

Package ‘mixgb’

December 2, 2024

Title Multiple Imputation Through 'XGBoost'

Version 1.5.2

Description Multiple imputation using 'XGBoost', subsampling, and predictive mean matching as described in Deng and Lumley (2023) [doi:10.1080/10618600.2023.2252501](https://doi.org/10.1080/10618600.2023.2252501). The package supports various types of variables, offers flexible settings, and enables saving an imputation model to impute new data. Data processing and memory usage have been optimised to speed up the imputation process.

URL <https://github.com/agnesdeng/mixgb>

BugReports <https://github.com/agnesdeng/mixgb/issues>

License GPL (>= 3)

Encoding UTF-8

LazyData true

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createNA	<i>Create missing values for a dataset</i>
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Description

This function creates missing values under the missing complete at random (MCAR) mechanism. It is for demonstration purposes only.

Usage

```
createNA(data, var.names = NULL, p = 0.3)
```

Arguments

data	A complete data frame.
var.names	The names of variables where missing values will be generated.
p	The proportion of missing values in the data frame or the proportions of missing values corresponding to the variables specified in var.names.

Value

A data frame with artificial missing values

Examples

```
# Create 30% MCAR data across all variables in a dataset
withNA.df <- createNA(data = iris, p = 0.3)

# Create 30% MCAR data in a specified variable in a dataset
withNA.df <- createNA(data = iris, var.names = c("Sepal.Length"), p = 0.3)

# Create MCAR data in several specified variables in a dataset
withNA.df <- createNA(
  data = iris,
```

```
var.names = c("Sepal.Length", "Petal.Width", "Species"),  
p = c(0.3, 0.2, 0.1)  
)
```

data_clean

Data cleaning

Description

The function `'data_clean()'` serves the purpose of performing a preliminary check and fix some evident issues. However, the function cannot resolve all data quality-related problems.

Usage

```
data_clean(rawdata, levels.tol = 0.2)
```

Arguments

<code>rawdata</code>	A data frame.
<code>levels.tol</code>	Tolerant proportion of the number of levels to the number of observations in a multiclass variable. Default: 0.2

Value

A preliminary cleaned dataset

Examples

```
rawdata <- nhanes3  
  
rawdata[4, 4] <- NaN  
rawdata[5, 5] <- Inf  
rawdata[6, 6] <- -Inf  
  
cleandata <- data_clean(rawdata = rawdata)
```

default_params

Auxiliary function for validating xgb.params

Description

Auxiliary function for setting up the default XGBoost-related hyperparameters for `mixgb` and checking the `xgb.params` argument in `mixgb()`. For more details on XGBoost hyperparameters, please refer to [XGBoost documentation on parameters](#).

Usage

```

default_params(
  device = "cpu",
  tree_method = "hist",
  eta = 0.3,
  gamma = 0,
  max_depth = 3,
  min_child_weight = 1,
  max_delta_step = 0,
  subsample = 0.7,
  sampling_method = "uniform",
  colsample_bytree = 1,
  colsample_bylevel = 1,
  colsample_bynode = 1,
  lambda = 1,
  alpha = 0,
  max_leaves = 0,
  max_bin = 256,
  num_parallel_tree = 1,
  nthread = -1
)

```

Arguments

device	Can be either "cpu" or "cuda". For ther options please refer to XGBoost documentation on parameters .
tree_method	Options: "auto", "exact", "approx", and "hist". Default: "hist".
eta	Step size shrinkage. Default: 0.3.
gamma	Minimum loss reduction required to make a further partition on a leaf node of the tree. Default: 0
max_depth	Maximum depth of a tree. Default: 3.
min_child_weight	Minimum sum of instance weight needed in a child. Default: 1.
max_delta_step	Maximum delta step. Default: 0.
subsample	Subsampling ratio of the data. Default: 0.7.
sampling_method	The method used to sample the data. Default: "uniform".
colsample_bytree	Subsampling ratio of columns when constructing each tree. Default: 1.
colsample_bylevel	Subsampling ratio of columns for each level. Default: 1.
colsample_bynode	Subsampling ratio of columns for each node. Default: 1.
lambda	L2 regularization term on weights. Default: 1.
alpha	L1 regularization term on weights. Default: 0.

max_leaves	Maximum number of nodes to be added (Not used when tree_method = "exact"). Default: 0.
max_bin	Maximum number of discrete bins to bucket continuous features (Only used when tree_method is either "hist", "approx" or "gpu_hist"). Default: 256.
num_parallel_tree	The number of parallel trees used for boosted random forests. Default: 1.
nthread	The number of CPU threads to be used. Default: -1 (all available threads).

Value

A list of hyperparameters.

Examples

```
default_params()

xgb.params <- list(device = "cuda", subsample = 0.9, nthread = 2)
default_params(device = xgb.params$device,
               subsample = xgb.params$subsample,
               nthread = xgb.params$nthread)

xgb.params <- do.call("default_params", xgb.params)
xgb.params
```

default_params_cran *Auxiliary function for validating xgb.params compatible with XGBoost CRAN version*

Description

Auxiliary function for setting up the default XGBoost-related hyperparameters for mixgb and checking the xgb.params argument in mixgb(). For more details on XGBoost hyperparameters, please refer to [XGBoost documentation on parameters](#).

Usage

```
default_params_cran(
  eta = 0.3,
  gamma = 0,
  max_depth = 3,
  min_child_weight = 1,
  max_delta_step,
  subsample = 0.7,
  sampling_method = "uniform",
  colsample_bytree = 1,
  colsample_bylevel = 1,
  colsample_bynode = 1,
```

```

lambda = 1,
alpha = 0,
tree_method = "auto",
max_leaves = 0,
max_bin = 256,
predictor = "auto",
num_parallel_tree = 1,
gpu_id = 0,
nthread = -1
)

```

Arguments

eta	Step size shrinkage. Default: 0.3.
gamma	Minimum loss reduction required to make a further partition on a leaf node of the tree. Default: 0
max_depth	Maximum depth of a tree. Default: 3.
min_child_weight	Minimum sum of instance weight needed in a child. Default: 1.
max_delta_step	Maximum delta step. Default: 0.
subsample	Subsampling ratio of the data. Default: 0.7.
sampling_method	The method used to sample the data. Default: "uniform".
colsample_bytree	Subsampling ratio of columns when constructing each tree. Default: 1.
colsample_bylevel	Subsampling ratio of columns for each level. Default: 1.
colsample_bynode	Subsampling ratio of columns for each node. Default: 1.
lambda	L2 regularization term on weights. Default: 1.
alpha	L1 regularization term on weights. Default: 0.
tree_method	Options: "auto", "exact", "approx", and "hist". Default: "hist".
max_leaves	Maximum number of nodes to be added (Not used when tree_method = "exact"). Default: 0.
max_bin	Maximum number of discrete bins to bucket continuous features (Only used when tree_method is either "hist", "approx" or "gpu_hist"). Default: 256.
predictor	Default: "auto"
num_parallel_tree	The number of parallel trees used for boosted random forests. Default: 1.
gpu_id	Which GPU device should be used. Default: 0.
nthread	The number of CPU threads to be used. Default: -1 (all available threads).

Value

A list of hyperparameters.

Examples

```

default_params_cran()

xgb.params <- list(subsample = 0.9, gpu_id = 1)
default_params_cran(subsample = xgb.params$subsample, gpu_id = xgb.params$gpu_id)

xgb.params <- do.call("default_params_cran", xgb.params)
xgb.params

```

`impute_new`*Impute new data with a saved mixgb imputer object*

Description

Impute new data with a saved mixgb imputer object

Usage

```

impute_new(
  object,
  newdata,
  initial.newdata = FALSE,
  pmm.k = NULL,
  m = NULL,
  verbose = FALSE
)

```

Arguments

<code>object</code>	A saved imputer object created by <code>mixgb(..., save.models = TRUE)</code>
<code>newdata</code>	A data.frame or data.table. New data with missing values.
<code>initial.newdata</code>	Whether to use the information from the new data to initially impute the missing values of the new data. By default, this is set to <code>FALSE</code> , the original data passed to <code>mixgb()</code> will be used for initial imputation.
<code>pmm.k</code>	The number of donors for predictive mean matching. If <code>NULL</code> (the default), the <code>pmm.k</code> value in the saved imputer object will be used.
<code>m</code>	The number of imputed datasets. If <code>NULL</code> (the default), the <code>m</code> value in the saved imputer object will be used.
<code>verbose</code>	Verbose setting for <code>mixgb</code> . If <code>TRUE</code> , will print out the progress of imputation. Default: <code>FALSE</code> .

Value

A list of `m` imputed datasets for new data.

Examples

```

set.seed(2022)
n <- nrow(nhanes3)
idx <- sample(1:n, size = round(0.7 * n), replace = FALSE)
train.data <- nhanes3[idx, ]
test.data <- nhanes3[-idx, ]

params <- list(max_depth = 3, subsample = 0.7, nthread = 2)
mixgb.obj <- mixgb(data = train.data, m = 2, xgb.params = params, nrounds = 10,
                  save.models = TRUE, save.models.folder = tempdir())

# obtain m imputed datasets for train.data
train.imputed <- mixgb.obj$imputed.data
train.imputed

# use the saved imputer to impute new data
test.imputed <- impute_new(object = mixgb.obj, newdata = test.data)
test.imputed

```

mixgb

Multiple imputation through XGBoost

Description

This function is used to generate multiply-imputed datasets using XGBoost, subsampling and predictive mean matching (PMM).

Usage

```

mixgb(
  data,
  m = 5,
  maxit = 1,
  ordinalAsInteger = FALSE,
  pmm.type = NULL,
  pmm.k = 5,
  pmm.link = "prob",
  initial.num = "normal",
  initial.int = "mode",
  initial.fac = "mode",
  save.models = FALSE,
  save.vars = NULL,
  save.models.folder = NULL,
  verbose = F,
  xgb.params = list(),
  nrounds = 100,
  early_stopping_rounds = NULL,
  print_every_n = 10L,

```



```

    xgboost_verbosity = 0,
    ...
)

```

Arguments

<code>data</code>	A <code>data.frame</code> or <code>data.table</code> with missing values
<code>m</code>	The number of imputed datasets. Default: 5
<code>maxit</code>	The number of imputation iterations. Default: 1
<code>ordinalAsInteger</code>	Whether to convert ordinal factors to integers. By default, <code>ordinalAsInteger = FALSE</code> . Setting <code>ordinalAsInteger = TRUE</code> may speed up the imputation process for large datasets.
<code>pmm.type</code>	The type of predictive mean matching (PMM). Possible values: <ul style="list-style-type: none"> • <code>NULL</code> (default): Imputations without PMM; • <code>0</code>: Imputations with PMM type 0; • <code>1</code>: Imputations with PMM type 1; • <code>2</code>: Imputations with PMM type 2; • <code>"auto"</code>: Imputations with PMM type 2 for numeric/integer variables; imputations without PMM for categorical variables.
<code>pmm.k</code>	The number of donors for predictive mean matching. Default: 5
<code>pmm.link</code>	The link for predictive mean matching in binary variables <ul style="list-style-type: none"> • <code>"prob"</code> (default): use probabilities; • <code>"logit"</code>: use logit values.
<code>initial.num</code>	Initial imputation method for numeric type data: <ul style="list-style-type: none"> • <code>"normal"</code> (default); • <code>"mean"</code>; • <code>"median"</code>; • <code>"mode"</code>; • <code>"sample"</code>.
<code>initial.int</code>	Initial imputation method for integer type data: <ul style="list-style-type: none"> • <code>"mode"</code> (default); • <code>"sample"</code>.
<code>initial.fac</code>	Initial imputation method for factor type data: <ul style="list-style-type: none"> • <code>"mode"</code> (default); • <code>"sample"</code>.
<code>save.models</code>	Whether to save imputation models for imputing new data later on. Default: <code>FALSE</code>
<code>save.vars</code>	For the purpose of imputing new data, the imputation models for response variables specified in <code>save.vars</code> will be saved. The values in <code>save.vars</code> can be a vector of names or indices. By default, only the imputation models for variables with missing values in the original data will be saved (<code>save.vars = NULL</code>). To save imputation models for all variables, users can specify <code>save.vars = colnames(data)</code> .

save.models.folder	Users can specify a directory to save all imputation models. Models will be saved in JSON format by internally calling <code>xgb.save()</code> , which is recommended by XGBoost.
verbose	Verbose setting for mixgb. If TRUE, will print out the progress of imputation. Default: FALSE.
xgb.params	A list of XGBoost parameters. For more details, please check XGBoost documentation on parameters .
nrounds	The maximum number of boosting iterations for XGBoost. Default: 100
early_stopping_rounds	An integer value k. XGBoost training will stop if the validation performance has not improved for k rounds. Default: 10.
print_every_n	Print XGBoost evaluation information at every nth iteration if <code>xgboost_verbose > 0</code> .
xgboost_verbose	Verbose setting for XGBoost training: 0 (silent), 1 (print information) and 2 (print additional information). Default: 0
...	Extra arguments to be passed to XGBoost

Value

If `save.models = FALSE`, this function will return a list of `m` imputed datasets. If `save.models = TRUE`, it will return an object with imputed datasets, saved models and parameters.

Examples

```
# obtain m multiply datasets without saving models
params <- list(max_depth = 3, subsample = 0.7, nthread = 2)
mixgb.data <- mixgb(data = nhanes3, m = 2, xgb.params = params, nrounds = 10)

# obtain m multiply imputed datasets and save models for imputing new data later on
mixgb.obj <- mixgb(data = nhanes3, m = 2, xgb.params = params, nrounds = 10,
  save.models = TRUE, save.models.folder = tempdir())
```

mixgb_cv

Use cross-validation to find the optimal nrounds

Description

Use cross-validation to find the optimal nrounds for an Mixgb imputer. Note that this method relies on the complete cases of a dataset to obtain the optimal nrounds.

Usage

```

mixgb_cv(
  data,
  nfold = 5,
  nrounds = 100,
  early_stopping_rounds = 10,
  response = NULL,
  select_features = NULL,
  xgb.params = list(),
  stringsAsFactors = FALSE,
  verbose = TRUE,
  ...
)

```

Arguments

data	A data.frame or a data.table with missing values.
nfold	The number of subsamples which are randomly partitioned and of equal size. Default: 5
nrounds	The max number of iterations in XGBoost training. Default: 100
early_stopping_rounds	An integer value k. Training will stop if the validation performance has not improved for k rounds.
response	The name or the column index of a response variable. Default: NULL (Randomly select an incomplete variable).
select_features	The names or the indices of selected features. Default: NULL (Select all the other variables in the dataset).
xgb.params	A list of XGBoost parameters. For more details, please check XGBoost documentation on parameters .
stringsAsFactors	A logical value indicating whether all character vectors in the dataset should be converted to factors.
verbose	A logical value. Whether to print out cross-validation results during the process.
...	Extra arguments to be passed to XGBoost.

Value

A list of the optimal nrounds, evaluation.log and the chosen response.

Examples

```

params <- list(max_depth = 3, subsample = 0.7, nthread = 2)
cv.results <- mixgb_cv(data = nhanes3, xgb.params = params)
cv.results$best.nrounds

imputed.data <- mixgb(data = nhanes3, m = 3, xgb.params = params,
  nrounds = cv.results$best.nrounds)

```

nhanes3

A small subset of the NHANES III (1988-1994) newborn data

Description

This dataset is a small subset of nhanes3_newborn. It is for demonstration purposes only. More information on NHANES III data can be found on <https://www.cdc.gov/Nchs/Data/Nhanes3/7a/doc/mimodels.pdf>

Usage

```
data(nhanes3)
```

Format

A data frame of 500 rows and 6 variables. Three variables have missing values.

HSAGEIR Age at interview (screener) - qty (months). An integer variable from 2 to 11.

HSSEX Sex. A factor variable with levels 1 (Male) and 2 (Female).

DMARETHN Race-ethnicity. A factor variable with levels 1 (Non-Hispanic white), 2 (Non-Hispanic black), 3 (Mexican-American) and 4 (Other).

BMPHEAD Head circumference (cm). Numeric.

BMPRECUM Recumbent length (cm). Numeric.

BMPWT Weight (kg). Numeric.

Source

<https://www.cdc.gov/nchs/nhanes/nhanes3/datafiles.aspx>

References

U.S. Department of Health and Human Services (DHHS). National Center for Health Statistics. Third National Health and Nutrition Examination Survey (NHANES III, 1988-1994): Multiply Imputed Data Set. CD-ROM, Series 11, No. 7A. Hyattsville, MD: Centers for Disease Control and Prevention, 2001. Includes access software: Adobe Systems, Inc. Acrobat Reader version 4.

nhanes3_newborn	<i>NHANES III (1988-1994) newborn data</i>
-----------------	--

Description

This dataset is extracted from the NHANES III (1988-1994) for the age class Newborn (under 1 year). Please note that this example dataset only contains selected variables and is for demonstration purposes only.

Usage

```
data(nhanes3_newborn)
```

Format

A data frame of 2107 rows and 16 variables. Nine variables have missing values.

HSHSIZER Household size. An integer variable from 1 to 10.

HSAGEIR Age at interview (screener) - qty (months). An integer variable from 2 to 11.

HSSEX Sex. A factor variable with levels 1 (Male) and 2 (Female).

DMARACER Race. A factor variable with levels 1 (White), 2 (Black) and 3 (Other).

DMAETHNR Ethnicity. A factor variable with levels 1 (Mexican-American), 2 (Other Hispanic) and 3 (Not Hispanic).

DMARETHN Race-ethnicity. A factor variable with levels 1 (Non-Hispanic white), 2 (Non-Hispanic black), 3 (Mexican-American) and 4 (Other).

BMPHEAD Head circumference (cm). Numeric.

BMPRECUM Recumbent length (cm). Numeric.

BMPSB1 First subscapular skinfold (mm). Numeric.

BMPSB2 Second subscapular skinfold (mm). Numeric.

BMPTR1 First triceps skinfold (mm). Numeric.

BMPTR2 Second triceps skinfold (mm). Numeric.

BMPWT Weight (kg). Numeric.

DMPPIR Poverty income ratio. Numeric.

HFF1 Does anyone who lives here smoke cigarettes in the home? A factor variable with levels 1 (Yes) and 2 (No).

HYD1 How is the health of subject person in general? An ordinal factor with levels 1 (Excellent), 2 (Very good), 3 (Good), 4 (Fair) and 5 (Poor).

Source

<https://www.cdc.gov/nchs/nhanes/nhanes3/datafiles.aspx>

References

U.S. Department of Health and Human Services (DHHS). National Center for Health Statistics. Third National Health and Nutrition Examination Survey (NHANES III, 1988-1994): Multiply Imputed Data Set. CD-ROM, Series 11, No. 7A. Hyattsville, MD: Centers for Disease Control and Prevention, 2001. Includes access software: Adobe Systems, Inc. Acrobat Reader version 4.

show_var	<i>Show multiply imputed values for a single variable</i>
----------	---

Description

Show *m* sets of imputed values for a specified variable.

Usage

```
show_var(imputation.list, var.name, original.data, true.values = NULL)
```

Arguments

<code>imputation.list</code>	A list of <i>m</i> imputed datasets returned by the <code>mixgb</code> imputer.
<code>var.name</code>	The name of a variable of interest.
<code>original.data</code>	The original data with missing data.
<code>true.values</code>	A vector of the true values (if known) of the missing values. In general, this is unknown.

Value

A `data.table` with *m* columns, each column represents the imputed values of all missing entries in the specified variable. If `true.values` is provided, the last column will be the true values of the missing values.

Examples

```
#obtain m multiply datasets
library(mixgb)
mixgb.data <- mixgb(data = nhanes3, m = 3)

imputed.BMPHEAD <- show_var(imputation.list = mixgb.data, var.name = "BMPHEAD",
  original.data = nhanes3)
```

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