Package ‘gcmr’

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R topics documented:
gcmr-package ......................................................... 2
arma.cormat .......................................................... 3
cluster.cormat ....................................................... 4
cormat.gcmr ......................................................... 5
epilepsy .............................................................. 5
gaussian.marg ...................................................... 6
gcmr ................................................................. 7
gcmr.options ....................................................... 10
HUR ................................................................. 11
ind.cormat .......................................................... 12
malaria ............................................................. 13
marginal.gcmr ..................................................... 14
matern.cormat ..................................................... 14
plot.gcmr .......................................................... 15
polio ............................................................... 17
**Description**

Fits Gaussian copula marginal regression models described in Song (2000) and Masarotto and Varin (2012; 2017).

**Details**

Gaussian copula models are frequently used to extend univariate regression models to the multivariate case. The principal merit of the approach is that the specification of the regression model is conveniently separated from the dependence structure described in the familiar form of the correlation matrix of a multivariate Gaussian distribution (Song 2000). This form of flexibility has been successfully employed in several complex applications including longitudinal data analysis, spatial statistics, genetics and time series. Some useful references can be found in Masarotto and Varin (2012; 2017), Song et al. (2013) and Nikoloulopoulos (2015).

This package contains R functions that implement the methodology discussed in Masarotto and Varin (2012) and Guolo and Varin (2014). The main function is `gcmr`, which fits Gaussian copula marginal regression models. Inference is performed through a likelihood approach. Computation of the exact likelihood is possible only for continuous responses, otherwise the likelihood function is approximated by importance sampling. See Masarotto and Varin (2017) for details.

**Author(s)**

Guido Masarotto and Cristiano Varin.

**References**


arma.cormat


---

**arma.cormat**  
*ARMA(p,q) Correlation*

**Description**

Sets ARMA(p,q) correlation in Gaussian copula regression models.

**Usage**

`arma.cormat(p, q)`

**Arguments**

- `p` order of the autoregressive component.
- `q` order of the moving average component.

**Value**

An object of class `cormat.gcmr` representing a correlation matrix with ARMA(p,q) structure.

**Author(s)**

Guido Masarotto and Cristiano Varin.

**References**


**See Also**

- `gcmr`
Description
Sets longitudinal/clustered data correlation in Gaussian copula regression models.

Usage
cluster.cormat(id, type = c("independence", "ar1", "ma1", "exchangeable", "unstructured"))

Arguments
id subject id. This is a vector of the same length of the number of observations. Please note that data must be sorted in way that observations from the same cluster are contiguous.
type a character string specifying the correlation structure. At the moment, the following are implemented:

 independence working independence.
ar1 autoregressive of order 1.
ma1 moving average of order 1.
exchangeable exchangeable.
unstructured unstructured.

Details
The correlation matrices are inherited from the \texttt{nlme} package (Pinheiro and Bates, 2000).

Value
An object of class \texttt{cormat.gcmr} representing a correlation matrix for longitudinal or clustered data.

Author(s)
Guido Masarotto and Cristiano Varin.

References
epilepsy

See Also
gcmr, n1me.

cormat.gcmr  Correlation Matrices for Gaussian Copula Regression Models

Description

Class of correlation matrices available in the gcmr package.

Value

At the moment, the following are implemented:

- ind.cormat: working independence.
- arma.cormat: ARMA(p,q).
- cluster.cormat: longitudinal/clustered data.
- matern.cormat: Matern spatial correlation.

Author(s)

Guido Masarotto and Cristiano Varin.

References


See Also
gcmr, ind.cormat, arma.cormat, cluster.cormat, matern.cormat.

epilepsy  Epiletic Seizures Data

Description

Longitudinal study on epiletic seizures (Thall and Vail, 1990; Diggle et al. 2002). The data consist into 59 individuals with five observations each: The baseline eight-week interval and measurements collected at subsequent visits every two-week.
Usage

```r
data(epilepsy)
```

Format

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>patient's id.</td>
</tr>
<tr>
<td>age</td>
<td>patient's age.</td>
</tr>
<tr>
<td>trt</td>
<td>indicator if the patient is treated with progabide (1) or with placebo (2).</td>
</tr>
<tr>
<td>counts</td>
<td>number of epileptic seizures.</td>
</tr>
<tr>
<td>time</td>
<td>observation period in weeks (8 for baseline and 2 for subsequent visits).</td>
</tr>
<tr>
<td>visit</td>
<td>indicator if observation at baseline (0) or subsequent visit (1).</td>
</tr>
</tbody>
</table>

Source


References


---

**gaussian.marg**

*Marginals in Gaussian Copula Marginal Regression Models*

Description

These functions set the marginals in Gaussian copula marginal regression models.

Usage

```r
beta.marg(link = "logit")
binomial.marg(link = "logit")
Gamma.marg(link = "inverse")
gaussian.marg(link = "identity")
negbin.marg(link = "log")
poisson.marg(link = "log")
weibull.marg(link = "log")
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>link</td>
<td>a specification for the model link function. See <code>family</code> for the special case of generalized linear models.</td>
</tr>
</tbody>
</table>
Details


For binomial marginals specified by `binomial.marg`, the response is specified as a factor when the first level denotes failure and all others success or as a two-column matrix with the columns giving the numbers of successes and failures.

Negative binomial marginals implemented in `negbin.marg` are parametrized such that \( \text{var}(Y) = E(Y) + kE(Y)^2 \).

For back-compatibility with previous versions of the `gcmr` package, short names for the marginals `bn.marg`, `gs.marg`, `nb.marg`, and `ps.marg` remain valid as an alternative to (preferred) longer versions `binomial.marg`, `gaussian.marg`, `negbin.marg`, and `poisson.marg`.

Value

An object of class `marginal.gcmr` representing the marginal component.

Author(s)

Guido Masarotto and Cristiano Varin.

References


See Also

`gcmr`, `betareg`.
Usage

gcmr(formula, data, subset, offset, marginal, 
cormat, start, fixed, options=gcmr.options(...), model=TRUE,...)

gcmr.fit(x=rep(1, NROW(y)), y, z=NULL, offset=NULL, 
marginal, cormat, start, fixed, options=gcmr.options())

Arguments

formula a symbolic description of the model to be fitted of type \( y \sim x \) or \( y \sim x \mid z \), for 
details see below.
data an optional data frame, list or environment (or object coercible by \texttt{as.data.frame} 
to a data frame) containing the variables in the model. If not found in data, the 
variables are taken from \texttt{environment(formula)}.
subset an optional vector specifying a subset of observations to be used in the fitting 
process.
offset optional numeric vector with an a priori known component to be included in the 
linear predictor for the mean. When appropriate, offset may also be a list of two 
offsets for the mean and precision equation, respectively.
x design matrix.
y vector of observations.
z optional design matrix for the dispersion/shape.
marginal an object of class \texttt{marginal.gcmr} specifying the marginal part of the model.
cormat an object of class \texttt{cormat.gcmr} representing the correlation matrix of the errors.
start optional numeric vector with starting values for the model parameters.
fixed optional numeric vector of the same length as the total number of parameters. If 
supplied, only \texttt{NA} entries in fixed will be varied.
options list of options passed to function \texttt{gcmr.options}.
model logical. If \texttt{TRUE}, then the model frame is returned.
... arguments passed to \texttt{gcmr.options}.

Details

Function \texttt{gcmr} computes maximum likelihood estimation in Gaussian copula marginal regression 
models. Computation of the exact likelihood is possible only for continuous responses, otherwise 
the likelihood function is approximated by importance sampling. See Masarotto and Varin (2012; 
2017) for details.

Standard formula \( y \sim x_1 + x_2 \) indicates that the mean response is modelled as a function of covari-
ates \( x_1 \) and \( x_2 \) through an appropriate link function. Extended formula \( y \sim x_1 + x_2 \mid z_1 + z_2 \) 
indicates that the dispersion (or the shape) parameter of the marginal distribution is modelled as a 
function of covariates \( z_1 \) and \( z_2 \). Dispersion (or shape) parameters are always modelled on log-
arithm scale. The model specification is inspired by beta regression as implemented in \texttt{betareg} 
(Cribari-Neto and Zeileis, 2010) through extended \texttt{Formula} objects (Zeileis and Croissant, 2010).
For binomial marginals specified by `binomial.marg` the response is specified as a factor when the first level denotes failure and all others success or as a two-column matrix with the columns giving the numbers of successes and failures.

gcmr.fit is the workhorse function: it is not normally called directly but can be more efficient where the response vector and design matrix have already been calculated.

**Value**

An object of class "gcmr" with the following components:

- `estimate` the maximum likelihood estimate.
- `maximum` the maximum likelihood value.
- `hessian` (minus) the Hessian at the maximum likelihood estimate.
- `jac` the Jacobian at the maximum likelihood estimate.
- `fitted.values` the fitted values.
- `marginal` the marginal model used.
- `cormat` the correlation matrix used.
- `fixed` the numeric vector indicating which parameters are constants.
- `ibeta` the indices of marginal parameters.
- `igamma` the indices of dependence parameters.
- `nbeta` the number of marginal parameters.
- `ngamma` the number of dependence parameters.
- `options` the fitting options used, see `gcmr.options`.
- `call` the matched call.
- `formula` the model formula.
- `terms` the terms objects for the fitted model.
- `levels` the levels of the categorical regressors.
- `model` the model frame, returned only if `model=TRUE`.
- `contrasts` the contrasts corresponding to `levels`.
- `y` the y vector used.
- `x` the model matrix used for the mean response.
- `z` the (optional) model matrix used for the dispersion/shape.
- `offset` the offset used.
- `n` the number of observations.
- `not.na` the vector of binary indicators of the available observations (not missing).

Functions `coefficients`, `logLik`, `fitted`, `vcov.gcmr` and `residuals.gcmr` can be used to extract various useful features of the value returned by `gcmr`. Function `plot.gcmr` produces various diagnostic plots for fitted gcmr objects.

**Author(s)**

Guido Masarotto and Cristiano Varin.
References


See Also
cormat.gcmr, marginal.gcmr, gcmr.options, Formula, betareg.

Examples

```r
## negative binomial model for longitudinal data
data(epilepsy)
gcmr(counts ~ offset(log(time)) + visit + trt + visit:trt, data = epilepsy,
   subset = (id != 49), marginal = negbin.marg, cormat = cluster.cormat(id, "arl"),
   options=gcmr.options(seed=123, nrep=100 ))
## Hidden Unemployment Rate (HUR) data (Rocha and Cribari-Neto, 2009)
## beta regression with ARMA(1,3) errors
data(HUR)
trend <- scale(time(HUR))
gcmr(HUR ~ trend | trend, marginal = beta.marg, cormat = arma.cormat(1, 3))
```

---

gcmr.options | Setting Options for Fitting Gaussian Copula Marginal Regression Models

Description

Sets options that affect the fitting of Gaussian copula marginal regression models.

Usage

```r
gcmr.options(seed = round(runif(1, 1, 1e+05)), nrep = c(100, 1000),
   no.se = FALSE, method = c("BFGS", "Nelder-Mead", "CG"), ...)
```
Arguments

seed   seed of the pseudorandom generator used in the importance sampling algorithm for likelihood approximation in case of discrete responses.

nrep   Monte Carlo size of the importance sampling algorithm for likelihood approximation in case of discrete responses. nrep can be a vector so that the model is fitted with a sequence of different Monte Carlo sizes. In this case, the starting values for optimization of the likelihood are taken from the previous fitting. A reasonable strategy is to fit the model with a small Monte Carlo size to obtain sensible starting values and then refit with a larger Monte Carlo size. The default value is 100 for the first optimization and 1000 for the second and definitive optimization.

no.se  logical. Should standard errors be computed and returned or not?

method  a character string specifying the method argument passed to optim. The default optimization routine is the quasi-Newton algorithm BFGS. See optim for details.

Value

A list containing the options.

Author(s)

Guido Masarotto and Cristiano Varin.

References


See Also

gcmr

---

**HUR**

*Hidden Unemployment in Sao Paulo*

Description

Rate of hidden unemployment due to substandard work conditions in Sao Paulo, Brazil (Rocha and Cribari-Neto, 2009).

Usage

data(HUR)
Source

Institute of Applied Economic Research (Ipea), Brazil. Data obtained from the IPEAdata website http://www.ipeadata.gov.br.

References


---

### ind.cormat

#### Description

Sets working independence correlation in Gaussian copula marginal regression models.

#### Usage

    ind.cormat()

#### Value

An object of class `cormat.gcmr` representing an identity correlation matrix.

#### Author(s)

Guido Masarotto and Cristiano Varin.

#### References


#### See Also

    gcmr.
malaria

Gambia Malaria Data

Description

Malaria prevalence in children in Gambia. The data are constructed from the gambia dataframe in the geor package (Diggle and Ribeiro, 2007) by village aggregation.

Usage

data(malaria)

Format

A data frame with the 65 observations with the following variables

- x: x-coordinate of the village (UTM).
- y: y-coordinate of the village (UTM).
- cases: number of sampled children with malaria in each village.
- size: number of sampled children in each village.
- age: mean age of the sampled children in each village.
- netuse: frequency of sampled children who regularly sleep under a bed-net in each village.
- treated: frequency of sampled children whose bed-net is treated.
- green: measure of vegetation green-ness in the immediate vicinity of the village.
- phc: indicator variable denoting the presence (1) or absence (0) of a health center in the village.
- area: indicator of the village area (Diggle et al., 2002).

Source


References


Examples

data(malaria)
marginal.gcml

Marginals for Gaussian Copula Marginal Regression

Description

Class of marginals available in the gcml library.

Value

At the moment, the following are implemented:

- beta.marg: beta marginals.
- binomial.marg: binomial marginals.
- Gamma.marg: Gamma marginals.
- gaussian.marg: Gaussian marginals.
- negbin.marg: negative binomial marginals.
- poisson.marg: Poisson marginals.
- weibull.marg: Weibull marginals.

Author(s)

Guido Masarotto and Cristiano Varin.

References


See Also

- gcml, beta.marg, binomial.marg, gaussian.marg, Gamma.marg, negbin.marg, poisson.marg, weibull.marg.

matern.cormat

Matern Spatial Correlation

Description

Sets a Matern spatial correlation matrix in Gaussian copula marginal regression models.

Usage

matern.cormat(D, alpha = 0.5)
Arguments

- **D**: matrix with values of the distances between pairs of data locations.
- **alpha**: value of the shape parameter of the Matern correlation class. The default alpha = 0.5 corresponds to an exponential correlation model.

Details

The Matérn correlation function is inherited from the geor package (Diggle and Ribeiro, 2007).

Value

An object of class `cormat_gcmr` representing a Matern correlation matrix.

Author(s)

Guido Masarotto and Cristiano Varin.

References


See Also

- `gcmr`, `matern`.

---

**plot.gcmr**

*Plot Diagnostics for Gaussian Copula Marginal Regression*

Description

Various types of diagnostic plots for Gaussian copula regression.

Usage

```r
## S3 method for class 'gcmr'
plot(x, which = if (!time.series) 1:4 else c(1, 3, 5, 6),
caption = c("Residuals vs indices of obs.", "Residuals vs linear predictor",
"Normal plot of residuals", "Predicted vs observed values",
"Autocorrelation plot of residuals", "Partial ACF plot of residuals"),
main = "", ask = prod(par("mfcol")) < length(which) && dev.interactive(),
level = 0.95, col.lines = "gray",
time.series = inherits(x$cormat, "arma.gcmr"), ...)
```
Arguments

- **x**: a fitted model object of class `gcmr`.
- **which**: select one, or more, of the six available plots. The default choice adapts to the correlation structure and selects four plots depending on the fact that the data are a regular time series or not.
- **caption**: captions to appear above the plots.
- **main**: title to each plot in addition to the above caption.
- **ask**: if TRUE, then the user is asked before each plot.
- **level**: confidence level in the normal probability plot. The default is 0.95.
- **col.lines**: color for lines. The default is "gray".
- **time.series**: if TRUE, four plots suitable for time series data are displayed. The default is TRUE when the correlation matrix corresponds to that of ARMA(p,q) process and FALSE otherwise.
- **...**: other parameters to be passed through to plotting functions.

Details

The plot method for `gcmr` objects produces six types of diagnostic plots selectable through the `which` argument. Available choices are: Quantile residuals vs indices of the observations (`which`=1); Quantile residuals vs linear predictor (`which`=2); Normal probability plot of quantile residuals (`which`=3); Fitted vs observed values (`which`=4); Autocorrelation plot of quantile residuals (`which`=5); Partial autocorrelation plot of quantile residuals (`which`=6). The latter two plots make sense for regular time series data only.

The normal probability plot is computed via function `qqPlot` from the package `car` (Fox and Weisberg, 2011).

Author(s)

Guido Masarotto and Cristiano Varin.

References


See Also

`gcmr`. 
Examples

```r
## beta regression with ARMA(1,3) errors
data(HUR)
trend <- scale(time(HUR))
m <- gcmr(HUR ~ trend | trend, marginal = beta.marg, cormat = arma.cormat(1, 3))
## normal probability plot
plot(m, 3)
## autocorrelation function of residuals
plot(m, 5)
```

### polio

#### Polio Time Series

Description


Usage

```r
data(polio)
```

Format

A data frame with the 168 monthly observations (from January 1970 to December 1983) with the following variables

- `y`: time series of polio incidences.
- `t*10^(-3)`: linear trend multiplied by factor $10^{-3}$.
- `cos(2*pi*t/12)`: cosine annual seasonal component.
- `sin(2*pi*t/12)`: sine annual seasonal component.
- `cos(2*pi*t/6)`: cosine semi-annual seasonal component.
- `sin(2*pi*t/6)`: sine semi-annual seasonal component.

Source


Examples

```r
data(polio)
```
Description
Computes the profile log-likelihood for mean response parameters of a Gaussian copula marginal regression model.

Usage

```r
## S3 method for class 'gcmr'
profile(fitted, which, low, up, npoints = 10,
       display = TRUE, alpha = 0.05, progress.bar = TRUE, ...)
```

Arguments

- `fitted`: a fitted Gaussian copula marginal regression model of class `gcmr`.
- `which`: the index of the regression parameter which should be profiled.
- `low`: the lower limit used in computation of the profile log-likelihood. If this is missing, then the lower limit is set equal to the estimate minus three times its standard error.
- `up`: the upper limit used in computation of the profile log-likelihood. If this is missing, then the upper limit is set equal to the estimate plus three times its standard error.
- `npoints`: number of points used in computation of the profile log-likelihood. Default is 10.
- `display`: should the profile log-likelihood be displayed or not? default is TRUE.
- `alpha`: the significance level, default is 0.05.
- `progress.bar`: logical. If TRUE, a text progress bar is displayed.
- `...`: further arguments passed to `plot`.

Details
If the display is requested, then the profile log-likelihood is smoothed by cubic spline interpolation.

Value
A list with the following components:

- `points`: points at which the profile log-likelihood is evaluated.
- `profile`: values of the profile log-likelihood.

Author(s)
Guido Masarotto and Cristiano Varin.

References


residuals.gcmr

See Also
gcmr

Examples

```r
## spatial binomial data
## Not run:
data(malaria)
D <- sp::spDists(cbind(malaria$x, malaria$y))/1000
m <- gcmr(cbind(cases, size-cases) ~ netuse+I(green/100)+phc, data=malaria,
marginal=binomial, marg, cormat=matern, cormat(D), options=gcmr.options(seed=987))
prof <- profile(m, which = 2)
prof

## End(Not run)
```

residuals.gcmr

Quantile Residuals for Gaussian Copula Marginal Regression

Description

Computes various type of quantile residuals for validation of a fitted Gaussian copula marginal regression model, as described in Masarotto and Varin (2012; 2017).

Usage

```r
## S3 method for class 'gcmr'
residuals(object, type=c("conditional","marginal"),
method=c("random","mid"),...)
```

Arguments

- `object`: an object of class `gcmr`, typically the result of a call to `gcmr`.
- `type`: the type of quantile residuals which should be returned. The alternatives are: "conditional" (default) and "marginal".
- `method`: different methods available for quantile residuals in case of discrete responses: "random" for randomized quantile residuals (default), and "mid" for mid interval quantile residuals as defined in Zucchini and MacDonald (2009).
- `...`: further arguments passed to or from other methods.

Details

Quantile residuals are defined in Dunn and Smyth (1996). Two different types are available:

- `conditional`: quantile residuals that account for the dependence.
- `marginal`: quantile residuals that do not account for the dependence.
Conditional quantile residuals are normal quantiles of Rosenblatt (1952) transformations and they are appropriate for validation of the marginal regression models discussed in Masarotto and Varin (2012; 2017). If the responses are discrete, then the conditional quantile residuals are not well defined. This difficulty is overcome by randomized quantile residuals available through option method="random". Alternatively, Zucchini and MacDonald (2009) suggest the use of mid interval quantile residuals (method="mid").

**Note**

Differently from randomized quantile residuals, mid quantile residuals are not realizations of uncorrelated standard normal variables under model conditions.

It is appropriate to inspect several sets of randomized quantile residuals before to take a decision about the model.

See Masarotto and Varin (2012; 2017) for more details.

**Author(s)**

Guido Masarotto and Cristiano Varin.

**References**


**See Also**

`gcmr`

**Examples**

```r
## spatial binomial data
## Not run:
data(malaria)
D <- sp::spDist(cbind(malaria$x, malaria$y))/1000
m <- gcmr(cbind(cases, size-cases) ~ netuse+I(100-netuse)+phc, data=malaria, marginal=binomial.marg, cormat=matern.cormat(D))
res <- residuals(m)
## normal probability plot
qqnorm(res)
qqline(res)
## or better via plot.gcmr
```
plot(m, which = 3)

## End(Not run)

### scotland

**Scotland Lip Cancer Data**

**Description**


**Usage**

```r
data(scotland)
```

**Format**

A data frame with the 56 observations with the following variables:

- `observed`: observed cases in each county.
- `expected`: expected cases in each county.
- `AFF`: proportion of the population employed in agriculture, fishing, or forestry.
- `latitude`: county latitude.
- `longitude`: county longitude.

**Source**


**References**


**Examples**

```r
data(scotland)
```

### summary.gcmr

**Methods for gcmr Objects**

**Description**

Methods for extracting information from fitted beta regression model objects of class "gcmr".
Usage

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

## S3 method for class 'gcmr'
coef(object, ...)
## S3 method for class 'gcmr'
vcov(object, ...)
## S3 method for class 'gcmr'
bread(x, ...)
## S3 method for class 'gcmr'
estfun(x, ...)
```

Arguments

- `object, x` a fitted marginal regression model of class `gcmr`.
- `...` additional arguments, but currently not used.

Value

The function `summary.gcmr` returns an object of class "summary.glm", a list with some components of the `gcmr` object, plus

- `coefficients` a list with components marginal and copula containing the maximum likelihood estimates of the marginal and Gaussian copula parameters, respectively.
- `aic` Akaike Information Criterion.

Function `coef` returns the estimated coefficients and `vcov` their variance-covariance matrix. Functions `bread` and `estfun` extract the components of the robust sandwich variance matrix that can be computed with the `sandwich` package (Zeileis, 2004; 2006).

Author(s)

Guido Masarotto and Cristiano Varin.

References


See Also

`bread, estfun, gcmr, sandwich`
Examples

```r
data(epilepsy)
fit <- gcmr(counts ~ offset(log(time)) + visit + trt + visit:trt, data = epilepsy, 
subset = (id != 49), marginal = negbin.marg, cormat = cluster.cormat(id, "ar1"), 
options=gcmr.options(seed=123, nrep=c(25,100)))
summary(fit)
```
Index

*Topic datasets
- malaria, 13
- polio, 17
- scotland, 21

*Topic models
- residuals.gcmr, 19

*Topic nonlinear
- arma.cormat, 3
- cluster.cormat, 4
- cormat.gcmr, 5
- gaussian.marg, 6
- gcmr, 7
- gcmr.options, 10
- ind.cormat, 12
- marginal.gcmr, 14
- matern.cormat, 14
- profile.gcmr, 17

*Topic package
gcmr-package, 2

*Topic regression
- arma.cormat, 3
- cluster.cormat, 4
- cormat.gcmr, 5
- gaussian.marg, 6
- gcmr, 7
- gcmr.options, 10
- ind.cormat, 12
- marginal.gcmr, 14
- matern.cormat, 14
- profile.gcmr, 17
- residuals.gcmr, 19
- bn.marg(gaussian.marg), 6
- bread, 22
- bread.gcmr(summary.gcmr), 21
- car, 16
- cluster.cormat, 4, 5
- coef, 22
- coef.gcmr(summary.gcmr), 21
- coefficients, 9
- coeftest.gcmr(summary.gcmr), 21
- cormat.gcmr, 3, 4, 5, 8, 10, 12, 15
- epilepsy, 5
- estfun, 22
- estfun.gcmr(summary.gcmr), 21
- family, 6
- fitted, 9
- Formula, 8, 10
- Gamma.marg, 14
- Gamma.marg(gaussian.marg), 6
- gaussian.marg, 6, 14
- gcmr, 2, 3, 5, 7, 8, 9, 11, 12, 14–16, 18–20, 22
- gcmr-package, 2
- gcmr.options, 8–10, 10
- gs.marg(gaussian.marg), 6
- HUR, 11
- ind.cormat, 5, 12
- logLik, 9
- logLik.gcmr(summary.gcmr), 21
- malaria, 13
- marginal.gcmr, 7, 8, 10, 14
- matern, 15
- matern.cormat, 5, 14
- model.frame.gcmr(summary.gcmr), 21

arma.cormat, 3, 5
as.data.frame, 8
beta.marg, 14
beta.marg(gaussian.marg), 6
betareg, 7, 8, 10
binomial.marg, 9, 14
binomial.marg(gaussian.marg), 6
model.matrix.gcmr (summary.gcmr), 21
nb.marg (gaussian.marg), 6
negbin.marg, 14
negbin.marg (gaussian.marg), 6
nlme, 4, 5
optim, 11
plot.gcmr, 9, 15
poisson.marg, 14
poisson.marg (gaussian.marg), 6
polio, 17
print.gcmr (summary.gcmr), 21
print.summary.gcmr (summary.gcmr), 21
profile.gcmr, 17
ps.marg (gaussian.marg), 6
qqPlot, 16
residuals.gcmr, 9, 19
sandwich, 22
scotland, 21
summary.gcmr, 21
terms.gcmr (summary.gcmr), 21
vcov, 22
vcov.gcmr, 9
vcov.gcmr (summary.gcmr), 21
weibull.marg, 14
weibull.marg (gaussian.marg), 6