrix

**Description**

Convert a mlresult to matrix

**Usage**

```r
## S3 method for class 'mlresult'
as.matrix(x, ...)
```

**Arguments**

- `x` The mlresult object
- `...` ignored

**Value**

matrix

### as.mlresult

Convert a matrix prediction in a multi label prediction

**Description**

Convert a matrix prediction in a multi label prediction

**Usage**

```r
as.mlresult(predictions, probability = TRUE, ...)
```

**Arguments**

- `predictions` a Matrix or data.frame contained the scores/probabilities values. The columns are the labels and the rows are the examples.
- `probability` A logical value. If TRUE the predicted values are the score between 0 and 1, otherwise the values are bipartition 0 or 1. (Default: TRUE)
- `...` ignored
- `threshold` A single value between 0 and 1 or a list with threshold values contained one value per label (Default: 0.5). Only used when the predictions are not a mlresult.
as.probability

Value

An object of type mlresult

Methods (by class)

• default: Default mlresult transform method
• mlresult: change the mlresult type

Examples

predictions <- matrix(rnorm(100), ncol = 10)
colnames(predictions) <- paste('label', 1:10, sep='')

# Create a mlresult from a matrix
mlresult <- as.mlresult(predictions)
mlresult <- as.mlresult(predictions, probability = FALSE)
mlresult <- as.mlresult(predictions, probability = FALSE, threshold = 0.6)

# Change the current type of a mlresult
mlresult <- as.mlresult(mlresult, probability = TRUE)

as.probability

Convert a mlresult to a probability matrix

Description

Convert a mlresult to a probability matrix

Usage

as.probability(mlresult)

Arguments

mlresult The mlresult object

Value

matrix with probabilities values
as.ranking  
*Convert a mlresult to a ranking matrix*

Description

Convert a mlresult to a ranking matrix

Usage

as.ranking(mlresult, ties.method = "min", ...)

Arguments

- **mlresult**: The mlresult object
- **ties.method**: A character string specifying how ties are treated (Default: "min"). see `rank` to more details.
- **...**: Others parameters passed to the `rank` method.

Value

matrix with ranking values

baseline  
*Baseline reference for multilabel classification*

Description

Create a baseline model for multilabel classification.

Usage

baseline(
  mdata,
  metric = c("general", "F1", "hamming-loss", "subset-accuracy", "ranking-loss"),
  ...
)

Arguments

- **mdata**: A mldr dataset used to train the binary models.
- **metric**: Define the strategy used to predict the labels. The possible values are: 'general', 'F1', 'hamming-loss' or 'subset-accuracy'. See the description for more details. (Default: 'general').
- **...**: not used
**Details**

Baseline is a naive multi-label classifier that maximize/minimize a specific measure without induces a learning model. It uses the general information about the labels in training dataset to estimate the labels in a test dataset.

The follow strategies are available:

- **general**  Predict the k most frequent labels, where k is the integer most close of label cardinality.
- **F1**  Predict the most frequent labels that obtain the best F1 measure in training data. In the original paper, the authors use the less frequent labels.
- **hamming-loss**  Predict the labels that are associated with more than 50% of instances.
- **subset-accuracy**  Predict the most common labelset.
- **ranking-loss**  Predict a ranking based on the most frequent labels.

**Value**

An object of class `BASELINEmodel` containing the set of fitted models, including:

- **labels**  A vector with the label names.
- **predict**  A list with the labels that will be predicted.

**References**


**Examples**

```r
model <- baseline(toyml)
pred <- predict(model, toyml)

## Change the metric
model <- baseline(toyml, "F1")
model <- baseline(toyml, "subset-accuracy")
```

---

**Binary Relevance for multi-label Classification**

**Description**

Create a Binary Relevance model for multilabel classification.
Usage

\[
\text{br(mdata, base.algorithm = getOption("utiml.base.algorithm", "SVM"), ...},
\text{cores = getOption("utiml.cores", 1), seed = getOption("utiml.seed", NA))}
\]

Arguments

- **mdata**: A mldr dataset used to train the binary models.
- **base.algorithm**: A string with the name of the base algorithm (Default: `getOption("utiml.base.algorithm", "SVM")`)
- **...**: Others arguments passed to the base algorithm for all subproblems
- **cores**: The number of cores to parallelize the training. (Default: `getOption("utiml.cores", 1)`)
- **seed**: An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `getOption("utiml.seed", NA)`)

Details

Binary Relevance is a simple and effective transformation method to predict multi-label data. This is based on the one-versus-all approach to build a specific model for each label.

Value

An object of class `BRmodel` containing the set of fitted models, including:

- **labels**: A vector with the label names.
- **models**: A list of the generated models, named by the label names.

References


See Also

Other Transformation methods: `brplus()`, `cc()`, `clr()`, `dbr()`, `ebr()`, `ecc()`, `eps()`, `esl()`, `homer()`, `lift()`, `lp()`, `mbr()`, `ns()`, `ppt()`, `prudent()`, `ps()`.

Examples

```r
model <- br(toyml, "RANDOM")
pred <- predict(model, toyml)
```
# Use SVM as base algorithm
model <- br(toyml, "SVM")
pred <- predict(model, toyml)

# Change the base algorithm and use 2 CORES
model <- br(toyml[1:50], 'RF', cores = 2, seed = 123)

# Set a parameters for all subproblems
model <- br(toyml, 'KNN', k=5)

---

### brplus

**BR+ or BRplus for multi-label Classification**

**Description**

Create a BR+ classifier to predict multi-label data. This is a simple approach that enables the binary classifiers to discover existing label dependency by themselves. The main idea of BR+ is to increment the feature space of the binary classifiers to let them discover existing label dependency by themselves.

**Usage**

```r
brplus(
  mdata,
  base.algorithm =getOption("utiml.base.algorithm", "SVM"),
  ..., cores =getOption("utiml.cores", 1),
  seed =getOption("utiml.seed", NA)
)
```

**Arguments**

- `mdata` A mlr dataset used to train the binary models.
- `base.algorithm` A string with the name of the base algorithm. (Default: `getOption("utiml.base.algorithm", "SVM")`)
- `...` Others arguments passed to the base algorithm for all subproblems.
- `cores` The number of cores to parallelize the training. Values higher than 1 require the `parallel` package. (Default: `getOption("utiml.cores", 1)`)
- `seed` An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `getOption("utiml.seed", NA)`)  

**Details**

This implementation has different strategy to predict the final set of labels for unlabeled examples, as proposed in original paper.
Value

An object of class BRPmodel containing the set of fitted models, including:

- freq  The label frequencies to use with the 'Stat' strategy
- initial The BR model to predict the values for the labels to initial step
- models A list of final models named by the label names.

References


See Also

Other Transformation methods: br(), cc(), clr(), dbr(), ebr(), ecc(), eps(), esl(), homer(), lift(), lp(), mbr(), ns(), ppt(), prudent(), ps(), rakel(), rdbr(), rpc()

Other Stacking methods: mbr()

Examples

# Use SVM as base algorithm
model <- brplus(toyml, "RANDOM")
pred <- predict(model, toyml)

# Use Random Forest as base algorithm and 2 cores
model <- brplus(toyml, 'RF', cores = 2, seed = 123)

---

cc

Classifier Chains for multi-label Classification

Description

Create a Classifier Chains model for multilabel classification.

Usage

cc(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  chain = NA,
  ...
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
Arguments

mdata  A mlr dataset used to train the binary models.
base.algorithm  A string with the name of the base algorithm. (Default: options("utiml.base.algorithm", "SVM"))
chain  A vector with the label names to define the chain order. If empty the chain is the default label sequence of the dataset. (Default: NA)
...  Others arguments passed to the base algorithm for all subproblems.
cores  The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
seed  An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

Details

Classifier Chains is a Binary Relevance transformation method based to predict multi-label data. This is based on the one-versus-all approach to build a specific model for each label. It is different from BR method due the strategy of extended the attribute space with the 0/1 label relevances of all previous classifiers, forming a classifier chain.

Value

An object of class CCmodel containing the set of fitted models, including:

chain  A vector with the chain order.
labels  A vector with the label names in expected order.
models  A list of models named by the label names.

References


See Also

Other Transformation methods: brplus(), br(), clr(), dbr(), ebr(), ecc(), eps(), esl(), homer(), lift(), lp(), mbr(), ns(), ppt(), prudent(), ps(), rakel(), rdbr(), rpc()

Examples

model <- cc(toyml, "RANDOM")
pred <- predict(model, toyml)

# Use a specific chain with C5.0 classifier
mychain <- sample(rownames(toyml$labels))
model <- cc(toyml, 'C5.0', mychain)

# Set a specific parameter
model <- cc(toyml, 'KNN', k=5)

# Run with multiple-cores
model <- cc(toyml, 'RF', cores = 2, seed = 123)

---

**clr**

*Calibrated Label Ranking (CLR) for multi-label Classification*

**Description**

Create a CLR model for multilabel classification.

**Usage**

```r
clr(
  mdata,
  base.algorithm =getOption("utiml.base.algorithm", "SVM"),
  ..., 
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

**Arguments**

- **mdata**: A mldr dataset used to train the binary models.
- **base.algorithm**: A string with the name of the base algorithm. (Default: `options("utiml.base.algorithm", "SVM")`) Others arguments passed to the base algorithm for all subproblems
- **cores**: The number of cores to parallelize the training. Values higher than 1 require the `parallel` package. (Default: `options("utiml.cores", 1)`) An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `options("utiml.seed", NA)`) An artificial calibration label, separates the relevant from the irrelevant labels.

**Details**

CLR is an extension of label ranking that incorporates the calibrated scenario.
compute_multilabel_predictions

Value

An object of class RPCmodel containing the set of fitted models, including:

- **labels** A vector with the label names.
- **rpcmodel** A RPC model.
- **brmodel** A BR model used to calibrated the labels.

References


See Also

Other Transformation methods: brplus(), br(), cc(), db(), ebr(), ecc(), eps(), esl(), homer(), lift(), lp(), mbr(), ns(), ppt(), prudent(), ps(), rakel(), rdbr(), rpc()

Other Pairwise methods: rpc()

Examples

```r
model <- clr(toyml, "RANDOM")
pred <- predict(model, toyml)
```

---

compute_multilabel_predictions

*Compute the multi-label ensemble predictions based on some vote schema*

Description

Compute the multi-label ensemble predictions based on some vote schema

Usage

```r
compute_multilabel_predictions(
  predictions,
  vote.schema = "maj",
  probability = getOption("utiml.use.probs", TRUE)
)
```
compute_multilabel_predictions

Arguments

- **predictions**: A list of multi-label predictions (mlresult).
- **vote.schema**: Define the way that ensemble must compute the predictions. The default valid options are:
  - `'avg'`: Compute the mean of probabilities and the bipartitions
  - `'maj'`: Compute the majority of votes
  - `'max'`: Compute the higher probability for each instance/label
  - `'min'`: Compute the lower probability for each instance/label
  (Default: `'maj'`)
- **probability**: A logical value. If `TRUE` the predicted values are the score between 0 and 1, otherwise the values are bipartition 0 or 1.

Value

A mlresult with computed predictions.

Note

You can create your own vote schema, just create a method that receive two matrix (bipartitions and probabilities) and return a list with the final bipartitions and probabilities.

Remember that this method will compute the ensemble votes for each label. Thus the bipartition and probability matrix passed as argument for this method is related with the bipartitions and probabilities for a single label.

Examples

```r
model <- br(toyml, "KNN")
predictions <- list(
predict(model, toyml[1:10], k=1),
predict(model, toyml[1:10], k=3),
predict(model, toyml[1:10], k=5)
)
result <- compute_multilabel_predictions(predictions, "maj")

## Random choice
random_choice <- function (bipartition, probability) {
cols <- sample(seq(ncol(bipartition)), nrow(bipartition), replace = TRUE)
list(
bipartition = bipartition[cbind(seq(nrow(bipartition)), cols)],
probability = probability[cbind(seq(nrow(probability)), cols)]
)
}
result <- compute_multilabel_predictions(predictions, "random_choice")
```
create_holdout_partition

Create a holdout partition based on the specified algorithm

Description

This method creates multi-label dataset for train, test, validation or other proposes the partition method defined in method. The number of partitions is defined in partitions parameter. Each instance is used in only one partition of division.

Usage

create_holdout_partition(
  mdata,
  partitions = c(train = 0.7, test = 0.3),
  method = c("random", "iterative", "stratified")
)

Arguments

- **mdata**: A mldr dataset.
- **partitions**: A list of percentages or a single value. The sum of all values does not be greater than 1. If a single value is informed then the complement of them is applied to generated the second partition. If two or more values are informed and the sum of them is lower than 1 the partitions will be generated with the informed proportion. If partitions have names, they are used to name the return. (Default: c(train=0.7, test=0.3)).
- **method**: The method to split the data. The default methods are:
  - **random**: Split randomly the folds.
  - **iterative**: Split the folds considering the labels proportions individually. Some specific label can not occurs in all folds.
  - **stratified**: Split the folds considering the labelset proportions.

You can also create your own partition method. See the note and example sections to more details. (Default: "random")

Value

A list with at least two datasets sampled as specified in partitions parameter.

Note

To create your own split method, you need to build a function that receive a mldr object and a list with the proportions of examples in each fold and return an other list with the index of the elements for each fold.
create_kfold_partition

This method creates the k-fold partition based on the specified algorithm.

Create the k-folds partition based on the specified algorithm.
Usage

create_kfold_partition(
  mdata,
  k = 10,
  method = c("random", "iterative", "stratified")
)

Arguments

mdata A mldr dataset.
k The number of desirable folds. (Default: 10)
method The method to split the data. The default methods are:
  random Split randomly the folds.
  iterative Split the folds considering the labels proportions individually. Some specific label can not occurs in all folds.
  stratified Split the folds considering the labelset proportions.

You can also create your own partition method. See the note and example sections to more details. (Default: "random")

Value

An object of type kFoldPartition.

Note

To create your own split method, you need to build a function that receive a mldr object and a list with the proportions of examples in each fold and return an other list with the index of the elements for each fold.

References


See Also

How to create the datasets from folds
Other sampling: create_holdout_partition(), create_random_subset(), create_subset()

Examples

k10 <- create_kfold_partition(toyml, 10)
k5 <- create_kfold_partition(toyml, 5, "stratified")

sequential_split <- function (mdata, r) {
  S <- list()

  # Code to implement sequential_split function
create_random_subset

Create a random subset of a dataset

Description
Create a random subset of a dataset

Usage
create_random_subset(
  mdata,
  instances,
  attributes = mdata$measures$num.inputs,
  replacement = FALSE
)

Arguments

  mdata       A mldr dataset
  instances   The number of expected instances
  attributes  The number of expected attributes. (Default: all attributes)
  replacement A boolean value to define sample with replacement or not. (Default: FALSE)

Value
A new mldr subset

See Also
Other sampling: create_holdout_partition(), create_kfold_partition(), create_subset()

Examples
small.toy <- create_random_subset(toyml, 10, 3)
medium.toy <- create_random_subset(toyml, 50, 5)
create_subset

Description

Create a subset of a dataset

Usage

create_subset(mdata, rows, cols = NULL)

Arguments

mdata  A mldr dataset
rows  A vector with the instances indexes (names or indexes).
cols  A vector with the attributes indexes (names or indexes).

Value

A new mldr subset

Note

It is not necessary specify the labels attributes because they are included by default.

See Also

Other sampling: create_holdout_partition(), create_kfold_partition(), create_random_subset()

Examples

## Create a dataset with the 20 first examples and the 7 first attributes
small.toy <- create_subset(toyml, seq(20), seq(7))

## Create a random dataset with 50 examples and 5 attributes
random.toy <- create_subset(toyml, sample(100, 50), sample(10, 5))
Multi-label cross-validation

Description

Perform the cross validation procedure for multi-label learning.

Usage

```r
cv(
  mdata,
  method,
  ...,
  cv.folds = 10,
  cv.sampling = c("random", "iterative", "stratified"),
  cv.results = FALSE,
  cv.predictions = FALSE,
  cv.measures = "all",
  cv.cores = getOption("utiml.cores", 1),
  cv.seed = getOption("utiml.seed", NA)
)
```

Arguments

- `mdata`: A mldr dataset.
- `method`: The multi-label classification method. It also accepts the name of the method as a string.
- `...`: Additional parameters required by the method.
- `cv.folds`: Number of folds. (Default: 10)
- `cv.sampling`: The method to split the data. The default methods are:
  - `random`: Split randomly the folds.
  - `iterative`: Split the folds considering the labels proportions individually. Some specific label can not occurs in all folds.
  - `stratified`: Split the folds considering the labelset proportions.
  (Default: "random")
- `cv.results`: Logical value indicating if the folds results should be reported (Default: FALSE).
- `cv.predictions`: Logical value indicating if the predictions should be reported (Default: FALSE).
- `cv.measures`: The measures names to be computed. Call `multilabel_measures()` to see the expected measures. You can also use "bipartition", "ranking", "label-based", "example-based", "macro-based", "micro-based" and "label-problem" to include a set of measures. (Default: "all").
- `cv.cores`: The number of cores to parallelize the cross validation procedure. (Default: `options("utiml.cores", 1)`)
- `cv.seed`: An optional integer used to set the seed. (Default: `options("utiml.seed", NA)`)
**Value**

If cv.results and cv.prediction are FALSE, the return is a vector with the expected multi-label measures, otherwise, a list contained the multi-label and the other expected results (the label measures and/or the prediction object) for each fold.

**See Also**

Other evaluation: `multilabel_confusion_matrix()`, `multilabel_evaluate()`, `multilabel_measures()`

**Examples**

```r
# Run 10 folds for BR method
res1 <- cv(toyml, br, base.algorithm="RANDOM", cv.folds=10)

# Run 3 folds for RAkEL method and get the fold results and the prediction
res2 <- cv(mdata=toyml, method="rakel", base.algorithm="RANDOM", k=2, m=10, cv.folds=3, cv.results=TRUE, cv.predictions=TRUE)
```

---

**dbr**  
*Dependent Binary Relevance (DBR) for multi-label Classification*

**Description**

Create a DBR classifier to predict multi-label data. This is a simple approach that enables the binary classifiers to discover existing label dependency by themselves. The idea of DBR is exactly the same used in BR+ (the training method is the same, excepted by the argument estimate.models that indicate if the estimated models must be created).

**Usage**

```r
dbr(
  mdata,  
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),  
  estimate.models = TRUE,  
  ...,  
  cores = getOption("utiml.cores", 1),  
  seed = getOption("utiml.seed", NA)
)
```

**Arguments**

- `mdata`  
  A mldr dataset used to train the binary models.

- `base.algorithm`  
  A string with the name of the base algorithm. (Default: `options("utiml.base.algorithm", "SVM")`)
estimates.models
Logical value indicating whether is necessary build Binary Relevance classifier for estimate process. The default implementation use BR as estimators, however when other classifier is desirable then use the value FALSE to skip this process. (Default: TRUE).

... Others arguments passed to the base algorithm for all subproblems.
cores The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
seed An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

Value
An object of class DBRmodel containing the set of fitted models, including:

labels A vector with the label names.
estimation The BR model to estimate the values for the labels. Only when the estimate.models = TRUE.
models A list of final models named by the label names.

References

See Also
Recursive Dependent Binary Relevance
Other Transformation methods: brplus(), br(), cc(), clr(), ebr(), ecc(), eps(), esl(), homer(), lift(), lp(), mbr(), ns(), ppt(), prudent(), ps(), rakel(), rdbr(), rpc()

Examples
model <- dbr(toyml, "RANDOM")
pred <- predict(model, toyml)

# Use Random Forest as base algorithm and 2 cores
model <- dbr(toyml, 'RF', cores = 2)
**ebr**  
*Ensemble of Binary Relevance for multi-label Classification*

**Description**
Create an Ensemble of Binary Relevance model for multilabel classification.

**Usage**
```r
ebr(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  m = 10,
  subsample = 0.75,
  attr.space = 0.5,
  replacement = TRUE,
  ...
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

**Arguments**
- **mdata**  
  A mldr dataset used to train the binary models.
- **base.algorithm**  
  A string with the name of the base algorithm. (Default: `options("utiml.base.algorithm", "SVM")`)
- **m**  
  The number of Binary Relevance models used in the ensemble. (Default: 10)
- **subsample**  
  A value between 0.1 and 1 to determine the percentage of training instances that must be used for each classifier. (Default: 0.75)
- **attr.space**  
  A value between 0.1 and 1 to determine the percentage of attributes that must be used for each classifier. (Default: 0.50)
- **replacement**  
  Boolean value to define if use sampling with replacement to create the data of the models of the ensemble. (Default: TRUE)
- **cores**  
  Others arguments passed to the base algorithm for all subproblems.
- **seed**  
  An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `options("utiml.seed", NA)`)  

**Details**
This model is composed by a set of Binary Relevance models. Binary Relevance is a simple and effective transformation method to predict multi-label data.
Value

An object of class `EBRmodel` containing the set of fitted BR models, including:

- **models** A list of BR models.
- **nrow** The number of instances used in each training dataset.
- **ncol** The number of attributes used in each training dataset.
- **rounds** The number of interactions.

Note

If you want to reproduce the same classification and obtain the same result will be necessary set a flag `utiml.mc.set.seed` to `FALSE`.

References


See Also

Other Transformation methods: `brplus()`, `br()`, `cc()`, `clr()`, `dbr()`, `ecc()`, `eps()`, `esl()`, `homer()`, `lift()`, `lp()`, `mbr()`, `ns()`, `ppt()`, `prudent()`, `ps()`, `rakel()`, `rdbr()`, `rpc()`

Other Ensemble methods: `ecc()`, `eps()`

Examples

```r
model <- ebr(toyml, "RANDOM")
pred <- predict(model, toyml)

# Use C5.0 with 90% of instances and only 5 rounds
model <- ebr(toyml, 'C5.0', m = 5, subsample = 0.9)

# Use 75% of attributes
model <- ebr(toyml, attr.space = 0.75)

# Running in 2 cores and define a specific seed
model1 <- ebr(toyml, cores=2, seed = 312)
```
**ecc**

*Ensemble of Classifier Chains for multi-label Classification*

Description

Create an Ensemble of Classifier Chains model for multilabel classification.

Usage

```r
ecc(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  m = 10,
  subsample = 0.75,
  attr.space = 0.5,
  replacement = TRUE,
  ...
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

Arguments

- `mdata` A mldr dataset used to train the binary models.
- `base.algorithm` A string with the name of the base algorithm. (Default: `getOption("utiml.base.algorithm", "SVM")`) 
- `m` The number of Classifier Chains models used in the ensemble. (Default: 10) 
- `subsample` A value between 0.1 and 1 to determine the percentage of training instances that must be used for each classifier. (Default: 0.75) 
- `attr.space` A value between 0.1 and 1 to determine the percentage of attributes that must be used for each classifier. (Default: 0.50) 
- `replacement` Boolean value to define if use sampling with replacement to create the data of the models of the ensemble. (Default: TRUE) 
- `cores` The number of cores to parallelize the training. Values higher than 1 require the `parallel` package. (Default: `getOption("utiml.cores", 1)`) 
- `seed` An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `getOption("utiml.seed", NA)`) 

Details

This model is composed by a set of Classifier Chains models. Classifier Chains is a Binary Relevance transformation method based to predict multi-label data. It is different from BR method due the strategy of extended the attribute space with the 0/1 label relevances of all previous classifiers, forming a classifier chain.
Value

An object of class ECCmodel containing the set of fitted CC models, including:

- **rounds**  The number of interactions
- **models**  A list of BR models.
- **nrow** The number of instances used in each training dataset
- **ncol** The number of attributes used in each training dataset

Note

If you want to reproduce the same classification and obtain the same result will be necessary set a flag utiml.mc.set.seed to FALSE.

References


See Also

Other Transformation methods: brplus(), br(), cc(), clr(), dbr(), ebr(), eps(), esl(), homer(), lift(), lp(), mbr(), ns(), ppt(), prudent(), ps(), rakel(), rdbr(), rpc()

Other Ensemble methods: ebr(), eps()

Examples

# Use all default values
model <- ecc(toyml, "RANDOM")
pred <- predict(model, toyml)

# Use C5.0 with 100% of instances and only 5 rounds
model <- ecc(toyml, 'C5.0', m = 5, subsample = 1)

# Use 75% of attributes
model <- ecc(toyml, attr.space = 0.75)

# Running in 2 cores and define a specific seed
model1 <- ecc(toyml, cores=2, seed=123)
Description

Create an Ensemble of Pruned Set model for multilabel classification.

Usage

```r
esps(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  m = 10,
  subsample = 0.75,
  p = 3,
  strategy = c("A", "B"),
  b = 2,
  ...,
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

Arguments

- **mdata**: A mldr dataset used to train the binary models.
- **base.algorithm**: A string with the name of the base algorithm. (Default: `getOption("utiml.base.algorithm", "SVM")`)
- **m**: The number of Pruned Set models used in the ensemble.
- **subsample**: A value between 0.1 and 1 to determine the percentage of training instances that must be used for each classifier. (Default: 0.63)
- **p**: Number of instances to prune. All labelsets that occurs p times or less in the training data is removed. (Default: 3)
- **strategy**: The strategy (A or B) for processing infrequent labelsets. (Default: A).
- **b**: The number used by the strategy for processing infrequent labelsets.
- **...**: Others arguments passed to the base algorithm for all subproblems.
- **cores**: The number of cores to parallelize the training. Values higher than 1 require the `parallel` package. (Default: `getOption("utiml.cores", 1)`)
- **seed**: An optional integer used to set the seed. (Default: `getOption("utiml.seed", NA)"")

Details

Pruned Set (PS) is a multi-class transformation that remove the less common classes to predict multi-label data. The ensemble is created with different subsets of the original multi-label data.
Value

An object of class EPSmodel containing the set of fitted models, including:

- **rounds** The number of interactions
- **models** A list of PS models.

References


See Also

Other Transformation methods: `brplus()`, `br()`, `cc()`, `clr()`, `dbre()`, `ebr()`, `ecc()`, `esl()`, `homer()`, `lift()`, `lp()`, `mbr()`, `ns()`, `ppt()`, `prudent()`, `ps()`, `rakel()`, `rdbr()`, `rpc()`

Other Powerset: `lp()`, `ppt()`, `ps()`, `rakel()`

Other Ensemble methods: `ebr()`, `ecc()`

Examples

```r
model <- esl(toyml, "RANDOM")
pred <- predict(model, toyml)

# Change default configurations
model <- esl(toyml, "RF", m=15, subsample=0.4, p=4, strategy="B", b=1)
```

---

### esl

**Ensemble of Single Label**

**Description**

Create an Ensemble of Single Label model for multilabel classification.

**Usage**

```r
esl(
mdata, 
base.algorithm =getOption("utiml.base.algorithm", "SVM"), 
m = 10, 
w = 1, 
..., 
cores = getOption("utiml.cores", 1), 
seed = getOption("utiml.seed", NA)
)
```
Arguments

- `mdata`  A mlr dataset used to train the binary models.
- `base.algorithm`  A string with the name of the base algorithm (Default: `options("utiml.base.algorithm", "SVM")`)
- `m`  The number of members used in the ensemble. (Default: 10)
- `w`  The weight given to the choice of the less frequent labels. When it is 0, the labels will be random choose, when it is 1 the complement of the label frequency is used as the probability to choose each label. Values greater than 1 will privilege the less frequent labels. (Default: 1)
- `...`  Others arguments passed to the base algorithm for all subproblems
- `cores`  The number of cores to parallelize the training. (Default: `options("utiml.cores", 1)`)
- `seed`  An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `options("utiml.seed", NA)`)  

Details

ESL is an ensemble of multi-class model that uses the less frequent labels. This is based on the label ignore approach different members of the ensemble.

Value

An object of class `ESLmodel` containing the set of fitted models, including:

- `labels`  A vector with the labels’ frequencies.
- `models`  A list of the multi-class models.

See Also

Other Transformation methods: `brplus()`, `br()` , `cc()`, `clr()`, `dbr()`, `ebr()`, `ecc()`, `eps()`, `homer()`, `lift()`, `lp()`, `mbr()`, `ns()`, `ppt()`, `prudent()`, `ps()`, `rakel()`, `rdbr()`, `rpc()`  

Examples

```r
model <- esl(toyml, "RANDOM")
pred <- predict(model, toyml)

# Use SVM as base algorithm
model <- esl(toyml, "SVM")
pred <- predict(model, toyml)

# Change the base algorithm and use 2 CORES
model <- esl(toyml[1:50], 'RF', cores = 2, seed = 123)

# Set a parameters for all subproblems
model <- esl(toyml, 'KNN', k=5)
```
fill_sparse_mldata  

Description
Transform a sparse dataset filling NA values to 0 or " values based on the column type. Text columns with numeric values will be modified to numerical.

Usage
fill_sparse_mldata(mdata)

Arguments
mdata  
The mldr dataset to be filled.

Value
a new mldr object.

See Also
Other pre process: normalize_mldata(), remove_attributes(), remove_labels(), remove_skewness_labels(), remove_unique_attributes(), remove_unlabeled_instances(), replace_nominal_attributes()

Examples
sparse.toy <- toyml
sparse.toy$dataset$ratt10[sample(100, 30)] <- NA
complete.toy <- fill_sparse_mldata(sparse.toy)

fixed_threshold  

Apply a fixed threshold in the results

Description
Transform a prediction matrix with scores/probabilities in a mlresult applying a fixed threshold. A global fixed threshold can be used of all labels or different fixed thresholds, one for each label.

Usage
fixed_threshold(prediction, threshold = 0.5, probability = FALSE)

## Default S3 method:
fixed_threshold(prediction, threshold = 0.5, probability = FALSE)

## S3 method for class 'mlresult'
fixed_threshold(prediction, threshold = 0.5, probability = FALSE)
**fixed_threshold**

**Arguments**

- **prediction**  A matrix with scores/probabilities where the columns are the labels and the rows are the instances.
- **threshold**  A single value between 0 and 1 or a list with threshold values contained one value per label.
- **probability**  A logical value. If TRUE the predicted values are the score between 0 and 1, otherwise the values are bipartition 0 or 1. (Default: FALSE)

**Value**

A mlresult object.

**Methods (by class)**

- default: Fixed Threshold for matrix or data.frame
- mlresult: Fixed Threshold for mlresult

**References**


**See Also**

Other threshold: lcard_threshold(), mcut_threshold(), pcut_threshold(), rcut_threshold(), scut_threshold(), subset_correction()

**Examples**

```r
# Create a prediction matrix with scores
result <- matrix(
  data = rnorm(9, 0.5, 0.2),
  ncol = 3,
  dimnames = list(NULL, c('lb1', 'lb2', 'lb3'))
)

# Use 0.5 as threshold
fixed_threshold(result)

# Use an threshold for each label
fixed_threshold(result, c(0.4, 0.6, 0.7))
```
**foodtruck**

*Foodtruck multi-label dataset.*

**Description**

The foodtruck multi-label dataset is a real multi-label dataset, which uses habits and personal information to predict food truck cuisines.

**Usage**

foodtruck

**Format**

A mldr object with 407 instances, 21 features and 12 labels:

**Details**

General Information

- Cardinality: 2.28
- Density: 0.19
- Distinct multi-labels: 117
- Number of single labelsets: 74
- Max frequency: 114

**Source**


---

**homer**

*Hierarchy Of Multilabel classifier (HOMER)*

**Description**

Create a Hierarchy Of Multilabel classifier (HOMER).
Usage

homer(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  clusters = 3,
  method = c("balanced", "clustering", "random"),
  iteration = 100,
  ...
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)

Arguments

mdata
A mldr dataset used to train the binary models.

base.algorithm
A string with the name of the base algorithm. (Default: options("utiml.base.algorithm", "SVM"))

clusters
Number maximum of nodes in each level. (Default: 3)

method
The strategy used to organize the labels (create the meta-labels). The options are: "balanced", "clustering" and "random". (Default: "balanced").

iteration
The number max of iterations, used by balanced or clustering methods.

cores
The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))

seed
An optional integer used to set the seed. (Default: options("utiml.seed", NA))

Details

HOMER is an algorithm for effective and computationally efficient multilabel classification in domains with many labels. It constructs a hierarchy of multilabel classifiers, each one dealing with a much smaller set of labels.

Value

An object of class HOMERmodel containing the set of fitted models, including:

labels    A vector with the label names.
clusters   The number of nodes in each level
models     The Hierarchy of BR models.

References

See Also
Other Transformation methods: `brplus()`, `br()`, `cc()`, `clr()`, `dbr()`, `ebr()`, `ecc()`, `eps()`, `esl()`, `lift()`, `lp()`, `mbr()`, `ns()`, `ppt()`, `prudent()`, `ps()`, `rakel()`, `rdbr()`, `rpc()`

Examples
```r
model <- homer(toyml, "RANDOM")
pred <- predict(model, toyml)

## Change default configurations
model <- homer(toyml, "RF", clusters=5, method="clustering", iteration=10)
```

### is.bipartition

Test if a mlresult contains crisp values as default

**Description**
Test if a mlresult contains crisp values as default

**Usage**

```r
is.bipartition(mlresult)
```

**Arguments**

- `mlresult` The mlresult object

**Value**

- logical value

### is.probability

Test if a mlresult contains score values as default

**Description**
Test if a mlresult contains score values as default

**Usage**

```r
is.probability(mlresult)
```

**Arguments**

- `mlresult` The mlresult object
### lcard_threshold

**Value**

logical value

---

**Threshold based on cardinality**

### Description

Find and apply the best threshold based on cardinality of training set. The threshold is choice based on how much the average observed label cardinality is close to the average predicted label cardinality.

### Usage

```r
lcard_threshold(prediction, cardinality, probability = FALSE)
```

```r
## Default S3 method:
lcard_threshold(prediction, cardinality, probability = FALSE)

## S3 method for class 'mlresult'
lcard_threshold(prediction, cardinality, probability = FALSE)
```

### Arguments

- **prediction**: A matrix or `mlresult`.
- **cardinality**: A real value of training dataset label cardinality, used to define the threshold value.
- **probability**: A logical value. If `TRUE` the predicted values are the score between 0 and 1, otherwise the values are bipartition 0 or 1. (Default: `FALSE`)

### Value

A `mlresult` object.

### Methods (by class)

- `default`: Cardinality Threshold for matrix or `data.frame`
- `mlresult`: Cardinality Threshold for `mlresult`

### References


### See Also

Other threshold: `fixed_threshold()`, `mcut_threshold()`, `pcut_threshold()`, `rcut_threshold()`, `scut_threshold()`, `subset_correction()`
Examples

```r
prediction <- matrix(runif(16), ncol = 4)
lcard_threshold(prediction, 2.1)
```

---

**Description**

Create a multi-label learning with Label specIfic FeaTures (LIFT) model.

**Usage**

```r
lift(
    mdata,
    base.algorithm = getOption("utiml.base.algorithm", "SVM"),
    ratio = 0.1,
    ...,
    cores = getOption("utiml.cores", 1),
    seed = getOption("utiml.seed", NA)
)
```

**Arguments**

- `mdata`: A mldr dataset used to train the binary models.
- `base.algorithm`: A string with the name of the base algorithm. (Default: `getOption("utiml.base.algorithm", "SVM")`)
- `ratio`: Control the number of clusters being retained. Must be between 0 and 1. (Default: 0.1)
- `...`: Others arguments passed to the base algorithm for all subproblems.
- `cores`: The number of cores to parallelize the training. Values higher than 1 require the `parallel` package. (Default: `getOption("utiml.cores", 1)`)  
- `seed`: An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `getOption("utiml.seed", NA)`)  

**Details**

LIFT firstly constructs features specific to each label by conducting clustering analysis on its positive and negative instances, and then performs training and testing by querying the clustering results.

**Value**

An object of class `LIFTmodel` containing the set of fitted models, including:

- `labels`: A vector with the label names.
- `models`: A list of the generated models, named by the label names.
lp

References

See Also
Other Transformation methods: brplus(), br(), cc(), clr(), dbr(), ebr(), ecc(), eps(), esl(), homer(), lp(), mbr(), ns(), ppt(), prudent(), ps(), rakel(), rdbr(), rpc()

Examples
model <- lift(toyml, "RANDOM")
pred <- predict(model, toyml)

# Running lift with a specific ratio
model <- lift(toyml, "RF", 0.15)

lp

Label Powerset for multi-label Classification

Description
Create a Label Powerset model for multilabel classification.

Usage
lp(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  ..., cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)

Arguments
mdata A mldr dataset used to train the binary models.
base.algorithm A string with the name of the base algorithm. (Default: options("utiml.base.algorithm", "SVM"))
... Others arguments passed to the base algorithm for all subproblems
cores Not used
seed An optional integer used to set the seed. (Default: options("utiml.seed", NA))
Details

Label Powerset is a simple transformation method to predict multi-label data. This is based on the
multi-class approach to build a model where the classes are each labelset.

Value

An object of class LPmodel containing the set of fitted models, including:

- **labels** A vector with the label names.
- **model** A multi-class model.

References

Pattern Recognition, 37(9), 1757-1771.

See Also

Other Transformation methods: brplus(), br(), cc(), clr(), dbr(), ebr(), ecc(), eps(),
esl(), homer(), lift(), mbr(), ns(), ppt(), prudent(), ps(), rakel(), rdbbr(), rpc()
Other Powerset: eps(), ppt(), ps(), rakel()

Examples

```r
model <- lp(toyml, "RANDOM")
pred <- predict(model, toyml)
```

Description

Create a Meta-BR (MBR) classifier to predict multi-label data. To this, two round of Binary Rele-
vance is executed, such that, the first step generates new attributes to enrich the second prediction.

Usage

```r
mbr(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  folds = 1,
  phi = 0,
  ...,
  predict.params = list(),
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```
**Arguments**

- `mdata` A mlr dataset used to train the binary models.
- `base.algorithm` A string with the name of the base algorithm. (Default: `options("utiml.base.algorithm", "SVM")`)
- `folds` The number of folds used in internal prediction. If this value is 1 all dataset will be used in the first prediction. (Default: 1)
- `phi` A value between 0 and 1 to determine the correlation coefficient. The value 0 include all labels in the second phase and the 1 only the predicted label. (Default: 0)
- `predict.params` A list of default arguments passed to the predictor algorithm. (Default: `list()`)
- `cores` The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: `options("utiml.cores", 1)`)
- `seed` An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `options("utiml.seed", NA)`)

**Details**

This implementation use complete training set for both training and prediction steps of 2BR. However, the phi parameter may be used to remove labels with low correlations on the second step.

**Value**

An object of class `MBRmodel` containing the set of fitted models, including:

- `labels` A vector with the label names.
- `phi` The value of phi parameter.
- `correlation` The matrix of label correlations used in combination with phi parameter to define the labels used in the second step.
- `basemodel` The BRModel used in the first iteration.
- `models` A list of models named by the label names used in the second iteration.

**References**


**See Also**

Other Transformation methods: `brplus()`, `br()`, `cc()`, `clr()`, `dbr()`, `ebr()`, `ecc()`, `eps()`, `esl()`, `homer()`, `lift()`, `lp()`, `ns()`, `ppt()`, `prudent()`, `ps()`, `rakel()`, `rdbr()`, `rpc()`

Other Stacking methods: `brplus()`
Examples

```r
model <- mbr(toyml, "RANDOM")
pred <- predict(model, toyml)

# Use 10 folds and different phi correlation with C5.0 classifier
model <- mbr(toyml, 'C5.0', 10, 0.2)

# Run with 2 cores
model <- mbr(toyml, "SVM", cores = 2, seed = 123)

# Set a specific parameter
model <- mbr(toyml, 'KNN', k=5)
```

---

**mcut_threshold**  
Maximum Cut Thresholding (MCut)

Description

The Maximum Cut (MCut) automatically determines a threshold for each instance that selects a subset of labels with higher scores than others. This leads to the selection of the middle of the interval defined by these two scores as the threshold.

Usage

```r
mcut_threshold(prediction, probability = FALSE)
```

## Default S3 method:
```r
mcut_threshold(prediction, probability = FALSE)
```

## S3 method for class 'mlresult'
```r
mcut_threshold(prediction, probability = FALSE)
```

Arguments

- **prediction**: A matrix or mlresult.
- **probability**: A logical value. If TRUE the predicted values are the score between 0 and 1, otherwise the values are bipartition 0 or 1. (Default: FALSE)

Value

A mlresult object.

Methods (by class)

- **default**: Maximum Cut Thresholding (MCut) method for matrix
- **mlresult**: Maximum Cut Thresholding (MCut) for mlresult
References

See Also
Other threshold: `fixed_threshold()`, `lcard_threshold()`, `pcut_threshold()`, `rcut_threshold()`, `scut_threshold()`, `subset_correction()`

Examples
```r
prediction <- matrix(runif(16), ncol = 4)
mcut_threshold(prediction)
```

---

**merge_mlconfmat**

Join a list of multi-label confusion matrix

**Description**
Join a list of multi-label confusion matrix

**Usage**

```r
merge_mlconfmat(object, ...)
```

**Arguments**

- `object` A mlconfmat object or a list of mlconfmat objects
- `...` mlconfmat objects

**Value**
mlconfmat

---

**mldata**

Fix the mldr dataset to use factors

**Description**
Fix the mldr dataset to use factors

**Usage**

```r
mldata(mdata)
```
Arguments

mdata A mldr dataset.

Value

A mldr object

Examples

```
toyml <- mldata(toyml)
```

Description

Create a ML-KNN classifier to predict multi-label data. It is a multi-label lazy learning, which is derived from the traditional K-nearest neighbor (KNN) algorithm. For each unseen instance, its K nearest neighbors in the training set are identified and based on statistical information gained from the label sets of these neighboring instances, the maximum a posteriori (MAP) principle is utilized to determine the label set for the unseen instance.

Usage

```
mlknn(
mdata, 
k = 10, 
s = 1, 
distance = "euclidean", 
..., 
cores = getOption("utiml.cores", 1), 
seed = getOption("utiml.seed", NA)
)
```

Arguments

mdata A mldr dataset used to train the binary models.

k The number of neighbors. (Default: 10)

s Smoothing parameter controlling the strength of uniform prior. When it is set to be 1, we have the Laplace smoothing. (Default: 1).

distance The name of method used to compute the distance. See dist to the list of options. (Default: "euclidean")

... Not used.

cores Ignored because this method does not support multi-core.

seed Ignored because this method is deterministic.
Value

An object of class `MLKNNmodel` containing the set of fitted models, including:

labels A vector with the label names.
prior The prior probability of each label to occur.
posterior The posterior probability of each label to occur given that k neighbors have it.

References


Examples

```r
model <- mlknn(toyml, k=3)
pred <- predict(model, toyml)
```

Usage

`mlpredict(model, newdata, ...)`

Arguments

model An object model returned by some mltrain method, its class determine the name of this method.
newdata A data.frame with the new data to be predicted.
... Others arguments passed to the predict method.

Value

A matrix with the probabilities of each class value/example, where the rows are the examples and the columns the class values.
How to create a new prediction base method

First is necessary to know the class of model generate by the respective train method, because this name determines the method name. It must start with 'mlpredict.', followed by the model class name, e.g. a model with class 'fooModel' must be called as mlpredict.fooModel.

After defined the name, you need to implement your prediction base method. The model built on mltrein is available on model parameter and the newdata is the data to be predict.

The return of this method must be a data.frame with two columns called "prediction" and "probability". The first column contains the predicted class and the second the probability/score/confidence of this prediction. The rows represents the examples.

Examples

# Create a method that predict always the first class
# The model must be of the class 'fooModel'
mlpredict.FooModel <- function (model, newdata, ...) {
  # Predict the first class with a random confidence
  data.frame(
    prediction = rep(model$classes[1], nrow(newdata)),
    probability = sapply(runif(nrow(newdata)), function (score) {
      max(score, 1 - score)
    }),
    row.names = rownames(newdata)
  )
}

# Create a SVM predict method using the e1071 package (the class of SVM model
# from e1071 package is 'svm')
library(e1071)
mlpredict.svm <- function (dataset, newdata, ...) {
  result <- predict(model, newdata, probability = TRUE, ...)
  attr(result, 'probabilities')
}
Usage

mltrain(object, ...)

Arguments

object A mltransformation object. This is used as a list and contains at least five values:

object$data A data.frame with the train data, where the columns are the attributes and the rows are the examples.

object$labelname The name of the class column.

object$labelindex The column index of the class.

object$mldataset The name of multi-label dataset.

object$mlmethod The name of the multi-label method.

Others values may be specified by the multi-label method.

...

Others arguments passed to the base method.

Value

A model object. The class of this model can be of any type, however, this object will be passed to the respective mlpredict method.

How to create a new train base method

First, is necessary to define a name of your classifier, because this name determines the method name. The base method name must start with mltrain.base followed by the designed name, e.g. a 'FOO' classify must be defined as mltrain.baseFOO (we suggest always use upper case names).

Next, your method must receive at least two parameters (object, ...). Use object$data[, object$labelindex] or object$data[, object$labelname] to access the labels values and use object$data[, -object$labelindex] to access the predictive attributes. If you need to know which are the multi-label dataset and method, use object$mldataset and object$mlmethod, respectively.

Finally, your method should return a model that will be used by the mlpredict method. Remember, that your method may be used to build binary and multi-class models.

Examples

# Create a empty model of type FOO
mltrain.baseFOO <- function (object, ...) {
  mymodel <- list(
    classes = as.character(unique(object$data[, object$labelindex]))
  )
  class(mymodel) <- 'FooModel'
  mymodel
}

# Using this base method with Binary Relevance
brmodel <- br(toyml, 'FOO')
# Create a SVM method using the e1071 package
library(e1071)
mltrain.baseSVM <- function (object, ...) {
  traindata <- object$data[, -object$labelindex]
  labelldata <- object$data[, object$labelindex]
  model <- svm(traindata, labelldata, probability = TRUE, ...)
  model
}

multilabel_confusion_matrix

Compute the confusion matrix for a multi-label prediction

Description

The multi-label confusion matrix is an object that contains the prediction, the expected values and also a lot of pre-processed information related with these data.

Usage

multilabel_confusion_matrix(mdata, mlresult)

Arguments

mdata A mldr dataset
mlresult A mlresult prediction

Value

A mlconfmat object that contains:

Z  The bipartition matrix prediction.
Fx  The score/probability matrix prediction.
R  The ranking matrix prediction.
Y  The expected matrix bipartition.
TP  The True Positive matrix values.
FP  The False Positive matrix values.
TN  The True Negative matrix values.
FN  The False Negative matrix values.
Zi  The total of positive predictions for each instance.
Yi  The total of positive expected for each instance.
TPi The total of True Positive predictions for each instance.
FPi  The total of False Positive predictions for each instance.
TNi  The total of True Negative predictions for each instance.
FNi  The total False Negative predictions for each instance.
Zl   The total of positive predictions for each label.
Yl   The total of positive expected for each label.
TPl  The total of True Positive predictions for each label.
FPl  The total of False Positive predictions for each label.
TNl  The total of True Negative predictions for each label.
FNl  The total False Negative predictions for each label.

See Also
Other evaluation: cv(), multilabel_evaluate(), multilabel_measures()

Examples

prediction <- predict(br(toyml), toyml)
mlconfmat <- multilabel_confusion_matrix(toyml, prediction)

# Label with the most number of True Positive values
which.max(mlconfmat$TPl)

# Number of wrong predictions for each label
errors <- mlconfmat$FPl + mlconfmat$FNl

# Examples predict with all labels
which(mlconfmat$Zi == toyml$measures$num.labels)

# You can join one or more mlconfmat
part1 <- create_subset(toyml, 1:50)
part2 <- create_subset(toyml, 51:100)
confmatp1 <- multilabel_confusion_matrix(part1, prediction[1:50, ])
confmatp2 <- multilabel_confusion_matrix(part2, prediction[51:100, ])
mlconfmat <- confmatp1 + confmatp2

multilabel_evaluate  Evaluate multi-label predictions

Description
This method is used to evaluate multi-label predictions. You can create a confusion matrix object or use directly the test dataset and the predictions. You can also specify which measures do you desire use.
Usage

multilabel_evaluate(object, ...)

## S3 method for class 'mldr'
multilabel_evaluate(object, mlresult, measures = c("all"), labels = FALSE, ...)

## S3 method for class 'mlconfmat'
multilabel_evaluate(object, measures = c("all"), labels = FALSE, ...)

Arguments

- **object**: A mldr dataset or a mlconfmat confusion matrix
- **...**: Extra parameters to specific measures.
- **mlresult**: The prediction result (Optional, required only when the mldr is used).
- **measures**: The measures names to be computed. Call multilabel_measures() to see the expected measures. You can also use "bipartition", "ranking", "label-based", "example-based", "macro-based", "micro-based" and "label-problem" to include a set of measures. (Default: "all").
- **labels**: Logical value defining if the label results should be also returned. (Default: FALSE)

Value

If labels is FALSE return a vector with the expected multi-label measures, otherwise, a list contained the multi-label and label measures.

Methods (by class)

- mldr: Default S3 method
- mlconfmat: Default S3 method

References


See Also

Other evaluation: cv(), multilabel_confusion_matrix(), multilabel_measures()
Examples

```
prediction <- predict(br(toyml), toyml)

# Compute all measures
multilabel_evaluate(toyml, prediction)
multilabel_evaluate(toyml, prediction, labels=TRUE) # Return a list

# Compute bipartition measures
multilabel_evaluate(toyml, prediction, "bipartition")

# Compute multilples measures
multilabel_evaluate(toyml, prediction, c("accuracy", "F1", "macro-based"))

# Compute the confusion matrix before the measures
cm <- multilabel_confusion_matrix(toyml, prediction)
multilabel_evaluate(cm)
multilabel_evaluate(cm, "example-based")
multilabel_evaluate(cm, c("hamming-loss", "subset-accuracy", "F1"))
```

---

```
multilabel_measures   Return the name of all measures
```

Description

Return the name of all measures

Usage

```
multilabel_measures()
```

Value

array of character contained the measures names.

See Also

Other evaluation: `cv()`, `multilabel_confusion_matrix()`, `multilabel_evaluate()`
multilabel_prediction

Create a mlresult object

Description

Create a mlresult object

Usage

multilabel_prediction(
  bipartitions,
  probabilities,
  probability = getOption("utiml.use.probs", TRUE),
  empty.prediction = getOption("utiml.empty.prediction", FALSE)
)

Arguments

bipartitions  The matrix of predictions (bipartition values), only 0 and 1
probabilities The matrix of probability/confidence of a prediction, between 0..1
probability   A logical value. If TRUE the predicted values are the score between 0 and 1, otherwise the values are bipartition 0 or 1. (Default: getOption("utiml.use.probs", TRUE))
empty.prediction
A logical value. If TRUE the predicted values may contains empty values, otherwise at least one label will be positive for each instance.

Value

An object of type mlresult

Examples

probs <- matrix(
  runif(90), ncol=3, dimnames = list(1:30, c("y1", "y2", "y3"))
)
preds <- matrix(
  as.numeric(probs > 0.5), ncol=3, dimnames = list(1:30, c("y1", "y2", "y3"))
)
multilabel_prediction(probs, preds)
normalize_mldata

Normalize numerical attributes

Description

Normalize all numerical attributes to values between 0 and 1. The highest value is changed to 1 and the lowest value to 0.

Usage

normalize_mldata(mdata)

Arguments

mdata The mldr dataset to be normalized.

Value

a new mldr object.

See Also

Other pre process: fill_sparse_mldata(), remove_attributes(), remove_labels(), remove_skewness_labels(), remove_unique_attributes(), remove_unlabeled_instances(), replace_nominal_attributes()

Examples

norm.toy <- normalize_mldata(toyml)

ns

Nested Stacking for multi-label Classification

Description

Create a Nested Stacking model for multilabel classification.

Usage

ns(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  chain = NA,
  ...
  predict.params = list(),
  cores = NULL,
  seed = getOption("utiml.seed", NA)
)

Arguments

- `mdata`: A mlr dataset used to train the binary models.
- `base.algorithm`: A string with the name of the base algorithm. (Default: `options("utiml.base.algorithm", "SVM")`)
- `chain`: A vector with the label names to define the chain order. If empty the chain is the default label sequence of the dataset. (Default: `NA`)
- `...`: Others arguments passed to the base algorithm for all subproblems.
- `predict.params`: A list of default arguments passed to the predict algorithm. (default: `list()`)
- `cores`: Ignored because this method does not support multi-core.
- `seed`: An optional integer used to set the seed. (Default: `options("utiml.seed", NA)`)  

Details

Nested Stacking is based on Classifier Chains transformation method to predict multi-label data. It differs from CC to predict the labels values in the training step and to regularize the output based on the labelsets available on training data.

Value

An object of class `NSmodel` containing the set of fitted models, including:

- `chain`: A vector with the chain order
- `labels`: A vector with the label names in expected order
- `labelset`: The matrix containing only labels values
- `models`: A list of models named by the label names.

References


See Also

Other Transformation methods: `brplus()`, `br()`, `cc()`, `clr()`, `dbr()`, `ebr()`, `ecc()`, `eps()`, `esl()`, `homer()`, `lift()`, `lp()`, `mbr()`, `ppt()`, `prudent()`, `ps()`, `rake1()`, `rdb()`, `rpc()`

Examples

```r
model <- ns(toyml, "RANDOM")
pred <- predict(model, toyml)

# Use a specific chain with C5.0 classifier
mychain <- sample(rownames(toyml$labels))
model <- ns(toyml, 'C5.0', mychain)
```
# Set a specific parameter
model <- ns(toyml, 'KNN', k=5)

**partition_fold**

Create the multi-label dataset from folds

**Description**

This is a simple way to use k-fold cross validation.

**Usage**

```r
partition_fold(kfold, n, has.validation = FALSE)
```

**Arguments**

- **kfold**: A `kFoldPartition` object obtained from use of the method `create_kfold_partition`.
- **n**: The number of the fold to separated train and test subsets.
- **has.validation**: Logical value that indicate if a validation dataset will be used. (Default: FALSE)

**Value**

A list contained train and test mldr dataset:
- **train**: The mldr dataset with train examples, that includes all examples except those that are in test and validation samples.
- **test**: The mldr dataset with test examples, defined by the number of the fold.
- **validation**: Optionally, only if `has.validation = TRUE`. The mldr dataset with validation examples.

**Examples**

```r
folds <- create_kfold_partition(toyml, 10)

# Using the first partition
dataset <- partition_fold(folds, 1)
names(dataset)
## [1] "train"  "test"

# All iterations
for (i in 1:10) {
  dataset <- partition_fold(folds, i)
  #dataset$train
  #dataset$test
}

# Using 3 folds validation
dataset <- partition_fold(folds, 3, TRUE)
# dataset$train, dataset$test, #dataset$validation
```
pcut_threshold

Proportional Thresholding (PCut)

Description

Define the proportion of examples for each label will be positive. The Proportion Cut (PCut) method can be a label-wise or global method that calibrates the threshold(s) from the training data globally or per label.

Usage

```r
pcut_threshold(prediction, ratio, probability = FALSE)
## Default S3 method:
pcut_threshold(prediction, ratio, probability = FALSE)
## S3 method for class 'mlresult'
pcut_threshold(prediction, ratio, probability = FALSE)
```

Arguments

- **prediction**: A matrix or mlresult.
- **ratio**: A single value between 0 and 1 or a list with ratio values contained one value per label.
- **probability**: A logical value. If `TRUE` the predicted values are the score between 0 and 1, otherwise the values are bipartition 0 or 1. (Default: `FALSE`)

Value

A mlresult object.

Methods (by class)

- `default`: Proportional Thresholding (PCut) method for matrix
- `mlresult`: Proportional Thresholding (PCut) for mlresult

References


**ppt**  

See Also  

Other threshold: `fixed_threshold()`, `lcard_threshold()`, `mcut_threshold()`, `rcut_threshold()`, `scut_threshold()`, `subset_correction()`

Examples  

```r  
prediction <- matrix(runif(16), ncol = 4)  
pcut_threshold(prediction, .45)  
```
predict.BASELINEmodel

Value

An object of class `PPTmodel` containing the set of fitted models, including:

- **labels** A vector with the label names.
- **model** A LP model contained only the most common labelsets.

References


See Also

Other Transformation methods: `brplus()`, `br()`, `cc()`, `clr()`, `dbr()`, `ebr()`, `ecc()`, `eps()`, `esl()`, `homer()`, `lift()`, `lp()`, `mbr()`, `ns()`, `prudent()`, `ps()`, `rakel()`, `rdbr()`, `rpc()`

Other Powerset: `eps()`, `lp()`, `ps()`, `rakel()`

Examples

```r
model <- ppt(toyml, "RANDOM")
pred <- predict(model, toyml)

## Change default configurations
model <- ppt(toyml, "RF", p=4, info.loss=TRUE)
```

Description

This function predicts values based upon a model trained by `baseline`.

Usage

```r
## S3 method for class 'BASELINEmodel'
predict(object, newdata, probability = getOption("utiml.use.probs", TRUE), ...)
```

Arguments

- **object** Object of class `BASELINEmodel`.
- **newdata** An object containing the new input data. This must be a matrix, data.frame or a mldr object.
- **probability** Logical indicating whether class probabilities should be returned. (Default: `getOption("utiml.use.probs", TRUE)`) not used.
predict.BRmodel

Value
An object of type mlresult, based on the parameter probability.

See Also
Baseline

Examples
model <- baseline(toyml)
pred <- predict(model, toyml)

predict.BRmodel  Predict Method for Binary Relevance

Description
This function predicts values based upon a model trained by \textit{br}.

Usage

## S3 method for class 'BRmodel'
predict(
  object,
  newdata,
  probability = getOption("utiml.use.probs", TRUE),
  ...,  
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)

Arguments

object
> Object of class ‘BRmodel’.

newdata
> An object containing the new input data. This must be a matrix, data.frame or a mldr object.

probability
> Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))

...  
> Others arguments passed to the base algorithm prediction for all subproblems.

twores
> The number of cores to parallelize the training. Values higher than 1 require the \textit{parallel} package. (Default: options("utiml.cores", 1))

seed
> An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

Value
An object of type mlresult, based on the parameter probability.
Predict Method for BR+ (brplus)

This function predicts values based upon a model trained by brplus.

Usage

```r
## S3 method for class 'BRPmodel'
predict(
  object,
  newdata,
  strategy = c("Dyn", "Stat", "Ord", "NU"),
  order = list(),
  probability =getOption("utiml.use.probs", TRUE),
  ...,
  cores =getOption("utiml.cores", 1),
  seed =getOption("utiml.seed", NA)
)
```

Arguments

- `object` Object of class 'BRPmodel'.
- `newdata` An object containing the new input data. This must be a matrix, data.frame or a mldr object.
predict.BRPmodel

strategy The strategy prefix to determine how to estimate the values of the augmented features of unlabeled examples. The possible values are: 'Dyn', 'Stat', 'Ord' or 'NU'. See the description for more details. (Default: 'Dyn').

order The label sequence used to update the initial labels results based on the final results. This argument is used only when the strategy = 'Ord' (Default: list())

probability Logical indicating whether class probabilities should be returned. (Default:getOption("utiml.use.probs", TRUE))

... Others arguments passed to the base algorithm prediction for all subproblems.

cores The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))

seed An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

Details

The strategies of estimate the values of the new features are separated in two groups:

**No Update** (NU) This use the initial prediction of BR to all labels. This name is because no modification is made to the initial estimates of the augmented features during the prediction phase

**With Update** This strategy update the initial prediction in that the final predict occurs. There are three possibilities to define the order of label sequences:

**Specific order** (Ord) The order is define by the user, require a new argument called order.

**Static order** (Stat) Use the frequency of single labels in the training set to define the sequence, where the least frequent labels are predicted first

**Dynamic order** (Dyn) Takes into account the confidence of the initial prediction for each independent single label, to define a sequence, where the labels predicted with less confidence are updated first.

Value

An object of type mlresult, based on the parameter probability.

References


See Also

BR+
Examples

```r
# Predict SVM scores
model <- brplus(toyml, "RANDOM")
pred <- predict(model, toyml)

# Predict SVM bipartitions and change the method to use No Update strategy
pred <- predict(model, toyml, strategy = 'NU', probability = FALSE)

# Predict using a random sequence to update the labels
labels <- sample(rownames(toyml$labels))
pred <- predict(model, toyml, strategy = 'Ord', order = labels)

# Passing a specif parameter for SVM predict method
pred <- predict(model, toyml, na.action = na.fail)
```

predict.CCmodel

**Predict Method for Classifier Chains**

**Description**

This function predicts values based upon a model trained by cc.

**Usage**

```r
# S3 method for class 'CCmodel'
predict(
  object,
  newdata,
  probability = getOption("utiml.use.probs", TRUE),
  ...
  cores = NULL,
  seed = getOption("utiml.seed", NA)
)
```

**Arguments**

- **object**: Object of class 'CCmodel'.
- **newdata**: An object containing the new input data. This must be a matrix, data.frame or a mldr object.
- **probability**: Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
- **...**: Others arguments passed to the base algorithm prediction for all subproblems.
- **cores**: Ignored because this method does not support multi-core.
- **seed**: An optional integer used to set the seed. (Default: options("utiml.seed", NA))
predict.CLRmodel

Value

An object of type mlresult, based on the parameter probability.

Note

The Classifier Chains prediction can not be parallelized

See Also

Classifier Chains (CC)

Examples

model <- cc(toyml, "RANDOM")
pred <- predict(model, toyml)

# Predict SVM bipartitions
pred <- predict(model, toyml, prob = FALSE)

# Passing a specif parameter for SVM predict algorithm
pred <- predict(model, toyml, na.action = na.fail)

predict.CLRmodel  
Predict Method for CLR

Description

This function predicts values based upon a model trained by clr.

Usage

## S3 method for class 'CLRmodel'
predict(
  object,
  newdata,
  probability = getOption("utiml.use.probs", TRUE),
  ...,  
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
predict.DBRmodel

Arguments

object Object of class 'CLRmodel'.
newdata An object containing the new input data. This must be a matrix, data.frame or a
mlr object.
probability Logical indicating whether class probabilities should be returned. (Default: 
getOption("utiml.use.probs", TRUE))
... Others arguments passed to the base algorithm prediction for all subproblems.
cores The number of cores to parallelize the training. Values higher than 1 require the 
parallel package. (Default: options("utiml.cores", 1))
seed An optional integer used to set the seed. This is useful when the method is run 
in parallel. (Default: options("utiml.seed", NA))

Value

An object of type mlresult, based on the parameter probability.

See Also

Binary Relevance (BR)

Examples

model <- clr(toyml, "RANDOM")
pred <- predict(model, toyml)

---

predict.DBRmodel 

Predict Method for DBR

Description

This function predicts values based upon a model trained by dbr. In general this method is a
restricted version of predict.BRPmodel using the 'NU' strategy.

Usage

### S3 method for class 'DBRmodel'
predict(
  object,
  newdata,
  estimative = NULL,
  probability = getOption("utiml.use.probs", TRUE),
  ...,
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
Arguments

- **object**: Object of class `DBRmodel`.
- **newdata**: An object containing the new input data. This must be a matrix, data.frame or a mlr object.
- **estimative**: A matrix containing the bipartition result of other multi-label classification algorithm or an mlresult object with the predictions.
- **probability**: Logical indicating whether class probabilities should be returned. (Default: `getOption("utiml.use.probs", TRUE)`)  
- **...**: Others arguments passed to the base algorithm prediction for all subproblems.
- **cores**: The number of cores to parallelize the training. Values higher than 1 require the `parallel` package. (Default: `options("utiml.cores", 1)`)  
- **seed**: An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `options("utiml.seed", NA)`)  

Details

As a new feature is possible to use other multi-label classifier to predict the estimate values of each label. To this use the prediction argument to inform a result of other multi-label algorithm.

Value

An object of type mlresult, based on the parameter probability.

References


See Also

Dependent Binary Relevance (DBR)

Examples

```r
# Predict SVM scores
model <- dbr(toyml)
pred <- predict(model, toyml)

# Passing a specific parameter for SVM predict algorithm
pred <- predict(model, toyml, na.action = na.fail)

# Using other classifier (EBR) to make the labels estimatives
estimative <- predict(ebr(toyml), toyml)
model <- dbr(toyml, estimate.models = FALSE)
pred <- predict(model, toyml, estimative = estimative)
```
predict.EBRmodel  Predict Method for Ensemble of Binary Relevance

Description

This method predicts values based upon a model trained by ebr.

Usage

```r
## S3 method for class 'EBRmodel'
predict(
  object,
  newdata,
  vote.schema = "maj",
  probability = getOption("utiml.use.probs", TRUE),
  ..., core = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

Arguments

- **object**: Object of class 'EBRmodel'.
- **newdata**: An object containing the new input data. This must be a matrix, data.frame or a mldr object.
- **vote.schema**: Define the way that ensemble must compute the predictions. The default valid options are: c("avg", "maj", "max", "min"). If NULL then all predictions are returned. (Default: "maj")
- **probability**: Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
- **...**: Others arguments passed to the base algorithm prediction for all subproblems.
- **cores**: The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
- **seed**: An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

Value

An object of type mlresult, based on the parameter probability.

See Also

Ensemble of Binary Relevance (EBR) Compute Multi-label Predictions
Examples

# Predict SVM scores
model <- ebr(toyml)
pred <- predict(model, toyml)

# Predict SVM bipartitions running in 2 cores
pred <- predict(model, toyml, prob = FALSE, cores = 2)

# Return the classes with the highest score
pred <- predict(model, toyml, vote = 'max')

predict.ECCmodel  
Predict Method for Ensemble of Classifier Chains

Description

This method predicts values based upon a model trained by ecc.

Usage

## S3 method for class 'ECCmodel'
predict(
  object,
  newdata,
  vote.schema = "maj",
  probability = getOption("utiml.use.probs", TRUE),
  ...,  
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)

Arguments

object Object of class 'ECCmodel'.
newdata An object containing the new input data. This must be a matrix, data.frame or a mldr object.
vote.schema Define the way that ensemble must compute the predictions. The default valid options are: c("avg", "maj", "max", "min"). If NULL then all predictions are returned. (Default: "maj")
probability Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
... Others arguments passed to the base algorithm prediction for all subproblems.
cores The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
seed An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))
Value

An object of type mlresult, based on the parameter probability.

See Also

Ensemble of Classifier Chains (ECC)

Examples

```r
# Predict SVM scores
model <- ecc(toyml)
pred <- predict(model, toyml)

# Predict SVM bipartitions running in 2 cores
pred <- predict(model, toyml, probability = FALSE, cores = 2)

# Return the classes with the highest score
pred <- predict(model, toyml, vote.schema = 'max')
```

predict.EPSmodel  

**Predict Method for Ensemble of Pruned Set Transformation**

Description

This function predicts values based upon a model trained by `eps`. Different from the others methods the probability value, is actually, the sum of all probability predictions such as it is described in the original paper.

Usage

```r
## S3 method for class 'EPSmodel'
predict(
  object,
  newdata,
  threshold = 0.5,
  probability = getOption("utiml.use.probs", TRUE),
  ...,
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

Arguments

- `object`  
  Object of class `EPSmodel`.
- `newdata`  
  An object containing the new input data. This must be a matrix, data.frame or a mldr object.
predict.ESLmodel

threshold  A threshold value for producing bipartitions. (Default: 0.5)
probability Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
... Others arguments passed to the base algorithm prediction for all subproblems.
cores The number of cores to parallelize the prediction. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
seed An optional integer used to set the seed. (Default: options("utiml.seed", NA))

Value
An object of type mlresult, based on the parameter probability.

See Also
Ensemble of Pruned Set (EPS)

Examples
model <- eps(toyml, "RANDOM")
pred <- predict(model, toyml)

predict.ESLmodel  Predict Method for Ensemble of Single Label

Description
This function predicts values based upon a model trained by esl.

Usage
## S3 method for class 'ESLmodel'
predict(
oobject,
newdata,
probability = getOption("utiml.use.probs", TRUE),
...,  
cores = getOption("utiml.cores", 1),
seed = getOption("utiml.seed", NA)  
)
Arguments

object Object of class 'ESLmodel'.
newdata An object containing the new input data. This must be a matrix, data.frame or a mlr object.
probability Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
... Others arguments passed to the base algorithm prediction for all subproblems.
cores The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
seed An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

Value

An object of type mlresult, based on the parameter probability.

See Also

Ensemble of Single Label (ESL)

Examples

model <- esl(toyml, "RANDOM")
pred <- predict(model, toyml)

predict.HOMERmodel Predict Method for HOMER

Description

This function predicts values based upon a model trained by homer.

Usage

## S3 method for class 'HOMERmodel'
predict(
  object, 
  newdata, 
  probability = getOption("utiml.use.probs", TRUE), 
  ..., 
  cores = getOption("utiml.cores", 1), 
  seed = getOption("utiml.seed", NA) 
)
Arguments

object Object of class 'HOMERmodel'.
newdata An object containing the new input data. This must be a matrix, data.frame or a mldr object.
probability Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
... Others arguments passed to the base algorithm prediction for all subproblems.
cores The number of cores to parallelize the prediction. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
seed An optional integer used to set the seed. (Default: options("utiml.seed", NA))

Value

An object of type mlresult, based on the parameter probability.

See Also

Hierarchy Of Multilabel classifier (HOMER)

Examples

model <- homer(toyml, "RANDOM")
pred <- predict(model, toyml)
predict.LPmodel

Arguments

object Object of class 'LIFTmodel'.
newdata An object containing the new input data. This must be a matrix, data.frame or a mldr object.
probability Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
... Others arguments passed to the base algorithm prediction for all subproblems.
cores The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
seed An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

Value

An object of type mlresult, based on the parameter probability.

See Also

LIFT

Examples

model <- lift(toyml, "RANDOM")
pred <- predict(model, toyml)
predict.MBRmodel

Arguments

object Object of class 'LPmodel'.
newdata An object containing the new input data. This must be a matrix, data.frame or a mldr object.
probability Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
... Others arguments passed to the base algorithm prediction for all subproblems.
cores Not used
seed An optional integer used to set the seed. (Default: options("utiml.seed", NA))

Value
An object of type mlresult, based on the parameter probability.

See Also
Label Powerset (LP)

Examples

model <- lp(toyml, "RANDOM")
pred <- predict(model, toyml)

predict.MBRmodel Predict Method for Meta-BR/2BR

Description
This function predicts values based upon a model trained by mbr.

Usage

## S3 method for class 'MBRmodel'
predict(
  object,
  newdata,
  probability = getOption("utiml.use.probs", TRUE),
  ..., cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
Arguments

object      Object of class 'MBRmodel'.
newdata     An object containing the new input data. This must be a matrix, data.frame or a mldr object.
probability Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
...         Others arguments passed to the base algorithm prediction for all subproblems.
cores       The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
seed        An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

Value

An object of type mresult, based on the parameter probability.

See Also

Meta-BR (MBR or 2BR)

Examples

# Predict SVM scores
model <- mbr(toyml)
pred <- predict(model, toyml)

# Predict SVM bipartitions
pred <- predict(model, toyml, probability = FALSE)

# Passing a specif parameter for SVM predict algorithm
pred <- predict(model, toyml, na.action = na.fail)
predict.NSmodel

Usage

```r
## S3 method for class 'MLKNNmodel'
predict(
  object,
  newdata,
  probability = getOption("utiml.use.probs", TRUE),
  ..., 
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

Arguments

- **object**: Object of class 'MLKNNmodel'.
- **newdata**: An object containing the new input data. This must be a matrix, data.frame or a mlr object.
- **probability**: Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
- **...**: Not used.
- **cores**: Ignored because this method does not support multi-core.
- **seed**: Ignored because this method is deterministic.

Value

An object of type mlresult, based on the parameter probability.

See Also

- ML-KNN

Examples

```r
model <- mlknn(toyml)
pred <- predict(model, toyml)
```

Description

This function predicts values based upon a model trained by ns. The scores of the prediction was adapted once this method uses a correction of labelsets to predict only classes present on training data. To more information about this implementation see subset_correction.
Usage

```r
## S3 method for class 'NSmodel'
predict(
  object,
  newdata,
  probability = getOption("utiml.use.probs", TRUE),
  ..., 
  cores = NULL,
  seed = getOption("utiml.seed", NA)
)
```

Arguments

- `object`: Object of class 'NSmodel'.
- `newdata`: An object containing the new input data. This must be a matrix, data.frame or a mldr object.
- `probability`: Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
- `...`: Others arguments passed to the base algorithm prediction for all subproblems.
- `cores`: Ignored because this method does not support multi-core.
- `seed`: An optional integer used to set the seed. (Default: options("utiml.seed", NA))

Value

An object of type mlresult, based on the parameter probability.

See Also

- Nested Stacking (NS)

Examples

```r
model <- ns(toyml, "RANDOM")
pred <- predict(model, toyml)

# Predict SVM bipartitions
pred <- predict(model, toyml, probability = FALSE)

# Passing a specif parameter for SVM predict algorithm
pred <- predict(model, toyml, na.action = na.fail)
```
### predict.PPTmodel

**Predict Method for Pruned Problem Transformation**

#### Description

This function predicts values based upon a model trained by \texttt{ppt}.

#### Usage

```r
## S3 method for class 'PPTmodel'
predict(
  object,
  newdata,
  probability = getOption("utiml.use.probs", TRUE),
  ..., 
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

#### Arguments

- **object**: Object of class 'PPTmodel'.
- **newdata**: An object containing the new input data. This must be a matrix, data.frame or a mldr object.
- **probability**: Logical indicating whether class probabilities should be returned. (Default: \texttt{getOption("utiml.use.probs", TRUE)})
- **...**: Others arguments passed to the base algorithm prediction for all subproblems.
- **cores**: Not used
- **seed**: An optional integer used to set the seed. (Default: \texttt{options("utiml.seed", NA)})

#### Value

An object of type mlresult, based on the parameter probability.

#### See Also

Pruned Problem Transformation (PPT)

#### Examples

```r
model <- ppt(toyml, "RANDOM")
pred <- predict(model, toyml)
```
predict.PruDentmodel  

Predict Method for PruDent

Description
This function predicts values based upon a model trained by prudent.

Usage
## S3 method for class 'PruDentmodel'
predict(
  object,
  newdata,
  probability = getOption("utiml.use.probs", TRUE),
  ..., 
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)

Arguments
  object          Object of class 'PruDentmodel'.
  newdata         An object containing the new input data. This must be a matrix, data.frame or a mldr object.
  probability     Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
  ...             Others arguments passed to the base algorithm prediction for all subproblems.
  cores           The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
  seed            An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

Value
An object of type mlresult, based on the parameter probability.

See Also

PruDent

Examples

# Predict SVM scores
model <- prudent(toyml)
pred <- predict(model, toyml)
# Predict SVM bipartitions
pred <- predict(model, toyml, probability = FALSE)

# Passing a specif parameter for SVM predict algorithm
pred <- predict(model, toyml, na.action = na.fail)

## predict.PSmodel

*Predict Method for Pruned Set Transformation*

**Description**

This function predicts values based upon a model trained by `ps`.

**Usage**

```r
## S3 method for class 'PSmodel'
predict(
  object,
  newdata,
  probability = getOption("utiml.use.probs", TRUE),
  ..., 
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

**Arguments**

- **object**: Object of class `PSmodel`.
- **newdata**: An object containing the new input data. This must be a matrix, data.frame or a mldr object.
- **probability**: Logical indicating whether class probabilities should be returned. (Default: `getOption("utiml.use.probs", TRUE)`)  
- **...**: Others arguments passed to the base algorithm prediction for all subproblems.
- **cores**: Not used.
- **seed**: An optional integer used to set the seed. (Default: `options("utiml.seed", NA)`)  

**Value**

An object of type mldrresult, based on the parameter probability.

**See Also**

`Pruned Set (PS)`
Examples

```r
model <- ps(toyml, "RANDOM")
pred <- predict(model, toyml)
```

**predict.RAkELmodel**

*Predict Method for RAkEL*

**Description**

This function predicts values based upon a model trained by `rakel`.

**Usage**

```r
## S3 method for class 'RAkELmodel'
predict(
  object,
  newdata,
  probability = getOption("utiml.use.probs", TRUE),
  ..., 
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

**Arguments**

- `object`: Object of class 'RAkELmodel'.
- `newdata`: An object containing the new input data. This must be a matrix, data.frame or a mldr object.
- `probability`: Logical indicating whether class probabilities should be returned. (Default: `getOption("utiml.use.probs", TRUE)`)
- `...`: Others arguments passed to the base algorithm prediction for all subproblems.
- `cores`: The number of cores to parallelize the prediction. Values higher than 1 require the `parallel` package. (Default: `options("utiml.cores", 1)`)
- `seed`: An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `options("utiml.seed", NA)`)

**Value**

An object of type mlresult, based on the parameter `probability`.

**See Also**

- Random k Labelsets (RAkEL)

**Examples**

```r
model <- rakel(toyml, "RANDOM")
pred <- predict(model, toyml)
```
Description

This function predicts values based upon a model trained by rdbr. In general this method is a recursive version of predict.DBRmodel.

Usage

```r
## S3 method for class 'RDBRmodel'
predict(
  object,  
  newdata,  
  estimative = NULL,  
  max.iterations = 5,  
  batch.mode = FALSE,  
  probability =getOption("utiml.use.probs", TRUE),  
  ...,  
  cores =getOption("utiml.cores", 1),  
  seed =getOption("utiml.seed", NA)  
)
```

Arguments

- **object**: Object of class `RDBRmodel`.
- **newdata**: An object containing the new input data. This must be a matrix, data.frame or a mldr object.
- **estimative**: A matrix containing the bipartition result of other multi-label classification algorithm or an mlresult object with the predictions.
- **max.iterations**: The maximum allowed iterations of the RDBR technique. (Default: 5)
- **batch.mode**: Logical value to determine if use the batch re-estimation. If FALSE then use the stochastic re-estimation strategy. (Default: FALSE)
- **probability**: Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
- **cores**: Others arguments passed to the base algorithm prediction for all subproblems.
- **seed**: An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))
Details

Two versions of the update strategy of the estimated labels are implemented. The batch re-estimates the labels only when a complete current label vector is available. The stochastic uses re-estimated labels as soon as they become available. This second does not support parallelize the prediction, however stabilizes earlier than batch mode.

Value

An object of type mlresult, based on the parameter probability.

References


See Also

Recursive Dependent Binary Relevance (RDBR)

Examples

```r
# Predict SVM scores
model <- rdbr(toyml)
pred <- predict(model, toyml)

# Passing a specif parameter for SVM predict algorithm
pred <- predict(model, toyml, na.action = na.fail)

# Use the batch mode and increase the max number of iteration to 10
pred <- predict(model, toyml, max.iterations = 10, batch.mode = TRUE)

# Using other classifier (EBR) to made the labels estimatives
estimative <- predict(ebr(toyml), toyml, probability = FALSE)
model <- rdbr(toyml, estimate.models = FALSE)
pred <- predict(model, toyml, estimative = estimative)
```
### S3 method for class 'RPCmodel'

```r
default predict(  
  object,  
  newdata,  
  probability =getOption("utiml.use.probs", TRUE),  
  ...,  
  cores =getOption("utiml.cores", 1),  
  seed =getOption("utiml.seed", NA)  
)
```

### Arguments

- `object` Object of class 'RPCmodel'.
- `newdata` An object containing the new input data. This must be a matrix, data.frame or a mldr object.
- `probability` Logical indicating whether class probabilities should be returned. (Default: getOption("utiml.use.probs", TRUE))
- `...` Others arguments passed to the base algorithm prediction for all subproblems.
- `cores` The number of cores to parallelize the training. Values higher than 1 require the `parallel` package. (Default: options("utiml.cores", 1))
- `seed` An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

### Value

An object of type mlresult, based on the parameter `probability`.

### See Also

- **Binary Relevance (BR)**

### Examples

```r
model <- rpc(toyml, "RANDOM")
pred <- predict(model, toyml)
```

---

**print.BRmodel**  
*Print BR model*

### Description

Print BR model
print.BRPmodel

Usage

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

Arguments

x The br model
...

Value

No return value, called for print model’s detail

print.BRPmodel

Print BRP model

Description

Print BRP model

Usage

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

Arguments

x The brp model
...

Value

No return value, called for print model’s detail
**print.CCmodel**

Print CC model

**Usage**

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

**Arguments**

- `x` The cc model
- `...` ignored

**Value**

No return value, called for print model's detail

---

**print.CLReqmodel**

Print CLR model

**Usage**

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

**Arguments**

- `x` The br model
- `...` ignored

**Value**

No return value, called for print model's detail
print.DBRmodel  

Description
Print DBR model

Usage

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

Arguments

x The dbr model
...

Value
No return value, called for print model’s detail

print.EBRmodel  

Description
Print EBR model

Usage

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

Arguments

x The ebr model
...

Value
No return value, called for print model’s detail
### print.ECCmodel

#### Description
Print ECC model

#### Usage
```r
## S3 method for class 'ECCmodel'
print(x, ...)
```

#### Arguments
- **x**
  - The ecc model
- **...**
  - ignored

#### Value
No return value, called for print model’s detail

### print.EPSmodel

#### Description
Print EPS model

#### Usage
```r
## S3 method for class 'EPSmodel'
print(x, ...)
```

#### Arguments
- **x**
  - The ps model
- **...**
  - ignored

#### Value
No return value, called for print model’s detail
print.ESLmodel

Print ESL model

Description

Print ESL model

Usage

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

Arguments

x
The esl model

... ignored

Value

No return value, called for print model’s detail

print.kFoldPartition

Print a kFoldPartition object

Description

Print a kFoldPartition object

Usage

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

Arguments

x
The kFoldPartition object

... ignored

Value

No return value, called for print folds’ detail
**print.LIFTmodel**

*Print LIFT model*

---

**Description**

Print LIFT model

**Usage**

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

**Arguments**

- `x`: The lift model
- `...`: ignored

**Value**

No return value, called for print model’s detail

---

**print.LPmodel**

*Print LP model*

---

**Description**

Print LP model

**Usage**

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

**Arguments**

- `x`: The lp model
- `...`: ignored

**Value**

No return value, called for print model’s detail
print.majorityModel  
**Print Majority model**

**Description**
Print Majority model

**Usage**
```r
## S3 method for class 'majorityModel'
print(x, ...)
```

**Arguments**
- `x` The base model
- `...` ignored

**Value**
No return value, called for print model’s detail

print.MBRmodel  
**Print MBR model**

**Description**
Print MBR model

**Usage**
```r
## S3 method for class 'MBRmodel'
print(x, ...)
```

**Arguments**
- `x` The mbr model
- `...` ignored

**Value**
No return value, called for print model’s detail
print.mlconfmat

Print a Multi-label Confusion Matrix

Description
Print a Multi-label Confusion Matrix

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

Arguments
- **x**: The mlconfmat
- **...**: ignored

Value
No return value, called for print a confusion matrix

print.MLKNNmodel

Print MLKNN model

Description
Print MLKNN model

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

Arguments
- **x**: The mlknn model
- **...**: ignored

Value
No return value, called for print model’s detail
### print.mlresult

**Print the mlresult**

**Description**

Print the mlresult

**Usage**

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

**Arguments**

- `x` The mlresult to print
- `...` Extra parameters for print method

**Value**

No return value, called for print a prediction result

### print.NSmodel

**Print NS model**

**Description**

Print NS model

**Usage**

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

**Arguments**

- `x` The ns model
- `...` ignored

**Value**

No return value, called for print model’s detail
print.PPTmodel

Description
Print PPT model

Usage

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

Arguments

x The ppt model
...

Value
No return value, called for print model's detail

print.PruDentmodel

Description
Print PruDent model

Usage

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

Arguments

x The prudent model
...

Value
No return value, called for print model's detail
print.PSmodel  
Print PS model

Description
Print PS model

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

Arguments

  x   The ps model

  ...  ignored

Value
No return value, called for print model’s detail

print.RAkelmodel  
Print RAkEL model

Description
Print RAkEL model

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

Arguments

  x   The rakel model

  ...  ignored

Value
No return value, called for print model’s detail
print.randomModel  

Print Random model

Description
Print Random model

Usage

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

Arguments

x  The base model
...

Value
No return value, called for print model’s detail

print.RDBRmodel  

Print RDBR model

Description
Print RDBR model

Usage

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

Arguments

x  The rdbr model
...

Value
No return value, called for print model’s detail
print.RPCmodel  Print RPC model

Description

Print RPC model

Usage

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

Arguments

- `x`  The br model
- `...`  ignored

Value

No return value, called for print model’s detail

prudent  PruDent classifier for multi-label Classification

Description

Create a PruDent classifier to predict multi-label data. To this, two round of Binary Relevance is executed, such that, the first iteration generates new attributes to enrich the second prediction.

Usage

```r
prudent(
  mdata,
  base.algorithm =getOption("utiml.base.algorithm", "SVM"),
  phi = 0,
  ..., 
  cores =getOption("utiml.cores", 1),
  seed =getOption("utiml.seed", NA)
)
```
prudent

Arguments

- mdata: A mlr dataset used to train the binary models.
- base.algorithm: A string with the name of the base algorithm. (Default: options("utiml.base.algorithm", "SVM"))
- phi: A value between 0 and 1 to determine the information gain. The value 0 include all labels in the second phase and the 1 none.
- cores: The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))
- seed: An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: options("utiml.seed", NA))

Details

In the second phase only labels whose information gain is greater than a specific phi value is added.

Value

An object of class PruDentmodel containing the set of fitted models, including:

- labels: A vector with the label names.
- phi: The value of phi parameter.
- IG: The matrix of Information Gain used in combination with phi parameter to define the labels used in the second step.
- basemodel: The BRModel used in the first iteration.
- metamodels: A list of models named by the label names used in the second iteration.

References


See Also

Other Transformation methods: brplus(), br(), cc(), clr(), dbr(), ebr(), ecc(), eps(), esl(), homer(), lift(), lp(), mbr(), ns(), ppt(), ps(), rakel(), rdbr(), rpc()

Examples

```r
model <- prudent(toyml, "RANDOM")
pred <- predict(model, toyml)

# Use different phi correlation with C5.0 classifier
model <- prudent(toyml, 'C5.0', 0.3)

# Set a specific parameter
model <- prudent(toyml, 'KNN', k=5)
```
**ps**

*Pruned Set for multi-label Classification*

**Description**

Create a Pruned Set model for multilabel classification.

**Usage**

```r
ps(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  p = 3,
  strategy = c("A", "B"),
  b = 2,
  ...,
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

**Arguments**

- `mdata`: A mldr dataset used to train the binary models.
- `base.algorithm`: A string with the name of the base algorithm. (Default: `getOption("utiml.base.algorithm", "SVM")`)
- `p`: Number of instances to prune. All labelsets that occurs p times or less in the training data is removed. (Default: 3)
- `strategy`: The strategy (A or B) for processing infrequent labelsets. (Default: A).
- `b`: The number used by the strategy for processing infrequent labelsets.
- `...`: Others arguments passed to the base algorithm for all subproblems.
- `cores`: Not used
- `seed`: An optional integer used to set the seed. (Default: `getOption("utiml.seed", NA)`)  

**Details**

Pruned Set (PS) is a multi-class transformation that remove the less common classes to predict multi-label data.

**Value**

An object of class `PSmodel` containing the set of fitted models, including:

- `labels`: A vector with the label names.
- `model`: A LP model contained only the most common labelsets.
rakel

References


See Also

Other Transformation methods: brplus(), br(), cc(), clr(), dbr(), ebr(), ecc(), eps(), esl(), homer(), lift(), lp(), mbr(), ns(), ppt(), prudent(), rakel(), rdbr(), rpc()
Other Powerset: eps(), lp(), ppt(), rakel()

Examples

model <- ps(toyml, "RANDOM")
pred <- predict(model, toyml)

##Change default configurations
model <- ps(toyml, "RF", p=4, strategy="B", b=1)

rakel

Random k-labelsets for multilabel classification

Description

Create a RAkEL model for multilabel classification.

Usage

rakel(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  k = 3,
  m = 2 * mdata$measures$num.labels,
  overlapping = TRUE,
  ...
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)

Arguments

mdata A mldr dataset used to train the binary models.
base.algorithm A string with the name of the base algorithm. (Default: options("utiml.base.algorithm", "SVM"))
k The number of labels used in each labelset. (Default: 3)
The number of LP models. Used when overlapping is TRUE, otherwise it is ignored. (Default: 2 * length(labels))

overlapping Logical value, that defines if the method must overlapping the labelsets. If FALSE the method uses disjoint labelsets. (Default: TRUE)

... Others arguments passed to the base algorithm for all subproblems.

cores The number of cores to parallelize the training. Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))

seed An optional integer used to set the seed. This is useful when the method is running in parallel. (Default: options("utiml.seed", NA))

Details
RAndom k labELsets is an ensemble of LP models where each classifier is trained with a small set of labels, called labelset. Two different strategies for constructing the labelsets are the disjoint and overlapping labelsets.

Value
An object of class RAkELmodel containing the set of fitted models, including:

labels A vector with the label names.

labelsets A list with the labelsets used to build the LP models.

model A list of the generated models, named by the label names.

References

See Also
Other Transformation methods: brplus(), br(), cc(), clr(), dbr(), ebr(), ecc(), eps(), esl(), homer(), lift(), lp(), mbr(), ns(), ppt(), prudent(), ps(), rdbr(), rpc()
Other Powerset: eps(), lp(), ppt(), ps()

Examples
model <- rakel(toyml, "RANDOM")
pred <- predict(model, toyml)

## SVM using k = 4 and m = 100
model <- rakel(toyml, "SVM", k=4, m=100)

## Random Forest using disjoint labelsets
model <- rakel(toyml, "RF", overlapping=FALSE)
Description

The Rank Cut (RCut) method is an instance-wise strategy, which outputs the k labels with the highest scores for each instance at the deployment.

Usage

rcut_threshold(prediction, k, probability = FALSE)

## Default S3 method:
rcut_threshold(prediction, k, probability = FALSE)

## S3 method for class 'mlresult'
rcut_threshold(prediction, k, probability = FALSE)

Arguments

- **prediction**: A matrix or mlresult.
- **k**: The number of elements that will be positive.
- **probability**: A logical value. If TRUE the predicted values are the score between 0 and 1, otherwise the values are bipartition 0 or 1. (Default: FALSE)

Value

A mlresult object.

Methods (by class)

- default: Rank Cut (RCut) threshold method for matrix
- mlresult: Rank Cut (RCut) threshold method for mlresult

References


See Also

Other threshold: fixed_threshold(), lcard_threshold(), mcut_threshold(), pcut_threshold(), scut_threshold(), subset_correction()
Examples

```r
classification <- matrix(runif(16), ncol = 4)
rcut_threshold(classification, 2)
```

---

**rdbr**  
*Recursive Dependent Binary Relevance (RDBR) for multi-label Classification*

**Description**

Create a RDBR classifier to predict multi-label data. This is a recursive approach that enables the binary classifiers to discover existing label dependency by themselves. The idea of RDBR is running DBR recursively until the results stabilization of the result.

**Usage**

```r
rdbr(
  mdata,
  base.algorithm = getOption("utiml.base.algorithm", "SVM"),
  estimate.models = TRUE,
  ...,
  cores = getOption("utiml.cores", 1),
  seed = getOption("utiml.seed", NA)
)
```

**Arguments**

- `mdata`  
  A mldr dataset used to train the binary models.

- `base.algorithm`  
  A string with the name of the base algorithm. (Default: `getOption("utiml.base.algorithm", "SVM")`)

- `estimate.models`  
  Logical value indicating whether is necessary build Binary Relevance classifier for estimate process. The default implementation use BR as estimators, however when other classifier is desirable then use the value `FALSE` to skip this process. (Default: `TRUE`).

- `...`  
  Others arguments passed to the base algorithm for all subproblems.

- `cores`  
  The number of cores to parallelize the training. Values higher than 1 require the `parallel` package. (Default: `options("utiml.cores", 1)`)

- `seed`  
  An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `options("utiml.seed", NA)`)

**Details**

The train method is exactly the same of DBR the recursion is in the predict method.
Value

An object of class \texttt{RDBRmodel} containing the set of fitted models, including:

- **labels**: A vector with the label names.
- **estimation**: The BR model to estimate the values for the labels. Only when the \texttt{estimate.models} = \texttt{TRUE}.
- **models**: A list of final models named by the label names.

References


See Also

\texttt{Dependent Binary Relevance (DBR)}

Other Transformation methods: \texttt{brplus()}, \texttt{br()}, \texttt{cc()}, \texttt{clr()}, \texttt{dbr()}, \texttt{ebr()}, \texttt{ecc()}, \texttt{eps()}, \texttt{esl()}, \texttt{homer()}, \texttt{lift()}, \texttt{lp()}, \texttt{mbr()}, \texttt{ns()}, \texttt{ppt()}, \texttt{prudent()}, \texttt{ps()}, \texttt{rakel()}, \texttt{rpc()}

Examples

```r
model <- rdbr(toyml, "RANDOM")
pred <- predict(model, toyml)

# Use Random Forest as base algorithm and 2 cores
model <- rdbr(toyml, 'RF', cores = 2, seed = 123)
```

remove\_attributes

**Remove attributes from the dataset**

Description

Remove specified attributes generating a new multi-label dataset.

Usage

```r
remove\_attributes(mdata, attributes)
```

Arguments

- **mdata**: The mlr dataset to remove labels.
- **attributes**: Attributes indexes or attributes names to be removed.
remove_labels

Value

a new mlr object.

Note

If invalid attributes names or indexes were informed, they will be ignored.

See Also

Other pre process: fill_sparse_mldata(), normalize_mldata(), remove_labels(), remove_skewness_labels(), remove_unique_attributes(), remove_unlabeled_instances(), replace_nominal_attributes()

Examples

toyml1 <- remove_labels(toyml, c("y1","y5"))
toyml2 <- remove_labels(toyml, c(11, 15))
remove_skewness_labels

Remove unusual or very common labels

Description
Remove the labels that have smaller number of positive or negative examples based on a specific threshold value.

Usage

remove_skewness_labels(mdata, t = 1)

Arguments

mdata The mldr dataset to remove the skewness labels.
t Threshold value. Number of minimum examples positive and negative.

Value

a new mldr object.

See Also
Other pre process: fill_sparse_mldata(), normalize_mldata(), remove_attributes(), remove_labels(), remove_unique_attributes(), remove_unlabeled_instances(), replace_nominal_attributes()

Examples

remove_skewness_labels(toyml, 20)

remove_unique_attributes

Remove unique attributes

Description
Remove the attributes that have a single value for all instances. Empty and NA values are considered different values.

Usage

remove_unique_attributes(mdata)
remove_unlabeled_instances

Arguments

mdata The mlr dataset to remove.

Value

a new mlr object.

See Also

Other pre process: fill_sparse_mldata(), normalize_mldata(), remove_attributes(), remove_labels(), remove_skewness_labels(), remove_unlabeled_instances(), replace_nominal_attributes()

Examples

alt.toy <- toyml
alt.toy$dataset$ratt10 <- mean(alt.toy$dataset$ratt10)
new.toy <- remove_unique_attributes(alt.toy)

eval(e(quote(remove_unlabeled_instances(alt.toy))))
replace_nominal_attributes

Replace nominal attributes Replace the nominal attributes by binary attributes.

Description

Replace nominal attributes Replace the nominal attributes by binary attributes.

Usage

replace_nominal_attributes(mdata, ordinal.attributes = list())

Arguments

mdata The mldr dataset to remove.
ordinal.attributes Not yet, but it will be used to specify which attributes need to be replaced.

Value

a new mldr object.

See Also

Other pre process: fill_sparse_mldata(), normalize_mldata(), remove_attributes(), remove_labels(), remove_skewness_labels(), remove_unique_attributes(), remove_unlabeled_instances()

Examples

new.toy <- toyml
new.column <- as.factor(sample(c("a","b","c"), 100, replace = TRUE))
new.toy$dataset$ratt10 <- new.column
head(replace_nominal_attributes(new.toy))

rpc

Ranking by Pairwise Comparison (RPC) for multi-label Classification

Description

Create a RPC model for multilabel classification.
Usage

rpc(mdata, 
    base.algorithm = getOption("utiml.base.algorithm", "SVM"), 
    ..., 
    cores = getOption("utiml.cores", 1), 
    seed = getOption("utiml.seed", NA) 
)

Arguments

- **mdata**: A mldr dataset used to train the binary models.
- **base.algorithm**: A string with the name of the base algorithm. (Default: `options("utiml.base.algorithm", "SVM")`)
- **...**: Others arguments passed to the base algorithm for all subproblems
- **cores**: The number of cores to parallelize the training. Values higher than 1 require the `parallel` package. (Default: `options("utiml.cores", 1)`) 
- **seed**: An optional integer used to set the seed. This is useful when the method is run in parallel. (Default: `options("utiml.seed", NA)`) 

Details

RPC is a simple transformation method that uses pairwise classification to predict multi-label data. This is based on the one-versus-one approach to build a specific model for each label combination.

Value

An object of class `RPCmodel` containing the set of fitted models, including:

- **labels**: A vector with the label names.
- **models**: A list of the generated models, named by the label names.

References


See Also

Other Transformation methods: `brplus()`, `br()`, `cc()`, `clr()`, `dbr()`, `ebr()`, `ecc()`, `eps()`, `esl()`, `homer()`, `lift()`, `lp()`, `mbr()`, `ns()`, `ppt()`, `prudent()` `ps()`, `rakel()`, `rdbr()`

Other Pairwise methods: `clr()`

Examples

```r
model <- rpc(toyml, "RANDOM")
pred <- predict(model, toyml)
```
scut_threshold  

SCut Score-based method

Description

This is a label-wise method that adjusts the threshold for each label to achieve a specific loss function using a validation set or cross validation.

Usage

```r
scut_threshold(
  prediction,
  expected,
  loss.function = NA,
  cores = getOption("utiml.cores", 1)
)
```

```r
## Default S3 method:
scut_threshold(
  prediction,
  expected,
  loss.function = NA,
  cores = getOption("utiml.cores", 1)
)
```

```r
## S3 method for class 'mlresult'
scut_threshold(
  prediction,
  expected,
  loss.function = NA,
  cores = getOption("utiml.cores", 1)
)
```

Arguments

- **prediction**: A matrix or mlresult.
- **expected**: The expected labels for the prediction. May be a matrix with the label values or a mldr object.
- **loss.function**: A loss function to be optimized. If you want to use your own error function see the notes and example. (Default: Mean Squared Error)
- **cores**: The number of cores to parallelize the computation Values higher than 1 require the parallel package. (Default: options("utiml.cores", 1))

Details

Different from the others threshold methods instead of return the bipartition results, it returns the threshold values for each label.
Value

A numeric vector with the threshold values for each label

Methods (by class)

- default: Default scut_threshold
- mlresult: Mlresult scut_threshold

Note

The loss function is a R method that receive two vectors, the expected values of the label and the predicted values, respectively. Positive values are represented by the 1 and the negative by the 0.

References


See Also

Other threshold: fixed_threshold(), lcard_threshold(), mcut_threshold(), pcut_threshold(), rcut_threshold(), subset_correction()

Examples

```r
names <- list(1:10, c("a", "b", "c"))
prediction <- matrix(runif(30), ncol = 3, dimnames = names)
classes <- matrix(sample(0:1, 30, rep = TRUE), ncol = 3, dimnames = names)
thresholds <- scut_threshold(prediction, classes)
fixed_threshold(prediction, thresholds)

# Penalizes only FP predictions
mylossfunc <- function (real, predicted) {
  mean(predicted - real * predicted)
}
prediction <- predict(br(toyml, "RANDOM"), toyml)
scut_threshold(prediction, toyml, loss.function = mylossfunc, cores = 2)
```
**subset_correction**

**Subset Correction of a predicted result**

**Description**

This method restricts a multi-label learner to predict only label combinations whose existence is present in the (training) data. To this all labelsets that are predicted but are not found on training data is replaced by the most similar labelset.

**Usage**

```r
subset_correction(mlresult, train_y, probability = FALSE)
```

**Arguments**

- `mlresult`: An object of mlresult that contains the scores and bipartition values.
- `train_y`: A matrix/data.frame with all labels values of the training dataset or a mldr train dataset.
- `probability`: A logical value. If `TRUE` the predicted values are the score between 0 and 1, otherwise the values are bipartition 0 or 1. (Default: `FALSE`)

**Details**

If the most similar is not unique, those label combinations with higher frequency in the training data are preferred. The Hamming loss distance is used to determine the difference between the labelsets.

**Value**

A new mlresult where all results are present in the training labelsets.

**Note**

The original paper describes a method to create only bipartitions result, but we adapted the method to change the scores. Based on the `base.threshold` value the scores higher than the threshold value, but must be lower are changed to respect this restriction. If `NULL` this correction will be ignored.

**References**


**See Also**

Other threshold: `fixed_threshold()`, `lcard_threshold()`, `mcut_threshold()`, `pcut_threshold()`, `rcut_threshold()`, `scut_threshold()`
Examples

```r
prediction <- predict(br(toyml, "RANDOM"), toyml)
subset_correction(prediction, toyml)
```

---

**summary.mltransformation**

*Summary method for mltransformation*

### Description

Summary method for mltransformation

### Usage

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

### Arguments

- `object` A transformed dataset
- `...` additional arguments affecting the summary produced.

### Value

No return value, called for print model’s detail

---

**toyml**

*Toy multi-label dataset.*

---

**Description**

A toy multi-label dataset is a synthetic dataset generated by the tool [http://sites.labic.icmc.usp.br/mldatagen/](http://sites.labic.icmc.usp.br/mldatagen/) using the Hyperspheres strategy. Its purpose is to be used for small tests and examples.

### Usage

```r
toyml
```
Format

A mldr object with 100 instances, 10 features and 5 labels:

- **att1**: Relevant numeric attribute between (-1 and 1)
- **att2**: Relevant numeric attribute between (-1 and 1)
- **att3**: Relevant numeric attribute between (-1 and 1)
- **att4**: Relevant numeric attribute between (-1 and 1)
- **att5**: Relevant numeric attribute between (-1 and 1)
- **att6**: Relevant numeric attribute between (-1 and 1)
- **att7**: Relevant numeric attribute between (-1 and 1)
- **iatt8**: Irrelevant numeric attribute between (-1 and 1)
- **iatt9**: Irrelevant numeric attribute between (-1 and 1)
- **ratt10**: Redundant numeric attribute between (-1 and 1)
- **y1**: Label 'y1' - Frequency: 0.17
- **y2**: Label 'y2' - Frequency: 0.78
- **y3**: Label 'y3' - Frequency: 0.19
- **y4**: Label 'y4' - Frequency: 0.69
- **y5**: Label 'y5' - Frequency: 0.17

Details

General Information

- Cardinality: 2
- Density: 0.4
- Distinct multi-labels: 18
- Number of single labelsets: 5
- Max frequency: 23

Source

Generated by [http://sites.labic.icmc.usp.br/mldatagen/](http://sites.labic.icmc.usp.br/mldatagen/) Configuration:

- Strategy: Hyperspheres
- Relevant Features: 7
- Irrelevant Features: 2
- Redundant Features: 1
- Number of Labels (q): 5
- Number of Instances: 100
- Noise (from 0 to 1): 0.05
- Maximum Radius/Half-Edge of the Hyperspheres/Hypercubes: 0.8
- Minimum Radius/Half-Edge of the Hyperspheres/Hypercubes: ((q/10)+1)/q
Description

The utiml package is a framework for the application of classification algorithms to multi-label data. Like the well known MULAN used with Weka, it provides a set of multi-label procedures such as sampling methods, transformation strategies, threshold functions, pre-processing techniques and evaluation metrics. The package was designed to allow users to easily perform complete multi-label classification experiments in the R environment.

Details

Currently, the main methods supported are:

1. **Classification methods**: ML Baselines, Binary Relevance (BR), BR+, Classifier Chains, Calibrated Label Ranking (CLR), Dependent Binary Relevance (DBR), Ensemble of Binary Relevance (EBR), Ensemble of Classifier Chains (ECC), Ensemble of Pruned Set (EPS), Hierarchy Of Multilabel classifiers (HOMER), Label specific Features (LIFT), Label Powerset (LP), Meta-Binary Relevance (MBR or 2BR), Multi-label KNN (ML-KNN), Nested Stacking (NS), Pruned Problem Transformation (PPT), Pruned and Confident Stacking Approach (Prudent), Pruned Set (PS), Random k-labelsets (RAkEL), Recursive Dependent Binary Relevance (RDBR), Ranking by Pairwise Comparison (RPC)

2. **Evaluation methods**: Performing a cross-validation procedure, Confusion Matrix, Evaluate, Supported measures

3. **Pre-process utilities**: Fill sparse data, Normalize data, Remove attributes, Remove labels, Remove skewness labels, Remove unique attributes, Remove unlabeled instances, Replace nominal attributes

4. **Sampling methods**: Create holdout partitions, Create k-fold partitions, Create random subset, Create subset, Partition fold

5. **Threshold methods**: Fixed threshold, Cardinality threshold, MCUT, PCUT, RCUT, SCUT, Subset correction

However, there are other utilities methods not previously cited as `as.bipartition`, `as.mlresult`, `as.ranking`, `multilabel_prediction`, etc. More details and examples are available on utiml repository.

Notes

We use the `mlDr` package, to manipulate multi-label data. See its documentation to more information about handle multi-label dataset.

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• Adriano Rivolli <rivolli@utfpr.edu.br>

This package is a result of my PhD at Institute of Mathematics and Computer Sciences (ICMC) at the University of Sao Paulo, Brazil.

PhD advisor: Andre C. P. L. F. de Carvalho

---

### utiml_measure_names

**Return the name of measures**

**Description**

Return the name of measures

**Usage**

```r
utiml_measure_names(measures = c("all"))
```

**Arguments**

- `measures`: The group of measures (Default: "all").

**Value**

array of character contained the measures names.

**Examples**

```r
utiml_measure_names()
utiml_measure_names("bipartition")
utiml_measure_names(c("micro-based", "macro-based"))
```
Filter a Multi-Label Result

Description

If column filter is performed, then the result will be a matrix. Otherwise, the result will be a mlresult.

Usage

```r
## S3 method for class 'mlresult'
mlresult[rowFilter = T, colFilter, ...]
```

Arguments

- `mlresult` A mlresult object
- `rowFilter` A list of rows to filter
- `colFilter` A list of columns to filter
- `...` Extra parameters to be used as the filter

Value

mlresult or matrix. If column filter is performed, then the result will be a matrix. Otherwise, the result will be a mlresult.
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