Package ‘DALEX’

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Title  moDel Agnostic Language for Exploration and eXplanation

Version  2.3.0

Description  Unverified black box model is the path to the failure. Opaqueness leads to distrust. Distrust leads to ignorance. Ignorance leads to rejection. DALEX package xrays any model and helps to explore and explain its behaviour. Machine Learning (ML) models are widely used and have various applications in classification or regression. Models created with boosting, bagging, stacking or similar techniques are often used due to their high performance. But such black-box models usually lack of direct interpretability. DALEX package contains various methods that help to understand the link between input variables and model output. Implemented methods help to explore model on the level of a single instance as well as a level of the whole dataset. All model explainers are model agnostic and can be compared across different models. DALEX package is the cornerstone for ‘DrWhy.AI’ universe of packages for visual model exploration. Find more details in (Biecek 2018) <arXiv:1806.08915>.

License  GPL

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RoxygenNote  7.1.1

Depends  R (>= 3.5)

Imports  ggplot2, iBreakDown (>= 1.3.1), ingredients (>= 2.0)

Suggests  gower, ranger, testthat, methods


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

NeedsCompilation  no

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apartments

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apartments | Apartments Data

**Description**

Datasets apartments and apartments_test are artificial, generated from the same model. Structure of the dataset is copied from real dataset from PBImisc package, but they were generated in a way to mimic effect of Anscombe quartet for complex black box models.

**Usage**

```r
data(apartments)
```

**Format**

a data frame with 1000 rows and 6 columns

**Details**

- `m2.price` - price per square meter
- `surface` - apartment area in square meters
- `n.rooms` - number of rooms (correlated with surface)
- `district` - district in which apartment is located, factor with 10 levels
- `floor` - floor
- `construction.date` - construction year

---

**colors_discrete_drwhy**  DrWhy color palettes for ggplot objects

**Description**

DrWhy color palettes for ggplot objects

**Usage**

```r
colors_discrete_drwhy(n = 2)
colors_diverging_drwhy()
colors_breakdown_drwhy()
```

**Arguments**

- `n` number of colors for color palette
Value

color palette as vector of characters

---

dragons

<table>
<thead>
<tr>
<th>dragons</th>
<th>Dragon Data</th>
</tr>
</thead>
</table>

Description

Datasets dragons and dragons_test are artificial, generated from the same ground truth model, but with sometimes different data distribution.

Usage

data(dragons)

Format

a data frame with 2000 rows and 8 columns

Details

Values are generated in a way to:
- have nonlinearity in year_of_birth and height
- have concept drift in the test set

- year_of_birth - year in which the dragon was born. Negative year means year BC, e.g.: -1200 = 1201 BC
- year_of_discovery - year in which the dragon was found.
- height - height of the dragon in yards.
- weight - weight of the dragon in tons.
- scars - number of scars.
- colour - colour of the dragon.
- number_of_lost_teeth - number of teeth that the dragon lost.
- life_length - life length of the dragon.
explain.default

Create Model Explainer

Description

Black-box models may have very different structures. This function creates a unified representation of a model, which can be further processed by functions for explanations.

Usage

```r
explain.default(
  model,
  data = NULL,
  y = NULL,
  predict_function = NULL,
  predict_function_target_column = NULL,
  residual_function = NULL,
  weights = NULL,
  ..., 
  label = NULL,
  verbose = TRUE,
  precalculate = TRUE,
  colorize = TRUE,
  model_info = NULL,
  type = NULL
)
```

```r
explain(
  model,
  data = NULL,
  y = NULL,
  predict_function = NULL,
  predict_function_target_column = NULL,
  residual_function = NULL,
  weights = NULL,
  ..., 
  label = NULL,
  verbose = TRUE,
  precalculate = TRUE,
  colorize = TRUE,
  model_info = NULL,
  type = NULL
)
```

Arguments

- `model` object - a model to be explained
data  
data.frame or matrix - data which will be used to calculate the explanations. If not provided then will be extracted from the model. Data should be passed without target column (this shall be provided as the y argument). NOTE: If target variable is present in the data, some of the functionalities may not work properly.

y  
numeric vector with outputs / scores. If provided then it shall have the same size as data

predict_function  
function that takes two arguments: model and new data and returns numeric vector with predictions. By default it is yhat.

predict_function_target_column  
Character or numeric containing either column name or column number in the model prediction object of the class that should be considered as positive (ie. the class that is associated with probability 1). If NULL, the second column of the output will be taken for binary classification. For a multiclass classification setting that parameter cause switch to binary classification mode with 1 vs others probabilities.

residual_function  
function that takes four arguments: model, data, target vector y and predict function (optionally). It should return a numeric vector with model residuals for given data. If not provided, response residuals \((y - \hat{y})\) are calculated. By default it is residual_function_default.

weights  
numeric vector with sampling weights. By default it’s NULL. If provided then it shall have the same length as data

...  
other parameters

label  
character - the name of the model. By default it’s extracted from the ‘class’ attribute of the model

verbose  
logical. If TRUE (default) then diagnostic messages will be printed

precalculate  
logical. If TRUE (default) then predicted_values and residual are calculated when explainer is created. This will happen also if verbose is TRUE. Set both verbose and precalculate to FALSE to omit calculations.

colorize  
logical. If TRUE (default) then WARNINGS, ERRORS and NOTES are colorized. Will work only in the R console.

model_info  
a named list (package, version, type) containing information about model. If NULL, DALEX will seek for information on it’s own.

type  
type of a model, either classification or regression. If not specified then type will be extracted from model_info.

Details

Please NOTE, that the model is the only required argument. But some explanations may expect that other arguments will be provided too.
Value

An object of the class explainer. It’s a list with following fields:

- `model` the explained model.
- `data` the dataset used for training.
- `y` response for observations from `data`.
- `weights` sample weights for data. NULL if weights are not specified.
- `y_hat` calculated predictions.
- `residuals` calculated residuals.
- `predict_function` function that may be used for model predictions, shall return a single numerical value for each observation.
- `residual_function` function that returns residuals, shall return a single numerical value for each observation.
- `class` class/classes of a model.
- `label` label of explainer.
- `model_info` named list containing basic information about model, like package, version of package and type.

References


Examples

```r
# simple explainer for regression problem
aps_lm_model4 <- lm(m2.price ~ ., data = apartments)
aps_lm_explainer4 <- explain(aps_lm_model4, data = apartments, label = "model_4v")
aps_lm_explainer4

# various parameters for the explain function
# all defaults
aps_lm <- explain(aps_lm_model4)

# silent execution
aps_lm <- explain(aps_lm_model4, verbose = FALSE)

# set target variable
aps_lm <- explain(aps_lm_model4, data = apartments, label = "model_4v", y = apartments$m2.price)
aps_lm <- explain(aps_lm_model4, data = apartments, label = "model_4v", y = apartments$m2.price, predict_function = predict)

# user provided predict_function
aps_ranger <- ranger::ranger(m2.price ~ ., data = apartments, num.trees = 50)
custom_predict <- function(X.model, newdata) {
```


```r
predict(X.model, newdata)$predictions
}
aps_ranger_exp <- explain(aps_ranger, data = apartments, y = apartments$m2.price,
  predict_function = custom_predict)

# user provided residual_function
aps_ranger <- ranger::ranger(m2.price ~ ., data = apartments, num.trees = 50)
custom_residual <- function(X.model, newdata, y, predict_function) {
  abs(y - predict_function(X.model, newdata))
}
aps_ranger_exp <- explain(aps_ranger, data = apartments,
  y = apartments$m2.price,
  residual_function = custom_residual)

# binary classification
titanic_ranger <- ranger::ranger(as.factor(survived) ~ ., data = titanic_imputed, num.trees = 50,
  probability = TRUE)
# keep in mind that for binary classification y parameter has to be numeric with 0 and 1 values
titanic_ranger_exp <- explain(titanic_ranger, data = titanic_imputed, y = titanic_imputed$survived)

# multiclass task
hr_ranger <- ranger::ranger(status ~ ., data = HR, num.trees = 50, probability = TRUE)
# keep in mind that for multiclass y parameter has to be a factor,
# with same levels as in training data
hr_ranger_exp <- explain(hr_ranger, data = HR, y = HR$status)

# set model_info
model_info <- list(package = "stats", ver = "3.6.2", type = "regression")
aps_lm_model4 <- lm(m2.price ~ ., data = apartments)
aps_lm_explainer4 <- explain(aps_lm_model4, data = apartments, label = "model_4v",
  model_info = model_info)

# simple function
aps_fun <- function(x) 58*x$surface
aps_fun_explainer <- explain(aps_fun, data = apartments, y = apartments$m2.price, label="sfun")
model_performance(aps_fun_explainer)

# set model_info
model_info <- list(package = "stats", ver = "3.6.2", type = "regression")
aps_lm_model4 <- lm(m2.price ~ ., data = apartments)
aps_lm_explainer4 <- explain(aps_lm_model4, data = apartments, label = "model_4v",
  model_info = model_info)
aps_lm_explainer4 <- explain(aps_lm_model4, data = apartments, label = "model_4v",
  weights = as.numeric(apartments$construction.year > 2000))

# more complex model
library("ranger")
aps_ranger_model4 <- ranger(m2.price ~ ., data = apartments, num.trees = 50)
aps_ranger_explainer4 <- explain(aps_ranger_model4, data = apartments, label = "model_ranger")
aps_ranger_explainer4
```
**FIFA 20 preprocessed data**

**Description**

The `fifa` dataset is a preprocessed `players_20.csv` dataset which comes as a part of "FIFA 20 complete player dataset" at Kaggle.

**Usage**

```r
data(fifa)
```

**Format**

A data frame with 5000 rows, 42 columns and rownames.

**Details**

It contains 5000 'overall' best players and 43 variables. These are:

- `short_name` (rownames)
- `nationality` of the player (not used in modeling)
- `overall`, `potential`, `value_eur`, `wage_eur` (4 potential target variables)
- `age`, `height`, `weight`, `attacking skills`, `defending skills`, `goalkeeping skills` (37 variables)

It is advised to leave only one target variable for modeling.

**Source:** [https://www.kaggle.com/stefanoleone992/fifa-20-complete-player-dataset](https://www.kaggle.com/stefanoleone992/fifa-20-complete-player-dataset)

All transformations:

1. Take 43 columns: `[3, 5, 7:9, 11:14, 45:78]` (R indexing)
2. Take rows with `value_eur > 0`
3. Convert `short_name` to ASCII
4. Remove rows with duplicated `short_name` (keep first)
5. Sort rows on `overall` and take top 5000
6. Set `short_name` column as rownames
7. Transform `nationality` to factor
8. Reorder columns

**Source**

The `players_20.csv` dataset was downloaded from the Kaggle site and went through few transformations. The complete dataset was obtained from [https://www.kaggle.com/stefanoleone992/fifa-20-complete-player-dataset#players_20.csv](https://www.kaggle.com/stefanoleone992/fifa-20-complete-player-dataset#players_20.csv) on January 1, 2020.
**HR**

*Human Resources Data*

**Description**

Datasets HR and HR_test are artificial, generated from the same model. Structure of the dataset is based on a real data, from Human Resources department with information which employees were promoted, which were fired.

**Usage**

```r
data(HR)
```

**Format**

a data frame with 10000 rows and 6 columns

**Details**

Values are generated in a way to:
- have interaction between age and gender for the 'fired' variable
- have non monotonic relation for the salary variable
- have linear effects for hours and evaluation.

- gender - gender of an employee.
- age - age of an employee in the moment of evaluation.
- hours - average number of working hours per week.
- evaluation - evaluation in the scale 2 (bad) - 5 (very good).
- salary - level of salary in the scale 0 (lowest) - 5 (highest).
- status - target variable, either 'fired' or 'promoted' or 'ok'.

**install_dependencies**

*Install all dependencies for the DALEX package*

**Description**

By default 'heavy' dependencies are not installed along DALEX. This function silently install all required packages.

**Usage**

```r
install_dependencies(packages = c("ingredients", "iBreakDown", "ggpubr"))
```

**Arguments**

- `packages` which packages shall be installed?
**loss_cross_entropy**  
*Calculate Loss Functions*

**Description**
Calculate Loss Functions

**Usage**

```r
loss_cross_entropy(observed, predicted, p_min = 1e-04, na.rm = TRUE)
loss_sum_of_squares(observed, predicted, na.rm = TRUE)
loss_root_mean_square(observed, predicted, na.rm = TRUE)
loss_accuracy(observed, predicted, na.rm = TRUE)
loss_one_minus_auc(observed, predicted)
loss_default(x)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>observed</td>
<td>observed scores or labels, these are supplied as explainer specific y</td>
</tr>
<tr>
<td>predicted</td>
<td>predicted scores, either vector of matrix, these are returned from the model specific predict_function()</td>
</tr>
<tr>
<td>p_min</td>
<td>for cross entropy, minimal value for probability to make sure that log will not explode</td>
</tr>
<tr>
<td>na.rm</td>
<td>logical, should missing values be removed?</td>
</tr>
<tr>
<td>x</td>
<td>either an explainer or type of the model. One of &quot;regression&quot;, &quot;classification&quot;, &quot;multiclass&quot;.</td>
</tr>
</tbody>
</table>

**Value**

numeric - value of the loss function

**Examples**

```r
library("ranger")
titanic_ranger_model <- ranger(survived~., data = titanic_imputed, num.trees = 50, probability = TRUE)
loss_one_minus_auc(titanic_imputed$survived, yhat(titanic_ranger_model, titanic_imputed))

HR_ranger_model_multi <- ranger(status~., data = HR, num.trees = 50, probability = TRUE)
loss_cross_entropy(as.numeric(HR$status), yhat(HR_ranger_model_multi, HR))
```
model_diagnostics  

Dataset Level Model Diagnostics

Description

This function performs model diagnostic of residuals. Residuals are calculated and plotted against predictions, true y values or selected variables. Find information how to use this function here: https://ema.drwhy.ai/residualDiagnostic.html.

Usage

model_diagnostics(explainer, variables = NULL, ...)

Arguments

explainer a model to be explained, preprocessed by the explain function
variables character - name of variables to be explained. Default NULL stands for all variables
... other parameters

Value

An object of the class model_diagnostics. It's a data frame with residuals and selected variables.

References


Examples

library(DALEX)
apartments_lm_model <- lm(m2.price ~ ., data = apartments)
explainer_lm <- explain(apartments_lm_model,
data = apartments,
y = apartments$m2.price)
diag_lm <- model_diagnostics(explainer_lm)
diag_lm
plot(diag_lm)

library("ranger")
apartments_ranger_model <- ranger(m2.price ~ ., data = apartments)
explainer_ranger <- explain(apartments_ranger_model,
data = apartments,
y = apartments$m2.price)
diag_ranger <- model_diagnostics(explainer_ranger)
diag_ranger
plot(diag_ranger)
model_info

plot(diag_ranger, diag_lm)
plot(diag_ranger, diag_lm, variable = "y")
plot(diag_ranger, diag_lm, variable = "construction.year")
plot(diag_ranger, variable = "y", yvariable = "y_hat")
plot(diag_ranger, variable = "y", yvariable = "abs_residuals")
plot(diag_ranger, variable = "ids")

---

model_info

Extract info from model

Description

This generic function lets users extract base information about a model. The function returns a named list of class model_info that contains information about the package of the model, version, and task type. For wrappers like mlr or caret, both package and wrapper information is stored.

Usage

model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'lm'
model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'randomForest'
model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'svm'
model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'glm'
model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'lrm'
model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'glmnet'
model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'cv.glmnet'
model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'ranger'
model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'gbm'
model_info(model, is_multiclass = FALSE, ...)
## S3 method for class 'model_fit'
model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'train'
model_info(model, is_multiclass = FALSE, ...)

## S3 method for class 'rpart'
model_info(model, is_multiclass = FALSE, ...)

## Default S3 method:
model_info(model, is_multiclass = FALSE, ...)

### Arguments

- `model`: model object
- `is_multiclass`: if TRUE and task is classification, then multitask classification is set. Else is omitted. If `model_info` was executed within explain function, DALEX will recognize subtype on its own.
- `...`: another arguments

Currently supported packages are:

- `class cv.glmnet` and `glmnet` - models created with `glmnet` package
- `class glm` - generalized linear models
- `class lrm` - models created with `rms` package
- `class model_fit` - models created with `parsnip` package
- `class lm` - linear models created with `stats::lm`
- `class ranger` - models created with `ranger` package
- `class randomForest` - random forest models created with `randomForest` package
- `class svm` - support vector machines models created with the `e1071` package
- `class train` - models created with `caret` package
- `class gbm` - models created with `gbm` package

### Value

A named list of class `model_info`

### Examples

```r
aps_lm_model4 <- lm(m2.price ~., data = apartments)
model_info(aps_lm_model4)
```

```r
library("ranger")
model_regr_rf <- ranger::ranger(status~., data = HR, num.trees = 50, probability = TRUE)
model_info(model_regr_rf, is_multiclass = TRUE)
```
### Description

From DALEX version 1.0 this function calls the `feature_importance` Find information how to use this function here: [https://ema.drwhy.ai/featureImportance.html](https://ema.drwhy.ai/featureImportance.html).

### Usage

```r
model_parts(
  explainer,
  loss_function = loss_default(explainer$model_info$type),
  ..., 
  type = "variable_importance",
  N = n_sample,
  n_sample = 1000
)
```

### Arguments

- **explainer**: a model to be explained, preprocessed by the `explain` function
- **loss_function**: a function that will be used to assess variable importance. By default it is 1-AUC for classification, cross entropy for multilabel classification and RMSE for regression. Custom, user-made loss function should accept two obligatory parameters (observed, predicted), where observed states for actual values of the target, while predicted for predicted values. If attribute "loss_accuracy" is associated with function object, then it will be plotted as name of the loss function.
- **...**: other parameters
- **type**: character, type of transformation that should be applied for dropout loss. `variable_importance` and `raw_results` raw drop losses, ratio returns `drop_loss/drop_loss_full_model` while difference returns `drop_loss - drop_loss_full_model`
- **N**: number of observations that should be sampled for calculation of variable importance. If NULL then variable importance will be calculated on whole dataset (no sampling).
- **n_sample**: alias for `N` held for backwards compatibility. number of observations that should be sampled for calculation of variable importance.

### Value

An object of the class `feature_importance`. It’s a data frame with calculated average response.
References


Examples

# regression
library("ranger")
apartments_ranger_model <- ranger(m2.price~., data = apartments, num.trees = 50)
explainer_ranger <- explain(apartments_ranger_model, data = apartments[-1], 
y = apartments$m2.price, label = "Ranger Apartments")
model_parts_ranger_aps <- model_parts(explainer_ranger, type = "raw")
head(model_parts_ranger_aps, 8)
plot(model_parts_ranger_aps)

# binary classification
titanic_glm_model <- glm(survived~., data = titanic_imputed, family = "binomial")
explainer_glm_titanic <- explain(titanic_glm_model, data = titanic_imputed[-8], 
y = titanic_imputed$survived)
logit <- function(x) exp(x)/(1+exp(x))
custom_loss <- function(observed, predicted){
  sum((observed - logit(predicted))^2)
}
attr(custom_loss, "loss_name") <- "Logit residuals"
model_parts_glm_titanic <- model_parts(explainer_glm_titanic, type = "raw", 
  loss_function = custom_loss)
head(model_parts_glm_titanic, 8)
plot(model_parts_glm_titanic)

# multilabel classification
HR_ranger_model_HR <- ranger(status~., data = HR, num.trees = 50, 
  probability = TRUE)
explainer_ranger_HR <- explain(HR_ranger_model_HR, data = HR[-6], 
y = HR$status, label = "Ranger HR")
model_parts_ranger_HR <- model_parts(explainer_ranger_HR, type = "raw")
head(model_parts_ranger_HR, 8)
plot(model_parts_ranger_HR)
**model_performance**

**Description**

Function `model_performance()` calculates various performance measures for classification and regression models. For classification models following measures are calculated: F1, accuracy, recall, precision and AUC. For regression models following measures are calculated: mean squared error, R squared, median absolute deviation.

**Usage**

```r
model_performance(explainer, ..., cutoff = 0.5)
```

**Arguments**

- **explainer** a model to be explained, preprocessed by the `explain` function
- **...** other parameters
- **cutoff** a cutoff for classification models, needed for measures like recall, precision, ACC, F1. By default 0.5.

**Value**

An object of the class `model_performance`.

It's a list with following fields:

- **residuals** - data frame that contains residuals for each observation
- **measures** - list with calculated measures that are dedicated for the task, whether it is regression, binary classification or multiclass classification.
- **type** - character that specifies type of the task.

**References**


**Examples**

```r
# regression
library("ranger")
apartments_ranger_model <- ranger(m2.price~., data = apartments, num.trees = 50)
explainer_ranger_apartments <- explain(apartments_ranger_model, data = apartments[,-1], y = apartments$m2.price, label = "Ranger Apartments")
model_performance_ranger_aps <- model_performance(explainer_ranger_apartments)
plot(model_performance_ranger_aps)
plot(model_performance_ranger_aps, geom = "boxplot")
plot(model_performance_ranger_aps, geom = "histogram")

# binary classification
```
titanic_glm_model <- glm(survived~., data = titanic_imputed, family = "binomial")
explainer_glm_titanic <- explain(titanic_glm_model, data = titanic_imputed[, -8],
y = titanic_imputed$survived)
model_performance_glm_titanic <- model_performance(explainer_glm_titanic)
plot(model_performance_glm_titanic)
plot(model_performance_glm_titanic, geom = "boxplot")
plot(model_performance_glm_titanic, geom = "histogram")

# multilabel classification
HR_ranger_model <- ranger(status~., data = HR, num.trees = 50,
  probability = TRUE)
explainer_ranger_HR <- explain(HR_ranger_model, data = HR[, -6],
y = HR$status, label = "Ranger HR")
model_performance_ranger_HR <- model_performance(explainer_ranger_HR)
plot(model_performance_ranger_HR)
plot(model_performance_ranger_HR, geom = "boxplot")
plot(model_performance_ranger_HR, geom = "histogram")

---

**model_profile**  
*Dataset Level Variable Profile as Partial Dependence or Accumulated Local Dependence Explanations*

**Description**

This function calculates explanations on a dataset level set that explore model response as a function of selected variables. The explanations can be calculated as Partial Dependence Profile or Accumulated Local Dependence Profile. Find information how to use this function here: [https://ema.drwhy.ai/partialDependenceProfiles.html](https://ema.drwhy.ai/partialDependenceProfiles.html). The variable_profile function is a copy of model_profile.

**Usage**

```r
model_profile(  
  explainer,  
  variables = NULL,  
  N = 100,  
  ...,  
  groups = NULL,  
  k = NULL,  
  center = TRUE,  
  type = "partial")
```
variable_profile(
  explainer,
  variables = NULL,
  N = 100,
  ..., 
  groups = NULL,
  k = NULL,
  center = TRUE,
  type = "partial"
)

single_variable(explainer, variable, type = "pdp", ...)

Arguments

explainer a model to be explained, preprocessed by the explain function
variables character - names of variables to be explained
N number of observations used for calculation of aggregated profiles. By default 100. Use NULL to use all observations.
... other parameters that will be passed to ingredients::aggregate_profiles
groups a variable name that will be used for grouping. By default NULL which means that no groups shall be calculated
k number of clusters for the hclust function (for clustered profiles)
center shall profiles be centered before clustering
type the type of variable profile. Either partial, conditional or accumulated.
variable deprecated, use variables instead

Details

Underneath this function calls the partial_dependence or accumulated_dependence functions from the ingredients package.

Value

An object of the class model_profile. It’s a data frame with calculated average model responses.

References


Examples

titanic_glm_model <- glm(survived~., data = titanic_imputed, family = "binomial")
explainer_glm <- explain(titanic_glm_model, data = titanic_imputed)
model_profile_glm_fare <- model_profile(explainer_glm, "fare")
plot(model_profile_glm_fare)
library("ranger")
titanic_ranger_model <- ranger(survived~., data = titanic_imputed, num.trees = 50,
    probability = TRUE)
explainer_ranger <- explain(titanic_ranger_model, data = titanic_imputed)
model_profile_ranger <- model_profile(explainer_ranger)
plot(model_profile_ranger, geom = "profiles")

model_profile_ranger_1 <- model_profile(explainer_ranger, type = "partial",
    variables = c("age", "fare"))
plot(model_profile_ranger_1, variables = c("age", "fare"), geom = "points")

model_profile_ranger_2 <- model_profile(explainer_ranger, type = "partial", k = 3)
plot(model_profile_ranger_2, geom = "profiles")

model_profile_ranger_3 <- model_profile(explainer_ranger, type = "partial", groups = "gender")
plot(model_profile_ranger_3, geom = "profiles")

model_profile_ranger_4 <- model_profile(explainer_ranger, type = "accumulated")
plot(model_profile_ranger_4, geom = "profiles")

# Multiple profiles
model_profile_ranger_fare <- model_profile(explainer_ranger, "fare")
plot(model_profile_ranger_fare, model_profile_glm_fare)

plot.list

Plot List of Explanations

Description

Plot List of Explanations

Usage

## S3 method for class 'list'
plot(x, ...)

Arguments

  x      a list of explanations of the same class
  ...    other parameters

Value

An object of the class ggplot.
Examples

library("ranger")
titanic_ranger_model <- ranger(survived~., data = titanic_imputed, num.trees = 50,
   probability = TRUE)
explainer_ranger <- explain(titanic_ranger_model, data = titanic_imputed[,-8],
   y = titanic_imputed$survived)
mp_ranger <- model_performance(explainer_ranger)

explainer_ranger2 <- explain(titanic_ranger_model2, data = titanic_imputed[,-8],
   y = titanic_imputed$survived,
   label = "ranger2")
mp_ranger2 <- model_performance(explainer_ranger2)

plot(list(mp_ranger, mp_ranger2), geom = "prc")
plot(list(mp_ranger, mp_ranger2), geom = "roc")
tmp <- list(mp_ranger, mp_ranger2)
names(tmp) <- c("ranger", "ranger2")
plot(tmp)

plot.model_diagnostics

Plot Dataset Level Model Diagnostics

Description

Plot Dataset Level Model Diagnostics

Usage

## S3 method for class 'model_diagnostics'
plot(x, ..., variable = "y_hat", yvariable = "residuals", smooth = TRUE)

Arguments

x a data.frame to be explained, preprocessed by the model_diagnostics function
...
variable character - name of the variable on OX axis to be explained, by default y_hat
yvariable character - name of the variable on OY axis, by default residuals
smooth logical shall the smooth line be added

Value

an object of the class model_diagnostics_explainer.
Examples

```r
apartments_lm_model <- lm(m2.price ~ ., data = apartments)
explainer_lm <- explain(apartments_lm_model,
data = apartments,
y = apartments$m2.price)
diag_lm <- model_diagnostics(explainer_lm)
diag_lm
plot(diag_lm)

library("ranger")
apartments_ranger_model <- ranger(m2.price ~ ., data = apartments)
explainer_ranger <- explain(apartments_ranger_model,
data = apartments,
y = apartments$m2.price)
diag_ranger <- model_diagnostics(explainer_ranger)
diag_ranger
plot(diag_ranger)
plot(diag_ranger, diag_lm)
plot(diag_ranger, diag_lm, variable = "y")
plot(diag_ranger, diag_lm, variable = "construction.year")
plot(diag_ranger, variable = "y", yvariable = "y_hat")
```

---

**plot.model_parts**

*Plot Variable Importance Explanations*

**Description**

Plot Variable Importance Explanations

**Usage**

```r
## S3 method for class 'model_parts'
plot(x, ...)
```

**Arguments**

- `x` an object of the class `model_parts`
- `...` other parameters described below

**Value**

An object of the class `ggplot`. 
Plot options

**variable_importance:**
- `max_vars` maximal number of features to be included in the plot. default value is 10
- `show_boxplots` logical if TRUE (default) boxplot will be plotted to show permutation data.
- `bar_width` width of bars. By default 10
- `desc_sorting` logical. Should the bars be sorted descending? By default TRUE
- `title` the plot’s title, by default 'Feature Importance'
- `subtitle` a character. Plot subtitle. By default NULL - then subtitle is set to "created for the XXX, YYY model", where XXX, YYY are labels of given explainers.

---

plot.model_performance

*Plot Dataset Level Model Performance Explanations*

**Description**

Plot Dataset Level Model Performance Explanations

**Usage**

```r
## S3 method for class 'model_performance'
plot(
x,
..., geom = "ecdf",
show_outliers = 0,
ptlabel = "name",
lossFunction = loss_function,
loss_function = function(x) sqrt(mean(x^2))
)
```

**Arguments**

- `x` a model to be explained, preprocessed by the `explain` function
- `...` other parameters
- `geom` either "prc", "roc", "ecdf", "boxplot", "gain", "lift" or "histogram" determines how residuals shall be summarized
- `show_outliers` number of largest residuals to be presented (only when `geom = boxplot`).
- `ptlabel` either "name" or "index" determines the naming convention of the outliers
- `lossFunction` alias for `loss_function` held for backwards compatibility.
- `loss_function` function that calculates the loss for a model based on model residuals. By default it’s the root mean square. NOTE that this argument was called `lossFunction`. 
Value

An object of the class model_performance.

Examples

```r
library("ranger")
titanic_ranger_model <- ranger(survived~., data = titanic_imputed, num.trees = 50,
   probability = TRUE)
explainer_ranger <- explain(titanic_ranger_model, data = titanic_imputed[,\-8],
   y = titanic_imputed$survived)
mp_ranger <- model_performance(explainer_ranger)
plot(mp_ranger)
plot(mp_ranger, geom = "boxplot", show_outliers = 1)

mp_ranger2 <- model_performance(explainer_ranger2)
plot(mp_ranger, mp_ranger2, geom = "prc")
plot(mp_ranger, mp_ranger2, geom = "roc")
plot(mp_ranger, mp_ranger2, geom = "lift")
plot(mp_ranger, mp_ranger2, geom = "gain")
plot(mp_ranger, mp_ranger2, geom = "boxplot")
plot(mp_ranger, mp_ranger2, geom = "histogram")
plot(mp_ranger, mp_ranger2, geom = "ecdf")

mp_glm <- model_performance(explainer_glm)
plot(mp_glm)

mp_lm <- model_performance(explainer_lm)
plot(mp_lm)
```
Description

Plot Dataset Level Model Profile Explanations

Usage

```r
## S3 method for class 'model_profile'
plot(x, ..., geom = "aggregates")
```

Arguments

- `x`: a variable profile explanation, created with the `model_profile` function
- `...`: other parameters
- `geom`: either "aggregates", "profiles", "points" determines which will be plotted

Value

An object of the class ggplot.

Examples

```r
titanic_glm_model <- glm(survived~., data = titanic_imputed, family = "binomial")
explainer_glm <- explain(titanic_glm_model, data = titanic_imputed)
expl_glm <- model_profile(explainer_glm, "fare")
plot(expl_glm)

library("ranger")
titanic_ranger_model <- ranger(survived~., data = titanic_imputed, num.trees = 50,
probability = TRUE)
explainer_ranger <- explain(titanic_ranger_model, data = titanic_imputed)
expl_ranger <- model_profile(explainer_ranger)
plot(expl_ranger)
plot(expl_ranger, geom = "aggregates")

vp_ra <- model_profile(explainer_ranger, type = "partial", variables = c("age", "fare"))
plot(vp_ra, variables = c("age", "fare"), geom = "points")

vp_ra <- model_profile(explainer_ranger, type = "partial", k = 3)
plot(vp_ra)
```
plot(vp_ra, geom = "profiles")
plot(vp_ra, geom = "points")

vp_ra <- model_profile(explainer_ranger, type = "partial", groups = "gender")
plot(vp_ra)
plot(vp_ra, geom = "profiles")
plot(vp_ra, geom = "points")

vp_ra <- model_profile(explainer_ranger, type = "accumulated")
plot(vp_ra)
plot(vp_ra, geom = "profiles")
plot(vp_ra, geom = "points")

---

plot.predict_diagnostics

Plot Instance Level Residual Diagnostics

Description

Plot Instance Level Residual Diagnostics

Usage

## S3 method for class 'predict_diagnostics'
plot(x, ...)

Arguments

x an object with instance level residual diagnostics created with predict_diagnostics function

... other parameters that will be passed to plot.ceteris_paribus_explain.

Value

an ggplot2 object of the class gg.

Examples

library("ranger")
titanic_glm_model <- ranger(survived ~ gender + age + class + fare + sibsp + parch,
data = titanic_imputed)
explainer_glm <- explain(titanic_glm_model,
data = titanic_imputed,
y = titanic_imputed$survived)
johny_d <- titanic_imputed[24, c("gender", "age", "class", "fare", "sibsp", "parch")]

plot.predict_parts

pl <- predict_diagnostics(explainer_glm, johny_d, variables = NULL)
plot(pl)

pl <- predict_diagnostics(explainer_glm, johny_d,
               neighbors = 10,
               variables = c("age", "fare"))
plot(pl)

pl <- predict_diagnostics(explainer_glm,
               johny_d,
               neighbors = 10,
               variables = c("class", "gender"))
plot(pl)

plot.predict_parts    Plot Variable Attribution Explanations

Description
Plot Variable Attribution Explanations

Usage
## S3 method for class 'predict_parts'
plot(x, ...)

Arguments
x    an object of the class predict_parts
...
other parameters described below

Value
An object of the class ggplot.

Plot options
break_down:
- max_features maximal number of features to be included in the plot. default value is 10
- 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.
- add_contributions if TRUE, variable contributions will be added to the plot.
- shift_contributions number describing how much labels should be shifted to the right, as a fraction of range. By default equal to 0.05.
Plot Variable Profile Explanations

Description
Plot Variable Profile Explanations

Usage
```r
## S3 method for class 'predict_profile'
plot(x, ...)  
```

Arguments

- **x**: an object of the class `predict_profile`
- **...**: other parameters

Value
An object of the class `ggplot`.

- vcolors If `NA` (default), DrWhy colors are used.
- vnames a character vector, if specified then will be used as labels on OY axis. By default `NULL`.
- digits number of decimal places (`round`) or significant digits (`signif`) to be used.
- rounding_function a function to be used for rounding numbers.
- plot_distributions if `TRUE` then distributions of conditional proportions will be plotted. This requires `keep_distributions=TRUE` in the `break_down`, `local_attributions`, or `local_interactions`.
- baseline if numeric then vertical line starts in baseline.
- title a character. Plot title. By default "Break Down profile".
- subtitle a character. Plot subtitle. By default `NULL` - then subtitle is set to "created for the XXX, YYY model", where XXX, YYY are labels of given explainers.
- max_vars alias for the `max_features` parameter.

shap:

- show_boxplots logical if `TRUE` (default) boxplot will be plotted to show uncertainty of attributions.
- vcolors If `NA` (default), DrWhy colors are used.
- max_features maximal number of features to be included in the plot. default value is 10
- max_vars alias for the `max_features` parameter.

oscillations:

- bar_width width of bars. By default 10

---

```r
plot.predict_profile
```
**Plot options**

**ceteris_paribus:**
- color a character. Either name of a color or name of a variable that should be used for coloring
- size a numeric. Size of lines to be plotted
- alpha a numeric between 0 and 1. Opacity of lines
- facet_ncol number of columns for the `facet_wrap`
- variables if not NULL then only variables will be presented
- variable_type a character. If numerical then only numerical variables will be plotted. If categorical then only categorical variables will be plotted.
- title a character. Plot title. By default "Ceteris Paribus profile".
- subtitle a character. Plot subtitle. By default NULL - then subtitle is set to "created for the XXX, YYY model", where XXX, YYY are labels of given explainers.
- categorical_type a character. How categorical variables shall be plotted? Either "lines" (default) or "bars".

---

**predict.explainer**  
**Predictions for the Explainer**

**Description**

This is a generic `predict()` function works for `explainer` objects.

**Usage**

```r
## S3 method for class 'explainer'
predict(object, newdata, ...)
model_prediction(explainer, new_data, ...)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>a model to be explained, object of the class <code>explainer</code></td>
</tr>
<tr>
<td>newdata</td>
<td>data.frame or matrix - observations for prediction</td>
</tr>
<tr>
<td>...</td>
<td>other parameters that will be passed to the predict function</td>
</tr>
<tr>
<td>explainer</td>
<td>a model to be explained, object of the class <code>explainer</code></td>
</tr>
<tr>
<td>new_data</td>
<td>data.frame or matrix - observations for prediction</td>
</tr>
</tbody>
</table>

**Value**

An numeric matrix of predictions
**Examples**

```r
HR_glm_model <- glm(status == "fired"., data = HR, family = "binomial")
explainer_glm <- explain(HR_glm_model, data = HR)
predict(explainer_glm, HR[1:3,])

library("ranger")
HR_ranger_model <- ranger(status~., data = HR, num.trees = 50, probability = TRUE)
explainer_ranger <- explain(HR_ranger_model, data = HR)
predict(explainer_ranger, HR[1:3,])
model_prediction(explainer_ranger, HR[1:3,])
```

---

**predict_diagnostics**  
*Instance Level Residual Diagnostics*

**Description**

This function performs local diagnostic of residuals. For a single instance its neighbors are identified in the validation data. Residuals are calculated for neighbors and plotted against residuals for all data. Find information how to use this function here: [https://ema.drwhy.ai/localDiagnostics.html](https://ema.drwhy.ai/localDiagnostics.html).

**Usage**

```r
predict_diagnostics(
  explainer,
  new_observation,
  variables = NULL,
  ..., nbins = 20,
  neighbors = 50,
  distance = gower::gower_dist
)

individual_diagnostics(
  explainer,
  new_observation,
  variables = NULL,
  ..., nbins = 20,
  neighbors = 50,
  distance = gower::gower_dist
)
```
**predict_diagnostics**

**Arguments**

- **explainer**: a model to be explained, preprocessed by the `explain` function
- **new_observation**: a new observation for which predictions need to be explained
- **variables**: character - name of variables to be explained
- **...**: other parameters
- **nbins**: number of bins for the histogram. By default 20
- **neighbors**: number of neighbors for histogram. By default 50.
- **distance**: the distance function, by default the `gower_dist()` function.

**Value**

An object of the class 'predict_diagnostics'. It's a data frame with calculated distribution of residuals.

**References**


**Examples**

```r
library("ranger")
titanic_glm_model <- ranger(survived ~ gender + age + class + fare + sibsp + parch, 
data = titanic_imputed)
explainer_glm <- explain(titanic_glm_model, 
data = titanic_imputed, 
y = titanic_imputed$survived)
johny_d <- titanic_imputed[24, c("gender", "age", "class", "fare", "sibsp", "parch")]
id_johny <- predict_diagnostics(explainer_glm, johny_d, variables = NULL)
id_johny
plot(id_johny)

id_johny <- predict_diagnostics(explainer_glm, johny_d, 
neighbors = 10, 
variables = c("age", "fare"))
id_johny
plot(id_johny)

id_johny <- predict_diagnostics(explainer_glm, johny_d, 
neighbors = 10, 
variables = c("class", "gender"))
id_johny
plot(id_johny)
```
Instance Level Parts of the Model Predictions

Description

Instance Level Variable Attributions as Break Down, SHAP or Oscillations explanations. Model prediction is decomposed into parts that are attributed for particular variables. From DALEX version 1.0 this function calls the `break_down` or `shap` functions from the iBreakDown package or `ceteris_paribus` from the ingredients package. Find information how to use the `break_down` method here: https://ema.drwhy.ai/breakDown.html. Find information how to use the `shap` method here: https://ema.drwhy.ai/shapley.html. Find information how to use the `oscillations` method here: https://ema.drwhy.ai/ceterisParibusOscillations.html.

Usage

```r
predict_parts(
  explainer,
  new_observation,
  ..., 
  N = if (substr(type, 1, 4) == "osci") 500 else NULL,
  type = "break_down"
)
```

```r
predict_parts_oscillations(explainer, new_observation, ...)
```

```r
predict_parts_oscillations_uni( 
  explainer,
  new_observation,
  variable_splits_type = "uniform",
  ...
)
```

```r
predict_parts_oscillations_emp( 
  explainer,
  new_observation,
  variable_splits = NULL,
  variables = colnames(explainer$data),
  ...
)
```

```r
predict_parts_break_down(explainer, new_observation, ...)
```

```r
predict_parts_break_down_interactions(explainer, new_observation, ...)
```

```r
predict_parts_shap(explainer, new_observation, ...)
```

```r variable_attribution(
```
predict_parts

explainer,
new_observation,
...
N = if (substr(type, 1, 4) == "osci") 500 else NULL,
type = "break_down"
)

Arguments

explainer a model to be explained, preprocessed by the explain function
new_observation a new observation for which predictions need to be explained
... other parameters that will be passed to iBreakDown::break_down
N the maximum number of observations used for calculation of attributions. By
default NULL (use all) or 500 (for oscillations).
type the type of variable attributions. Either shap, oscillations, oscillations_uni,
oscillations_emp, break_down or break_down_interactions.
variable_splits_type how variable grids shall be calculated? Will be passed to ceteris_paribus.
variable_splits named list of splits for variables. It is used by oscillations based measures. Will
be passed to ceteris_paribus.
variables names of variables for which splits shall be calculated. Will be passed to ceteris_paribus.

Value

Depending on the type there are different classes of the resulting object. It's a data frame with
calculated average response.

References

drwhy.ai/

Examples

library(DALEX)

new_dragon <- data.frame(
    year_of_birth = 200,
    height = 80,
    weight = 12.5,
    scars = 0,
    number_of_lost_teeth = 5
)

model_lm <- lm(life_length ~ year_of_birth + height +
    weight + scars + number_of_lost_teeth,
data = dragons)
predict_profile

Instance Level Profile as Ceteris Paribus

Description

This function calculated individual profiles aka Ceteris Paribus Profiles. From DALEX version 1.0 this function calls the ceteris_paribus from the ingredients package. Find information how to use this function here: https://ema.drwhy.ai/ceterisParibus.html.

Usage

predict_profile(
  explainer,
  new_observation,
  variables = NULL,
  ..., 
  type = "ceteris_paribus",
  variable_splits_type = "uniform"
)

individual_profile(
  explainer,
predict_profile

new_observation,
variables = NULL,
...,  
type = "ceteris_paribus",
variable_splits_type = "uniform"
)

Arguments

explainer a model to be explained, preprocessed by the explain function
new_observation a new observation for which predictions need to be explained
variables character - names of variables to be explained
... other parameters
type character, currently only the ceteris_paribus is implemented
variable_splits_type how variable grids shall be calculated? Use "quantiles" (default) for percentiles or "uniform" to get uniform grid of points. Will be passed to 'ingredients'.

Value

An object of the class ceteris_paribus_explainer. It's a data frame with calculated average response.

References


Examples

new_dragon <- data.frame(year_of_birth = 200,
height = 80,
weight = 12.5,
scars = 0,
number_of_lost_teeth = 5)
dragon_lm_model4 <- lm(life_length ~ year_of_birth + height +
weight + scars + number_of_lost_teeth,
data = dragons)
dragon_lm_explainer4 <- explain(dragon_lm_model4, data = dragons, y = dragons$year_of_birth,
label = "model_4v")
dragon_lm_predict4 <- predict_profile(dragon_lm_explainer4,
new_observation = new_dragon,
variables = c("year_of_birth", "height", "scars"))
head(dragon_lm_predict4)
plot(dragon_lm_predict4,
variables = c("year_of_birth", "height", "scars"))
library("ranger")
dragon_ranger_model4 <- ranger(life_length ~ year_of_birth + height +
weight + scars + number_of_lost_teeth,
data = dragons, num.trees = 50)
dragon_ranger_explainer4 <- explain(dragon_ranger_model4, data = dragons, y = dragons$year_of_birth,
label = "model_ranger")
dragon_ranger_predict4 <- predict_profile(dragon_ranger_explainer4,
new_observation = new_dragon,
variables = c("year_of_birth", "height", "scars"))
head(dragon_ranger_predict4)
plot(dragon_ranger_predict4,
variables = c("year_of_birth", "height", "scars"))
Examples

```r
aps_lm_model4 <- lm(m2.price~, data = apartments)
aps_lm_explainer4 <- explain(aps_lm_model4, data = apartments, y = apartments$m2.price,
                            label = "model_4v")
aps_lm_explainer4

library("ranger")
titanic_ranger_model <- ranger(survived~., data = titanic_imputed, num.trees = 50,
                               probability = TRUE)
explainer_ranger <- explain(titanic_ranger_model, data = titanic_imputed[,-8],
                            y = titanic_imputed$survived,
                            label = "model_ranger")
explainer_ranger
```

---

### print.model_diagnostics

**Print Dataset Level Model Diagnostics**

**Description**

Generic function

**Usage**

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

**Arguments**

- `x` an object with dataset level residual diagnostics created with `model_diagnostics` function
- `...` other parameters

### print.model_info

**Print model_info**

**Description**

Function prints object of class `model_info` created with `model_info`
print.model_performance

Print Dataset Level Model Performance Summary

Usage

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

Arguments

x - an object of class model_info
...
- other parameters

Examples

library("ranger")
titanic_ranger_model <- ranger(survived~., data = titanic_imputed, num.trees = 100,
probability = TRUE)
# It's a good practice to pass data without target variable
explainer_ranger <- explain(titanic_ranger_model, data = titanic_imputed[, -8],
y = titanic_imputed$survived)
# resulting dataframe has predicted values and residuals
mp_ex_rn <- model_performance(explainer_ranger)
mp_ex_rn
plot(mp_ex_rn)
**print.model_profile**

*Print Dataset Level Model Profile*

**Description**

Generic function

**Usage**

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

**Arguments**

- `x`: an object with dataset level profile created with `model_profile` function
- `...`: other parameters

---

**print.predict_diagnostics**

*Print Instance Level Residual Diagnostics*

**Description**

Generic function

**Usage**

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

**Arguments**

- `x`: an object with instance level residual diagnostics created with `predict_diagnostics` function
- `...`: other parameters
DrWhy Theme for ggplot objects

Description

DrWhy Theme for ggplot objects

Usage

theme_drwhy()

theme_ema()

theme_drwhy_vertical()

theme_ema_vertical()

Value

theme for ggplot2 objects

Passengers and Crew on the RMS Titanic Data

Description

The `titanic` data is a complete list of passengers and crew members on the RMS Titanic. It includes a variable indicating whether a person did survive the sinking of the RMS Titanic on April 15, 1912.

Usage

data(titanic)

data(titanic_imputed)

Format

a data frame with 2207 rows and 9 columns
Details

This dataset was copied from the stablelearner package and went through few variable transformations. Levels in embarked was replaced with full names, sibsp, parch and fare were converted to numerical variables and values for crew were replaced with 0. If you use this dataset please cite the original package.

From stablelearner: The website https://www.encyclopedia-titanica.org offers detailed information about passengers and crew members on the RMS Titanic. According to the website 1317 passengers and 890 crew member were aboard. 8 musicians and 9 employees of the shipyard company are listed as passengers, but travelled with a free ticket, which is why they have NA values in fare. In addition to that, fare is truly missing for a few regular passengers.

- gender a factor with levels male and female.
- age a numeric value with the persons age on the day of the sinking.
- class a factor specifying the class for passengers or the type of service aboard for crew members.
- embarked a factor with the persons place of of embarkment (Belfast/Cherbourg/Queenstown/Southampton).
- country a factor with the persons home country.
- fare a numeric value with the ticket price (0 for crew members, musicians and employees of the shipyard company).
- sibsp an ordered factor specifying the number if siblings/spouses aboard; adopted from Vanderbild data set (see below).
- parch an ordered factor specifying the number of parents/children aboard; adopted from Vanderbild data set (see below).
- survived a factor with two levels (no and yes) specifying whether the person has survived the sinking.

NOTE: The titanic_imputed dataset use following imputation rules.

- Missing ‘age’ is replaced with the mean of the observed ones, i.e., 30.
- For sibsp and parch, missing values are replaced by the most frequently observed value, i.e., 0.
- For fare, mean fare for a given class is used, i.e., 0 pounds for crew, 89 pounds for the 1st, 22 pounds for the 2nd, and 13 pounds for the 3rd class.

Source

This dataset was copied from the stablelearner package and went through few variable transformations. The complete list of persons on the RMS titanic was downloaded from https://www.encyclopedia-titanica.org on April 5, 2016. The information given in sibsp and parch was adopted from a data set obtained from https://biostat.app.vumc.org/wiki/Main/DataSets.

References

https://www.encyclopedia-titanica.org and https://CRAN.R-project.org/package=stablelearner
**update_data**  
*Update data of an explainer object*

**Description**

Function allows users to update data and y of any explainer in a unified way. It doesn’t require knowledge about structure of an explainer.

**Usage**

```r
update_data(explainer, data, y = NULL, verbose = TRUE)
```

**Arguments**

- `explainer` - explainer object that is supposed to be updated.
- `data` - new data, is going to be passed to an explainer
- `y` - new y, is going to be passed to an explainer
- `verbose` - logical, indicates if information about update should be printed

**Value**

updated explainer object

**Examples**

```r
aps_lm_model4 <- lm(m2.price ~ ., data = apartments)
aps_lm_explainer4 <- explain(aps_lm_model4, data = apartments, label = "model_4v")
explainer <- update_data(aps_lm_explainer4, data = apartmentsTest, y = apartmentsTest$m2.price)
```

---

**update_label**  
*Update label of explainer object*

**Description**

Function allows users to update label of any explainer in a unified way. It doesn’t require knowledge about structure of an explainer.

**Usage**

```r
update_label(explainer, label, verbose = TRUE)
```

**Examples**

```r
aps_lm_model4 <- lm(m2.price ~ ., data = apartments)
aps_lm_explainer4 <- explain(aps_lm_model4, data = apartments, label = "model_4v")
explainer <- update_data(aps_lm_explainer4, data = apartmentsTest, y = apartmentsTest$m2.price)
```
variable_effect

Arguments
- explainer - explainer object that is supposed to be updated.
- label - new label, is going to be passed to an explainer
- verbose - logical, indicates if information about update should be printed

Value
updated explainer object

Examples
aps_lm_model4 <- lm(m2.price ~ ., data = apartments)
aps_lm_explainer4 <- explain(aps_lm_model4, data = apartments, label = "model_4v")
explainer <- update_label(aps_lm_explainer4, label = "lm")

variable_effect

Dataset Level Variable Effect as Partial Dependency Profile or Accumulated Local Effects

Description
From DALEX version 1.0 this function calls the accumulated_dependence or partial_dependence from the ingredients package. Find information how to use this function here: https://ema.drwhy.ai/partialDependenceProfiles.html.

Usage
variable_effect(explainer, variables, ..., type = "partial_dependency")

variable_effect_partial_dependency(explainer, variables, ...)

variable_effect_accumulated_dependency(explainer, variables, ...)

Arguments
- explainer - a model to be explained, preprocessed by the 'explain' function
- variables - character - names of variables to be explained
- ... - other parameters
- type - character - type of the response to be calculated. Currently following options are implemented: 'partial_dependency' for Partial Dependency and 'accumulated_dependency' for Accumulated Local Effects

Value
An object of the class 'aggregated_profiles_explainer'. It’s a data frame with calculated average response.
References


Examples

titanic(glm_model) <- glm(survived~., data = titanic_imputed, family = "binomial")
explainer(glm_model) <- explain(titanic(glm_model), data = titanic_imputed)
expl_glm <- variable_effect(explainer(glm_model, "fare", "partial_dependency")
plot(expl_glm)

library("ranger")
titanic_ranger_model <- ranger(survived~., data = titanic_imputed, num.trees = 50,
probability = TRUE)
explainer_ranger <- explain(titanic_ranger_model, data = titanic_imputed)
expl_ranger <- variable_effect(explainer_ranger, variables = "fare",
type = "partial_dependency")
plot(expl_ranger)
plot(expl_ranger, expl_glm)

# Example for factor variable (with factorMerger)
expl_ranger_factor <- variable_effect(explainer_ranger, variables = "class")
plot(expl_ranger_factor)

---

**yhat**

*Wrap Various Predict Functions*

**Description**

This function is a wrapper over various predict functions for different models and different model structures. The wrapper returns a single numeric score for each new observation. To do this it uses different extraction techniques for models from different classes, like for classification, random forest is forces the output to be probabilities not classes itself.

**Usage**

```r
yhat(X.model, newdata, ...)
```

## S3 method for class 'lm'

```r
yhat(X.model, newdata, ...)
```

## S3 method for class 'randomForest'

```r
yhat(X.model, newdata, ...)
```

## S3 method for class 'svm'
yhat(X.model, newdata, ...)

## S3 method for class 'gbm'
yhat(X.model, newdata, ...)

## S3 method for class 'glm'
yhat(X.model, newdata, ...)

## S3 method for class 'cv.glmnet'
yhat(X.model, newdata, ...)

## S3 method for class 'glmnet'
yhat(X.model, newdata, ...)

## S3 method for class 'ranger'
yhat(X.model, newdata, ...)

## S3 method for class 'model_fit'
yhat(X.model, newdata, ...)

## S3 method for class 'train'
yhat(X.model, newdata, ...)

## S3 method for class 'lrm'
yhat(X.model, newdata, ...)

## S3 method for class 'rpart'
yhat(X.model, newdata, ...)

## S3 method for class `function`
yhat(X.model, newdata, ...)

## Default S3 method:
yhat(X.model, newdata, ...)

Arguments

- **X.model** object - a model to be explained
- **newdata** data.frame or matrix - observations for prediction
- **...** other parameters that will be passed to the predict function

Details

Currently supported packages are:

- class `cv.glmnet` and `glmnet` - models created with `glmnet` package,
- class `glm` - generalized linear models created with `glm`,
- class `model_fit` - models created with `parsnip` package,
• class lm - linear models created with lm,
• class ranger - models created with ranger package,
• class randomForest - random forest models created with randomForest package,
• class svm - support vector machines models created with the e1071 package,
• class train - models created with caret package,
• class gbm - models created with gbm package,
• class lrm - models created with rms package,
• class rpart - models created with rpart package.

Value

An numeric matrix of predictions
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