Package: glmmML (via r-universe)

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Maintainer Göran Broström <goran.brostrom@umu.se>

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Author Göran Broström [aut, cre], Jianming Jin [ctb], Henrik Holmberg [ctb]

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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(zeros**2)? Default is TRUE.

Details

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

Value

A list vith 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)
```

glmmboot *Generalized Linear Models with fixed effects grouping*

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 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.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	See glm.
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'.
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)

G\"oran Brostr\"om and Henrik Holmberg

References

Brostr\"om, 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))
```

glmmbootFit *Generalized Linear Models with fixed effects grouping*

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 moddel 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 glm.
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 glm.control 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 *No* (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 recomended absolute *minimum value* 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

sigma.sd	Its standard error
variance	The estimated variance-covariance matrix. The last column/row corresponds to the standard deviation of the random effects (sigma)
aic	AIC
bootP	Bootstrap p value from testing the null hypothesis of no random effect (sigma = 0)
deviance	Deviance
mixed	Logical
df.residual	Degrees of freedom
cluster.null.deviance	Deviance from a glm 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.
cluster.null.df	Its degrees of freedom
posterior.modes	Estimated posterior modes of the random effects
terms	The terms object
info	From hessian inversion. Should be 0. If not, no variances could be estimated. You could try fixing sigma at the estimated value and rerun.
prior	Which prior was used?
call	The function call
x	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)

G\"oran Brostr\"om

References

Brostr\"om, 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 Matrixand 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

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

Details

In the optimisation, "vmmin" (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.glmmboot *Prints a 'glmmML' object.*

Description

A glmmboot object is the output of `glmmboot`.

Usage

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

Arguments

`x`	The glmmboot 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

glmmboot

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

Description

A glmmML object is the output of `glmmML`.

Usage

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

Arguments

`x`	The glmmML 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

glmmML

`summary.glmmboot` *Summary of a glmmboot object*

Description

It simply calls `print.glmmboot`

Usage

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

Arguments

`object`	A glmmboot object
`...`	Additional arguments

Details

A summary method will be written soon.

Value

Nothing is returned.

Note

Preliminary

Author(s)

Göran Broström

See Also

print.glmmboot

`summary.glmmML` *Summary of a glmmML object*

Description

It simply calls `print.glmmML`

Usage

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

Arguments

`object`	A glmmML object
`...`	Additional arguments

Value

Nothing is returned.

Note

Preliminary

Author(s)

Göran Broström

See Also

`print.glmmML`

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