Package ‘hnp’

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Description Generates (half-)normal plots with simulation envelopes using different diagnostics from a range of different fitted models. A few example datasets are included.

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Half-Normal Plots with Simulation Envelopes

Description

Generates (half-)normal plots with simulation envelopes for common diagnostics from fitted models for a range of model classes. The function `hnp()` is written so that it is relatively easy to extend it to new model classes and different diagnostics that are not already implemented. A few example datasets are included. The main functions are `hnp` and `plot.hnp`.

Details

Package: hnp
Type: Package
Version: 1.2-6
Date: 2018-05-21
License: GPL version 2 or newer

Package includes two functions, `hnp` and `plot.hnp`, as well as seven data sets extracted from Demétrio et al (2014). Explanation on how to produce the half-normal plots with simulation envelopes can be found in Demétrio and Hinde (1997) and on the `hnp` function documentation. Data sets are based on entomology studies and the focus is on overdispersed data. Details on overdispersion models can be found in Hinde and Demétrio (1998). Special thanks to FAPESP and CNPq for funding.

Author(s)

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References


Coffee berry borer trapping data

Description

Data on counts of coffee berry borer obtained using different traps through time.

Usage

data(cbb)

Format

A data frame with 288 observations on the following 4 variables.

<table>
<thead>
<tr>
<th>week</th>
<th>numeric</th>
<th>week of observation (1 to 24)</th>
</tr>
</thead>
<tbody>
<tr>
<td>block</td>
<td>factor</td>
<td>levels I II III IV</td>
</tr>
<tr>
<td>trap</td>
<td>factor</td>
<td>levels CV F SF</td>
</tr>
<tr>
<td>count</td>
<td>numeric</td>
<td>number of observed insects</td>
</tr>
</tbody>
</table>

Details

The coffee berry borer is a major pest of commercial coffee. The insect directly attacks the coffee fruit in development causing severe losses in bean production and quality. This data set was obtained in an experiment conducted by Mota (2013), where three types of traps (SF, F, CV) were randomized in each of four equidistant lines (blocks) of a coffee field. Each week, over a 24 week period, the insects were removed from the traps and counted.

Source


References

Mota, L. H. C. (2013) Desenvolvimento de armadilha de auto-inoculacao para o controlde de Hypothenemus hampei (Ferrari, 1867) (Coleoptera: Curculionidae) com Beauveria bassiana (Bals.) Vuil (Ascomycota: Hypocreales) em tecido sinetico. Master’s dissertation, ESALQ-USP

Examples

data(cbb)
# exploratory plot
require(latticeExtra)
trellis.par.set(strip.background=list(col="lightgrey"))
useOuterStrips(xyplot(count ~ week | block + trap, data=cbb,
  layout=c(3,1),type="l", col=1, xlab="Week", ylab="Insect counts"))
# Poisson fit
model1 <- glm(count ~ block + trap*factor(week),
              data=cbb, family=poisson)
anova(model1, test="Chisq")
sum(resid(model1, ty="pearson")^2)
summary(model1)
hnp(model1, sim=19, conf=1)

## Not run:
hnp(model1) # default call
## End(Not run)

# Quasi-Poisson fit
model2 <- glm(count ~ block + trap*factor(week), data=cbb,
              family=quasipoisson)
anova(model2, test="F")
summary(model2)
hnp(model2, sim=19, conf=1)

## Not run:
hnp(model2) # default call
## End(Not run)

## for discussion on the analysis of this data set,
## see Demetrio et al. (2014)

---

### chryso

**Chrysoperla externa mortality data**

#### Description

Mortality of the predator *Chrysoperla externa* on different doses of lime sulphur, a substance used to control pests on trees.

#### Usage

data(chryso)

#### Format

A data frame with 24 observations on the following 4 variables.

- **dead**: numeric, count of dead *C. externa* specimens
- **alive**: numeric, count of alive *C. externa* specimens
- **conc**: numeric, lime sulphur concentration
- **log.conc**: numeric, natural logarithm of lime sulphur concentration
Details

The neuropteran *Chrysoperla externa* is a predator that acts as a natural enemy of the brown citrus aphid, *Toxoptera citricida*, which is among the most important citrus pests worldwide. A possible strategy to control *T. citricida* populations would be to use a substance called lime sulphur and the *C. externa* predator in combination, which may be beneficial as long as the lime sulphur has less effect on the predator than the prey. To explore this, Battel (2012) conducted an experiment with first-instar larvae of *Chrysoperla externa* exposed to different levels of lime sulphur. Specifically, twenty-four Orange Jessamine (*Murraya paniculata*) plants were sprayed with different concentrations (conc) of lime sulphur and up to seven first-instar larvae were placed on each plant. The experiment was set up in a completely randomized design with four treatments: lime sulphur concentrations at 0ppm (water control), 60ppm, 600ppm, and 6000ppm. The plants were observed until the predators reached the second instar and the number of larvae that died on each plant was recorded.

Source


References


Examples

data(chryso)

# fit model using conc levels both on log-scale and
# as a factor to produce simple analysis of deviance
model <- glm(cbind(dead, alive) ~ log.conc + factor(conc),
             family=binomial, data=chryso)
anova(model, test="Chisq")
# test adequacy of factor model using deviance and X2
1-pchisq(deviance(model), df.residual(model))
(X2 <- sum(residuals(model, type="pearson")^2))
1-pchisq(X2, df.residual(model))

model1 <- glm(cbind(dead, alive) ~ log.conc,
             family=binomial, data=chryso)
par(mfrow=c(1,2), cex=1.4)
with(chryso, plot(jitter(log.conc), dead/(dead+alive),
       ylab="Proportion dead", xlab="log(conc+1)"))
x <- seq(0, 8.7, .1)
pr <- predict(model1, data.frame(log.conc=x), ty="response")
lines(x, pr)
# half-normal plot
hnp(model1, xlab="Half-normal scores",
    ylab="Deviance residuals", pch=4)
```r
require(MASS)
dose.p(model1[, p=.10)

logLC10 <- dose.p(model1[, p=.10)
LC10 <- exp(logLC10[1]) - 1

#95% CI on log-dose scale using transformation
c(logLC10[1]+2*attr(logLC10,'SE'),
   logLC10[1]+2*attr(logLC10,'SE'))

#95% CI on dose scale using transformation
c(exp(logLC10[1]+2*attr(logLC10,'SE'))-1,
   exp(logLC10[1]+2*attr(logLC10,'SE'))-1)

## for discussion on the analysis of this data set,
## see Demetrio et al. (2014)
```

---

**corn**

*Corn damage data*

**Description**

Corn grain damage by the maize weevil, a major pest of stored maize worldwide.

**Usage**

data(corn)

**Format**

A data frame with 40 observations on the following 3 variables.

- **extract**: factor with levels leaf, branch, seed and control
- **m**: numeric total number of corn grains
- **y**: numeric number of damaged corn grains

**Details**

A major pest of stored maize in Brazil is *Sitophilus zeamais*. In an experiment to assess the insecticide action of organic extracts of *Annona mucosa* (*Annonaceae*), Petri dishes containing 10g of corn were treated with extracts prepared with different parts of the plant (seeds, leaves and branches) at a concentration of 1500mg/kg or just water (control), using a completely randomized design with 10 replicates. Then 20 *Sitophilus zeamais* adults were placed in each Petri dish and, after 60 days, the numbers of damaged and undamaged corn grains were counted, see Ribeiro et al (2013).

**Source**

References


Examples

data(corn)

# Binomial fit
model1 <- glm(cbind(y, m-y) ~ extract, family=binomial,
              data=corn)
anova(model1, test="Chisq")
hnp(model1, pch=4, main="Binomial: Logit",
    xlab="Half-normal scores", ylab="Deviance residuals")

# Quasi-binomial fit
model2 <- glm(cbind(y, m-y) ~ extract, family=quasibinomial,
              data=corn)
anova(model2, test="F")
summary(model2)$dispersion # estimated phi

# half-normal plots
par(mfrow=c(1,2),cex=1.4, cex.main=0.9, pty="s")
hnp(model1, pch=4, main="(a) Binomial: Logit",
    xlab="Half-normal scores", ylab="Deviance residuals")
hnp(model2, pch=4, main="(b) Quasibinomial: Logit",
    xlab="Half-normal scores", ylab="Deviance residuals")

anova(model1, test="Chisq") # binomial model
anova(model2, test="F") # quasi-binomial model
summary(model1) # binomial model
summary(model2) # quasi-binomial model

# now with factor level parameterisation
summary(update(model1,.~.-1))
summary(update(model2,.~.-1))

## for discussion on the analysis of this data set,
## see Demetrio et al. (2014)

fungi

Diaphorina citri mortality data
Description

Mortality of the Citrus psyllid, *Diaphorina citri*, a major pest of Citrus worldwide, when exposed to different concentrations of two fungi species, *Beauveria bassiana* and *Isaria fumosorosea*.

Usage

data(fungi)

Format

A data frame with 30 observations on the following 5 variables.

- `y` numeric number of dead insects
- `m` numeric total number of insects
- `conc` numeric fungi concentration (in conidia/ml)
- `lconc` numeric natural logarithm of fungi concentration
- `species` factor levels *isaria* and *beauveria*, fungi species

Details

The Citrus psyllid *Diaphorina citri* is a vector of Huanglongbing, known as greening disease. An alternative to chemical control is to use solutions of fungi conidia as a biological control strategy. D’Alessandro (2014) conducted a completely randomized experiment to assess how different conidia concentrations ($10^4$, $10^5$, $10^6$, $10^7$, and $10^8$ conidia/ml) of two fungi species, *Beauveria bassiana* and *Isaria fumosorosea*, infected *D. citri* adults. Each experimental unit consisted of around 20 *D. citri* adults, which were placed on *Citrus limonia* plants. The insects were pulverized with the solutions and after 10 days the number of dead insects and dead insects due to fungus infection were observed. Note that in this case the conidia concentrations are obtained in successive dilutions and therefore small variations in the number of conidia per ml may contribute additional variability to the data. Such additional variability may be accounted for in the model by including an additive random effect in the linear predictor.

Source


References


Examples

data(fungi)

# Binomial fit
model1 <- glm(cbind(y, m-y) ~ lconc*species, family=binomial, data=fungi)
anova(model1, test="Chisq")
sum(resid(model1, ty="pearson")^2)
1 - pchisq(sum(resid(model1, ty="pearson")^2), 20)
hnp(model1)

# Quasi-binomial fit
model2 <- glm(cbind(y, m-y) ~ lconc*species,
               family=quasibinomial, data=fungi)
anova(model2, test="F")
hnp(model2)

## Not run:
# Logistic-normal fit
require(lme4)
fungi$ind <- factor(!nrow(fungi))
model3 <- glmer(cbind(y, m-y) ~ lconc*species + (1|ind),
                family=binomial, data=fungi)
summary(model3)
hnp(model3)

## End(Not run)

## for discussion on the analysis of this data set,
## see Demetrio et al. (2014)

---

**hnp**

**Half-Normal Plots with Simulation Envelopes**

### Description

Produces a (half-)normal plot from a fitted model object for a range of different models. Extendable to non-implemented model classes.

### Usage

```r
hnp(object, sim = 99, conf = 0.95, resid.type, maxit, 
    halfnormal = T, scale = F, plot.sim = T, verb.sim = F, 
    warn = F, how.many.out = F, print.on = F, paint.out = F, 
    col.paint.out, newclass = F, diagfun, simfun, fitfun, ...)
```

### Arguments

- **object**: fitted model object or numeric vector.
- **sim**: number of simulations used to compute envelope. Default is 99.
- **conf**: confidence level of the simulated envelope. Default is 0.95.
- **resid.type**: type of residuals to be used; must be one of "deviance", "pearson", "response", "working", "simple", "student", or "standard". Not all model type and residual type combinations are allowed. Defaults are "student" for `aov` and `lm` objects, "deviance" for `glm`, `glm.nb`, `lmer`, `glmer` and `aodml` objects, "simple" for `gamlss` objects, "response" for `glmmadmb` and `vglm` objects, "pearson" for `zeroinfl` and `hurdle` objects.
maxit maximum number of iterations of the estimation algorithm. Defaults are 25 for glm, glm.nb, gamlss and vglm objects, 300 for glmmadmb, lmer and glmer objects, 3000 for aodml objects, 10000 for zeroinfl and hurdle objects.

halfnormal logical. If TRUE, a half-normal plot is produced. If FALSE, a normal plot is produced. Default is TRUE.

scale logical. If TRUE and if object is a numeric vector, simulates from a normal distribution with mean and variance estimated from object. If FALSE, uses a standard normal distribution to simulate from. Default is FALSE.

plot.sim logical. Should the (half-)normal plot be plotted? Default is TRUE.

verb.sim logical. If TRUE, prints each step of the simulation procedure. Default is FALSE.

warn logical. If TRUE, shows warning messages in the simulation process. Default is FALSE.

how.many.out logical. If TRUE, the number of points out of the envelope is printed. Default is FALSE.

print.on logical. If TRUE, the number of points out of the envelope is printed on the plot. Default is FALSE.

paint.out logical. If TRUE, points out of the simulation envelope are plotted in a different color. Default is FALSE.

col.paint.out If paint.out=TRUE, sets the color of points out of the envelope. Default is "red".

newclass logical. If TRUE, use diagfun, simfun, and fitfun to extract diagnostics (typically residuals), generate simulated data using fitted model parameters, and fit the desired model. Default is FALSE.

diagfun user-defined function used to obtain the diagnostic measures from the fitted model object (only used when newclass=TRUE). Default is resid.

simfun user-defined function used to simulate a random sample from the model estimated parameters (only used when newclass=TRUE).

fitfun user-defined function used to re-fit the model to simulated data (only used when newclass=TRUE).

... extra graphical arguments passed to plot.hnp.

Details

A relatively easy way to assess goodness-of-fit of a fitted model is to use (half-)normal plots of a model diagnostic, e.g., different types of residuals, Cook's distance, leverage. These plots are obtained by plotting the ordered absolute values of a model diagnostic versus the expected order statistic of a half-normal distribution,

$$
\Phi^{-1}\left(\frac{i + n - 1/8}{2 * n + 1/2}\right)
$$

(for a half-normal plot) or the normal distribution,

$$
\Phi^{-1}\left(\frac{i + 3/8}{n + 1/4}\right)
$$
Atkinson (1985) proposed the addition of a simulated envelope, which is such that under the correct model the plot for the observed data is likely to fall within the envelope. The objective is not to provide a region of acceptance, but some sort of guidance to what kind of shape to expect.

Obtaining the simulated envelope is simple and consists of (1) fitting a model; (2) extracting model diagnostics and calculating sorted absolute values; (3) simulating 99 (or more) response variables using the same model matrix, error distribution and fitted parameters; (4) fitting the same model to each simulated response variable and obtaining the same model diagnostics, again sorted absolute values; (5) computing the desired percentiles (e.g., 2.5 and 97.5) at each value of the expected order statistic to form the envelope.

This function handles different model classes and more will be implemented as time goes by. So far, the following models are included:

**Continuous data:**

- Normal: functions `lm`, `aov` and `glm` with family=gaussian
- Gamma: function `glm` with family=Gamma
- Inverse gaussian: function `glm` with family=inverse.gaussian

**Proportion data:**

- Binomial: function `glm` with family=binomial
- Quasi-binomial: function `glm` with family=quasibinomial
- Beta-binomial: package VGAM - function vglm, with family=beta; package aods3 - function aodml, with family="bb"; package gamlss - function gamlss, with family=BB; package glmmADMB - function glmmadmb, with family="betabinomial"
- Zero-inflated binomial: package VGAM - function vglm, with family=zibinomial; package gamlss - function gamlss, with family=ZIBI; package glmmADMB - function glmmadmb, with family="binomial" and zeroInfl=TRUE
- Zero-inflated beta-binomial: package gamlss - function gamlss, with family=ZIBB; package glmmADMB - function glmmadmb, with family="betabinomial" and zeroInfl=TRUE

**Count data:**

- Poisson: function `glm` with family=poisson
- Quasi-Poisson: function `glm` with family=quasipoisson

This function handles different model classes and more will be implemented as time goes by. So far, the following models are included:
Negative binomial: package MASS - function \texttt{glm.nb}; package aods3 - function aodml, with family=\texttt{"nb"} and \texttt{phi.scale=\texttt{"inverse"}}

Zero-inflated Poisson: package pscl - function zeroinfl, with dist=\texttt{"poisson"}

Zero-inflated negative binomial: package pscl - function zeroinfl, with dist=\texttt{"negbin"}

Hurdle Poisson: package pscl - function hurdle, with dist=\texttt{"poisson"}

Hurdle negative binomial: package pscl - function hurdle, with dist=\texttt{"negbin"}

Mixed models:

Linear mixed models: package lme4, function \texttt{lmer}

Generalized linear mixed models: package lme4, function \texttt{glmer} with family=\texttt{poisson} or \texttt{binomial}

Users can also use a numeric vector as object and \texttt{hnp} will generate the (half-)normal plot with a simulated envelope using the standard normal distribution (\texttt{scale=F}) or $N(\mu, \sigma^2)$ (\texttt{scale=T}).

Implementing a new model class is done by providing three functions to \texttt{hnp}: diagfun - to obtain model diagnostics, simfun - to simulate random variables and fitfun - to refit the model to simulated variables. The way these functions must be written is shown in the Examples section.

\textbf{Value}

\texttt{hnp} returns an object of class "\texttt{hnp}", which is a list containing the following components:

- \texttt{x}: quantiles of the (half-)normal distribution
- \texttt{lower}: lower envelope band
- \texttt{median}: median envelope band
- \texttt{upper}: upper envelope band
- \texttt{residuals}: diagnostic measures in absolute value and in order
- \texttt{out.index}: vector indicating which points are out of the envelope
- \texttt{col.paint.out}: color of points which are outside of the envelope (used if \texttt{paint.out=TRUE})
- \texttt{how.many.out}: logical. Equals \texttt{TRUE} if \texttt{how.many.out=TRUE} in the \texttt{hnp} call
- \texttt{total}: length of the diagnostic measure vector
- \texttt{out}: number of points out of the envelope
- \texttt{print.on}: logical. Equals \texttt{TRUE} if \texttt{print.on=TRUE} in the \texttt{hnp} call
- \texttt{paint.out}: logical. Equals \texttt{TRUE} if \texttt{paint.out=TRUE} in the \texttt{hnp} call
- \texttt{all.sim}: matrix with all diagnostics obtained in the simulations. Each column represents one simulation
Note

See documentation on example data sets for simple analyses and goodness-of-fit checking using hnp.

Author(s)

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References


See Also

plot.hnp, cbb, chryso, corn, fungi, oil, progeny, wolbachia

Examples

```r
## Simple Poisson regression
set.seed(100)
counts <- c(rpois(5, 2), rpois(5, 4), rpois(5, 6), rpois(5, 8))
treatment <- gl(4, 5)
fit <- glm(counts ~ treatment, family=poisson)
anova(fit, test="Chisq")

## half-normal plot
hnp(fit)

## or save it in an object and then use the plot method
my.hnp <- hnp(fit, print.on=TRUE, plot=FALSE)
plot(my.hnp)

## changing graphical parameters
plot(my.hnp, lty=2, pch=4, cex=1.2)
plot(my.hnp, lty=c(2,3,2), pch=4, cex=1.2, col=c(2,2,2,1))
plot(my.hnp, main="Half-normal plot", xlab="Half-normal scores",
     ylab="Deviance residuals", legpos="bottomright")

## Using a numeric vector
my.vec <- rnorm(20, 4, 4)
hnp(my.vec) # using N(0,1)
```
hnp(my.vec, scale=TRUE) # using N(μ, σ^2)

## Implementing new classes
## Users provide three functions - diagfun, simfun and fitfun,
## in the following way:
##
## diagfun <- function(obj) {
## userfunction(obj, other_arguments)
## # e.g., resid(obj, type="pearson")
## }
##
## simfun <- function(n, obj) {
## userfunction(n, other_arguments) # e.g., rpois(n, fitted(obj))
## }
##
## fitfun <- function(y.) {
## userfunction(y. ~ linear_predictor, other_arguments, data=data)
## # e.g., glm(y. ~ block + factor1 * factor2, family=poisson,
## # data=mydata)
## }
##
## when response is binary:
## fitfun <- function(y.) {
## userfunction(cbind(y., m-y.) ~ linear_predictor,
## other_arguments, data=data)
## # e.g., glm(cbind(y., m-y.) ~ treatment - 1,
## # family=binomial, data=data)
## }
##
## # Not run:
## Example no. 1: Using Cook’s distance as a diagnostic measure
y <- rpois(30, lambda=rep(c(.5, 1.5, 5), each=10))
tr <- gl(3, 10)
fit1 <- glm(y ~ tr, family=poisson)

# diagfun
d.fun <- function(obj) cooks.distance(obj)

# simfun
s.fun <- function(n, obj) {
  lam <- fitted(obj)
  rpois(n, lambda=lam)
}

# fitfun
my.data <- data.frame(y, tr)
f.fun <- function(y.) glm(y. ~ tr, family=poisson, data=my.data)

# hnp call
hnp(fit1, newclass=TRUE, diagfun=d.fun, simfun=s.fun, fitfun=f.fun)

## Example no. 2: Implementing gamma model using package gamlss
# load package
require(gamlss)

# model fitting
y <- rGA(30, mu=rep(c(.5, 1.5, 5), each=10), sigma=.5)
tr <- gl(3, 10)
fit2 <- gamlss(y ~ tr, family=GA)

# diagfun
d.fun <- function(obj) resid(obj) # this is the default if no
# diagfun is provided

# simfun
s.fun <- function(n, obj) {
  mu <- obj$mu.fv
  sig <- obj$sigma.fv
  rGA(n, mu=mu, sigma=sig)
}

# fitfun
my.data <- data.frame(y, tr)
f.fun <- function(y.) gamlss(y. ~ tr, family=GA, data=my.data)

# hnp call
hnp(fit2, newclass=TRUE, diagfun=d.fun, simfun=s.fun, fitfun=f.fun, data=data.frame(y, tr))

## Example no. 3: Implementing binomial model in gamlss
# model fitting
y <- rBI(30, bd=50, mu=rep(c(.2, .5, .9), each=10))
m <- 50
tr <- gl(3, 10)
fit3 <- gamlss(cbind(y, m-y) ~ tr, family=BI)

# diagfun
d.fun <- function(obj) resid(obj)

# simfun
s.fun <- function(n, obj) {
  mu <- obj$mu.fv
  bd <- obj$bd
  rBI(n, bd=bd, mu=mu)
}

# fitfun
my.data <- data.frame(y, tr, m)
f.fun <- function(y.) gamlss(cbind(y., m-y.) ~ tr,
                            family=BI, data=my.data)

# hnp call
hnp(fit3, newclass=TRUE, diagfun=d.fun, simfun=s.fun, fitfun=f.fun)

## End(Not run)
**newhnp**

**hnp-internal**  
*Internal function to prepare hnp objects*

**Description**

This is an internally called function used to prepare hnp objects for plotting.

**Author(s)**

Rafael A. Moral <rafael_moral@yahoo.com.br>, John Hinde and Clarice G. B. Demétrio

**newhnp**  
*Method for non-implemented model classes*

**Description**

Uses user defined functions to produce the (half-)normal plot with simulated envelope.

**Usage**

```r
newhnp(object, sim=99, conf=.95, halfnormal=T, plot.sim=T, verb.sim=F, how.many.out=F, print.on=F, paint.out=F, col.paint.out, diagfun, simfun, fitfun, ...)```

**Arguments**

- **object**: fitted model object or numeric vector.
- **sim**: number of simulations used to compute envelope. Default is 99.
- **conf**: confidence level of the simulated envelope. Default is 0.95.
- **halfnormal**: logical. If **TRUE**, a half-normal plot is produced. If **FALSE**, a normal plot is produced. Default is **TRUE**.
- **plot.sim**: logical. Should the (half-)normal plot be plotted? Default is **TRUE**.
- **verb.sim**: logical. If **TRUE**, prints each step of the simulation procedure. Default is **FALSE**.
- **how.many.out**: logical. If **TRUE**, the number of points out of the envelope is printed. Default is **FALSE**.
- **print.on**: logical. If **TRUE**, the number of points out of the envelope is printed on the plot. Default is **FALSE**.
- **paint.out**: logical. If **TRUE**, points out of the simulation envelope are plotted in a different color. Default is **FALSE**.
- **col.paint.out**: If **paint.out=TRUE**, sets the color of points out of the envelope. Default is "red".
- **diagfun**: user-defined function used to obtain the diagnostic measures from the fitted model object (only used when **newclass=TRUE**). Default is `resid`. 
Details

By providing three user-defined functions, `newhnp` produces the half-normal plot with simulated envelope for a model whose class is not yet implemented in the package.

The first function, `diagfun`, must extract the desired model diagnostics from a model fit object. The second function, `simfun`, must return the response variable (numeric vector or matrix), simulated using the same error distributions and estimated parameters from the fitted model. The third and final function, `fitfun`, must return a fitted model object. See the Examples section.

Author(s)

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Examples

```r
## Implementing new classes
## Users provide three functions - diagfun, simfun and fitfun,
## in the following way:
##
## diagfun <- function(obj) {
##   userfunction(obj, other_arguments)
##   # e.g., resid(obj, type="pearson")
## }
##
## simfun <- function(n, obj) {
##   userfunction(n, other_arguments) # e.g., rpois(n, fitted(obj))
## }
##
## fitfun <- function(y.) {
##   userfunction(y. ~ linear_predictor, other_arguments, data=data)
##   # e.g., glm(y. ~ block * factor1 * factor2, family=poisson,
##   # data=mydata)
## }
##
## when response is binary:
##
## fitfun <- function(y.) {
##   userfunction(cbind(y., m-y.) ~ linear_predictor,
##   other_arguments, data=data)
##   # e.g., glm(cbind(y., m-y.) ~ treatment - 1,
##   # family=binomial, data=data)
## }
##
## Not run:
## Example no. 1: Using Cook’s distance as a diagnostic measure
y <- rpois(30, lambda=rep(c(.5, 1.5, 5), each=10))
```

tr <- gl(3, 10)
fit1 <- glm(y ~ tr, family=poisson)

# diagfun
d.fun <- function(obj) cooks.distance(obj)

# simfun
s.fun <- function(n, obj) {
  lam <- fitted(obj)
  rpois(n, lambda=lam)
}

# fitfun
my.data <- data.frame(y, tr)
f.fun <- function(y.) glm(y. ~ tr, family=poisson, data=my.data)

# hnp call
hnp(fit1, newclass=TRUE, diagfun=d.fun, simfun=s.fun, fitfun=f.fun)

## Example no. 2: Implementing gamma model using package gamlss

# load package
require(gamlss)

# model fitting
y <- rGA(30, mu=rep(c(.5, 1.5, 5), each=10), sigma=.5)
tr <- gl(3, 10)
fit2 <- gamlss(y ~ tr, family=GA)

# diagfun
d.fun <- function(obj) resid(obj) # this is the default if no
# diagfun is provided

# simfun
s.fun <- function(n, obj) {
  mu <- obj$mu.fv
  sig <- obj$sigma.fv
  rGA(n, mu=mu, sigma=sig)
}

# fitfun
my.data <- data.frame(y, tr)
f.fun <- function(y.) gamlss(y. ~ tr, family=GA, data=my.data)

# hnp call
hnp(fit2, newclass=TRUE, diagfun=d.fun, simfun=s.fun, fitfun=f.fun, data=data.frame(y, tr))

## Example no. 3: Implementing binomial model in gamlss

# model fitting
y <- rBI(30, bd=50, mu=rep(c(.2, .5, .9), each=10))
m <- 50
tr <- gl(3, 10)
fit3 <- gamlss(cbind(y, m-y) ~ tr, family=BI)
# diagfun
d.fun <- function(obj) resid(obj)

# simfun
s.fun <- function(n, obj) {
  mu <- obj$mu.fv
  bd <- obj$bd
  rBI(n, bd=bd, mu=mu)
}

# fitfun
my.data <- data.frame(y, tr, m)

f.fun <- function(y.) gamlss(cbind(y., m-y.) ~ tr,
                 family=BI, data=my.data)

# hnp call
hnp(fit3, newclass=TRUE, diagfun=d.fun, simfun=s.fun, fitfun=f.fun)

## End(Not run)

diagfun

d.fun <- function(obj) resid(obj)

simfun

s.fun <- function(n, obj) {
  mu <- obj$mu.fv
  bd <- obj$bd
  rBI(n, bd=bd, mu=mu)
}

fitfun

my.data <- data.frame(y, tr, m)

f.fun <- function(y.) gamlss(cbind(y., m-y.) ~ tr,
                 family=BI, data=my.data)

# hnp call
hnp(fit3, newclass=TRUE, diagfun=d.fun, simfun=s.fun, fitfun=f.fun)

## End(Not run)

---

**Diaphorina citri oviposition data**

---

**Description**

Effects of three agricultural oils on *Diaphorina citri* oviposition.

**Usage**

data(oil)

**Format**

A data frame with 70 observations on the following 2 variables.

- **y** numeric number of eggs laid
- **treat** factor treatments applied in the experiment

**Details**

In an experiment to assess the effect of three agricultural oils on the oviposition of *Diaphorina citri*, seventy Orange Jessamine (*Murraya paniculata*) plants were sprayed with solutions of the mineral oils Oppa and Iharol, and the vegetable oil Nortox. The experiment used the oils in concentrations of 0.5 and 1.0 percent and a control of plain water set out in a completely randomized design with ten replicates. Following treatment, when the plants were dry, ten pregnant females of *D. citri* were released on each plant. After five days, the insects were removed and the total number of eggs on each plant was observed, see Amaral et al (2012). This is an example of aggregated data as the number of eggs is the sum over the (unrecorded) numbers of eggs deposited each day and the
possibility of day to day variation may contribute additional variability to the recorded counts.

Source


References


Examples

data(oil)

# Poisson fit
model1 <- glm(y ~ treat, family=poisson, data=oil)
anova(model1, test="Chisq")
sum(resid(model1, ty=“pearson”)^2)

# Quasi-Poisson fit
model2 <- glm(y ~ treat, family=quasipoisson, data=oil)
summary(model2)
anova(model2,test="F")
summary(model2)$dispersion

# Negative binomial fit
require(MASS)
model3 <- glm.nb(y ~ treat, data=oil)
thetahat <- summary(model3)$theta
anova(model3, test="F")

# half-normal plots
par(mfrow=c(1,3),cex=1.4, cex.main=0.9)
hnp(model1,pch=4, main="(a) Poisson",
  xlab="Half-normal scores", ylab="Deviance residuals")
hnp(model2,pch=4, main="(b) Quasi-Poisson",
  xlab="Half-normal scores", ylab="")
hnp(model3,pch=4, main="(c) Negative binomial",
  xlab="Half-normal scores", ylab="")

## Not run:
# using aods3
require(aods3)
model3b <- aodml(y ~ treat, family="nb", phi.scale="inverse",
  fixpar=list(8, 1.086148), data=oil)
hnp(model3b)

## End(Not run)
## for discussion on the analysis of this data set,
## see Demetrio et al. (2014)

---

### Orange tissue-culture experiment data

**Description**

Number of embryos of orange variety *Caipira* produced with different sugar types.

**Usage**

```r
data("orange")
```

**Format**

A data frame with 150 observations on the following 4 variables.

- **block**: a factor with levels 1 2 3 4 5
- **sugar**: a factor with levels Maltose Glucose Lactose Galactose Sucrose Glycerol
- **dose**: a numeric vector
- **embryos**: a numeric vector

**Details**

To study the effect of six sugars (maltose, glucose, galactose, lactose, sucrose and glycerol) on the stimulation of somatic embryos from callus cultures, the number of embryos after approximately four weeks was observed. The experiment was set up in a completely randomized block design with five blocks and the six sugars at dose levels of 18, 37, 75, 110 and 150 mM for the first five and 6, 12, 24, 36 and 50 mM for glycerol, see Tomaz (2001). The main interest was in the dose-response relationship.

**Source**


**References**

Examples

```r
data(orange)
require(gamlss)
fit_nbI <- gamlss(embryos ~ block + poly(dose, 2) * sugar, 
                family=NBII(), data=orange)

d.fun <- function(obj) resid(obj)
s.fun <- function(n, obj) {
  mu <- obj$mu.fv
  sigma <- obj$sigma.fv
  rNBII(n, mu, sigma)
}
f.fun <- function(y.) {
  gamlss(y. ~ block + poly(dose, 2) * sugar, family=NBII(), data=orange)
}

## Not run:
plot.hnp(fit_nbI, newclass=TRUE, diagfun=d.fun, simfun=s.fun, fitfun=f.fun)
## End(Not run)
fit_pred <- gamlss(embryos ~ poly(dose, 2) * sugar, family=NBII(), data=orange)
orange.pred <- rbind(expand.grid(sugar=levels(orange$sugar)[-6], dose=18:150),
                     expand.grid(sugar="Glycerol", dose=6:50))
orange.pred$pred <- predict(fit_pred, newdata=orange.pred, type="response")
require(latticeExtra)
trellis.par.set(strip.background=list(col="lightgrey"))
xyplot(embryos ~ dose | sugar, scales=list(relation="free"), layout=c(3,2),
       data=orange, col=1, xlab="Dose levels", ylab="Number of embryos") +
       as.layer(xyplot(pred ~ dose | sugar, type="l", col=1, data=orange.pred))
```

---

plot.hnp

**Plot Method for hnp Objects**

**Description**

The plot method for objects of class hnp.

**Usage**

```r
## S3 method for class 'hnp'
plot(x, cex, pch, colour, lty, lwd, type,
     xlab, ylab, main, legpos, legcex, ...)
```
Arguments

- **x**: object of class "hnp".
- **cex**: character expansion size.
- **pch**: character string or vector of one character or integer for plotting characters, see `points`.
- **colour**: vector of colours.
- **lty**: vector of line types.
- **lwd**: vector of line widths.
- **type**: type of plot for each envelope band and points. Default is `c("l","l","l","p")`.
- **xlab**: title for x axis, as in `plot`.
- **ylab**: title for y axis, as in `plot`.
- **main**: plot title.
- **legpos**: if `print.on=TRUE`, represents the position where the information should be printed ("topright", "topleft", "bottomright", "bottomleft"), as in `legend`.
- **legcex**: if `print.on=TRUE`, character expansion size of `legend`.
- **...**: extra graphical arguments passed to `matplot`.

Value

None.

Author(s)

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References


See Also

- `hnp`
Examples

## Simple Poisson regression
set.seed(100)
counts <- c(rpois(5, 2), rpois(5, 4), rpois(5, 6), rpois(5, 8))
treatment <- gl(4, 5)
fit <- glm(counts ~ treatment, family=poisson)
anova(fit, test="Chisq")

## half-normal plot
hnp(fit)

## or save it in an object and then use the plot method
my.hnp <- hnp(fit, print.on=TRUE, plot=FALSE)
plot(my.hnp)

## changing graphical parameters
plot(my.hnp, lty=2, pch=4, cex=1.2)
plot(my.hnp, lty=c(2,3,2), pch=4, cex=1.2, col=c(2,2,2,1))
plot(my.hnp, main="Half-normal plot", xlab="Half-normal scores",
     ylab="Deviance residuals", legpos="bottomright")

---

**progeny**  
**Sitophilus zeamais progeny**

Description

Progeny of *Sitophilus zeamais*, the maize weevil, when treated with different organic extracts

Usage

data(progeny)

Format

A data frame with 40 observations on the following 2 variables.

<table>
<thead>
<tr>
<th>extract</th>
<th>factor</th>
<th>levels</th>
<th>y</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>leaf, branch, seed and control</td>
<td>numeric</td>
</tr>
</tbody>
</table>

Details

Petri dishes containing 10g of corn were treated with extracts prepared with different parts of the plant *Annona mucosa* (seeds, leaves and branches) at a concentration of 1500 mg/kg or just water (control), using a completely randomized design with 10 replicates. Then 20 *S. zeamais* adults were placed in each Petri dish and the focus is on the numbers of emerged insects (progeny) after 60 days, see Ribeiro et al (2013).
wolbachia

Source


References


Examples

data(progeny)

# Poisson fit
model1 <- glm(y ~ extract, family=poisson, data=progeny)
anova(model1, test="Chisq")

# Quasi-Poisson fit
model2 <- glm(y ~ extract, family=quasipoisson, data=progeny)
summary(model2)$dispersion
anova(model2, test="F")

# half-normal plots
par(mfrow=c(1,2),cex=1.4, cex.main=0.9, pty='s')
hnp(model1, pch=4, main="(a) Poisson; log-linear",
    xlab="Half-normal scores", ylab="Deviance residuals")
hnp(model2, pch=4, main="(b) Quasi-Poisson; log-linear",
    xlab="Half-normal scores", ylab="Deviance residuals")

anova(model1, test="Chisq") # Poisson model
anova(model2, test="F") # quasi-Poisson model
summary(model1) # Poisson model
summary(model2) # quasi-Poisson model

# now with factor level parameterisation
summary(update(model1,.~.-1))
summary(update(model2,.~.-1))

## for discussion on the analysis of this data set,
## see Demetrio et al. (2014)

wolbachia      Trichogramma galloi parasitism data
Description

Viability of *Trichogramma galloi*, a parasitoid wasp, when infected with *Wolbachia*, a bacteria known to change its reproductive aspects.

Usage

data(wolbachia)

Format

A data frame with 106 observations on the following 3 variables.

- y numeric; number of eggs with an orifice
- m numeric; total number of parasitised eggs
- treat a factor with levels m+f+, m+f-, f+, m-f- and f-, where m stands for male, f stands for female, + means infected and - means non-infected; f+ and f- represent virgin infected and non-infected females, respectively.

Details

The bacteria *Wolbachia* is commonly found in various insect species and has the ability to change reproductive aspects of its host. When it infects the wasp *Trichogramma galloi* it is known to induce thelykous parthenogenesis, i.e., only females are produced from unfertilized eggs. Souza (2011) conducted an experiment to assess the effects of *Wolbachia* on the viability of *T. galloi* eggs. Around 100 *Diatraea saccharalis* eggs (the host) were offered to infected (+) or non-infected (-) parasitoid couples or virgin females every day until the death of the female. The parasitised eggs, easily identifiable because they become dark, were then kept on moist filter paper for twenty days when counts were then made of the number of eggs that had an orifice, which meant that an adult parasitoid had emerged and thus the parasitoid was viable.

Source


References


Examples

data(wolbachia)

# Binomial fit
model1 <- glm(cbind(y, m-y) ~ treat, family=binomial, data=wolbachia)
anova(model1, test="Chisq")

# Quasi-binomial fit
model2 <- glm(cbind(y, m-y) ~ treat, family=quasibinomial, data=wolbachia)
summary(model2)
anova(model2, test="F")

## half normal plots
par(mfrow=c(1,2), cex=1.2, cex.main=1.1)
hnp(model1, print=TRUE, pch=4, main="(a) Binomial",
    xlab="Half-normal scores", ylab="Deviance residuals")
hnp(model2, print=TRUE, pch=4, main="(b) Quasi-binomial",
    xlab="Half-normal scores", ylab="")

## Not run:
# Beta-binomial fit
### using package aods3
require(aods3)
model3 <- aodml(cbind(y, m-y) ~ treat, family='bb', data=wolbachia)
hnp(model3, print=TRUE, pch=4,
    xlab="Half-normal scores", ylab='Deviance residuals')

### using package VGAM
require(VGAM)
model3a <- vglm(cbind(y, m-y) ~ treat, family=betabinomial,
    data=wolbachia)
summary(model3a)
1/(1+exp(-coef(model3a)[2])) # phi estimate
hnp(model3a, data=wolbachia)

## End(Not run)

## for discussion on the analysis of this data set,
## see Demetrio et al. (2014)
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