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- Introduction
- 2 Logistic Regression with a Single Predictor
 - Coronary Heart Disease
 - The Logistic Regression Model
 - Fitting with glm
 - Plotting Model Fit
 - Interpreting Model Coefficients
- Assessing Model Fit in Logistic Regression
 - The Deviance Statistic
 - Comparing Models
 - Test of Model Fit
- 4 Logistic Regression with Several Predictors
- Generalized Linear Models
- 6 Classification Via Logistic Regression
- Classifying Several Groups with Multinomial Logistic Regression

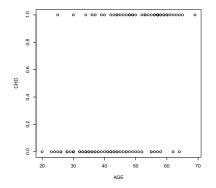
Introduction

- Logistic Regression deals with the case where the dependent variable is binary, and the conditional distribution is binomial.
- Recall that, for a random variable Y having a binomial distribution with parameters n (the number of trials), and p (the probability of "success", the mean of Y is np and the variance of Y is np(1-p).
- Therefore, if the conditional distribution of Y given a predictor X is binomial, then the mean function and variance functions will be necessarily related.
- Moreover, since, for a given value of n, the mean of the conditional distribution is necessarily bounded by 0 and n, it follows that a linear function will generally fail to fit at large values of the predictor.
- So, special methods are called for.



- As an example, consider some data relating age to the presence of coronary disease.
- The independent variable is the age of the subject, and the dependent variable is binary, reflecting the presence or absence of coronary heart disease.

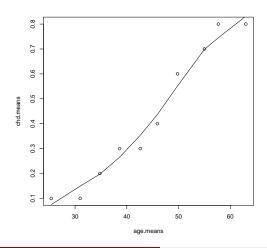
```
> chd.data <- read.table(
+ "http://www.statpower.net/R312/chdage.txt", header=T)
> attach(chd.data)
> plot(AGE,CHD)
```



- The general trend, that age is related to coronary heart disease, seems clear from the plot, but it is difficult to see the precise nature of the relationship.
- We can get a crude but somewhat more revealing picture of the relationship between the two variables by collecting the data in groups of ten observations and plotting mean age against the proportion of individuals with CHD.

```
> age.means <- rep(0,10)
> chd.means <- rep(0,10)
> for(i in 0:9)age.means[i+1]<-mean(
+ chd.data[(10*i+1):(10*i+10),2])
> age.means
[1] 25.4 31.0 34.8 38.6 42.6 45.9 49.8 55.0 57.7 63.0
> for(i in 0:9)chd.means[i+1]<-mean(
+ chd.data[(10*i+1):(10*i+10),3])
> chd.means
[1] 0.1 0.1 0.2 0.3 0.3 0.4 0.6 0.7 0.8 0.8
```

```
> plot(age.means,chd.means)
> lines(lowess(age.means,chd.means,iter=1,f=2/3))
```



- For notational simplicity, suppose we have a single predictor, and define p(x) = Pr(Y = 1|X = x) = E(Y|X = x).
- Suppose that, instead of the probability of heart disease, we consider the odds as a function of age.
- Odds range from zero to infinity, so the problem fitting a linear model to the upper asymptote can be eliminated.
- If we go one step further and consider the logarithm of the odds, we now have a dependent variable that ranges from $-\infty$ to $+\infty$.

- Suppose we try to fit a linear regression model to the log-odds variable.
- Our model would now be

$$logit(p(x)) = log\left(\frac{p(x)}{1 - p(x)}\right) = \beta_0 + \beta_1 x \tag{1}$$

If we can successfully fit this linear model, then we also have successfully fit a nonlinear model for p(x), since the logit function is invertible, so after taking $\log it^{-1}$ of both sides, we obtain

$$p(x) = \operatorname{logit}^{-1}(\beta_0 + \beta_1 x) \tag{2}$$

where

$$\log it^{-1}(w) = \frac{\exp(w)}{1 + \exp(w)} = \frac{1}{1 + \exp(-w)}$$
(3)

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The above system generalizes to more than one predictor, i.e.,

$$p(\mathbf{x}) = \mathsf{E}(Y|X = \mathbf{x}) = \mathsf{logit}^{-1}(\beta'\mathbf{x}) \tag{4}$$

- It turns out that the system we have just described is a special case of what is now termed a *generalized linear model*.
- In the context of generalized linear model theory, the logit function that "linearizes" the binomial proportions $p(\mathbf{x})$ is called a *link function*.
- In this module, we shall pursue logistic regression primarily from the practical standpoint of obtaining estimates and interpreting the results.
- Logistic regression is applied very widely in the medical and social sciences, and entire books on applied logistic regression are available.

Fitting with glm

- Fitting a logistic regression model in R is straightforward.
- You use the glm function and specify the binomial distribution family and the logit link function.

Fitting with glm

```
> fit.chd <- glm(CHD ~AGE, family=binomial(link="logit"))
> summarv(fit.chd)
Call:
glm(formula = CHD ~ AGE, family = binomial(link = "logit"))
Deviance Residuals:
   Min
            10 Median 30
                                   Max
-1.9407 -0.8538 -0.4735 0.8392 2.2518
Coefficients:
          Estimate Std. Error z value Pr(>|z|)
(Intercept) -5.12630 1.11205 -4.61 4.03e-06 ***
AGE.
          Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '. 0.1 ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 136.66 on 99 degrees of freedom
Residual deviance: 108.88 on 98 degrees of freedom
AIC: 112.88
```

= 900 €

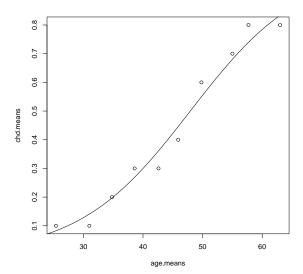
Number of Fisher Scoring iterations: 4

Plotting Model Fit

- Remember that the coefficient estimates are for the transformed model. They provide a linear fit for logit(p(x)), not for p(x).
 However, if we define an inverse logit function, we can transform our model back to the original metric.
- Below, we plot the mean AGE against the mean CHD for groups of 10 observations, then superimpose the logistic regression fit, transformed back into the probability metric.

```
> pdf("Scatterplot02.pdf")
> logit.inverse <- function(x){1/(1+exp(-x))}
> plot(age.means,chd.means)
> lines(AGE,logit.inverse(predict(fit.chd)))
```

Plotting Model Fit



Binary Predictor

- Suppose there is a single predictor, and it is categorical (0,1). How can one interpret the coefficient β_1 ?
- Consider the *odds ratio*, the ratio of the odds when x = 1 to the odds when x = 0.
- According to our model, $logit(p(x)) = exp(\beta_0 + \beta_1 x)$, so the log of the odds ratio is given by

$$\log(OR) = \log \left[\frac{p(1)/(1-p(1))}{p(0)/(1-p(0))} \right]$$

$$= \log \left[p(1)/(1-p(1)) \right] - \log \left[p(0)/(1-p(0)) \right]$$

$$= \log it(p(1)) - \log it(p(0))$$

$$= \beta_0 + \beta_1 \times 1 - (\beta_0 + \beta_1 \times 0)$$

$$= \beta_1$$
(5)

Binary Predictor

Exponentiating both sides, we get

$$OR = \exp(\beta_1) \tag{6}$$

- Suppose that X represents the presence or absence of a medical treatment, and $\beta_1=2$. This means that the odds ratio is $\exp(2)=7.389$. If the event is survival, this implies that the odds of surviving are 7.389 times as high when the treatment is present than when it is not.
- You can see why logistic regression is very popular in medical research, and why there is a tradition of working in the "odds metric."

Continuous Predictor

- In our coronary heart disease data set, the predictor is continuous.
- Interpreting model coefficients when a predictor is continuous is more difficult.
- Recalling the form of the fitted function for p(x), we see that it does not have a constant slope.
- By taking derivatives, we compute the slope as $\beta_1 p(x)(1-p(x))$. Hence, the steepest slope is at p(x)=1/2, at which $x=-\beta_0/\beta_1$, and the actual slope is $\beta_1/4$.
- In toxicology, this is called LD_{50} , because it is the dose at which the probability of death is 1/2.

Continuous Predictor

- So a rough "rule of thumb" is that when X is near the middle of its range, a unit change in X results in a change of $\beta_1/4$ units in p(x).
- More precise calculations can be achieved with the aid of R and the logit⁻¹ function.

Continuous Predictor

Example (CHD vs. AGE)

- We saw that, in our CHD data, the estimated value of β_1 is 0.1069, and the estimated value of β_0 is -5.1263.
- This suggests that, around the age of 45, an increase of 1 year in AGE corresponds roughly to an increase of 0.0267 in the probability of coronary heart disease.
- Let's do the calculations by hand, using R.

Continuous Predictor

- The numbers demonstrate that, in the "linear zone" near the center of the plot, the rule of thumb works quite well.
- The rule implies that for every increase of 4 units in AGE, there will be roughly a β_1 increase in the probability of coronary heart disease.
- We can simplify the calculations on the preceding slide by using the predict function on the fit object.

Continuous Predictor

Example (CHD vs. AGE)

- Suppose we wish to obtain predicted probabilities for ages 45 through 50.
- We set up a data frame with the new AGE data. Note that you must use the exact same name as the predictor variable in the data frame you analyzed.

```
> my.data <- data.frame(45:50)
> colnames(my.data) <- c("AGE")
> rownames(my.data) <- as.character(my.data$AGE)</pre>
```

- Using the predict function is straightforward.
- However, to obtain the values in the correct (probability) metric, we must remember to use the type = "response" option!

Assessing Model Fit in Logistic Regression

Deviance

- In multiple linear regression, the residual sum of squares provides the basis for tests for comparing mean functions.
- In logistic regression, the residual sum of squares is replaced by the *deviance*, which is often called G^2 . Suppose there are k data groupings based on $n_i, i = 1, \ldots, k$ binomial observations. The deviance is defined for logistic regression to be

$$G^{2} = 2\sum_{i=1}^{k} \left[y_{i} \log \left(\frac{y_{i}}{\hat{y}_{i}} \right) + (n_{i} - y_{i}) \log \left(\frac{n_{i} - y_{i}}{n_{i} - \hat{y}_{i}} \right) \right]$$
(7)

where $\hat{y}_i = n_i \hat{p}(\mathbf{x}_i)$ are the fitted numbers of successes in n_i trials in the *i*th grouping.

• The degrees of freedom associated with the analysis is the number of groupings n used in the calculation minus the number of free parameters in β that were estimated.

Comparing Models

- Comparing models in logistic regression is similar to regular linear regression.
- For two nested models, the difference in deviances is treated as a chi-square with degrees of freedom equal to the difference in the degrees of freedom for the two models.

Test of Model Fit

- When the number of trials $n_i > 1$, the deviance G^2 can be used to provide a goodness-of-fit test for a logistic regression model.
- The test compares the null hypothesis that the mean function used is adequate versus the alternative that a separate parameter needs to be fit for each value of i (this latter case is called the saturated model).
- When all the n_i are large enough, G^2 can be compared with the χ^2_{n-p} distribution to get an approximate p-value.

Test of Model Fit

• An alternative statistic is the Pearson X^2

$$X^{2} = \sum_{i=1}^{k} \left[(y_{i} - \hat{y}_{i})^{2} \left(\frac{1}{\hat{y}_{i}} + \frac{1}{n_{i} - \hat{y}_{i}} \right) \right]$$
$$= \sum_{i=1}^{k} \frac{n_{i}(y_{i}/n_{i} - \hat{\theta}(\mathbf{x}_{i}))^{2}}{\hat{\theta}(\mathbf{x}_{i})(1 - \hat{\theta}(\mathbf{x}_{i}))}$$
(8)

• According to ALR, X^2 and G^2 have the same large-sample distribution and often give the same inferences. But in small samples, there may be differences, and sometimes X^2 may be preferred for testing goodness-of-fit.

- As an example of logistic predictors, Weisberg presents data from the famous Titanic disaster. (Frank Harrell presents a much more detailed analysis of the Titanic in his superb book *Regression Modeling* Strategies).
- Of 2201 known passengers and crew, only 711 are reported to have survived.
- The data in the file titanic.txt from Dawson (1995) classify the people on board the ship according to their Sex as Male or Female, Age, either child or adult, and Class, either first, second, third, or crew.
- Not all combinations of the three factors occur in the data, since no children were members of the crew. For each age/sex/class combination, the number of people M and the number surviving Surv are also reported.
- The data are shown in Table 12.5.

TABLE 12.5 Data from the Titanic Disaster of 1912. Each Cell Gives Surv/M, the Number of Survivors, and the Number of People in the Cell

	Female		Male	
Class	Adult	Child	Adult	Child
Crew	20/23	NA	192/862	NA
First	140/144	1/1	57/175	5/5
Second	80/93	13/13	14/168	11/11
Third	76/165	14/31	75/462	13/48

- ALR fits a sequence of 5 models to these data.
- Since almost all the m_i exceed 1, we can use either G^2 or X^2 as a goodness-of-fit test for these models.
- The first two mean functions, the main effects only model, and the main effects plus the ${\it Class} \times {\it Sex}$ interaction, clearly do not fit the data because the values of ${\it G}^2$ and ${\it X}^2$ are both much larger then their df, and the corresponding ${\it p}$ -values from the χ^2 distribution are 0 to several decimal places.
- The third model, which adds the Class × Age interaction, has both G² and X² smaller than its df, with p-values of about 0.64, so this mean function seems to match the data well.
- Adding more terms can only reduce the value of G^2 and X^2 , and adding the third interaction decreases these statistics to 0 to the accuracy shown.
- Adding the three-factor interaction fits one parameter for each cell, effectively estimating the probability of survival by the observed probability of survival in each cell. This will give an exact fit to the data.

```
> library(alr3)
Loading required package:
                             car
> library(xtable)
> mysummary <- function(m){c(df=m$df.residual,G2=m$deviance,
                               X2=sum(residuals(m,type="pearson")^2) )}
> m1 <- glm(cbind(Surv,N-Surv)~Class+Age+Sex, data=titanic, family=binomial())
> m2 <- update(m1,~.+Class:Sex)</pre>
> m3 <- update(m2,~.+Class:Age)</pre>
> m4 <- update(m3,~.+Age:Sex)</pre>
> m5 <- update(m4,~Class:Age:Sex)</pre>
> ans <- mysummary(m1)</pre>
> ans <- rbind(ans,mysummary(m2))</pre>
> ans <- rbind(ans,mysummary(m3))</pre>
> ans <- rbind(ans,mysummary(m4))</pre>
> ans <- rbind(ans,mysummary(m5))</pre>
> row.names(ans) <- c( "Main effects only",
+ "Main Effects + Class:Sex",
+ "Main Effects + Class:Sex + Class:Age",
+ "Main Effects + All 2 Factor Interactions",
+ "Main Effects + All 2 and 3 Factor Interactions")
```

```
> options(scipen=1.digits=3)
> summary(m3)
glm(formula = cbind(Surv, N - Surv) ~ Class + Age + Sex + Class:Sex +
   Class: Age, family = binomial(), data = titanic)
Deviance Residuals:
0.0000 0.0000 0.0000 0.0001 0.0000 0.0000
         8
                     9
                            10
0.0000 0.0001 0.0000 0.0000 -0.8745 0.8265
  13 14
0.3806 -0.3043
Coefficients: (1 not defined because of singularities)
                    Estimate Std. Error z value
(Intercept)
                    1.897
                                 0.619 3.06
ClassFirst
                      1.658
                                 0.800 2.07
ClassSecond
                     -0.080
                                 0.688 -0.12
ClassThird
                     -2 115
                                0 637 -3 32
AgeChild
                      0.338
                                0.269 1.26
SexMale
                     -3.147
                                 0.625 -5.04
ClassFirst:SexMale
                     -1.136
                                 0.821 -1.38
ClassSecond:SexMale
                    -1.068
                                 0.747 -1.43
ClassThird:SexMale
                      1.762
                                 0.652
ClassFirst:AgeChild
                     22.424 16495.727
ClassSecond: AgeChild 24.422 13007.888
                                        0.00
ClassThird:AgeChild
                       NΔ
                   Pr(>|z|)
                    0.0022 **
(Intercept)
                    0.0383 *
ClassSecond
                    0.9073
ClassThird
                    0.0009 ***
                    0.2094
SexMale
ClassFirst:SexMale
                    0.1662
ClassSecond: SexMale
                    0.1525
                    0.0069 **
ClassThird:SexMale
ClassFirst:AgeChild
                    0.9989
ClassSecond: AgeChild 0.9985
ClassThird:AgeChild
Signif. codes: 0 '*** 0.001 '** 0.01 '* 0.05 '. 0.1 ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 671.9622 on 13 degrees of freedom
Residual deviance: 1.6854 on 3 degrees of freedom
AIC: 70.31
Number of Fisher Scoring iterations: 21
```

The Titanic Disaster

> xtable(ans)

	df	G2	X2
Main effects only	8.00	112.57	103.83
$Main\;Effects + Class : Sex$	5.00	45.90	42.77
${\sf Main\ Effects+Class:Sex+Class:Age}$	3.00	1.69	1.72
Main Effects + All 2 Factor Interactions	2.00	0.00	0.00
Main Effects + All 2 and 3 Factor Interactions		0.00	0.00

Generalized Linear Models

- Both the multiple linear regression model discussed earlier in this book and the logistic regression model discussed in this chapter are particular instances of a generalized linear model.
- Generalized linear models all share three basic characteristics:

Generalized Linear Models

- The distribution of the response Y, given a set of terms X, is distributed according to an exponential family distribution. The important members of this class include the normal and binomial distributions we have already encountered, as well as the Poisson and gamma distributions.
- ② The response Y depends on the terms X only through the linear combination $\beta'\mathbf{X}$.
- **3** The mean $E(Y|X=x)=m(\beta'x)$ for some kernel mean function m. For the multiple linear regression model, m is the identity function, and for logistic regression, it is the logistic function. There is considerable flexibility in selecting the kernel mean function. Most presentations of generalized linear models discuss the link function, which technically is defined as the *inverse* of m rather than m itself.

- In some previous lectures, we discussed *discriminant analysis* and its use as a method of *classification*.
- Since binary logistic regression provides a predicted probability of the two binary outcomes, one may classify observations using logistic regression, as we demonstrate in the following example.
- We download some data representing measurements of human skulls dating back to ancient Egypt.
- This subset of the original data set may be downloaded from the website.

```
> Egypt <- read.csv(
+ "http://www.statpower.net/R312/Egypt.csv"
+ )</pre>
```

Egyptian Skull Data

Below is the key information on the data

```
> names(Egypt)
[1] "Group" "mb"     "bh"     "bl"     "nh"
> #Group 1 = circa 4000 BC
> #Group 2 = circa 3300 BC
> #mb: maximum breadth of the skull.
> #bh: basibregmatic height of the skull.
> #bl: basialiveolar length of the skull.
> #nh: nasal heights of the skull.
```

Egyptian Skull Data

 We predict the probabilities for membership in the 4000 B.C. or 3300 B.C. epochs from the skull measurements.

```
> Egypt$Group <- Egypt$Group-1 #convert to binary variable
> fit <- glm(Group ~ .. data = Egypt, family=binomial(link="logit"))
> summary(fit)
Call:
glm(formula = Group ~ ., family = binomial(link = "logit"), data = Egypt)
Deviance Residuals:
   Min
             10 Median
                                     Max
-1.4402 -1.1406 -0.0959 1.1515
                                 1.4905
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) 1.83842 10.97726 0.17
                                        0.87
           0.05763 0.05791 1.00 0.32
mb
         -0.04345 0.06064 -0.72 0.47
bh
b1
          -0.00904 0.05210 -0.17 0.86
                     0.10147 -0.54 0.59
nh
          -0.05468
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 83.178 on 59 degrees of freedom
Residual deviance: 81.492 on 55 degrees of freedom
ATC: 91.49
Number of Fisher Scoring iterations: 4
```

Egyptian Skull Data

- None of the coefficients is statistically significant, suggesting that this logistic regression will not do a very good job of classifying the skulls.
- We can produce a classification table in a very straightforward manner from the fit object.
- As expected, the performance is not much better than chance.

```
> Class <- predict(fit,type="response")>.5
> table(Egypt$Group,Class)

Class
   FALSE TRUE
0   18  12
1  14  16
```

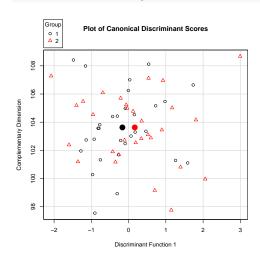
Egyptian Skull Data

Let's try discriminant analysis on the data and see what happens.

• The plot of the scores on the next slide shows that there is not much separation between the groups in discriminant space.

Egyptian Skull Data

```
> D <- Make.D(Group)
> H <- Make.H(Group)
> Plot.Discriminant.Scores(x,D,H,Group)
```



Egyptian Skull Data

• The canonical table confirms the lack of statistical significance.

• In their sign and relative size, the standardized discriminant weights closely match the pattern of the logistic regression weights.

```
> print(Standardized.Discriminant.Weights(x,D,H))
   mb   bh   bl   nh
0.832 -0.577 -0.138 -0.457
```

Egyptian Skull Data

- The bottom line is that in quite a few situations, logistic regression will produce results similar to linear discriminant analysis.
- Logistic regression, however, makes fewer statistical assumptions. It does not require continuous predictors, and it therefore naturally does not require multivariate normality.

Multinomial Logistic Regression

Football Data

- The binary logistic regression model involving two outcomes generalizes to the multinomial logistic regression model.
- A rudimentary procedure to fit multinomial regression models is available in the nnet library.
- Here we quickly demonstrate classifying the football data.

Multinomial Logistic Regression

Football Data

Here is the code.

```
> fb.data <- read.table(
    "http://www.statpower.net/R312/football.txt",header=T,sep=",")
> names(fb.data)
[1] "GROUP" "WDIM"
                     "CIRCUM" "FBEYE" "EYEHD"
[6] "EARHD" "JAW"
> library(nnet)
> mod <- multinom(GROUP ~.,fb.data)
# weights: 24 (14 variable)
initial value 98.875106
iter 10 value 53.052168
iter 20 value 51 037137
iter 30 value 50.193419
iter 40 value 50.102582
iter 50 value 50.086496
final value 50.072216
converged
> table(fb.data$GROUP.predict(mod))
  1 27 2 1
  2 1 20 9
 3 2 8 20
```

Multinomial Logistic Regression

Football Data

```
> summary(mod)
Call:
multinom(formula = GROUP ~ ., data = fb.data)
Coefficients:
  (Intercept) WDIM CIRCUM FBEYE EYEHD EARHD JAW
    26.4 3.91 -0.259 1.6 -2.31 -1.89 -4.13
        21.6 5.21 -0.435 1.7 -1.58 -2.05 -5.19
Std. Errors:
  (Intercept) WDIM CIRCUM FBEYE EYEHD EARHD JAW
        5.44 1.97 0.519 1.31 0.650 0.869 1.98
        5.87 1.98 0.489 1.28 0.604 0.852 1.98
Residual Deviance: 100
ATC: 128
```