

## 22S:166 Computing in Statistics

### More on R

Lecture 6  
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## Lists in R

- lists are R objects that contain other named R objects
- often used to return results of functions when different parts of the results are of different types and lengths

## Example: Using the glm function for generalized linear models

```
> help(glm)

glm                package:stats                R Documentation

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 = glm.control(...), model = TRUE,
method = "glm.fit", x = FALSE, y = TRUE, contrasts = NULL, ...)
```

### Arguments:

**formula:** a symbolic description of the model to be fit. The details of model specification are given below.

**family:** a description of the error distribution and link function to be used in the model. This can be a character string naming a family function, a family function or the result of a call to a family function. (See 'family' for details of family functions.)

**data:** an optional data frame, list or environment (or object coercible by 'as.data.frame' to a data frame) containing the variables in the model. If not found in 'data', the variables are taken from 'environment(formula)', typically the environment from which 'glm' is called.

**weights:** an optional vector of weights to be used in the fitting process. Should be 'NULL' or a numeric vector.

**method:** the method to be used in fitting the model. The default method 'glm.fit' uses iteratively reweighted least squares (IWLS). The only current alternative is 'model.frame' which returns the model frame and does no fitting.

**intercept:** logical. Should an intercept be included in the \_null\_model?

...: 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 duplicates removed. 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.

A specification of the form 'first:second' indicates the 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'.

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: Akaike's `_An Information Criterion_`, minus twice the maximized log-likelihood plus twice the number of coefficients (so assuming that the dispersion is known).

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

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 case weights initially supplied.

df.residual: the residual degrees of freedom.

df.null: the residual degrees of freedom for the null model.

y: the 'y' vector used. (It is a vector even for a binomial model.)

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.

## Value:

'glm' returns an object of class inheriting from "glm" which inherits from the class "lm". See later in this section.

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.

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.

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

## A worked example

### Create the data frame for analysis

```
> 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(69,35,26,21,18,16,13,12,12))
```

### Assign output of glm function to an object

```
> clot.glm <- glm(lot1 ~ log(u), data=clotting, family=Gamma)
> names(clot.glm)
 [1] "coefficients"      "residuals"        "fitted.values"
 [4] "effects"           "R"                 "rank"
 [7] "qr"                "family"            "linear.predictors"
[10] "deviance"          "aic"               "null.deviance"
[13] "iter"              "weights"           "prior.weights"
[16] "df.residual"       "df.null"           "y"
[19] "converged"         "boundary"          "model"
[22] "call"              "formula"           "terms"
[25] "data"              "offset"            "control"
[28] "method"            "contrasts"        "xlevels"
```

### Extract items from the list object

```
> clot.glm$coefficients
(Intercept)    log(u)
-0.01655438  0.01534311
> coefficients(clot.glm)
(Intercept)    log(u)
-0.01655438  0.01534311
> clot.glm[[1]]
(Intercept)    log(u)
i-0.01655438  0.01534311
> clot.glm$residuals
      1          2          3          4          5
3.219040e-04 -1.669367e-03 -1.245089e-03 -8.626301e-04  1.353040e-03
      6          7          8          9
-4.456895e-05  1.314957e-03  1.879617e-03  1.414312e-03

> clot.glm$call
glm(formula = lot1 ~ log(u), family = Gamma, data = clotting)
```

## Apply generic R function to the object

```
> summary(clot.glm)
```

Call:

```
glm(formula = lot1 ~ log(u), family = Gamma, data = clotting)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-0.04008	-0.03756	-0.02637	0.02905	0.08641

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.0165544	0.0009275	-17.85	4.28e-07 ***
log(u)	0.0153431	0.0004150	36.98	2.75e-09 ***

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for Gamma family taken to be 0.002446013)

Null deviance: 3.512826 on 8 degrees of freedom  
Residual deviance: 0.016730 on 7 degrees of freedom  
AIC: 37.99

Number of Fisher Scoring iterations: 3

## Writing your own R functions

- structure of a function

```
function( <arguments> )
{
  <body of function>
  <object to return>
}
```

- invoking the R editor to write a function

```
<function name> <- function(){}

```

```
<function name> <- edit(<function name>)
```

example

```
quadratic <- function( a,b,c ){}
```

```
quadratic <- edit(quadratic)
```