Package: separationplot (via r-universe)

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| Author Brian D. Greenhill, Michael D. Ward and Audrey Sacks | | | | |
| Maintainer Brian Greenhill | | | | |
| Depends RColorBrewer, Hmisc, MASS, foreign | | | | |
| Description Visual representations of model fit or predictive success in the form of ``separation plots." See Greenhill, Brian, Michael D. Ward, and Audrey Sacks. ``The separation plot: A new visual method for evaluating the fit of binary models." American Journal of Political Science 55.4 (2011): 991-1002. | | | | |
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separationplot-package

Separation Plots

Description

Visual representations of model fit or predictive success in the form of "separation plots." See Greenhill, Brian, Michael D. Ward, and Audrey Sacks. "The separation plot: A new visual method for evaluating the fit of binary models." American Journal of Political Science 55.4 (2011): 991-1002.

Details

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two outcome levels

A package to create "separation plots" as described in Greenhill, Ward, and Sacks (2011).

Author(s)

Brian D. Greenhill, Michael D. Ward and Audrey Sacks Maintainer: Brian Greenhill spreenhill@albany.edu

References

Greenhill, Brian, Michael D. Ward, and Audrey Sacks. "The separation plot: A new visual method for evaluating the fit of binary models." American Journal of Political Science 55.4 (2011): 991-1002.

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Examples

```
# Very simple example from the introduction to the paper: separationplot(pred=c(0.774, 0.364, 0.997, 0.728, 0.961, 0.422), actual=c(0,0,1,0,1,1), shuffle=FALSE, line=FALSE, type="rect", rectborder=1)
```

separationplot

Generate a Separation Plot

Description

This is the core function for the generation of a separation plot.

Usage

```
separationplot(pred, actual, type = "line", line = T, lwd1 = 0.5, lwd2 = 0.5, heading = "", xlab = "", shuffle = T, width = 9, height = 1.2, col0 = "#FEF0D9", col1 = "#E34A33", flag = NULL, flagcol = 1, file = NULL, newplot = T, locate = NULL, rectborder = NA, show.expected = F, zerosfirst = T, BW=F)
```

Arguments

height

| pred | Vector of predicted probabilities (on a continuous 0 to 1 scale). |
|---------|--|
| actual | Vector of actual outcomes (each element must be either 0 or 1). |
| type | Should the individual lines on the separation plot be plotted as line segments (type="line") or rectangles (type="rect"), or should the probabilities in different regions of the plot be grouped into distinct bands (type="bands")? |
| line | Should a trace line be added to the plot? |
| lwd1 | The width of the individual line segments (only when type="line"). |
| lwd2 | The width of the trace line (only when line=T). |
| heading | An optional title for the plot. |
| xlab | An option x-axis label. |
| shuffle | If shuffle=T, the order of rows in the results data is randomized to break up any pre-existing patterns that may distort the appearance of the results in the special case where many of the observations share the same fitted values. This happens, for example, when the original dataframe is organized in such a way that all the cases with the event of interest come before the cases without the event. Note that when shuffle=T, the random number seed is reset to 1 each time this function is called. This ensures that replicable results can be obtained even when the order of observations is randomized. |
| width | Width of the plot space (in inches). |

Height of the plot space (in inches).

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| col0 | Color of the predicted probabilities corresponding to 0s in the actual vector. The default color has been chosen from one of the palettes on https://colorbrewer2.org/ . |
|---------------|--|
| col1 | Color of the predicted probabilities corresponding to 1s in the actual vector. The default color has been chosen from one of the palettes on https://colorbrewer2.org/ . |
| flag | A vector of row number(s) in the actual vector corresponding to the observations to flag. |
| flagcol | A vector of colors for the flags. |
| file | The name and file path of where the pdf output should be written, if desired. If file=NULL the output will be written to the screen. |
| newplot | Should a new plotting space be opened up for the separation plot? Select newplot=F if you want the separation plot to be added to currently open output device. |
| locate | Number of lines (if any) on the separation plot that you want to identify with the mouse using the locator function. |
| rectborder | When type="rect", the value of this argument is passed to the border argument of the rect function used to draw the line segments. The default setting (rectborder=NA) suppresses the drawing of borders around the individual segments of the plot. |
| show.expected | If show.expected=T, a marker is added to the plot showing the expected total number of events. The expected number of events is calculated by simply summing (and rounding) the predicted probabilities over all observations. |
| zerosfirst | When type="line", should the 0s be plotted in the background, and the 1s in the foreground, or vice-versa? This will affect the output when the number of observations is very large relative to the size of the plot. |
| BW | Should the Black and White color scheme be implemented? |

Details

Please see the paper by Greenhill, Ward and Sacks (2011) for more information on the features of the separation plot.

Value

resultsmatrix

The dataframe containing the data used to generate the separation plot. The first column is the vector of predicted probabilities, the second is the vector of actual outcomes, the third indicates which observations have been flagged using the flag argument above, the fourth gives the position of each observation on the horizontal axis of the separation plot, and the fifth gives the color used to plot each observation.

Author(s)

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References

Greenhill, Brian, Michael D. Ward, and Audrey Sacks. "The separation plot: A new visual method for evaluating the fit of binary models." American Journal of Political Science 55.4 (2011): 991-1002.

See Also

See sp.categorical for plotting separation plots for models with polytomous dependent variables.

Examples

```
# Create a separation plot for a simple logit model:
library(MASS)
set.seed(1)
Sigma <- matrix(c(1,0.78,0.78,1),2,2)
a<-(mvrnorm(n=500, rep(0, 2), Sigma))
a[,2][a[,2]>0.75]<-1
a[,2][a[,2]<=0.75]<-0
a[,1]<-a[,1]-min(a[,1])
a[,1]<-a[,1]/max(a[,1])

cor(a) # should be 0.55

model1<-glm(a[,2]~a[,1], family=binomial(link = "logit"))
library(Hmisc)
somers2(model1$fitted.values, model1$y)
separationplot(pred=model1$fitted.values, actual=model1$y, type="rect", line=TRUE, show.expected=TRUE, heading="Example 1")</pre>
```

sp.categorical

Separation plots for variables with more than two outcome levels

Description

This function generates separation plots for polytomous dependent variables.

Usage

```
sp.categorical(pred, actual, file = NULL, cex = 1.5, ...)
```

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Arguments

| pred | A matrix of fitted values. Each row represents one observation, and each column represents the probability of obtaining that outcome. The column names correspond to the outcome categories. |
|--------|--|
| actual | A vector containing the actual outcomes corresponding to each observation. |
| file | The name and file path of where the pdf output should be written, if desired. If file=NULL the output will be written to the screen. |
| cex | Character expansion factor used for the outcome category labels. |
| | Additional arguments passed to separationplot. |

Details

This function is a wrapper for separationplot that generates a series of separation plots for each outcome category for a variable with more than two outcomes.

Please see the paper by Greenhill, Ward and Sacks for more information on the features of the separation plot.

Value

None. This function is used for its side effects only.

Author(s)

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References

Greenhill, Brian, Michael D. Ward, and Audrey Sacks. "The separation plot: A new visual method for evaluating the fit of binary models." American Journal of Political Science 55.4 (2011): 991-1002.

See Also

See separationplot for a description of the core function for generating separation plots.

Examples

```
# This example borrows code from the example given in the documentation for the polr() function
# that uses the "housing" dataset:
options(contrasts = c("contr.treatment", "contr.poly"))
house.plr <- polr(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)

sp.categorical(pred=house.plr$fitted.values,
actual=as.character(house.plr$model[,1]), type="rect", lwd2=2)
# not a very good fit!</pre>
```

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