

Package ‘vivid’

July 22, 2025

Title Variable Importance and Variable Interaction Displays

Version 0.2.9

Language en-US

Description A suite of plots for displaying variable importance and two-way variable interaction jointly. Can also display partial dependence plots laid out in a pairs plot or 'zenplots' style.

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Encoding UTF-8

Imports condvis2, ggplot2, GGally, RColorBrewer, colorspace, stats,
DendSer, ggalt, dplyr, igraph, flashlight, ggnewscale, sp

Suggests intergraph (>= 2.0-2), network (>= 1.12.0), sna (>= 2.3-2),
mlr, MASS, tidymodels, e1071, gridExtra, lemon, mlr3,
mlr3learners, scales, ranger, vip, knitr, rmarkdown,
randomForest, testthat (>= 3.0.0), labeling, zenplots, covr,
xgboost, bartMachine, caret, gbm, keras

VignetteBuilder knitr

RoxygenNote 7.2.3

Config/testthat/edition 3

URL <https://alaninglis.github.io/vivid/>

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-07-31 11:50:02 UTC

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as.data.frame.vivid	<i>as.data.frame.vivid</i>
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Description

Takes a matrix of class vivid and turn it into a data frame containing variable names, Vimp and Vint values, and the row and column index from the original matrix.

Usage

```
## S3 method for class 'vivid'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

- x A matrix of class 'vivid' to be converted to a data frame.
- row.names NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
- optional Logical. If TRUE, setting row names and converting column names (to syntactic names: see make.names) is optional. Note that all of R's base package as.data.frame() methods use optional only for column names treatment, basically with the meaning of data.frame(*, check.names = !optional). See also the make.names argument of the matrix method.
- ... Additional arguments to be passed to or from methods.

Value

A data frame of Vimp and Vint values and their index from the vivid matrix.

Examples

```
library(ranger)
aq <- na.omit(airquality)
aq <- aq[1:20,]# for speed
rF <- ranger(Ozone ~ ., data = aq, importance = "permutation")
myMat <- vivi(fit = rF, data = aq, response = "Ozone")
myDf <- as.data.frame(myMat)
myDf
```

pdpPairs

*pdpPairs***Description**

Creates a pairs plot showing bivariate pdp on upper diagonal, ice/univariate pdp on the diagonal and data on the lower diagonal

Usage

```
pdpPairs(
  data,
  fit,
  response,
  vars = NULL,
  pal = rev(RColorBrewer::brewer.pal(11, "RdYlBu")),
  fitlims = "pdp",
  gridSize = 10,
  nmax = 500,
  class = 1,
  nIce = 30,
  colorVar = NULL,
  comboImage = FALSE,
  predictFun = NULL,
  convexHull = FALSE,
  probability = FALSE
)
```

Arguments

<code>data</code>	Data frame used for fit.
<code>fit</code>	A supervised machine learning model, which understands <code>condvis2::CVpredict</code>
<code>response</code>	The name of the response for the fit.
<code>vars</code>	The variables to plot (and their order), defaults to all variables other than response.
<code>pal</code>	A vector of colors to show predictions, for use with <code>scale_fill_gradientn</code>

<code>fitlims</code>	Specifies the fit range for the color map. Options are a numeric vector of length 2, "pdp" (default), in which cases limits are calculated from the pdp, or "all", when limits are calculated from the observations and pdp. Predictions outside fitlims are squished on the color scale.
<code>gridSize</code>	The size of the grid for evaluating the predictions.
<code>nmax</code>	Uses sample of nmax data rows for the pdp. Default is 500. Use all rows if NULL.
<code>class</code>	Category for classification, a factor level, or a number indicating which factor level.
<code>nIce</code>	Number of ice curves to be plotted, defaults to 30.
<code>colorVar</code>	Which variable to colour the predictions by.
<code>comboImage</code>	If TRUE draws pdp for mixed variable plots as an image, otherwise an interaction plot.
<code>predictFun</code>	Function of (fit, data) to extract numeric predictions from fit. Uses <code>condvis2::CVpredict</code> by default, which works for many fit classes.
<code>convexHull</code>	If TRUE, then the convex hull is computed and any points outside the convex hull are removed.
<code>probability</code>	if TRUE, then returns the partial dependence for classification on the probability scale. If FALSE (default), then the partial dependence is returned on a near logit scale.

Value

A pairs plot

Examples

```
# Load in the data:
aq <- na.omit(airquality)
f <- lm(Ozone ~ ., data = aq)
pdpPairs(aq, f, "Ozone")

# Run a ranger model:
library(ranger)
library(MASS)
Boston1 <- Boston[, c(4:6, 8, 13:14)]
Boston1$chas <- factor(Boston1$chas)
fit <- ranger(medv ~ ., data = Boston1, importance = "permutation")
pdpPairs(Boston1[1:30, ], fit, "medv")
pdpPairs(Boston1[1:30, ], fit, "medv", comboImage = TRUE)
viv <- vivi(Boston1, fit, "medv")
# show top variables only
pdpPairs(Boston1[1:30, ], fit, "medv", comboImage = TRUE, vars = rownames(viv)[1:4])

library(ranger)
rf <- ranger(Species ~ ., data = iris, probability = TRUE)
pdpPairs(iris, rf, "Species") # prediction probs for first class, setosa
```

```
pdpPairs(iris, rf, "Species", class = "versicolor") # prediction probs versicolor
```

pdpVars

pdpVars

Description

Displays the individual conditional expectation (ICE) curves and aggregated partial dependence for each variable in a grid.

Usage

```
pdpVars(
  data,
  fit,
  response,
  vars = NULL,
  pal = rev(RColorBrewer::brewer.pal(11, "RdYlBu")),
  gridSize = 10,
  nmax = 500,
  class = 1,
  nIce = 30,
  predictFun = NULL,
  limits = NULL,
  colorVar = NULL,
  draw = TRUE,
  probability = FALSE
)
```

Arguments

<code>data</code>	Data frame used for fit.
<code>fit</code>	A supervised machine learning model, which understands <code>condvis2::CVpredict</code>
<code>response</code>	The name of the response for the fit.
<code>vars</code>	The variables to plot (and their order), defaults to all variables other than response.
<code>pal</code>	A vector of colors to show predictions, for use with <code>scale_fill_gradientn</code>
<code>gridSize</code>	The size of the grid for evaluating the predictions.
<code>nmax</code>	Uses sample of <code>nmax</code> data rows for the pdp. Default is 500. Use all rows if <code>NULL</code> .
<code>class</code>	Category for classification, a factor level, or a number indicating which factor level.
<code>nIce</code>	Number of ice curves to be plotted, defaults to 30.

<code>predictFun</code>	Function of (fit, data) to extract numeric predictions from fit. Uses <code>condvis2::CVpredict</code> by default, which works for many fit classes.
<code>limits</code>	A vector determining the limits of the predicted values.
<code>colorVar</code>	Which variable to colour the predictions by.
<code>draw</code>	If FALSE, then the plot will not be drawn. Default is TRUE.
<code>probability</code>	if TRUE, then returns the partial dependence for classification on the probability scale. If FALSE (default), then the partial dependence is returned on a near logit scale.

Value

A grid displaying ICE curves and univariate partial dependence.

Examples

```
# Load in the data:
aq <- na.omit(airquality)
fit <- lm(Ozone ~ ., data = aq)
pdpVars(aq, fit, "Ozone")

# Classification
library(ranger)
rfClassif <- ranger(Species ~ ., data = iris, probability = TRUE)
pdpVars(iris, rfClassif, "Species", class = 3)

pp <- pdpVars(iris, rfClassif, "Species", class = 2, draw = FALSE)
pp[[1]]
pdpVars(iris, rfClassif, "Species", class = 2, colorVar = "Species")
```

pdpZen

Create a zenplot displaying partial dependence values.

Description

Constructs a zigzag expanded navigation plot (zenplot) displaying partial dependence values.

Usage

```
pdpZen(
  data,
  fit,
  response,
  zpath = NULL,
  pal = rev(RColorBrewer::brewer.pal(11, "RdYlBu")),
  fitlims = "pdp",
  gridSize = 10,
```

```

    nmax = 500,
    class = 1,
    comboImage = FALSE,
    rug = TRUE,
    predictFun = NULL,
    convexHull = FALSE,
    probability = FALSE,
    ...
)

```

Arguments

<code>data</code>	Data frame used for fit
<code>fit</code>	A supervised machine learning model, which understands <code>condvis2::CVpredict</code>
<code>response</code>	The name of the response for the fit
<code>zpath</code>	Plot shows consecutive pairs of these variables. Defaults to all variables other than response. Recommend constructing <code>zpath</code> with <code>calcZpath</code> .
<code>pal</code>	A vector of colors to show predictions, for use with <code>scale_fill_gradientn</code>
<code>fitlims</code>	Specifies the fit range for the color map. Options are a numeric vector of length 2, "pdp" (default), in which cases limits are calculated from the pdp, or "all", when limits are calculated from the observations and pdp predictions outside <code>fitlims</code> are squished on the color scale.
<code>gridSize</code>	The size of the grid for evaluating the predictions.
<code>nmax</code>	Uses sample of <code>nmax</code> data rows for the pdp. Default is 500. Use all rows if NULL.
<code>class</code>	Category for classification, a factor level, or a number indicating which factor level.
<code>comboImage</code>	If TRUE draws pdp for mixed variable plots as an image, otherwise an interaction plot.
<code>rug</code>	If TRUE adds rugs for the data to the pdp plots
<code>predictFun</code>	Function of (fit, data) to extract numeric predictions from fit. Uses <code>condvis2::CVpredict</code> by default, which works for many fit classes.
<code>convexHull</code>	If TRUE, then the convex hull is computed and any points outside the convex hull are removed.
<code>probability</code>	if TRUE, then returns the partial dependence for classification on the probability scale. If FALSE (default), then the partial dependence is returned on a near logit scale.
<code>...</code>	passed on to <code>zenplot</code>

Value

A zenplot of partial dependence values.

Examples

```
## Not run:
# To use this function, install zenplots and graph from Bioconductor.
if (!requireNamespace("graph", quietly = TRUE)) {
  install.packages("BiocManager")
  BiocManager::install("graph")
}
install.packages("zenplots")

library(MASS)
library(ranger)
Boston1 <- Boston
Boston1$chas <- factor(Boston1$chas)
rf <- ranger(medv ~ ., data = Boston1)
pdpZen(Boston1[1:30, ], rf, response = "medv", zpath = names(Boston1)[1:4], comboImage = T)
# Find the top variables in rf
set.seed(123)
viv <- vivi(Boston1, rf, "medv", nmax = 30) # use 30 rows, for speed
pdpZen(Boston1, rf, response = "medv", zpath = rownames(viv)[1:4], comboImage = T)
zpath <- zPath(viv, cutoff = .2) # find plots whose interaction score exceeds .2
pdpZen(Boston1, rf, response = "medv", zpath = zpath, comboImage = T)

## End(Not run)
```

vip2vivid

vip2vivid

Description

Takes measured importance and interactions from the vip package and turns them into a matrix which can be used for plotting. Accepts any of the variable importance methods supplied by vip.

Usage

```
vip2vivid(importance, interaction, reorder = TRUE)
```

Arguments

importance	Measured importance from the vip package using vi function.
interaction	Measured interaction from the vip package using vint function.
reorder	If TRUE (default) uses DendSer to reorder the matrix of interactions and variable importances.

Value

A matrix of interaction values, with importance on the diagonal.

Examples

```
## Not run:
library(ranger)
library(vip)
aq <- na.omit(airquality) # get data
nameAq <- names(aq[-1]) # get feature names

rF <- ranger(Ozone ~ ., data = aq, importance = "permutation") # create ranger random forest fit
vImp <- vi(rF) # vip importance
vInt <- vint(rF, feature_names = nameAq) # vip interaction

vip2vivid(vImp, vInt)

## End(Not run)
```

vivi

vivi

Description

Creates a matrix displaying variable importance on the diagonal and variable interaction on the off-diagonal.

Usage

```
vivi(
  data,
  fit,
  response,
  gridSize = 50,
  importanceType = "agnostic",
  nmax = 500,
  reorder = TRUE,
  class = 1,
  predictFun = NULL,
  normalized = FALSE,
  numPerm = 4,
  showVimpError = FALSE,
  vars = NULL
)
```

Arguments

<code>data</code>	Data frame used for fit.
<code>fit</code>	A supervised machine learning model, which understands <code>condvis2::CVpredict</code>
<code>response</code>	The name of the response for the fit.
<code>gridSize</code>	The size of the grid for evaluating the predictions.

<code>importanceType</code>	Used to select the importance metric. By default, an agnostic importance measure is used. If an embedded metric is available, then setting this argument to the importance metric will use the selected importance values in the vivid-matrix. Please refer to the examples given for illustration. Alternatively, set to equal "agnostic" (the default) to override embedded importance measures and return agnostic importance values.
<code>nmax</code>	Maximum number of data rows to consider. Default is 500. Use all rows if NULL.
<code>reorder</code>	If TRUE (default) uses DendSer to reorder the matrix of interactions and variable importances.
<code>class</code>	Category for classification, a factor level, or a number indicating which factor level.
<code>predictFun</code>	Function of (fit, data) to extract numeric predictions from fit. Uses <code>convis2::CVpredict</code> by default, which works for many fit classes.
<code>normalized</code>	Should Friedman's H-statistic be normalized or not. Default is FALSE.
<code>numPerm</code>	Number of permutations to perform for agnostic importance. Default is 4.
<code>showVimpError</code>	Logical. If TRUE, and <code>numPerm > 1</code> then a tibble containing the variable names, their importance values, and the standard error for each importance is printed to the console.
<code>vars</code>	A vector of variable names to be assessed.

Details

If the argument `importanceType = 'agnostic'`, then an agnostic permutation importance (1) is calculated. Friedman's H statistic (2) is used for measuring the interactions. This measure is based on partial dependence curves and relates the interaction strength of a pair of variables to the total effect strength of that variable pair.

Value

A matrix of interaction values, with importance on the diagonal.

References

- 1: Fisher A., Rudin C., Dominici F. (2018). All Models are Wrong but many are Useful: Variable Importance for Black-Box, Proprietary, or Misspecified Prediction Models, using Model Class Reliance. Arxiv.
- 2: Friedman, J. H. and Popescu, B. E. (2008). "Predictive learning via rule ensembles." The Annals of Applied Statistics. JSTOR, 916–54.

Examples

```
aq <- na.omit(airquality)
f <- lm(Ozone ~ ., data = aq)
m <- vivi(fit = f, data = aq, response = "Ozone") # as expected all interactions are zero
viviHeatmap(m)
```

```
# Select importance metric
library(randomForest)
rf1 <- randomForest(Ozone~., data = aq, importance = TRUE)
m2 <- vivi(fit = rf1, data = aq, response = 'Ozone',
           importanceType = '%IncMSE') # select %IncMSE as the importance measure
viviHeatmap(m2)

library(ranger)
rf <- ranger(Species ~ ., data = iris, importance = "impurity", probability = TRUE)
vivi(fit = rf, data = iris, response = "Species") # returns agnostic importance
vivi(fit = rf, data = iris, response = "Species",
     importanceType = "impurity") # returns selected 'impurity' importance.
```

vividReorder

vividReorder

Description

Reorders a square matrix so that values of high importance and interaction strength are pushed to the top left of the matrix.

Usage

```
vividReorder(d)
```

Arguments

d A matrix such as that returned by vivi

Value

A reordered version of d.

Examples

```
f <- lm(Sepal.Length ~ ., data = iris[, -5])
m <- vivi(fit = f, data = iris[, -5], response = "Sepal.Length")
corimp <- abs(cor(iris[, -5])[1, -1])
viviUpdate(m, corimp) # use correlation as importance and reorder
```

viviHeatmap

viviHeatmap

Description

Plots a Heatmap showing variable importance on the diagonal and variable interaction on the off-diagonal.

Usage

```
viviHeatmap(
  mat,
  intPal = rev(colorspace::sequential_hcl(palette = "Purples 3", n = 100)),
  impPal = rev(colorspace::sequential_hcl(palette = "Greens 3", n = 100)),
  intLims = NULL,
  impLims = NULL,
  border = FALSE,
  angle = 0
)
```

Arguments

mat	A matrix, such as that returned by <code>vivi</code> , of values to be plotted.
intPal	A vector of colours to show interactions, for use with <code>scale_fill_gradientn</code> .
impPal	A vector of colours to show importance, for use with <code>scale_fill_gradientn</code> .
intLims	Specifies the fit range for the color map for interaction strength.
impLims	Specifies the fit range for the color map for importance.
border	Logical. If TRUE then draw a black border around the diagonal elements.
angle	The angle to rotate the x-axis labels. Defaults to zero.

Value

A heatmap plot showing variable importance on the diagonal and variable interaction on the off-diagonal.

Examples

```
library(ranger)
aq <- na.omit(airquality)
rF <- ranger(Ozone ~ ., data = aq, importance = "permutation")
myMat <- vivi(fit = rF, data = aq, response = "Ozone")
viviHeatmap(myMat)
```

viviNetwork

*viviNetwork***Description**

Create a Network plot displaying variable importance and variable interaction.

Usage

```
viviNetwork(
  mat,
  intThreshold = NULL,
  intLims = NULL,
  impLims = NULL,
  intPal = rev(colorspace::sequential_hcl(palette = "Purples 3", n = 100)),
  impPal = rev(colorspace::sequential_hcl(palette = "Greens 3", n = 100)),
  removeNode = FALSE,
  layout = igraph::layout_in_circle,
  cluster = NULL,
  nudge_x = 0.05,
  nudge_y = 0.03,
  edgeWidths = 1:4
)
```

Arguments

<code>mat</code>	A matrix, such as that returned by <code>vivi</code> , of values to be plotted.
<code>intThreshold</code>	Remove edges with weight below this value if provided.
<code>intLims</code>	Specifies the fit range for the color map for interaction strength.
<code>impLims</code>	Specifies the fit range for the color map for importance.
<code>intPal</code>	A vector of colours to show interactions, for use with <code>scale_fill_gradientn</code> .
<code>impPal</code>	A vector of colours to show importance, for use with <code>scale_fill_gradientn</code> .
<code>removeNode</code>	If TRUE, then removes nodes with no connecting edges when thresholding interaction values.
<code>layout</code>	igraph layout function or a numeric matrix with two columns, one row per node. Defaults to <code>igraph::layout_as_circle</code>
<code>cluster</code>	Either a vector of cluster memberships for nodes or an igraph clustering function.
<code>nudge_x</code>	Nudge (centered) labels by this amount, outward horizontally.
<code>nudge_y</code>	Nudge (centered) labels by this amount, outward vertically.
<code>edgeWidths</code>	A vector specifying the scaling of the edges for the displayed graph. Values must be positive.

Value

A plot displaying interaction strength between variables on the edges and variable importance on the nodes.

Examples

```
library(ranger)
aq <- na.omit(airquality)
rF <- ranger(Ozone ~ ., data = aq, importance = "permutation")
myMat <- vivi(fit = rF, data = aq, response = "Ozone")
viviNetwork(myMat)
```

viviUpdate	<i>viviUpdate</i>
------------	-------------------

Description

Creates a matrix displaying updated variable importance on the diagonal and variable interaction on the off-diagonal.

Usage

```
viviUpdate(mat, newImp, reorder = TRUE)
```

Arguments

mat	A matrix, such as that returned by vivi.
newImp	A named vector of variable importances.
reorder	If TRUE (default) uses DendSer to reorder the matrix of interactions and variable importances.

Value

A matrix of values, of class vivid, with updated variable importances.

Examples

```
f <- lm(Sepal.Length ~ ., data = iris[, -5])
m <- vivi(iris[, -5], f, "Sepal.Length")
corimp <- abs(cor(iris[, -5])[1, -1])
viviUpdate(m, corimp) # use correlation as updated importance
```

zPath

zPath

Description

Constructs a zenpath for connecting and displaying pairs.

Usage

```
zPath(
  viv,
  cutoff = NULL,
  method = c("greedy.weighted", "strictly.weighted"),
  connect = TRUE
)
```

Arguments

viv	A matrix, created by vivi to be used to calculate the path.
cutoff	Do not include any variables that are below the cutoff interaction value.
method	String indicating the method to use. The available methods are: "greedy.weighted": Sort all pairs according to a greedy (heuristic) Euler path with x as weights visiting each edge precisely once. "strictly.weighted": Strictly respect the order of the weights - so the first, second, third, and so on, adjacent pair of numbers of the output of zenpath() corresponds to the pair with largest, second-largest, third-largest, and so on, weight. see zenpath
connect	If connect is TRUE, connect the edges from separate eulerians (strictly.weighted only).

Details

Construct a path of indices to visit to order variables

Value

Returns a zpath from viv showing pairs with viv entry over the cutoff

Examples

```
## Not run:
# To use this function, install zenplots and graph from Bioconductor.
if (!requireNamespace("graph", quietly = TRUE)) {
  install.packages("BiocManager")
  BiocManager::install("graph")
}
install.packages("zenplots")
```

```
aq <- na.omit(airquality) * 1.0

# Run an mlr3 ranger model:
library(mlr3)
library(mlr3learners)
library(ranger)
ozonet <- TaskRegr$new(id = "airQ", backend = aq, target = "Ozone")
ozonel <- lrn("regr.ranger", importance = "permutation")
ozonef <- ozonel$train(ozonet)

viv <- vivi(aq, ozonef, "Ozone")

# Calculate Zpath:
zpath <- zPath(viv, .8)
zpath

## End(Not run)
```

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