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Description Select data analysis plots, under a standardized calling interface implemented on top of 'ggplot2' and 'plotly'. Plots of interest include: 'ROC', gain curve, scatter plot with marginal distributions, conditioned scatter plot with marginal densities, box and stem with matching theoretical distribution, and density with matching theoretical distribution.

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Contents

WVPlots-package *WVPlots: Common Plots for Analysis*

Description

Select data analysis plots, under a standardized calling interface implemented on top of ggplot2 and plotly. Plots of interest include: ROC, gain curve, scatter plot with marginal distributions, conditioned scatter plot with marginal densities. box and stem with matching theoretical distribution, density with matching theoretical distribution.

Details

For more information:

- vignette(package='WVPlots')
- RShowDoc('WVPlots_examples',package='WVPlots')
- Website: https://github.com/WinVector/WVPlots

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See Also

Useful links:

- https://github.com/WinVector/WVPlots
- https://winvector.github.io/WVPlots/
- Report bugs at https://github.com/WinVector/WVPlots/issues

`BinaryYScatterPlot` *Plot a scatter plot of a binary variable with smoothing curve.*

Description

Plot the scatter plot of a binary variable with a smoothing curve.

Usage

```
BinaryYScatterPlot(
  frame,
  xvar,
  yvar,
  title,
  ...,
  se = FALSE,
  use_glm = TRUE,
  point_color = "black",
  smooth_color = "blue"
)
```

Arguments

`frame`	data frame to get values from
`xvar`	name of the independent column in frame
`yvar`	name of the dependent (output or result to be modeled) column in frame
`title`	title to place on plot
`...`	no unnamed argument, added to force named binding of later arguments.
`se`	if TRUE, add error bars (defaults to FALSE). Ignored if useGLM is TRUE
`use_glm`	if TRUE, "smooths" with a one-variable logistic regression (defaults to TRUE)
`point_color`	color for points
`smooth_color`	color for smoothing line

Details

The points are jittered for legibility. By default, a logistic regression fit is used, so that the smoothing curve represents the probability of y == 1 (as fit by the logistic regression). If `use_glm` is set to FALSE, a standard smoothing curve (either loess or a spline fit) is used.

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}
```

```
set.seed(34903490)
x = rnorm(50)
y = 0.5*x^2 + 2*x + rnorm(length(x))
frm = data.frame(x=x,y=y,yC=y>=as.numeric(quantile(y,probs=0.8)))
frm$absY <- abs(frm$y)
frm$posY = frm$y > 0
frm$costX = 1
WVPlots::BinaryYScatterPlot(frm, "x", "posY",
   title="Example 'Probability of Y' Plot")
```

`ClevelandDotPlot` *Plot a Cleveland dot plot.*

Description

Plot counts of a categorical variable.

Usage

```
ClevelandDotPlot(
  frm,
  xvar,
  title,
  ...,
  sort = -1,
  limit_n = NULL,
  stem = TRUE,
  color = "black"
)
```

Arguments

`frm`	data frame to get values from
`xvar`	name of the independent (input or model) column in frame
`title`	title to place on plot
`...`	no unnamed argument, added to force named binding of later arguments.
`sort`	if TRUE sort data
`limit_n`	if not NULL number of items to plot
`stem`	if TRUE add stems/whiskers to plot
`color`	color for points and stems

Details

Assumes that xvar is a factor or can be coerced to one (character or integral).

- sort < 0 sorts the factor levels in decreasing order (most frequent level first)
- sort > 0 sorts the factor levels in increasing order (good when used in conjunction with coord_flip())
- sort = 0 leaves the factor levels in "natural order" – usually alphabetical
- stem = FALSE will plot only the dots, without the stem to the y=0 line.
- limit_n = NULL plots all the levels, N an integer limits to the top N most populous levels

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
# discrete variable: letters of the alphabet
# frequencies of letters in English
# source: http://en.algoritmy.net/article/40379/Letter-frequency-English
letterFreqs = c(8.167, 1.492, 2.782, 4.253, 12.702, 2.228,
                2.015, 6.094, 6.966, 0.153, 0.772, 4.025, 2.406, 6.749, 7.507, 1.929,
                0.095, 5.987, 6.327, 9.056, 2.758, 0.978, 2.360, 0.150, 1.974, 0.074)
letterFreqs = letterFreqs/100
letterFrame = data.frame(letter = letters, freq=letterFreqs)
# now let's generate letters according to their letter frequencies
N = 1000
randomDraws = data.frame(draw=1:N,
  letter=sample(letterFrame$letter, size=N,
  replace=TRUE, prob=letterFrame$freq))
WVPlots::ClevelandDotPlot(randomDraws, "letter",
  title = "Example Cleveland-style dot plot")

# # Note the use of sort = 0. Also note that the graph omits counts
# # with no occurrences (5, and 7)
# WVPlots::ClevelandDotPlot(mtcars, "carb", sort = 0, "Example of counting integer values")

# # For counting integer values while including counts with no occurrences,
# # use Discrete Distribution.
# WVPlots::DiscreteDistribution(mtcars, "carb", "Better way to count integer values")
```

ConditionalSmoothedScatterPlot

Plot a scatter plot with smoothing line.

Description

Plot a scatter plot with a smoothing line; the smoothing window is aligned either left, center or right.

Usage

```
ConditionalSmoothedScatterPlot(
  frame,
  xvar,
  yvar,
  groupvar = NULL,
  title = "ConditionalSmoothedScatterPlot",
  ...,
  k = 3,
  align = "center",
  point_color = "black",
  point_alpha = 0.2,
  smooth_color = "black",
  palette = "Dark2"
)
```

Arguments

frame	data frame to get values from
xvar	name of the independent column in frame. Assumed to be regularly spaced
yvar	name of the dependent (output or result to be modeled) column in frame
groupvar	name of the grouping column in frame. Can be NULL for an unconditional plot
title	title for plot
...	no unnamed argument, added to force named binding of later arguments.
k	width of smoothing window. Must be odd for a center-aligned plot. Defaults to 3
align	smoothing window alignment: 'center', 'left', or 'right'. Defaults to 'center'
point_color	color of points, when groupvar is NULL. Set to NULL to turn off points.
point_alpha	alpha/opaqueness of points.
smooth_color	color of smoothing line, when groupvar is NULL
palette	name of Brewer palette, when groupvar is non-NULL (can be NULL)

Details

xvar is the continuous independent variable and yvar is the dependent binary variable. Smoothing is by a square window of width k.

If palette is NULL, and groupvar is non-NULL, plot colors will be chosen from the default ggplot2 palette. Setting palette to NULL allows the user to choose a non-Brewer palette, for example with scale_fill_manual.

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

y = c(1,2,3,4,5,10,15,18,20,25)
x = seq_len(length(y))
df = data.frame(x=x, y=y, group=x>5)
WVPlots::ConditionalSmoothedScatterPlot(df, "x", "y", NULL,
   title="left smooth, one group", align="left")
# WVPlots::ConditionalSmoothedScatterPlot(df, "x", "y", "group",
#    title="left smooth, two groups", align="left")
```

`DiscreteDistribution` *Plot distribution of a single discrete numerical variable.*

Description

Similar to calling `ClevelandDotPlot` with `sort = 0` on a numerical x variable that takes on a discrete set of values.

Usage

```
DiscreteDistribution(frm, xvar, title, ..., stem = TRUE, color = "black")
```

Arguments

`frm`	data frame to get values from
`xvar`	numeric: name of the variable whose distribution is to be plotted
`title`	title to place on plot
`...`	no unnamed argument, added to force named binding of later arguments.
`stem`	if TRUE add whisker/stems to plot
`color`	color of points and stems

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

frmx = data.frame(x = rbinom(1000, 20, 0.5))
WVPlots::DiscreteDistribution(frmx, "x","Discrete example")
```

DoubleDensityPlot *Plot two density plots conditioned on an outcome variable.*

Description

Plot two density plots conditioned on a binary outcome variable.

Usage

```
DoubleDensityPlot(
  frame,
  xvar,
  truthVar,
  title,
  ...,
  truth_target = NULL,
  palette = "Dark2"
)
```

Arguments

frame	data frame to get values from
xvar	name of the independent (input or model) column in frame
truthVar	name of the dependent (output or result to be modeled) column in frame
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
truth_target	if not NULL compare to this scalar value.
palette	name of Brewer palette (can be NULL)

Details

The use case for this visualization is to plot the distribution of a predictive model score (usually the predicted probability of a desired outcome) conditioned on the actual outcome. However, you can use it to compare the distribution of any numerical quantity conditioned on a binary feature. See the examples.

The plot will degrade gracefully in degenerate conditions, for example when only one category is present.

If palette is NULL, plot colors will be chosen from the default ggplot2 palette. Setting palette to NULL allows the user to choose a non-Brewer palette, for example with scale_fill_manual.

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

mpg = ggplot2::mpg
mpg$trans = gsub("\\(.*$", '', mpg$trans)
WVPlots::DoubleDensityPlot(mpg, "cty", "trans", "City driving mpg by transmission type")

if (FALSE) {
# redo the last plot with a custom palette
cmap = c("auto" = "#b2df8a", "manual" = "#1f78b4")
plt = WVPlots::DoubleDensityPlot(mpg, "cty", "trans",
              palette = NULL,
              title="City driving mpg by transmission type")
plt + ggplot2::scale_color_manual(values=cmap) +
      ggplot2::scale_fill_manual(values=cmap)

set.seed(34903490)
x = rnorm(50)
y = 0.5*x^2 + 2*x + rnorm(length(x))
frm = data.frame(score=x,
   truth=(y>=as.numeric(quantile(y,probs=0.8))),
   stuck=TRUE,
   rare=FALSE)
frm[1,'rare'] = TRUE
WVPlots::DoubleDensityPlot(frm, "score", "truth", title="Example double density plot")
}
```

DoubleHistogramPlot *Plot two histograms conditioned on an outcome variable.*

Description

Plot two histograms conditioned on a binary outcome variable.

Usage

```
DoubleHistogramPlot(
  frame,
  xvar,
  truthVar,
  title,
  ...,
  palette = "Dark2",
  breaks = 40
)
```

Arguments

frame	data frame to get values from
xvar	name of the independent (input or model) column in frame
truthVar	name of the dependent (output or result to be modeled) column in frame
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
palette	name of Brewer palette (can be NULL)
breaks	breaks to pass to histogram

Details

To distinguish the two conditions, one histogram is plotted upside-down.

The use case for this visualization is to plot a predictive model score (usually the predicted probability of a desired outcome) conditioned on the actual outcome. However, you can use it to compare any numerical quantity conditioned on a binary feature.

If palette is NULL, plot colors will be chosen from the default ggplot2 palette. Setting palette to NULL allows the user to choose a non-Brewer palette, for example with scale_fill_manual.

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
x = rnorm(50)
y = 0.5*x^2 + 2*x + rnorm(length(x))
frm = data.frame(x=x,y=y,yC=y>=as.numeric(quantile(y,probs=0.8)))
frm$absY <- abs(frm$y)
frm$posY = frm$y > 0
frm$costX = 1
WVPlots::DoubleHistogramPlot(frm, "x", "yC", title="Example double histogram plot")

if (FALSE) {
# redo the plot with a custom palette
plt = WVPlots::DoubleHistogramPlot(frm, "x", "yC", palette=NULL,
                              title="Example double histogram plot")
cmap = c("TRUE" = "#b2df8a", "FALSE" = "#1f78b4")
plt + ggplot2::scale_color_manual(values=cmap) +
      ggplot2::scale_fill_manual(values=cmap)
}
```

GainCurvePlot *Plot the cumulative gain curve of a sort-order.*

Description

Plot the cumulative gain curve of a sort-order.

Usage

```
GainCurvePlot(
  frame,
  xvar,
  truthVar,
  title,
  ...,
  estimate_sig = FALSE,
  large_count = 1000,
  truth_target = NULL,
  model_color = "darkblue",
  wizard_color = "darkgreen",
  shadow_color = "darkgray"
)
```

Arguments

frame	data frame to get values from
xvar	name of the independent (input or model score) column in frame
truthVar	name of the dependent (output or result to be modeled) column in frame
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
estimate_sig	logical, if TRUE compute significance.
large_count	numeric, upper bound target for number of plotting points.
truth_target	if not NULL compare to this scalar value.
model_color	color for the model curve
wizard_color	color for the "wizard" (best possible) curve
shadow_color	color for the shaded area under the curve

Details

The use case for this visualization is to compare a predictive model score to an actual outcome (either binary (0/1) or continuous). In this case the gain curve plot measures how well the model score sorts the data compared to the true outcome value.

The x-axis represents the fraction of items seen when sorted by score, and the y-axis represents the cumulative summed true outcome represented by the items seen so far. See, for example, https://www.ibm.com/docs/SSLVMB_24.0.0/spss/tutorials/mlp_bankloan_outputtype_02.html.

For comparison, GainCurvePlot also plots the "wizard curve": the gain curve when the data is sorted according to its true outcome.

To improve presentation quality, the plot is limited to approximately large_count points (default: 1000). For larger data sets, the data is appropriately randomly sampled down before plotting.

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
y = abs(rnorm(20)) + 0.1
x = abs(y + 0.5*rnorm(20))
frm = data.frame(model=x, value=y)
WVPlots::GainCurvePlot(frm, "model", "value",
   title="Example Continuous Gain Curve")
```

GainCurvePlotC *Plot the cumulative gain curve of a sort-order with costs.*

Description

Plot the cumulative gain curve of a sort-order with costs.

Usage

```
GainCurvePlotC(
  frame,
  xvar,
  costVar,
  truthVar,
  title,
  ...,
  estimate_sig = FALSE,
  large_count = 1000,
  model_color = "darkblue",
  wizard_color = "darkgreen",
  shadow_color = "darkgray"
)
```

Arguments

frame	data frame to get values from
xvar	name of the independent (input or model score) column in frame
costVar	cost of each item (drives x-axis sum)
truthVar	name of the dependent (output or result to be modeled) column in frame
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
estimate_sig	logical, if TRUE compute significance
large_count	numeric, upper bound target for number of plotting points
model_color	color for the model curve
wizard_color	color for the "wizard" (best possible) curve
shadow_color	color for the shaded area under the curve

Details

GainCurvePlotC plots a cumulative gain curve for the case where items have an additional cost, in addition to an outcome value.

The x-axis represents the fraction of total cost experienced when items are sorted by score, and the y-axis represents the cumulative summed true outcome represented by the items seen so far.

For comparison, GainCurvePlotC also plots the "wizard curve": the gain curve when the data is sorted according to its true outcome/cost (the optimal sort order).

To improve presentation quality, the plot is limited to approximately large_count points (default: 1000). For larger data sets, the data is appropriately randomly sampled down before plotting.

See Also

GainCurvePlot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
y = abs(rnorm(20)) + 0.1
x = abs(y + 0.5*rnorm(20))
frm = data.frame(model=x, value=y)
frm$costs=1
frm$costs[1]=5
WVPlots::GainCurvePlotC(frm, "model", "costs", "value",
   title="Example Continuous Gain CurveC")
```

GainCurvePlotList *Plot the cumulative gain curves of a sort-order.*

Description

Plot the cumulative gain curves of a sort-order.

Usage

```
GainCurvePlotList(
  frame,
  xvars,
  truthVar,
  title,
  ...,
  truth_target = NULL,
  palette = "Dark2"
)

GainCurveListPlot(
  frame,
  xvars,
  truthVar,
  title,
  ...,
  truth_target = NULL,
  palette = "Dark2"
)
```

Arguments

frame	data frame to get values from
xvars	name of the independent (input or model score) columns in frame
truthVar	name of the dependent (output or result to be modeled) column in frame
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
truth_target	if not NULL compare to this scalar value.
palette	color palette for the model curves

Details

The use case for this visualization is to compare a predictive model score to an actual outcome (either binary (0/1) or continuous). In this case the gain curve plot measures how well the model score sorts the data compared to the true outcome value.

The x-axis represents the fraction of items seen when sorted by score, and the y-axis represents the gain seen so far (cumulative value of model over cummulative value of random selection)..

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
y = abs(rnorm(20)) + 0.1
x = abs(y + 0.5*rnorm(20))
frm = data.frame(model=x, value=y)
WVPlots::GainCurvePlotList(frm, c("model", "value"), "value",
   title="Example Continuous gain Curves")
```

`GainCurvePlotWithNotation` *Plot the cumulative gain curve of a sort-order with extra notation*

Description

Plot the cumulative gain curve of a sort-order with extra notation.

Usage

```
GainCurvePlotWithNotation(
  frame,
  xvar,
  truthVar,
  title,
  gainx,
  labelfun,
  ...,
  sort_by_model = TRUE,
  estimate_sig = FALSE,
  large_count = 1000,
  model_color = "darkblue",
  wizard_color = "darkgreen",
  shadow_color = "darkgray",
  crosshair_color = "red",
  text_color = "black"
)
```

Arguments

`frame`	data frame to get values from
`xvar`	name of the independent (input or model score) column in frame
`truthVar`	name of the dependent (output or result to be modeled) column in frame

title	title to place on plot
gainx	the point on the x axis corresponding to the desired label
labelfun	a function to return a label for the marked point
...	no unnamed argument, added to force named binding of later arguments.
sort_by_model	logical, if TRUE use the model to calculate gainy, else use wizard.
estimate_sig	logical, if TRUE compute significance
large_count	numeric, upper bound target for number of plotting points
model_color	color for the model curve
wizard_color	color for the "wizard" (best possible) curve
shadow_color	color for the shaded area under the curve
crosshair_color	color for the annotation location lines
text_color	color for the annotation text

Details

This is the standard gain curve plot (see GainCurvePlot) with a label attached to a particular value of x. The label is created by a function labelfun, which takes as inputs the x and y coordinates of a label and returns a string (the label).

By default, uses the model to calculate the y value of the calculated point; to use the wizard curve, set sort_by_model = FALSE

See Also

GainCurvePlot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
y = abs(rnorm(20)) + 0.1
x = abs(y + 0.5*rnorm(20))
frm = data.frame(model=x, value=y)
gainx = 0.25  # get the predicted top 25% most valuable points as sorted by the model
# make a function to calculate the label for the annotated point
labelfun = function(gx, gy) {
  pctx = gx*100
  pcty = gy*100

  paste("The predicted top ", pctx, "% most valuable points by the model\n",
        "are ", pcty, "% of total actual value", sep='')
}
WVPlots::GainCurvePlotWithNotation(frm, "model", "value",
```

```
   title="Example Gain Curve with annotation",
   gainx=gainx,labelfun=labelfun)

# now get the top 25% actual most valuable points

labelfun = function(gx, gy) {
  pctx = gx*100
  pcty = gy*100

  paste("The actual top ", pctx, "% most valuable points\n",
        "are ", pcty, "% of total actual value", sep='')
}

WVPlots::GainCurvePlotWithNotation(frm, "model", "value",
   title="Example Gain Curve with annotation",
   gainx=gainx,labelfun=labelfun, sort_by_model=FALSE)
```

`HexBinPlot` *Build a hex bin plot*

Description

Build a hex bin plot with rational color coding.

Usage

```
HexBinPlot(
  d,
  xvar,
  yvar,
  title,
  ...,
  lightcolor = "#deebf7",
  darkcolor = "#000000",
  bins = 30,
  binwidth = NULL,
  na.rm = FALSE
)
```

Arguments

`d`	data frame
`xvar`	name of x variable column
`yvar`	name of y variable column
`title`	plot title
`...`	not used, forces later arguments to bind by name

lightcolor	light color for least dense areas
darkcolor	dark color for most dense areas
bins	passed to geom_hex
binwidth	passed to geom_hex
na.rm	passed to geom_hex

Details

Builds a standard ggplot2 hexbin plot, with a color scale such that dense areas are colored darker (the default ggplot2 fill scales will color dense areas lighter).

The user can choose an alternate color scale with endpoints lightcolor and darkcolor; it is up to the user to make sure that lightcolor is lighter than darkcolor.

Requires the hexbin package.

Value

a ggplot2 hexbin plot

See Also

geom_hex

Examples

```
if(requireNamespace("hexbin", quietly = TRUE)) {
   if (requireNamespace('data.table', quietly = TRUE)) {
    # don't multi-thread during CRAN checks
     data.table::setDTthreads(1)
   }
   set.seed(634267)
   dframe = data.frame(x = rnorm(1000), y = rnorm(1000))
   print(HexBinPlot(dframe, "x", "y", "Example hexbin"))

   diamonds = ggplot2::diamonds
   print(HexBinPlot(diamonds, "carat", "price", "Diamonds example"))

   # change the colorscale
    print(HexBinPlot(diamonds, "carat", "price", "Diamonds example",
                     lightcolor="#fed98e",
                     darkcolor="#993404"))
}
```

`LiftCurvePlot` *Plot the cumulative lift curve of a sort-order.*

Description

Plot the cumulative lift curve of a sort-order.

Usage

```
LiftCurvePlot(
  frame,
  xvar,
  truthVar,
  title,
  ...,
  large_count = 1000,
  include_wizard = TRUE,
  truth_target = NULL,
  model_color = "darkblue",
  wizard_color = "darkgreen"
)
```

Arguments

`frame`	data frame to get values from
`xvar`	name of the independent (input or model score) column in frame
`truthVar`	name of the dependent (output or result to be modeled) column in frame
`title`	title to place on plot
`...`	no unnamed argument, added to force named binding of later arguments.
`large_count`	numeric, upper bound target for number of plotting points
`include_wizard`	logical, if TRUE plot the ideal or wizard plot.
`truth_target`	if not NULL compare to this scalar value.
`model_color`	color for the model curve
`wizard_color`	color for the "wizard" (best possible) curve

Details

The use case for this visualization is to compare a predictive model score to an actual outcome (either binary (0/1) or continuous). In this case the lift curve plot measures how well the model score sorts the data compared to the true outcome value.

The x-axis represents the fraction of items seen when sorted by score, and the y-axis represents the lift seen so far (cumulative value of model over cummulative value of random selection)..

For comparison, `LiftCurvePlot` also plots the "wizard curve": the lift curve when the data is sorted according to its true outcome.

To improve presentation quality, the plot is limited to approximately `large_count` points (default: 1000). For larger data sets, the data is appropriately randomly sampled down before plotting.

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
y = abs(rnorm(20)) + 0.1
x = abs(y + 0.5*rnorm(20))
frm = data.frame(model=x, value=y)
WVPlots::LiftCurvePlot(frm, "model", "value",
   title="Example Continuous Lift Curve")
```

`LiftCurvePlotList` *Plot the cumulative lift curves of a sort-order.*

Description

Plot the cumulative lift curves of a sort-order.

Usage

```
LiftCurvePlotList(
  frame,
  xvars,
  truthVar,
  title,
  ...,
  truth_target = NULL,
  palette = "Dark2"
)

LiftCurveListPlot(
  frame,
  xvars,
  truthVar,
  title,
  ...,
  truth_target = NULL,
  palette = "Dark2"
)
```

Arguments

`frame`	data frame to get values from
`xvars`	name of the independent (input or model score) columns in frame

truthVar	name of the dependent (output or result to be modeled) column in frame
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
truth_target	if not NULL compare to this scalar value.
palette	color palette for the model curves

Details

The use case for this visualization is to compare a predictive model score to an actual outcome (either binary (0/1) or continuous). In this case the lift curve plot measures how well the model score sorts the data compared to the true outcome value.

The x-axis represents the fraction of items seen when sorted by score, and the y-axis represents the lift seen so far (cumulative value of model over cummulative value of random selection)..

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
y = abs(rnorm(20)) + 0.1
x = abs(y + 0.5*rnorm(20))
frm = data.frame(model=x, value=y)
WVPlots::LiftCurvePlotList(frm, c("model", "value"), "value",
   title="Example Continuous Lift Curves")
```

LogLogPlot *Log-log plot*

Description

Plot a trend on log-log paper.

Usage

```
LogLogPlot(
  frame,
  xvar,
  yvar,
  title,
  ...,
  use_coord_trans = FALSE,
  point_color = "black",
  linear_color = "#018571",
```

```
  quadratic_color = "#a6611a",
  smoothing_color = "blue"
)
```

Arguments

frame	data frame to get values from
xvar	name of the independent (input or model) column in frame
yvar	name of the dependent (output or result to be modeled) column in frame
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
use_coord_trans	logical if TRUE, use coord_trans instead of coord_trans(x = "log10", y = "log10") instead of scale_x_log10() + scale_y_log10() (useful when there is not enough range to show ticks).
point_color	the color of the data points
linear_color	the color of the linear growth lines
quadratic_color	the color of the quadratic growth lines
smoothing_color	the color of the smoothing line through the data

Details

This plot is intended for plotting functions that are observed costs or durations as a function of problem size. In this case we expect the ideal or expected cost function to be non-decreasing. Any negative trends are assumed to arise from the noise model. The graph is specialized to compare non-decreasing linear and non-decreasing quadratic growth.

Some care must be taken in drawing conclusions from log-log plots, as the transform is fairly violent. Please see: "(Mar's Law) Everything is linear if plotted log-log with a fat magic marker" (from Akin's Laws of Spacecraft Design https://spacecraft.ssl.umd.edu/akins_laws.html), and "So You Think You Have a Power Law" http://bactra.org/weblog/491.html.

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(5326)
frm = data.frame(x = 1:20)
frm$y <- 5 + frm$x + 0.2 * frm$x * frm$x + 0.1*abs(rnorm(nrow(frm)))
WVPlots::LogLogPlot(frm, "x", "y", title="Example Trend")
```

`MetricPairPlot` *Plot the relationship between two metrics.*

Description

Plot the relationship between two metrics.

Usage

```
MetricPairPlot(
  frame,
  xvar,
  truthVar,
  title,
  ...,
  x_metric = "false_positive_rate",
  y_metric = "true_positive_rate",
  truth_target = TRUE,
  points_to_plot = NULL,
  linecolor = "black"
)
```

Arguments

`frame`	data frame to get values from
`xvar`	name of the independent (input or model) column in frame
`truthVar`	name of the column to be predicted
`title`	title to place on plot
`...`	no unnamed argument, added to force named binding of later arguments.
`x_metric`	metric to be plotted. See Details for the list of allowed metrics
`y_metric`	metric to be plotted. See Details for the list of allowed metrics
`truth_target`	truth value considered to be positive.
`points_to_plot`	how many data points to use for plotting. Defaults to NULL (all data)
`linecolor`	character: name of line color

Details

Plots two classifier metrics against each other, showing achievable combinations of performance metrics. For example, plotting true_positive_rate vs false_positive_rate recreates the ROC plot.

`MetricPairPlot` can plot a number of metrics. Some of the metrics are redundant, in keeping with the customary terminology of various analysis communities.

- sensitivity: fraction of true positives that were predicted to be true (also known as the true positive rate)

- specificity: fraction of true negatives to all negatives (or 1 - false_positive_rate)
- precision: fraction of predicted positives that are true positives
- recall: same as sensitivity or true positive rate
- accuracy: fraction of items correctly decided
- false_positive_rate: fraction of negatives predicted to be true over all negatives
- true_positive_rate: fraction of positives predicted to be true over all positives
- false_negative_rate: fraction of positives predicted to be all false over all positives
- true_negative_rate: fraction negatives predicted to be false over all negatives

`points_to_plot` specifies the approximate number of datums used to create the plots as an absolute count; for example setting `points_to_plot = 200` uses approximately 200 points, rather than the entire data set. This can be useful when visualizing very large data sets.

See Also

ThresholdPlot, PRTPlot, ROCPlot, PRPlot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

# data with two different regimes of behavior
d <- rbind(
  data.frame(
    x =  rnorm(1000),
    y = sample(c(TRUE, FALSE), prob = c(0.02, 0.98), size = 1000, replace = TRUE)),
  data.frame(
    x =  rnorm(200) + 5,
    y = sample(c(TRUE, FALSE), size = 200, replace = TRUE))
)

# Sensitivity/Specificity examples
MetricPairPlot(d, 'x', 'y',
   x_metric = 'false_positive_rate',
   y_metric = 'true_positive_rate',
   truth_target = TRUE,
   title = 'ROC equivalent')
if(FALSE) {
ThresholdPlot(d, 'x', 'y',
   title = 'Sensitivity/Specificity',
   metrics = c('sensitivity', 'specificity'),
   truth_target = TRUE)
ROCPlot(d, 'x', 'y',
   truthTarget = TRUE,
   title = 'ROC example')

# Precision/Recall examples
```

```
ThresholdPlot(d, 'x', 'y',
   title = 'precision/recall',
   metrics = c('recall', 'precision'),
   truth_target = TRUE)
MetricPairPlot(d, 'x', 'y',
   x_metric = 'recall',
   y_metric = 'precision',
   title = 'recall/precision',
   truth_target = TRUE)
PRPlot(d, 'x', 'y',
   truthTarget = TRUE,
   title = 'p/r plot')
}
```

`PairPlot` *Build a pair plot*

Description

Creates a matrix of scatterplots, one for each possible pair of variables.

Usage

```
PairPlot(
  d,
  meas_vars,
  title,
  ...,
  group_var = NULL,
  alpha = 1,
  palette = "Dark2",
  point_color = "darkgray"
)
```

Arguments

`d`	data frame
`meas_vars`	the variables to be plotted
`title`	plot title
`...`	not used, forces later arguments to bind by name
`group_var`	variable for grouping and colorcoding
`alpha`	alpha for points on plot
`palette`	name of a brewer palette (NULL for ggplot2 default coloring)
`point_color`	point color for monochrome plots (no grouping)

Details

If palette is NULL, and group_var is non-NULL, plot colors will be chosen from the default ggplot2 palette. Setting palette to NULL allows the user to choose a non-Brewer palette, for example with scale_color_manual.

Value

a ggplot2 pair plot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

# PairPlot(iris, colnames(iris)[1:4], "Example plot", group_var = "Species")

# custom palette
colormap = c('#a6611a', '#dfc27d', '#018571')
PairPlot(iris, colnames(iris)[1:4], "Example plot",
         group_var = "Species", palette=NULL) +
         ggplot2::scale_color_manual(values=colormap)

# # no color-coding
# PairPlot(iris, colnames(iris)[1:4], "Example plot")
```

PlotDistCountBinomial *Plot count data with a theoretical binomial*

Description

Compares empirical count data to a binomial distribution

Usage

```
PlotDistCountBinomial(
  frm,
  xvar,
  trial_size,
  title,
  ...,
  p = NULL,
  limit_to_observed_range = FALSE,
  count_color = "black",
  binom_color = "blue"
)
```

Arguments

frm	data frame to get values from
xvar	column of frm that counts the number of successes for each trial
trial_size	the number of "coin flips" in a trial
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
p	mean of the binomial. If NULL, use empirical mean
limit_to_observed_range	If TRUE, limit plot to observed counts
count_color	color of empirical distribution
binom_color	color of theoretical binomial

Details

This function is useful for comparing the number of successes that occur in a series of trials, all of the same size, to a binomial of a given success-probability.

Plots the empirical distribution of successes, and a theoretical matching binomial. If the mean of the binomial, p, is given, the binomial with success-probability p is plotted. Otherwise, p is taken to be the pooled success rate of the data: `sum(frm[[xvar]]) / (trial_size*nrow(frm))`. The mean of the binomial is reported in the subtitle of the plot (to three significant figures).

If `limit_to_observed_range` is TRUE, the range of the plot will only cover the range of the empirical data. Otherwise, the range of the plot will be `0:trial_size` (the default).

See Also

PlotDistHistBeta, PlotDistDensityBeta,

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(23590)
class_size = 35
nclasses = 100
true_frate = 0.4
fdata = data.frame(n_female = rbinom(nclasses, class_size, true_frate), stringsAsFactors = FALSE)

title = paste("Distribution of count of female students, class size =", class_size)
# compare to empirical p
PlotDistCountBinomial(fdata, "n_female", class_size, title)

if(FALSE) {
  # compare to theoretical p of 0.5
  PlotDistCountBinomial(fdata, "n_female", class_size, title,
```

```
                      p = 0.5)

  # Example where the distribution is not of a true single binomial
  fdata2 = rbind(data.frame(n_female = rbinom(50, class_size, 0.25)),
                 data.frame(n_female = rbinom(10, class_size, 0.60)),
                 stringsAsFactors = FALSE )
  PlotDistCountBinomial(fdata2, "n_female", class_size, title)
}
```

`PlotDistCountNormal` *Plot distribution details as a histogram plus matching normal*

Description

Compares empirical data to a normal distribution with the same mean and standard deviation.

Usage

```
PlotDistCountNormal(
  frm,
  xvar,
  title,
  ...,
  binWidth = c(),
  hist_color = "black",
  normal_color = "blue",
  mean_color = "blue",
  sd_color = "blue"
)
```

Arguments

`frm`	data frame to get values from
`xvar`	name of the independent (input or model) column in frame
`title`	title to place on plot
`...`	no unnamed argument, added to force named binding of later arguments.
`binWidth`	width of histogram bins
`hist_color`	color of empirical histogram
`normal_color`	color of matching theoretical normal
`mean_color`	color of mean line
`sd_color`	color of 1-standard deviation lines (can be NULL)

Details

Plots the histograms of the empirical distribution and of the matching normal distribution. Also plots the mean and plus/minus one standard deviation.

Bin width for the histogram is calculated automatically to yield approximately 50 bins across the range of the data, unless the `binWidth` argument is explicitly passed in. `binWidth` is reported in the subtitle of the plot.

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(52523)
d <- data.frame(wt=100*rnorm(100))
PlotDistCountNormal(d,'wt','example')

# # no sd lines
# PlotDistCountNormal(d, 'wt', 'example', sd_color=NULL)
```

PlotDistDensityBeta *Plot empirical rate data as a density with the matching beta distribution*

Description

Compares empirical rate data to a beta distribution with the same mean and standard deviation.

Usage

```
PlotDistDensityBeta(
  frm,
  xvar,
  title,
  ...,
  curve_color = "lightgray",
  beta_color = "blue",
  mean_color = "blue",
  sd_color = "darkgray"
)
```

Arguments

`frm`	data frame to get values from
`xvar`	name of the independent (input or model) column in frame

title	title to place on plot
...	force later arguments to bind by name
curve_color	color for empirical density curve
beta_color	color for matching theoretical beta
mean_color	color for mean line
sd_color	color for 1-standard deviation lines (can be NULL)

Details

Plots the empirical density, the theoretical matching beta, the mean value, and plus/minus one standard deviation from the mean.

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(52523)
N = 100
pgray = 0.1  # rate of gray horses in the population
herd_size = round(runif(N, min=25, 50))
ngray = rbinom(N, herd_size, pgray)
hdata = data.frame(n_gray=ngray, herd_size=herd_size)

# observed rate of gray horses in each herd
hdata$rate_gray = with(hdata, ngray/herd_size)

title = "Observed prevalence of gray horses in population"

PlotDistDensityBeta(hdata, "rate_gray", title) +
  ggplot2::geom_vline(xintercept = pgray, linetype=4, color="maroon") +
  ggplot2::annotate("text", x=pgray+0.01, y=0.01, hjust="left",
                    label = paste("True prevalence =", pgray))

# # no sd lines
# PlotDistDensityBeta(hdata, "rate_gray", title,
#                     sd_color=NULL)
```

PlotDistDensityNormal *Plot an empirical density with the matching normal distribution*

Description

Compares empirical data to a normal distribution with the same mean and standard deviation.

Usage

```
PlotDistDensityNormal(
  frm,
  xvar,
  title,
  ...,
  adjust = 0.5,
  curve_color = "lightgray",
  normal_color = "blue",
  mean_color = "blue",
  sd_color = "darkgray"
)
```

Arguments

frm	data frame to get values from
xvar	name of the independent (input or model) column in frame
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
adjust	passed to geom_density; controls smoothness of density plot
curve_color	color for empirical density curve
normal_color	color for theoretical matching normal
mean_color	color of mean line
sd_color	color for 1-standard deviation lines (can be NULL)

Details

Plots the empirical density, the theoretical matching normal, the mean value, and plus/minus one standard deviation from the mean.

See Also

geom_density

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(52523)
d <- data.frame(wt=100*rnorm(100))
PlotDistDensityNormal(d,'wt','example')

# # no sd lines
# PlotDistDensityNormal(d, 'wt', 'example', sd_color=NULL)
```

PlotDistHistBeta *Plot empirical rate data as a histogram plus matching beta*

Description

Compares empirical rate data to a beta distribution with the same mean and standard deviation.

Usage

```
PlotDistHistBeta(
  frm,
  xvar,
  title,
  ...,
  bins = 30,
  hist_color = "darkgray",
  beta_color = "blue",
  mean_color = "blue",
  sd_color = "darkgray"
)
```

Arguments

frm	data frame to get values from
xvar	name of the independent (input or model) column in frame
title	title to place on plot
...	force later arguments to bind by name
bins	passed to geom_histogram(). Default: 30
hist_color	color of empirical histogram
beta_color	color of matching theoretical beta
mean_color	color of mean line
sd_color	color of 1-standard devation lines (can be NULL)

Details

Plots the histogram of the empirical distribution and the density of the matching beta distribution. Also plots the mean and plus/minus one standard deviation.

The number of bins for the histogram defaults to 30. The binwidth can also be passed in instead of the number of bins.

Value

ggplot2 plot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(52523)
N = 100
pgray = 0.1  # rate of gray horses in the population
herd_size = round(runif(N, min=25, 50))
ngray = rbinom(N, herd_size, pgray)
hdata = data.frame(n_gray=ngray, herd_size=herd_size)

# observed rate of gray horses in each herd
hdata$rate_gray = with(hdata, n_gray/herd_size)

title = "Observed prevalence of gray horses in population"

PlotDistHistBeta(hdata, "rate_gray", title) +
  ggplot2::geom_vline(xintercept = pgray, linetype=4, color="maroon") +
  ggplot2::annotate("text", x=pgray+0.01, y=0.01, hjust="left",
                    label = paste("True prevalence =", pgray))

# # no sd lines
# PlotDistHistBeta(hdata, "rate_gray", title,
#                      sd_color=NULL)
```

`plotlyROC` *Use* `plotly` *to produce a ROC plot.*

Description

Note: any `arrange_` warning is a version incompatibility between `plotly` and `dplyr`.

Usage

```
plotlyROC(
  d,
  predCol,
  outcomeCol,
  outcomeTarget,
  title,
  ...,
  estimate_sig = FALSE
)
```

Arguments

d	dataframe
predCol	name of column with numeric predictions
outcomeCol	name of column with truth
outcomeTarget	value considered true
title	character title for plot
...	no unnamed argument, added to force named binding of later arguments.
estimate_sig	logical, if TRUE estimate and display significance of difference from AUC 0.5.

Value

plotly plot

See Also

ROCPlot

Examples

```
if(FALSE && requireNamespace("plotly", quietly = TRUE)) {
   if (requireNamespace('data.table', quietly = TRUE)) {
    # don't multi-thread during CRAN checks
     data.table::setDTthreads(1)
   }
   set.seed(34903490)
   x = rnorm(50)
   y = 0.5*x^2 + 2*x + rnorm(length(x))
   frm = data.frame(x=x,yC=y>=as.numeric(quantile(y,probs=0.8)))
   plotlyROC(frm, 'x', 'yC', TRUE, 'example plot', estimate_sig = TRUE)
}
```

---

plot_fit_trajectory *Plot the trajectory of a model fit.*

Description

Plot a history of model fit performance over the a trajectory of times.

Usage

```
plot_fit_trajectory(
  d,
  column_description,
  title,
  ...,
  epoch_name = "epoch",
  needs_flip = c(),
  pick_metric = NULL,
  discount_rate = NULL,
  draw_ribbon = FALSE,
  draw_segments = FALSE,
  val_color = "#d95f02",
  train_color = "#1b9e77",
  pick_color = "#e6ab02"
)
```

Arguments

d	data frame to get values from.
column_description	description of column measures (data.frame with columns measure, validation, and training).
title	character title for plot.
...	force later arguments to be bound by name
epoch_name	name for epoch or trajectory column.
needs_flip	character array of measures that need to be flipped.
pick_metric	character metric to maximize.
discount_rate	numeric what fraction of over-fit to subtract from validation performance.
draw_ribbon	present the difference in training and validation performance as a ribbon rather than two curves? (default FALSE)
draw_segments	logical if TRUE draw over-fit/under-fit segments.
val_color	color for validation performance curve
train_color	color for training performance curve
pick_color	color for indicating optimal stopping point

Details

This visualization can be applied to any staged machine learning algorithm. For example one could plot the performance of a gradient boosting machine as a function of the number of trees added. The fit history data should be in the form given in the example below.

The example below gives a fit plot for a history report from Keras R package. Please see https://win-vector.com/2017/12/23/plotting-deep-learning-model-performance-trajectories/ for some examples and details.

Value

ggplot2 plot

See Also

plot_Keras_fit_trajectory

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

d <- data.frame(
  epoch    = c(1,         2,         3,         4,         5),
  val_loss = c(0.3769818, 0.2996994, 0.2963943, 0.2779052, 0.2842501),
  val_acc  = c(0.8722000, 0.8895000, 0.8822000, 0.8899000, 0.8861000),
  loss     = c(0.5067290, 0.3002033, 0.2165675, 0.1738829, 0.1410933),
  acc      = c(0.7852000, 0.9040000, 0.9303333, 0.9428000, 0.9545333) )

cT <- data.frame(
  measure =    c("minus binary cross entropy", "accuracy"),
  training =   c("loss",                       "acc"),
  validation = c("val_loss",                   "val_acc"),
  stringsAsFactors = FALSE)

plt <- plot_fit_trajectory(
  d,
  column_description = cT,
  needs_flip = "minus binary cross entropy",
  title = "model performance by epoch, dataset, and measure",
  epoch_name = "epoch",
  pick_metric = "minus binary cross entropy",
  discount_rate = 0.1)

print(plt)
```

---

plot_Keras_fit_trajectory

Plot the trajectory of a Keras model fit.

Description

Plot a history of model fit performance over the number of training epochs.

Usage

```
plot_Keras_fit_trajectory(
  d,
  title,
  ...,
  epoch_name = "epoch",
  lossname = "loss",
  loss_pretty_name = "minus binary cross entropy",
  perfname = "acc",
  perf_pretty_name = "accuracy",
  pick_metric = loss_pretty_name,
  fliploss = TRUE,
  discount_rate = NULL,
  draw_ribbon = FALSE,
  val_color = "#d95f02",
  train_color = "#1b9e77",
  pick_color = "#e6ab02"
)
```

Arguments

d	data frame to get values from.
title	character title for plot.
...	force later arguments to be bound by name
epoch_name	name for epoch or trajectory column.
lossname	name of training loss column (default 'loss')
loss_pretty_name	name for loss on graph (default 'minus binary cross entropy')
perfname	name of training performance column (default 'acc')
perf_pretty_name	name for performance metric on graph (default 'accuracy')
pick_metric	character: metric to maximize (NULL for no pick line - default loss_pretty_name)
fliploss	flip the loss so that "larger is better"? (default TRUE)
discount_rate	numeric: what fraction of over-fit to subtract from validation performance.
draw_ribbon	present the difference in training and validation performance as a ribbon rather than two curves? (default FALSE)
val_color	color for validation performance curve
train_color	color for training performance curve
pick_color	color for indicating optimal stopping point

Details

Assumes a performance matrix that carries information for both training and validation loss, and an additional training and validation performance metric, in the format that a Keras history object returns.

By default, flips the loss so that better performance is larger for both the loss and the performance metric, and then draws a vertical line at the minimum validation loss (maximum flipped validation loss). If you choose not to flip the loss, you should not use the loss as the pick_metric.

The example below gives a fit plot for a history report from Keras R package. Please see https://winvector.github.io/FluidData/PlotExample/KerasPerfPlot.html for some details.

Value

ggplot2 plot

See Also

plot_fit_trajectory

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

# example data (from Keras)
d <- data.frame(
  val_loss = c(0.3769818, 0.2996994, 0.2963943, 0.2779052, 0.2842501),
  val_acc  = c(0.8722000, 0.8895000, 0.8822000, 0.8899000, 0.8861000),
  loss     = c(0.5067290, 0.3002033, 0.2165675, 0.1738829, 0.1410933),
  acc      = c(0.7852000, 0.9040000, 0.9303333, 0.9428000, 0.9545333) )

plt <- plot_Keras_fit_trajectory(
  d,
  title = "model performance by epoch, dataset, and measure")

print(plt)
```

PRPlot *Plot Precision-Recall plot.*

Description

Plot Precision-Recall plot.

Usage

```
PRPlot(frame, xvar, truthVar, truthTarget, title, ..., estimate_sig = FALSE)
```

Arguments

frame	data frame to get values from
xvar	name of the independent (input or model) column in frame
truthVar	name of the dependent (output or result to be modeled) column in frame
truthTarget	value we consider to be positive
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
estimate_sig	logical, if TRUE compute significance

Details

See https://www.nature.com/articles/nmeth.3945 for a discussion of precision and recall, and how the precision/recall plot relates to the ROC plot.

In addition to plotting precision versus recall, PRPlot reports the best achieved F1 score, and plots an isoline corresponding to that F1 score.

See Also

ROCPlot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
x = rnorm(50)
y = 0.5*x^2 + 2*x + rnorm(length(x))
frm = data.frame(x=x,y=y,yC=y>=as.numeric(quantile(y,probs=0.8)))
frm$absY <- abs(frm$y)
frm$posY = frm$y > 0
frm$costX = 1
WVPlots::PRPlot(frm, "x", "yC", TRUE, title="Example Precision-Recall plot")
```

PRTPlot *Plot Precision-Recall or Enrichment-Recall as a function of threshold.*

Description

Plot classifier performance metrics as a function of threshold.

Usage

```
PRTPlot(
  frame,
  predVar,
  truthVar,
  truthTarget,
  title,
  ...,
  plotvars = c("precision", "recall"),
  thresholdrange = c(-Inf, Inf),
  linecolor = "black"
)
```

Arguments

frame	data frame to get values from
predVar	name of the column of predicted scores
truthVar	name of the column of actual outcomes in frame
truthTarget	value we consider to be positive
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
plotvars	variables to plot, must be at least one of the measures listed below. Defaults to c("precision", "recall")
thresholdrange	range of thresholds to plot.
linecolor	line color for the plot

Details

For a classifier, the precision is what fraction of predicted positives are true positives; the recall is what fraction of true positives the classifier finds, and the enrichment is the ratio of classifier precision to the average rate of positives. Plotting precision-recall or enrichment-recall as a function of classifier score helps identify a score threshold that achieves an acceptable tradeoff between precision and recall, or enrichment and recall.

In addition to precision/recall, PRTPlot can plot a number of other metrics:

- precision: fraction of predicted positives that are true positives
- recall: fraction of true positives that were predicted to be true
- enrichment: ratio of classifier precision to prevalence of positive class
- sensitivity: the same as recall (also known as the true positive rate)
- specificity: fraction of true negatives to all negatives (or 1 - false_positive_rate)
- false_positive_rate: fraction of negatives predicted to be true over all negatives

For example, plotting sensitivity/false_positive_rate as functions of threshold will "unroll" an ROC Plot.

Plots are in a single column, in the order specified by plotvars.

See Also

ThresholdPlot, ROCPlot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

df <- iris
df$isVersicolor <- with(df, Species=='versicolor')
model = glm(isVersicolor ~ Petal.Length + Petal.Width + Sepal.Length + Sepal.Width,
            data=df, family=binomial)
df$pred = predict(model, newdata=df, type="response")

WVPlots::PRTPlot(df, "pred", "isVersicolor", TRUE, title="Example Precision-Recall threshold plot")

if (FALSE) {
WVPlots::PRTPlot(df, "pred", "isVersicolor", TRUE,
                 plotvars = c("sensitivity", "specificity", "false_positive_rate"),
                 title="Sensitivity/specificity/FPR as functions of threshold")
}
```

ROCPlot *Plot receiver operating characteristic plot.*

Description

Plot receiver operating characteristic plot.

Usage

```
ROCPlot(
  frame,
  xvar,
  truthVar,
  truthTarget,
  title,
  ...,
  estimate_sig = FALSE,
  returnScores = FALSE,
  nrep = 100,
  parallelCluster = NULL,
  curve_color = "darkblue",
  fill_color = "black",
  diag_color = "black",
```

```
  add_beta_ideal_curve = FALSE,
  beta_ideal_curve_color = "#fd8d3c",
  add_beta1_ideal_curve = FALSE,
  beta1_ideal_curve_color = "#f03b20",
  add_symmetric_ideal_curve = FALSE,
  symmetric_ideal_curve_color = "#bd0026",
  add_convex_hull = FALSE,
  convex_hull_color = "#404040",
  ideal_plot_step_size = 0.001
)
```

Arguments

frame	data frame to get values from
xvar	name of the independent (input or model) column in frame
truthVar	name of the dependent (output or result to be modeled) column in frame
truthTarget	value we consider to be positive
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
estimate_sig	logical, if TRUE estimate and display significance of difference from AUC 0.5.
returnScores	logical if TRUE return detailed permutedScores
nrep	number of permutation repetitions to estimate p values.
parallelCluster	(optional) a cluster object created by package parallel or package snow.
curve_color	color of the ROC curve
fill_color	shading color for the area under the curve
diag_color	color for the AUC=0.5 line (x=y)
add_beta_ideal_curve	logical, if TRUE add the beta(a, b), beta(c, d) ideal curve found by moment matching.
beta_ideal_curve_color	color for ideal curve.
add_beta1_ideal_curve	logical, if TRUE add the beta(1, a), beta(b, 2) ideal curve defined in doi:10.1177/0272989X15582210
beta1_ideal_curve_color	color for ideal curve.
add_symmetric_ideal_curve	logical, if TRUE add the ideal curve as discussed in https://win-vector.com/2020/09/13/why-working-with-auc-is-more-powerful-than-one-might-think/.
symmetric_ideal_curve_color	color for ideal curve.
add_convex_hull	logical, if TRUE add convex hull to plot

convex_hull_color
: color for convex hull curve

ideal_plot_step_size
: step size used in ideal plots

Details

See https://www.nature.com/articles/nmeth.3945 for a discussion of true positive and false positive rates, and how the ROC plot relates to the precision/recall plot.

See Also

PRTPlot, ThresholdPlot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

beta_example <- function(
  n,
  shape1_pos, shape2_pos,
  shape1_neg, shape2_neg) {
  d <- data.frame(
    y = sample(
      c(TRUE, FALSE),
      size = n,
      replace = TRUE),
    score = 0.0
  )
  d$score[d$y] <- rbeta(sum(d$y), shape1 = shape1_pos, shape2 = shape2_pos)
  d$score[!d$y] <- rbeta(sum(!d$y), shape1 = shape1_neg, shape2 = shape2_neg)
  d
}

d1 <- beta_example(
  100,
  shape1_pos = 6,
  shape2_pos = 5,
  shape1_neg = 1,
  shape2_neg = 2)

ROCPlot(
   d1,
   xvar = "score",
   truthVar = "y", truthTarget = TRUE,
   title="Example ROC plot",
   estimate_sig = TRUE,
   add_beta_ideal_curve = TRUE,
   add_convex_hull = TRUE)
```

ROCPlotList *Compare multiple ROC plots.*

Description

Plot multiple receiver operating characteristic curves from the same data.frame.

Usage

```
ROCPlotList(
  frame,
  xvar_names,
  truthVar,
  truthTarget,
  title,
  ...,
  palette = "Dark2"
)

ROCPlotPairList(
  frame,
  xvar_names,
  truthVar,
  truthTarget,
  title,
  ...,
  palette = "Dark2"
)

ROCListPlot(
  frame,
  xvar_names,
  truthVar,
  truthTarget,
  title,
  ...,
  palette = "Dark2"
)
```

Arguments

frame	data frame to get values from
xvar_names	names of the independent (input or model) columns in frame
truthVar	name of the dependent (output or result to be modeled) column in frame
truthTarget	value we consider to be positive
title	title to place on plot

...	no unnamed argument, added to force named binding of later arguments.
palette	name of a brewer palette (NULL for ggplot2 default coloring)

Details

The use case for this function is to compare the performance of two models when applied to a data set, where the predictions from both models are columns of the same data frame.

If palette is NULL, plot colors will be chosen from the default ggplot2 palette. Setting palette to NULL allows the user to choose a non-Brewer palette, for example with scale_color_manual.

See Also

ROCPlot, ROCPlotPair, ROCPlotPair2

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
x1 = rnorm(50)
x2 = rnorm(length(x1))
x3 = rnorm(length(x1))
y = 0.2*x2^2 + 0.5*x2 + x1 + rnorm(length(x1))
frm = data.frame(
   x1 = x1,
   x2 = x2,
   x3 = x3,
   yC = y >= as.numeric(quantile(y,probs=0.8)))
WVPlots::ROCPlotList(
   frame = frm,
   xvar_names = c("x1", "x2", "x3"),
   truthVar = "yC", truthTarget = TRUE,
   title = "Example ROC list plot")
```

ROCPlotPair *Compare two ROC plots.*

Description

Plot two receiver operating characteristic curves from the same data.frame.

Usage

```
ROCPlotPair(
  frame,
  xvar1,
  xvar2,
  truthVar,
  truthTarget,
  title,
  ...,
  estimate_sig = FALSE,
  returnScores = FALSE,
  nrep = 100,
  parallelCluster = NULL,
  palette = "Dark2"
)
```

Arguments

`frame`	data frame to get values from
`xvar1`	name of the first independent (input or model) column in frame
`xvar2`	name of the second independent (input or model) column in frame
`truthVar`	name of the dependent (output or result to be modeled) column in frame
`truthTarget`	value we consider to be positive
`title`	title to place on plot
`...`	no unnamed argument, added to force named binding of later arguments.
`estimate_sig`	logical, if TRUE estimate and display significance of difference from AUC 0.5.
`returnScores`	logical if TRUE return detailed permutedScores
`nrep`	number of permutation repetitions to estimate p values.
`parallelCluster`	(optional) a cluster object created by package parallel or package snow.
`palette`	name of a brewer palette (NULL for ggplot2 default coloring)

Details

The use case for this function is to compare the performance of two models when applied to a data set, where the predictions from both models are columns of the same data frame.

If `palette` is NULL, plot colors will be chosen from the default ggplot2 palette. Setting `palette` to NULL allows the user to choose a non-Brewer palette, for example with `scale_color_manual`.

See Also

`ROCPlot`

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
x1 = rnorm(50)
x2 = rnorm(length(x1))
y = 0.2*x2^2 + 0.5*x2 + x1 + rnorm(length(x1))
frm = data.frame(x1=x1,x2=x2,yC=y>=as.numeric(quantile(y,probs=0.8)))
# WVPlots::ROCPlot(frm, "x1", "yC", TRUE, title="Example ROC plot")
# WVPlots::ROCPlot(frm, "x2", "yC", TRUE, title="Example ROC plot")
WVPlots::ROCPlotPair(frm, "x1", "x2", "yC", TRUE,
   title="Example ROC pair plot", estimate_sig = TRUE)
```

ROCPlotPair2 *Compare two ROC plots.*

Description

Plot two receiver operating characteristic curves from different data frames.

Usage

```
ROCPlotPair2(
  nm1,
  frame1,
  xvar1,
  truthVar1,
  truthTarget1,
  nm2,
  frame2,
  xvar2,
  truthVar2,
  truthTarget2,
  title,
  ...,
  estimate_sig = TRUE,
  returnScores = FALSE,
  nrep = 100,
  parallelCluster = NULL,
  palette = "Dark2"
)
```

Arguments

nm1	name of first model
frame1	data frame to get values from
xvar1	name of the first independent (input or model) column in frame
truthVar1	name of the dependent (output or result to be modeled) column in frame
truthTarget1	value we consider to be positive
nm2	name of second model
frame2	data frame to get values from
xvar2	name of the first independent (input or model) column in frame
truthVar2	name of the dependent (output or result to be modeled) column in frame
truthTarget2	value we consider to be positive
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
estimate_sig	logical, if TRUE estimate and display significance of difference from AUC 0.5.
returnScores	logical if TRUE return detailed permutedScores
nrep	number of permutation repetitions to estimate p values.
parallelCluster	(optional) a cluster object created by package parallel or package snow.
palette	name of Brewer palette to color curves (can be NULL)

Details

Use this curve to compare model predictions to true outcome from two data frames, each of which has its own model predictions and true outcome columns.

If palette is NULL, plot colors will be chosen from the default ggplot2 palette. Setting palette to NULL allows the user to choose a non-Brewer palette, for example with scale_color_manual.

See Also

ROCPlot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
x1 = rnorm(50)
x2 = rnorm(length(x1))
y = 0.2*x2^2 + 0.5*x2 + x1 + rnorm(length(x1))
frm = data.frame(x1=x1,x2=x2,yC=y>=as.numeric(quantile(y,probs=0.8)))
# WVPlots::ROCPlot(frm, "x1", "yC", TRUE, title="Example ROC plot")
```

```
# WVPlots::ROCPlot(frm, "x2", "yC", TRUE, title="Example ROC plot")
WVPlots::ROCPlotPair2('train',frm, "x1", "yC", TRUE,
                      'test', frm, "x2", "yC", TRUE,
                      title="Example ROC pair plot", estimate_sig = TRUE)
```

`ScatterBoxPlot` *Plot a scatter box plot.*

Description

Plot a boxplot with the data points superimposed.

Usage

```
ScatterBoxPlot(
  frm,
  xvar,
  yvar,
  title,
  ...,
  pt_alpha = 0.3,
  pt_color = "black",
  box_color = "black",
  box_fill = "lightgray"
)
```

Arguments

`frm`	data frame to get values from
`xvar`	name of the independent column in frame; assumed discrete
`yvar`	name of the continuous column in frame
`title`	plot title
`...`	(doesn't take additional arguments, used to force later arguments by name)
`pt_alpha`	transparency of points in scatter plot
`pt_color`	point color
`box_color`	boxplot line color
`box_fill`	boxplot fill color (can be NA for no fill)

Details

`xvar` is a discrete variable and `yvar` is a continuous variable.

See Also

`ScatterBoxPlotH`

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

classes = c("a", "b", "c")
means = c(2, 4, 3)
names(means) = classes
label = sample(classes, size=1000, replace=TRUE)
meas = means[label] + rnorm(1000)
frm2 = data.frame(label=label,
                  meas = meas)
WVPlots::ScatterBoxPlot(frm2, "label", "meas", pt_alpha=0.2, title="Example Scatter/Box plot")
```

`ScatterBoxPlotH` *Plot a scatter box plot in horizontal mode.*

Description

Plot a boxplot with the data points superimposed. Box plots are aligned horizontally.

Usage

```
ScatterBoxPlotH(
  frm,
  xvar,
  yvar,
  title,
  ...,
  pt_alpha = 0.3,
  pt_color = "black",
  box_color = "black",
  box_fill = "lightgray"
)
```

Arguments

`frm`	data frame to get values from
`xvar`	name of the continuous column in frame
`yvar`	name of the independent column in frame; assumed discrete
`title`	plot title
`...`	(doesn't take additional arguments, used to force later arguments by name)
`pt_alpha`	transparency of points in scatter plot
`pt_color`	point color
`box_color`	boxplot line color
`box_fill`	boxplot fill color (can be NA for no fill)

Details

xvar is a continuous variable and yvar is a discrete variable.

See Also

ScatterBoxPlot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

classes = c("a", "b", "c")
means = c(2, 4, 3)
names(means) = classes
label = sample(classes, size=1000, replace=TRUE)
meas = means[label] + rnorm(1000)
frm2 = data.frame(label=label,
                  meas = meas)
WVPlots::ScatterBoxPlotH(frm2, "meas", "label",  pt_alpha=0.2, title="Example Scatter/Box plot")
```

ScatterHist *Plot a scatter plot with marginals.*

Description

Plot a scatter plot with optional smoothing curves or contour lines, and marginal histogram/density plots. Based on https://win-vector.com/2015/06/11/wanted-a-perfect-scatterplot-with-marginals/. See also ggExtra::ggMarginal.

Usage

```
ScatterHist(
  frame,
  xvar,
  yvar,
  title,
  ...,
  smoothmethod = "lm",
  estimate_sig = FALSE,
  minimal_labels = TRUE,
  binwidth_x = NULL,
  binwidth_y = NULL,
  adjust_x = 1,
```

```
  adjust_y = 1,
  point_alpha = 0.5,
  contour = FALSE,
  point_color = "black",
  hist_color = "gray",
  smoothing_color = "blue",
  density_color = "blue",
  contour_color = "blue"
)
```

Arguments

frame	data frame to get values from
xvar	name of the independent (input or model) column in frame
yvar	name of the dependent (output or result to be modeled) column in frame
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
smoothmethod	(optional) one of 'auto', 'loess', 'gam', 'lm', 'identity', or 'none'.
estimate_sig	logical if TRUE and smoothmethod is 'identity' or 'lm', report goodness of fit and significance of relation.
minimal_labels	logical drop some annotations
binwidth_x	numeric binwidth for x histogram
binwidth_y	numeric binwidth for y histogram
adjust_x	numeric adjust x density plot
adjust_y	numeric adjust y density plot
point_alpha	numeric opaqueness of the plot points
contour	logical if TRUE add a 2d contour plot
point_color	color for scatter plots
hist_color	fill color for marginal histograms
smoothing_color	color for smoothing line
density_color	color for marginal density plots
contour_color	color for contour plots

Details

If smoothmethod is:

- 'auto', 'loess' or 'gam': the appropriate smoothing curve is added to the scatterplot.
- 'lm' (the default): the best fit line is added to the scatterplot.
- 'identity': the line x = y is added to the scatterplot. This is useful for comparing model predictions to true outcome.
- 'none': no smoothing line is added to the scatterplot.

If estimate_sig is TRUE and smoothmethod is:

- 'lm': the R-squared of the linear fit is reported.
- 'identity': the R-squared of the exact relation between xvar and yvar is reported.

Note that the identity R-squared is NOT the square of the correlation between xvar and yvar (which includes an implicit shift and scale). It is the coefficient of determination between xvar and yvar, and can be negative. See https://en.wikipedia.org/wiki/Coefficient_of_determination for more details. If xvar is the output of a model to predict yvar, then the identity R-squared, not the lm R-squared, is the correct measure.

If smoothmethod is neither 'lm' or 'identity' then estimate_sig is ignored.

Value

plot grid

See Also

ScatterHistC

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
x = rnorm(50)
y = 0.5*x^2 + 2*x + rnorm(length(x))
frm = data.frame(x=x,y=y)
WVPlots::ScatterHist(frm, "x", "y",
  title= "Example Fit",
  smoothmethod = "gam",
  contour = TRUE)

if (FALSE) {
# Same plot with custom colors
WVPlots::ScatterHist(frm, "x", "y",
  title= "Example Fit",
  smoothmethod = "gam",
  contour = TRUE,
  point_color = "#006d2c", # dark green
  hist_color = "#6baed6", # medium blue
  smoothing_color = "#54278f", # dark purple
  density_color = "#08519c", # darker blue
  contour_color = "#9e9ac8") # lighter purple
}
```

`ScatterHistC` *Plot a conditional scatter plot with marginals.*

Description

Plot a scatter plot conditioned on a discrete variable, with marginal conditional density plots.

Usage

```
ScatterHistC(
  frame,
  xvar,
  yvar,
  cvar,
  title,
  ...,
  annot_size = 3,
  colorPalette = "Dark2",
  adjust_x = 1,
  adjust_y = 1
)
```

Arguments

`frame`	data frame to get values from
`xvar`	name of the x variable
`yvar`	name of the y variable
`cvar`	name of condition variable
`title`	title to place on plot
`...`	no unnamed argument, added to force named binding of later arguments.
`annot_size`	numeric scale annotation text (if present)
`colorPalette`	name of a Brewer palette (see https://colorbrewer2.org/)
`adjust_x`	numeric: adjust x density plot
`adjust_y`	numeric: adjust y density plot

Details

`xvar` and `yvar` are the coordinates of the points, and `cvar` is the discrete conditioning variable that indicates which category each point (x,y) belongs to.

Value

plot grid

See Also

ScatterHist

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
frm = data.frame(x=rnorm(50),y=rnorm(50))
frm$cat <- frm$x+frm$y>0
WVPlots::ScatterHistC(frm, "x", "y", "cat",
                      title="Example Conditional Distribution")
```

ScatterHistN *Plot a height scatter plot with marginals.*

Description

Plot a scatter plot conditioned on a continuous variable, with marginal conditional density plots.

Usage

```
ScatterHistN(
  frame,
  xvar,
  yvar,
  zvar,
  title,
  ...,
  annot_size = 3,
  colorPalette = "RdYlBu",
  nclus = 3,
  adjust_x = 1,
  adjust_y = 1
)
```

Arguments

frame	data frame to get values from
xvar	name of the x variable
yvar	name of the y variable
zvar	name of height variable
title	title to place on plot

...	no unnamed argument, added to force named binding of later arguments.
annot_size	numeric: scale annotation text (if present)
colorPalette	name of a Brewer palette (see https://colorbrewer2.org/)
nclus	scalar: number of z-clusters to plot
adjust_x	numeric: adjust x density plot
adjust_y	numeric: adjust y density plot

Details

xvar and yvar are the coordinates of the points, and zvar is the continuous conditioning variable. zvar is partitioned into nclus disjoint ranges (by default, 3), which are then treated as discrete categories.The scatterplot and marginal density plots are color-coded by these categories.

See Also

ScatterHistC

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(34903490)
frm = data.frame(x=rnorm(50),y=rnorm(50))
frm$z <- frm$x+frm$y
WVPlots::ScatterHistN(frm, "x", "y", "z", title="Example Joint Distribution")
```

ShadedDensity *Plot the distribution of a variable with a tail shaded*

Description

Plot the distribution of a variable with a tail shaded. Annotate with the area of the shaded region.

Usage

```
ShadedDensity(
  frame,
  xvar,
  threshold,
  title,
  ...,
  tail = "left",
  linecolor = "darkgray",
```

```
  shading = "darkblue",
  annotate_area = TRUE
)
```

Arguments

frame	data frame to get values from
xvar	name of the variable to be density plotted
threshold	boundary value for the tail
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
tail	which tail to shade, 'left' (default) or 'right'
linecolor	color of density curve
shading	color of shaded region and boundaries
annotate_area	if TRUE (default), report the area of the shaded region

See Also

ShadedDensityCenter

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(52523)
d = data.frame(meas=rnorm(100))
threshold = -1.5
WVPlots::ShadedDensity(d, "meas", threshold,
                       title="Example shaded density plot, left tail")
if (FALSE) {
WVPlots::ShadedDensity(d, "meas", -threshold, tail="right",
                       title="Example shaded density plot, right tail")
}
```

ShadedDensityCenter *Plot the distribution of a variable with a center region shaded*

Description

Plot the distribution of a variable with a center region shaded. Annotate with the area of the shaded region.

Usage

```
ShadedDensityCenter(
  frame,
  xvar,
  boundaries,
  title,
  ...,
  linecolor = "darkgray",
  shading = "darkblue",
  annotate_area = TRUE
)
```

Arguments

frame	data frame to get values from
xvar	name of the variable to be density plotted
boundaries	vector of the min and max boundaries of the shaded region
title	title to place on plot
...	no unnamed argument, added to force named binding of later arguments.
linecolor	color of density curve
shading	color of shaded region and boundaries
annotate_area	if TRUE (default), report the area of the shaded region

See Also

ShadedDensity

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

set.seed(52523)
d = data.frame(meas=rnorm(100))
boundaries = c(-1.5, 1.5)
WVPlots::ShadedDensityCenter(d, "meas", boundaries,
                      title="Example center-shaded density plot")
```

ShadowHist *Plot a Shadow Histogram Plot*

Description

Plot a histogram of a continuous variable xvar, faceted on a categorical conditioning variable, condvar. Each faceted plot also shows a "shadow plot" of the unconditioned histogram for comparison.

Usage

```
ShadowHist(
  frm,
  xvar,
  condvar,
  title,
  ...,
  ncol = 1,
  monochrome = FALSE,
  palette = "Dark2",
  fillcolor = "darkblue",
  bins = 30,
  binwidth = NULL
)
```

Arguments

frm	data frame to get values from.
xvar	name of the primary continuous variable
condvar	name of conditioning variable (categorical variable, controls faceting).
title	title to place on plot.
...	no unnamed argument, added to force named binding of later arguments.
ncol	numeric: number of columns in facet_wrap.
monochrome	logical: if TRUE, all facets filled with same color
palette	character: if monochrome==FALSE, name of brewer color palette (can be NULL)
fillcolor	character: if monochrome==TRUE, name of fill color
bins	number of bins. Defaults to thirty.
binwidth	width of the bins. Overrides bins.

Details

Currently supports only the bins and binwidth arguments (see geom_histogram), but not the center, boundary, or breaks arguments.

By default, the facet plots are arranged in a single column. This can be changed with the optional ncol argument.

If palette is NULL, and monochrome is FALSE, plot colors will be chosen from the default ggplot2 palette. Setting palette to NULL allows the user to choose a non-Brewer palette, for example with scale_fill_manual. For consistency with previous releases, ShadowHist defaults to monochrome = FALSE, while ShadowPlot defaults to monochrome = TRUE.

Please see here for some interesting discussion https://drsimonj.svbtle.com/plotting-background-data-for-group

Value

a ggplot2 histogram plot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

ShadowHist(iris, "Petal.Length", "Species",
           title = "Petal Length distribution by Species")

if (FALSE) {
# make all the facets the same color
ShadowHist(iris, "Petal.Length", "Species",
           monochrome=TRUE,
           title = "Petal Length distribution by Species")
}
```

ShadowPlot *Plot a Shadow Bar Plot*

Description

Plot a bar chart of row counts conditioned on the categorical variable condvar, faceted on a second categorical variable, refinevar. Each faceted plot also shows a "shadow plot" of the totals conditioned on condvar alone.

Usage

```
ShadowPlot(
  frm,
  condvar,
```

```
  refinevar,
  title,
  ...,
  monochrome = TRUE,
  palette = "Dark2",
  fillcolor = "darkblue",
  ncol = 1
)
```

Arguments

frm	data frame to get values from.
condvar	name of the primary conditioning variable (a categorical variable, controls x-axis).
refinevar	name of the second or refining conditioning variable (also a categorical variable, controls faceting).
title	title to place on plot.
...	no unnamed argument, added to force named binding of later arguments.
monochrome	logical: if TRUE, all facets filled with same color
palette	character: if monochrome==FALSE, name of brewer color palette (can be NULL)
fillcolor	character: if monochrome==TRUE, name of fill color for bars
ncol	numeric: number of columns in facet_wrap.

Details

This plot enables comparisons of subpopulation totals across both condvar and refinevar simultaneously.

By default, the facet plots are arranged in a single column. This can be changed with the optional ncol argument.

If palette is NULL, and monochrome is FALSE, plot colors will be chosen from the default ggplot2 palette. Setting palette to NULL allows the user to choose a non-Brewer palette, for example with scale_fill_manual. For consistency with previous releases, ShadowPlot defaults to monochrome = TRUE, while ShadowHist defaults to monochrome = FALSE.

Please see here for some interesting discussion https://drsimonj.svbtle.com/plotting-background-data-for-group

Value

a ggplot2 bar chart counting examples grouped by condvar, faceted by refinevar.

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}
```

```
ShadowPlot(mtcars, "carb", "cyl",
           title = "Number of example cars by carb and cyl counts")

if (FALSE) {
# colorcode the facets
ShadowPlot(mtcars, "carb", "cyl",
           monochrome = FALSE,
           title = "Number of example cars by carb and cyl counts")
}
```

`simulate_aes_string` *Simulate the deprecated* `ggplot2::aes_string()`.

Description

Use to allow replacing code of the form `ggplot2::aes_string(...)` with code of the form `ggplot2::aes(!!!simulate_a`
Purpose is to get out of the way of the deprecation and possible future removal of `ggplot2::aes_string()`.
Inspired by the research of https://stackoverflow.com/a/74424353/6901725.

Usage

```
simulate_aes_string(...)
```

Arguments

`...`	named string arguments to turn into symbols using ‘rlang::data_sym()‘.

Value

some rlang NSE that simulates string values at great complexity (but needed for newer ggplot2()).

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

d <- data.frame(x = c(1, 2, 3), y = c(4, 5, 6))
xvar <- 'x'  # the idea is, this is passed in and not known at coding time
yvar <- 'y'
# what we want:
#  ggplot2::ggplot(data = d, mapping = ggplot2::aes_string(x = xvar, y = yvar)) +
#     ggplot2::geom_point()
# The required "tidy evaluation ideoms[sic] with `aes()`".
ggplot2::ggplot(data = d, mapping = ggplot2::aes(!!!simulate_aes_string(x = xvar, y = yvar))) +
   ggplot2::geom_point()
```

`ThresholdPlot` *Plot classifier metrics as a function of thresholds.*

Description

Plot classifier metrics as a function of thresholds.

Usage

```
ThresholdPlot(
  frame,
  xvar,
  truthVar,
  title,
  ...,
  metrics = c("sensitivity", "specificity"),
  truth_target = TRUE,
  points_to_plot = NULL,
  monochrome = TRUE,
  palette = "Dark2",
  linecolor = "black"
)
```

Arguments

`frame`	data frame to get values from
`xvar`	column of scores
`truthVar`	column of true outcomes
`title`	title to place on plot
`...`	no unnamed argument, added to force named binding of later arguments.
`metrics`	metrics to be computed. See Details for the list of allowed metrics
`truth_target`	truth value considered to be positive.
`points_to_plot`	how many data points to use for plotting. Defaults to NULL (all data)
`monochrome`	logical: if TRUE, all subgraphs plotted in same color
`palette`	character: if monochrome==FALSE, name of brewer color palette (can be NULL)
`linecolor`	character: if monochrome==TRUE, name of line color

Details

By default, `ThresholdPlot` plots sensitivity and specificity of a a classifier as a function of the decision threshold. Plotting sensitivity-specificity (or other metrics) as a function of classifier score helps identify a score threshold that achieves an acceptable tradeoff among desirable properties.

`ThresholdPlot` can plot a number of metrics. Some of the metrics are redundant, in keeping with the customary terminology of various analysis communities.

- sensitivity: fraction of true positives that were predicted to be true (also known as the true positive rate)
- specificity: fraction of true negatives to all negatives (or 1 - false_positive_rate)
- precision: fraction of predicted positives that are true positives
- recall: same as sensitivity or true positive rate
- accuracy: fraction of items correctly decided
- false_positive_rate: fraction of negatives predicted to be true over all negatives
- true_positive_rate: fraction of positives predicted to be true over all positives
- false_negative_rate: fraction of positives predicted to be all false over all positives
- true_negative_rate: fraction negatives predicted to be false over all negatives

For example, plotting sensitivity/false_positive_rate as functions of threshold will "unroll" an ROC Plot.

`ThresholdPlot` can also plot distribution diagnostics about the scores:

- fraction: the fraction of datums that scored greater than a given threshold
- cdf: CDF or `1 - fraction`; the fraction of datums that scored less than a given threshold

Plots are in a single column, in the order specified by `metrics`.

`points_to_plot` specifies the approximate number of datums used to create the plots as an absolute count; for example setting `points_to_plot = 200` uses approximately 200 points, rather than the entire data set. This can be useful when visualizing very large data sets.

See Also

PRTPlot

Examples

```
if (requireNamespace('data.table', quietly = TRUE)) {
 # don't multi-thread during CRAN checks
  data.table::setDTthreads(1)
}

# data with two different regimes of behavior
d <- rbind(
  data.frame(
    x =  rnorm(1000),
    y = sample(c(TRUE, FALSE), prob = c(0.02, 0.98), size = 1000, replace = TRUE)),
  data.frame(
    x =  rnorm(200) + 5,
    y = sample(c(TRUE, FALSE), size = 200, replace = TRUE))
)

# Sensitivity/Specificity examples
ThresholdPlot(d, 'x', 'y',
   title = 'Sensitivity/Specificity',
   metrics = c('sensitivity', 'specificity'),
```

```
   truth_target = TRUE)
if(FALSE) {
MetricPairPlot(d, 'x', 'y',
   x_metric = 'false_positive_rate',
   y_metric = 'true_positive_rate',
   truth_target = TRUE,
   title = 'ROC equivalent')
ROCPlot(d, 'x', 'y',
   truthTarget = TRUE,
   title = 'ROC example')

# Precision/Recall examples
ThresholdPlot(d, 'x', 'y',
   title = 'precision/recall',
   metrics = c('recall', 'precision'),
   truth_target = TRUE)
MetricPairPlot(d, 'x', 'y',
   x_metric = 'recall',
   y_metric = 'precision',
   title = 'recall/precision',
   truth_target = TRUE)
PRPlot(d, 'x', 'y',
   truthTarget = TRUE,
   title = 'p/r plot')
}
```

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