

Package ‘hglm’

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Type Package

Title Hierarchical Generalized Linear Models

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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 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.

License GPL

LazyLoad yes

Depends Matrix, MASS

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hglm-package

Hierarchical Generalized Linear Models

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](#). Currently, only the extended quasi likelihood (EQL; Lee et al., 2006) estimation method is available which is also the REML for linear mixed models.

Details

Package: hglm
Type: Package
Version: 1.2-2
Date: 2011-07-01
License: GPL
LazyLoad: yes
Depends: Matrix, MASS

This is version 1.2-2 of the hglm package.

Author(s)

Moudud Alam, Xia Shen, Lars Ronnegard
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References

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

See Also

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

Beta	<i>Extended Beta Family</i>
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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

<code>hglm</code>	<i>Fitting Hierarchical Generalized Linear Models</i>
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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-4, maxit = 20, startval = NULL, fixed = NULL, random = NULL,
     X.disp = NULL, disp = NULL, link.disp = "log", data = NULL,
     weights = NULL, fix.disp=NULL, offset = NULL,
     RandC = NULL, sparse = TRUE, vcovmat = 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). Currently only EQL is available as the estimation method.
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 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.
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.
...	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-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). 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.

Author(s)

Moudud Alam, Lars Ronnegard, Xia Shen

References

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

See Also

[hglm2](#)

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)
```

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-4, maxit = 20, startval = NULL,
      X.disp = NULL, disp = NULL, link.disp = "log",
      weights = NULL, fix.disp = NULL, offset = NULL,
      sparse = TRUE, vcovmat = 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). Currently only EQL is available as the estimation method.
conv	numeric. The convergence criteria (change in linear predictor between iterations).

<code>maxit</code>	numeric. Maximum number of iterations in the hglm algorithm.
<code>startval</code>	numeric. A vector of starting values in the following order: fixed effects, random effect, variance of random effects, variance of residuals.
<code>X.disp</code>	matrix. The design matrix for the fixed effects in the dispersion part of the model.
<code>disp</code>	formula. A one-sided formula specifying the fixed effects in the dispersion part of the model.
<code>link.disp</code>	character. The link function for the dispersion part of the model.
<code>weights</code>	numeric. Prior weights to be specified in weighted regression.
<code>fix.disp</code>	numeric. A numeric value if the dispersion parameter of the mean model is known, e.g., 1 for binomial and Poisson model.
<code>offset</code>	An offset for the linear predictor of the mean model.
<code>sparse</code>	logical. If TRUE, the computation is to be carried out by using sparse matrix technique.
<code>vcovmat</code>	logical. If TRUE, the variance-covariance matrix is exported.
<code>...</code>	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 currections 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 Z 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.

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.

Author(s)

Moudud Alam, Xia Shen, Lars Ronnegard

References

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

See Also

[hglm](#)

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)

```

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 = 4, lcol = 2, ...)
```

Arguments

x	the hglm object to be plotted
pch	symbol used in the plots
pcol	color of points
lcol	color of lines
...	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)

```

pump

Pump reliability data set from Gaver and O’Muircheartaigh (1987)

Description

The ‘pump’ data set presents the failures of pumps in several systems of the water reactor nuclear plant Farley 1.

Format

The ‘pump’ data set contains 4 columns and 10 rows. A short description of the data columns are given below.

System The system number.

S Number of pumps failures.

t Time (in thousand hours) of operation.

Gr Pump groups; two levels: 1 = operated continuously, 0 = operated intermittently.

Source

Gaver, D P. and O’Muircheartaigh, I. G. 1987. Robust Empirical Bayes Analyses of Event Rates, *Technometrics* 29(1),1–15

References

Lee, Y. and Nelder, J. A. 1996. Hierarchical generalized linear models, *Journal of the Royal Statistical Association (B, Theory and Methods)* 58(4), 619–678.

QTLMAS

Simulated Data Set for the QTLMAS 2009 Workshop

Description

The data was simulated for the QTLMAS 2009 workshop in Wageningen, The Netherlands. The data was made available at <http://www.qtlmas2009.wur.nl/UK/Dataset/> and consists of markers, trait values and pedigree information. The original data set consisted of several traits and markers from several chromosomes, whereas the current data set included in this package consists of one trait ("P265"), pedigree information and data from 90 markers on chromosome number 1. There are 2025 individuals in the pedigree where 1000 individuals have trait values.

Format

A matrix containing 1000 rows and 2116 columns. The first column contains the trait values. Columns 2 to 2026 contains matrix Z, i.e. the pedigree information (as the Colesky factorization of the additive relationship matrix). Columns 2027 to 2116 contains matrix Z.marker, i.e. the marker information for the 90 markers on chromosome 1.

Source

QTLMAS 2009 Workshop <http://www.qtlmas2009.wur.nl/UK/Dataset/>

References

Coster, A., Bastiaansen J., Calus M., Maliepaard C. and Bink M. 2009. QTLMAS 2009: Simulated dataset. (submitted)

 salamander

Salamander mating data set from McCullagh and Nelder (1989)

Description

'salamander' data set presents the outcome of an experiment which was conducted at the University of Chicago in 1986 to study the extent at which mountain dusky salamanders from different populations would interbreed. More detailed description of the data is given in its original source, McCullagh and Nelder (1989).

Format

'salamander' data set contains 6 columns and 360 rows. A brief description of the data columns is given below.

Season The seasons, Spring and Summer of 1986, when the experiment was carried out.

Experiment Experiment number; 1,2,3.

TypeM Type of the male salamander; Rough Butt=R and White Side=W

TypeF Type of the female salamander; Rough Butt=R and White Side=W

Cross Cross between female and male type e.g. Cross=WR mean a White Side female was crossed with a Rough Butt male.

Male Identification number of the male salamander.

Female Identification number of the female salamander.

Mate Whether a mating was observed, Yes=1 and No=0.

Source

McCullagh P. and Nelder, J. A. 1989. *Generalized Linear Models*, Section 14.5, Chapman and Hall/CRC.

 seeds

Seeds germination data set from Crowder (1978)

Description

The data set was initially presented in Crowder (1978) to demonstrate the problem of over dispersion with binomial response and its solution via beta-binomial ANOVA. Later, the data set is used by many others including Breslow and Clayton (1993) and Lee and Nelder (1996) to demonstrate the usefulness of the Generalized Linear Mixed (and hierarchical) model. The seeds data set was originally obtained from a 2 by 2 factorial layout. The experiment was conducted on two types of seeds, *O. aegyptiaca* 75 and *O. aegyptiaca* 73, and two root extracts, bean and cucumber with an equal dilution, 1/125. Experimental units (plates) were prepared with the specific root extracts and a batch of certain seeds was brushed into the plates. The outcome is the count of germinated seed out of the total number of seeds applied in each plate.

Format

The seeds data set contains 5 columns and 21 rows. A short description of the data columns are given below.

plate Plate number.

seed Seed type; 2 levels: O75 (*O. aegyptiaca* 75) and O73 (*O. aegyptiaca* 73).

extract Type of roots extract; 2 levels: Bean and Cucumber.

r Response; number of seeds germinated in each plate.

n Total number of seeds applied in each plate.

Source

Crowder, M. J. 1978. Beta-binomial Anova for proportions, *Journal of the Royal Statistical Society (C, Applied Statistics)* 27(1), 34–37.

References

Breslow, N. E. and Clayton, D. G. 1993. Approximate inference in generalized linear mixed models, *Journal of the American Statistical Association* 88, 9–25.

Lee, Y. and Nelder, J. A. 1996. Hierarchical generalized linear models, *Journal of the Royal Statistical Association (B, Theory and Methods)* 58(4), 619–678.

 semiconductor

Semiconductor data set from GenStat.

Description

The semiconductor data set is obtained from a $2^{(6-2)}$ factorial design conducted in a semiconductor plant. The design variables, Lamination (3 factors; Temperature, Time and Pressure) and Firing (3 factors; Temperature, Cycle Time and Dew Point), are each taken at two levels. The goal of the original data analysis was to model the curvature or camber (taken in $1e-4$ in./in.) as a function of the design variables. The data set is taken from GenStat 11.1. It is also used in Lee et al. (2006) where Mayers et al. (2002) is referred to as the the original source of the data.

Format

This data set contains 64 rows and the following columns

Device Substrate device

x1 Lamination Temperature; two levels +1 and -1.

x2 Lamination Time; two levels: +1 and -1.

x3 Lamination Pressure; two levels: +1 and -1.

x4 Firing Temperature; two levels: +1 and -1.

x5 Firing Cycle Time; two levels: +1 and -1.

x6 Firing Dew Point; two levels: +1 and -1.

y Camber measure; in $1e-4$ in./in.

Source

GenStat(R) Release 11.1. VSN International Limited.

References

Lee, Y. and Nelder J. A., and Pawitan, Y. 2006. *Generalized Linear Models with Random Effectes*, Chapman and Hall/CRC.

Mayers, P. H., Montgomery, D. C. and Vining G. G. 2002. *Generalized Linear Models with Application in Engineering and Science*, John Wiley and Sons.

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