A Generalized Linear Model for Bernoulli Response Data

Consider the Gauss-Markov linear model with normal errors:

$$\boldsymbol{y} = \boldsymbol{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}, \quad \boldsymbol{\epsilon} \sim N(\boldsymbol{0}, \sigma^2 \boldsymbol{I}).$$

Another way to write this model is

$$\forall\ i = 1, \ldots, n, \quad y_i \sim N(\mu_i, \sigma^2), \quad \mu_i = \boldsymbol{x}_i'\boldsymbol{\beta},$$

and $y_1, \ldots, y_n$ are independent.

This is a special case of what is known as a generalized linear model.

Here is another special case:

$$\forall\ i = 1, \ldots, n, \quad y_i \sim \text{Bernoulli}(\pi_i),$$

$$\pi_i = \frac{\exp(\boldsymbol{x}_i'\boldsymbol{\beta})}{1 + \exp(\boldsymbol{x}_i'\boldsymbol{\beta})},$$

and $y_1, \ldots, y_n$ are independent.

In each example, all responses are independent, and each response is a draw from one type of distribution whose parameters may depend on explanatory variables through a linear predictor $\boldsymbol{x}_i'\boldsymbol{\beta}$.

The second model, for the case of a binary response, is often called a logistic regression model.

Binary responses are common (success/failure, survive/die, good customer/bad customer, win/lose, etc.)

The logistic regression model can help us understand how explanatory variables are related to the probability of “success.”

Example: Disease Outbreak Study

Source: *Applied Linear Statistical Models*, 4th edition, by Neter, Kutner, Nachtsheim, Wasserman (1996)

In a health study to investigate an epidemic outbreak of a disease that is spread by mosquitoes, individuals were randomly sampled within two sectors in a city to determine if the person had recently contracted the disease under study.

Response Variable

$$
\begin{aligned}
y_i &= 0 \text{ (person } i \text{ does not have the disease)} \\
y_i &= 1 \text{ (person } i \text{ has the disease)}
\end{aligned}
$$

Potential Explanatory Variables

- age in years
- socioeconomic status

$$\begin{aligned} 1 &= \text{upper} \\ 2 &= \text{middle} \\ 3 &= \text{lower} \end{aligned}$$

- sector (1 or 2)

Questions of Interest

The potential explanatory variables and the response were recorded for 196 randomly selected individuals.

Are any of these variables associated with the probability of disease and if so how?

We will demonstrate how to use R to fit a logistic regression model to this dataset.

Before delving more deeply into logistic regression, we will review the basic facts of the Bernoulli distribution.

$y \sim \text{Bernoulli}(\pi)$ has probability mass function

$$Pr(y = k) = f(k) = \begin{cases} \pi^k(1-\pi)^{1-k} & \text{for } k \in \{0, 1\} \\ 0 & \text{otherwise} \end{cases}$$

Thus,

$$Pr(y = 0) = f(0) = \pi^0(1-\pi)^{1-0} = 1 - \pi$$

and

$$Pr(y = 1) = f(1) = \pi^1(1-\pi)^{1-1} = \pi.$$

The variance of y is a function of the mean of y.

$$E(y) = \sum_{k=0}^{1} kf(k) = 0 \cdot (1-\pi) + 1 \cdot \pi = \pi$$

$$E(y^2) = \sum_{k=0}^{1} k^2 f(k) = 0^2 \cdot (1-\pi) + 1^2 \cdot \pi = \pi$$

$$\text{Var}(y) = E(y^2) - [E(y)]^2 = \pi - \pi^2 = \pi(1-\pi)$$

The Logistic Regression Model

For $i = 1, \ldots, n$, $y_i \sim \text{Bernoulli}(\pi_i)$,

where

$$\pi_i = \frac{\exp(\boldsymbol{x}_i'\boldsymbol{\beta})}{1 + \exp(\boldsymbol{x}_i'\boldsymbol{\beta})}$$

and $y_1, \ldots, y_n$ are independent.

The Logit Function

The function

$$g(\pi) = \log\left(\frac{\pi}{1-\pi}\right)$$

is called the *logit function*.

The logit function maps the interval $(0, 1)$ to the real line $(-\infty, \infty)$.

π is a probability, so $\log(\frac{\pi}{1-\pi})$ is the log(odds), where the odds of an event $A \equiv \frac{Pr(A)}{1-Pr(A)}$.

Note that

$$
\begin{aligned}
g(\pi) &= \log\left(\frac{\pi}{1-\pi}\right) \\
&= \log\left[\frac{\exp(\boldsymbol{x}_i'\boldsymbol{\beta})}{1+\exp(\boldsymbol{x}_i'\boldsymbol{\beta})} \Bigg/ \frac{1}{1+\exp(\boldsymbol{x}_i'\boldsymbol{\beta})}\right] \\
&= \log[\exp(\boldsymbol{x}_i'\boldsymbol{\beta})] = \boldsymbol{x}_i'\boldsymbol{\beta}.
\end{aligned}
$$

Thus, the logistic regression model says that,

$$y_i \sim \text{Bernoulli}(\pi_i), \text{ where}$$

$$\log\left(\frac{\pi_i}{1-\pi_i}\right) = \boldsymbol{x}_i'\boldsymbol{\beta}$$

In Generalized Linear Models terminology, the logit is called the link function because it “links” the mean of y_i (i.e., π_i) to the linear predictor $\boldsymbol{x}_i'\boldsymbol{\beta}$.

For Generalized Linear Models, it is not necessary that the mean of y_i be a linear function of $\boldsymbol{\beta}$.

Rather, some function of the mean of y_i is a linear function of $\boldsymbol{\beta}$.

For logistic regression, that function is

$$\text{logit}(\pi_i) = \log\left(\frac{\pi_i}{1-\pi_i}\right) = \boldsymbol{x}_i'\boldsymbol{\beta}.$$

When the response is Bernoulli or more generally, binomial, the logit link function is one natural choice. However, other link functions can be considered.

Some common choices (that are also available in R) include the following:

1. logit:

$$\log\left(\frac{\pi}{1-\pi}\right) = \boldsymbol{x}'\boldsymbol{\beta}.$$

2. probit:

$$\Phi^{-1}(\pi) = \boldsymbol{x}'\boldsymbol{\beta},$$

where $\Phi^{-1}(\cdot)$ is the inverse of $N(0,1)$ CDF.

3. Complementary log-log (cloglog in R):

$$\log(-\log(1-\pi)) = \boldsymbol{x}'\boldsymbol{\beta}.$$

Although any of these link functions (or others) can be used, the logit link has some advantages when it comes to interpreting the results (as we will discuss later).

Thus, the logit link is a good choice if it can provide a good fit to the data.

The log likelihood function for logistic regression is

$$
\begin{aligned}
\ell(\boldsymbol{\beta} \mid \boldsymbol{y}) &= \sum_{i=1}^{n} \log[\pi_i^{y_i}(1-\pi_i)^{1-y_i}] \\
&= \sum_{i=1}^{n} [y_i \log(\pi_i) + (1-y_i)\log(1-\pi_i)] \\
&= \sum_{i=1}^{n} [y_i\{\log(\pi_i) - \log(1-\pi_i)\} + \log(1-\pi_i)] \\
&= \sum_{i=1}^{n} \left[y_i \log\left(\frac{\pi_i}{1-\pi_i}\right) + \log(1-\pi_i)\right] \\
&= \sum_{i=1}^{n} [y_i\, \boldsymbol{x}_i'\boldsymbol{\beta} - \log(1+\exp\{\boldsymbol{x}_i'\boldsymbol{\beta}\})]
\end{aligned}
$$

For Generalized Linear Models, Fisher's Scoring Method is typically used to obtain an MLE for $\boldsymbol{\beta}$, denoted as $\hat{\boldsymbol{\beta}}$.

Fisher's Scoring Method is a variation of the Newton-Raphson algorithm in which the Hessian matrix (matrix of second partial derivatives) is replaced by its expected value (-Fisher Information matrix).

For generalized Linear Models, Fisher's scoring method results in an iterative weighted least squares procedure.

The algorithm is presented for the general case in Section 2.5 of *Generalized Linear Models* 2nd Edition (1989) by McCullough and Nelder.

For sufficiently large samples, $\hat{\boldsymbol{\beta}}$ is approximately normal with mean $\boldsymbol{\beta}$ and a variance-covariance matrix that can be approximated by the estimated inverse of the Fisher Information Matrix.

Inference can be conducted using the Wald approach or via likelihood ratio testing as discussed in our course notes on likelihood-related topics.

Interpretation of Logistic Regression Parameters

Let $\boldsymbol{x} = [x_1, x_2, \ldots, x_{j-1}, x_j \qquad , x_{j+1}, \ldots, x_p]'$.

Let $\tilde{\boldsymbol{x}} = [x_1, x_2, \ldots, x_{j-1}, x_j + 1, x_{j+1}, \ldots, x_p]'$.

In other words, $\tilde{\boldsymbol{x}}$ is the same as $\boldsymbol{x}$ except that the jth explanatory variable has been increased by one unit.

Let $\pi = \frac{\exp(\boldsymbol{x}'\boldsymbol{\beta})}{1+\exp(\boldsymbol{x}'\boldsymbol{\beta})}$ and $\tilde{\pi} = \frac{\exp(\tilde{\boldsymbol{x}}'\boldsymbol{\beta})}{1+\exp(\tilde{\boldsymbol{x}}'\boldsymbol{\beta})}$.

The Odds Ratio

$$
\begin{aligned}
\frac{\tilde{\pi}}{1-\tilde{\pi}} \bigg/ \frac{\pi}{1-\pi} &= \exp\left\{\log\left(\frac{\tilde{\pi}}{1-\tilde{\pi}} \bigg/ \frac{\pi}{1-\pi}\right)\right\} \\
&= \exp\left\{\log\left(\frac{\tilde{\pi}}{1-\tilde{\pi}}\right) - \log\left(\frac{\pi}{1-\pi}\right)\right\} \\
&= \exp\{\tilde{\boldsymbol{x}}'\boldsymbol{\beta} - \boldsymbol{x}'\boldsymbol{\beta}\} \\
&= \exp\{(x_j + 1)\beta_j - x_j\beta_j\} \\
&= \exp\{\beta_j\}.
\end{aligned}
$$

Thus, $\frac{\tilde{\pi}}{1-\tilde{\pi}} = \exp(\beta_j)\frac{\pi}{1-\pi}$.

All other explanatory variables held constant, the odds of success at $x_j + 1$ are $\exp(\beta_j)$ times the odds of success at x_j.

This is true regardless of the initial value x_j.

A one unit increase in the jth explanatory variable (with all other explanatory variables held constant) is associated with a multiplicative change in the odds of success by the factor $\exp(\beta_j)$.

If (L_j, U_j) is a $100(1-\alpha)\%$ confidence interval for β_j, then

$$(\exp(L_j), \exp(U_j))$$

is a $100(1-\alpha)\%$ confidence interval for $\exp(\beta_j)$.

Also, note that

$$\begin{aligned}\pi &= \frac{\exp(\boldsymbol{x}'\boldsymbol{\beta})}{1+\exp(\boldsymbol{x}'\boldsymbol{\beta})} = \frac{1}{\frac{1}{\exp(\boldsymbol{x}'\boldsymbol{\beta})}+1} \\ &= \frac{1}{1+\exp(-\boldsymbol{x}'\boldsymbol{\beta})}.\end{aligned}$$

Thus, if (L_j, U_j) is a $100(1-\alpha)\%$ confidence interval for $\boldsymbol{x}'\boldsymbol{\beta}$, then a $100(1-\alpha)\%$ confidence interval for π is

$$\left(\frac{1}{1+\exp(-L_j)}, \frac{1}{1+\exp(-U_j)}\right).$$

```
d=read.delim(
"http://www.public.iastate.edu/~dnett/S511/Disease.txt")

head(d)

  id age ses sector disease savings
1  1  33   1      1       0       1
2  2  35   1      1       0       1
3  3   6   1      1       0       0
4  4  60   1      1       0       1
5  5  18   3      1       1       0
6  6  26   3      1       0       0

d$ses=as.factor(d$ses)
d$sector=as.factor(d$sector)
```

```
o=glm(disease~age+ses+sector,
       family=binomial(link=logit),
       data=d)



summary(o)

Call:
glm(formula = disease ~ age + ses + sector, family =
binomial(link = logit),
    data = d)

Deviance Residuals:
    Min        1Q    Median        3Q       Max
-1.6576  -0.8295  -0.5652   1.0092   2.0842
```

```
Coefficients:
             Estimate Std. Error z value Pr(>|z|)    
(Intercept) -2.293933   0.436769  -5.252 1.50e-07 ***
age          0.026991   0.008675   3.111 0.001862 ** 
ses2         0.044609   0.432490   0.103 0.917849    
ses3         0.253433   0.405532   0.625 0.532011    
sector2      1.243630   0.352271   3.530 0.000415 ***

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 236.33  on 195  degrees of freedom
Residual deviance: 211.22  on 191  degrees of freedom
AIC: 221.22

Number of Fisher Scoring iterations: 3
```

```
coef(o)
(Intercept)         age        ses2        ses3     sector2
-2.29393347  0.02699100  0.04460863  0.25343316  1.24363036

v=vcov(o)
round(v,3)
            (Intercept)    age   ses2   ses3 sector2
(Intercept)       0.191 -0.002 -0.083 -0.102  -0.080
age              -0.002  0.000  0.000  0.000   0.000
ses2             -0.083  0.000  0.187  0.072   0.003
ses3             -0.102  0.000  0.072  0.164   0.039
sector2          -0.080  0.000  0.003  0.039   0.124


confint(o)
Waiting for profiling to be done...
                  2.5 %      97.5 %
(Intercept) -3.19560769 -1.47574975
age          0.01024152  0.04445014
ses2        -0.81499026  0.89014587
ses3        -0.53951033  1.05825383
sector2      0.56319260  1.94992969
```

```
oreduced=glm(disease~age+sector,
       family=binomial(link=logit),
       data=d)

anova(oreduced,o,test="Chisq")
Analysis of Deviance Table

Model 1: disease ~ age + sector
Model 2: disease ~ age + ses + sector
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1       193     211.64
2       191     211.22  2   0.4193    0.8109
```

```
o=oreduced

anova(o,test="Chisq")
Analysis of Deviance Table

Model: binomial, link: logit

Response: disease

Terms added sequentially (first to last)


       Df Deviance Resid. Df Resid. Dev P(>|Chi|)
NULL                     195     236.33
age     1   12.013       194     224.32 0.0005283 ***
sector  1   12.677       193     211.64 0.0003702 ***
```

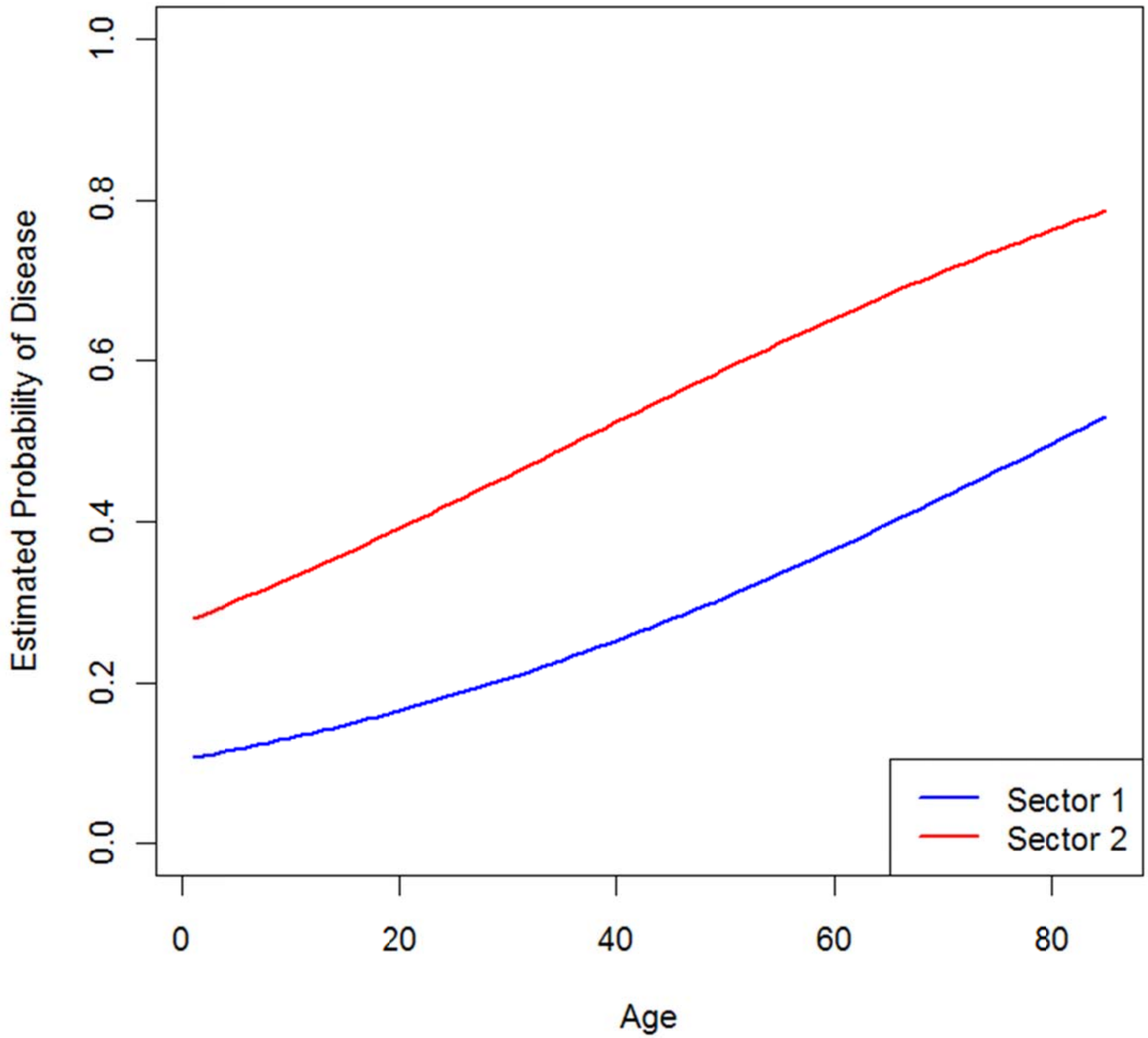
```
head(model.matrix(o))
  (Intercept) age sector2
1           1  33       0
2           1  35       0
3           1   6       0
4           1  60       0
5           1  18       0
6           1  26       0

b=coef(o)
b
(Intercept)         age     sector2
-2.15965912  0.02681289  1.18169345

ci=confint(o)
Waiting for profiling to be done...
ci
                  2.5 %      97.5 %
(Intercept) -2.86990940 -1.51605906
age          0.01010532  0.04421365
sector2      0.52854584  1.85407936
```

```
#How should we interpret our estimate of
#the slope coefficient on age?

exp(b[2])
     age
1.027176

#All else equal, the odds of disease are
#about 1.027 times greater for someone age
#x+1 than for someone age x. An increase of
#one year in age is associated with an
#increase in the odds of disease by about 2.7%.
#A 95% confidence interval for the multiplicative
#increase factor is

exp(ci[2,])
   2.5 %   97.5 %
1.010157 1.045206
```

```
#How should we interpret our estimate of
#the slope coefficient on sector?

exp(b[3])
sector2
3.25989

#All else equal, the odds of disease are
#about 3.26 times greater for someone
#living in sector 2 than for someone living
#in sector 1.

#A 95% confidence interval for the multiplicative
#increase factor is

exp(ci[3,])
   2.5 %   97.5 %
1.696464 6.385816
```

```
#Estimate the probability that a randomly
#selected 40-year-old living in sector 2
#has the disease.

x=c(1,40,1)

1/(1+exp(-t(x)%*%b))
          [,1]
[1,] 0.5236198

#Approximate 95% confidence interval
#for the probability in question.

sexb=sqrt(t(x)%*%vcov(o)%*%x)

cixb=c(t(x)%*%b-2*sexb,t(x)%*%b+2*sexb)

1/(1+exp(-cixb))

[1] 0.3965921 0.6476635
```

```
#Plot estimated probabilities as a function
#of age for each sector.

x=1:85
plot(x,1/(1+exp(-(b[1]+b[2]*x))),ylim=c(0,1),
     type="l",col=4,lwd=2,xlab="Age",
     ylab="Estimated Probability of Disease")
lines(x,1/(1+exp(-(b[1]+b[2]*x+b[3]))),col=2,lwd=2)
legend("bottomright",legend=c("Sector 1","Sector 2"),
       col=c(4,2),lwd=2)
```



1.0
0.8
0.6
0.4
0.2
0.0
Estimated Probability of Disease
0
20
40
60
80
Age
Sector 1
Sector 2