Fitting Generalized Linear Models

Description

glm is used to fit generalized linear models, specified by giving a symbolic description of the linear predictor and a description of the error distribution.

Usage

glm(formula, family = gaussian, data, weights, subset,
    na.action, start = NULL, etastart, mustart, offset,
    control = list(...), model = TRUE, method = "glm.fit",
    x = FALSE, y = TRUE, singular.ok = TRUE, contrasts = NULL, ...)

glm.fit(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)

## S3 method for class 'glm'
weights(object, type = c("prior", "working"), ...)
start starting values for the parameters in the linear predictor.
etastart starting values for the linear predictor.
mustart starting values for the vector of means.
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.
control a list of parameters for controlling the fitting process. For glm.fit this is passed to glm.control.
model a logical value indicating whether model frame should be included as a component of the returned value.
method the method to be used in fitting the model. The default method "glm.fit" uses iteratively reweighted least squares (IWLS): the alternative "model.frame" returns the model frame and does no fitting. User-supplied fitting functions can be supplied either as a function or a character string naming a function, with a function which takes the same arguments as glm.fit. If specified as a character string it is looked up from within the stats namespace.
x, y For glm: logical values indicating whether the response vector and model matrix used in the fitting process should be returned as components of the returned value. For glm.fit: x is a design matrix of dimension n * p, and y is a vector of observations of length n.
singular.ok logical; if FALSE a singular fit is an error.
contrasts an optional list. See the contrasts.arg of model.matrix.default.
intercept logical. Should an intercept be included in the null model?
object an object inheriting from class "glm".
type character, partial matching allowed. Type of weights to extract from the fitted model object. Can be abbreviated.
... For glm: arguments to be used to form the default control argument if it is not supplied directly. For weights: further arguments passed to or from other methods.

Details
A typical predictor has the form response ~ terms where response is the (numeric) response vector and terms is a series of terms which specifies a linear predictor for response.
For binomial and quasibinomial families the response can also be 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. A terms specification of the form first + second indicates all the terms in first together with all the terms in second with any duplicates removed.
A specification of the form first:second indicates the set of terms obtained by taking the interactions of all terms in first with all terms in second. The specification first*second indicates the cross of first and second. This is the same as first + second + first:second.
The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a terms object as the formula.
Non-NULL weights can be used to indicate that different observations have different dispersions (with the values in weights being inversely proportional to the dispersions); or equivalently, when the elements of weights are positive integers w_i, that each response y_i is the mean of w_i unit-weight observations. For a
binomial GLM prior weights are used to give the number of trials when the response is the proportion of successes: they would rarely be used for a Poisson GLM.

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

If more than one of etastart, start and mustart is specified, the first in the list will be used. It is often advisable to supply starting values for a quasi family, and also for families with unusual links such as gaussian("log").

All of weights, subset, offset, etastart and mustart are evaluated in the same way as variables in formula, that is first in data and then in the environment of formula.

For the background to warning messages about 'fitted probabilities numerically 0 or 1 occurred' for binomial GLMs, see Venables & Ripley (2002, pp. 197–8).

Value

glm returns an object of class inheriting from "glm" which inherits from the class "lm". See later in this section. If a non-standard method is used, the object will also inherit from the class (if any) returned by that function.

The function summary (i.e., summary.glm) can be used to obtain or print a summary of the results and the function anova (i.e., anova.glm) to produce an analysis of variance table.

The generic accessor functions coefficients, effects, fitted.values and residuals can be used to extract various useful features of the value returned by glm.

weights extracts a vector of weights, one for each case in the fit (after subsetting and na.action).

An object of class "glm" is a list containing at least the following components:

coefficients a named vector of coefficients
residuals the working residuals, that is the residuals in the final iteration of the IWLS fit. Since cases with zero weights are omitted, their working residuals are NA.
fitted.values the fitted mean values, obtained by transforming the linear predictors by the inverse of the link function.
rank the numeric rank of the fitted linear model.
family the family object used.
linear.predictors the linear fit on link scale.
deviance up to a constant, minus twice the maximized log-likelihood. Where sensible, the constant is chosen so that a saturated model has deviance zero.
aic A version of Akaike's An Information Criterion, minus twice the maximized log-likelihood plus twice the number of parameters, computed by the aic component of the family. For binomial and Poison families the dispersion is fixed at one and the number of parameters is the number of coefficients. For gaussian, Gamma and inverse gaussian families the dispersion is estimated from the residual deviance, and the number of parameters is the number of coefficients plus one. For a gaussian family the MLE of the dispersion is used so this is a valid value of AIC, but for Gamma and inverse gaussian families it is not. For families fitted by quasi-likelihood the value is NA.
null.deviance The deviance for the null model, comparable with deviance. The null model will include the offset, and an intercept if there is one in the model. Note that this will be incorrect if the link function depends on the data other than through the fitted mean: specify a zero offset to
force a correct calculation.

iter  the number of iterations of IWLS used.
weights  the working weights, that is the weights in the final iteration of the IWLS fit.
prior.weights  the weights initially supplied, a vector of 1s if none were.
df.residual  the residual degrees of freedom.
df.null  the residual degrees of freedom for the null model.
y  if requested (the default) the y vector used. (It is a vector even for a binomial model.)
x  if requested, the model matrix.
model  if requested (the default), the model frame.
converged  logical. Was the IWLS algorithm judged to have converged?
boundary  logical. Is the fitted value on the boundary of the attainable values?
call  the matched call.
formula  the formula supplied.
terms  the terms object used.
data  the data argument.
offset  the offset vector used.
control  the value of the control argument used.
method  the name of the fitter function used, currently always "glm.fit".
contrasts  (where relevant) the contrasts used.
xlevels  (where relevant) a record of the levels of the factors used in fitting.
na.action  (where relevant) information returned by model.frame on the special handling of NAs.

In addition, non-empty fits will have components qr, R and effects relating to the final weighted linear fit.

Objects of class "glm" are normally of class c("glm", "lm"), that is inherit from class "lm", and well-designed methods for class "lm" will be applied to the weighted linear model at the final iteration of IWLS. However, care is needed, as extractor functions for class "glm" such as residuals and weights do not just pick out the component of the fit with the same name.

If a binomial glm model was specified by giving a two-column response, the weights returned by prior.weights are the total numbers of cases (factored by the supplied case weights) and the component y of the result is the proportion of successes.

Fitting functions

The argument method serves two purposes. One is to allow the model frame to be recreated with no fitting. The other is to allow the default fitting function glm.fit to be replaced by a function which takes the same arguments and uses a different fitting algorithm. If glm.fit is supplied as a character string it is used to search for a function of that name, starting in the stats namespace.

The class of the object return by the fitter (if any) will be prepended to the class returned by glm.
Author(s)
The original R implementation of glm was written by Simon Davies working for Ross Ihaka at the University of Auckland, but has since been extensively re-written by members of the R Core team.

The design was inspired by the S function of the same name described in Hastie & Pregibon (1992).

References

See Also
anova.glm, summary.glm, etc. for glm methods, and the generic functions anova, summary, effects, fitted.values, and residuals.

lm for non-generalized linear models (which SAS calls GLMs, for ‘general’ linear models).
loglin and loglm (package MASS) for fitting log-linear models (which binomial and Poisson GLMs are) to contingency tables.
bigglm in package biglm for an alternative way to fit GLMs to large datasets (especially those with many cases).
esoph, infert and predict.glm have examples of fitting binomial glms.

Examples
## Dobson (1990) Page 93: Randomized Controlled Trial:
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
print(d.AD <- data.frame(treatment, outcome, counts))
glm.D93 <- glm(counts ~ outcome + treatment, family = poisson())
anova(glm.D93)
summary(glm.D93)

## an example with offsets from Venables & Ripley (2002, p.189)
utils::data(anorexia, package = "MASS")
anorex.1 <- glm(Postwt ~ Prewt + Treat + offset(Prewt),
               family = gaussian, data = anorexia)
summary(anorex.1)

# A Gamma example, from McCullagh & Nelder (1989, pp. 300-2)
clotting <- data.frame(
    u = c(5,10,15,20,30,40,60,80,100),
    lot1 = c(118,58,42,35,27,25,21,19,18),
    lot2 = c(58,39,30,20,20,20,17,16,15),
    lot3 = c(42,35,27,25,20,20,17,16,15))
lot2 = c(69,35,26,21,18,13,12,12))
summary(glm(lot1 ~ log(u), data = clotting, family = Gamma))
summary(glm(lot2 ~ log(u), data = clotting, family = Gamma))
## Aliased ("S"ingular) -> 1 NA coefficient
(fS <- glm(lot2 ~ log(u) + log(u^2), data = clotting, family = Gamma))
tools::assertError(update(fS, singular.ok=FALSE), verbose=interactive())
## -> .. "singular fit encountered"

## Not run:
## for an example of the use of a terms object as a formula
demo(glm.vr)

## End(Not run)