

# Package ‘mmmgee’

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**Title** Simultaneous Inference for Multiple Linear Contrasts in GEE Models

**Version** 1.20

**Imports** stats, methods, Matrix, mvtnorm

**Suggests** geepack, testthat

**Description** Provides global hypothesis tests, multiple testing procedures and simultaneous confidence intervals for multiple linear contrasts of regression coefficients in a single generalized estimating equation (GEE) model or across multiple GEE models. GEE models are fit by a modified version of the 'geeM' package.

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 datasim

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*Simulated Data Set With Three Endpoints*


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## Description

A data set was simulated with repeated observations of a continuous outcome variable Y.lin, a count data outcome Y.poi and a binary outcome Y.bin. In the simulation, the mean of an outcome variable depends on the binary grouping variable gr.lang and one of the continuous predictors x1, x2 and x3. Observations of all outcomes in the same subject, indicated by the variable id, are correlated. Also x1, x2 and x3 are correlated within subjects. Data are independent between subjects. The example code shows how to fit a marginal GEE model for each outcome variable and how to test, with different methods, the null hypothesis that the grouping variable has no effect on any of the three endpoints.

## Usage

```
data(datasim)
```

## Format

A data frame.

## Examples

```
data(datasim)
head(datasim)
mod1<-geem2(Y.lin~gr.lang+x1,id=id,data=datasim,family="gaussian",corstr="exchangeable")
mod2<-geem2(Y.poi~gr.lang+x2,id=id,data=datasim,family="poisson",corstr="exchangeable")
mod3<-geem2(Y.bin~gr.lang+x3,id=id,data=datasim,family="binomial",corstr="exchangeable")
L1<-L2<-L3<-matrix(c(0,1,0),nrow=1)
mmmgee.test(list(mod1,mod2,mod3),L=list(L1,L2,L3),statistic="Wald",type="maximum",
biascorr=TRUE,asymptotic=FALSE,closed.test=TRUE)
## Not run:
mmmgee.test(list(mod1,mod2,mod3),L=list(L1,L2,L3),statistic="score",closed.test=TRUE)
mmmgee.test(list(mod1,mod2,mod3),L=list(L1,L2,L3),statistic="score",type="quadratic",
closed.test=TRUE)
mmmgee.test(list(mod1,mod2,mod3),L=list(L1,L2,L3),statistic="Wald",type="quadratic",
biascorr=TRUE,asymptotic=FALSE,closed.test=TRUE)
mmmgee.test(list(mod1,mod2,mod3),L=list(L1,L2,L3),statistic="Wald",type="quadratic",
scaled=TRUE,biascorr=TRUE,asymptotic=FALSE,closed.test=TRUE)

## End(Not run)
```

## Description

geem2 is a modified version of [geem](#) to fit generalized estimating equation models and to provide objects that can be used for simultaneous inference across multiple marginal models using [mmmgee](#) and [mmmgee.test](#). Like geem, geem2 estimates coefficients and nuisance parameters using generalized estimating equations. The link and variance functions can be specified by the user and the syntax is similar to [glm](#).

## Usage

```
geem2(formula, id, waves = NULL, data = parent.frame(),
      family = gaussian, corstr = "independence", Mv = 1,
      weights = NULL, corr.mat = NULL, init.beta = NULL,
      init.alpha = NULL, init.phi = 1, scale.fix = FALSE,
      nodummy = FALSE, sandwich = TRUE, useP = TRUE, maxit = 20,
      tol = 1e-05, restriction = NULL, conv.criterion = c("ratio",
      "difference"))
```

## Arguments

formula	a formula expression similar to that for <a href="#">glm</a> , of the form response~predictors. An offset is allowed, as in glm.
id	a vector identifying the clusters. By default, data are assumed to be sorted such that observations in a cluster are in consecutive rows and higher numbered rows in a cluster are assumed to be later. If NULL, then each observation is assigned its own cluster.
waves	a non-negative integer vector identifying components of a cluster. For example, this could be a time ordering. If integers are skipped within a cluster, then dummy rows with weight 0 are added in an attempt to preserve the correlation structure (except if corstr = "exchangeable" or "independent"). This can be skipped by setting nodummy=TRUE. When assessing missing values, waves are assumed to start at 1, starting at a larger integer is therefore computationally inefficient.
data	an optional data frame containing the variables in the model.
family	will determine the link and variance functions. The argument can be one of three options: a family object, a character string, or a list of functions. For more information on how to use family objects, see <a href="#">family</a> . If the supplied argument is a character string, then the string should correspond to one of the family objects. In order to define a link function, a list must be created with the components (LinkFun, VarFun, InvLink, InvLinkDeriv), all of which are vectorized functions. If the components in the list are not named as (LinkFun, VarFun, InvLink, InvLinkDeriv), then geem2 assumes that the functions are given in that order. LinkFun and VarFun are the link and variance functions.

	InvLink and InvLinkDeriv are the inverse of the link function and the derivative of the inverse of the link function and so are decided by the choice of the link function.
corstr	a character string specifying the correlation structure. Allowed structures are: "independence", "exchangeable", "ar1", "m-dependent", "unstructured", "fixed", and "userdefined". Any unique substring may be supplied. If "fixed" or "userdefined", then <code>corr.mat</code> must be specified. If "m-dependent", then <code>Mv</code> is relevant.
Mv	for "m-dependent", the value for m.
weights	A vector of weights for the inverse of the scale factor each observation. If an observation is assigned weight 0, it is excluded from the calculations of any parameters. Observations with a NA in any variable will be assigned a weight of 0. Note that weights are defined differently in <code>geem2</code> and <code>geem</code> , see details.
corr.mat	the correlation matrix for "fixed". Matrix should be symmetric with dimensions $\geq$ the maximum cluster size. If the correlation structure is "userdefined", then this is a matrix describing which correlations are the same. In that case, all entries have to be integers, and values less or equal zero indicate a correlation of zero. The information regarding the user-defined structure are extracted from the upper triangle of the provided matrix.
init.beta	an optional vector with the initial values of beta. If not specified, then the intercept will be set to <code>InvLink(mean(response))</code> . <code>init.beta</code> must be specified if not using an intercept.
init.alpha	an optional scalar or vector giving the initial values for the correlation. If provided along with <code>Mv &gt; 1</code> or unstructured correlation, then the user must ensure that the vector is of the appropriate length.
init.phi	an optional initial scale parameter. If not supplied, initialized to 1.
scale.fix	if set to TRUE, then the scale parameter is fixed at the value of <code>init.phi</code> . See details.
nodummy	if set to TRUE, then dummy rows will not be added based on the values in waves.
sandwich	if TRUE, calculate robust variance.
useP	if set to FALSE, do not use the n-p correction for dispersion and correlation estimates, as in Liang and Zeger. This can be useful when the number of observations is small, as subtracting p may yield correlations greater than 1.
maxit	maximum number of iterations.
tol	tolerance in calculation of coefficients.
restriction	either a contrast matrix or a list of a contrast matrix and a right hand side vector, defining a restriction on the regression coefficients. See details.
conv.criterion	convergence criterion, either "ratio" or "difference". The default is "ratio", using the relative change in regression coefficient estimates as convergence criterion, like in <code>geem</code> . With "difference" the maximum absolute difference in regression coefficient estimates is used. The latter is required if some coefficient is 0, e.g. by estimation under some restriction.

## Details

The function is a modification of [geem](#) from the `geeM` package, such that additional output is returned that is required for the calculation of covariance matrix across multiple marginal models. In particular the contributions of each subject to the estimating equation are made available in the output. Internal functions regarding the calculation of matrix inverses were modified to improve the handling of missing data.

In `geem2`, weights are defined as scale weights, similar to most other software. Note that, in contrast, the current version of `geem` (version 0.10.1) uses residual weights.

The scale parameter `phi` is used in estimating the residual working correlation parameters and in estimating the model based (naïv) covariance matrix of the regression coefficients. Similar as in most other software, requesting `scale.fix=TRUE` only has an impact on the latter, while the working correlation is still estimated using an empirical scale factor for the residuals. In contrast, `geem` uses the fixed scale factor also when estimating the working correlation.

`geem2` allows for estimation of regression coefficients under linear restrictions  $L\beta = r$ , where  $L$  is a contrast matrix,  $\beta$  the vector of regression coefficients and  $r$  a real valued right hand side vector. Using the argument `restriction`,  $L$  and  $r$  can be specified. If only  $L$  is specified,  $r$  is assumed as null vector. The functionality is in particular required to calculate the generalized score test for linear hypotheses about  $\beta$ . Use `conv.criterion="difference"` if any regression coefficient is restricted to 0.

## Value

A list with class `geem2`, similar to the output of `geem` from the `geeM` package. The additional slot `sandwich.args` contains components to calculate the sandwich variance estimator for the fitted model and across models if applied in the multiple marginal model framework.

## Note

The option to fit a model with linear restrictions concerning the coefficients is implemented to enable the calculation of a generalized score test. It may also be used to obtain estimates of the coefficients under restrictions. The model based and robust variance estimates of the restricted coefficient estimates are found in the slots `restricted.naiv.var` and `restricted.var`, respectively. Note that the variance of estimates restricted to a single value is supposed to be zero, however the calculated variance estimate may deviate from zero within machine accuracy.

## Author(s)

The `geem` function was written by Lee McDaniel and Nick Henderson, modifications for `geem2` are by Robin Ristl <[robin.ristl@meduniwien.ac.at](mailto:robin.ristl@meduniwien.ac.at)>

## References

Lee S. McDaniel, Nicholas C. Henderson, Paul J. Rathouz. Fast pure R implementation of GEE: application of the matrix package. *The R journal* 5.1 (2013): 181.

## See Also

[mmmgee](#), [geem](#), [mmmgee.test](#)

## Examples

```
data(keratosis)
m1<-geem2(clearance~trt,id=id,data=keratosis,family=binomial,corstr="independence")
summary(m1)
m2<-geem2(pain~trt,id=id,data=keratosis[keratosis$lesion==1,],family=gaussian,corstr="independence")
summary(m2)
geem2(pain~trt,id=id,data=keratosis[keratosis$lesion==1,],family=gaussian,corstr="exchangeable")
#
data(datasim)
mod1<-geem2(Y.lin~gr.lang+x1,id=id,data=datasim,family="gaussian",corstr="exchangeable")
summary(mod1)
mod2<-geem2(Y.poi~gr.lang+x2,id=id,data=datasim,family="poisson",corstr="unstructured")
summary(mod2)
mod3<-geem2(Y.bin~gr.lang+x3,id=id,data=datasim,family="binomial",corstr="user",
corr.mat=matrix(c(1,2,3,0, 2,1,2,3, 3,2,1,2, 0,3,2,1),4,4))
summary(mod3)
```

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keratosis

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*Simulated Data Set for a Study of Actinic Keratosis Treatments*


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## Description

A data set simulated under the planning assumptions for a study comparing four radiation regimens for a photodynamic treatment of actinic keratosis. Each patient receives each treatment in a different skin patch and each patch contains four lesions. Variables are patient identifier (id), treatment (trt), lesion identifier within a patient (lesion), the binary outcome clearance success (1=success, 0=no success) reported for each lesion and the metric outcome pain (larger values indicating more pain) reported for each skin patch. The aim of the study is to compare the treatments B, C and D to the reference treatment A in terms of both outcomes.

## Usage

```
data(keratosis)
```

## Format

A data frame.

## Examples

```
data(keratosis)
head(keratosis)
```

**Description**

Calculate the covariance matrix for a stacked vector of regression coefficients from multiple marginal GEE models fitted with [geem2](#).

**Usage**

```
mmmgee(x, biascorr = FALSE)
```

**Arguments**

x	a list of geem objects fitted with geem2. The geem objects must be different models calculated with data from the same subjects. In particular, the parameter id in the call to geem2 must refer to the same subjects in each model.
biascorr	logical, if TRUE, a bias corrected covariance matrix is calculate by extending the method due to Mancl and DeRouen to multiple models. See references.

**Value**

A list with class mmmgee containing the following components:

beta	The stacked vector of regression coefficient estimates from the models in x.
V	The estimated covariance matrix of the regression coefficient estimates.
A	The outer component of $V = ABA$ .
B	The inner component of $V = ABA$ .
biascorr	The value of the input argument biascorr (logical).
n	A vector with the number of clusters in each model in x.
p	A vector with number of regression coefficients in each model in x.

**Author(s)**

Robin Ristl, <[robin.ristl@meduniwien.ac.at](mailto:robin.ristl@meduniwien.ac.at)>

**References**

Lloyd A. Mancl, Timothy A. DeRouen. A covariance estimator for GEE with improved small sample properties. Biometrics, 2001, 57(1):126-134.

**See Also**

[geem2](#), [mmmgee.test](#)

## Examples

```
data(keratoses)
m1<-geem2(clearance~trt,id=id,data=keratoses,family=binomial,corstr="independence")
m2<-geem2(pain~trt,id=id,data=keratoses[keratoses$lesion==1,],family=gaussian,corstr="independence")
mmmgee(x=list(m1,m2),biacorr=TRUE)
```

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mmmgee.test	<i>Hypothesis Tests for Linear Contrasts in Multiple Marginal GEE Models</i>
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## Description

Global hypothesis tests, multiple testing procedures and simultaneous confidence intervals for multiple linear contrasts of regression coefficients in a single generalized estimating equation (GEE) model or across multiple GEE models.

## Usage

```
mmmgee.test(x, L, r = NULL, statistic = c("wald", "score"),
  type = c("maximum", "quadratic"), asymptotic = TRUE,
  biacorr = FALSE, closed.test = FALSE, conf.int = FALSE,
  conf.level = 0.95, alternative = c("undirected", "greater", "less"),
  denomDF = NULL, scaled.F = FALSE, maxit = 20, tol = 10^(-8), ...)
```

## Arguments

x	a geem2 object fitted with geem2 or a list of geem2. In the latter case, the geem2 objects must be different models calculated with data from the same subjects. In particular, the parameter id in the call to geem2 must refer to the same subjects in each model.
L	a contrast matrix defining a contrast for the stacked vector of regression coefficients of the marginal models, or a list of contrast matrices. In the latter case, the list must contain one matrix for each model listed in x, in the same order as the models. When using the the score test and x is a list, L must be a list.
r	right hand side vector of the null hypothesis or a list of vectors resembling the right hand side of the null hypothesis. If not specified, r is assumed to be a null vector of appropriate length. See details.
statistic	either "wald" or "score", see details. The default is "wald".
type	either "maximum" or "quadratic", see details. The default is "maximum".
asymptotic	logical, if TRUE the reference distribution for the maximum-type Wald test statistic is a multivariate normal distribution and the reference distribution for the quadratic form Wald test statistic is a chi-squared distribution. If FALSE, a multivariate t-distribution or an F-distribution is used instead. Ignored for the Score test, see details.



<code>biascorr</code>	logical indicating whether the Mancl and DeRouen Bias correction should be used when estimating the joint covariance matrix via <a href="#">mmmgee</a> .
<code>closed.test</code>	logical, if TRUE, multiplicity adjusted p-values based on a closed test procedure using the selected type of test are calculated. With $k$ hypotheses this involves the computation of $2^k$ tests, which may require considerable computation time.
<code>conf.int</code>	logical. If TRUE simultaneous confidence intervals corresponding to a single step maximum-type test are calculated using a multivariate normal or t approximation, depending on <code>asymptotic</code> .
<code>conf.level</code>	the nominal simultaneous coverage probability of the confidence intervals.
<code>alternative</code>	one of "undirected", "greater", or "less". Determines the direction of maximum-type tests and of confidence intervals. The default is "undirected".
<code>denomDF</code>	Defaults to NULL. In that case, denominator degrees of freedom for the multivariate t-distribution or F-distribution are calculated as $\min(n-p)$ , where $n$ and $p$ are vectors of the number of independent clusters and the number of regression coefficients in the models in <code>x</code> . Alternatively, a numeric value may be entered to be used as denominator degrees of freedom.
<code>scaled.F</code>	logical. If TRUE and <code>type="quadratic"</code> and <code>asymptotic=FALSE</code> a scaled F distribution similar as for Hotelling's test is used. Ignored otherwise.
<code>maxit</code>	maximal number of iterations to be passed to <a href="#">geem2</a> . Only required when using the score test, where the models are refitted under the restriction of the null hypothesis.
<code>tol</code>	tolerance limit for the convergence criterion to be passed to <a href="#">geem2</a> . Only required when using the score test, where the models are refitted under the restriction of the null hypothesis.
<code>...</code>	additional arguments that are passed to <a href="#">pmvnorm</a> , <a href="#">qmvnorm</a> , <a href="#">pmvt</a> and <a href="#">qmvmt</a> . In particular the algorithm to solve the multivariate normal or t-distribution integrals may be selected.

## Details

The null hypothesis is  $H_0 : L\beta = r$  where  $L$  is a contrast matrix,  $\beta$  the stacked vector of regression coefficients from the marginal models and  $r$  a real values right hand side vector.  $L$  can be specified as matrix or, if it is a block diagonal matrix with each block corresponding to a contrast for one marginal GEE model, as list of the matrices on the diagonal. The right hand side  $r$  can be specified as vector or as list of vectors each corresponding to the part of the right hand side vector for one model.

When choosing `statistic="wald"` and `type="maximum"`, the maximum of the standardized entries of  $L\hat{\beta}$  is used as test statistic and the p-value is calculated from a multivariate normal or t-distribution (depending on `asymptotic` being TRUE or FALSE) with correlation matrix estimated for  $L\hat{\beta}$ . For the t-distribution, denominator degrees of freedom are used as specified in `denomDF`. When choosing `statistic="wald"` and `type="quadratic"`, a quadratic form of  $L\hat{\beta}$  and the inverse of the estimated covariance matrix of  $L\hat{\beta}$  is used as test statistic and the p-value is calculated from a chi-squared distribution or an F-distribution (depending on `asymptotic` being TRUE or FALSE).

With `statistic="score"`, generalized score tests are calculated by replacing  $L\hat{\beta}$  by the first order approximation  $LAU$  where  $U$  is the stacked estimating equation (the score) and  $A$  is the negative

inverse of the matrix of first derivatives of  $U$ , both evaluated at the location of constrained estimates for  $\beta$  under the null hypothesis. Analogous to the Wald statistic, a maximum-type and a quadratic form score test are available. For the score test the option `asymptotic` is ignored and the reference distribution is multivariate normal or chi-squared.

## Value

A list with class `mmmgeetest` containing the following components, if required:

`test` Contains a data frame with the test statistic, degrees of freedom (depending in the type of test) and the p-value. If closed test was required, a further data frame is reported with estimates, right hand side vector, unadjusted p-values and adjusted p-values for each line of  $H_0 : L\beta - r = 0$ .

`hypothesis` A list containing the contrast matrix  $L$  and the right hand side vector  $r$ .

`conf.int` The simultaneous confidence intervals.

`denomDF` The type and value of the denominator degrees of freedom used in the procedure.

`mmmgee` The `mmmgee` object containing in particular the estimated covariance matrix for the coefficients of the models in `x`. See [mmmgee](#).

## Note

A single value for the denominator degrees of freedom is calculated for the covariance matrix estimate across all contrasts. In the closed testing procedure, this value is used for the degrees of freedom associated with the covariance matrix of any subset of contrasts.

Usual linear models or generalized linear models can be regarded as special case of GEE models and can be included in the analysis framework. Note however that `mmmgee.test` always uses the robust sandwich covariance matrix estimate, even if the calculation of the sandwich covariance was suppressed in the model objects in `x`.

## Author(s)

Robin Ristl, <[robin.ristl@meduniwien.ac.at](mailto:robin.ristl@meduniwien.ac.at)>

## References

Dennis D. Boos. On generalized score tests. The American Statistician, 1992, 46(4):327-333.

Lloyd A. Mancl, Timothy A. DeRouen. A covariance estimator for GEE with improved small sample properties. Biometrics, 2001, 57(1):126-134.

## See Also

[geem2](#), [mmmgee](#)

## Examples

```

data(keratoses)
m1<-geem2(clearance~trt,id=id,data=keratoses,family=binomial,corstr="independence")
m2<-geem2(pain~trt,id=id,data=keratoses[keratoses$lesion==1,],family=gaussian,corstr="independence")
L1<-L2<-diag(1,4)[-1,]
mmmgee.test(x=m1,L=list(L1),statistic="wald",type="maximum")
mmmgee.test(x=m1,L=list(L1),statistic="score",type="maximum")
mmmgee.test(x=list(m1,m2),L=list(L1,L2),type="maximum",asymptotic=FALSE,biacorr=TRUE)
mmmgee.test(x=list(m1,m2),L=list(L1,L2),type="maximum",closed.test=TRUE)
mmmgee.test(x=list(m1,m2),L=list(L1,L2),type="maximum",asymptotic=FALSE,
alternative="less",conf.int=TRUE,denomDF=40)
mmmgee.test(x=list(m1,m2),L=list(L1,L2),type="quadratic",asymptotic=TRUE)
mmmgee.test(x=list(m1,m2),L=list(L1,L2),statistic="score",type="quadratic")
mmmgee.test(x=list(m1,m2),L=list(L1,L2),statistic="score",type="maximum")
#
## Not run:
data(datasim)
mod1<-geem2(Y.lin~gr.lang+x1,id=id,data=datasim,family="gaussian",corstr="exchangeable")
mod2<-geem2(Y.poi~gr.lang+x2,id=id,data=datasim,family="poisson",corstr="exchangeable")
mod3<-geem2(Y.bin~gr.lang+x3,id=id,data=datasim,family="binomial",corstr="exchangeable")
Li<-matrix(c(0,1,0),nrow=1)
mmmgee.test(list(mod1,mod2,mod3),L=list(Li,Li,Li),statistic="Wald",type="maximum",
biacorr=TRUE,asymptotic=FALSE,closed.test=TRUE)
mmmgee.test(list(mod1,mod2,mod3),L=list(Li,Li,Li),statistic="score",closed.test=TRUE)

## End(Not run)

```

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