

Package ‘vtreat’

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Type Package

Title A Statistically Sound 'data.frame' Processor/Conditioner

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Description A 'data.frame' processor/conditioner that prepares real-world data for predictive modeling in a statistically sound manner. 'vtreat' prepares variables so that data has fewer exceptional cases, making it easier to safely use models in production. Common problems 'vtreat' defends against: 'Inf', 'NA', too many categorical levels, rare categorical levels, and new categorical levels (levels seen during application, but not during training). Reference: ``vtreat': a data.frame Processor for Predictive Modeling", Zumel, Mount, 2016, <DOI:10.5281/zenodo.1173313>.

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<i>as_rquery_plan</i>	<i>Convert vtreatment plans into a sequence of rquery operations.</i>
-----------------------	---

Description

Convert vtreatment plans into a sequence of rquery operations.

Usage

```
as_rquery_plan(treatmentplans, ..., var_restriction = NULL)
```

Arguments

treatmentplans vtreat treatment plan or list of vtreat treatment plan sharing same outcome and outcome type.
... not used, force any later arguments to bind to names.
var_restriction character, if not null restrict to producing these variables.

Value

list(optree_generator (ordered list of functions), temp_tables (named list of tables))

See Also

[rquery_prepare](#)

Examples

```
if(requireNamespace("rquery", quietly = TRUE)) {  
  dTrainC <- data.frame(x= c('a', 'a', 'a', 'b', NA, 'b'),  
                       z= c(1, 2, NA, 4, 5, 6),  
                       y= c(FALSE, FALSE, TRUE, FALSE, TRUE, TRUE),  
                       stringsAsFactors = FALSE)  
  dTrainC$id <- seq_len(nrow(dTrainC))  
  treatmentsC <- designTreatmentsC(dTrainC, c("x", "z"), 'y', TRUE)  
  print(prepare(treatmentsC, dTrainC))  
  rqplan <- as_rquery_plan(list(treatmentsC))  
}
```

```

ops <- flatten_fn_list(rquery::local_td(dTrainC), rqplan$optree_generators)
cat(format(ops))
if(requireNamespace("rqdatatable", quietly = TRUE)) {
  treated <- rqdatatable::ex_data_table(ops, tables = rqplan$tables)
  print(treated[])
}
if(requireNamespace("DBI", quietly = TRUE) &&
  requireNamespace("RSQLite", quietly = TRUE)) {
  db <- DBI::dbConnect(RSQLite::SQLite(), ":memory:")
  source_data <- rquery::rq_copy_to(db, "dTrainC", dTrainC,
    overwrite = TRUE, temporary = TRUE)

  rest <- rquery_prepare(db, rqplan, source_data, "dTreatedC",
    extracols = "id")
  resd <- DBI::dbReadTable(db, rest$table_name)
  print(resd)

  rquery::rq_remove_table(db, source_data$table_name)
  rquery::rq_remove_table(db, rest$table_name)
  DBI::dbDisconnect(db)
}
}

```

buildEvalSets

Build set carve-up for out-of sample evaluation.

Description

Return a carve-up of `seq_len(nRows)`. Very useful for any sort of nested model situation (such as data prep, stacking, or super-learning).

Usage

```
buildEvalSets(nRows, ..., dframe = NULL, y = NULL,
  splitFunction = NULL, nSplits = 3)
```

Arguments

<code>nRows</code>	scalar, ≥ 1 number of rows to sample from.
<code>...</code>	no additional arguments, declared to forced named binding of later arguments.
<code>dframe</code>	(optional) original data.frame, passed to user <code>splitFunction</code> .
<code>y</code>	(optional) numeric vector, outcome variable (possibly to stratify on), passed to user <code>splitFunction</code> .
<code>splitFunction</code>	(optional) function taking arguments <code>nSplits</code> , <code>nRows</code> , <code>dframe</code> , and <code>y</code> ; returning a user desired split.
<code>nSplits</code>	integer, target number of splits.

Details

Also sets attribute "splitmethod" on return value that describes how the split was performed. attr(returnValue,'splitmethod') is one of: 'notsplit' (data was not split; corner cases like single row data sets), 'oneway' (leave one out holdout), 'kwaycross' (a simple partition), 'userfunction' (user supplied function was actually used), or a user specified attribute. Any user desired properties (such as stratification on y, or preservation of groups designated by original data row numbers) may not apply unless you see that 'userfunction' has been used.

The intent is the user splitFunction only needs to handle "easy cases" and maintain user invariants. If the user splitFunction returns NULL, throws, or returns an unacceptable carve-up then vtreat::buildEvalSets returns its own eval set plan. The signature of splitFunction should be splitFunction(nRows,nSplits,dframe,y) where nSplits is the number of pieces we want in the carve-up, nRows is the number of rows to split, dframe is the original dataframe (useful for any group control variables), and y is a numeric vector representing outcome (useful for outcome stratification).

Note that buildEvalSets may not always return a partition (such as one row dataframes), or if the user split function chooses to make rows eligible for application a different number of times.

Value

list of lists where the app portion of the sub-lists is a disjoint carve-up of seq_len(nRows) and each list as a train portion disjoint from app.

See Also

[kWayCrossValidation](#), [kWayStratifiedY](#), and [makekWayCrossValidationGroupedByColumn](#)

Examples

```
# use
buildEvalSets(200)

# longer example
# helper fns
# fit models using experiment plan to estimate out of sample behavior
fitModelAndApply <- function(trainData,applicaitonData) {
  model <- lm(y~x,data=trainData)
  predict(model,newdata=applicaitonData)
}
simulateOutOfSampleTrainEval <- function(d,fitApplyFn) {
  eSets <- buildEvalSets(nrow(d))
  evals <- lapply(eSets,
    function(ei) { fitApplyFn(d[ei$train,],d[ei$app,]) })
  pred <- numeric(nrow(d))
  for(eii in seq_len(length(eSets))) {
    pred[eSets[[eii]]$app] <- evals[[eii]]
  }
  pred
}

# run the experiment
```

```

set.seed(2352356)
# example data
d <- data.frame(x=rnorm(5),y=rnorm(5),
                outOfSampleEst=NA,inSampleEst=NA)

# fit model on all data
d$inSampleEst <- fitModelAndApply(d,d)
# compute in-sample R^2 (above zero, falsely shows a
# relation until we adjust for degrees of freedom)
1-sum((d$y-d$inSampleEst)^2)/sum((d$y-mean(d$y))^2)

d$outOfSampleEst <- simulateOutOfSampleTrainEval(d,fitModelAndApply)
# compute out-sample R^2 (not positive,
# evidence of no relation)
1-sum((d$y-d$outOfSampleEst)^2)/sum((d$y-mean(d$y))^2)

```

center_scale

Center and scale a set of variables.

Description

Center and scale a set of variables. Other columns are passed through.

Usage

```
center_scale(d, center, scale)
```

Arguments

d	data.frame to work with
center	named vector of variables to center
scale	named vector of variables to scale

Value

d with centered and scaled columns altered

Examples

```

d <- data.frame(x = 1:5,
               y = c('a', 'a', 'b', 'b', 'b'))
vars_to_transform = "x"
t <- base::scale(as.matrix(d[, vars_to_transform, drop = FALSE]),
                 center = TRUE, scale = TRUE)
t
centering <- attr(t, "scaled:center")

```

```
scaling <- attr(t, "scaled:scale")
center_scale(d, center = centering, scale = scaling)
```

designTreatmentsC *Build all treatments for a data frame to predict a categorical outcome.*

Description

Function to design variable treatments for binary prediction of a categorical outcome. Data frame is assumed to have only atomic columns except for dates (which are converted to numeric). Note: re-encoding high cardinality categorical variables can introduce undesirable nested model bias, for such data consider using [mkCrossFrameCExperiment](#).

Usage

```
designTreatmentsC(dframe, varlist, outcomename, outcometarget, ...,
  weights = c(), minFraction = 0.02, smFactor = 0, rareCount = 0,
  rareSig = NULL, collarProb = 0, codeRestriction = NULL,
  customCoders = NULL, splitFunction = NULL, ncross = 3,
  forceSplit = FALSE, catScaling = TRUE, verbose = TRUE,
  parallelCluster = NULL, use_parallel = TRUE)
```

Arguments

dframe	Data frame to learn treatments from (training data), must have at least 1 row.
varlist	Names of columns to treat (effective variables).
outcomename	Name of column holding outcome variable. <code>dframe[[outcomename]]</code> must be only finite non-missing values.
outcometarget	Value/level of outcome to be considered "success", and there must be a cut such that <code>dframe[[outcomename]]==outcometarget</code> at least twice and <code>dframe[[outcomename]]!=outcometarget</code> at least twice.
...	no additional arguments, declared to forced named binding of later arguments
weights	optional training weights for each row
minFraction	optional minimum frequency a categorical level must have to be converted to an indicator column.
smFactor	optional smoothing factor for impact coding models.
rareCount	optional integer, allow levels with this count or below to be pooled into a shared rare-level. Defaults to 0 or off.
rareSig	optional numeric, suppress levels from pooling at this significance value greater. Defaults to NULL or off.
collarProb	what fraction of the data (pseudo-probability) to collar data at if <code>doCollar</code> is set during prepare.treatmentplan .

codeRestriction	what types of variables to produce (character array of level codes, NULL means no restriction).
customCoders	map from code names to custom categorical variable encoding functions (please see https://github.com/WinVector/vtreat/blob/master/extras/CustomLevelCoders.md).
splitFunction	(optional) see vtreat::buildEvalSets .
ncross	optional scalar ≥ 2 number of cross validation splits use in rescaling complex variables.
forceSplit	logical, if TRUE force cross-validated significance calculations on all variables.
catScaling	optional, if TRUE use glm() linkspace, if FALSE use lm() for scaling.
verbose	if TRUE print progress.
parallelCluster	(optional) a cluster object created by package parallel or package snow.
use_parallel	logical, if TRUE use parallel methods (when parallel cluster is set).

Details

The main fields are mostly vectors with names (all with the same names in the same order):

- vars : (character array without names) names of variables (in same order as names on the other diagnostic vectors) - varMoves : logical TRUE if the variable varied during hold out scoring, only variables that move will be in the treated frame - #' - sig : an estimate significance of effect

See the vtreat vignette for a bit more detail and a worked example.

Columns that do not vary are not passed through.

Value

treatment plan (for use with prepare)

See Also

[prepare.treatmentplan](#), [designTreatmentsN](#), [designTreatmentsZ](#), [mkCrossFrameCExperiment](#)

Examples

```
dTrainC <- data.frame(x=c('a', 'a', 'a', 'b', 'b', 'b'),
  z=c(1,2,3,4,5,6),
  y=c(FALSE, FALSE, TRUE, FALSE, TRUE, TRUE))
dTestC <- data.frame(x=c('a', 'b', 'c', NA),
  z=c(10,20,30,NA))
treatmentsC <- designTreatmentsC(dTrainC,colnames(dTrainC), 'y', TRUE)
dTrainCTreated <- prepare(treatmentsC,dTrainC,pruneSig=0.99)
dTestCTreated <- prepare(treatmentsC,dTestC,pruneSig=0.99)
```

designTreatmentsN *build all treatments for a data frame to predict a numeric outcome*

Description

Function to design variable treatments for binary prediction of a numeric outcome. Data frame is assumed to have only atomic columns except for dates (which are converted to numeric). Note: each column is processed independently of all others. Note: re-encoding high cardinality categorical variables can introduce undesirable nested model bias, for such data consider using [mkCrossFrameNExperiment](#).

Usage

```
designTreatmentsN(dframe, varlist, outcomename, ..., weights = c(),
  minFraction = 0.02, smFactor = 0, rareCount = 0, rareSig = NULL,
  collarProb = 0, codeRestriction = NULL, customCoders = NULL,
  splitFunction = NULL, ncross = 3, forceSplit = FALSE,
  verbose = TRUE, parallelCluster = NULL, use_parallel = TRUE)
```

Arguments

dframe	Data frame to learn treatments from (training data), must have at least 1 row.
varlist	Names of columns to treat (effective variables).
outcomename	Name of column holding outcome variable. <code>dframe[[outcomename]]</code> must be only finite non-missing values and there must be a cut such that <code>dframe[[outcomename]]</code> is both above the cut at least twice and below the cut at least twice.
...	no additional arguments, declared to forced named binding of later arguments
weights	optional training weights for each row
minFraction	optional minimum frequency a categorical level must have to be converted to an indicator column.
smFactor	optional smoothing factor for impact coding models.
rareCount	optional integer, allow levels with this count or below to be pooled into a shared rare-level. Defaults to 0 or off.
rareSig	optional numeric, suppress levels from pooling at this significance value greater. Defaults to NULL or off.
collarProb	what fraction of the data (pseudo-probability) to collar data at if <code>doCollar</code> is set during prepare.treatmentplan .
codeRestriction	what types of variables to produce (character array of level codes, NULL means no restriction).
customCoders	map from code names to custom categorical variable encoding functions (please see https://github.com/WinVector/vtreat/blob/master/extras/CustomLevelCoders.md).
splitFunction	(optional) see <code>vtreat::buildEvalSets</code> .

ncross	optional scalar ≥ 2 number of cross validation splits use in rescoring complex variables.
forceSplit	logical, if TRUE force cross-validated significance calculations on all variables.
verbose	if TRUE print progress.
parallelCluster	(optional) a cluster object created by package parallel or package snow.
use_parallel	logical, if TRUE use parallel methods (when parallel cluster is set).

Details

The main fields are mostly vectors with names (all with the same names in the same order):

- vars : (character array without names) names of variables (in same order as names on the other diagnostic vectors) - varMoves : logical TRUE if the variable varied during hold out scoring, only variables that move will be in the treated frame - sig : an estimate significance of effect

See the vtreat vignette for a bit more detail and a worked example.

Columns that do not vary are not passed through.

Value

treatment plan (for use with prepare)

See Also

[prepare.treatmentplan](#), [designTreatmentsC](#), [designTreatmentsZ](#), [mkCrossFrameNExperiment](#)

Examples

```
dTrainN <- data.frame(x=c('a','a','a','a','b','b','b'),
  z=c(1,2,3,4,5,6,7),y=c(0,0,0,1,0,1,1))
dTestN <- data.frame(x=c('a','b','c',NA),
  z=c(10,20,30,NA))
treatmentsN = designTreatmentsN(dTrainN,colnames(dTrainN),'y')
dTrainNTreated <- prepare(treatmentsN,dTrainN,pruneSig=0.99)
dTestNTreated <- prepare(treatmentsN,dTestN,pruneSig=0.99)
```

designTreatmentsZ *Design variable treatments with no outcome variable.*

Description

Data frame is assumed to have only atomic columns except for dates (which are converted to numeric). Note: each column is processed independently of all others.

Usage

```
designTreatmentsZ(dframe, varlist, ..., minFraction = 0, weights = c(),
  rareCount = 0, collarProb = 0, codeRestriction = NULL,
  customCoders = NULL, verbose = TRUE, parallelCluster = NULL,
  use_parallel = TRUE)
```

Arguments

dframe	Data frame to learn treatments from (training data), must have at least 1 row.
varlist	Names of columns to treat (effective variables).
...	no additional arguments, declared to forced named binding of later arguments
minFraction	optional minimum frequency a categorical level must have to be converted to an indicator column.
weights	optional training weights for each row
rareCount	optional integer, allow levels with this count or below to be pooled into a shared rare-level. Defaults to 0 or off.
collarProb	what fraction of the data (pseudo-probability) to collar data at if doCollar is set during prepare.treatmentplan .
codeRestriction	what types of variables to produce (character array of level codes, NULL means no restriction).
customCoders	map from code names to custom categorical variable encoding functions (please see https://github.com/WinVector/vtreat/blob/master/extras/CustomLevelCoders.md).
verbose	if TRUE print progress.
parallelCluster	(optional) a cluster object created by package parallel or package snow.
use_parallel	logical, if TRUE use parallel methods (if parallel cluster is set).

Details

The main fields are mostly vectors with names (all with the same names in the same order):

- vars : (character array without names) names of variables (in same order as names on the other diagnostic vectors) - varMoves : logical TRUE if the variable varied during hold out scoring, only variables that move will be in the treated frame

See the vtreat vignette for a bit more detail and a worked example.

Columns that do not vary are not passed through.

Value

treatment plan (for use with prepare)

See Also

[prepare.treatmentplan](#), [designTreatmentsC](#), [designTreatmentsN](#)

Examples

```
dTrainZ <- data.frame(x=c('a','a','a','a','b','b',NA,'e','e'),
  z=c(1,2,3,4,5,6,7,NA,9))
dTestZ <- data.frame(x=c('a','x','c',NA),
  z=c(10,20,30,NA))
treatmentsZ = designTreatmentsZ(dTrainZ, colnames(dTrainZ),
  rareCount=0)
dTrainZTreated <- prepare(treatmentsZ, dTrainZ)
dTestZTreated <- prepare(treatmentsZ, dTestZ)
```

design_missingness_treatment

Design a simple treatment plan to indicate missingness and perform simple imputation.

Description

Design a simple treatment plan to indicate missingness and perform simple imputation.

Usage

```
design_missingness_treatment(dframe, ..., varlist = colnames(dframe),
  invalid_mark = "_invalid_", drop_constant_columns = FALSE)
```

Arguments

dframe	data.frame to drive design.
...	not used, forces later arguments to bind by name.
varlist	character, names of columns to process.
invalid_mark	character, name to use for NA levels and novel levels.
drop_constant_columns	logical, if TRUE drop columns that do not vary from the treatment plan.

Value

simple treatment plan.

See Also

[prepare.simple_plan](#)

Examples

```
d <- wrapr::build_frame(
  "x1", "x2", "x3" |
  1 , 4 , "A" |
  NA , 5 , "B" |
  3 , 6 , NA )

plan <- design_missingness_treatment(d)
prepare(plan, d)

prepare(plan, data.frame(x1=NA, x2=NA, x3="E"))
```

```
format.vtreatment      Display treatment plan.
```

Description

Display treatment plan.

Usage

```
## S3 method for class 'vtreatment'
format(x, ...)
```

Arguments

```
x          treatment plan
...        additional args (to match general signature).
```

```
getSplitPlanAppLabels read application labels off a split plan.
```

Description

read application labels off a split plan.

Usage

```
getSplitPlanAppLabels(nRow, plan)
```

Arguments

```
nRow      number of rows in original data.frame.
plan      split plan
```

Value

vector of labels

See Also

[kWayCrossValidation](#), [kWayStratifiedY](#), and [makekWayCrossValidationGroupedByColumn](#)

Examples

```
plan <- kWayStratifiedY(3,2,NULL,NULL)
getSplitPlanAppLabels(3,plan)
```

`kWayCrossValidation` *k-fold cross validation, a splitFunction in the sense of vtreat::buildEvalSets*

Description

k-fold cross validation, a `splitFunction` in the sense of `vtreat::buildEvalSets`

Usage

```
kWayCrossValidation(nRows, nSplits, dframe, y)
```

Arguments

<code>nRows</code>	number of rows to split (>1).
<code>nSplits</code>	number of groups to split into (>1,<=nRows).
<code>dframe</code>	original data frame (ignored).
<code>y</code>	numeric outcome variable (ignored).

Value

split plan

Examples

```
kWayCrossValidation(7,2,NULL,NULL)
```

kWayStratifiedY	<i>k-fold cross validation stratified on y, a splitFunction in the sense of vtreat::buildEvalSets</i>
-----------------	---

Description

k-fold cross validation stratified on y, a splitFunction in the sense of vtreat::buildEvalSets

Usage

```
kWayStratifiedY(nRows, nSplits, dframe, y)
```

Arguments

nRows	number of rows to split (>1)
nSplits	number of groups to split into (<nRows,>1).
dframe	original data frame (ignored).
y	numeric outcome variable try to have equidistributed in each split.

Value

split plan

Examples

```
set.seed(23255)
d <- data.frame(y=sin(1:100))
pStrat <- kWayStratifiedY(nrow(d),5,d,d$y)
problemAppPlan(nrow(d),5,pStrat,TRUE)
d$stratGroup <- vtreat::getSplitPlanAppLabels(nrow(d),pStrat)
pSimple <- kWayCrossValidation(nrow(d),5,d,d$y)
problemAppPlan(nrow(d),5,pSimple,TRUE)
d$simpleGroup <- vtreat::getSplitPlanAppLabels(nrow(d),pSimple)
summary(tapply(d$y,d$simpleGroup,mean))
summary(tapply(d$y,d$stratGroup,mean))
```

kWayStratifiedYReplace

k-fold cross validation stratified with replacement on y, a splitFunction in the sense of vtreat::buildEvalSets .

Description

Build a k-fold cross validation sample where training sets are the same size as the original data, and built by sampling disjoint from test/application sets (sampled with replacement).

Usage

```
kWayStratifiedYReplace(nRows, nSplits, dframe, y)
```

Arguments

nRows	number of rows to split (>1)
nSplits	number of groups to split into (<nRows,>1).
dframe	original data frame (ignored).
y	numeric outcome variable try to have equidistributed in each split.

Value

split plan

Examples

```
set.seed(23255)
d <- data.frame(y=sin(1:100))
pStrat <- kWayStratifiedYReplace(nrow(d),5,d,d$y)
```

makekWayCrossValidationGroupedByColumn

Build a k-fold cross validation splitter, respecting (never splitting) groupingColumn.

Description

Build a k-fold cross validation splitter, respecting (never splitting) groupingColumn.

Usage

```
makekWayCrossValidationGroupedByColumn(groupingColumnName)
```


Arguments

groupingColumnName
name of column to group by.

Value

splitting function in the sense of vtreat::buildEvalSets.

Examples

```
d <- data.frame(y=sin(1:100))
d$group <- floor(seq_len(nrow(d))/5)
splitter <- makekWayCrossValidationGroupedByColumn('group')
split <- splitter(nrow(d),5,d,d$y)
d$splitLabel <- vtreat::getSplitPlanAppLabels(nrow(d),split)
rowSums(table(d$group,d$splitLabel)>0)
```

mkCrossFrameCExperiment

Run categorical cross-frame experiment.

Description

Builds a [designTreatmentsC](#) treatment plan and a data frame prepared from dframe that is "cross" in the sense each row is treated using a treatment plan built from a subset of dframe disjoint from the given row. The goal is to try to and supply a method of breaking nested model bias other than splitting into calibration, training, test sets.

Usage

```
mkCrossFrameCExperiment(dframe, varlist, outcomename, outcometarget, ...,
  weights = c(), minFraction = 0.02, smFactor = 0, rareCount = 0,
  rareSig = 1, collarProb = 0, codeRestriction = NULL,
  customCoders = NULL, scale = FALSE, doCollar = FALSE,
  splitFunction = NULL, ncross = 3, forceSplit = FALSE,
  catScaling = TRUE, verbose = TRUE, parallelCluster = NULL,
  use_parallel = TRUE)
```

Arguments

dframe Data frame to learn treatments from (training data), must have at least 1 row.
varlist Names of columns to treat (effective variables).
outcomename Name of column holding outcome variable. dframe[[outcomename]] must be only finite non-missing values.

outcometarget	Value/level of outcome to be considered "success", and there must be a cut such that <code>dframe[[outcomename]]==outcometarget</code> at least twice and <code>dframe[[outcomename]]!=outcometarget</code> at least twice.
...	no additional arguments, declared to forced named binding of later arguments
weights	optional training weights for each row
minFraction	optional minimum frequency a categorical level must have to be converted to an indicator column.
smFactor	optional smoothing factor for impact coding models.
rareCount	optional integer, allow levels with this count or below to be pooled into a shared rare-level. Defaults to 0 or off.
rareSig	optional numeric, suppress levels from pooling at this significance value greater. Defaults to NULL or off.
collarProb	what fraction of the data (pseudo-probability) to collar data at if <code>doCollar</code> is set during <code>prepare.treatmentplan</code> .
codeRestriction	what types of variables to produce (character array of level codes, NULL means no restriction).
customCoders	map from code names to custom categorical variable encoding functions (please see https://github.com/WinVector/vtreat/blob/master/extras/CustomLevelCoders.md).
scale	optional if TRUE replace numeric variables with regression ("move to outcome-scale").
doCollar	optional if TRUE collar numeric variables by cutting off after a tail-probability specified by <code>collarProb</code> during treatment design.
splitFunction	(optional) see <code>vtreat::buildEvalSets</code> .
ncross	optional scalar ≥ 2 number of cross-validation rounds to design.
forceSplit	logical, if TRUE force cross-validated significance calculations on all variables.
catScaling	optional, if TRUE use <code>glm()</code> linkspace, if FALSE use <code>lm()</code> for scaling.
verbose	if TRUE print progress.
parallelCluster	(optional) a cluster object created by package <code>parallel</code> or package <code>snow</code> .
use_parallel	logical, if TRUE use parallel methods.

Value

list with treatments and crossFrame

See Also

[designTreatmentsC](#), [designTreatmentsN](#), [prepare.treatmentplan](#)

Examples

```

set.seed(23525)
zip <- paste('z',1:100)
N <- 200
d <- data.frame(zip=sample(zip,N,replace=TRUE),
                zip2=sample(zip,20,replace=TRUE),
                y=runif(N))
del <- runif(length(zip))
names(del) <- zip
d$y <- d$y + del[d$zip2]
d$yc <- d$y>=mean(d$y)
cC <- mkCrossFrameCExperiment(d,c('zip','zip2'),'yc',TRUE,
                             rareCount=2,rareSig=0.9)
cor(as.numeric(cC$crossFrame$yc),cC$crossFrame$zip_catB) # poor
cor(as.numeric(cC$crossFrame$yc),cC$crossFrame$zip2_catB) # better
treatments <- cC$treatments
dTrainV <- cC$crossFrame

```

mkCrossFrameMExperiment

Function to build multi-outcome vtreat cross frame and treatment plan.

Description

Please see vignette("MultiClassVtreat", package = "vtreat") <https://winvector.github.io/vtreat/articles/MultiClassVtreat.html>.

Usage

```

mkCrossFrameMExperiment(d, vars, y_name, ..., weights = c(),
                        minFraction = 0.02, smFactor = 0, rareCount = 0, rareSig = 1,
                        collarProb = 0, codeRestriction = NULL, customCoders = NULL,
                        scale = FALSE, doCollar = FALSE, splitFunction = NULL,
                        ncross = 3, forceSplit = FALSE, catScaling = FALSE,
                        y_dependent_treatments = c("catB"), verbose = FALSE,
                        parallelCluster = NULL, use_parallel = TRUE)

```

Arguments

d	data to learn from
vars	character, vector of independent variable column names.
y_name	character, name of outcome column.
...	not used, declared to forced named binding of later arguments
weights	optional training weights for each row

minFraction	optional minimum frequency a categorical level must have to be converted to an indicator column.
smFactor	optional smoothing factor for impact coding models.
rareCount	optional integer, allow levels with this count or below to be pooled into a shared rare-level. Defaults to 0 or off.
rareSig	optional numeric, suppress levels from pooling at this significance value greater. Defaults to NULL or off.
collarProb	what fraction of the data (pseudo-probability) to collar data at if doCollar is set during prepare.multinomial_plan .
codeRestriction	what types of variables to produce (character array of level codes, NULL means no restriction).
customCoders	map from code names to custom categorical variable encoding functions (please see https://github.com/WinVector/vtreat/blob/master/extras/CustomLevelCoders.md).
scale	optional if TRUE replace numeric variables with regression ("move to outcome-scale").
doCollar	optional if TRUE collar numeric variables by cutting off after a tail-probability specified by collarProb during treatment design.
splitFunction	(optional) see <code>vtreat::buildEvalSets</code> .
ncross	optional scalar ≥ 2 number of cross-validation rounds to design.
forceSplit	logical, if TRUE force cross-validated significance calculations on all variables.
catScaling	optional, if TRUE use <code>glm()</code> linkspace, if FALSE use <code>lm()</code> for scaling.
y_dependent_treatments	character what treatment types to build per-outcome level.
verbose	if TRUE print progress.
parallelCluster	(optional) a cluster object created by package <code>parallel</code> or package <code>snow</code> .
use_parallel	logical, if TRUE use parallel methods.

Value

`list(cross_frame, treatments_0, treatments_m)`

See Also

[prepare.multinomial_plan](#)

mkCrossFrameNExperiment

Run a numeric cross frame experiment.

Description

Builds a `designTreatmentsN` treatment plan and a data frame prepared from `dframe` that is "cross" in the sense each row is treated using a treatment plan built from a subset of `dframe` disjoint from the given row. The goal is to try to and supply a method of breaking nested model bias other than splitting into calibration, training, test sets.

Usage

```
mkCrossFrameNExperiment(dframe, varlist, outcomename, ..., weights = c(),
  minFraction = 0.02, smFactor = 0, rareCount = 0, rareSig = 1,
  collarProb = 0, codeRestriction = NULL, customCoders = NULL,
  scale = FALSE, doCollar = FALSE, splitFunction = NULL,
  ncross = 3, forceSplit = FALSE, verbose = TRUE,
  parallelCluster = NULL, use_parallel = TRUE)
```

Arguments

<code>dframe</code>	Data frame to learn treatments from (training data), must have at least 1 row.
<code>varlist</code>	Names of columns to treat (effective variables).
<code>outcomename</code>	Name of column holding outcome variable. <code>dframe[[outcomename]]</code> must be only finite non-missing values and there must be a cut such that <code>dframe[[outcomename]]</code> is both above the cut at least twice and below the cut at least twice.
<code>...</code>	no additional arguments, declared to forced named binding of later arguments
<code>weights</code>	optional training weights for each row
<code>minFraction</code>	optional minimum frequency a categorical level must have to be converted to an indicator column.
<code>smFactor</code>	optional smoothing factor for impact coding models.
<code>rareCount</code>	optional integer, allow levels with this count or below to be pooled into a shared rare-level. Defaults to 0 or off.
<code>rareSig</code>	optional numeric, suppress levels from pooling at this significance value greater. Defaults to NULL or off.
<code>collarProb</code>	what fraction of the data (pseudo-probability) to collar data at if <code>doCollar</code> is set during <code>prepare.treatmentplan</code> .
<code>codeRestriction</code>	what types of variables to produce (character array of level codes, NULL means no restriction).
<code>customCoders</code>	map from code names to custom categorical variable encoding functions (please see https://github.com/WinVector/vtreat/blob/master/extras/CustomLevelCoders.md).

scale	optional if TRUE replace numeric variables with regression ("move to outcome-scale").
doCollar	optional if TRUE collar numeric variables by cutting off after a tail-probability specified by collarProb during treatment design.
splitFunction	(optional) see vtreat::buildEvalSets .
ncross	optional scalar ≥ 2 number of cross-validation rounds to design.
forceSplit	logical, if TRUE force cross-validated significance calculations on all variables.
verbose	if TRUE print progress.
parallelCluster	(optional) a cluster object created by package parallel or package snow.
use_parallel	logical, if TRUE use parallel methods.

Value

treatment plan (for use with prepare)

See Also

[designTreatmentsC](#), [designTreatmentsN](#), [prepare.treatmentplan](#)

Examples

```
set.seed(23525)
zip <- paste('z',1:100)
N <- 200
d <- data.frame(zip=sample(zip,N,replace=TRUE),
                zip2=sample(zip,N,replace=TRUE),
                y=runif(N))
del <- runif(length(zip))
names(del) <- zip
d$y <- d$y + del[d$zip2]
d$yc <- d$y>=mean(d$y)
cN <- mkCrossFrameNExperiment(d,c('zip','zip2'),'y',
                             rareCount=2,rareSig=0.9)
cor(cN$crossFrame$y,cN$crossFrame$zip_catN) # poor
cor(cN$crossFrame$y,cN$crossFrame$zip2_catN) # better
treatments <- cN$treatments
dTrainV <- cN$crossFrame
```

novel_value_summary *Report new/novel appearances of character values.*

Description

Report new/novel appearances of character values.

Usage

```
novel_value_summary(dframe, trackedValues)
```

Arguments

`dframe` Data frame to inspect.

`trackedValues` optional named list mapping variables to know values, allows warnings upon novel level appearances (see [track_values](#))

Value

frame of novel occurrences

See Also

[prepare.treatmentplan](#), [track_values](#)

Examples

```
set.seed(23525)
zip <- c(NA, paste('z', 1:10, sep = "_"))
N <- 10
d <- data.frame(zip = sample(zip, N, replace=TRUE),
                zip2 = sample(zip, N, replace=TRUE),
                y = runif(N))
dSample <- d[1:5, , drop = FALSE]
trackedValues <- track_values(dSample, c("zip", "zip2"))
novel_value_summary(d, trackedValues)
```

oneWayHoldout	<i>One way holdout, a splitFunction in the sense of vtreat::buildEvalSets.</i>
---------------	--

Description

Note one way holdout can leak target expected values, so it should not be preferred in nested modeling situations. Also, doesn't respect nSplits.

Usage

```
oneWayHoldout(nRows, nSplits, dframe, y)
```

Arguments

nRows	number of rows to split (integer >1).
nSplits	number of groups to split into (ignored).
dframe	original data frame (ignored).
y	numeric outcome variable (ignored).

Value

split plan

Examples

```
oneWayHoldout(3, NULL, NULL, NULL)
```

patch_columns_into_frame	<i>Patch columns into data.frame.</i>
--------------------------	---------------------------------------

Description

Add columns from new_frame into old_frame, replacing any columns with matching names in orig_frame with values from new_frame.

Usage

```
patch_columns_into_frame(orig_frame, new_frame)
```

Arguments

orig_frame	data.frame to patch into.
new_frame	data.frame to take replacement columns from.

Value

patched data.frame

Examples

```
orig_frame <- data.frame(x = 1, y = 2)
new_frame <- data.frame(y = 3, z = 4)
patch_columns_into_frame(orig_frame, new_frame)
```

ppCoderC

Solve a categorical partial pooling problem.

Description

Please see <http://www.win-vector.com/blog/2017/09/custom-level-coding-in-vtreat/> and <http://www.win-vector.com/blog/2017/09/partial-pooling-for-lower-variance-variable-encoding/>.

Usage

```
ppCoderC(v, vcol, y, w = NULL)
```

Arguments

v	character variable name
vcol	character, independent or input variable
y	logical, dependent or outcome variable to predict
w	row/example weights

Value

scored training data column

 ppCoderN

Solve a numeric partial pooling problem.

Description

Please see <http://www.win-vector.com/blog/2017/09/custom-level-coding-in-vtreat/> and <http://www.win-vector.com/blog/2017/09/partial-pooling-for-lower-variance-variable-encoding/>.

Usage

```
ppCoderN(v, vcol, y, w = NULL)
```

Arguments

v	character variable name
vcol	character, independent or input variable
y	numeric, dependent or outcome variable to predict
w	row/example weights

Value

scored training data column

prepare

Apply treatments and restrict to useful variables.

Description

Apply treatments and restrict to useful variables.

Usage

```
prepare(treatmentplan, dframe, ...)
```

Arguments

treatmentplan	Plan built by designTreatmentsC() or designTreatmentsN()
dframe	Data frame to be treated
...	no additional arguments, declared to forced named binding of later arguments

See Also

[prepare.treatmentplan](#), [prepare.simple_plan](#), [prepare.multinomial_plan](#)

```
prepare.multinomial_plan
```

Function to apply mkCrossFrameMExperiment treatemnts.

Description

Please see vignette("MultiClassVtreat", package = "vtreat") <https://winvector.github.io/vtreat/articles/MultiClassVtreat.html>.

Usage

```
## S3 method for class 'multinomial_plan'
prepare(treatmentplan, dframe, ...,
  pruneSig = NULL, scale = FALSE, doCollar = FALSE,
  varRestriction = NULL, codeRestriction = NULL,
  trackedValues = NULL, extracols = NULL, parallelCluster = NULL,
  use_parallel = TRUE)
```

Arguments

treatmentplan	multinomial_plan from mkCrossFrameMExperiment.
dframe	new data to process.
...	not used, declared to forced named binding of later arguments
pruneSig	suppress variables with significance above this level
scale	optional if TRUE replace numeric variables with single variable model regressions ("move to outcome-scale"). These have mean zero and (for variables with significant less than 1) slope 1 when regressed (lm for regression problems/glm for classification problems) against outcome.
doCollar	optional if TRUE collar numeric variables by cutting off after a tail-probability specified by collarProb during treatment design.
varRestriction	optional list of treated variable names to restrict to
codeRestriction	optional list of treated variable codes to restrict to
trackedValues	optional named list mapping variables to know values, allows warnings upon novel level appearances (see track_values)
extracols	extra columns to copy.
parallelCluster	(optional) a cluster object created by package parallel or package snow.
use_parallel	logical, if TRUE use parallel methods.

Value

prepared data frame.

See Also

[mkCrossFrameMExperiment](#), [prepare](#)

prepare.simple_plan *Prepare a simple treatment.*

Description

Prepare a simple treatment.

Usage

```
## S3 method for class 'simple_plan'  
prepare(treatmentplan, dframe, ...)
```

Arguments

treatmentplan A simple treatment plan.
dframe data.frame to be treated.
... not used, present for S3 signature consistency.

See Also

[design_missingness_treatment](#), [prepare](#)

Examples

```
d <- wrapr::build_frame(  
  "x1", "x2", "x3" |  
  1   , 4   , "A"  |  
  NA  , 5   , "B"  |  
  3   , 6   , NA   )  
  
plan <- design_missingness_treatment(d)  
prepare(plan, d)  
  
prepare(plan, data.frame(x1=NA, x2=NA, x3="E"))
```

```
prepare.treatmentplan Apply treatments and restrict to useful variables.
```

Description

Use a treatment plan to prepare a data frame for analysis. The resulting frame will have new effective variables that are numeric and free of NaN/NA. If the outcome column is present it will be copied over. The intent is that these frames are compatible with more machine learning techniques, and avoid a lot of corner cases (NA,NaN, novel levels, too many levels). Note: each column is processed independently of all others. Also copies over outcome if present. Note: treatmentplan's are not meant for long-term storage, a warning is issued if the version of vtreat that produced the plan differs from the version running prepare().

Usage

```
## S3 method for class 'treatmentplan'
prepare(treatmentplan, dframe, ...,
        pruneSig = NULL, scale = FALSE, doCollar = FALSE,
        varRestriction = NULL, codeRestriction = NULL,
        trackedValues = NULL, extracols = NULL, parallelCluster = NULL,
        use_parallel = TRUE)
```

Arguments

treatmentplan	Plan built by designTreatmentsC() or designTreatmentsN()
dframe	Data frame to be treated
...	no additional arguments, declared to forced named binding of later arguments
pruneSig	suppress variables with significance above this level
scale	optional if TRUE replace numeric variables with single variable model regressions ("move to outcome-scale"). These have mean zero and (for variables with significant less than 1) slope 1 when regressed (lm for regression problems/glm for classification problems) against outcome.
doCollar	optional if TRUE collar numeric variables by cutting off after a tail-probability specified by collarProb during treatment design.
varRestriction	optional list of treated variable names to restrict to
codeRestriction	optional list of treated variable codes to restrict to
trackedValues	optional named list mapping variables to know values, allows warnings upon novel level appearances (see track_values)
extracols	extra columns to copy.
parallelCluster	(optional) a cluster object created by package parallel or package snow.
use_parallel	logical, if TRUE use parallel methods.

Value

treated data frame (all columns numeric- without NA, NaN)

See Also

[mkCrossFrameCExperiment](#), [mkCrossFrameNExperiment](#), [designTreatmentsC](#) [designTreatmentsN](#)
[designTreatmentsZ](#), [prepare](#)

Examples

```
dTrainN <- data.frame(x= c('a','a','a','a','b','b','b'),
                    z= c(1,2,3,4,5,6,7),
                    y= c(0,0,0,1,0,1,1))
dTestN <- data.frame(x= c('a','b','c',NA),
                    z= c(10,20,30,NA))
treatmentsN = designTreatmentsN(dTrainN,colnames(dTrainN), 'y')
dTrainNTreated <- prepare(treatmentsN, dTrainN, pruneSig= 0.2)
dTestNTreated <- prepare(treatmentsN, dTestN, pruneSig= 0.2)

dTrainC <- data.frame(x= c('a','a','a','b','b','b'),
                    z= c(1,2,3,4,5,6),
                    y= c(FALSE,FALSE,TRUE,FALSE,TRUE,TRUE))
dTestC <- data.frame(x= c('a','b','c',NA),
                    z= c(10,20,30,NA))
treatmentsC <- designTreatmentsC(dTrainC, colnames(dTrainC),'y',TRUE)
dTrainCTreated <- prepare(treatmentsC, dTrainC)
dTestCTreated <- prepare(treatmentsC, dTestC)

dTrainZ <- data.frame(x= c('a','a','a','b','b','b'),
                    z= c(1,2,3,4,5,6))
dTestZ <- data.frame(x= c('a','b','c',NA),
                    z= c(10,20,30,NA))
treatmentsZ <- designTreatmentsZ(dTrainZ, colnames(dTrainZ))
dTrainZTreated <- prepare(treatmentsZ, dTrainZ, codeRestriction= c('lev'))
dTestZTreated <- prepare(treatmentsZ, dTestZ, codeRestriction= c('lev'))
```

```
pre_comp_xval
```

Pre-computed cross-plan (so same split happens each time).

Description

Pre-computed cross-plan (so same split happens each time).

Usage

```
pre_comp_xval(nRows, nSplits, splitplan)
```

Arguments

nRows number of rows to split (integer >1).
nSplits number of groups to split into (ignored).
splitplan split plan to actually use

Value

splitplan

Examples

```
p1 <- oneWayHoldout(3,NULL,NULL,NULL)
p2 <- pre_comp_xval(3, 3, p1)
p2(3, 3)
```

```
print.multinomial_plan
```

Print treatmentplan.

Description

Print treatmentplan.

Usage

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

Arguments

x treatmentplan
... additional args (to match general signature).

`print.simple_plan` *Print treatmentplan.*

Description

Print treatmentplan.

Usage

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

Arguments

`x` `treatmentplan`
`...` additional args (to match general signature).

`print.treatmentplan` *Print treatmentplan.*

Description

Print treatmentplan.

Usage

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

Arguments

`x` `treatmentplan`
`...` additional args (to match general signature).

See Also

[designTreatmentsC](#), [designTreatmentsN](#), [designTreatmentsZ](#), [prepare.treatmentplan](#)

```
print.vtreatment      Print treatmentplan.
```

Description

Print treatmentplan.

Usage

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

Arguments

```
x          treatmentplan
...        additional args (to match general signature).
```

See Also

[designTreatmentsC](#), [designTreatmentsN](#), [designTreatmentsZ](#), [prepare.treatmentplan](#)

```
problemAppPlan      check if appPlan is a good carve-up of 1:nRows into nSplits groups
```

Description

check if appPlan is a good carve-up of 1:nRows into nSplits groups

Usage

```
problemAppPlan(nRows, nSplits, appPlan, strictCheck)
```

Arguments

```
nRows      number of rows to carve-up
nSplits    number of sets to carve-up into
appPlan    carve-up to critique
strictCheck logical, if true expect application data to be a carve-up and training data to be a maximal partition and to match nSplits.
```

Value

problem with carve-up (null if good)

See Also

[kWayCrossValidation](#), [kWayStratifiedY](#), and [makekWayCrossValidationGroupedByColumn](#)

Examples

```
plan <- kWayStratifiedY(3,2,NULL,NULL)
problemAppPlan(3,3,plan,TRUE)
```

rquery_prepare	<i>Materialize a treated data frame remotely.</i>
----------------	---

Description

Materialize a treated data frame remotely.

Usage

```
rquery_prepare(db, rqplan, data_source, result_table_name, ...,
  extracols = NULL, temporary = FALSE, overwrite = TRUE,
  attempt_nan_inf_mapping = FALSE, col_sample = NULL,
  return_ops = FALSE)
```

```
materialize_treated(db, rqplan, data_source, result_table_name, ...,
  extracols = NULL, temporary = FALSE, overwrite = TRUE,
  attempt_nan_inf_mapping = FALSE, col_sample = NULL,
  return_ops = FALSE)
```

Arguments

db	a db handle.
rqplan	an query plan produced by <code>as_rquery_plan()</code> .
data_source	relop, data source (usually a <code>relop_table_source</code>).
result_table_name	character, table name to land result in
...	force later arguments to bind by name.
extracols	extra columns to copy.
temporary	logical, if TRUE try to make result temporary.
overwrite	logical, if TRUE try to overwrite result.
attempt_nan_inf_mapping	logical, if TRUE attempt to map NaN and Infinity to NA/NULL (goot on PostgreSQL, not on Spark).
col_sample	sample of data to determine column types.
return_ops	logical, if TRUE return operator tree instead of materializing.

Value

description of treated table.

Functions

- `materialize_treated`: old name for `rquery_prepare` function

See Also

[as_rquery_plan](#), [rqdatatable_prepare](#)

run_vtreat_tests	<i>Run vtreat tests.</i>
------------------	--------------------------

Description

For all files with names of the form "`^test_+\\.R$`" in the package directory `unit_tests` run all functions with names of the form "`^test_+.$`" as RUnit tests. Attaches RUnit and `pkg`, requires RUnit. Stops on error.

Usage

```
run_vtreat_tests(..., verbose = TRUE, package_test_dirs = "unit_tests",
  test_dirs = character(0), stop_on_issue = TRUE,
  stop_if_no_tests = TRUE, require_RUnit_attached = FALSE,
  require_pkg_attached = TRUE, rngKind = "Mersenne-Twister",
  rngNormalKind = "Inversion")
```

Arguments

<code>...</code>	not used, force later arguments to bind by name.
<code>verbose</code>	logical, if TRUE print more.
<code>package_test_dirs</code>	directory names to look for in the installed package.
<code>test_dirs</code>	paths to look for tests in.
<code>stop_on_issue</code>	logical, if TRUE stop after errors or failures.
<code>stop_if_no_tests</code>	logical, if TRUE stop if no tests were found.
<code>require_RUnit_attached</code>	logical, if TRUE require RUnit be attached before testing.
<code>require_pkg_attached</code>	logical, if TRUE require <code>pkg</code> be attached before testing.
<code>rngKind</code>	pseudo-random number generator method name.
<code>rngNormalKind</code>	pseudo-random normal generator method name.

Details

Based on <https://github.com/RcppCore/Rcpp/blob/master/tests/doRUnit.R>. This version is GPL-3, works derived from it must be distributed GPL-3.

Value

RUnit test results (invisible).

solveIsotone	<i>Solve for best single-direction (non-decreasing or non-increasing) fit.</i>
--------------	--

Description

Return a vector of length y that is a function of x (differs at most where x differs) obeying the either the same order constraints or the opposite order constraints as x . This vector is picked as close to y (by square-distance) as possible.

Usage

```
solveIsotone(varName, x, y, w = NULL)
```

Arguments

varName	character, name of variable
x	numeric, factor, or character input (not empty, no NAs).
y	numeric (same length as x no NAs), output to match
w	numeric positive, same length as x (weights, can be NULL)

Details

Please see <https://github.com/WinVector/vtreat/blob/master/extras/MonotoneCoder.md>.

Value

isotonically adjusted y (non-decreasing)

Examples

```
if(requireNamespace("isotone", quietly = TRUE)) {
  solveIsotone('v', 1:3, c(1,2,1))
}
```

solveNonDecreasing	<i>Solve for best non-decreasing fit using isotone regression (from the "isotone" package https://CRAN.R-project.org/package=isotone).</i>
--------------------	---

Description

Return a vector of length y that is a function of x (differs at most where x differs) obeying the same order constraints as x. This vector is picked as close to y (by square-distance) as possible.

Usage

```
solveNonDecreasing(varName, x, y, w = NULL)
```

Arguments

varName	character, name of variable
x	numeric, factor, or character input (not empty, no NAs).
y	numeric or castable to such (same length as x no NAs), output to match
w	numeric positive, same length as x (weights, can be NULL)

Details

Please see <https://github.com/WinVector/vtreat/blob/master/extras/MonotoneCoder.md>.

Value

isotonically adjusted y (non-decreasing)

Examples

```
if(requireNamespace("isotone", quietly = TRUE)) {  
  solveNonDecreasing('v', 1:3, c(1,2,1))  
}
```

solveNonIncreasing *Solve for best non-increasing fit.*

Description

Return a vector of length y that is a function of x (differs at most where x differs) obeying the opposite order constraints as x. This vector is picked as close to y (by square-distance) as possible.

Usage

```
solveNonIncreasing(varName, x, y, w = NULL)
```

Arguments

varName	character, name of variable
x	numeric, factor, or character input (not empty, no NAs).
y	numeric (same length as x no NAs), output to match
w	numeric positive, same length as x (weights, can be NULL)

Details

Please see <https://github.com/WinVector/vtreat/blob/master/extras/MonotoneCoder.md>.

Value

isotonically adjusted y (non-decreasing)

Examples

```
if(requireNamespace("isotone", quietly = TRUE)) {  
  solveNonIncreasing('v', 1:3, c(1,2,1))  
}
```

solve_pieewise	<i>Solve as pieewise linear problem, numeric target.</i>
----------------	--

Description

Return a vector of length y that is a pieewise function of x. This vector is picked as close to y (by square-distance) as possible for a set of x-only determined cut-points. Cross-validates for a good number of segments.

Usage

```
solve_pieewise(varName, x, y, w = NULL)
```

Arguments

varName	character, name of variable
x	numeric input (not empty, no NAs).
y	numeric or castable to such (same length as x no NAs), output to match
w	numeric positive, same length as x (weights, can be NULL)

Value

segmented y prediction

solve_pieewisec	<i>Solve as pieewise logit problem, categorical target.</i>
-----------------	---

Description

Return a vector of length y that is a pieewise function of x. This vector is picked as close to y (by square-distance) as possible for a set of x-only determined cut-points. Cross-validates for a good number of segments.

Usage

```
solve_pieewisec(varName, x, y, w = NULL)
```

Arguments

varName	character, name of variable
x	numeric input (not empty, no NAs).
y	numeric or castable to such (same length as x no NAs), output to match
w	numeric positive, same length as x (weights, can be NULL)

Value

segmented y prediction

spline_variable *Spline variable numeric target.*

Description

Return a spline approximation of data.

Usage

```
spline_variable(varName, x, y, w = NULL)
```

Arguments

varName	character, name of variable
x	numeric input (not empty, no NAs).
y	numeric or castable to such (same length as x no NAs), output to match
w	numeric positive, same length as x (weights, can be NULL)

Value

spline y prediction

spline_variablec *Spline variable categorical target.*

Description

Return a spline approximation of the change in log odds.

Usage

```
spline_variablec(varName, x, y, w = NULL)
```

Arguments

varName	character, name of variable
x	numeric input (not empty, no NAs).
y	numeric or castable to such (same length as x no NAs), output to match
w	numeric positive, same length as x (weights, can be NULL)

Value

spline y prediction

square_window	<i>Build a square windows variable, numeric target.</i>
---------------	---

Description

Build a square moving average window (KNN in 1d). This is a high-frequency feature.

Usage

```
square_window(varName, x, y, w = NULL)
```

Arguments

varName	character, name of variable
x	numeric input (not empty, no NAs).
y	numeric or castable to such (same length as x no NAs), output to match
w	numeric positive, same length as x (weights, can be NULL) IGNORED

Value

segmented y prediction

Examples

```
d <- data.frame(x = c(NA, 1:6), y = c(0, 0, 0, 1, 1, 0, 0))
square_window("v", d$x, d$y)
```

square_windowc	<i>Build a square windows variable, categorical target.</i>
----------------	---

Description

Build a square moving average window (KNN in 1d). This is a high-frequency feature. Approximation of the change in log odds.

Usage

```
square_windowc(varName, x, y, w = NULL)
```

Arguments

varName	character, name of variable
x	numeric input (not empty, no NAs).
y	numeric or castable to such (same length as x no NAs), output to match
w	numeric positive, same length as x (weights, can be NULL) IGNORED

Value

segmented y prediction

Examples

```
d <- data.frame(x = c(NA, 1:6), y = c(0, 0, 0, 1, 1, 0, 0))
square_window("v", d$x, d$y)
```

track_values

Track unique character values for variables.

Description

Builds lists of observed unique character values of varlist variables from the data frame.

Usage

```
track_values(dframe, varlist)
```

Arguments

dframe	Data frame to learn treatments from (training data), must have at least 1 row.
varlist	Names of columns to treat (effective variables).

Value

named list of values seen.

See Also

[prepare.treatmentplan](#), [novel_value_summary](#)

Examples

```

set.seed(23525)
zip <- c(NA, paste('z', 1:100, sep = "_"))
N <- 500
d <- data.frame(zip = sample(zip, N, replace=TRUE),
               zip2 = sample(zip, N, replace=TRUE),
               y = runif(N))
dSample <- d[1:300, , drop = FALSE]
tplan <- designTreatmentsN(dSample,
                          c("zip", "zip2"), "y",
                          verbose = FALSE)
trackedValues <- track_values(dSample, c("zip", "zip2"))
# don't normally want to catch warnings,
# doing it here as this is an example
# and must not have unhandled warnings.
tryCatch(
  prepare(tplan, d, trackedValues = trackedValues),
  warning = function(w) { cat(paste(w, collapse = "\n")) })

```

value_variables_C

*Value variables for prediction a categorical outcome.***Description**

Value variables for prediction a categorical outcome.

Usage

```

value_variables_C(dframe, varlist, outcomename, outcometarget, ...,
  weights = c(), minFraction = 0.02, smFactor = 0, rareCount = 0,
  rareSig = 1, collarProb = 0, scale = FALSE, doCollar = FALSE,
  splitFunction = NULL, ncross = 3, forceSplit = FALSE,
  catScaling = TRUE, verbose = FALSE, parallelCluster = NULL,
  use_parallel = TRUE, customCoders = list(c.PiecewiseV.num =
  vtreat::solve_pieciwesc, n.PiecewiseV.num = vtreat::solve_pieciwise,
  c.knearest.num = vtreat::square_windowc, n.knearest.num =
  vtreat::square_window), codeRestriction = c("PiecewiseV", "knearest",
  "clean", "isBAD", "catB", "catP"))

```

Arguments

dframe	Data frame to learn treatments from (training data), must have at least 1 row.
varlist	Names of columns to treat (effective variables).
outcomename	Name of column holding outcome variable. dframe[[outcomename]] must be only finite non-missing values.

outcometarget	Value/level of outcome to be considered "success", and there must be a cut such that <code>dframe[[outcomename]]==outcometarget</code> at least twice and <code>dframe[[outcomename]]!=outcometarget</code> at least twice.
...	no additional arguments, declared to forced named binding of later arguments
weights	optional training weights for each row
minFraction	optional minimum frequency a categorical level must have to be converted to an indicator column.
smFactor	optional smoothing factor for impact coding models.
rareCount	optional integer, allow levels with this count or below to be pooled into a shared rare-level. Defaults to 0 or off.
rareSig	optional numeric, suppress levels from pooling at this significance value greater. Defaults to NULL or off.
collarProb	what fraction of the data (pseudo-probability) to collar data at if <code>doCollar</code> is set during <code>prepare.treatmentplan</code> .
scale	optional if TRUE replace numeric variables with regression ("move to outcome-scale").
doCollar	optional if TRUE collar numeric variables by cutting off after a tail-probability specified by <code>collarProb</code> during treatment design.
splitFunction	(optional) see <code>vtreat::buildEvalSets</code> .
ncross	optional scalar ≥ 2 number of cross-validation rounds to design.
forceSplit	logical, if TRUE force cross-validated significance calculations on all variables.
catScaling	optional, if TRUE use <code>glm()</code> linkspace, if FALSE use <code>lm()</code> for scaling.
verbose	if TRUE print progress.
parallelCluster	(optional) a cluster object created by package <code>parallel</code> or package <code>snow</code> .
use_parallel	logical, if TRUE use parallel methods.
customCoders	additional coders to use for variable importance estimate.
codeRestriction	codes to restrict to for variable importance estimate.

Value

table of variable valuations

value_variables_N	<i>Value variables for prediction a numeric outcome.</i>
-------------------	--

Description

Value variables for prediction a numeric outcome.

Usage

```
value_variables_N(dframe, varlist, outcomename, ..., weights = c(),
  minFraction = 0.02, smFactor = 0, rareCount = 0, rareSig = 1,
  collarProb = 0, scale = FALSE, doCollar = FALSE,
  splitFunction = NULL, ncross = 3, forceSplit = FALSE,
  verbose = FALSE, parallelCluster = NULL, use_parallel = TRUE,
  customCoders = list(c.PiecewiseV.num = vtreat::solve_pieciwsec,
  n.PiecewiseV.num = vtreat::solve_pieciwise, c.knearest.num =
  vtreat::square_windowc, n.knearest.num = vtreat::square_window),
  codeRestriction = c("PieciwiseV", "knearest", "clean", "isBAD", "catB",
  "catP"))
```

Arguments

dframe	Data frame to learn treatments from (training data), must have at least 1 row.
varlist	Names of columns to treat (effective variables).
outcomename	Name of column holding outcome variable. <code>dframe[[outcomename]]</code> must be only finite non-missing values and there must be a cut such that <code>dframe[[outcomename]]</code> is both above the cut at least twice and below the cut at least twice.
...	no additional arguments, declared to forced named binding of later arguments
weights	optional training weights for each row
minFraction	optional minimum frequency a categorical level must have to be converted to an indicator column.
smFactor	optional smoothing factor for impact coding models.
rareCount	optional integer, allow levels with this count or below to be pooled into a shared rare-level. Defaults to 0 or off.
rareSig	optional numeric, suppress levels from pooling at this significance value greater. Defaults to NULL or off.
collarProb	what fraction of the data (pseudo-probability) to collar data at if <code>doCollar</code> is set during prepare.treatmentplan .
scale	optional if TRUE replace numeric variables with regression ("move to outcome-scale").
doCollar	optional if TRUE collar numeric variables by cutting off after a tail-probability specified by <code>collarProb</code> during treatment design.
splitFunction	(optional) see <code>vtreat::buildEvalSets</code> .
ncross	optional scalar ≥ 2 number of cross-validation rounds to design.
forceSplit	logical, if TRUE force cross-validated significance calculations on all variables.
verbose	if TRUE print progress.
parallelCluster	(optional) a cluster object created by package <code>parallel</code> or package <code>snow</code> .
use_parallel	logical, if TRUE use parallel methods.
customCoders	additional coders to use for variable importance estimate.
codeRestriction	codes to restrict to for variable importance estimate.

Value

table of variable valuations

variable_values	<i>Return variable evaluations.</i>
-----------------	-------------------------------------

Description

Return variable evaluations.

Usage

```
variable_values(sf)
```

Arguments

sf scoreFrame from from vtreat treatments

Value

per-original variable evaluations

vnames	<i>New treated variable names from a treatmentplan\$treatment item.</i>
--------	---

Description

New treated variable names from a treatmentplan\$treatment item.

Usage

```
vnames(x)
```

Arguments

x vtreatment item

See Also

[designTreatmentsC](#) [designTreatmentsN](#) [designTreatmentsZ](#)

vorig	<i>Original variable name from a treatmentplan\$treatment item.</i>
-------	---

Description

Original variable name from a treatmentplan\$treatment item.

Usage

```
vorig(x)
```

Arguments

x vtreatment item.

See Also

[designTreatmentsC](#) [designTreatmentsN](#) [designTreatmentsZ](#)

vtreat	<i>vtreat: A Statistically Sound 'data.frame' Processor/Conditioner</i>
--------	---

Description

A 'data.frame' processor/conditioner that prepares real-world data for predictive modeling in a statistically sound manner. 'vtreat' prepares variables so that data has fewer exceptional cases, making it easier to safely use models in production. Common problems 'vtreat' defends against: 'Inf', 'NA', too many categorical levels, rare categorical levels, and new categorical levels (levels seen during application, but not during training). 'vtreat::prepare' should be used as you would use 'model.matrix'.

Details

For more information:

- `vignette('vtreat', package='vtreat')`
- `vignette(package='vtreat')`
- Website: <https://github.com/WinVector/vtreat>

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