Package ‘hglm’
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Type Package
Title Hierarchical Generalized Linear Models
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Author Moudud Alam, Lars Ronnegard, Xia Shen
Maintainer Xia Shen <xia.shen@ki.se>
Description Implemented here are procedures for fitting hierarchical generalized linear models (HGLM). It can be used for linear mixed models and generalized linear mixed models with random effects for a variety of links and a variety of distributions for both the outcomes and the random effects. Fixed effects can also be fitted in the dispersion part of the mean model. As statistical models, HGLMs were initially developed by Lee and Nelder (1996) <https://www.jstor.org/stable/2346105?seq=1>. We provide an implementation (Ronnegard, Alam and Shen 2010) <https://journal.r-project.org/archive/2010-2/RJournal_2010-2_Ronnegaard~etal.pdf> following Lee, Nelder and Pawitan (2006) <ISBN: 9781420011340> with algorithms extended for spatial modeling (Alam, Ronnegard and Shen 2015) <https://journal.r-project.org/archive/2015/RJ-2015-017/RJ-2015-017.pdf>.

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The hglm package is used to fit hierarchical generalized linear models. It can be used for linear mixed models and generalized linear models with random effects for a variety of links and a variety of distributions for both the outcomes and the random effects. Fixed effects can also be fitted in the dispersion part of the model. The function can be called either by specifying the design matrices or as a formula. The default estimation method is extended quasi likelihood (EQL; Lee et al., 2006) but from version 2.0 the EQL1 correction has been implemented as well.

**Author(s)**

Moudud Alam, Lars Ronnegard, Xia Shen

Maintainer: Xia Shen <xia.shen@ki.se>

**References**

Beta


Moudud Alam, Lars Ronnegard, Xia Shen (2014). *Fitting conditional and simultaneous autoregressive spatial models in hglm*. *Submitted*.

See Also

`hglm`, `hglm2`, `plot.hglm`

---

**Beta**

*Extended Beta Family*

**Description**

A function used in the `hglm` package which extends the usage of the Beta family.

**Usage**

```r
Beta(link = "logit")
```

**Arguments**

- `link`: the link function

**Value**

Output as for other GLM families
**CAR**  
*Conditional Autoregressive Family*

**Description**
A function used in the hglm package which extends the usage of the CAR family.

**Usage**
CAR(D, link = "identity", link.rand.disp = "inverse")

**Arguments**
- `D`: the D matrix of the Markov Random Field model.
- `link`: the link function for the random effects.
- `link.rand.disp`: the link function for the random effects dispersion parameter.

**Value**
Output specific for hglm fit, including eigen values and vectors of D.

**References**

---

**hglm**  
*Fitting Hierarchical Generalized Linear Models*

**Description**
hglm is used to fit hierarchical generalized linear models. It can be used for linear mixed models and generalized linear models with random effects for a variety of links and a variety of distributions for both the outcomes and the random effects. Fixed effects can also be fitted in the dispersion part of the model. The function can be called either by specifying the design matrices or as a formula.

**Usage**
hglm(X = NULL, y = NULL, Z = NULL, family = gaussian(link = identity),  
rand.family = gaussian(link = identity), method = "EQL",  
conv = 1e-6, maxit = 50, startval = NULL, fixed = NULL,  
random = NULL, X.disp = NULL, disp = NULL, link.disp = "log",  
X.rand.disp = NULL, rand.disp = NULL, link.rand.disp = "log",  
data = NULL, weights = NULL, fix.disp = NULL, offset = NULL,  
RandC = ncol(Z), sparse = TRUE, vcovmat = FALSE,  
calc.lik = FALSE, bigRR = FALSE, verbose = FALSE, ...)
Arguments

- **X** matrix. The design matrix for the fixed effects.
- **y** numeric. The dependent variable.
- **Z** matrix. The design matrix for the random effects.
- **family** family. The description of the error distribution and link function to be used in the mean part of the model. (See **family** for details of family functions.)
- **rand.family** family. The description of the distribution and link function to be used for the random effect.
- **method** character. Estimation method where EQL is the method of interconnected GLMs presented in Lee et al (2006). Apart from the default option EQL there is also an EQL1 option, which improves estimation for GLMMs (especially for Poisson models with a large number of levels in the random effects).
- **conv** numeric. The convergence criteria (change in linear predictor between iterations).
- **maxit** numeric. Maximum number of iterations in the hglm algorithm.
- **startval** numeric. A vector of starting values in the following order: fixed effects, random effect, variance of random effects, variance of residuals.
- **fixed** formula. A formula specifying the fixed effects part of the model.
- **random** formula. A one-sided formula specifying the random effects part of the model.
- **X.disp** matrix. The design matrix for the fixed effects in the residual dispersion part of the model.
- **disp** formula. A one-sided formula specifying the fixed effects in the residual dispersion part of the model.
- **link.disp** character. The link function for the residual dispersion part of the model.
- **X.rand.disp** matrix. The design matrix for the fixed effects in the random effects dispersion part of the model.
- **rand.disp** formula. A one-sided formula specifying the fixed effects in the random effects dispersion part of the model.
- **link.rand.disp** character. The link function for the random effects dispersion part of the model.
- **data** data.frame. The data frame to be used together with fixed and random.
- **weights** numeric. Prior weights to be specified in weighted regression.
- **fix.disp** numeric. A numeric value if the dispersion parameter of the mean model is known, e.g., 1 for binomial and Poisson model.
- **offset** An offset for the linear predictor of the mean model.
- **RandC** numeric. Integers (possibly a vector) specifying the number of column of Z to be used for each of the random-effect terms.
- **sparse** logical. If TRUE, the computation is to be carried out by using sparse matrix technique.
- **vcovmat** logical. If TRUE, the variance-covariance matrix is returned.
calc.like logical. If TRUE, likelihoods will be computed at convergence and will be shown via the print or summary methods on the output object.

bigRR logical. If TRUE, and only for the Gaussian model with one random effect term, a specific algorithm will be used for fast fitting high-dimensional (p > n) problems. See Shen et al. (2013) for more details of the method.

verbose logical. If TRUE, more information is printed during model fitting process.

... not used.

Details

Models for hglm are either specified symbolically using formula or by specifying the design matrices (X, Z and x.disp). The extended quasi likelihood (EQL) method is the default method for estimation of the model parameters. For the Gaussian-Gaussian linear mixed models, it is REML. It should be noted that the EQL estimator can be biased and inconsistent in some special cases e.g. binary pair matched response. A higher order correction might be useful to correct the bias of EQL (Lee et al. 2006). There is also an EQL1 option, which improves estimation for GLMMs (especially for Poisson models with a large number of levels in the random effects). The EQL1 method computes estimates by adjusting the working response as described in the appendix of Lee and Lee (2012).

By default, the dispersion parameter is estimated by the hglm and hglm2 functions. If the dispersion parameter of the mean model is to be held constant, for example if it is desired to be 1 for binomial and Poisson family, then fix.disp=value where, value=1 for the above example, should be used.

Interpretation of warning messages

Remove all NA before input to the hglm function.
- This message is important and tells the user to delete all lines with missing values from the input data.

Residuals numerically 0 are replaced by \textit{1e-8}. or
Hat-values numerically 1 are replaced by \textit{1 - 1e-8}.
- These messages are often not important as they usually reflect a numerical issue in an intermediate step of the iterative fitting algorithm. However, it is a good idea to check that there are no hat values equal to 1 in the final output.

Value

It returns an object of class hglm consisting of the following values.

fixef fixed effect estimates.
ranef random effect estimates.
RandC integers (possibly a vector) specified the number of column of Z to be used for each of the random-effect terms.
varFix dispersion parameter of the mean model (residual variance for LMM).
varRanef dispersion parameter of the random effects (variance of random effects for GLMM).
CAR.rho parameter estimate for a MRF spatial model.
CAR.tau parameter estimate for a MRF spatial model.
iter  number of iterations used.
Converge  specifies if the algorithm converged.
SeFe  standard errors of fixed effects.
SeRe  standard errors of random effects.
dfReFe  deviance degrees of freedom for the mean part of the model.
SummVC1  estimates and standard errors of the linear predictor in the dispersion model.
SummVC2  estimates and standard errors of the linear predictor for the dispersion parameter of the random effects.
dev  individual deviances for the mean part of the model.
hv  hatvalues for the mean part of the model.
resid  studentized residuals for the mean part of the model.
fv  fitted values for the mean part of the model.
disp.fv  fitted values for the dispersion part of the model.
disp.resid  standardized deviance residuals for the dispersion part of the model.
link.disp  link function for the dispersion part of the model.
vcov  the variance-covariance matrix.
likelihood  a list of log-likelihood values for model selection purposes, where $hlik$ is the log-h-likelihood, $pvh$ the adjusted profile log-likelihood profiled over random effects, $pbvh$ the adjusted profile log-likelihood profiled over fixed and random effects, and $caic$ the conditional AIC. (NOTE: In some earlier version (version <2.0) -2 times the log-likelihoods were reported.)
bad  the index of the influential observation.

Author(s)
Moudud Alam, Lars Ronnegard, Xia Shen

References


Moudud Alam, Lars Ronnegard, Xia Shen (2014). *Fitting conditional and simultaneous autoregressive spatial models in hglm*. *Submitted*. 

See Also

`hglm2`

Examples

```r
# Find more examples and instructions in the package vignette:
# vignette('hglm')

require(hglm)

# ---------------------------
# semiconductor example #
# ---------------------------

data(semiconductor)

m11 <- hglm(fixed = y ~ x1 + x3 + x5 + x6,
             random = ~ 1|Device,
             family = Gamma(link = log),
             disp = ~ x2 + x3, data = semiconductor)
summary(m11)
plot(m11, cex = .6, pch = 1,
     cex.axis = 1/.6, cex.lab = 1/.6,
     cex.main = 1/.6, mar = c(3, 4.5, 0, 1.5))

# ---------------------------
# redo it using hglm2 #
# ---------------------------

m12 <- hglm2(y ~ x1 + x3 + x5 + x6 + (1|Device),
             family = Gamma(link = log),
             disp = ~ x2 + x3, data = semiconductor)
summary(m12)

# ---------------------------
# redo it using matrix input #
# ---------------------------

attach(semiconductor)

m13 <- hglm(y = y, X = model.matrix(~ x1 + x3 + x5 + x6),
             Z = kronecker(diag(16), rep(1, 4)),
             X.disp = model.matrix(~ x2 + x3),
             family = Gamma(link = log))
summary(m13)
```

# ---------------------------
# verbose & likelihoods #
# ----------------------------------- #

m14 <- hglm(fixed = y ~ x1 + x3 + x5 + x6,
             random = ~ 1|Device,
             family = Gamma(link = log),
             disp = ~ x2 + x3, data = semiconductor,
             verbose = TRUE, calc.lik = TRUE)
summary(m14)

# ----------------------------------- #
# simulated example with 2 random effects terms #
# ----------------------------------- #
## Not run:
set.seed(911)
x1 <- rnorm(100)
x2 <- rnorm(100)
x3 <- rnorm(100)
z1 <- factor(rep(LETTERS[1:10], rep(10, 10))
z2 <- factor(rep(letters[1:5], rep(20, 5))
Z1 <- model.matrix(~ 0 + z1)
Z2 <- model.matrix(~ 0 + z2)
u1 <- rnorm(100, 0, sqrt(2))
u2 <- rnorm(5, 0, sqrt(3))
y <- 1 + 2*x1 + 3*x2 + Z1 %*% u1 + Z2 %*% u2 + rnorm(100, 0, sqrt(exp(x3)))
dd <- data.frame(x1 = x1, x2 = x2, x3 = x3, z1 = z1, z2 = z2, y = y)

(m21 <- hglm(X = cbind(rep(1, 100), x1, x2), y = y, Z = cbind(Z1, Z2),
            RandC = c(10, 5)))
summary(m21)
plot(m21)

# m21 is the same as:
(m21b <- hglm(X = cbind(rep(1, 100), x1, x2), y = y, Z = cbind(Z1, Z2),
            rand.family = list(gaussian(), gaussian()), RandC = c(10, 5))

(m22 <- hglm2(y ~ x1 + x2 + (1|z1) + (1|z2), data = dd, vcovmat = TRUE))
image(m22$vcov, main = 'Variance-covariance Matrix')
summary(m22)
plot(m22)

m31 <- hglm2(y ~ x1 + x2 + (1|z1) + (1|z2), disp = ~ x3, data = dd)
print (m31)
summary(m31)
plot(m31)

# ----------------------------------- #
# Markov random field (MRF) model #
# ----------------------------------- #
data(cancer)
logE <- log(E)
X11 <- model.matrix(~ Paff)
m41 <- hglm(X = X11, y = 0, Z = diag(length(0)),
            random = ~ 1|Device,
            family = Gamma(link = log),
            disp = ~ x2 + x3, data = semiconductor,
            verbose = TRUE, calc.lik = TRUE)
summary(m41)
hglmR

**Fitting Hierarchical Generalized Linear Models**

**Description**

hglmR is used to fit hierarchical generalized linear models. It extends the hglm function by allowing for several random effects, where the model is specified in \textit{lme4} convolution, and also by implementing sparse matrix techniques using the \texttt{Matrix} library.

**Usage**

\begin{verbatim}

\texttt{hglm2(meanmodel, data = NULL, family = gaussian(link = identity),}
\texttt{ rand.family = gaussian(link = identity), method = "EQL",}
\texttt{ conv = 1e-6, maxit = 50, startval = NULL,}
\texttt{ X.disp = NULL, disp = NULL, link.disp = "log",}
\texttt{ weights = NULL, fix.disp = NULL, offset = NULL,}
\texttt{ sparse = TRUE, vcovmat = FALSE, calc.like = FALSE,}
\texttt{ RandC = NULL, bigRR = FALSE, verbose = FALSE, ...)}

\end{verbatim}

**Arguments**

- \texttt{meanmodel} \hspace{1cm} formula. A two sided formula specifying the fixed and random terms in \texttt{lme4} convention, e.g. \texttt{y ~ x1 + (1|id)} indicates \texttt{y} as response, \texttt{x1} as the fixed effect and \texttt{(1|id)} represent a random intercept for each level of \texttt{id}.
- \texttt{data} \hspace{1cm} data.frame. An optional data frame from where the variables in the \texttt{meanmodel} (and possibly \texttt{disp}) are to be obtained. It is expected that the data frame does not contain any missing value.
family

family. The description of the error distribution and link function to be used in
the mean part of the model. (See family for details of family functions.)

rand.family

family. The description of the distribution and link function to be used for the
random effect.

method

character. Estimation method where EQL is the method of interconnected
GLMs presented in Lee et al (2006). Apart from the default option EQL there
is also an EQL1 option, which improves estimation for GLMMs (especially for
Poisson models with a large number of levels in the random effects).

conv

numeric. The convergence criteria (change in linear predictor between itera-
tions).

maxit

numeric. Maximum number of iterations in the hglm algorithm.

startval

numeric. A vector of starting values in the following order: fixed effects, ran-
dom effect, variance of random effects, variance of residuals.

X.disp

matrix. The design matrix for the fixed effects in the dispersion part of the
model.

disp

formula. A one-sided formula specifying the fixed effects in the dispersion
part of the model.

link.disp

character. The link function for the dispersion part of the model.

weights

numeric. Prior weights to be specified in weighted regression.

fix.disp

numeric. A numeric value if the dispersion parameter of the mean model is
known, e.g., 1 for binomial and Poisson model.

offset

An offset for the linear predictor of the mean model.

sparse

logical. If TRUE, the computation is to be carried out by using sparse matrix
technique.

vcovmat

logical. If TRUE, the variance-covariance matrix is exported.

calc.like

logical. If TRUE, likelihoods will be computed at convergence and will be shown
via the print or summary methods on the output object.

RandC

numeric. Necessary in old versions but can be neglected now. Integers (possi-
bly a vector) specifying the number of column of Z to be used for each of the
random-effect terms.

bigRR

logical. If TRUE, and only for the Gaussian model with one random effect term, a
specific algorithm will be used for fast fitting high-dimensional (p \gg n) problems. See
Shen et al. (2013) for more details of the method.

verbose

logical. If TRUE, more information is printed during model fitting process.

... not used.

Details

Models for hglm are either specified symbolically using formula or by specifying the design ma-
trices (X, Z and X.disp). Currently, only the extended quasi likelihood (EQL) method is available
for the estimation of the model parameters. Only for the Gaussian-Gaussina linear mixed models, it
is REML. It should be noted that the EQL estimator can be biased and inconsistent in some special
cases e.g. binary pair matched response. A higher order correction might be useful to correct the
bias of EQL (Lee et al. 2006). But, those corrections are not implemented in the current version. By default, the dispersion parameter is always estimated via EQL. If the dispersion parameter of the mean model is to be held constant, for example if it is desired to be 1 for binomial and Poisson family, then fix.disp=value where, value=1 for the above example, should be used.

Value

It returns an object of class hglm consisting of the following values.

- **fixef**: fixed effect estimates.
- **ranef**: random effect estimates.
- **RandC**: integers (possibly a vector) specified the number of column of Z to be used for each of the random-effect terms.
- **varFix**: dispersion parameter of the mean model (residual variance for LMM).
- **varRanef**: dispersion parameter of the random effects (variance of random effects for GLMM).
- **iter**: number of iterations used.
- **Converge**: specifies if the algorithm converged.
- **SeFe**: standard errors of fixed effects.
- **SeRe**: standard errors of random effects.
- **dfReFe**: deviance degrees of freedom for the mean part of the model.
- **SummVC1**: estimates and standard errors of the linear predictor in the dispersion model.
- **SummVC2**: estimates and standard errors of the linear predictor for the dispersion parameter of the random effects.
- **dev**: individual deviances for the mean part of the model.
- **hv**: hatvalues for the mean part of the model.
- **resid**: studentized residuals for the mean part of the model.
- **fv**: fitted values for the mean part of the model.
- **disp.fv**: fitted values for the dispersion part of the model.
- **disp.resid**: standardized deviance residuals for the dispersion part of the model.
- **link.disp**: link function for the dispersion part of the model.
- **vcov**: the variance-covariance matrix.
- **likelihood**: a list of log-likelihood values for model selection purposes, where $hlik$ is -2 times the log-h-likelihood, $pvh$ -2 times the adjusted profile log-likelihood profiled over random effects, $pvh$ -2 times the adjusted profile log-likelihood profiled over fixed and random effects, and $caic$ the conditional AIC.
- **bad**: the index of the influential observation.

Author(s)

Moudud Alam, Xia Shen, Lars Ronnegard
References


Xia Shen, Moudud Alam, Freddy Fikse and Lars Ronnegard (2013). **A novel generalized ridge regression method for quantitative genetics.** *Genetics.***

Moudud Alam, Lars Ronnegard, Xia Shen (2014). **Fitting conditional and simultaneous autoregressive spatial models in hglm.** Submitted.

See Also

hglm

Examples

```r
# Find more examples and instructions in the package vignette:
# vignette('hglm')

require(hglm)

# -------------------------- #
# semiconductor example #
# -------------------------- #

data(semiconductor)

m11 <- hglm(fixed = y ~ x1 + x3 + x5 + x6,
            random = ~ 1|Device,
            family = Gamma(link = log),
            disp = ~ x2 + x3, data = semiconductor)
summary(m11)
plot(m11, cex = .6, pch = 1,
     cex.axis = 1/.6, cex.lab = 1/.6,
     cex.main = 1/.6, mar = c(3, 4.5, 0, 1.5))

# -------------------------- #
# redo it using hglm2 #
# -------------------------- #

m12 <- hglm2(y ~ x1 + x3 + x5 + x6 + (1|Device),
             family = Gamma(link = log),
             disp = ~ x2 + x3, data = semiconductor)
summary(m12)
```

# redo it using matrix input

attach(semiconductor)

m13 <- hglm(y = y, X = model.matrix(~ x1 + x3 + x5 + x6),
    Z = kronecker(diag(16), rep(1, 4)),
    X.disp = model.matrix(~ x2 + x3),
    family = Gamma(link = log))

summary(m13)

m14 <- hglm(fixed = y ~ x1 + x3 + x5 + x6,
    random = ~ 1|Device,
    family = Gamma(link = log),
    disp = ~ x2 + x3, data = semiconductor,
    verbose = TRUE, calc.like = TRUE)

summary(m14)

# simulated example with 2 random effects terms

## Not run:

set.seed(912)
x1 <- rnorm(100)
x2 <- rnorm(100)
x3 <- rnorm(100)
z1 <- factor(rep(letters[1:10], rep(10, 10)))
z2 <- factor(rep(letters[1:5], rep(20, 5)))
Z1 <- model.matrix(~ 0 + z1)
Z2 <- model.matrix(~ 0 + z2)
u1 <- rnorm(10, 0, sqrt(2))
U2 <- rnorm(5, 0, sqrt(3))
y <- 1 + 2*x1 + 3*x2 + Z1%*%u1 + Z2%*%u2 + rnorm(100, 0, sqrt(exp(x3)))

dd <- data.frame(x1 = x1, x2 = x2, x3 = x3, z1 = z1, z2 = z2, y = y)

(m21 <- hglm(X = cbind(rep(1, 100), x1, x2), y = y, Z = cbind(Z1, Z2),
    RandC = c(10, 5)))

summary(m21)
plot(m21)

(m22 <- hglm2(y ~ x1 + x2 + (1|z1) + (1|z2), data = dd, vcovmat = TRUE))
image(m22$vcov, main = 'Variance-covariance Matrix')
summary(m22)
plot(m22)

m31 <- hglm2(y ~ x1 + x2 + (1|z1) + (1|z2), disp = ~ x3, data = dd)
print (m31)
summary(m31)
inverse.gamma

```
plot(m31)
## End(Not run)
```

---

**inverse.gamma**  
*Inverse Gamma Family*

**Description**

A function used in the hglm package for the inverse Gamma family.

**Usage**

```
inverse.gamma(link="inverse")
```

**Arguments**

`link` Link function.

**Value**

Output as for other GLM families

---

**inverse.sqrt**  
*Inverse Square Root Family*

**Description**

A function used in the hglm package for the inverse square root family.

**Usage**

```
inverse.sqrt()
```

**Value**

Output as for other GLM families
### logLik.hglm

*Extracts log-likelihood values*

#### Description

Extracts log-likelihood values from an existing hglm object hglm.obj.

#### Usage

```r
## S3 method for class 'hglm'
logLik(object, REML=NULL, ...)
```

#### Arguments

- `object` A fitted hglm object.
- `REML` The default NULL returns all computed log-likelihoods. The option REML=TRUE returns only the adjusted profile log-likelihood profiled over fixed and random effects.
- `...` This argument is not used.

#### Details

The use of log-likelihoods and cAIC is described in Lee, Nelder and Pawitan (2006).

#### Value

A list of log-likelihood values for model selection purposes, where $hlik$ is the log-h-likelihood, $pvh$ the adjusted profile log-likelihood profiled over random effects, $pbvh$ the adjusted profile log-likelihood profiled over fixed and random effects, and $cAIC$ the conditional AIC.

#### References


---

### lrt

*Likelihood-ratio test for variance components in hglm*

#### Description

Likelihood-ratio test for the estimated variance components (or other dispersion parameters) in hglm.

#### Usage

```r
lrt(hglm.obj1, hglm.obj2 = NULL)
```
**Arguments**

- `hglm.obj1` a fitted `hglm` object.
- `hglm.obj2` optional, another fitted `hglm` object to be tested against `hglm.obj1`.

**Details**

When `hglm.obj2 = NULL`, all the random effects variance components in `hglm.obj1` are tested against the null model with only fixed effects. The degree of freedom is determined by comparing the number of random effects terms in `hglm.obj1` and `hglm.obj2` or the null fixed-effects-only model. Note that the likelihood-ratio test statistic for variance estimates, which are bounded above zero, follows a 50:50 mixture distribution of chi-square with 0 and 1 degree of freedom (Self and Liang 1987 JASA).

**Value**

Printout summary of the likelihood-ratio test results. Test statistic, p-value, etc. are returned.

**References**


**Examples**

```r
require(hglm)

## Not run:
set.seed(911)
x1 <- rnorm(100)
x2 <- rnorm(100)
x3 <- rnorm(100)
z1 <- factor(rep(LETTERS[1:10], rep(10, 10)))
z2 <- factor(rep(letters[1:5], rep(20, 5)))
Z1 <- model.matrix(~ 0 + z1)
Z2 <- model.matrix(~ 0 + z2)
u1 <- rnorm(10, 0, sqrt(2))
u2 <- rnorm(5, 0, sqrt(3))
y <- 1 + 2*x1 + 3*x2 + Z1%*%u1 + Z2%*%u2 + rnorm(100, 0, sqrt(exp(x3)))
dd <- data.frame(x1 = x1, x2 = x2, x3 = x3, z1 = z1, z2 = z2, y = y)
m20 <- hglm(X = cbind(rep(1, 100), x1, x2), y = y, Z = Z1, calc.like = TRUE)
lrt(m20)
m21 <- hglm(X = cbind(rep(1, 100), x1, x2), y = y, Z = cbind(Z1, Z2),
            RandC = c(10, 5), calc.like = TRUE)
lrt(m20, m21)
```
Description

Plots residuals for the mean and dispersion models, individual deviances and hatvalues for hglm objects.

Usage

```r
## S3 method for class 'hglm'
plot(x, pch = "*", pcol = 'slateblue', lcol = 2,
     device = NULL, name = NULL, ...)
```

Arguments

- `x`: the hglm object to be plotted
- `pch`: symbol used in the plots
- `pcol`: color of points
- `lcol`: color of lines
- `device`: if NULL, plot on screen devices, if 'pdf', plot to PDF files in the current working directory.
- `name`: a string gives the main name of the PDF file when `device = 'pdf'`.
- `...`: graphical parameters

Details

A S3 generic plot method for hglm objects. It produces a set of diagnostic plots for a hierarchical model.

Author(s)

Xia Shen

Examples

```r
# semiconductor example

data(semiconductor)

h.gamma.normal <- hglm(fixed = y ~ x1 + x3 + x5 + x6,
                        random = ~ 1|Device,
                        family = Gamma(var = normal)
                       )
```

```r
plot(h.gamma.normal)
```
family = Gamma(link = log),
disp = ~ x2 + x3, data = semiconductor)

summary(h.gamma.normal)
plot(h.gamma.normal, cex = .6, pch = 1,
    cex.axis = 1/6, cex.lab = 1/6,
    cex.main = 1/6, mar = c(3, 4.5, 0, 1.5))

# -------------- #
# redo it using hglm2 #
# -------------- #

m1 <- hglm2(y ~ x1 + x3 + x5 + x6 + (1|Device),
    family = Gamma(link = log),
    disp = ~ x2 + x3, data = semiconductor)

summary(m1)
plot(m1, cex = .6, pch = 1,
    cex.axis = 1/6, cex.lab = 1/6,
    cex.main = 1/6, mar = c(3, 4.5, 0, 1.5))

# ------------------------------- #
# simulated example with 2 random effects terms #
# ------------------------------- #

## Not run:
set.seed(911)
x1 <- rnorm(100)
x2 <- rnorm(100)
x3 <- rnorm(100)
z1 <- factor(rep(LETTERS[1:10], rep(10, 10)))
z2 <- factor(rep(letters[1:5], rep(20, 5)))
Z1 <- model.matrix(~ 0 + z1)
Z2 <- model.matrix(~ 0 + z2)
u1 <- rnorm(100, 0, sqrt(2))
u2 <- rnorm(50, 0, sqrt(3))
y <- 1 + 2*x1 + 3*x2 + Z1*x1 + Z2*x2 + rnorm(100, 0, sqrt(exp(x3))

dd <- data.frame(x1 = x1, x2 = x2, x3 = x3, z1 = z1, z2 = z2, y = y)

(m2.1 <- hglm(X = cbind(rep(1, 100), x1, x2), y = y, Z = cbind(Z1, Z2),
    RandC = c(10, 5)))

summary(m2.1)
plot(m2.1)

(m2.2 <- hglm2(y ~ x1 + x2 + (1|z1) + (1|z2), data = dd, vcovmat = TRUE))
image(m2.2$vcov)
summary(m2.2)
plot(m2.2)

m3 <- hglm2(y ~ x1 + x2 + (1|z1) + (1|z2), disp = ~ x3, data = dd)
print(m3)
summary(m3)
plot(m3)

## End(Not run)
Simultaneous Autoregressive Family

Description

A function used in the hglm package which extends the usage of the SAR family.

Usage

SAR(D, link = "identity", link.rand.disp = "inverse.sqrt")

Arguments

D the D matrix of the SAR model.
link the link function for the random effects.
link.rand.disp the link function for the random effects dispersion parameter.

Value

Output specific for hglm fit, including eigen values and vectors of D.

References

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