Package 'logihist'

April 30, 2025

Type Package

Title Combined Graphs for Logistic Regression

Version 1.1

Date 2025-04-30

Depends ggplot2

Suggests popbio

Description Provides histograms, boxplots and dotplots as alternatives to scatterplots of data when plotting fitted logistic regressions.

NeedsCompilation no

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Repository CRAN

Date/Publication 2025-04-30 19:30:02 UTC

Contents

`logi.hist.plot2` *Plot logistic regression*

Description

Plot combined graphs for logistic regressions

Usage

```
logi.hist.plot2(independ, depend, logi.mod = 1, type = "dit",
boxp = TRUE, rug = FALSE, ylabel = "Probability", ylabel2 = "Frequency",
xlabel = "", mainlabel = "", las.h = 1, counts = FALSE, cex.p = 1,
pch.dit = 1, incre = 0.02, ...)
```

Arguments

`independ`	explanatory variable
`depend`	dependent variable, typically a logical vector
`logi.mod`	type of fitting, 1 = logistic; 2 = "gaussian" logistic
`type`	type of representation, "dit" = dot plot; "hist" = histogram
`boxp`	TRUE = with box plots, FALSE = without
`rug`	TRUE = with rug plots, FALSE = without
`ylabel`	y-axis label
`ylabel2`	2nd y-axis label
`xlabel`	x-axix label
`mainlabel`	overall title for plot
`las.h`	orientation of axes labels (0 = vertical, 1 = horizontal
`counts`	add counts above histogram bars
`cex.p`	size of points in dotplots
`pch.dit`	Either an integer specifying a symbol or a single character to be used as the default in plotting points. See `points` for possible values and their interpretation.
`incre`	increment, i.e., separation between neighbour points in the dotplot.
`...`	additional options passed to logi.hist

Value

A combined logistic regression plot

Note

This is a new version of function logi.hist.plot already available in the package **popbio**. In this new version, control of points in the dot plot is provided by the arguments `cex.p`, `pch.dit` and `incre`.

Author(s)

M. de la Cruz Rot

References

De la Cruz Rot, M. 2005. Improving the Presentation of Results of Logistic Regression with R. ESA Bulletin 86:41-48.

Examples

```
data(aq.trans, package="popbio")

aq.trans$survived<-aq.trans$fate!="dead"

a<-subset(aq.trans, leaf<50 & stage!="recruit", c(leaf,survived))

logi.hist.plot2(a$leaf,  a$survived,
type="hist", boxp=FALSE, counts=TRUE, int=10,
ylabel="Survival probability", ylabel2="Number of plants",
 xlab="Number of leaves" )

b<-glm(survived ~ leaf, binomial, data=a)
 summary(b)
```

`logihist` *Combined Graphs for Logistic Regression*

Description

Plot combined graphs for logistic regressions in the ggplot2 system.

Usage

```
logihist(x, y, scale.hist = 5, breaks = "Sturges", counts = TRUE, intervalo = 0,
   ylab2 = "Frequency", fillb = 1, colob = 1, sizeb = 1, pglm = FALSE, se = FALSE,
    sizeglm = 1, colglm = 1)
logibox(x, y, boxwd = 0.1, wiswd = 0.05, displac = 0, sizepat = 1, fillb = NA, colob = 1,
  colpat = 1, colbig = 1, colmed = 1, sizeb = 1, sizebig = 1, sizemed = 2, colout = 1,
   sizeout = 1, shapeout = 1, pglm = FALSE, se = FALSE, sizeglm = 1, colglm = 1)
logidot(x, y, incre = NULL, sizedot = NULL, coldot = 1, shapedot = 1, pglm = FALSE,
   se = FALSE, sizeglm = 1, colglm = 1)
```

Arguments

`x`	Either the predictor variable or a glm object.
`y`	If `x` is a predictor variable, y is the response variable, i.e., either a logic (FALSE and TRUE) vector or a vector of 1's and 0's.
`scale.hist`	Value to scale the maximum vertical size of histograms.
`breaks`	How to compute the breakpoints for the histograms. See `hist` in package **graphics**.
`counts`	Add counts above histogram bars (not implemented in this version).
`intervalo`	Width of histogram bins.
`ylab2`	Label for the y-axis of the histograms.

`fillb`	Color to fill the histogram bars or the boxes of the boxplots. Either a single value or a vector witth different values for the 0 and 1 cases.
`colob`	Color to delineate the histogram bars or the boxes of the boxplots. Either a single or double value.
`colpat`	Color of the line representing the whiskers in boxplots.
`colbig`	Color of the line representing the end of whiskers in boxplots.
`colmed`	Color of the line representing the median in boxplots.
`colout`	Color of the line representing the outliers in boxplots.
`sizeb`	Width of the lines that delineate the histogram bars or the boxes of the boxplots.
`boxwd`	Width of the boxes in boxplots.
`wiswd`	Size of the end of whiskers in boxplots.
`sizebig`	Width of the line representing the end of whiskers in boxplots.
`sizepat`	Width of the line representing the whiskers in boxplots.
`sizemed`	Width of the line representing the median in boxplots.
`sizeout`	Size of the points representing the outliers in boxplots.
`shapeout`	Shape of the points representing the outliers. See the entry for `pch` in `points`.
`displac`	Vertical displacement of boxplots along the y-axis.
`incre`	Separation among points in the dotplot.
`sizedot`	Size of points in the dotplot.
`coldot`	Color of points in the dotplot.
`shapedot`	Shape of the points in the dotplot. See the entry for `pch` in `points`.
`pglm`	Draw the fitted logistic curve? (TRUE or FALSE).
`se`	Draw the standard error around the fitted logistic curve?(TRUE or FALSE).
`sizeglm`	Width of the line for the fitted fitted logistic curve.
`colglm`	Color of the line for the fitted fitted logistic curve.

Details

The use of functions `logihist`, `logibox` or `logidot` will render a combined graph for logistic regression. Either a double histogram, a double boxplot or a double dotplot, which could be modified or integrated with other graphical elements of `ggplot2`.

Value

A combined graph for logistic regression.

Note

`logidot` would try to find the optimal size of dots to avoid overlaping. The default computed sizes and separation could be fine-tunned by the arguments `sizedot` and `incre`.

Author(s)

Marcelino de la Cruz

References

De la Cruz Rot, M. 2005. Improving the Presentation of Results of Logistic Regression with R. ESA Bulletin 86:41-48.

See Also

The original implementation of the `logi.hist.plot` function for the R graphic sytem in the package **popbio**.

Examples

```
# Get some data from package popbio
data(aq.trans, package="popbio")
aq.trans$survived<-aq.trans$fate!="dead"
a <-subset(aq.trans, leaf<50 & stage!="recruit", c(leaf,survived))


# Transform the "survived" variable in numeric
# This is necesary to correctly plot the combined graph.

a$survived <-a$survived*1

# Fit a logistic regression
glm.a<- glm(survived~leaf, data=a, family=binomial)


# Histograms
# From individual variables
# Modifying the appearence of histogram bins
logihist(a$leaf, a$survived)
logihist(a$leaf, a$survived, fillb="blue")
logihist(a$leaf, a$survived, fillb="blue", colob="blue")
logihist(a$leaf, a$survived, fillb=c("orange","blue"), colob=c("orange","blue"))
logihist(a$leaf, a$survived, fillb=c("orange","blue"), colob=c("orange","blue"),
scale.hist=2)
logihist(a$leaf,a$survived, fillb=c("orange","blue"), colob=c("orange","blue"),
  breaks=seq(0,50, by=2))

# Modifying the combined plot using functions from ggpplot2

logihist(a$leaf, a$survived, fillb=NA, sizeb=0.5, ylab2="Number of plants") +
   ylab("survived") + xlab("leaf") + stat_smooth(method = "glm", method.args =
   list(family = "binomial"), se=TRUE, linewidth=1, colour="black") + theme_light()


# The same from a glm object

logihist(glm.a, fillb=NA, sizeb=0.5, ylab2="Number of plants", se=TRUE)+
```

```
           theme_light()



# Dotplots
# Double dotplot from the individual variables, with different symbols for
#  0 and 1 categories (black and void, redand solid respectively).

logidot(a$leaf, a$survived, coldot=c(1,2), shapedot=c(1,19))


# Try with a larger dot.
logidot(a$leaf, a$survived, coldot=c(1,2), shapedot=c(1,19), sizedot=1)

# Add the fitted logistic curve and change the presentation using
# respectively a stat and a theme from ggplot2

logidot(a$leaf,a$survived, coldot=c(1,2),shapedot=c(1,19),  sizedot=1)+
    stat_smooth(method = "glm", method.args = list(family = "binomial"),
           se=FALSE, size=2) + theme_light() + ylab("leaf")+xlab("survived")

# Get the same graphic directly form the fitted glm object
logidot(glm.a, coldot=c(1,2),shapedot=c(1,19),  sizedot=1, sizeglm=2,
           colglm="blue") + theme_light()



# Boxplots
logibox(a$leaf,a$survived)+theme_light()+ stat_smooth(method = "glm",
           method.args = list(family = "binomial"),se=FALSE )+
   geom_jitter(height=0.02, size=0.5, colour="pink", alpha=0.5)
```

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