Package 'treeshap'

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Title Compute SHAP Values for Your Tree-Based Models Using the 'TreeSHAP' Algorithm

Version 0.4.0

Description An efficient implementation of the 'TreeSHAP' algorithm introduced by Lundberg et al., (2020) <doi:10.1038/s42256-019-0138-9>. It is capable of calculating SHAP (SHapley Additive exPlanations) values for tree-based models in polynomial time. Currently supported models include 'gbm', 'randomForest', 'ranger', 'xgboost', 'lightgbm'.

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URL https://modeloriented.github.io/treeshap/, https://github.com/ModelOriented/treeshap

BugReports https://github.com/ModelOriented/treeshap/issues

Depends R (>= 4.1.0)

Imports data.table, ggplot2, Rcpp

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Contents

`colors_discrete_drwhy` *DrWhy color palettes for ggplot objects*

Description

DrWhy color palettes for ggplot objects

Usage

```
colors_discrete_drwhy(n = 2)

colors_breakdown_drwhy()
```

Arguments

n	number of colors for color palette

Value

color palette as vector of characters

`fifa20` *Attributes of all players in FIFA 20*

Description

Dataset consists of 56 columns, 55 numeric and one of type factor `'work_rate'`. `value_eur` is a potential target feature.

Usage

```
fifa20
```

Format

A data frame with 18278 rows and 56 columns. Most of variables representing skills are in range from 0 to 100 and will not be described here. To list non obvious features:

overall Overall score of player's skills

potential Potential of a player, younger players tend to have higher level of potential

value_eur Market value of a player (in mln EUR)

international_reputation Range 1 to 5

weak_foot Range 1 to 5

skill_moves Range 1 to 5

work_rate Divided by slash levels of willingness to work in offense and defense respectively

Source

"Data has been scraped from the publicly available website https://sofifa.com" https://www.kaggle.com/stefanoleone992/fifa-20-complete-player-dataset

gbm.unify *Unify GBM model*

Description

Convert your GBM model into a standardized representation. The returned representation is easy to be interpreted by the user and ready to be used as an argument in `treeshap()` function.

Usage

```
gbm.unify(gbm_model, data)
```

Arguments

`gbm_model`	An object of gbm class. At the moment, models built on data with categorical features are not supported - please encode them before training.
`data`	Reference dataset. A `data.frame` or `matrix` with the same columns as in the training set of the model. Usually dataset used to train model.

Value

a unified model representation - a `model_unified.object` object

See Also

`lightgbm.unify` for `LightGBM` `models`

`xgboost.unify` for `XGBoost` `models`

`ranger.unify` for `ranger` `models`

`randomForest.unify` for `randomForest` `models`

Examples

```
if (requireNamespace("gbm", quietly = TRUE)) {
  library(gbm)
  data <- fifa20$data[colnames(fifa20$data) != 'work_rate']
  data['value_eur'] <- fifa20$target
  gbm_model <- gbm::gbm(
               formula = value_eur ~ .,
               data = data,
               distribution = "gaussian",
               n.trees = 20,
               interaction.depth = 4,
               n.cores = 1)
  unified_model <- gbm.unify(gbm_model, data)
  shaps <- treeshap(unified_model, data[1:2,])
  plot_contribution(shaps, obs = 1)
}
```

gpboost.unify *Unify GPBoost model*

Description

Convert your GPBoost model into a standardized representation. The returned representation is easy to be interpreted by the user and ready to be used as an argument in `treeshap()` function.

Usage

```
gpboost.unify(gpb_model, data, recalculate = FALSE)
```

Arguments

`gpb_model`	A gpboost model - object of class `gpb.Booster`
`data`	Reference dataset. A `data.frame` or `matrix` with the same columns as in the training set of the model. Usually dataset used to train model.
`recalculate`	logical indicating if covers should be recalculated according to the dataset given in data. Keep it `FALSE` if training data are used.

Value

a unified model representation - a `model_unified.object` object

See Also

`gbm.unify` for `GBM` `models`

`xgboost.unify` for `XGBoost` `models`

`lightgbm.unify` for `LightGBM` `models`

`ranger.unify` for `ranger` `models`

`randomForest.unify` for `randomForest` `models`

Examples

```
if (requireNamespace("gpboost", quietly = TRUE)) {
  library(gpboost)
  param_gpb <- list(objective = "regression", max_depth = 2,
                    force_row_wise = TRUE, num_iterations = 20)
  data_fifa <- fifa20$data[!colnames(fifa20$data) %in%
               c('work_rate', 'value_eur', 'gk_diving', 'gk_handling',
               'gk_kicking', 'gk_reflexes', 'gk_speed', 'gk_positioning')]
  data <- na.omit(cbind(data_fifa, fifa20$target))
  sparse_data <- as.matrix(data[,-ncol(data)])
  x <- gpboost::gpb.Dataset(sparse_data, label = as.matrix(data[,ncol(data)]))
  gpb_data <- gpboost::gpb.Dataset.construct(x)
  gpb_model <- gpboost::gpboost(data = gpb_data, params = param_gpb,
                                verbose = -1, num_threads = 1)
```

```
  unified_model <- gpboost.unify(gpb_model, sparse_data)
  shaps <- treeshap(unified_model, data[1:2, ])
  plot_contribution(shaps, obs = 1)
}
```

`is.model_unified` *Check whether object is a valid model_unified object*

Description

Does not check correctness of representation, only basic checks

Usage

```
is.model_unified(x)
```

Arguments

`x`	an object to check

Value

boolean

`is.treeshap` *Check whether object is a valid treeshap object*

Description

Does not check correctness of result, only basic checks

Usage

```
is.treeshap(x)
```

Arguments

`x`	an object to check

Value

boolean

lightgbm.unify *Unify LightGBM model*

Description

Convert your LightGBM model into a standardized representation. The returned representation is easy to be interpreted by the user and ready to be used as an argument in `treeshap()` function.

Usage

```
lightgbm.unify(lgb_model, data, recalculate = FALSE)
```

Arguments

`lgb_model`	A lightgbm model - object of class `lgb.Booster`
`data`	Reference dataset. A `data.frame` or `matrix` with the same columns as in the training set of the model. Usually dataset used to train model.
`recalculate`	logical indicating if covers should be recalculated according to the dataset given in data. Keep it `FALSE` if training data are used.

Value

a unified model representation - a `model_unified.object` object

See Also

`gbm.unify` for `GBM` `models`

`xgboost.unify` for `XGBoost` `models`

`ranger.unify` for `ranger` `models`

`randomForest.unify` for `randomForest` `models`

Examples

```
if (requireNamespace("lightgbm", quietly = TRUE) &&
 requireNamespace("jsonlite", quietly = TRUE)) {
  library(lightgbm)
  param_lgbm <- list(objective = "regression", max_depth = 2,
                     force_row_wise = TRUE, num_iterations = 20)
  data_fifa <- fifa20$data[!colnames(fifa20$data) %in%
               c('work_rate', 'value_eur', 'gk_diving', 'gk_handling',
               'gk_kicking', 'gk_reflexes', 'gk_speed', 'gk_positioning')]
  data <- na.omit(cbind(data_fifa, fifa20$target))
  sparse_data <- as.matrix(data[,-ncol(data)])
  x <- lightgbm::lgb.Dataset(sparse_data, label = as.matrix(data[,ncol(data)]))
  lgb_data <- lightgbm::lgb.Dataset.construct(x)
  lgb_model <- lightgbm::lightgbm(data = lgb_data, params = param_lgbm,
                                  verbose = -1, num_threads = 1)
```

```
  unified_model <- lightgbm.unify(lgb_model, sparse_data)
  shaps <- treeshap(unified_model, data[1:2, ])
  plot_contribution(shaps, obs = 1)
}
```

`model_unified.object` *Unified model representation*

Description

`model_unified` object produced by `*.unify` or `unify` function.

Value

List consisting of two elements:

model - A `data.frame` representing model with following columns:

`Tree`	0-indexed ID of a tree
`Node`	0-indexed ID of a node in a tree. In a tree the root always has ID 0
`Feature`	In case of an internal node - name of a feature to split on. Otherwise - NA
`Decision.type`	A factor with two levels: "<" and "<=". In case of an internal node - predicate used for splitting observations. Otherwise - NA
`Split`	For internal nodes threshold used for splitting observations. All observations that satisfy the predicate Decision.type(Split) ('< Split' / '<= Split') are proceeded to the node marked as 'Yes'. Otherwise to the 'No' node. For leaves - NA
`Yes`	Index of a row containing a child Node. Thanks to explicit indicating the row it is much faster to move between nodes
`No`	Index of a row containing a child Node
`Missing`	Index of a row containing a child Node where are proceeded all observations with no value of the dividing feature
`Prediction`	For leaves: Value of prediction in the leaf. For internal nodes: NA
`Cover`	Number of observations seen by the internal node or collected by the leaf for the reference dataset

data - Dataset used as a reference for calculating SHAP values. A dataset passed to the `*.unify`, `unify` or `set_reference_dataset` function with `data` argument. A `data.frame`.

Object has two also attributes set:

`model`	A string. By what package the model was produced.
`missing_support`	A boolean. Whether the model allows missing values to be present in explained dataset.

See Also

`unify`

model_unified_multioutput.object *Unified model representations for multi-output model*

Description

`model_unified_multioutput` object produced by `*.unify` or `unify` function.

Value

List consisting of `model_unified` objects, one for each individual output of a model. For survival models, the list is named using the time points, for which predictions are calculated.

See Also

`unify`

plot_contribution *SHAP value based Break-Down plot*

Description

This function plots contributions of features into the prediction for a single observation.

Usage

```
plot_contribution(
  treeshap,
  obs = 1,
  max_vars = 5,
  min_max = NA,
  digits = 3,
  explain_deviation = FALSE,
  title = "SHAP Break-Down",
  subtitle = ""
)
```

Arguments

`treeshap`	A treeshap object produced with the `treeshap` function. `treeshap.object`.
`obs`	A numeric indicating which observation should be plotted. Be default it's first observation.
`max_vars`	maximum number of variables that shall be presented. Variables with the highest importance will be presented. Remaining variables will be summed into one additional contribution. By default `5`.

min_max	a range of OX axis. By default NA, therefore it will be extracted from the contributions of x. But it can be set to some constants, useful if these plots are to be used for comparisons.
digits	number of decimal places (round) to be used.
explain_deviation	if TRUE then instead of explaining prediction and plotting intercept bar, only deviation from mean prediction of the reference dataset will be explained. By default FALSE.
title	the plot's title, by default 'SHAP Break-Down'.
subtitle	the plot's subtitle. By default no subtitle.

Value

a ggplot2 object

See Also

treeshap for calculation of SHAP values

plot_feature_importance, plot_feature_dependence, plot_interaction

Examples

```
if (requireNamespace("xgboost", quietly = TRUE) &&
 requireNamespace("scales", quietly = TRUE)) {
  library(xgboost)
  data <- fifa20$data[colnames(fifa20$data) != 'work_rate']
  target <- fifa20$target
  xgb_model <- xgboost::xgboost(
   x = as.matrix(data),
   y = target,
   objective = "reg:squarederror",
   max_depth = 3,
   nrounds = 20,
   nthreads = 1
  )
  unified_model <- xgboost.unify(xgb_model, as.matrix(data))
  x <- head(data, 1)
  shap <- treeshap(unified_model, x)
  plot_contribution(shap, 1, min_max = c(-5e5, 1.3e8))
}
```

---

plot_feature_dependence

SHAP value based Feature Dependence plot

Description

Depending on the value of a variable: how does it contribute into the prediction?

Usage

```
plot_feature_dependence(
  treeshap,
  variable,
  title = "Feature Dependence",
  subtitle = NULL
)
```

Arguments

treeshap	A treeshap object produced with the treeshap function. treeshap.object.
variable	name or index of variable for which feature dependence will be plotted.
title	the plot's title, by default 'Feature Dependence'.
subtitle	the plot's subtitle. By default no subtitle.

Value

a ggplot2 object

See Also

treeshap for calculation of SHAP values

plot_contribution, plot_feature_importance, plot_interaction

Examples

```
if (requireNamespace("xgboost", quietly = TRUE) &&
 requireNamespace("scales", quietly = TRUE)) {
  library(xgboost)
  data <- fifa20$data[colnames(fifa20$data) != 'work_rate']
  target <- fifa20$target
  xgb_model <- xgboost::xgboost(
   x = as.matrix(data),
   y = target,
   objective = "reg:squarederror",
   max_depth = 3,
   nrounds = 20,
   nthreads = 1
  )
  unified_model <- xgboost.unify(xgb_model, as.matrix(data))
  x <- head(data, 100)
  shaps <- treeshap(unified_model, x)
  plot_feature_dependence(shaps, variable = "overall")
}
```

plot_feature_importance *SHAP value based Feature Importance plot*

Description

This function plots feature importance calculated as means of absolute values of SHAP values of variables (average impact on model output magnitude).

Usage

```
plot_feature_importance(
  treeshap,
  desc_sorting = TRUE,
  max_vars = ncol(shaps),
  title = "Feature Importance",
  subtitle = NULL
)
```

Arguments

treeshap	A treeshap object produced with the treeshap function. treeshap.object.
desc_sorting	logical. Should the bars be sorted descending? By default TRUE.
max_vars	maximum number of variables that shall be presented. By default all are presented.
title	the plot's title, by default 'Feature Importance'.
subtitle	the plot's subtitle. By default no subtitle.

Value

a ggplot2 object

See Also

treeshap for calculation of SHAP values

plot_contribution, plot_feature_dependence, plot_interaction

Examples

```
if (requireNamespace("xgboost", quietly = TRUE) &&
 requireNamespace("scales", quietly = TRUE)) {
  library(xgboost)
  data <- fifa20$data[colnames(fifa20$data) != 'work_rate']
  target <- fifa20$target
  xgb_model <- xgboost::xgboost(
   x = as.matrix(data),
   y = target,
```

```
  objective = "reg:squarederror",
  max_depth = 3,
  nrounds = 20,
  nthreads = 1
 )
 unified_model <- xgboost.unify(xgb_model, as.matrix(data))
 shaps <- treeshap(unified_model, as.matrix(head(data, 3)))
 plot_feature_importance(shaps, max_vars = 4)
}
```

`plot_interaction` *SHAP Interaction value plot*

Description

This function plots SHAP Interaction value for two variables depending on the value of the first variable. Value of the second variable is marked with the color.

Usage

```
plot_interaction(
  treeshap,
  var1,
  var2,
  title = "SHAP Interaction Value Plot",
  subtitle = ""
)
```

Arguments

`treeshap`	A treeshap object produced with `treeshap(interactions = TRUE)` function. `treeshap.object`.
`var1`	name or index of the first variable - plotted on x axis.
`var2`	name or index of the second variable - marked with color.
`title`	the plot's title, by default `'SHAP Interaction Value Plot'`.
`subtitle`	the plot's subtitle. By default no subtitle.

Value

a `ggplot2` object

See Also

`treeshap` for calculation of SHAP Interaction values

`plot_contribution`, `plot_feature_importance`, `plot_feature_dependence`

Examples

```
if (requireNamespace("xgboost", quietly = TRUE) &&
 requireNamespace("scales", quietly = TRUE)) {
  data <- fifa20$data[colnames(fifa20$data) != 'work_rate']
  target <- fifa20$target
  xgb_model2 <- xgboost::xgboost(
   x = as.matrix(data),
   y = target,
   objective = "reg:squarederror",
   max_depth = 5,
   nrounds = 10,
   nthreads = 1
  )
  unified_model2 <- xgboost.unify(xgb_model2, data)
  inters <- treeshap(unified_model2, as.matrix(data[1:50, ]), interactions = TRUE)
  plot_interaction(inters, "dribbling", "defending")
}
```

`predict.model_unified` *Predict*

Description

Predict using unified_model representation.

Usage

```
## S3 method for class 'model_unified'
predict(object, x, ...)
```

Arguments

`object`	Unified model representation of the model created with a (model).unify function. `model_unified.object`
`x`	Observations to predict. A `data.frame` or `matrix` with the same columns as in the training set of the model.
`...`	other parameters

Value

a vector of predictions.

Examples

```
if (requireNamespace("gbm", quietly = TRUE)) {
  library(gbm)
  data <- fifa20$data[colnames(fifa20$data) != 'work_rate']
  data['value_eur'] <- fifa20$target
  gbm_model <- gbm::gbm(
    formula = value_eur ~ .,
    data = data,
    distribution = "laplace",
    n.trees = 20,
    interaction.depth = 4,
    n.cores = 1
  )
  unified <- gbm.unify(gbm_model, data)
  predict(unified, data[2001:2005, ])
}
```

`print.model_unified` *Prints model_unified objects*

Description

Prints model_unified objects

Usage

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

Arguments

`x`	a model_unified object
`...`	other arguments

Value

No return value, called for printing

print.model_unified_multioutput *Prints model_unified_multioutput objects*

Description

Prints model_unified_multioutput objects

Usage

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

Arguments

x	a model_unified_multioutput object
...	other arguments

Value

No return value, called for printing

print.treeshap *Prints treeshap objects*

Description

Prints treeshap objects

Usage

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

Arguments

x	a treeshap object
...	other arguments

Value

No return value, called for printing

print.treeshap_multioutput *Prints treeshap_multioutput objects*

Description

Prints treeshap_multioutput objects

Usage

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

Arguments

x	a treeshap_multioutput object
...	other arguments

Value

No return value, called for printing

randomForest.unify *Unify randomForest model*

Description

Convert your randomForest model into a standardized representation. The returned representation is easy to be interpreted by the user and ready to be used as an argument in `treeshap()` function.

Usage

```
randomForest.unify(rf_model, data)
```

Arguments

rf_model	An object of `randomForest` class. At the moment, models built on data with categorical features are not supported - please encode them before training.
data	Reference dataset. A `data.frame` or `matrix` with the same columns as in the training set of the model. Usually dataset used to train model.

Details

Binary classification models with a target variable that is a factor with two levels, 0 and 1, are supported

Value

a unified model representation - a model_unified.object object

See Also

lightgbm.unify for LightGBM models

gbm.unify for GBM models

xgboost.unify for XGBoost models

ranger.unify for ranger models

Examples

```
if (requireNamespace("randomForest", quietly = TRUE)) {
  library(randomForest)
  data_fifa <- fifa20$data[
    !colnames(fifa20$data) %in%
      c(
        'work_rate',
        'value_eur',
        'gk_diving',
        'gk_handling',
        'gk_kicking',
        'gk_reflexes',
        'gk_speed',
        'gk_positioning'
      )
  ]
  data <- na.omit(cbind(data_fifa, target = fifa20$target))

  rf <- randomForest::randomForest(
    target ~ .,
    data = data,
    maxnodes = 10,
    ntree = 10
  )
  unified_model <- randomForest.unify(rf, data)
  shaps <- treeshap(unified_model, data[1:2, ])
   # plot_contribution(shaps, obs = 1)
}
```

---

ranger.unify *Unify ranger model*

Description

Convert your ranger model into a standardized representation. The returned representation is easy to be interpreted by the user and ready to be used as an argument in treeshap() function.

Usage

```
ranger.unify(rf_model, data)
```

Arguments

rf_model	An object of ranger class. At the moment, models built on data with categorical features are not supported - please encode them before training.
data	Reference dataset. A data.frame or matrix with the same columns as in the training set of the model. Usually dataset used to train model.

Value

a unified model representation - a model_unified.object object

See Also

lightgbm.unify for LightGBM models

gbm.unify for GBM models

xgboost.unify for XGBoost models

randomForest.unify for randomForest models

Examples

```
if (requireNamespace("ranger", quietly = TRUE)) {
 library(ranger)
 data_fifa <- fifa20$data[!colnames(fifa20$data) %in%
                           c('work_rate', 'value_eur', 'gk_diving', 'gk_handling',
                            'gk_kicking', 'gk_reflexes', 'gk_speed', 'gk_positioning')]
 data <- na.omit(cbind(data_fifa, target = fifa20$target))

 rf <- ranger::ranger(target~., data = data, max.depth = 10, num.trees = 10)
 unified_model <- ranger.unify(rf, data)
 shaps <- treeshap(unified_model, data[1:2,])
 plot_contribution(shaps, obs = 1)
}
```

---

ranger_surv.unify *Unify ranger survival model*

Description

Convert your ranger model into a standardized representation. The returned representation is easy to be interpreted by the user and ready to be used as an argument in treeshap() function.

Usage

```
ranger_surv.unify(
  rf_model,
  data,
  type = c("risk", "survival", "chf"),
  times = NULL
)
```

Arguments

rf_model	An object of ranger class. At the moment, models built on data with categorical features are not supported - please encode them before training.
data	Reference dataset. A data.frame or matrix with the same columns as in the training set of the model. Usually dataset used to train model.
type	A character to define the type of model prediction to use. Either "risk" (default), which uses the risk score calculated as a sum of cumulative hazard function values, "survival", which uses the survival probability at certain time-points for each observation, or "chf", which used the cumulative hazard values at certain time-points for each observation.
times	A numeric vector of unique death times at which the prediction should be evaluated. By default unique.death.times from model are used.

Details

The survival forest implemented in the ranger package stores cumulative hazard functions (CHFs) in the leaves of survival trees, as proposed for Random Survival Forests (Ishwaran et al. 2008). The final model prediction is made by averaging these CHFs from all the trees. To provide explanations in the form of a survival function, the CHFs from the leaves are converted into survival functions (SFs) using the formula SF(t) = exp(-CHF(t)). However, it is important to note that averaging these SFs does not yield the correct model prediction as the model prediction is the average of CHFs transformed in the same way. Therefore, when you obtain explanations based on the survival function, they are only proxies and may not be fully consistent with the model predictions obtained using for example predict function.

Value

For type = "risk" a unified model representation is returned - a model_unified.object object. For type = "survival" or type = "chf" - a model_unified_multioutput.object object is returned, which is a list that contains unified model representation (model_unified.object object) for each time point. In this case, the list names are time points at which the survival function was evaluated.

See Also

ranger.unify for regression and classification ranger models

lightgbm.unify for LightGBM models

gbm.unify for GBM models

xgboost.unify for XGBoost models

randomForest.unify for randomForest models

Examples

```
if (requireNamespace("ranger", quietly = TRUE) &&
 requireNamespace("survival", quietly = TRUE)) {

  library(ranger)
  data_colon <- data.table::data.table(survival::colon)
  data_colon <- na.omit(data_colon[get("etype") == 2, ])
  surv_cols <- c("status", "time", "rx")

  feature_cols <- colnames(data_colon)[3:(ncol(data_colon) - 1)]

  train_x <- model.matrix(
    ~ -1 + .,
    data_colon[, .SD, .SDcols = setdiff(feature_cols, surv_cols[1:2])]
  )
  train_y <- survival::Surv(
    event = (data_colon[, get("status")] |>
               as.character() |>
               as.integer()),
    time = data_colon[, get("time")],
    type = "right"
  )

  rf <- ranger::ranger(
    x = train_x,
    y = train_y,
    data = data_colon,
    max.depth = 10,
    num.trees = 10
  )
  unified_model_risk <- ranger_surv.unify(rf, train_x, type = "risk")
  shaps <- treeshap(unified_model_risk, train_x[1:2,])

  # compute shaps for 3 selected time points
 unified_model_surv <- ranger_surv.unify(rf, train_x, type = "survival", times = c(23  , 50, 73))
  shaps_surv <- treeshap(unified_model_surv, train_x[1:2,])
}
```

---

set_reference_dataset *Set reference dataset*

Description

Change a dataset used as reference for calculating SHAP values. Reference dataset is initially set with data argument in unifying function. Usually reference dataset is dataset used to train the

model. Important property of reference dataset is that SHAP values for each observation add up to its deviation from mean prediction for a reference dataset.

Usage

```
set_reference_dataset(unified_model, x)
```

Arguments

unified_model	Unified model representation of the model created with a (model).unify function. (model_unified.object).
x	Reference dataset. A data.frame or matrix with the same columns as in the training set of the model.

Value

model_unified.object. Unified representation of the model as created with a (model).unify function, but with changed reference dataset (Cover column containing updated values).

See Also

lightgbm.unify for LightGBM models

gbm.unify for GBM models

xgboost.unify for XGBoost models

ranger.unify for ranger models

randomForest.unify for randomForest models

Examples

```
if (requireNamespace("gbm", quietly = TRUE)) {
  library(gbm)
  data <- fifa20$data[colnames(fifa20$data) != 'work_rate']
  data['value_eur'] <- fifa20$target
  gbm_model <- gbm::gbm(
  formula = value_eur ~ .,
    data = data,
    distribution = "laplace",
    n.trees = 20,
    interaction.depth = 4,
    n.cores = 1)
  unified <- gbm.unify(gbm_model, data)
  set_reference_dataset(unified, data[200:700, ])
}
```

theme_drwhy *DrWhy Theme for ggplot objects*

Description

DrWhy Theme for ggplot objects

Usage

```
theme_drwhy()

theme_drwhy_vertical()
```

Value

theme for ggplot2 objects

treeshap *Calculate SHAP values of a tree ensemble model.*

Description

Calculate SHAP values and optionally SHAP Interaction values.

Usage

```
treeshap(unified_model, x, interactions = FALSE, verbose = TRUE)
```

Arguments

unified_model	Unified data.frame representation of the model created with a (model).unify function. A model_unified.object object.
x	Observations to be explained. A data.frame or matrix object with the same columns as in the training set of the model. Keep in mind that objects different than data.frame or plain matrix will cause an error or unpredictable behavior.
interactions	Whether to calculate SHAP interaction values. By default is FALSE. Basic SHAP values are always calculated.
verbose	Whether to print progress bar to the console. Should be logical. Progress bar will not be displayed on Windows.

Value

A treeshap.object object (for single-output models) or treeshap_multioutput.object, which is a list of treeshap.object objects (for multi-output models). SHAP values can be accessed from treeshap.object with $shaps, and interaction values can be accessed with $interactions.

See Also

xgboost.unify for XGBoost models lightgbm.unify for LightGBM models gpboost.unify for GPBoost models gbm.unify for GBM models randomForest.unify for randomForest models ranger.unify for ranger models ranger_surv.unify for ranger survival models

Examples

```
if (requireNamespace("xgboost", quietly = TRUE)) {
  library(xgboost)
  data <- fifa20$data[colnames(fifa20$data) != 'work_rate']
  target <- fifa20$target

  # calculating simple SHAP values
  xgb_model <- xgboost::xgboost(
   x = as.matrix(data),
   y = target,
   objective = "reg:squarederror",
   max_depth = 3,
   nrounds = 20,
   nthreads = 1
  )
  unified_model <- xgboost.unify(xgb_model, as.matrix(data))
  treeshap1 <- treeshap(unified_model, head(data, 3))
  plot_contribution(treeshap1, obs = 1)
  treeshap1$shaps

  # It's possible to calcualte explanation over different part of the data set

  unified_model_rec <- set_reference_dataset(unified_model, data[1:1000, ])
  treeshap_rec <- treeshap(unified_model, head(data, 3))
  plot_contribution(treeshap_rec, obs = 1)

  # calculating SHAP interaction values
  xgb_model2 <- xgboost::xgboost(
   x = as.matrix(data),
   y = target,
   objective = "reg:squarederror",
   max_depth = 7,
   nrounds = 10,
   nthreads = 1
  )
  unified_model2 <- xgboost.unify(xgb_model2, as.matrix(data))
  treeshap2 <- treeshap(unified_model2, head(data, 3), interactions = TRUE)
  treeshap2$interactions
}
```

`treeshap.object` *treeshap results*

Description

`treeshap` object produced by `treeshap` function.

Value

List consisting of four elements:

shaps A `data.frame` with M columns, X rows (M - number of features, X - number of explained observations). Every row corresponds to SHAP values for a observation.

interactions An `array` with dimensions (M, M, X) (M - number of features, X - number of explained observations). Every `[, , i]` slice is a symmetric matrix - SHAP Interaction values for a observation. `[a, b, i]` element is SHAP Interaction value of features `a` and `b` for observation `i`. Is `NULL` if interactions where not calculated (parameter `interactions` set `FALSE`.)

unified_model An object of type `model_unified.object`. Unified representation of a model for which SHAP values were calculated. It is used by some of the plotting functions.

observations Explained dataset. `data.frame` or `matrix`. It is used by some of the plotting functions.

See Also

`treeshap`,

`plot_contribution`, `plot_feature_importance`, `plot_feature_dependence`, `plot_interaction`

---

treeshap_multioutput.object

treeshap results for multi-output model

Description

`treeshap_multioutput` object produced by `treeshap` function.

Value

List consisting of `treeshap` objects, one for each individual output of a model. For survival models, the list is named using the time points, for which TreeSHAP values are calculated.

See Also

`treeshap`,

`treeshap.object`

`unify` *Unify tree-based model*

Description

Convert your tree-based model into a standardized representation. The returned representation is easy to be interpreted by the user and ready to be used as an argument in `treeshap()` function.

Usage

```
unify(model, data, ...)
```

Arguments

`model`	A tree-based model object of any supported class (`gbm`, `lgb.Booster`, `randomForest`, `ranger`, or `xgb.Booster`).
`data`	Reference dataset. A `data.frame` or `matrix` with the same columns as in the training set of the model. Usually dataset used to train model.
`...`	Additional parameters passed to the model-specific unification functions.

Value

A unified model representation - a `model_unified.object` object (for single-output models) or `model_unified_multioutput.object`, which is a list of `model_unified.object` objects (for multi-output models).

See Also

`lightgbm.unify` for `LightGBM` `models`

`gpboost.unify` for `GPBoost` `models`

`gbm.unify` for `GBM` `models`

`xgboost.unify` for `XGBoost` `models`

`ranger.unify` for `ranger` `models`

`randomForest.unify` for `randomForest` `models`

Examples

```
if (
  requireNamespace("ranger", quietly = TRUE) &&
    requireNamespace("randomForest", quietly = TRUE)
) {
  library(ranger)
  data_fifa <- fifa20$data[
    !colnames(fifa20$data) %in%
      c(
        'work_rate',
```

```
          'value_eur',
          'gk_diving',
          'gk_handling',
          'gk_kicking',
          'gk_reflexes',
          'gk_speed',
          'gk_positioning'
        )
    ]
    data <- na.omit(cbind(data_fifa, target = fifa20$target))

    rf1 <- ranger::ranger(target ~ ., data = data, max.depth = 10, num.trees = 10)
    unified_model1 <- unify(rf1, data)
    shaps1 <- treeshap(unified_model1, data[1:2, ])
    plot_contribution(shaps1, obs = 1)

    rf2 <- randomForest::randomForest(
      target ~ .,
      data = data,
      maxnodes = 10,
      ntree = 10
    )
    unified_model2 <- unify(rf2, data)
    shaps2 <- treeshap(unified_model2, data[1:2, ])
    plot_contribution(shaps2, obs = 1)
  }
```

`xgboost.unify` *Unify XGBoost model*

Description

Convert your XGBoost model into a standardized representation. The returned representation is easy to be interpreted by the user and ready to be used as an argument in `treeshap()` function.

Usage

```
xgboost.unify(xgb_model, data, recalculate = FALSE)
```

Arguments

`xgb_model`	A XGBoost model - object of class `xgb.Booster`
`data`	Reference dataset. A `data.frame` or `matrix` with the same columns as in the training set of the model. Usually dataset used to train model.
`recalculate`	logical indicating if covers should be recalculated according to the dataset given in data. Keep it `FALSE` if training data are used.

Value

a unified model representation - a model_unified.object object

See Also

lightgbm.unify for LightGBM models

gbm.unify for GBM models

ranger.unify for ranger models

randomForest.unify for randomForest models

Examples

```
if (requireNamespace("xgboost", quietly = TRUE)) {
  library(xgboost)
  data <- fifa20$data[colnames(fifa20$data) != 'work_rate']
  target <- fifa20$target
  xgb_model <- xgboost::xgboost(
   x = as.matrix(data),
   y = target,
   objective = "reg:squarederror",
   max_depth = 3,
   nrounds = 20,
   nthreads = 1
  )
  unified_model <- xgboost.unify(xgb_model, as.matrix(data))
  shaps <- treeshap(unified_model, data[1:2,])
  plot_contribution(shaps, obs = 1)
}
```

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