Package 'brglm2'

March 19, 2020

Title Bias Reduction in Generalized Linear Models

Version 0.6.2

Description

Estimation and inference from generalized linear models based on various methods for bias reduction and maximum penalized likelihood with powers of the Jeffreys prior as penalty. The 'brglmFit' fitting method can achieve reduction of estimation bias by solving either the mean bias-reducing adjusted score equations in Firth (1993) <doi:10.1093/biomet/80.1.27> and Kosmidis and Firth (2009) <doi:10.1093/biomet/asp055>, or the median bias-reduction adjusted score equations in Kenne et al. (2016) <arXiv:1604.04768>, or through the direct subtraction of an estimate of the bias of the maximum likelihood estimator from the maximum likelihood estimates as in Cordeiro and McCullagh (1991) <http://www.jstor.org/stable/2345592>. See Kosmidis et al (2019) <doi:10.1007/s11222-019-09860-6> for more details. Estimation in all cases takes place via a quasi Fisher scoring algorithm, and S3 methods for the construction of of confidence intervals for the reduced-bias estimates are provided. In the special case of generalized linear models for binomial and multinomial responses (both ordinal and nominal), the adjusted score approaches return estimates with improved frequentist properties, that are also always finite, even in cases where the maximum likelihood estimates are infinite (e.g. complete and quasi-complete separation). 'brglm2' also provides pre-fit and post-fit methods for detecting separation and infinite maximum likelihood estimates in binomial response generalized linear models.

URL https://github.com/ikosmidis/brglm2

BugReports https://github.com/ikosmidis/brglm2/issues

Depends R (>= 3.3.0)

Imports MASS, stats, Matrix, graphics, nnet, enrichwith, lpSolveAPI, numDeriv

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.0.2

Suggests testthat, knitr, rmarkdown, covr

VignetteBuilder knitr

R topics documented:

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alligators	*Alligator food choice data*

Description

Alligator food choice data

Usage

    alligators

Format

A data frame with 80 rows and 5 variables:

foodchoice primary food type, in volume, found in an alligator's stomach, with levels `fish`, `invertebrate`, `reptile`, `bird`, `other`

lake lake of capture with levels `Hancock`, `Oklawaha`, `Trafford`, `George`

gender gender of the alligator with levels `Male` and `Female`

size size of the alligator with levels `<=2.3` meters long and `>2.3` meters long

freq number of alligators for each foodchoice, lake, gender and size combination

Source

The alligators data set is analyzed in Agresti (2002, Subsection~7.1.2).

References

Agresti, A. (2002). *Categorical Data Analysis*. Wiley Series in Probability and Statistics. Wiley

See Also

[brmultinom](#)

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bracl	*Bias reduction for adjacent category logit models for ordinal responses using the Poisson trick.*

Description

`bracl` is a wrapper of [brglmFit](#) that fits adjacent category logit models with or without proportional odds using implicit and explicit bias reduction methods. See Kosmidis & Firth (2011) for details.

Usage

```
bracl(
  formula,
  data,
  weights,
  subset,
  na.action,
  parallel = FALSE,
  contrasts = NULL,
  model = TRUE,
  x = TRUE,
  control = list(...),
  ...
)
```

Arguments

formula	a formula expression as for regression models, of the form response ~ predictors. The response should be a factor (preferably an ordered factor), which will be interpreted as an ordinal response, with levels ordered as in the factor. The model must have an intercept: attempts to remove one will lead to a warning and be ignored. An offset may be used. See the documentation of formula for other details.
data	an optional data frame in which to interpret the variables occurring in formula.
weights	optional case weights in fitting. Default to 1.
subset	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
na.action	a function to filter missing data.
parallel	if FALSE (default), then a non-proportional odds adjacent category model is fit, assuming different effects per category; if TRUE then a proportional odds adjacent category model is fit. See Details.
contrasts	a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.
model	logical for whether the model matrix should be returned.
x	should the model matrix be included with in the result (default is TRUE).
control	a list of parameters for controlling the fitting process. See brglmControl for details.
...	arguments to be used to form the default 'control' argument if it is not supplied directly.

Details

The bracl function fits adjacent category models, which assume multinomial observations with probabilities with proportional odds of the form

$$\log \frac{\pi_{ij}}{\pi_{ij+1}} = \alpha_j + \beta^T x_i$$

or with non-proportional odds of the form

$$\log \frac{\pi_{ij}}{\pi_{ij+1}} = \alpha_j + \beta_j^T x_i$$

where x_i is a vector of covariates and π_{ij} is the probability that category j is observed at the covariate setting i.

Author(s)

Ioannis Kosmidis <ioannis.kosmidis@warwick.ac.uk>

References

Kosmidis I, Kenne Pagui EC, Sartori N (2019). Mean and median bias reduction in generalized linear models. *arXiv e-prints*, arXiv:1804.04085. To appear in Statistics and Computing, <URL: https://arxiv.org/abs/1804.04085>.

Agresti, A. (2010). *Analysis of Ordinal Categorical Data* (2nd edition). Wiley Series in Probability and Statistics. Wiley.

Albert A. and Anderson J. A. (1984). On the Existence of Maximum Likelihood Estimates in Logistic Regression Models. *Biometrika*, **71** 1–10.

Kosmidis I. and Firth D. (2011). Multinomial logit bias reduction via the Poisson log-linear model. *Biometrika*, **98**, 755-759.

Palmgren, J. (1981). The Fisher Information Matrix for Log Linear Models Arguing Conditionally on Observed Explanatory Variables. *Biometrika*, **68**, 563-566.

See Also

multinom, brmultinom

Examples

```
data("stemcell", package = "brglm2")

# Adjacent category logit (non-proportional odds)
fit_bracl <- bracl(research ~ as.numeric(religion) + gender, weights = frequency,
                   data = stemcell, type = "ML")
# Adjacent category logit (proportional odds)
fit_bracl_p <- bracl(research ~ as.numeric(religion) + gender, weights = frequency,
                     data = stemcell, type = "ML", parallel = TRUE)
```

| brglm2 | *brglm2: Bias Reduction in Generalized Linear Models* |

Description

Estimation and inference from generalized linear models using implicit and explicit bias reduction methods (Kosmidis, 2014), and other penalized maximum likelihood methods. Currently supported methods include the mean bias-reducing adjusted scores approach in Firth (1993) and Kosmidis & Firth (2009), the median bias-reduction adjusted scores approach in Kenne Pagui et al. (2017), the correction of the asymptotic bias in Cordeiro & McCullagh (1991), the mixed bias-reduction adjusted scores approach in Kosmidis et al (2019), maximum penalized likelihood with powers of the Jeffreys prior as penalty, and maximum likelihood.

Details

In the special case of generalized linear models for binomial, Poisson and multinomial responses (both nominal and ordinal), mean and median bias reduction and maximum penalized likelihood return estimates with improved frequentist properties, that are also always finite, even in cases where the maximum likelihood estimates are infinite (e.g. complete and quasi-complete separation in multinomial regression; see also `detect_separation` and `check_infinite_estimates` for pre-fit and post-fit methods for the detection of infinite estimates in binomial response generalized linear models). Estimation in all cases takes place via a modified Fisher scoring algorithm, and S3 methods for the construction of confidence intervals for the reduced-bias estimates are provided.

The core model fitters are implemented by the functions `brglm_fit` (univariate generalized linear models), `brmultinom` (baseline category logit models for nominal multinomial responses), and `bracl` (adjacent category logit models for ordinal multinomial responses).

The similarly named **brglm** R package can only handle generalized linear models with binomial responses. Special care has been taken when developing **brglm2** in order not to have conflicts when the user loads **brglm2** and **brglm** simultaneously. The development and maintenance of the two packages will continue in parallel, until **brglm2** incorporates all **brglm** functionality and gets an appropriate wrapper to the `brglm::brglm` function.

Author(s)

Ioannis Kosmidis <ioannis.kosmidis@warwick.ac.uk>

References

Cordeiro G. M. & McCullagh, P. (1991). Bias correction in generalized linear models. *Journal of the Royal Statistical Society. Series B (Methodological)*, **53**, 629-643

Firth D. (1993). Bias reduction of maximum likelihood estimates, Biometrika, **80**, 27-38

Kenne Pagui E C, Salvan A and Sartori N (2016). Median bias reduction of maximum likelihood estimates. *arXiv*, **arXiv:1604.04768**

Kosmidis I and Firth D (2009). Bias reduction in exponential family nonlinear models. *Biometrika*, **96**, 793-804

Kosmidis I and Firth D (2010). A generic algorithm for reducing bias in parametric estimation. *Electronic Journal of Statistics*, **4**, 1097-1112

Kosmidis I (2014). Bias in parametric estimation: reduction and useful side-effects. *WIRE Computational Statistics*, **6**, 185-196

See Also

`brglm_fit`, `brmultinom`, `bracl`

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brglmControl	*Auxiliary function for* glm *fitting using the* brglmFit *method.*

Description

Typically only used internally by brglmFit, but may be used to construct a control argument.

Usage

```
brglmControl(
  epsilon = 1e-06,
  maxit = 100,
  trace = FALSE,
 type = c("AS_mixed", "AS_mean", "AS_median", "correction", "MPL_Jeffreys", "ML"),
  transformation = "identity",
  slowit = 1,
  response_adjustment = NULL,
  max_step_factor = 12,
  a = 1/2
)

brglm_control(
  epsilon = 1e-06,
  maxit = 100,
  trace = FALSE,
 type = c("AS_mixed", "AS_mean", "AS_median", "correction", "MPL_Jeffreys", "ML"),
  transformation = "identity",
  slowit = 1,
  response_adjustment = NULL,
  max_step_factor = 12,
  a = 1/2
)
```

Arguments

epsilon	positive convergence tolerance epsilon. Default is 1e-06.
maxit	integer giving the maximal number of iterations allowed. Default is 100.
trace	logical indicating if output should be produced for each iteration. Default is FALSE.
type	the type of fitting method to be used. The options are AS_mean (mean-bias reducing adjusted scores), AS_median (median-bias reducing adjusted scores), AS_mixed (bias reduction using mixed score adjustments; default), correction (asymptotic bias correction), MPL_Jeffreys (maximum penalized likelihood with powers of the Jeffreys prior as penalty) andML (maximum likelihood).
transformation	the transformation of the dispersion to be estimated. Default is identity. See Details.

slowit   a positive real used as a multiplier for the stepsize. The smaller it is the smaller
                    the steps are. Default is 1.

response_adjustment
                    a (small) positive constant or a vector of such. Default is NULL. See Details.

max_step_factor
                    the maximum number of step halving steps to consider. Default is 12.

a   power of the Jeffreys prior penalty. See Details.

Details

brglmControl provides default values and sanity checking for the various constants that control
the iteration and generally the behaviour of brglmFit.

When `trace` is true, calls to `cat` produce the output for each iteration. Hence, `options(digits =`
`*)` can be used to increase the precision.

`transformation` sets the transformation of the dispersion parameter for which the bias reduced
estimates are computed. Can be one of "identity", "sqrt", "inverse", "log" and "inverseSqrt". Cus-
tom transformations are accommodated by supplying a list of two expressions (transformation and
inverse transformation). See the examples for more details.

The value of `response_adjustment` is only relevant if brglmFit is called with `start = NULL`,
and `family` is binomial or poisson. For those models, an initial maximum likelihood fit is
obtained on adjusted data to provide starting values for the iteration in `brglmFit`. The value of
`response_adjustment` governs how the data is adjusted. Specifically, if `family` is `binomial`, then
the responses and totals are adjusted by and `2 * response_adjustment`, respectively; if `family` is
`poisson`, then the responses are adjusted by and `response_adjustment`. `response_adjustment`
`= NULL` (default) is equivalent to setting it to "number of parameters"/"number of observations".

. . When `type = "AS_mixed"` (default), mean bias reduction is used for the regression parameters,
and median bias reduction for the dispersion parameter, if that is not fixed. This adjustment has
been developed based on equivariance arguments (see, Kosmidis et al, 2019, Section 4) in order to
produce regression parameter estimates that are invariant to arbitrary contrasts, and estimates for the
dispersion parameter that are invariant to arbitrary non-linear transformations. `type = "AS_mixed"`
and `type = "AS_mean"` return the same results if brglmFit is called with `family` binomial or
poisson (i.e. families with fixed dispersion).

When `type = "MPL_Jeffreys"`, brglmFit will maximize the penalized log-likelihood

$$l(\beta, \phi) + a \log \det i(\beta, \phi)$$

where $i(\beta, \phi)$ is the expected information matrix about the regression parameters β and the disper-
sion parameter ϕ. See, `vignette("iteration", "brglm2")` for more information. The argument
a controls the amount of penalization and its default value is `a = 1/2`, corresponding to maxi-
mum penalized likelihood using a Jeffreys-prior penalty. See, Kosmidis & Firth (2019) for proofs
and discussion about the finiteness and shrinkage properties of the maximum penalized likelihood
estimators for binomial-response generalized linear models.

The estimates from `type = "AS_mean"` and `type = "MPL_Jeffreys"` with `a = 1/2` (default) are
identical for Poisson log-linear models and logistic regression models, i.e. for binomial and Poisson
regression models with canonical links. See, Firth (1993) for details.

`brglm_control` is an alias to `brglmControl`.

Value

a list with components named as the arguments, including symbolic expressions for the dispersion transformation (`Trans`) and its inverse (`inverseTrans`)

Author(s)

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References

Kosmidis I, Kenne Pagui EC, Sartori N (2019). Mean and median bias reduction in generalized linear models. *arXiv e-prints*, arXiv:1804.04085. To appear in Statistics and Computing, <URL: https://arxiv.org/abs/1804.04085>.

Kosmidis I and Firth D (2019). Jeffreys-prior penalty, finiteness and shrinkage in binomial-response generalized linear models. *arXiv e-prints*, arXiv:1812.01938

#' Firth D (1993). Bias reduction of maximum likelihood estimates. Biometrika, **80**, 27-38

See Also

brglm_fit and glm.fit

Examples

```
data("coalition", package = "brglm2")
## The maximum likelihood fit with log link
coalitionML <- glm(duration ~ fract + numst2, family = Gamma, data = coalition)

## Bias reduced estimation of the dispersion parameter
coalitionBRi <- glm(duration ~ fract + numst2, family = Gamma, data = coalition,
                    method = "brglmFit")
coef(coalitionBRi, model = "dispersion")

## Bias reduced estimation of log(dispersion)
coalitionBRl <- glm(duration ~ fract + numst2, family = Gamma, data = coalition,
                    method = "brglmFit", transformation = "log")
coef(coalitionBRl, model = "dispersion")

## Just for illustration: Bias reduced estimation of dispersion^0.25
my_transformation <- list(expression(dispersion^0.25), expression(transformed_dispersion^4))
coalitionBRc <- update(coalitionBRi, transformation = my_transformation)
coef(coalitionBRc, model = "dispersion")
```

---

brglmFit   *Fitting function for* glm *for reduced-bias estimation and inference*

Description

brglmFit is a fitting method for glm that fits generalized linear models using implicit and explicit bias reduction methods (Kosmidis, 2014), and other penalized maximum likelihood methods. Currently supported methods include the mean bias-reducing adjusted scores approach in Firth (1993) and Kosmidis & Firth (2009), the median bias-reduction adjusted scores approach in Kenne Pagui et al. (2017), the correction of the asymptotic bias in Cordeiro & McCullagh (1991), the mixed bias-reduction adjusted scores approach in Kosmidis et al (2019), maximum penalized likelihood with powers of the Jeffreys prior as penalty, and maximum likelihood. Estimation is performed using a quasi Fisher scoring iteration (see vignette("iteration","brglm2")), which, in the case of mean-bias reduction, resembles an iterative correction of the asymptotic bias of the Fisher scoring iterates.

Usage

```
brglmFit(
  x,
  y,
  weights = rep(1, nobs),
  start = NULL,
  etastart = NULL,
  mustart = NULL,
  offset = rep(0, nobs),
  family = gaussian(),
  control = list(),
  intercept = TRUE,
  fixed_totals = NULL,
  singular.ok = TRUE
)

brglm_fit(
  x,
  y,
  weights = rep(1, nobs),
  start = NULL,
  etastart = NULL,
  mustart = NULL,
  offset = rep(0, nobs),
  family = gaussian(),
  control = list(),
  intercept = TRUE,
  fixed_totals = NULL,
  singular.ok = TRUE
)
```

Arguments

x	x is a design matrix of dimension n * p.
y	y is a vector of observations of length n.
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
start	starting values for the parameters in the linear predictor. If NULL (default) then the maximum likelihood estimates are calculated and used as starting values.
etastart	applied only when start is not NULL. Starting values for the linear predictor to be passed to glm.fit when computing starting values using maximum likelihood.
mustart	applied only when start is not NULL. Starting values for the vector of means to be passed to glm.fit when computing starting values using maximum likelihood.
offset	this can be used to specify an *a priori* known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See model.offset.
family	a description of the error distribution and link function to be used in the model. For glm this can be a character string naming a family function, a family function or the result of a call to a family function. For glm.fit only the third option is supported. (See family for details of family functions.)
control	a list of parameters controlling the fitting process. See brglmControl for details.
intercept	logical. Should an intercept be included in the *null* model?
fixed_totals	effective only when family is poisson. Either NULL (no effect) or a vector that indicates which counts must be treated as a group. See Details for more information and brmultinom.
singular.ok	logical. If FALSE, a singular model is an error.

Details

A detailed description of the supported adjustments and the quasi Fisher scoring iteration is given in the iteration vignette (see, vignette("iteration","brglm2") or Kosmidis et al, 2019). A shorter description of the quasi Fisher scoring iteration is also given in one of the vignettes of the *enrichwith* R package (see, https://cran.r-project.org/package=enrichwith/vignettes/bias.html). Kosmidis and Firth (2010) describe a parallel quasi Newton-Raphson iteration with the same stationary point.

In the special case of generalized linear models for binomial, Poisson and multinomial responses, the adjusted score equations approach returns estimates with improved frequentist properties, that are also always finite, even in cases where the maximum likelihood estimates are infinite (e.g. complete and quasi-complete separation in multinomial regression). See, also, detect_separation and check_infinite_estimates for pre-fit and post-fit methods for the detection of infinite estimates in binomial response generalized linear models.

The type of score adjustment to be used is specified through the type argument (see brglmControl for details). The available options are

- type = "AS_mixed": the mixed bias-reducing score adjustments in Kosmidis et al (2019) that result in mean bias reduction for the regression parameters and median bias reduction for the dispersion parameter, if any; default.

- type = "AS_mean": the mean bias-reducing score adjustments in Firth, 1993 and Kosmidis & Firth, 2009. type = "AS_mixed" and type = "AS_mean" will return the same results when family is binomial or poisson, i.e. when the dispersion is fixed)

- type = "AS_median": the median-bias reducing score adjustments in Kenne Pagui et al. (2017)

- type = "MPL_Jeffreys": maximum penalized likelihood with powers of the Jeffreys prior as penalty.

- type = "ML": maximum likelihood

- type = "correction": asymptotic bias correction, as in Cordeiro & McCullagh (1991).

The null deviance is evaluated based on the fitted values using the method specified by the type argument (see brglmControl).

The family argument of the current version of brglmFit can accept any combination of family objects and link functions, including families with user-specified link functions, mis links, and power links, but excluding quasi, quasipoisson and quasibinomial families.

The description of method argument and the Fitting functions section in glm gives information on supplying fitting methods to glm.

fixed_totals to specify groups of observations for which the sum of the means of a Poisson model will be held fixed to the observed count for each group. This argument is used internally in brmultinom and bracl for baseline-category logit models and adjacent category logit models, respectively.

brglm_fit is an alias to brglmFit.

Author(s)

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References

Kosmidis I and Firth D (2019). Jeffreys-prior penalty, finiteness and shrinkage in binomial-response generalized linear models. *arXiv e-prints*, arXiv:1812.01938 <URL: http://arxiv.org/abs/1812.01938>.

Kosmidis I, Kenne Pagui EC, Sartori N (2019). Mean and median bias reduction in generalized linear models. *arXiv e-prints*, arXiv:1804.04085. To appear in Statistics and Computing, <URL: https://arxiv.org/abs/1804.04085>.

Cordeiro GM & McCullagh, P (1991). Bias correction in generalized linear models. *Journal of the Royal Statistical Society. Series B (Methodological)*, **53**, 629-643

Firth D (1993). Bias reduction of maximum likelihood estimates, Biometrika. **80**, 27-38

Kenne Pagui EC, Salvan A, and Sartori N (2017). Median bias reduction of maximum likelihood estimates. *Biometrika*, **104**, 923–938

Kosmidis I and Firth D (2009). Bias reduction in exponential family nonlinear models. *Biometrika*, **96**, 793-804

Kosmidis I and Firth D (2010). A generic algorithm for reducing bias in parametric estimation. *Electronic Journal of Statistics*, **4**, 1097-1112

Kosmidis I (2014). Bias in parametric estimation: reduction and useful side-effects. *WIRE Computational Statistics*, **6**, 185-196

See Also

`glm.fit` and `glm`

Examples

```
## The lizards example from ?brglm::brglm
data("lizards")
# Fit the model using maximum likelihood
lizardsML <- glm(cbind(grahami, opalinus) ~ height + diameter +
                 light + time, family = binomial(logit), data = lizards,
                 method = "glm.fit")
# Mean bias-reduced fit:
lizardsBR_mean <- glm(cbind(grahami, opalinus) ~ height + diameter +
                      light + time, family = binomial(logit), data = lizards,
                      method = "brglmFit")
# Median bias-reduced fit:
lizardsBR_median <- glm(cbind(grahami, opalinus) ~ height + diameter +
                        light + time, family = binomial(logit), data = lizards,
                        method = "brglmFit", type = "AS_median")
summary(lizardsML)
summary(lizardsBR_median)
summary(lizardsBR_mean)

# Maximum penalized likelihood with Jeffreys prior penalty
lizards_Jeffreys <- glm(cbind(grahami, opalinus) ~ height + diameter +
                        light + time, family = binomial(logit), data = lizards,
                        method = "brglmFit", type = "MPL_Jeffreys")
# lizards_Jeffreys is the same fit as lizardsBR_mean (see Firth, 1993)
all.equal(coef(lizardsBR_mean), coef(lizards_Jeffreys))

# Maximum penalized likelihood with powers of the Jeffreys prior as
# penalty. See Kosmidis & Firth (2019) for the finiteness and
# shrinkage properties of the maximum penalized likelihood
# estimators in binomial response models

a <- seq(0, 20, 0.5)
coefs <- sapply(a, function(a) {
    out <- glm(cbind(grahami, opalinus) ~ height + diameter +
            light + time, family = binomial(logit), data = lizards,
            method = "brglmFit", type = "MPL_Jeffreys", a = a)
    coef(out)
})
# Illustration of shrinkage as a grows
matplot(a, t(coefs), type = "l", col = 1, lty = 1)
abline(0, 0, col = "grey")
```

```
## Another example from
## King, Gary, James E. Alt, Nancy Elizabeth Burns and Michael Laver
## (1990).  "A Unified Model of Cabinet Dissolution in Parliamentary
## Democracies", _American Journal of Political Science_, **34**, 846-870


data("coalition", package = "brglm2")
# The maximum likelihood fit with log link
coalitionML <- glm(duration ~ fract + numst2, family = Gamma, data = coalition)
# The mean bias-reduced fit
coalitionBR_mean <- update(coalitionML, method = "brglmFit")
# The bias-corrected fit
coalitionBC <- update(coalitionML, method = "brglmFit", type = "correction")
# The median bias-corrected fit
coalitionBR_median <- update(coalitionML, method = "brglmFit", type = "AS_median")




## An example with offsets from Venables & Ripley (2002, p.189)
data("anorexia", package = "MASS")

anorexML <- glm(Postwt ~ Prewt + Treat + offset(Prewt),
                family = gaussian, data = anorexia)
anorexBC <- update(anorexML, method = "brglmFit", type = "correction")
anorexBR_mean <- update(anorexML, method = "brglmFit")
anorexBR_median <- update(anorexML, method = "brglmFit", type = "AS_median")

## All methods return the same estimates for the regression
## parameters because the maximum likelihood estimator is normally
## distributed around the `true` value under the model (hence, both
## mean and component-wise median unbiased). The Wald tests for
## anorexBC and anorexBR_mean differ from anorexML
## because the bias-reduced estimator of the dispersion is the
## unbiased, by degree of freedom adjustment (divide by n - p),
## estimator of the residual variance. The Wald tests from
## anorexBR_median are based on the median bias-reduced estimator
## of the dispersion that results from a different adjustment of the
## degrees of freedom (divide by n - p - 2/3)
summary(anorexML)
summary(anorexBC)
summary(anorexBR_mean)
summary(anorexBR_median)


## endometrial data from Heinze & Schemper (2002) (see ?endometrial)
data("endometrial", package = "brglm2")
endometrialML <- glm(HG ~ NV + PI + EH, data = endometrial,
                     family = binomial("probit"))
endometrialBR_mean <- update(endometrialML, method = "brglmFit",
                             type = "AS_mean")
endometrialBC <- update(endometrialML, method = "brglmFit",
                        type = "correction")
```

```
endometrialBR_median <- update(endometrialML, method = "brglmFit",
                               type = "AS_median")
summary(endometrialML)
summary(endometrialBC)
summary(endometrialBR_mean)
summary(endometrialBR_median)
```

| brmultinom | *Bias reduction for multinomial response models using the Poisson trick.* |

Description

brmultinom is a wrapper of [brglmFit](#) that fits multinomial regression models using implicit and explicit bias reduction methods. See Kosmidis & Firth (2011) for details.

Usage

```
brmultinom(
  formula,
  data,
  weights,
  subset,
  na.action,
  contrasts = NULL,
  ref = 1,
  model = TRUE,
  x = TRUE,
  control = list(...),
  ...
)
```

Arguments

formula	a formula expression as for regression models, of the form response ~ predictors. The response should be a factor or a matrix with K columns, which will be interpreted as counts for each of K classes. A log-linear model is fitted, with coefficients zero for the first class. An offset can be included: it should be a numeric matrix with K columns if the response is either a matrix with K columns or a factor with K >= 2 classes, or a numeric vector for a response factor with 2 levels. See the documentation of [formula](#)() for other details.
data	an optional data frame in which to interpret the variables occurring in formula.
weights	optional case weights in fitting.
subset	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
na.action	a function to filter missing data.

contrasts   a list of contrasts to be used for some or all of the factors appearing as variables
                 in the model formula.

ref   the reference category to use for multinomial regression. Either an integer, in
                 which case levels(response)[ref] is used as a baseline, or a character string. De-
                 fault is 1.

model   logical. If true, the model frame is saved as component model of the returned
                 object.

x   should the model matrix be included with in the result (default is TRUE).

control   a list of parameters for controlling the fitting process. See brglmControl for
                 details.

...   arguments to be used to form the default 'control' argument if it is not supplied
                 directly.

Details

The models brmultinom handles are also known as baseline-category logit models (see, Agresti,
2002, Section 7.1), because they model the log-odds of every category against a baseline cate-
gory. The user can control which baseline (or reference) category is used via the ref. By default
brmultinom uses the first category as reference.

The maximum likelihood estimates for the parameters of baseline-category logit models have in-
finite components with positive probability, which can result in problems in their estimation and
the use of inferential procedures (e.g. Wad tests). Albert and Andreson (1984) have categorized
the possible data patterns for such models into the exclusive and exhaustive categories of complete
separation, quasi-complete separation and overlap, and showed that infinite maximum likelihood
estimates result when complete or quasi-complete separation occurs.

The adjusted score approach to bias reduction that brmultinom implements (type = "AS_mean") is
an alternative to maximum likelihood that results in estimates with smaller asymptotic bias that are
also *always* finite, even in cases of complete or quasi-complete separation.

brmultinom is a wrapper of brglmFit that fits multinomial logit regression models through the
'Poisson trick' (see, for example, Palmgren, 1981; Kosmidis & Firth, 2011).

The implementation relies on the construction of an 'extended' model matrix for the log-linear
model and constraints on the sums of the Poisson means. Specifically, a log-linear model is fitted
on a Kronecker product (https://en.wikipedia.org/wiki/Kronecker_product) of the original
model matrix X implied by the formula, augmented by nrow(X) dummy variables.

The extended model matrix is sparse, and the **Matrix** package is used for its effective storage.

While brmultinom can be used for analyses using multinomial regression models, the current im-
plementation is more of a 'proof of concept' and is not expected to scale well with either of nrow(X),
ncol(X) or the number of levels in the categorical response.

Author(s)

Ioannis Kosmidis <ioannis.kosmidis@warwick.ac.uk>

References

Kosmidis I, Kenne Pagui EC, Sartori N (2019). Mean and median bias reduction in generalized linear models. *arXiv e-prints*, arXiv:1804.04085. To appear in Statistics and Computing, <URL: https://arxiv.org/abs/1804.04085>.

Agresti A. (2002). *Categorical data analysis* (2nd edition). Wiley Series in Probability and Statistics. Wiley.

Albert A. and Anderson J. A. (1984). On the Existence of Maximum Likelihood Estimates in Logistic Regression Models. *Biometrika*, **71** 1–10.

Kosmidis I. and Firth D. (2011). Multinomial logit bias reduction via the Poisson log-linear model. *Biometrika*, **98**, 755-759.

Palmgren, J. (1981). The Fisher Information Matrix for Log Linear Models Arguing Conditionally on Observed Explanatory Variables. *Biometrika*, **68**, 563-566.

See Also

[multinom](), [bracl]() for adjacent category logit models for ordinal responses

Examples

```
data("housing", package = "MASS")

# Maximum likelihood using nnet::multinom
houseML1nnet <- nnet::multinom(Sat ~ Infl + Type + Cont, weights = Freq,
                               data = housing)
# Maximum likelihood using brmultinom with baseline category 'Low'
houseML1 <- brmultinom(Sat ~ Infl + Type + Cont, weights = Freq,
                       data = housing, type = "ML", ref = 1)
# The estimates are numerically the same as houseML0
all.equal(coef(houseML1nnet), coef(houseML1), tolerance = 1e-04)

# Maximum likelihood using brmultinom with 'High' as baseline
houseML3 <- brmultinom(Sat ~ Infl + Type + Cont, weights = Freq,
                       data = housing, type = "ML", ref = 3)
# The fitted values are the same as houseML1
all.equal(fitted(houseML3), fitted(houseML1), tolerance = 1e-10)

# Bias reduction
houseBR3 <- update(houseML3, type = "AS_mean")
# Bias correction
houseBC3 <- update(houseML3, type = "correction")
```

---

check_infinite_estimates

Generic method for checking for infinite estimates

Description

Generic method for checking for infinite estimates

Usage

```
check_infinite_estimates(object, ...)
```

Arguments

object	a fitted model object (e.g. the result of a [glm](#) call).
...	other options to be passed to the method.

Note

check_infinite_estimates will be removed from **brglm2** at version 0.8. An new version of check_infinite_estimates is now maintained in the **detectseparation** R package at https://cran.r-project.org/package=detectseparation.

See Also

check_infinite_estimates.glm

---

check_infinite_estimates.glm

A simple diagnostic of whether the maximum likelihood estimates are infinite

---

Description

A simple diagnostic of whether the maximum likelihood estimates are infinite

Usage

```
## S3 method for class 'glm'
check_infinite_estimates(object, nsteps = 20, ...)
```

Arguments

object	the result of a [glm](#) call.
nsteps	starting from maxit = 1, the GLM is refitted for maxit = 2, maxit = 3, . . . , maxit = nsteps. Default value is 30.
...	currently not used.

Details

check_infinite_estimates attempts to identify the occurrence of infinite estimates in GLMs with binomial responses by successively refitting the model. At each iteration the maximum number of allowed IWLS iterations is fixed starting from 1 to nsteps (by setting control = glm.control(maxit = j), where j takes values 1, ..., nsteps in glm). For each value of maxit, the estimated asymptotic standard errors are divided to the corresponding ones from control = glm.control(maxit = 1). Then, based on the results in Lesaffre & Albert (1989), if the sequence of ratios in any column of the resultant matrix diverges, then complete or quasi-complete separation occurs and the maximum likelihood estimate for the corresponding parameter has value minus or plus infinity.

Note

check_infinite_estimates will be removed from **brglm2** at version 0.8. An new version of check_infinite_estimates is now maintained in the **detectseparation** R package at https://cran.r-project.org/package=detectseparation. In order to use the version in detect_separation load first **brglm2** and then **detectseparation**, i.e. library(brglm2); library(detectseparation).

References

Lesaffre, E., & Albert, A. (1989). Partial Separation in Logistic Discrimination. *Journal of the Royal Statistical Society. Series B (Methodological)*, **51**, 109-116

See Also

multinom, brmultinom

Examples

```
## endometrial data from Heinze & Schemper (2002) (see ?endometrial)
data("endometrial", package = "brglm2")
endometrialML <- glm(HG ~ NV + PI + EH, data = endometrial,
                     family = binomial("probit"))
## clearly the maximum likelihood estimate for the coefficient of
## NV is infinite
check_infinite_estimates(endometrialML)

## Not run:
## Aligator data (Agresti, 2002, Table~7.1)
data("alligator", package = "brglm2")
all_ml <- brmultinom(foodchoice ~ size + lake , weights = round(freq/3),
                     data = alligators, type = "ML", ref = 1)
## Clearly some estimated standard errors diverge as the number of
## Fisher scoring iterations increases
matplot(check_infinite_estimates(all_ml), type = "l", lty = 1,
        ylim = c(0.5, 1.5))

## End(Not run)
```

---

coalition *Coalition data*

Description

Coalition data

Usage

coalition

Format

An object of class data.frame with 314 rows and 7 columns.

Note

Data is as provided in the Zeilig R package (<https://cran.r-project.org/package=Zelig>)

References

King, G., Alt, J. E., Burns, N. E. and Laver, M. (1990). A Unified Model of Cabinet Dissolution in Parliamentary Democracies. *American Journal of Political Science*, **34**, 846-870.

King, G., Alt, J. E., Burns, N. E. and Laver, M. ICPSR Publication Related Archive, 1115.

See Also

[brglm_fit](#)

---

confint.brglmFit *Method for computing confidence intervals for one or more regression parameters in a* [brglmFit](#) *object*

Description

Method for computing confidence intervals for one or more regression parameters in a [brglmFit](#) object

Usage

```
## S3 method for class 'brglmFit'
confint(object, parm, level = 0.95, ...)
```

Arguments

`object`	a fitted model object.
`parm`	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
`level`	the confidence level required.
`...`	additional argument(s) for methods.

---

detect_separation	*Method for* glm *that tests for data separation and finds which parameters have infinite maximum likelihood estimates in generalized linear models with binomial responses*

Description

detect_separation is a method for glm that tests for the occurrence of complete or quasi-complete separation in datasets for binomial response generalized linear models, and finds which of the parameters will have infinite maximum likelihood estimates. detect_separation relies on the linear programming methods developed in Konis (2007).

Usage

```
detect_separation(
  x,
  y,
  weights = rep(1, nobs),
  start = NULL,
  etastart = NULL,
  mustart = NULL,
  offset = rep(0, nobs),
  family = gaussian(),
  control = list(),
  intercept = TRUE,
  singular.ok = TRUE
)

detectSeparation(
  x,
  y,
  weights = rep(1, nobs),
  start = NULL,
  etastart = NULL,
  mustart = NULL,
  offset = rep(0, nobs),
  family = gaussian(),
```

```
    control = list(),
    intercept = TRUE,
    singular.ok = TRUE
)
```

Arguments

x	x is a design matrix of dimension n * p.
y	y is a vector of observations of length n.
weights	an optional vector of 'prior weights' to be used in the fitting process. Should be NULL or a numeric vector.
start	currently not used.
etastart	currently not used.
mustart	currently not used.
offset	this can be used to specify an *a priori* known component to be included in the linear predictor during fitting. This should be NULL or a numeric vector of length equal to the number of cases. One or more offset terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See model.offset.
family	a description of the error distribution and link function to be used in the model. For glm this can be a character string naming a family function, a family function or the result of a call to a family function. For glm.fit only the third option is supported. (See family for details of family functions.)
control	a list of parameters controlling separation detection. See detect_separation_control for details.
intercept	logical. Should an intercept be included in the *null* model?
singular.ok	logical. If FALSE, a singular model is an error.

Details

For the definition of complete and quasi-complete separation, see Albert and Anderson (1984).

detect_separation is a wrapper to the separator function from the **safeBinaryRegression** R package, that can be passed directly as a method to the glm function. See, examples.

The interface to separator was designed by Ioannis Kosmidis after correspondence with Kjell Konis, and a port of separator has been included in **brglm2** under the permission of Kjell Konis.

detectSeparation is an alias for detect_separation.

Note

detect_separation will be removed from **brglm2** at version 0.8. A new version of detect_separation is now maintained in the **detectseparation** R package at https://cran.r-project.org/package=detectseparation. In order to use the version in detect_separation load first **brglm2** and then **detectseparation**, i.e. library(brglm2); library(detectseparation).

Author(s)

Ioannis Kosmidis [aut, cre] <ioannis.kosmidis@warwick.ac.uk>, Kjell Konis [ctb] <kjell.konis@me.com>

References

Konis K. (2007). *Linear Programming Algorithms for Detecting Separated Data in Binary Logistic Regression Models*. DPhil. University of Oxford. https://ora.ox.ac.uk/objects/uuid:8f9ee0d0-d78e-4101-9ab4-f9cbceed2a2a

Konis K. (2013). safeBinaryRegression: Safe Binary Regression. R package version 0.1-3. https://CRAN.R-project.org/package=safeBinaryRegression

See Also

brglm_fit, glm.fit and glm

Examples

```
## endometrial data from Heinze & Schemper (2002) (see ?endometrial)
data("endometrial", package = "brglm2")
endometrial_sep <- glm(HG ~ NV + PI + EH, data = endometrial,
                       family = binomial("logit"),
                       method = "detect_separation")
endometrial_sep
## The maximum likelihood estimate for NV is infinite
summary(update(endometrial_sep, method = "glm.fit"))

## Not run:
## Example inspired by unpublished microeconometrics lecture notes by
## Achim Zeileis https://eeecon.uibk.ac.at/~zeileis/
## The maximum likelihood estimate of sourhernyes is infinite
data("MurderRates", package = "AER")
murder_sep <- glm(I(executions > 0) ~ time + income +
                  noncauc + lfp + southern, data = MurderRates,
                  family = binomial(), method = "detect_separation")
murder_sep
## which is also evident by the large estimated standard error for NV
murder_glm <- update(murder_sep, method = "glm.fit")
summary(murder_glm)
## and is also reveal by the divergence of the NV column of the
## result from the more computationally intensive check
check_infinite_estimates(murder_glm)
## Mean bias reduction via adjusted scores results in finite estimates
update(murder_glm, method = "brglm_fit")

## End(Not run)
```

detect_separation_control

> *Auxiliary function for the* [glm](glm) *interface when* method *is* detect_separation.

Description

Typically only used internally by detect_separation but may be used to construct a control argument.

Usage

```
detect_separation_control(
  linear_program = c("primal", "dual"),
  purpose = c("find", "test"),
  beta_tolerance = sqrt(.Machine$double.eps)
)

detectSeparationControl(
  linear_program = c("primal", "dual"),
  purpose = c("find", "test"),
  beta_tolerance = sqrt(.Machine$double.eps)
)
```

Arguments

linear_program	should detect_separation solve the "primal" or "dual" linear program for separation detection?
purpose	should detect_separation simply "test" for separation or also "find" which parameters are infinite?
beta_tolerance	maximum absolute variable value from the linear program, before separation is declared.

---

endometrial   *Histology grade and risk factors for 79 cases of endometrial cancer*

Description

Histology grade and risk factors for 79 cases of endometrial cancer

Usage

```
endometrial
```

Format

A data frame with 79 rows and 4 variables:

NV neovasculization with coding 0 for absent and 1 for present

PI pulsality index of arteria uterina

EH endometrium height

HG histology grade with coding 0 for low grade and 1 for high grade

Source

The packaged data set was downloaded in .dat format from http://www.stat.ufl.edu/~aa/glm/data. The latter link provides the data sets used in Agresti (2015).

The endometrial data set was first analyzed in Heinze and Schemper (2002), and was originally provided by Dr E. Asseryanis from the Medical University of Vienna.

References

Agresti, A. (2015). *Foundations of Linear and Generalized Linear Models*. Wiley Series in Probability and Statistics. Wiley

Heinze, G., & Schemper, M. (2002). A Solution to the Problem of Separation in Logistic Regression. *Statistics in Medicine*, **21**, 2409–2419

See Also

brglm_fit

---

lizards   *Habitat preferences of lizards*

Description

The lizards data frame has 23 rows and 6 columns. Variables grahami and opalinus are counts of two lizard species at two different perch heights, two different perch diameters, in sun and in shade, at three times of day.

Usage

```
lizards
```

Format

An object of class data.frame with 23 rows and 6 columns.

Details

- grahami. count of grahami lizards
- opalinus. count of opalinus lizards
- height. a factor with levels `<5ft`, `>=5ft`
- diameter. a factor with levels `<=2in`, `>2in`
- light. a factor with levels `sunny`, `shady`
- time. a factor with levels `early`, `midday`, `late`

Source

McCullagh, P. and Nelder, J. A. (1989) _Generalized Linear Models_ (2nd Edition). London: Chapman and Hall.

Originally from

Schoener, T. W. (1970) Nonsynchronous spatial overlap of lizards in patchy habitats. _Ecology_ *51*, 408-418.

See Also

brglm_fit

---

mis   *A* `link-glm` *object for misclassified responses in binomial regression models*

Description

[mis](mis) is a `link-glm` object that specifies the link function in Neuhaus (1999, expression~(8)) for handling misclassified responses in binomial regression models using maximum likelihood. A prior specification of the sensitivity and specificity is required.

Usage

```
mis(link = "logit", sensitivity = 1, specificity = 1)
```

Arguments

link	the baseline link to be used.
sensitivity	the probability of observing a success given that a success actually took place given any covariate values.
specificity	the probability of observing a failure given that a failure actually took place given any covariate values.

Details

`sensitivity + specificity` should be greater or equal to 1, otherwise it is implied that the procedure producing the responses performs worse than chance in terms of misclassification.

References

Neuhaus J. M. (1999). Bias and efficiency loss due to misclassified responses in binary regression. Biometrika, **86**, 843-855

See Also

glm, brglm_fit

Examples

```
## Define a few links with some misclassification
logit_mis <- mis(link = "logit", sensitivity = 0.9, specificity = 0.9)

lizards_f <- cbind(grahami, opalinus) ~ height + diameter + light + time

lizardsML <- glm(lizards_f, family = binomial(logit), data = lizards)

lizardsML_mis <- update(lizardsML, family = binomial(logit_mis),
                        start = coef(lizardsML))

## A notable change is coefficients is noted here compared to when
## specificity and sensitity are 1
coef(lizardsML)
coef(lizardsML_mis)

## Bias reduction is also possible
update(lizardsML_mis, method = "brglmFit", type = "AS_mean",
       start = coef(lizardsML))

update(lizardsML_mis, method = "brglmFit", type = "AS_median",
       start = coef(lizardsML))
```

---

predict.bracl   *Predict method for* bracl *fits*

Description

Obtain class and probability predictions from a fitted adjacent category logits model.

Usage

```
## S3 method for class 'bracl'
predict(object, newdata, type = c("class", "probs"), ...)
```

Arguments

`object`	a fitted object of class inheriting from `"bracl"`.
`newdata`	optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted linear predictors are used.
`type`	the type of prediction required. The default is `"class"`, which produces predictions of the response category at the covariate values supplied in `"newdata"`, selecting the category with the largest probability; the alternative `"probs"` returns all category probabilities at the covariate values supplied in `"newdata"`.
`...`	further arguments passed to or from other methods.

Details

If `newdata` is omitted the predictions are based on the data used for the fit.

Value

If `type = "class"` a vector with the predicted response categories; if `type = "probs"` a matrix of probabilities for all response categories at `newdata`.

Examples

```
data("stemcell", package = "brglm2")

# Adjacent category logit (non-proportional odds)
fit_bracl <- bracl(research ~ as.numeric(religion) + gender, weights = frequency,
                   data = stemcell, type = "ML")
# Adjacent category logit (proportional odds)
fit_bracl_p <- bracl(research ~ as.numeric(religion) + gender, weights = frequency,
                     data = stemcell, type = "ML", parallel = TRUE)

# New data
newdata <- expand.grid(gender = c("male", "female"),
                       religion = c("liberal", "moderate", "fundamentalist"))

# Predictions
sapply(c("class", "probs"), function(what) predict(fit_bracl, newdata, what))
sapply(c("class", "probs"), function(what) predict(fit_bracl_p, newdata, what))
```

---

predict.brmultinom   *Predict method for* brmultinom *fits*

Description

Obtain class and probability predictions from a fitted baseline category logits model.

Usage

```
## S3 method for class 'brmultinom'
predict(object, newdata, type = c("class", "probs"), ...)
```

Arguments

`object`	a fitted object of class inheriting from "brmultinom".
`newdata`	optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted linear predictors are used.
`type`	the type of prediction required. The default is "class", which produces predictions of the response category at the covariate values supplied in "newdata", selecting the category with the largest probability; the alternative "probs" returns all category probabilities at the covariate values supplied in "newdata".
`...`	further arguments passed to or from other methods.

Details

If newdata is omitted the predictions are based on the data used for the fit.

Value

If type = "class" a vector with the predicted response categories; if type = "probs" a matrix of probabilities for all response categories at newdata.

Examples

```
data("housing", package = "MASS")

# Maximum likelihood using brmultinom with baseline category 'Low'
houseML1 <- brmultinom(Sat ~ Infl + Type + Cont, weights = Freq,
                       data = housing, type = "ML", ref = 1)

# New data
newdata <- expand.grid(Infl = c("Low", "Medium"),
                       Type = c("Tower", "Atrium", "Terrace"),
                       Cont = c("Low", NA, "High"))

## Predictions
sapply(c("class", "probs"), function(what) predict(houseML1, newdata, what))
```

---

residuals.brmultinom   *Residuals for multinomial logistic regression and adjacent category logit models*

Description

Residuals for multinomial logistic regression and adjacent category logit models

Usage

```
## S3 method for class 'brmultinom'
residuals(object, type = c("pearson", "response", "deviance", "working"), ...)

## S3 method for class 'bracl'
residuals(object, type = c("pearson", "response", "deviance", "working"), ...)
```

Arguments

object	the object coming out of [bracl](#) and [brmultinom](#).
type	the type of residuals which should be returned. The options are: "pearson" (default), "response", "deviance", "working". See Details.
...	Currently not used.

Details

The residuals computed are the residuals from the equivalent Poisson log-linear model fit, organized in a form that matches the output of fitted(object, type = "probs"). As a result, the output is residuals defined in terms of the object and expected multinomial counts.

See Also

brmultinom bracl

---

stemcell   *Opinion on Stem Cell Research and Religious Fundamentalism*

Description

A data set from the 2006 General Social Survey that shows the relationship in the United States between opinion about funding stem cell research and the fundamentalism/liberalism of one's religious beliefs, stratified by gender.

Usage

```
stemcell
```

Format

A data frame with 24 rows and 4 variables:

research opinion about funding stem cell research with levels `definitely`, `probably`, `probably not`, `definitely not`

gender the gender of the respondent with levels `female` and `male`

religion the fundamentalism/liberalism of one's religious beliefs with levels `fundamentalist`, `moderate`, `liberal`

frequency the number of times a respondent fell in each of the combinations of levels for `research`, `religion` and `gender`

Source

The `stemcell` data set is analyzed in Agresti (2010, Subsection~4.1.5).

References

Agresti, A. (2010). *Analysis of Ordinal Categorical Data* (2nd edition). Wiley Series in Probability and Statistics. Wiley

See Also

bracl

---

summary.brglmFit   summary *method for* brglmFit *objects*

Description

summary method for brglmFit objects

Usage

```
## S3 method for class 'brglmFit'
summary(
  object,
  dispersion = NULL,
  correlation = FALSE,
  symbolic.cor = FALSE,
  ...
)
```

Arguments

object	an object of class "glm", usually, a result of a call to [glm]().
dispersion	the dispersion parameter for the family used. Either a single numerical value or NULL (the default), when it is inferred from object (see 'Details').
correlation	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
symbolic.cor	logical. If TRUE, print the correlations in a symbolic form (see [symnum]()) rather than as numbers.
...	further arguments passed to or from other methods.

Details

The interface of the summary method for [brglmFit]() objects is identical to that of [glm]() objects. The summary method for [brglmFit]() objects computes the p-values of the individual Wald statistics based on the standard normal distribution, unless the family is Gaussian, in which case a t distribution with appropriate degrees of freedom is used.

See Also

[summary.glm]() and [glm]()

Examples

```
## For examples see examples(brglmFit)
```

---

vcov.brglmFit	*Return the variance-covariance matrix for the regression parameters in a* [brglmFit]() *object*

Description

Return the variance-covariance matrix for the regression parameters in a [brglmFit]() object

Usage

```
## S3 method for class 'brglmFit'
vcov(object, model = c("mean", "full", "dispersion"), complete = TRUE, ...)
```

Arguments

object	a fitted model object, typically. Sometimes also a [summary]() object of such a fitted model.
model	character specifying for which component of the model coefficients should be extracted.

complete   for the aov, lm, glm, mlm, and where applicable summary.lm etc methods: log-ical indicating if the full variance-covariance matrix should be returned also in case of an over-determined system where some coefficients are undefined and coef(.) contains NAs correspondingly. When complete = TRUE, vcov() is compatible with coef() also in this singular case.

...   additional arguments for method functions. For the glm method this can be used to pass a dispersion parameter.

Details

The options for model are "mean" for mean regression parameters only (default), "dispersion" for the dispersion parameter (or the transformed dispersion; see brglm_control), and "mean" for both the mean regression and the (transformed) dispersion parameters.

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