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 scatterplots of data when plotting fitted logistic regressions.
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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-axis 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

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, shap dot = 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.
**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 over-lapping. The default computed sizes and separation could be fine-tunned by the arguments `sizedot` and `inre`.
Author(s)

Marcelino de la Cruz

References


See Also

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

Examples

```r
# 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 necessary 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 appearance 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
```
# Dotplots
# Double dotplot from the individual variables, with different symbols for
# 0 and 1 categories (black and void, red and 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 from 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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