

**A Handbook of Statistical Analyses Using R**  
— **2nd Edition**

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## Logistic Regression and Generalised Linear Models: Blood Screening, Women's Role in Society, Colonic Polyps, and Driving and Back Pain

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### 7.1 Introduction

### 7.2 Logistic Regression and Generalised Linear Models

### 7.3 Analysis Using R

#### 7.3.1 ESR and Plasma Proteins

We can now fit a logistic regression model to the data using the `glm` function. We start with a model that includes only a single explanatory variable, `fibrinogen`. The code to fit the model is

```
R> plasma_glm_1 <- glm(ESR ~ fibrinogen, data = plasma,
+                      family = binomial())
```

The formula implicitly defines a parameter for the global mean (the intercept term) as discussed in Chapter 5 and Chapter 6. The distribution of the response is defined by the `family` argument, a binomial distribution in our case. (The default link function when the binomial family is requested is the logistic function.)

From the results in Figure 7.2 we see that the regression coefficient for `fibrinogen` is significant at the 5% level. An increase of one unit in this variable increases the log-odds in favour of an ESR value greater than 20 by an estimated 1.83 with 95% confidence interval

```
R> confint(plasma_glm_1, parm = "fibrinogen")
      2.5 % 97.5 %
0.339  3.998
```

These values are more helpful if converted to the corresponding values for the odds themselves by exponentiating the estimate

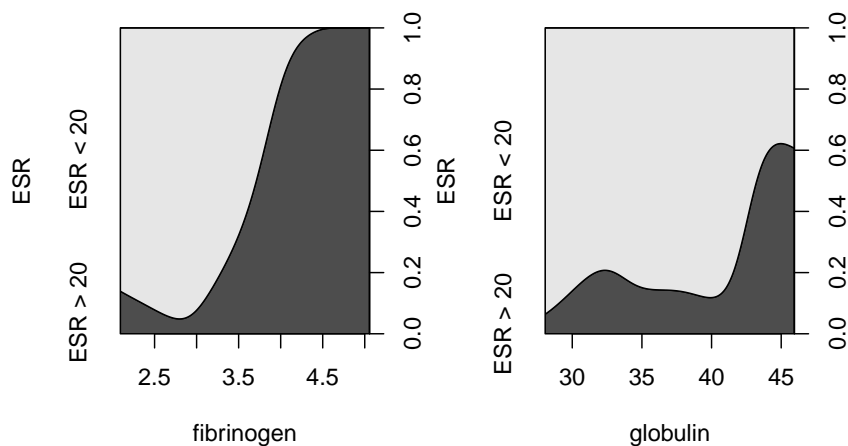
```
R> exp(coef(plasma_glm_1)["fibrinogen"])
fibrinogen
      6.22
```

and the confidence interval

```
R> exp(confint(plasma_glm_1, parm = "fibrinogen"))
```

#### 4 LOGISTIC REGRESSION AND GENERALISED LINEAR MODELS

```
R> data("plasma", package = "HSAUR2")
R> layout(matrix(1:2, ncol = 2))
R> cdplot(ESR ~ fibrinogen, data = plasma)
R> cdplot(ESR ~ globulin, data = plasma)
```



**Figure 7.1** Conditional density plots of the erythrocyte sedimentation rate (ESR) given fibrinogen and globulin.

```
2.5 % 97.5 %
1.4  54.5
```

The confidence interval is very wide because there are few observations overall and very few where the ESR value is greater than 20. Nevertheless it seems likely that increased values of fibrinogen lead to a greater probability of an ESR value greater than 20.

We can now fit a logistic regression model that includes both explanatory variables using the code

```
R> plasma_glm_2 <- glm(ESR ~ fibrinogen + globulin,
+ data = plasma, family = binomial())
```

and the output of the `summary` method is shown in Figure 7.3.

The coefficient for gamma globulin is not significantly different from zero. Subtracting the residual deviance of the second model from the corresponding value for the first model we get a value of 1.87. Tested using a  $\chi^2$ -distribution with a single degree of freedom this is not significant at the 5% level and so we conclude that gamma globulin is not associated with ESR level. In R, the task of comparing the two nested models can be performed using the `anova` function

---

```
R> summary(plasma_glm_1)
Call:
glm(formula = ESR ~ fibrinogen, family = binomial(), data = plasma)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -6.845     2.770   -2.47  0.013
fibrinogen    1.827     0.901    2.03  0.043

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 30.885  on 31  degrees of freedom
Residual deviance: 24.840  on 30  degrees of freedom
AIC: 28.84

Number of Fisher Scoring iterations: 5
```

---

**Figure 7.2** R output of the `summary` method for the logistic regression model fitted to ESR and fibrinogen.

---

```
R> summary(plasma_glm_2)
Call:
glm(formula = ESR ~ fibrinogen + globulin, family = binomial(),
    data = plasma)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -12.792     5.796   -2.21  0.027
fibrinogen    1.910     0.971    1.97  0.049
globulin      0.156     0.120    1.30  0.193

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 30.885  on 31  degrees of freedom
Residual deviance: 22.971  on 29  degrees of freedom
AIC: 28.97

Number of Fisher Scoring iterations: 5
```

---

**Figure 7.3** R output of the `summary` method for the logistic regression model fitted to ESR and both globulin and fibrinogen.

```
R> anova(plasma_glm_1, plasma_glm_2, test = "Chisq")
```

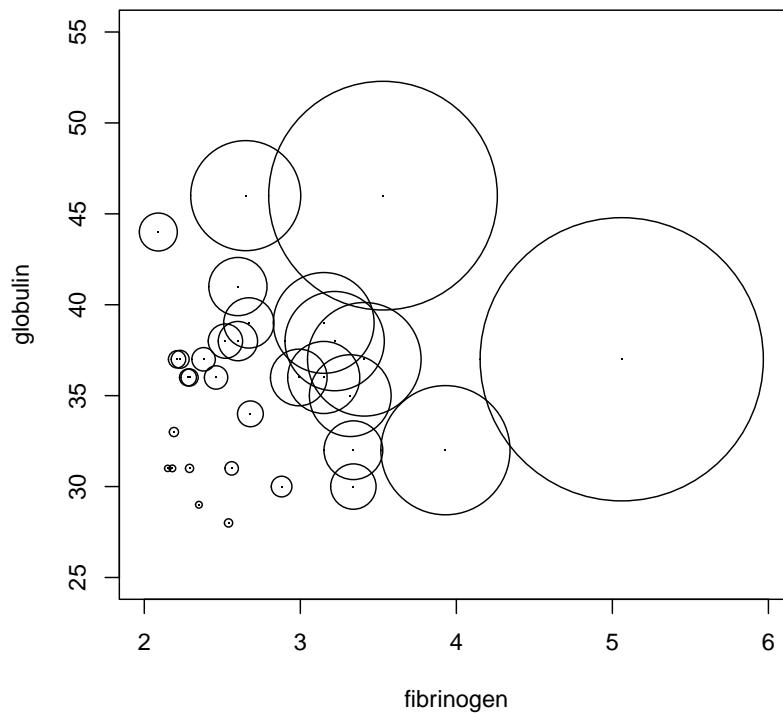
*Analysis of Deviance Table*

```
Model 1: ESR ~ fibrinogen
Model 2: ESR ~ fibrinogen + globulin
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1         30         24.8
2         29         23.0  1      1.87    0.17
```

Nevertheless we shall use the predicted values from the second model and plot them against the values of *both* explanatory variables using a *bubbleplot* to illustrate the use of the `symbols` function. The estimated conditional proba-

6 LOGISTIC REGRESSION AND GENERALISED LINEAR MODELS

```
R> plot(globulin ~ fibrinogen, data = plasma, xlim = c(2, 6),  
+       ylim = c(25, 55), pch = ".")  
R> symbols(plasma$fibrinogen, plasma$globulin, circles = prob,  
+         add = TRUE)
```



**Figure 7.4** Bubbleplot of fitted values for a logistic regression model fitted to the plasma data.

bility of a ESR value larger 20 for all observations can be computed, following formula (??), by

```
R> prob <- predict(plasma_glm_2, type = "response")
```

and now we can assign a larger circle to observations with larger probability as shown in Figure 7.4. The plot clearly shows the increasing probability of an ESR value above 20 (larger circles) as the values of fibrinogen, and to a lesser extent, gamma globulin, increase.

### 7.3.2 Women's Role in Society

Originally the data in Table ?? would have been in a completely equivalent form to the data in Table ?? data, but here the individual observations have been grouped into counts of numbers of agreements and disagreements for the two explanatory variables, `gender` and `education`. To fit a logistic regression model to such grouped data using the `glm` function we need to specify the number of agreements and disagreements as a two-column matrix on the left hand side of the model formula. We first fit a model that includes the two explanatory variables using the code

```
R> data("womensrole", package = "HSAUR2")
R> fm1 <- cbind(agree, disagree) ~ gender + education
R> womensrole_glm_1 <- glm(fm1, data = womensrole,
+                           family = binomial())
```

---

```
R> summary(womensrole_glm_1)

Call:
glm(formula = fm1, family = binomial(), data = womensrole)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   2.5094     0.1839   13.65 <2e-16
genderFemale  -0.0114     0.0841   -0.14  0.89
education     -0.2706     0.0154  -17.56 <2e-16

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 451.722 on 40 degrees of freedom
Residual deviance: 64.007 on 38 degrees of freedom
AIC: 208.1

Number of Fisher Scoring iterations: 4
```

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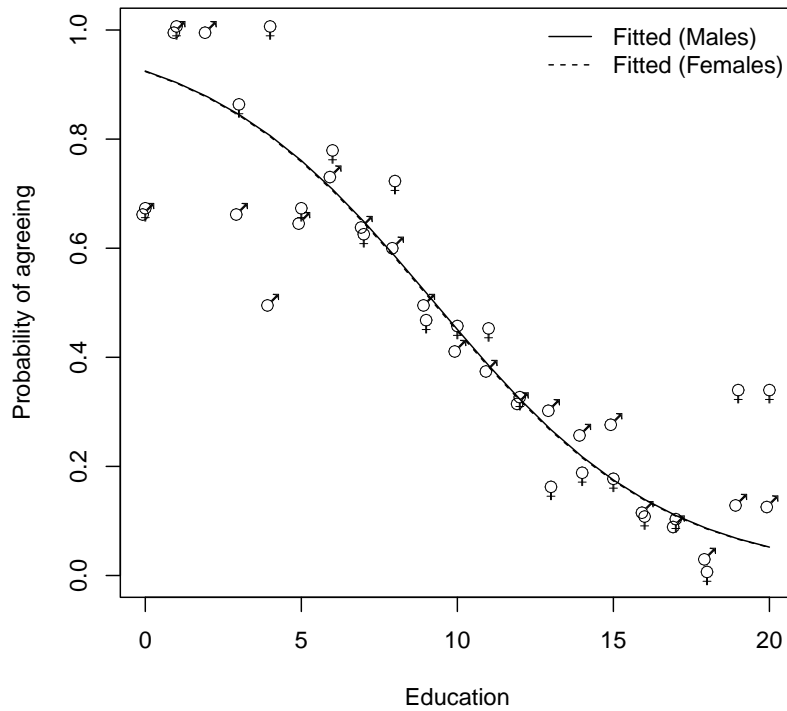
**Figure 7.5** R output of the `summary` method for the logistic regression model fitted to the `womensrole` data.

From the `summary` output in Figure 7.5 it appears that education has a highly significant part to play in predicting whether a respondent will agree with the statement read to them, but the respondent's gender is apparently unimportant. As years of education increase the probability of agreeing with the statement declines. We now are going to construct a plot comparing the observed proportions of agreeing with those fitted by our fitted model. Because we will reuse this plot for another fitted object later on, we define a function which plots years of education against some fitted probabilities, e.g.,

```
R> role.fitted1 <- predict(womensrole_glm_1, type = "response")
and labels each observation with the person's gender:
1 R> myplot <- function(role.fitted) {
2 +   f <- womensrole$gender == "Female"
3 +   plot(womensrole$education, role.fitted, type = "n",
```

8 LOGISTIC REGRESSION AND GENERALISED LINEAR MODELS

R> myplot(role.fitted1)



**Figure 7.6** Fitted (from `womensrole_glm_1`) and observed probabilities of agreeing for the `womensrole` data.

```

4 +         ylab = "Probability of agreeing",
5 +         xlab = "Education", ylim = c(0,1))
6 +     lines(womensrole$education[!f], role.fitted[!f], lty = 1)
7 +     lines(womensrole$education[f], role.fitted[f], lty = 2)
8 +     lgtxt <- c("Fitted (Males)", "Fitted (Females)")
9 +     legend("topright", lgtxt, lty = 1:2, bty = "n")
10 +     y <- womensrole$agree / (womensrole$agree +
11 +                             womensrole$disagree)
12 +     text(womensrole$education, y, ifelse(f, "\\VE", "\\MA"),
13 +          family = "HersheySerif", cex = 1.25)
14 + }

```

In lines 3–5 of function `myplot`, an empty scatterplot of education and fitted



probabilities (`type = "n"`) is set up, basically to set the scene for the following plotting actions. Then, two lines are drawn (using function `lines` in lines 6 and 7), one for males (with line type 1) and one for females (with line type 2, i.e., a dashed line), where the logical vector `f` describes both genders. In line 9 a legend is added. Finally, in lines 12 and 13 we plot ‘observed’ values, i.e., the frequencies of agreeing in each of the groups (`y` as computed in lines 10 and 11) and use the Venus and Mars symbols to indicate gender.

The two curves for males and females in Figure 7.6 are almost the same reflecting the non-significant value of the regression coefficient for gender in `womensrole_glm_1`. But the observed values plotted on Figure 7.6 suggest that there might be an interaction of education and gender, a possibility that can be investigated by applying a further logistic regression model using

```
R> fm2 <- cbind(agree,disagree) ~ gender * education
R> womensrole_glm_2 <- glm(fm2, data = womensrole,
+                           family = binomial())
```

The `gender` and `education` interaction term is seen to be highly significant, as can be seen from the `summary` output in Figure 7.7.

---

```
R> summary(womensrole_glm_2)

Call:
glm(formula = fm2, family = binomial(), data = womensrole)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    2.0982    0.2355   8.91 <2e-16
genderFemale    0.9047    0.3601   2.51 0.0120
education     -0.2340    0.0202 -11.59 <2e-16
genderFemale:education -0.0814    0.0311  -2.62 0.0089

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 451.722 on 40 degrees of freedom
Residual deviance: 57.103 on 37 degrees of freedom
AIC: 203.2

Number of Fisher Scoring iterations: 4
```

---

**Figure 7.7** R output of the `summary` method for the logistic regression model fitted to the `womensrole` data.

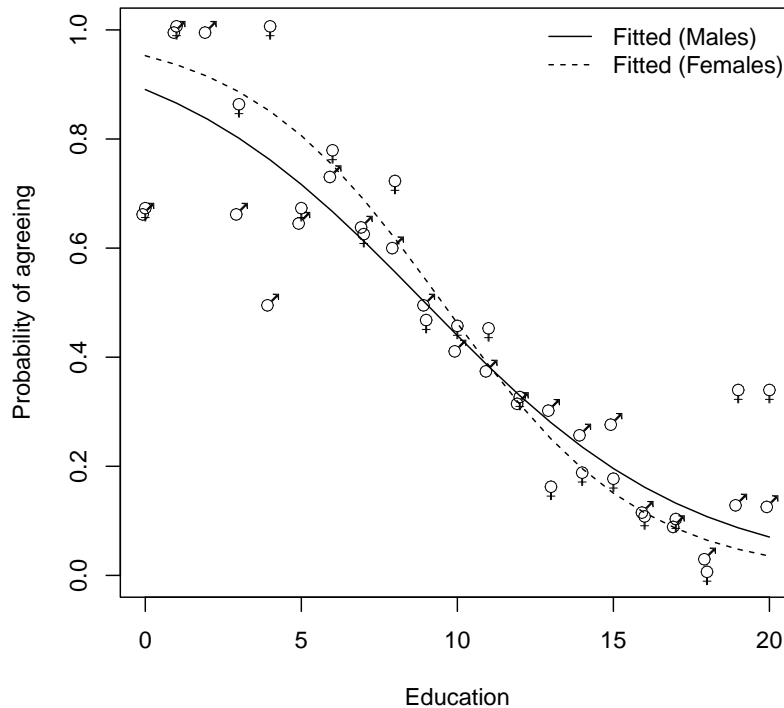
We can obtain a plot of deviance residuals plotted against fitted values using the following code above Figure 7.9. The residuals fall into a horizontal band between  $-2$  and  $2$ . This pattern does not suggest a poor fit for any particular observation or subset of observations.

### 7.3.3 Colonic Polyps

The data on colonic polyps in Table ?? involves *count* data. We could try to model this using multiple regression but there are two problems. The first is that a response that is a count can take only positive values, and secondly

10 LOGISTIC REGRESSION AND GENERALISED LINEAR MODELS

```
R> role.fitted2 <- predict(womensrole_glm_2, type = "response")
R> myplot(role.fitted2)
```



**Figure 7.8** Fitted (from `womensrole_glm_2`) and observed probabilities of agreeing for the `womensrole` data.

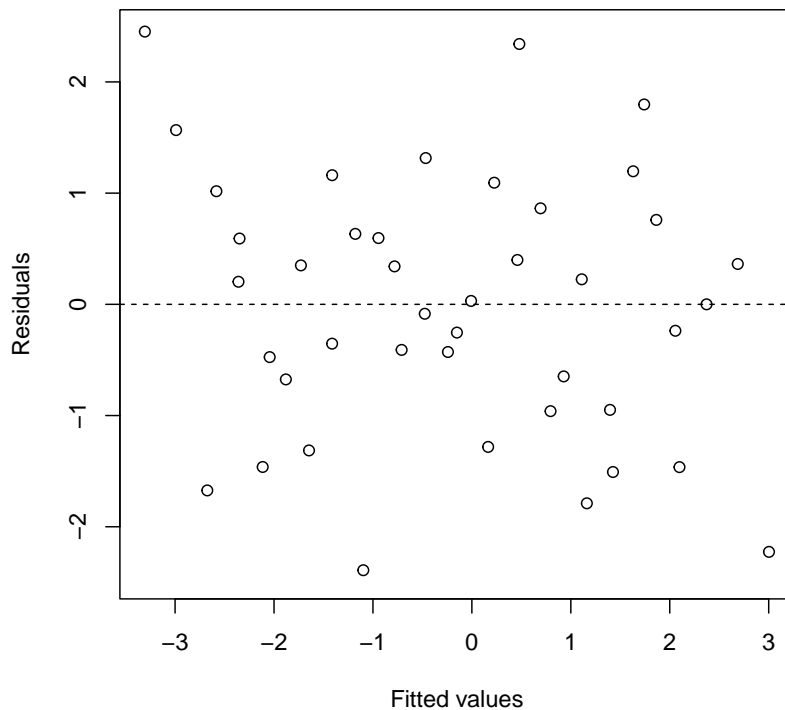
such a variable is unlikely to have a normal distribution. Instead we will apply a GLM with a log link function, ensuring that fitted values are positive, and a Poisson error distribution, i.e.,

$$P(y) = \frac{e^{-\lambda} \lambda^y}{y!}.$$

This type of GLM is often known as *Poisson regression*. We can apply the model using

```
R> data("polyps", package = "HSAUR2")
R> polyps_glm_1 <- glm(number ~ treat + age, data = polyps,
+ family = poisson())
```

```
R> res <- residuals(womensrole_glm_2, type = "deviance")
R> plot(predict(womensrole_glm_2), res,
+       xlab="Fitted values", ylab = "Residuals",
+       ylim = max(abs(res)) * c(-1,1))
R> abline(h = 0, lty = 2)
```



**Figure 7.9** Plot of deviance residuals from logistic regression model fitted to the `womensrole` data.

(The default link function when the Poisson family is requested is the log function.)

We can deal with overdispersion by using a procedure known as *quasi-likelihood*, which allows the estimation of model parameters without fully knowing the error distribution of the response variable. McCullagh and Nelder (1989) give full details of the quasi-likelihood approach. In many respects it simply allows for the estimation of  $\phi$  from the data rather than defining it

## 12 LOGISTIC REGRESSION AND GENERALISED LINEAR MODELS

```
R> summary(polyps_glm_1)

Call:
glm(formula = number ~ treat + age, family = poisson(), data = polyps)

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  4.52902    0.14687   30.84 <2e-16
treatdrug   -1.35908    0.11764  -11.55 <2e-16
age         -0.03883    0.00596   -6.52  7e-11

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 378.66 on 19 degrees of freedom
Residual deviance: 179.54 on 17 degrees of freedom
AIC: 273.9

Number of Fisher Scoring iterations: 5
```

**Figure 7.10** R output of the `summary` method for the Poisson regression model fitted to the `polyps` data.

to be unity for the binomial and Poisson distributions. We can apply quasi-likelihood estimation to the colonic polyps data using the following R code

```
R> polyps_glm_2 <- glm(number ~ treat + age, data = polyps,
+                      family = quasipoisson())
R> summary(polyps_glm_2)

Call:
glm(formula = number ~ treat + age, family = quasipoisson(),
    data = polyps)

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  4.5290    0.4811    9.41 3.7e-08
treatdrug   -1.3591    0.3853   -3.53 0.0026
age         -0.0388    0.0195   -1.99 0.0628

(Dispersion parameter for quasipoisson family taken to be 10.7)

Null deviance: 378.66 on 19 degrees of freedom
Residual deviance: 179.54 on 17 degrees of freedom
AIC: NA

Number of Fisher Scoring iterations: 5
```

The regression coefficients for both explanatory variables remain significant but their estimated standard errors are now much greater than the values given in Figure 7.10. A possible reason for overdispersion in these data is that polyps do not occur independently of one another, but instead may ‘cluster’ together.

#### 7.3.4 Driving and Back Pain

A frequently used design in medicine is the matched case-control study in which each patient suffering from a particular condition of interest included in the study is matched to one or more people without the condition. The most commonly used matching variables are age, ethnic group, mental status etc. A design with  $m$  controls per case is known as a  $1 : m$  matched study. In many cases  $m$  will be one, and it is the  $1 : 1$  matched study that we shall concentrate on here where we analyse the data on low back pain given in Table ???. To begin we shall describe the form of the logistic model appropriate for case-control studies in the simplest case where there is only one binary explanatory variable.

With matched pairs data the form of the logistic model involves the probability,  $\varphi$ , that in matched pair number  $i$ , for a given value of the explanatory variable the member of the pair is a case. Specifically the model is

$$\text{logit}(\varphi_i) = \alpha_i + \beta x.$$

The odds that a subject with  $x = 1$  is a case equals  $\exp(\beta)$  times the odds that a subject with  $x = 0$  is a case.

The model generalises to the situation where there are  $q$  explanatory variables as

$$\text{logit}(\varphi_i) = \alpha_i + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_q x_q.$$

Typically one  $x$  is an explanatory variable of real interest, such as past exposure to a risk factor, with the others being used as a form of statistical control in addition to the variables already controlled by virtue of using them to form matched pairs. This is the case in our back pain example where it is the effect of car driving on lower back pain that is of most interest.

The problem with the model above is that the number of parameters increases at the same rate as the sample size with the consequence that maximum likelihood estimation is no longer viable. We can overcome this problem if we regard the parameters  $\alpha_i$  as of little interest and so are willing to forgo their estimation. If we do, we can then create a *conditional likelihood function* that will yield maximum likelihood estimators of the coefficients,  $\beta_1, \dots, \beta_q$ , that are consistent and asymptotically normally distributed. The mathematics behind this are described in Collett (2003).

The model can be fitted using the `clogit` function from package **survival**; the results are shown in Figure 7.11.

```
R> library("survival")
R> backpain_glm <- clogit(I(status == "case") ~
+   driver + suburban + strata(ID), data = backpain)
```

The response has to be a logical (TRUE for cases) and the `strata` command specifies the matched pairs.

The estimate of the odds ratio of a herniated disc occurring in a driver relative to a nondriver is 1.93 with a 95% confidence interval of (1.09, 3.44).

## 14 LOGISTIC REGRESSION AND GENERALISED LINEAR MODELS

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```
R> print(backpain_glm)

Call:
clogit(I(status == "case") ~ driver + suburban + strata(ID),
      data = backpain)

      coef exp(coef) se(coef) z      p
driveryes  0.7      1.9    0.3 2 0.03
suburbanyes 0.3      1.3    0.2 1 0.26

Likelihood ratio test=10 on 2 df, p=0.008
n= 434, number of events= 217
```

---

**Figure 7.11** R output of the `print` method for the conditional logistic regression model fitted to the `backpain` data.

Conditional on residence we can say that the risk of a herniated disc occurring in a driver is about twice that of a nondriver. There is no evidence that where a person lives affects the risk of lower back pain.

### 7.4 Summary

Generalised linear models provide a very powerful and flexible framework for the application of regression models to a variety of non-normal response variables, for example, logistic regression to binary responses and Poisson regression to count data.

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## Bibliography

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- Collett, D. (2003), *Modelling Binary Data*, London, UK: Chapman & Hall/CRC, 2nd edition.
- McCullagh, P. and Nelder, J. A. (1989), *Generalized Linear Models*, London, UK: Chapman & Hall/CRC.