

Package ‘htmglm’

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Type Package

Title Hypothesis Testing for McGLMs

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Description Performs hypothesis testing for multivariate covariance generalized linear models (McGLMs). McGLM is a general framework for non-normal multivariate data analysis, designed to handle multivariate response variables, along with a wide range of temporal and spatial correlation structures defined in terms of a covariance link function combined with a matrix linear predictor involving known matrices. The models take non-normality into account in the conventional way by means of a variance function, and the mean structure is modelled by means of a link function and a linear predictor. The models are fitted using an efficient Newton scoring algorithm based on quasi-likelihood and Pearson estimating functions, using only second-moment assumptions. This provides a unified approach to a wide variety of different types of response variables and covariance structures, including multivariate extensions of repeated measures, time series, longitudinal, spatial and spatio-temporal structures. The package offers a user-friendly interface for fitting McGLMs similar to the `glm()` R function.

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URL <https://github.com/lineu96/htmglm>

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apc	<i>Generate Matrix of All Pairwise Comparisons (Tukey contrasts)</i>
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Description

This function takes a matrix where each line defines a linear function of the parameters to estimate a marginal mean (aka least squares mean) and return the matrix that define the contrasts among these means. All pairwise contrasts are returned (aka Tukey contrasts). The matrix with these contrasts can be passed to `glht::multcomp()` to estimate them or used in explicit matricial calculus.

Usage

```
apc(lfm, lev = NULL)
```

Arguments

<code>lfm</code>	a $k \times p$ matrix where each line defines a linear function to estimate a lsmean. In general, these matrices are obtained by using <code>doBy::LSmatrix()</code> .
<code>lev</code>	a character vector with length equals to the numbers of lines of <code>lfm</code> matrix, (k). Default is <code>NULL</code> and the row names of <code>codelfm</code> is used. If row names is also <code>NULL</code> , incremental integer values are used to identify the comparisons.

Value

a $K \times p$ matrix with the linear functions that define all pairwise contrasts. K is $\binom{k}{2}$.

Author(s)

Walmes Zeviani, <walmes@ufpr.br>.

See Also

doBy::LSmatrix().

Examples

```
X <- diag(3)
rownames(X)
apc(X)

rownames(X) <- letters[nrow(X):1]
apc(X)

apc(X, lev = LETTERS[1:nrow(X)])

# Objects from doBy::LSmatrix() have an "grid" attribute.
attr(X, "grid") <- data.frame(n = LETTERS[1:nrow(X)])
rownames(X) <- NULL
apc(X)
```

mc_anova_dispersion *ANOVA tables for dispersion components.*

Description

Performs Wald tests to generate analysis-of-variance tables of the significance for the dispersion components by response variables for model objects produced by mcglm.

Usage

```
mc_anova_dispersion(object, p_var, names, verbose = TRUE)
```

Arguments

object	An object of mcglm class.
p_var	A list of indices that indicate how the dispersion parameters are related. Parameters with the same index are tested together.
names	Names to be shown in the table.
verbose	a logical if TRUE print some information about the tests performed. Default verbose = TRUE.

Value

Type III ANOVA table for dispersion components of mcglm objects.

Author(s)

Lineu Alberto Cavazani de Freitas, <lineuacf@gmail.com>

See Also

mc_anova_I, mc_anova_II and mc_anova_III.

Examples

```

library(mcgml)
library(Matrix)
library(htmcgml)

data("soya", package = "mcgml")

form.grain <- grain ~ water * pot
form.seed <- seeds ~ water * pot

soya$viabilepeasP <- soya$viabilepeas / soya$totalpeas
form.peas <- viablepeasP ~ water * pot

Z0 <- mc_id(soya)
Z1 <- mc_mixed(~0 + factor(block), data = soya)

fit_joint <- mcgml(linear_pred = c(form.grain,
                                form.seed,
                                form.peas),
                  matrix_pred = list(c(Z0, Z1),
                                    c(Z0, Z1),
                                    c(Z0, Z1)),
                  link = c("identity",
                          "log",
                          "logit"),
                  variance = c("constant",
                              "tweedie",
                              "binomialP"),
                  Ntrial = list(NULL,
                                NULL,
                                soya$totalpeas),
                  power_fixed = c(TRUE, TRUE, TRUE),
                  data = soya)

mc_anova_dispersion(fit_joint,
p_var = list(c(0,1), c(0,1), c(0,1)),
names = list(c('tau10', 'tau11'),
             c('tau20', 'tau21'),
             c('tau30', 'tau31')))

```

mc_anova_I	<i>ANOVA type I table for mcglm objects via Wald test.</i>
------------	--

Description

Performs Wald tests to generate type-I analysis-of- variance tables per response for model objects produced by mcglm.

Usage

```
mc_anova_I(object, verbose = TRUE)
```

Arguments

object	An object of mcglm class.
verbose	a logical if TRUE print some information about the tests performed. Default verbose = TRUE.

Value

Type I ANOVA table for mcglm objects.

Author(s)

Lineu Alberto Cavazani de Freitas, <lineuacf@gmail.com>

See Also

mc_anova_II, mc_anova_III and mc_anova_disp.

Examples

```
library(mcglm)
library(Matrix)
library(htmcglm)

data("soya", package = "mcglm")

form.grain <- grain ~ water * pot
form.seed <- seeds ~ water * pot

soya$viablepeasP <- soya$viablepeas / soya$totalpeas
form.peas <- viablepeasP ~ water * pot

Z0 <- mc_id(soya)
Z1 <- mc_mixed(~0 + factor(block), data = soya)

fit_joint <- mcglm(linear_pred = c(form.grain,
```

```

        form.seed,
        form.peas),
matrix_pred = list(c(Z0, Z1),
                  c(Z0, Z1),
                  c(Z0, Z1)),
link = c("identity",
        "log",
        "logit"),
variance = c("constant",
            "tweedie",
            "binomialP"),
Ntrial = list(NULL,
              NULL,
              soya$totalpeas),
power_fixed = c(TRUE, TRUE, TRUE),
data = soya)

mc_anova_I(fit_joint)

```

mc_anova_II

ANOVA type II table for mcglm objects via Wald test.

Description

Performs Wald tests to generate type-II analysis-of- variance tables per response for model objects produced by mcglm.

Usage

```
mc_anova_II(object, verbose = TRUE)
```

Arguments

object	An object of mcglm class.
verbose	a logical if TRUE print some information about the tests performed. Default verbose = TRUE.

Value

Type II ANOVA table for mcglm objects.

Author(s)

Lineu Alberto Cavazani de Freitas, <lineuacf@gmail.com>

See Also

mc_anova_I, mc_anova_III and mc_anova_disp.

Examples

```

library(mcglm)
library(Matrix)
library(htmcglm)

data("soya", package = "mcglm")

form.grain <- grain ~ water * pot
form.seed <- seeds ~ water * pot

soya$viabilepeasP <- soya$viabilepeas / soya$totalpeas
form.peas <- viablepeasP ~ water * pot

Z0 <- mc_id(soya)
Z1 <- mc_mixed(~0 + factor(block), data = soya)

fit_joint <- mcglm(linear_pred = c(form.grain,
                                form.seed,
                                form.peas),
                  matrix_pred = list(c(Z0, Z1),
                                    c(Z0, Z1),
                                    c(Z0, Z1)),
                  link = c("identity",
                           "log",
                           "logit"),
                  variance = c("constant",
                               "tweedie",
                               "binomialP"),
                  Ntrial = list(NULL,
                                NULL,
                                soya$totalpeas),
                  power_fixed = c(TRUE, TRUE, TRUE),
                  data = soya)

mc_anova_II(fit_joint)

```

mc_anova_III

ANOVA type III table for mcglm objects via Wald test.

Description

Performs Wald tests to generate type-III analysis-of- variance tables per response for model objects produced by mcglm.

Usage

```
mc_anova_III(object, verbose = TRUE)
```

Arguments

object An object of mcglm class.
 verbose a logical if TRUE print some information about the tests performed. Default
 verbose = TRUE.

Value

Type III ANOVA table for mcglm objects.

Author(s)

Lineu Alberto Cavazani de Freitas, <lineuacf@gmail.com>

See Also

mc_anova_I, mc_anova_II and mc_anova_disp.

Examples

```
library(mcglm)
library(Matrix)
library(htmcglm)

data("soya", package = "mcglm")

form.grain <- grain ~ water * pot
form.seed <- seeds ~ water * pot

soya$viaiblepeasP <- soya$viaiblepeas / soya$totalpeas
form.peas <- viablepeasP ~ water * pot

Z0 <- mc_id(soya)
Z1 <- mc_mixed(~0 + factor(block), data = soya)

fit_joint <- mcglm(linear_pred = c(form.grain,
                                   form.seed,
                                   form.peas),
                  matrix_pred = list(c(Z0, Z1),
                                     c(Z0, Z1),
                                     c(Z0, Z1)),
                  link = c("identity",
                           "log",
                           "logit"),
                  variance = c("constant",
                               "tweedie",
                               "binomialP"),
                  Ntrial = list(NULL,
                                NULL,
                                soya$totalpeas),
                  power_fixed = c(TRUE, TRUE, TRUE),
```



```
data = soya)

mc_anova_III(fit_joint)
```

mc_linear_hypothesis *Test Linear Hypothesis*

Description

Performs Wald tests for testing a linear hypothesis for model objects produced by mcglm.

Usage

```
mc_linear_hypothesis(object, hypothesis, verbose = TRUE)
```

Arguments

object	An object of mcglm class.
hypothesis	A vector of strings with the hypotheses to be tested.
verbose	a logical if TRUE print some information about the tests performed. Default verbose = TRUE.

Value

Table result of the hypothesis test specified.

Author(s)

Lineu Alberto Cavazani de Freitas, <lineuacf@gmail.com>

Examples

```
library(mcglm)
library(Matrix)
library(htmcglm)

data("soya", package = "mcglm")

form.grain <- grain ~ water * pot
form.seed <- seeds ~ water * pot

soya$viabilepeasP <- soya$viabilepeas / soya$totalpeas
form.peas <- viablepeasP ~ water * pot

Z0 <- mc_id(soya)
Z1 <- mc_mixed(~0 + factor(block), data = soya)
```

```

fit_joint <- mcglm(linear_pred = c(form.grain,
                                form.seed,
                                form.peas),
                  matrix_pred = list(c(Z0, Z1),
                                    c(Z0, Z1),
                                    c(Z0, Z1)),
                  link = c("identity",
                           "log",
                           "logit"),
                  variance = c("constant",
                               "tweedie",
                               "binomialP"),
                  Ntrial = list(NULL,
                                NULL,
                                soya$totalpeas),
                  power_fixed = c(TRUE, TRUE, TRUE),
                  data = soya)

mc_linear_hypothesis(object = fit_joint,
                     hypothesis = c('beta11 = 0'))

mc_linear_hypothesis(object = fit_joint,
                     hypothesis = c('beta11 = 0',
                                     'beta12 = 0'))

mc_linear_hypothesis(object = fit_joint,
                     hypothesis = c('beta11 = 0',
                                     'beta12 = 0',
                                     'beta21 = 0',
                                     'beta22 = 0',
                                     'beta31 = 0',
                                     'beta32 = 0'))

mc_linear_hypothesis(object = fit_joint,
                     hypothesis = c('beta11 = beta21'))

mc_linear_hypothesis(object = fit_joint,
                     hypothesis = c('tau11 = 0'))

mc_linear_hypothesis(object = fit_joint,
                     hypothesis = c('tau11 = 0',
                                     'tau21 = 0',
                                     'tau31 = 0'))

mc_linear_hypothesis(object = fit_joint,
                     hypothesis = c('tau12 = tau22'))

```

Description

Performs Wald tests to generate multivariate analysis-of -variance tables of the significance for the dispersion components for model objects produced by mcglm.

Usage

```
mc_manova_dispersion(object, p_var, names, verbose = TRUE)
```

Arguments

object	An object of mcglm class.
p_var	A vector of indices that indicate how the dispersion parameters are related. Parameters with the same index are tested together.
names	Names to be shown in the table.
verbose	a logical if TRUE print some information about the tests performed. Default verbose = TRUE.

Value

Type III MANOVA table for dispersion components of mcglm objects.

Author(s)

Lineu Alberto Cavazani de Freitas, <lineuacf@gmail.com>

See Also

mc_manova_I, mc_manova_II and mc_manova_III.

Examples

```
library(mcglm)
library(Matrix)
library(htmcglm)

data("soya", package = "mcglm")

form.grain <- grain ~ water * pot
form.seed <- seeds ~ water * pot

soya$viabilepeasP <- soya$viabilepeas / soya$totalpeas
form.peas <- viablepeasP ~ water * pot

Z0 <- mc_id(soya)
Z1 <- mc_mixed(~0 + factor(block), data = soya)

fit_joint <- mcglm(linear_pred = c(form.grain,
                                  form.seed,
                                  form.peas),
```

```

matrix_pred = list(c(Z0, Z1),
                  c(Z0, Z1),
                  c(Z0, Z1)),
link = c("identity",
         "log",
         "logit"),
variance = c("constant",
            "tweedie",
            "binomialP"),
Ntrial = list(NULL,
              NULL,
              soya$totalpeas),
power_fixed = c(TRUE, TRUE, TRUE),
data = soya)

mc_manova_dispersion(fit_joint,
                    p_var = c(0,1),
                    names = c('tau11', 'tau21'))

```

mc_manova_I

MANOVA type I table for mcglm objects via Wald test.

Description

Performs Wald tests to generate multivariate type-I analysis-of-variance tables for model objects produced by mcglm.

Usage

```
mc_manova_I(object, verbose = TRUE)
```

Arguments

object	An object of mcglm class.
verbose	a logical if TRUE print some information about the tests performed. Default verbose = TRUE.

Value

Type I MANOVA table for mcglm objects.

Author(s)

Lineu Alberto Cavazani de Freitas, <lineuacf@gmail.com>

See Also

mc_manova_II, mc_manova_III and mc_manova_disp.

Examples

```

library(mcglm)
library(Matrix)
library(htmcglm)

data("soya", package = "mcglm")

form.grain <- grain ~ water * pot
form.seed <- seeds ~ water * pot

soya$viaiblepeasP <- soya$viaiblepeas / soya$totalpeas
form.peas <- viaiblepeasP ~ water * pot

Z0 <- mc_id(soya)
Z1 <- mc_mixed(~0 + factor(block), data = soya)

fit_joint <- mcglm(linear_pred = c(form.grain,
                                form.seed,
                                form.peas),
                  matrix_pred = list(c(Z0, Z1),
                                    c(Z0, Z1),
                                    c(Z0, Z1)),
                  link = c("identity",
                          "log",
                          "logit"),
                  variance = c("constant",
                              "tweedie",
                              "binomialP"),
                  Ntrial = list(NULL,
                                NULL,
                                soya$totalpeas),
                  power_fixed = c(TRUE, TRUE, TRUE),
                  data = soya)

mc_manova_I(fit_joint)

```

mc_manova_II

MANOVA type II table for mcglm objects via Wald test.

Description

Performs Wald tests to generate multivariate type-II analysis-of-variance tables for model objects produced by mcglm.

Usage

```
mc_manova_II(object, verbose = TRUE)
```

Arguments

object An object of mcglm class.
 verbose a logical if TRUE print some information about the tests performed. Default
 verbose = TRUE.

Value

Type II MANOVA table for mcglm objects.

Author(s)

Lineu Alberto Cavazani de Freitas, <lineuacf@gmail.com>

See Also

mc_manova_I, mc_manova_III and mc_manova_disp.

Examples

```
library(mcglm)
library(Matrix)
library(htmcglm)

data("soya", package = "mcglm")

form.grain <- grain ~ water * pot
form.seed <- seeds ~ water * pot

soya$viaiblepeasP <- soya$viaiblepeas / soya$totalpeas
form.peas <- viablepeasP ~ water * pot

Z0 <- mc_id(soya)
Z1 <- mc_mixed(~0 + factor(block), data = soya)

fit_joint <- mcglm(linear_pred = c(form.grain,
                                  form.seed,
                                  form.peas),
                  matrix_pred = list(c(Z0, Z1),
                                     c(Z0, Z1),
                                     c(Z0, Z1)),
                  link = c("identity",
                           "log",
                           "logit"),
                  variance = c("constant",
                               "tweedie",
                               "binomialP"),
                  Ntrial = list(NULL,
                                NULL,
                                soya$totalpeas),
                  power_fixed = c(TRUE, TRUE, TRUE),
```

```
data = soya)
mc_manova_III(fit_joint)
```

mc_manova_III	<i>MANOVA type III table for mcglm objects via Wald test.</i>
---------------	---

Description

Performs Wald tests to generate multivariate type-III analysis-of-variance tables for model objects produced by mcglm.

Usage

```
mc_manova_III(object, verbose = TRUE)
```

Arguments

object	An object of mcglm class.
verbose	a logical if TRUE print some information about the tests performed. Default verbose = TRUE.

Value

Type III MANOVA table for mcglm objects.

Author(s)

Lineu Alberto Cavazani de Freitas, <lineuacf@gmail.com>

See Also

mc_manova_I, mc_manova_II and mc_manova_disp.

Examples

```
library(mcglm)
library(Matrix)
library(htmcglm)

data("soya", package = "mcglm")

form.grain <- grain ~ water * pot
form.seed <- seeds ~ water * pot

soya$viabilepeasP <- soya$viabilepeas / soya$totalpeas
form.peas <- viablepeasP ~ water * pot
```

```

Z0 <- mc_id(soya)
Z1 <- mc_mixed(~0 + factor(block), data = soya)

fit_joint <- mcglm(linear_pred = c(form.grain,
                                  form.seed,
                                  form.peas),
                  matrix_pred = list(c(Z0, Z1),
                                     c(Z0, Z1),
                                     c(Z0, Z1)),
                  link = c("identity",
                           "log",
                           "logit"),
                  variance = c("constant",
                               "tweedie",
                               "binomialP"),
                  Ntrial = list(NULL,
                                NULL,
                                soya$totalpeas),
                  power_fixed = c(TRUE, TRUE, TRUE),
                  data = soya)

mc_manova_III(fit_joint)

```

mc_multcomp

Multiple comparisons test for each response.

Description

Performs a multiple comparisons test to compare differences between treatment levels for each response for model objects produced by mcglm.

Usage

```
mc_multcomp(object, effect, data, verbose = TRUE)
```

Arguments

object	An object of mcglm class.
effect	A list of vector of variables. For each configuration of these the estimate will be calculated.
data	Data frame with the dataset used in the model.
verbose	a logical if TRUE print some information about the tests performed. Default verbose = TRUE.

Value

Table of multiple comparisons.


```
          c('pot')),
  data = soya)

mc_multcomp(object = fit_joint,
  effect = list(c('water', 'pot'),
               c('water', 'pot'),
               c('water', 'pot')),
  data = soya)
```

mc_mult_multcomp *Multivariate multiple comparisons test.*

Description

Performs a multiple comparisons test to compare differences between treatment levels for all responses of model objects produced by mcglm.

Usage

```
mc_mult_multcomp(object, effect, data, verbose = TRUE)
```

Arguments

object	An object of mcglm class.
effect	A vector of variables. For each configuration of these the estimate will be calculated.
data	Data frame with the dataset used in the model.
verbose	a logical if TRUE print some information about the tests performed. Default verbose = TRUE.

Value

Table of multiple comparisons.

Author(s)

Lineu Alberto Cavazani de Freitas, <lineuacf@gmail.com>

See Also

mc_multcomp.

Examples

```
library(mcgml)
library(Matrix)
library(htmcgml)

data("soya", package = "mcgml")

form.grain <- grain ~ water * pot
form.seed <- seeds ~ water * pot

soya$viabilepeasP <- soya$viabilepeas / soya$totalpeas
form.peas <- viablepeasP ~ water * pot

Z0 <- mc_id(soya)
Z1 <- mc_mixed(~0 + factor(block), data = soya)

fit_joint <- mcgml(linear_pred = c(form.grain,
                                  form.seed,
                                  form.peas),
                  matrix_pred = list(c(Z0, Z1),
                                     c(Z0, Z1),
                                     c(Z0, Z1)),
                  link = c("identity",
                           "log",
                           "logit"),
                  variance = c("constant",
                                "tweedie",
                                "binomialP"),
                  Ntrial = list(NULL,
                                NULL,
                                soya$totalpeas),
                  power_fixed = c(TRUE, TRUE, TRUE),
                  data = soya)

mc_mult_multcomp(object = fit_joint,
                 effect = c('water'),
                 data = soya)

mc_mult_multcomp(object = fit_joint,
                 effect = c('pot'),
                 data = soya)

mc_mult_multcomp(object = fit_joint,
                 effect = c('water', 'pot'),
                 data = soya)
```

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