

Package ‘hglm’

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Type Package

Title Hierarchical Generalized Linear Models

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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_Roennegaard-et-al.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>>.

BugReports https://r-forge.r-project.org/tracker/?group_id=558

License GPL (>= 2)

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hglm-package	<i>Hierarchical Generalized Linear Models</i>
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Description

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.

Details

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Author(s)

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References

Lars Ronnegard, Xia Shen and Moudud Alam (2010). **hglm: A Package for Fitting Hierarchical Generalized Linear Models**. *The R Journal*, **2**(2), 20-28.

Youngjo Lee, John A Nelder and Yudi Pawitan (2006) *Generalized Linear Models with Random Effect: a unified analysis via h-likelihood*. Chapman and Hall/CRC.

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](#), [hglm2](#), [plot.hglm](#)

Beta

Extended Beta Family

Description

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

Usage

```
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

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

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.like = 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 ($p \gg n$) 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 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 1e-8. or

Hat-values numerically 1 are replaced by 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.

<code>fixef</code>	fixed effect estimates.
<code>ranef</code>	random effect estimates.
<code>RandC</code>	integers (possibly a vector) specified the number of column of <code>Z</code> to be used for each of the random-effect terms.
<code>varFix</code>	dispersion parameter of the mean model (residual variance for LMM).
<code>varRanef</code>	dispersion parameter of the random effects (variance of random effects for GLMM).
<code>CAR.rho</code>	parameter estimate for a MRF spatial model.
<code>CAR.tau</code>	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

Lars Ronnegard, Xia Shen and Moudud Alam (2010). **hglm: A Package for Fitting Hierarchical Generalized Linear Models**. *The R Journal*, **2**(2), 20-28.

Youngjo Lee, John A Nelder and Yudi Pawitan (2006) *Generalized Linear Models with Random Effect: a unified analysis via h-likelihood*. Chapman and Hall/CRC.

Xia Shen, Moudud Alam, Freddy Fikse and Lars Ronnegard (2013). **A novel generalized ridge regression method for quantitative genetics**. *Genetics* **193**(4), ?1255-1268.

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

Woojoo Lee and Youngjo Lee (2012). **Modifications of REML algorithm for hglms.** *Statistics and Computing* **22**, 959-966.

See Also

[hglm2](#)

Examples

```
# 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.like = 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(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)

# 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)),

```

```

        family = poisson(), rand.family = CAR(D = nbr),
        offset = logE, conv = 1e-9, maxit = 200, fix.disp = 1)
summary(m41)

data(ohio)
m42 <- hglm(fixed = MedianScore ~ 1,
           random = ~ 1 | district,
           rand.family = CAR(D = ohioDistrictDistMat),
           data = ohioMedian)
summary(m42)
require(sp)
districtShape <- as.numeric(substr(as.character(ohioShape@data$UNSDIDFP), 3, 7))
CARfit <- matrix(m42$ranef + m42$fixef, dimnames = list(rownames(ohioDistrictDistMat), NULL))
ohioShape@data$CAR <- CARfit[as.character(districtShape),]
ohioShape@data$CAR[353] <- NA # remove estimate of Lake Erie
splot(ohioShape, zcol = "CAR", main = "Fitted values from CAR",
      col.regions = heat.colors(1000)[1000:1], cuts = 1000)

## End(Not run)

```

hglm2

Fitting Hierarchical Generalized Linear Models

Description

hglm2 is used to fit hierarchical generalized linear models. hglm2 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 lme4 convention, and also by implementing sparse matrix techniques using the Matrix library.

Usage

```

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

```

Arguments

meanmodel	formula. A two sided formula specifying the fixed and random terms in lme4 convention, e.g. $y \sim x1 + (1 id)$ indicates y as response, $x1$ as the fixed effect and $(1 id)$ represent a random intercept for each level of id .
data	data.frame. An optional data frame from where the variables in the meanmodel (and possibly 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 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.
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 (possibly 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 matrices (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.

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

Author(s)

Moudud Alam, Xia Shen, Lars Ronnegard

References

Lars Ronnegard, Xia Shen and Moudud Alam (2010). **hglm: A Package for Fitting Hierarchical Generalized Linear Models**. *The R Journal*, **2**(2), 20-28.

Youngjo Lee, John A Nelder and Yudi Pawitan (2006) *Generalized Linear Models with Random Effect: a unified analysis via h-likelihood*. Chapman and Hall/CRC.

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

```
# 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.like = 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(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)

```

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

<i>inverse.gamma</i>	<i>Inverse Gamma Family</i>
----------------------	-----------------------------

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

<i>inverse.sqrt</i>	<i>Inverse Square Root Family</i>
---------------------	-----------------------------------

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	<i>Extracts log-likelihood values</i>
-------------	---------------------------------------

Description

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

Usage

```
## 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

Youngjo Lee, John A Nelder and Yudi Pawitan (2006) *Generalized Linear Models with Random Effect: a unified analysis via h-likelihood*. Chapman and Hall/CRC.

lrt	<i>Likelihood-ratio test for variance components in hglm</i>
-----	--

Description

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

Usage

```
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

Self, S. G., & Liang, K.-Y. (1987). Asymptotic Properties of Maximum Likelihood Estimators and Likelihood Ratio Tests Under Nonstandard Conditions. *Journal of the American Statistical Association*, **82**(398), 605-610.

Examples

```
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)
```

```
## End(Not run)
```

```
plot.hglm
```

Plot Hierarchical Generalized Linear Model Objects

Description

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

Usage

```
## 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

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

data(semiconductor)

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

```

        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(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)

(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)

```

SAR

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

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

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