

# Package ‘interpretR’

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**Type** Package

**Title** Binary Classifier and Regression Model Interpretation Functions

**Version** 0.2.5

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**Depends** randomForest

**Imports** AUC, stats, graphics

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**Description** Compute permutation- based performance measures and create partial dependence plots for (cross-validated) 'randomForest' and 'ada' models.

**License** GPL (>= 2)

**RoxygenNote** 7.2.3

**NeedsCompilation** no

**Repository** CRAN

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interpretR-package	<i>Partial Dependence Plots and Permutation-Based Performance Measures</i>
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**Description**

Compute permutation-based performance measures (for binary classification) and create partial dependence plots (cross-validated classification and regression models). Currently only binary classification and regression models estimated with the package `randomForest` are supported. Binary classification models estimated with `ada` are also supported.

**Author(s)**

Authors: Michel Ballings, and Dirk Van den Poel, Maintainer: <Michel.Ballings@GMail.com>

**See Also**

[parDepPlot](#), [variableImportance](#)

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interpretRNews	<i>Display the NEWS file</i>
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**Description**

`interpretRNews` shows the NEWS file of the `interpretR` package.

**Usage**

```
interpretRNews()
```

**Author(s)**

Authors: Michel Ballings and Dirk Van den Poel, Maintainer: <Michel.Ballings@GMail.com>

**See Also**

[parDepPlot](#)

**Examples**

```
interpretRNews()
```

parDepPlot

*Model interpretation functions: Partial Dependence Plots***Description**

parDepPlot creates partial dependence plots for binary (cross-validated) classification models and regression models. Currently only binary classification models estimated with the packages randomForest and ada are supported. In addition randomForest regression models are supported.

**Usage**

```
parDepPlot(
  x.name,
  object,
  data,
  rm.outliers = TRUE,
  fact = 1.5,
  n.pt = 50,
  robust = FALSE,
  ci = FALSE,
  u.quant = 0.75,
  l.quant = 0.25,
  xlab = substr(x.name, 1, 50),
  ylab = NULL,
  main = if (any(class(object) %in% c("randomForest", "ada")))
    paste("Partial Dependence on", substr(x.name, 1, 20)) else
    paste("Cross-Validated Partial Dependence on", substr(x.name, 1, 10)),
  logit = TRUE,
  ylim = NULL,
  ...
)
```

**Arguments**

x.name	the name of the predictor as a character string for which a partial dependence plot has to be created.
object	can be a model or a list of cross- validated models. Currently only binary classification models built using the packages randomForest and ada are supported.
data	a data frame containing the predictors for the model or a list of data frames for cross-validation with length equal to the number of models.
rm.outliers	boolean, remove the outliers in x.name. Outliers are values that are smaller than $\max(Q1 - \text{fact} * \text{IQR}, \min)$ or greater than $\min(Q3 + \text{fact} * \text{IQR}, \max)$ . Overridden if xlim is used.
fact	factor to use in rm.outliers. The default is 1.5.
n.pt	if x.name is a continuous predictor, the number of points that will be used to plot the curve.

<code>robust</code>	if TRUE then the median is used to plot the central tendency (recommended when <code>logit=FALSE</code> ). If FALSE the mean is used.
<code>ci</code>	boolean. Should a confidence interval based on quantiles be plotted? This only works if <code>robust=TRUE</code> .
<code>u.quant</code>	Upper quantile for <code>ci</code> . This only works if <code>ci=TRUE</code> and <code>robust=TRUE</code> .
<code>l.quant</code>	Lower quantile for <code>ci</code> . This only works if <code>ci=TRUE</code> and <code>robust=TRUE</code> .
<code>xlab</code>	label for the x-axis. Is determined automatically if NULL.
<code>ylab</code>	label for the y-axis.
<code>main</code>	main title for the plot.
<code>logit</code>	boolean. Should the y-axis be on a logit scale or not? If FALSE, it is recommended to set <code>robust=TRUE</code> . Only applicable for classification.
<code>ylim</code>	The y limits of the plot
<code>...</code>	other graphical parameters for plot.

### Details

For classification, the response variable in the model is always assumed to take on the values {0,1}. Resulting partial dependence plots always refer to class 1. Whenever strange results are obtained the user has three options. First set `rm.outliers=TRUE`. Second, if that doesn't help, set `robust=TRUE`. Finally, if that doesn't help, the user can also try setting `ci=TRUE`. Areas with larger confidence intervals typically indicate problem areas. These options help the user tease out the root of strange results and converge to better parameter values.

### Author(s)

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### References

The code in this function uses part of the code from the `partialPlot` function in `randomForest`. It is expanded and generalized to support cross-validation and other packages.

### See Also

[variableImportance](#)

### Examples

```
library(randomForest)
#Prepare data
data(iris)
iris <- iris[1:100,]
iris$Species <- as.factor(ifelse(factor(iris$Species)=="setosa",0,1))

#Cross-validated models
#Estimate 10 models and create 10 test sets
data <- list()
rf <- list()
```

```

for (i in 1:10) {
  ind <- sample(nrow(iris),50)
  rf[[i]] <- randomForest(Species~., iris[ind,])
  data[[i]] <- iris[-ind,]
}

parDepPlot(x.name="Petal.Width", object=rf, data=data)

#Single model
#Estimate a single model
ind <- sample(nrow(iris),50)
rf <- randomForest(Species~., iris[ind,])
parDepPlot(x.name="Petal.Width", object=rf, data=iris[-ind,])

```

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variableImportance	<i>Permutation- based Variable Importance Measures</i>
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### Description

variableImportance produces permutation- based variable importance measures (currently only for binary classification models from the package randomForest and only for the performance measure AUROC)

### Usage

```

variableImportance(
  object = NULL,
  xdata = NULL,
  ydata = NULL,
  CV = 3,
  measure = "AUROC",
  sort = TRUE
)

```

### Arguments

object	A model. Currently only binary classification models from the package randomForest.
xdata	A data frame containing the predictors for the model.
ydata	A factor containing the response variable.
CV	Cross-validation. How many times should the data be permuted and the decrease in performance be calculated? Afterwards the mean is taken. CV should be higher for very small samples to ensure stability.
measure	Currently only Area Under the Receiver Operating Characteristic Curve (AUROC) is supported.
sort	Logical. Should the results be sorted from high to low?

**Details**

Currently only binary classification models from `randomForest` are supported. Also, currently only AUROC is supported. Definition of `MeanDecreaseAUROC`: for the entire ensemble the AUROC is recorded on the provided `xdata`. The same is subsequently done after permuting each variable (iteratively, for each variable separately). Then the latter is subtracted from the former. This is called the Decrease in AUROC. If we do this for multiple CV, it becomes the Mean Decrease in AUROC.

**Value**

A data frame containing the variable names and the mean decrease in AUROC

**Author(s)**

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**See Also**

[parDepPlot](#)

**Examples**

```
#Prepare data
data(iris)
iris <- iris[1:100,]
iris$Species <- as.factor(ifelse(factor(iris$Species)=="setosa",0,1))
#Estimate model
library(randomForest)
ind <- sample(nrow(iris),50)
rf <- randomForest(Species~., iris[ind,])
#Obtain variable importances
variableImportance(object=rf, xdata=iris[-ind,names(iris) != "Species"],
ydata=iris[-ind,]$Species)
```

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