Package 'doMIsaul'

July 20, 2021

Title Do Multiple Imputation-Based Semisupervised and Unsupervised
Learning

Version 1.0.0

Description Algorithms for (i) unsupervised learning for dataset with
missing data and/or left-censored data, using multiple imputation and
consensus clustering ; (ii) semisupervised learning with a survival
endpoint (right-censored) for complete or incomplete datasets, using
multiple imputation and consensus clustering in the latter case.

License GPL (>= 3)

URL https://github.com/LilithF/doMIsaul

BugReports https://github.com/LilithF/doMIsaul/issues

Imports aricode,
arules,
clusterCrit,
clusteval,
dplyr,
ggplot2,
Gmedian,
graphics,
MASS,
methods,
mice,
NbClust,
ncvreg,
plyr,
scales,
stats,
survival,
utils,
withr

Suggests censReg,
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igraph,
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R topics documented:

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cleanUp_partition   *Remove small clusters (i.e. unclassified observations for which no consensus was obtained)*

Description

Remove small clusters (i.e. unclassified observations for which no consensus was obtained)

Usage

```
cleanUp_partition(
  partition,
  min.cluster.size = 10,
  level.order = NULL,
  Unclassified = c(NA, "Unclassified")
)
```

Arguments

partition   the partition to clean (vector).

min.cluster.size

     Minimum cluster size (i.e., smaller clusters will be discarded)

level.order   optional. If you supply a variable the cluster levels will be ordinated according to the mean values for the variable

Unclassified   string for the label of the unclassified observations. defaults value is NA.

Value

The cleaned up partition (factor).

Examples

```
part <- factor(kmeans(iris[, 1:4], 8)$cluster)
summary(part)
part.clean <- cleanUp_partition(part, Unclassified = "Unclassified")
```

CVE_LP	*Cross-validation for cox regression using the linear predictor estimator with wrapper for warnings handling*

Description

Cross-validation for cox regression using the linear predictor estimator with wrapper for warnings handling

Usage

```
CVE_LP(x)
```

Arguments

x   list of 3 named elements : data (data containing columns time and status), partition (dataframe with 1 column), nfolds (number of fold for cross-validation).

Value

numeric, cross-validation error

Examples

```
data(cancer, package = "survival")
cancer$status <- cancer$status - 1
part <- data.frame(Cl= factor(cancer[, "sex"]), stringsAsFactors = TRUE)
CVE_LP(list(data = cancer, partition = part, nfolds = 10))
```

---

evaluate_partition_semisup

Evaluation of a semisupervised obtained partition in comparison to reference partitions

---

Description

Evaluate number of clusters, ARI, AUC difference, c-index and CPE, with Supervised, unsupervised and Semisupervised reference partitions

Usage

```
evaluate_partition_semisup(
  partition,
  ref.unsup,
  ref.sup,
  ref.semisup,
  data.surv,
  TMIN = 2,
  TMAX = 5
)
```

Arguments

partition	Vector containing cluster ids of the partition to evaluate.
ref.unsup	Vector: Unsupervised reference partition (i.e. data structure).
ref.sup	Vector: Supervised reference partition (i.e. using survival parameters).
ref.semisup	Vector: Semisupervised reference partition (i.e. combining both).
data.surv	dataframe with variables time and status.
TMIN	time point to start analyzing AUC.
TMAX	time point to analyze AUC.

Value

a list of named performances values

Examples

```
library(survival) # survival should be loaded in the environment
data(cancer, package = "survival")
cancer$status <- cancer$status - 1
res <- evaluate_partition_semisup (
  partition = factor(rep(c(1,2,3), each = 50)),
  ref.unsup = factor(rep(c(1,2,3), times = c(100, 25, 25))),
```

```
      ref.sup = factor(rep(c(1,2), times = c(50, 100))),
      ref.semisup = factor(rep(c(3, 2, 1), times = c(120, 10, 20))),
      data.surv = cancer[1:150, c("time", "status")] )
```

---

evaluate_partition_unsup
Comparison of an unsupervised obtained partition to a reference par-
tition.

Description

Compares partitions on number of cluster, ARI and percentage of unclassified observations.

Usage

```
evaluate_partition_unsup(
  partition,
  partition.ref,
  is.missing = NULL,
  is.cens = NULL
)
```

Arguments

`partition`	vector (factor): the partition to evaluate.
`partition.ref`	reference partition 1 (ex partition on complete data or true partition if known).
`is.missing`	boolean vector identifying observations with missing data (coded `TRUE`), from those without (coded `FALSE`).
`is.cens`	the incomplete dataframe with NA for missing and left-censored data (or the complete datasets if all data were observed).

Value

A list containing the following elements : `Nbclust`: number of clusters of the partition; `ARI`: ARI value on cases classified by both partitions ; `ARI.cc`: ARI value on cases complete AND classified by both partitions ; `ARI.nona`; ARI on cases with no missing data AND classified by both partitions; `ARI.nocens`: ARI on cases with no censored data AND classified by both partitions ; `Per.Unclass`: Percentage of observations unclassified in the partition ; `Per.Unclass.cc`: Among complete cases, percentage of observations unclassified in the partition ; `Per.Unclass.na`: Among cases with missing data, percentage of observations unclassified in the partition ; `Per.Unclass.cens`: Among cases with censored data, percentage of observations unclassified in the partition ; `Per.Unclass.ic`: Among incomplete cases, percentage of observations unclassified in the partition

Examples

```
res <- evaluate_partition_unsup(
  partition = factor(rep(c(1,2,3), each = 50)),
  partition.ref = factor(rep(c(1,2,3), times = c(100, 25, 25))))

## With missing data
res2 <- evaluate_partition_unsup(
```

```
  partition = factor(rep(c(1,2,3), each = 50)),
  partition.ref = factor(rep(c(1,2,3), times = c(100, 25, 25))),
  is.missing = sample(c(TRUE, FALSE), 150, replace = TRUE, prob = c(.2,.8)))

## With missing and censored data
  missing.indicator <- sample(c(TRUE, FALSE), 150,
   replace = TRUE, prob = c(.2,.8))
  Censor.indicator <- data.frame(
   X1 = runif(150, 1, 5),
   X2 = runif(150, 6, 8),
   X3 = runif(150, 3, 9))
  Censor.indicator$X1[missing.indicator] <- NA
  Censor.indicator$X1[
  sample(c(TRUE, FALSE), 150,replace = TRUE, prob = c(.1,.9))] <- NA
  Censor.indicator$X2[
  sample(c(TRUE, FALSE), 150,replace = TRUE, prob = c(.3,.7))] <- NA
  Censor.indicator$X3[
  sample(c(TRUE, FALSE), 150,replace = TRUE, prob = c(.05,.95))] <- NA
res3 <- evaluate_partition_unsup(
  partition = factor(rep(c(1,2,3), each = 50)),
  partition.ref = factor(rep(c(1,2,3), times = c(100, 25, 25))),
  is.missing = missing.indicator,
  is.cens = Censor.indicator)

## With missing and censored data and unclassifed observations
res4 <- evaluate_partition_unsup(
  partition = factor(rep(c(1,2, NA,3), times = c(50, 40, 20, 40))),
  partition.ref = factor(rep(c(1,2,3), times = c(100, 25, 25))),
  is.missing = missing.indicator,
  is.cens = Censor.indicator)
```

---

  initiate_centers   *Initiate centers for clustering algorithm*

Description

Initiate centers for clustering algorithm

Usage

```
initiate_centers(data, N = 1000, t = 1, k, algorithms = NULL, seeds.N = NULL)
```

Arguments

data	Dataset that clustering will be applied on
N	Integer. Number clustering initialization (set of centers) to generate
t	Numeric between 0 and 1. weight coefficient between only random centers (t=1) and only centers from clustering (t=0).
k	Vector of size N containing the number of centers for each initialization.
algorithms	list of algorithm(s) (size N * (1-t) to generate centers if t!=1, given as characters. Possible values are km for K-means, kmed for K-medians, hclust.mean, hclust.med for hierarchical clustering with mean or median position of the center.
seeds.N	(optional) vector of size N containing seeds for each initialization.

Value

list of size N containing coordinates of centers for clustering initialization.

Examples

```
Cent.init <- initiate_centers(data = iris[, 1:4], N = 10,
                              k = sample(c(2:7), 10, replace = TRUE))
```

---

mice.impute.cens	*Impute left censored data with MICE*

Description

Function from `Lapidus et al.` for imputing left-censored data with mice

Usage

```
mice.impute.cens(
  y,
  ry,
  x,
  lod.j,
  lod.name = "lod",
  REDRAW = FALSE,
  wy = NULL,
  ...
)
```

Arguments

y	Vector to be imputed
ry	Logical vector of length `length(y)` indicating the the subset y[ry] of elements in y to which the imputation model is fitted. The ry generally distinguishes the observed (TRUE) and missing values (FALSE) in y.
x	Numeric design matrix with `length(y)` rows with predictors for y. Matrix x may have no missing values.
lod.j	censoring value.
lod.name	suffix name used for the censored variable.
REDRAW	Boolean indicating whether values should be redrawn if some are over the censoring limit
wy	Logical vector of length `length(y)`. A TRUE value indicates locations in y for which imputations are created.
...	Other named arguments.

Value

Vector with imputed data, same type as y, and of length `sum(wy)`.

MImpute   *Wrapper functions for multivariate imputation with survival data or*
                            left-censored data

Description

Performs imputation of the missing data using MICE and returns a list in the correct format for
the `unsupMI()` and `seMIsupcox()`functions. `MImpute` performs imputation for datasets with miss-
ing data only. `MImpute_surv` performs imputation for a dataset with survival data. The Nelson
Aalen estimator is calculated and used as predictor in the imputation, Time is not used as pre-
dictor. `MImpute_lcens` performs imputation for a dataset with left-censored data. Note that with
`MImpute_lcens` pmm imputation is performed for variables not affected by left-censoring.

Usage

```
MImpute(
  data,
  mi.m,
  method = NULL,
  predMat = NULL,
  maxit = 10,
  return.midsObject = FALSE
)

MImpute_surv(
  data,
  mi.m,
  time.status.names = c("time", "status"),
  return.midsObject = FALSE
)

MImpute_lcens(
  data,
  data.lod,
  standards,
  mi.m,
  mice.log = 10,
  maxit = 10,
  return.midsObject = FALSE
)
```

Arguments

`data`	Dataframe with incomplete data. (for `MImpute_lcens`, with `NA` for both missing and left-censored data).
`mi.m`	Number of imputations to perform.
`method`	Optional. single string, or a vector of strings specifying the imputation method to be used for each column in data (passed to `mice()`). If `NULL` default mice setting are used.

predMat	Optional. supply a `predictorMatrix` (passed to `mice()`). If NULL default mice setting are used.
maxit	passed to `mice()`.
return.midsObject	
	Boolean
time.status.names	
	Names of the variables for time and status (in that order).
data.lod	Dataframe containing indicators of which observation are left-censored (censoring value for such observations and any other values for not censored observations). The colnames should correspond to variables in `data`. The variables that are left-censored are thus given in `data` (with left-censored data as NA) and in `data.lod` with random values for observed data and the LOD for left-censored data. Note that if the data are to be logged (`is.numeric(mice.log)`), only the argument `data` will be logged, therefore, the LOD values given here should be given as `log(LOD)` with the correct number of decimals: `round(log(LOD),mice.log)`.
standards	Dataframe of 1 row containing the LOD values (not logged, whatever the value for `mice.log`).
mice.log	set to `FALSE` if the imputation should be performed on unlogged data. Otherwise, number of decimal to save after taking the log of data (should be 10 unless for specific reasons) ; in that case the data will be unlogged after imputation.

Value

If `return.midsObject == FALSE` a list of size mi.m, containing the imputed datasets. If `return.midsObject == TRUE` a list of 2, the first element (`imputed.data`) being the list of size mi.m as described in the previous sentence, the 2nd element (`mids.obj`) containing the `mids` object as returned by `mice()`

Examples

```
data(cancer, package = "survival")
cancer.imp <- MImpute(cancer[, -c(1:3)], 3)

## MImpute_surv
data(cancer, package = "survival")
cancer$status <- cancer$status - 1
cancer.imp <- MImpute_surv(cancer, 3)

## MImpute_lcens
toy <- iris[, 1:4]
# censor on variables 3 and 4, with LOD at quantile .1 and .2.
LODs <- toy[1, ]
LODs[1, ] <-c(NA, NA, quantile(toy[,3], .2), quantile(toy[,4], .1))
# Censor indicator
Censored <- data.frame(Petal.Length = runif(150, 50,60),
                       Petal.Width = runif(150, 50,60))
Censored[toy[,3] < LODs[1, 3], 1] <- LODs[1, 3]
Censored[toy[,4] < LODs[1, 4], 2] <- LODs[1, 4]
# NA for censored data
toy[toy[,3] < LODs[1, 3], 3] <- NA
toy[toy[,4] < LODs[1, 4], 4] <- NA
# Additional missing data
toy[sample(1:nrow(toy), 30), 1] <- NA
toy[sample(1:nrow(toy), 30), 3] <- NA
toy[sample(1:nrow(toy), 30), 4] <- NA
```

```
toy.imp <- MImpute_lcens(data = toy, data.lod = Censored, standards = LODs,
                         mi.m = 3, mice.log = FALSE)
```

MultiCons   *MultiCons Consensus Clustering Algorithm*

Description

Performs MultiCons clustering, from Al-Najdi et Al. For some reason, if you want to use `mclust` clustering the package needs to be loaded manually

Usage

```
MultiCons(
  DB,
  Clust_entry = FALSE,
  Clustering_selection = c("kmeans", "pam", "OPTICS", "agghc", "AGNES", "DIANA",
    "MCLUST", "CMeans", "FANNY", "BaggedClust"),
  num_algo = 10,
  maxClust = 10,
  sim.indice = "jaccard",
  returnAll = FALSE,
  Plot = TRUE,
  verbose = FALSE
)
```

Arguments

DB	Either data or dataframe of partitions.
Clust_entry	Is DB partitions (TRUE) or data (FALSE).
Clustering_selection	
	If DB is data, clustering algorithm to select among. Must be included in default value.
num_algo	Number of clustering algorithms to perform.
maxClust	Maximum number of clusters.
sim.indice	Index for defining best partition.
returnAll	Should all partitions (TRUE) or only the best (FALSE) be returned.
Plot	Should tree be plotted.
verbose	Passed on to `mclust` and other functions.

Value

A list of 2: performances and partitions. If `returnAll` is `TRUE`, both elements of the list contain results for all levels of the tree, else they only contain the results for the best level of the tree.

Examples

```
library(mclust)
### With clustering algorithm choices
MultiCons(iris[, 1:4],
          Clustering_selection = c("kmeans", "pam", "DIANA", "MCLUST"),
          Plot = TRUE)
### With a manual clustering entry
parts <- data.frame(factor(rep(c(1,2,3), each = 50)),
                    factor(rep(c(1,2,3), times = c(100, 25, 25))),
                    factor(rep(c(1,2), times = c(50, 100))),
                    factor(rep(c(3, 2, 1), times = c(120, 10, 20))),
                    stringsAsFactors = TRUE)
MultiCons(parts, Clust_entry = TRUE, Plot = TRUE)
```

---

   partition_generation   *Unsupervised partition with K selection*

Description

Generates a partition using clust.algo algorithm, with k.crit for selecting the number of clusters

Usage

```
partition_generation(data, LOG, clust.algo, k.crit)
```

Arguments

data	dataframe to cluster
LOG	logical. Should all columns of the dataset be logged before applying clustering algorithms?
clust.algo	vector of strings: name of clustering algorithms to use (use "km" for k-means, "kmed" for K-medians, "hc" for hclust and/or "mclust" for mclust).
k.crit	string. Criterion to select the optimal number of clusters (for each imputed dataset). Use "ch" for Calinski and Harabasz criterion (not available for mclust), "CritCF" for CritCF or bic for BIC (mclust only).

Value

a dataframe with one column for each algorithm in clust.algo, containing the cluster IDs.

Examples

```
partition_generation(iris[, 1:4], LOG = FALSE,
                     clust.algo = c("km", "hc"), k.crit = "ch")
```

---

plot_boxplot   ggplot *type boxplots for each vars.cont by partition level.*

Description

ggplot type boxplots for each vars.cont by partition level.

Usage

```
plot_boxplot(
  data,
  partition.name,
  vars.cont,
  vars.cont.names = NULL,
  unclass.name = "Unclassified",
  include.unclass = FALSE,
  add.n = FALSE,
  nc.facet = 10
)
```

Arguments

data	The dataset.
partition.name	string. Name of the partition (in data). The partition variable should be a factor.
vars.cont	vector of strings. variables to plot (continuous only).
vars.cont.names	
	Optional. Names for displaying the continuous variables. (given in the same order than vars.cont)
unclass.name	If applicable, name for the unclassified observations in the partition.
include.unclass	
	boolean, should boxplot be displayed for the unclassified or should they be excluded from the plot.
add.n	Boolean. Should the number of samples per cluster be indicated on the x axis and color legend.
nc.facet	integer. Number of columns in the facet_wrap()

Value

ggplot object.

Examples

```
data(cancer, package = "survival")
cancer$status <- factor(cancer$status)
plot_boxplot(data = cancer, partition.name = "status",
                vars.cont = c("age", "meal.cal", "wt.loss"))

## With unclassifieds
cancer$status.2 <- as.character(cancer$status)
cancer$status.2[sample(1:nrow(cancer), 30)] <- "Unclassif."
```

```
cancer$status.2 <- factor(cancer$status.2)
plot_boxplot(data = cancer, partition.name = "status.2",
                vars.cont = c("age", "meal.cal", "wt.loss"),
                unclass.name = "Unclassif.", include.unclass = TRUE)

## With unclassifieds (as NA)
cancer$status.3 <- cancer$status
cancer$status.3[sample(1:nrow(cancer), 30)] <- NA
plot_boxplot(data = cancer, partition.name = "status.3",
                vars.cont = c("age", "meal.cal", "wt.loss"),
                unclass.name = NA, include.unclass = TRUE, add.n = TRUE)
```

---

plot_frequency	ggplot *type barplots representing frequencies for each vars.cat by partition level.*

Description

ggplot type barplots representing frequencies for each vars.cat by partition level.

Usage

```
plot_frequency(
  data,
  partition.name,
  vars.cat,
  vars.cat.names = NULL,
  binary.simplify = TRUE,
  unclass.name = "Unclassified",
  include.unclass = FALSE
)
```

Arguments

data   The dataset.

partition.name   string. Name of the partition (in data). The partition variable should be a factor.

vars.cat   vector of strings. variables to plot (categorical only).

vars.cat.names   Optional. Names for displaying the categorical variables. (given in the same order than `vars.cat`)

binary.simplify

                  boolean. Should only the 1st level be kept for binary variables in `vars.cat`?

unclass.name   If applicable, name for the unclassified observations in the partition.

include.unclass

                  boolean, should boxplot be displayed for the unclassified or should they be excluded from the plot.

Value

ggplot object.

Examples

```
data(cancer, package = "survival")
cancer$status <- factor(cancer$status)
plot_frequency(data = cancer, partition.name = "status",
                    vars.cat = c("sex", "ph.ecog"))

## With unclassifieds
cancer$status.2 <- as.character(cancer$status)
cancer$status.2[sample(1:nrow(cancer), 30)] <- "Unclassif."
cancer$status.2 <- factor(cancer$status.2)
plot_frequency(data = cancer, partition.name = "status.2",
                vars.cat = c("sex", "ph.ecog"),
                unclass.name = "Unclassif.", include.unclass = TRUE)

## With unclassifieds (as NA)
cancer$status.3 <- cancer$status
cancer$status.3[sample(1:nrow(cancer), 30)] <- NA
plot_frequency(data = cancer, partition.name = "status.3",
                vars.cat = c("sex", "ph.ecog"),
                unclass.name = NA, include.unclass = TRUE)

plot_frequency(data = cancer, partition.name = "status.3",
                vars.cat = c("sex", "ph.ecog", "ph.karno"),
                binary.simplify = FALSE,
                unclass.name = NA, include.unclass = FALSE)
```

---

plot_MIpca   *Plot a PCA from a multiply imputed dataset.*

Description

plot_MIpca plots only mean value while plot_MIpca_all plots all values for the selected observations.

Usage

```
plot_MIpca(
  data.list,
  obs.sel,
  color.var = NULL,
  pca.varsel = NULL,
  pc.sel = c(1, 2)
)

plot_MIpca_all(
  data.list,
  obs.sel,
  pca.varsel = NULL,
  color.var = NULL,
  pc.sel = c(1, 2),
  alpha = 0.4
)
```

Arguments

`data.list`	The list of the imputed datasets.
`obs.sel`	The selection of observations to highlight. If `NULL`, no observations are selected; if `numeric`, the vector corresponds to the observations' row number to highlight, if `character`, the string should be of type a condition (TRUE/FALSE) on the dataset to select the observations, where the dataset is referred to as "DATA" (ex: `obs.sel = "DATA$X1>3"`).
`color.var`	Either `NULL` to color according to `obs.sel`, "none" to use no color, or a vector of size `nrow(data.list[[1]])` (a factor).
`pca.varsel`	optional. A vector of strings containing the names of the variables to use for the PCA. If `NULL` all variables in the dataset will be used.
`pc.sel`	Numeric vector of size 2 containing the indexes of the principal components to plot. Default is PC1 and PC2.
`alpha`	Transparency level for plotting the point of the selected observations.

Value

A `ggplot` object.

Examples

```
data(cancer, package = "survival")
cancer.imp <- MImpute(cancer[, -c(1:3)], 6)
plot_MIpca(cancer.imp, 1:10,
    pca.varsel = c("age", "sex", "ph.ecog", "meal.cal",  "wt.loss"))

## not run ##
# plot_MIpca(cancer.imp, obs.sel = NULL, color.var = factor(cancer$status),
#     pca.varsel = c("age", "sex", "ph.ecog", "meal.cal",  "wt.loss"))
data(cancer, package = "survival")
cancer.imp <- MImpute(cancer[, -c(1:3)], 6)
plot_MIpca_all(cancer.imp, 1:10,
    pca.varsel = c("age", "sex", "ph.ecog", "meal.cal",  "wt.loss"))
```

---

seMIsupcox   *Semisupervised learning for a right censored endpoint*

Description

MultiCons consensus based method for MI-Semisupervised clustering. The final partition is a consensus of the Pareto-optimal solutions.

Usage

```
seMIsupcox(
  Impute = FALSE,
  Impute.m = 5,
  center.init = TRUE,
  center.init.N = 500,
  center.init.Ks = 2:7,
```

```
    X,
    CVE.fun = "LP",
    Y,
    nfolds = 10,
    save.path = NULL,
    Unsup.Sup.relImp = list(relImp.55 = c(0.5, 0.5)),
    plot.cons = FALSE,
    cleanup.partition = TRUE,
    min.cluster.size = 10,
    level.order = NULL,
    Unclassified = "Unclassified",
    return.detail = FALSE
)
```

Arguments

Impute	Boolean. Default is FALSE to indicate that the user performed the imputation and provides the imputed data. If TRUE, the imputation will be performed within the call using the `MImpute_surv()` function. Note that if Impute is TRUE, `center.init` is also forced to TRUE as the center coordinates may depend on the imputation.
Impute.m	Used only if Impute is TRUE; number of imputations to perform
center.init	Either a User supplied List of dataframe containing the cluster centers coordinates (for example as obtained with `initiate_centers()`, Or TRUE to initiate the centers within the call of the function (performed with `initiate_centers()`). Note that if TRUE a random initialization will be performed. For a finer tuning of the center initialization the user should generate and provide the list of centers coordinates.
center.init.N	Used only if `center.init` is TRUE. The number to initialization to produce. Default to 500.
center.init.Ks	Used only if `center.init` is TRUE. Vector of number of clusters to generate for the initialization. Default to 2 to 7 clusters.
X	Data, in the form of a list of data.frame(s). The list should be one length 1 if data are complete or if Impute is TRUE, of should be a list of imputed dataframes if data are incomplete. If columns named "time" and "status" are present they will be discarded for the clustering.
CVE.fun	string indicating how to calculate the cross validation error : only LP is available and stands for linear predictor approach (using the `ncvreg` package).
Y	Passed to CVE.fun, Outcome data: should be dataframe or matrix with 2 columns: "time" and "status".
nfolds	Number of folds for cross-validation.
save.path	Path indicating where objectives values for each iteration should be saved. If null the values are not saved.
Unsup.Sup.relImp	
	List of weights for the unsupervised and supervised objectives for the Pareto optimal solution. Default is to use only one set of weights : same weight.
plot.cons	Logical. Should the consensus tree be plotted?
cleanup.partition	
	should the partition be trimmed of small clusters. (The consensus may generate small clusters of observations for which there is no consensus on the cluster assignation)

min.cluster.size

> if cleanup.partition == TRUE: Minimum cluster size (i.e., smaller clusters will be discarded)

level.order   if cleanup.partition == TRUE: optional. If you supply a variable the cluster levels will be ordinated according to the mean values for the variable

Unclassified   if cleanup.partition == TRUE string for the label of the unclassified observations. defaults value is NA.

return.detail   logical. Should the detail of imputation specific partition be returned, in supplement to the final consensus partition?

Value

A vector containing the final cluster IDs. Or if return.detail == TRUE, a list containing Consensus: the final cluster ID, Detail: the clusters obtained for each imputed dataset, Imputed.data a list containing the imputed datasets.

Examples

```
data(cancer, package = "survival")
cancer$status <- cancer$status - 1
cancer <- cancer[, -1]
## With imputation included
## not run ##
# res <- seMIsupcox(X = list(cancer), Y = cancer[, c("time", "status")],
#                   Impute = TRUE, Impute.m = 3, center.init = TRUE,
#                   nfolds = 10, center.init.N = 100)


### With imputation and center initialization not included
## 1 imputation
cancer.imp <- MImpute_surv(cancer, 3)

## 2 Center initialization
N <- 100
center.number <- sample(2:6, size = N, replace = TRUE)
the.seeds <- runif(N) * 10^9
sel.col <- which(!colnames(cancer) %in% c("time", "status"))
inits <- sapply(1:length(cancer.imp), function(mi.i) {
 initiate_centers(data = cancer.imp[[mi.i]][, sel.col],
                  N = N, t = 1, k = center.number,
                  seeds.N = the.seeds)},
              USE.NAMES = TRUE, simplify = FALSE)

## 3 learning
## not run ##
# res1 <- seMIsupcox(X = cancer.imp, Y = cancer[, c("time", "status")],
#                    Impute = FALSE, center.init = inits, nfolds = 10,
#                    cleanup.partition = FALSE)
# res2 <- seMIsupcox(X = cancer.imp, Y = cancer[, c("time", "status")],
#                    center.init = inits, nfolds = 10)
```

---

table_categorical   *Display table with comparison of the partition with categorical vari-*
ables.

Description

Display table with comparison of the partition with categorical variables.

Usage

```
table_categorical(
  data,
  partition.name,
  vars.cat,
  vars.cat.names = NULL,
  na.value = "",
  nb.dec = 1,
  text.pval = FALSE
)
```

Arguments

data	The dataset.
partition.name	string. Name of the partition (in data). The partition variable should be a factor.
vars.cat	vector of strings. variables to compare to (categorical only).
vars.cat.names	Optional. Names for displaying the categorical variables. (in the same order than vars.cat)
na.value	Value to use for the empty cases (e.g. "" or NA).
nb.dec	digit. Number of decimals for the percentage.
text.pval	boolean. Set to TRUEto display "p=", to FALSE to display only the value.

Value

table with n and percentage values per level of the partition and chi square test p-values.

Examples

```
data(cancer, package = "survival")
cancer$status <- factor(cancer$status)
table_categorical(data = cancer, partition.name = "status",
                  vars.cat = c("sex", "ph.ecog"))
```

---

table_continuous   *Display table with comparison of the partition with continuous variables.*

Description

Display table with comparison of the partition with continuous variables.

Usage

```
table_continuous(
  data,
  partition.name,
  vars.cont,
  vars.cont.names = NULL,
  na.value = "",
  nb.dec = 1,
  text.pval = FALSE
)
```

Arguments

data	The dataset.
partition.name	string. Name of the partition (in data). The partition variable should be a factor.
vars.cont	vector of strings. variables to compare to (continuous only).
vars.cont.names	Optional. Names for displaying the continuous variables. (in the same order than vars.cont)
na.value	Value to use for the empty cases (e.g. ″″ or NA).
nb.dec	digit. Number of decimals for the mean and quartile values.
text.pval	boolean. Set to TRUEto display ″p=″, to FALSE to display only the value.

Value

table with mean and Q1 Q3 values per level of the partition and ANOVA test p-values.

Examples

```
data(cancer, package = "survival")
cancer$status <- factor(cancer$status)
table_continuous(data = cancer, partition.name = "status",
                 vars.cont = c("age", "meal.cal", "wt.loss"))
```

unsupMI	*Unsupervised learning for incomplete dataset*

Description

Unsupervised clustering for multiply imputed datasets using `MultiCons` consensus (Faucheux et al. 2021 procedure)

Usage

```
unsupMI(
  Impute = FALSE,
  Impute.m = 5,
  cens.data.lod = NULL,
  cens.standards = NULL,
  cens.mice.log = 10,
  data,
  log.data = FALSE,
  algo = "km",
  k.crit = "ch",
  comb.cons = FALSE,
  plot.cons = FALSE,
  return.detail = FALSE,
  not.to.use = c("time", "status"),
  cleanup.partition = TRUE,
  min.cluster.size = 10,
  level.order = NULL,
  Unclassified = "Unclassified"
)
```

Arguments

Impute	Default is `FALSE` to indicate that the user performed the imputation and provides the imputed data. Otherwise string (`"MImpute"`, `"MImpute_surv"` or `"MImpute_lcens"`) to perform the imputation within the call using the `MImpute()`, `MImpute_surv()` or `MImpute_lcens()` function.
Impute.m	Used only if Impute is not `FALSE` ; number of imputations to perform
cens.data.lod	passed to `MImpute_lcens()` if Impute == `MImpute_lcens`
cens.standards	passed to `MImpute_lcens()` if Impute == `MImpute_lcens`
cens.mice.log	passed to `MImpute_lcens()` if Impute == `MImpute_lcens`
data	Data, in the form of a list of data.frame(s). The list should be one length 1 if data are complete or if Impute is not `FALSE`, it should be a list of imputed dataframes if data are incomplete and imputed. If some columns are in `not.to.use`, they will be discarded for the clustering.
log.data	logical. Should all columns of the dataset be logged before applying clustering algorithms?
algo	vector of strings: name of clustering algorithms to use (use `"km"` for k-means, `"kmed"` for K-medians, `"hc"` for `hclust` and/or `"mclust"` for `mclust`).

k.crit	string. Criterion to select the optimal number of clusters (for each imputed dataset). Use "ch" for Calinski and Harabasz criterion (not available for mclust), "CritCF" for CritCF or "bic" for BIC (mclust only).
comb.cons	logical. Forced to FALSE if length(algo)<2. Use TRUE to perform an additional consensus from all partitions generates, whatever the algorithm.
plot.cons	logical. Use TRUE to print the MultiCons tree. Note that if all partitions are identical across the imputation no consensus will be performed and therefore not plot will be obtained even if plot.cons = TRUE.
return.detail	logical. Should the detail of imputation specific partition and the imputed data be returned, in the supplement to the final consensus partition?
not.to.use	vector of strings : names of the columns that should be discarded for the learning step.
cleanup.partition	
	should the partition be trimmed of small clusters. (The consensus may generate small clusters of observations for which there is no consensus on the cluster assignation)
min.cluster.size	
	if cleanup.partition == TRUE: Minimum cluster size (i.e., smaller clusters will be discarded)
level.order	if cleanup.partition == TRUE: optional. If you supply a variable the cluster levels will be ordinated according to the mean values for the variable
Unclassified	if cleanup.partition == TRUE string for the label of the unclassified observations. defaults value is NA.

Value

if length(algo)>1 a vector of final cluster ID ; if length(algo)>1 a data.frame with each column being the final cluster ID for the corresponding algorithm. Or if return.detail == TRUE, a list containing Consensus : the final cluster ID (or data.frame), Detail: the clusters obtained for each imputed dataset, Imputed.data a list containing the imputed datasets.

Examples

```
## With imputation included
data(cancer, package = "survival")
cancer$status <- cancer$status - 1
res.0 <- unsupMI(data = list(cancer), Impute = "MImpute_surv",
                 cleanup.partition = FALSE)


### With imputation not included
## 1 imputation
cancer.imp <- MImpute_surv(cancer, 3)
## 2 learning
res <- unsupMI(data = cancer.imp, cleanup.partition = FALSE)
summary(factor(res))
res.1 <- unsupMI(data = cancer.imp)
summary(factor(res.1))

## 2.bis learning with several algorithms
res.2 <- unsupMI(data = cancer.imp, algo = c("km", "hc"), comb.cons = TRUE,
                 plot.cons = TRUE)
```

```
## Alternative: perform imputation within
## not run ##
# res <- unsupMI(Impute = "MImpute_surv", data = list(cancer))
```

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