

Package ‘glmmML’

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Description Binomial and Poisson regression for clustered data, fixed and random effects with bootstrapping.

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ghq

Gauss-Hermite

Description

Calculates the zeros and weights needed for Gauss-Hermite quadrature.

Usage

```
ghq(n.points = 1, modified = TRUE)
```

Arguments

n.points	Number of points.
modified	Multiply by $\exp(\text{zeros}^2)$? Default is TRUE.

Details

Based on a Fortran 66 subroutine written by professor Jianming Jin.

Value

A list with components

zeros	The zeros (abscissas).
weights	The weights

Note

The code is modified to suit the purpose of glmmML, with the permission of professor Jin.

Author(s)

Jianming Jin, Univ. of Illinois, Urbana-Campaign

References

Gauss-Hermite

See Also

[glmmML](#)

Examples

```
ghq(15, FALSE)
```

Description

Fits grouped GLMs with fixed group effects. The significance of the grouping is tested by simulation, with a bootstrap approach.

Usage

```
glmmboot(formula, family = binomial, data, cluster, weights, subset, na.action,
offset, contrasts = NULL, start.coef = NULL,
control = list(epsilon = 1e-08, maxit = 200, trace = FALSE), boot = 0)
```

Arguments

formula	a symbolic description of the model to be fit. The details of model specification are given below.
family	Currently, the only valid values are <code>binomial</code> and <code>poisson</code> . The binomial family allows for the <code>logit</code> and <code>cloglog</code> links.
data	an optional data frame containing the variables in the model. By default the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>'glmmML'</code> is called.
cluster	Factor indicating which items are correlated.
weights	Case weights.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	See <code>glm</code> .
offset	this can be used to specify an a priori known component to be included in the linear predictor during fitting.
contrasts	an optional list. See the <code>'contrasts.arg'</code> of <code>'model.matrix.default'</code> .
start.coef	starting values for the parameters in the linear predictor. Defaults to zero.
control	Controls the convergence criteria. See glm.control for details.
boot	number of bootstrap replicates. If equal to zero, no test of significance of the grouping factor is performed.

Details

The simulation is performed by simulating new response vectors from the fitted probabilities without clustering, and comparing the maximized log likelihoods. The maximizations are performed by profiling out the grouping factor. It is a very fast procedure, compared to `glm`, when the grouping factor has many levels.

Value

The return value is a list, an object of class 'glmmboot'.

coefficients	Estimated regression coefficients
logLik	the max log likelihood
cluster.null.deviance	Deviance without the clustering
frail	The estimated cluster effects
bootLog	The logLik values from the bootstrap samples
bootP	Bootstrap p value
variance	Variance covariance matrix
sd	Standard error of regression parameters
boot_rep	No. of bootstrap replicates
mixed	Logical
deviance	Deviance
df.residual	Its degrees of freedom
aic	AIC
boot	Logical
call	The function call

Note

There is no overall intercept for this model; each cluster has its own intercept. See `frail`

Author(s)

Göran Broström and Henrik Holmberg

References

Broström, G. and Holmberg, H. (2011). Generalized linear models with clustered data: Fixed and random effects models. *Computational Statistics and Data Analysis* 55:3123-3134.

See Also

`link{glmmML}`, `optim`, `lmer` in *Matrix*, and `glmmPQL` in *MASS*.

Examples

```
## Not run:
id <- factor(rep(1:20, rep(5, 20)))
y <- rbinom(100, prob = rep(runif(20), rep(5, 20)), size = 1)
x <- rnorm(100)
dat <- data.frame(y = y, x = x, id = id)
res <- glmmboot(y ~ x, cluster = id, data = dat, boot = 5000)
## End(Not run)
##system.time(res.glm <- glm(y ~ x + id, family = binomial))
```

Description

'glmmbootFit' is the workhorse in the function glmmboot. It is suitable to call instead of 'glmmboot', e.g. in simulations.

Usage

```
glmmbootFit(X, Y, weights = rep(1, NROW(Y)),
  start.coef = NULL, cluster = rep(1, length(Y)),
  offset = rep(0, length(Y)), family = binomial(),
  control = list(epsilon = 1.e-8, maxit = 200, trace
    = FALSE), boot = 0)
```

Arguments

X	The design matrix (n * p).
Y	The response vector of length n.
weights	Case weights.
start.coef	start values for the parameters in the linear predictor (except the intercept).
cluster	Factor indicating which items are correlated.
offset	this can be used to specify an a priori known component to be included in the linear predictor during fitting.
family	Currently, the only valid values are binomial and poisson. The binomial family allows for the logit and cloglog links.
control	A list. Controls the convergence criteria. See glm.control for details.
boot	number of bootstrap replicates. If equal to zero, no test of significance of the grouping factor is performed. If non-zero, it should be large, at least, say, 2000.

Value

A list with components

coefficients	Estimated regression coefficients (note: No intercept).
logLik	The maximised log likelihood.
cluster.null.deviance	deviance from a model without cluster.
frail	The estimated cluster effects.
bootLog	The maximised bootstrap log likelihood values. A vector of length boot.
bootP	The bootstrap p value.
variance	The variance-covariance matrix of the fixed effects (no intercept).
sd	The standard errors of the coefficients.
boot_rep	The number of bootstrap replicates.

Note

A profiling approach is used to estimate the cluster effects.

Author(s)

Göran Broström

See Also

[glmmboot](#)

Examples

```
## Not run
x <- matrix(rnorm(1000), ncol = 1)
id <- rep(1:100, rep(10, 100))
y <- rbinom(1000, size = 1, prob = 0.4)
fit <- glmmbootFit(x, y, cluster = id, boot = 200)
summary(fit)
## End(Not run)
## Should show no effects. And boot too small.
```

glmmML

Generalized Linear Models with random intercept

Description

Fits GLMs with random intercept by Maximum Likelihood and numerical integration via Gauss-Hermite quadrature.

Usage

```
glmmML(formula, family = binomial, data, cluster, weights,
cluster.weights, subset, na.action,
offset, contrasts = NULL, prior = c("gaussian", "logistic", "cauchy"),
start.coef = NULL, start.sigma = NULL, fix.sigma = FALSE, x = FALSE,
control = list(epsilon = 1e-08, maxit = 200, trace = FALSE),
method = c("Laplace", "ghq"), n.points = 8, boot = 0)
```

Arguments

formula	a symbolic description of the model to be fit. The details of model specification are given below.
family	Currently, the only valid values are binomial and poisson. The binomial family allows for the logit and cloglog links.
data	an optional data frame containing the variables in the model. By default the variables are taken from 'environment(formula)', typically the environment from which 'glmmML' is called.

cluster	Factor indicating which items are correlated.
weights	Case weights. Defaults to one.
cluster.weights	Cluster weights. Defaults to one.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	See <code>glm</code> .
start.coef	starting values for the parameters in the linear predictor. Defaults to zero.
start.sigma	starting value for the mixing standard deviation. Defaults to 0.5.
fix.sigma	Should sigma be fixed at start.sigma?
x	If TRUE, the design matrix is returned (as x).
offset	this can be used to specify an a priori known component to be included in the linear predictor during fitting.
contrasts	an optional list. See the 'contrasts.arg' of 'model.matrix.default'.
prior	Which "prior" distribution (for the random effects)? Possible choices are "gaussian" (default), "logistic", and "cauchy".
control	Controls the convergence criteria. See <code>glm.control</code> for details.
method	There are two choices "Laplace" (default) and "ghq" (Gauss-Hermite).
n.points	Number of points in the Gauss-Hermite quadrature. If n.points == 1, the Gauss-Hermite is the same as Laplace approximation. If method is set to "Laplace", this parameter is ignored.
boot	Do you want a bootstrap estimate of cluster effect? The default is <i>No</i> (boot = 0). If you want to say yes, enter a positive integer here. It should be equal to the number of bootstrap samples you want to draw. A recommended absolute <i>minimum value</i> is boot = 2000.

Details

The integrals in the log likelihood function are evaluated by the Laplace approximation (default) or Gauss-Hermite quadrature. The latter is now fully adaptive; however, only approximate estimates of variances are available for the Gauss-Hermite (n.points > 1) method.

For the binomial families, the response can be a two-column matrix, see the help page for `glm` for details.

Value

The return value is a list, an object of class 'glmmML'. The components are:

boot	No. of boot replicates
converged	Logical
coefficients	Estimated regression coefficients
coef.sd	Their standard errors
sigma	The estimated random effects' standard deviation

<code>sigma.sd</code>	Its standard error
<code>variance</code>	The estimated variance-covariance matrix. The last column/row corresponds to the standard deviation of the random effects (<code>sigma</code>)
<code>aic</code>	AIC
<code>bootP</code>	Bootstrap p value from testing the null hypothesis of no random effect (<code>sigma = 0</code>)
<code>deviance</code>	Deviance
<code>mixed</code>	Logical
<code>df.residual</code>	Degrees of freedom
<code>cluster.null.deviance</code>	Deviance from a <code>glm</code> with no clustering. Subtracting deviance gives a test statistic for the null hypothesis of no clustering. Its asymptotic distribution is a symmetric mixture a constant at zero and a chi-squared distribution with one df. The printed p-value is based on this.
<code>cluster.null.df</code>	Its degrees of freedom
<code>posterior.modes</code>	Estimated posterior modes of the random effects
<code>terms</code>	The terms object
<code>info</code>	From hessian inversion. Should be 0. If not, no variances could be estimated. You could try fixing <code>sigma</code> at the estimated value and rerun.
<code>prior</code>	Which prior was used?
<code>call</code>	The function call
<code>x</code>	The design matrix if asked for, otherwise not present

Note

The optimization may not converge with the default value of `start.sigma`. In that case, try different start values for `sigma`. If still no convergence, consider the possibility to fix the value of `sigma` at several values and study the profile likelihood.

Author(s)

Göran Broström

References

Broström, G. and Holmberg, H. (2011). Generalized linear models with clustered data: Fixed and random effects models. *Computational Statistics and Data Analysis* 55:3123-3134.

See Also

[glmmboot](#), [glm](#), [optim](#), [lmer](#) in Matrix and [glmmPQL](#) in MASS.

Examples

```
id <- factor(rep(1:20, rep(5, 20)))
y <- rbinom(100, prob = rep(runif(20), rep(5, 20)), size = 1)
x <- rnorm(100)
dat <- data.frame(y = y, x = x, id = id)
glmmML(y ~ x, data = dat, cluster = id)
```

glmmML.fit

*Generalized Linear Model with random intercept***Description**

This function is called by `glmmML`, but it can also be called directly by the user.

Usage

```
glmmML.fit(X, Y, weights = rep(1, NROW(Y)), cluster.weights = rep(1, NROW(Y)),
  start.coef = NULL, start.sigma = NULL,
  fix.sigma = FALSE,
  cluster = NULL, offset = rep(0, nobs), family = binomial(),
  method = 1, n.points = 1,
  control = list(epsilon = 1.e-8, maxit = 200, trace = FALSE),
  intercept = TRUE, boot = 0, prior = 0)
```

Arguments

<code>X</code>	Design matrix of covariates.
<code>Y</code>	Response vector. Or two-column matrix.
<code>weights</code>	Case weights. Defaults to one.
<code>cluster.weights</code>	Cluster weights. Defaults to one.
<code>start.coef</code>	Starting values for the coefficients.
<code>start.sigma</code>	Starting value for the mixing standard deviation.
<code>fix.sigma</code>	Should sigma be fixed at <code>start.sigma</code> ?
<code>cluster</code>	The clustering variable.
<code>offset</code>	The offset in the model.
<code>family</code>	Family of distributions. Defaults to binomial with logit link. Other possibilities are binomial with cloglog link and poisson with log link.
<code>method</code>	Laplace (1) or Gauss-hermite (0)?
<code>n.points</code>	Number of points in the Gauss-Hermite quadrature. Default is <code>n.points = 1</code> , which is equivalent to Laplace approximation.
<code>control</code>	Control of the iterations. See glm.control .
<code>intercept</code>	Logical. If TRUE, an intercept is fitted.
<code>boot</code>	Integer. If > 0, bootstrapping with <code>boot</code> replicates.
<code>prior</code>	Which prior distribution? 0 for "gaussian", 1 for "logistic", 2 for "cauchy".

Details

In the optimisation, "vmmmin" (in C code) is used.

Value

A list. For details, see the code, and glmmML.

Author(s)

Göran Broström

References

Broström (2003)

See Also

[glmmML](#), [glmmPQL](#), and [lmer](#).

Examples

```
x <- cbind(rep(1, 14), rnorm(14))
y <- rbinom(14, prob = 0.5, size = 1)
id <- rep(1:7, 2)

glmmML.fit(x, y, cluster = id)
```

print.glmboot *Prints a 'glmmML' object.*

Description

A glmboot object is the output of glmboot.

Usage

```
## S3 method for class 'glmboot'
print(x, digits = max(3, getOption("digits") - 3), na.print = "", ...)
```

Arguments

x	The glmboot object
digits	Number of printed digits.
na.print	How to print NAs
...	Additional parameters, which are ignored.

Details

Nothing in particular.

Value

A short summary of the object is printed.

Note

This is the only summary method available for the moment.

Author(s)

Göran Broström

See Also

[glmboot](#)

<code>print.glmML</code>	<i>Prints a 'glmML' object.</i>
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Description

A glmML object is the output of glmML.

Usage

```
## S3 method for class 'glmML'  
print(x, digits = max(3, getOption("digits") - 3), na.print = "", ...)
```

Arguments

<code>x</code>	The glmML object
<code>digits</code>	Number of printed digits.
<code>na.print</code>	How to print NAs
<code>...</code>	Additional parameters, which are ignored.

Details

Nothing in particular.

Value

A short summary of the object is printed.

Note

This is the only summary method available for the moment.

Author(s)

Göran Broström

See Also

[glmML](#)

summary.glmboot

Summary of a glmboot object

Description

It simply calls `print.glmboot`

Usage

```
## S3 method for class 'glmboot'  
summary(object, ...)
```

Arguments

<code>object</code>	A glmboot object
<code>...</code>	Additional arguments

Details

A summary method will be written soon.

Value

Nothing is returned.

Note

Preliminary

Author(s)

Göran Broström

See Also

[print.glmboot](#)

summary.glmML *Summary of a glmML object*

Description

It simply calls `print.glmML`

Usage

```
## S3 method for class 'glmML'
summary(object, ...)
```

Arguments

<code>object</code>	A glmML object
<code>...</code>	Additional arguments

Value

Nothing is returned.

Note

Preliminary

Author(s)

Göran Broström

See Also

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