Package 'logihist'

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Type Package

Title Combined Graphs for Logistic Regression

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Depends ggplot2

Suggests popbio

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

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NeedsCompilation no

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R topics documented:

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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 appeerence 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, size=1, colour="black")+theme_light()


# The same fromm 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 an 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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