Logistic Regression Ch5

F.A. BarriosInstituto de Neurobiología UNAM

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```
library(tidyverse)
library(here)
library(wesanderson)
library(rstatix)
library(HSAUR2)
library(car)
library(multcomp)

setwd("~/Dropbox/GitHub/Class2020")
wcgs <- read_csv("DataRegressBook/Chap2/wcgs.csv")
```

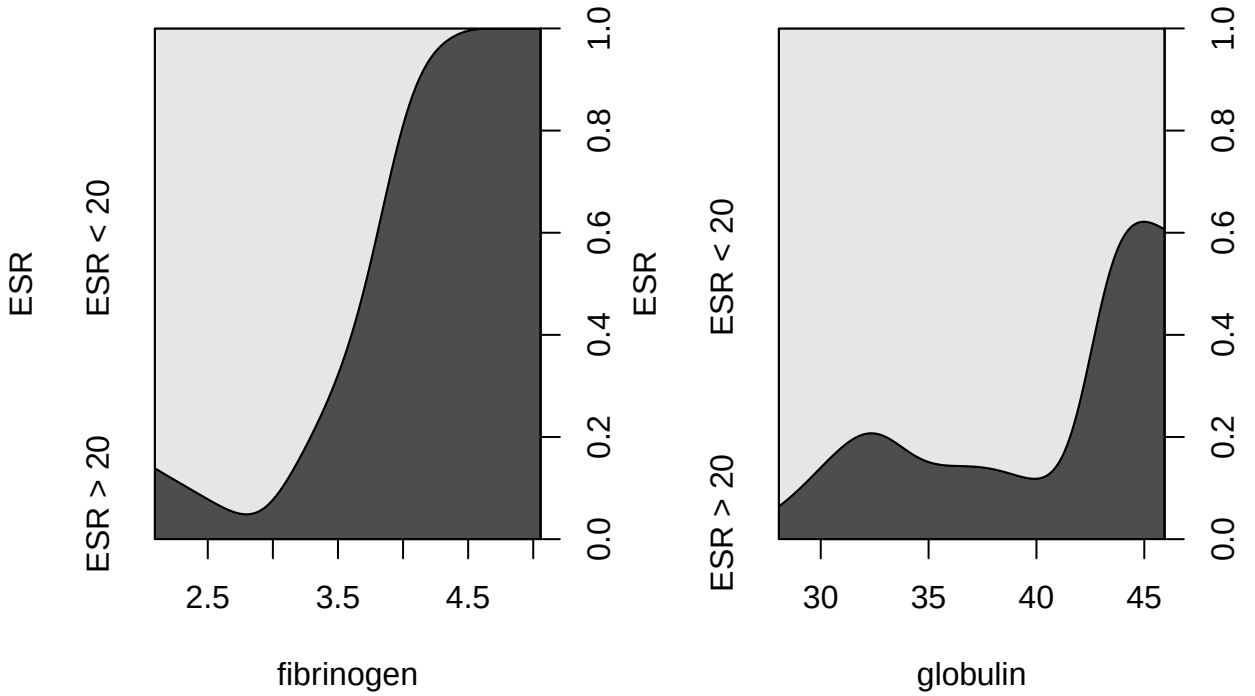
Logistic Regression

Example from HSAUR (Chapter 7, in HSAUR3)

Introduction

The erythrocyte sedimentation rate (ESR) is the rate at which red blood cells (erythrocytes) settle out of suspension in the blood plasma, when measured under standard conditions. If the ESR increases when the level of certain proteins in the blood plasma rise in association with conditions such as rheumatic diseases, chronic infections, and malignant diseases, its determination might be useful in screening blood samples taken from people suspected of suffering from one of the conditions mentioned. The absolute value of the ESR is not of great importance; rather, less than 20mm/hr indicates a 'healthy' individual. To asses whether the ESR is a useful diagnostic tool, Collett and Jemain (1985) collected the data in HSAUR2. The question of interest is whether there is any association between the probability of an ESR reading greater than 20mm/hr and the levels of the two plasma proteins. If there is not then the determination of ESR would not be useful for diagnostic purposes.

```
# Using plasma data from HSAUR
data("plasma", package = "HSAUR2")
layout(matrix(1:2, ncol = 2))
# cdplot computes and plots conditional densities describing how the conditional distribution of a cate
cdplot(ESR ~ fibrinogen, data = plasma)
cdplot(ESR ~ globulin, data = plasma)
```



To estimate a logistic regression model in R the glm (General Linear Model) is used, for binomial distribution the glm() function defalut to a logistic model.

```
# glm general linear model default is logistic for binomial distribution

plasma_glm01 <- glm(ESR ~ fibrinogen, data = plasma, family = binomial())
summary(plasma_glm01)
```

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

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.9298  -0.5399  -0.4382  -0.3356   2.4794

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -6.8451     2.7703  -2.471   0.0135 *
fibrinogen    1.8271     0.9009   2.028   0.0425 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(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
```

From these results we see that the regression coefficients for fibrinogen is significant at the 5% level. An increase of one unit in this variable increases the log-odds on favor of an ESR value greater then 20 by estimated 1.83 with 95% confidence interval:

```r
# coeff fibrinogen is sifnificative 5%
# one unit change in this variable increases the log-odds in favor of ESR > 20mm/hr by 1.83
confint(plasma_glm01, parm = "fibrinogen")
```

```
    2.5 %    97.5 %
0.3387619 3.9984921
```

```r
exp(coef(plasma_glm01)["fibrinogen"])
```

```
fibrinogen
  6.215715
```

```r
exp(confint(plasma_glm01, parm = "fibrinogen"))
```

```
    2.5 %    97.5 %
 1.403209 54.515884
```

These are the values of the odds themselves (by exponentiating the estimate). So **increased values of fibrinogen lead to a grater probability of an ESR value greater than 20**.

```r
# full model with two variables
plasma_glm02 <- glm(ESR ~ fibrinogen + globulin, data = plasma, family = binomial())
summary(plasma_glm02)
```

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

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.9683  -0.6122  -0.3458  -0.2116   2.2636

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -12.7921     5.7963  -2.207   0.0273 *
fibrinogen    1.9104     0.9710   1.967   0.0491 *
globulin      0.1558     0.1195   1.303   0.1925
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(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: 28.971

Number of Fisher Scoring iterations: 5
```

Comparing the residual deviance of the models: residual deviance 01: 24.84 residual deviance 02: 22.971 -> 1.869 (1.87), to test for significance R take the lgm with a χ^2 the 1.87 we conclude that **the globulin has no influence in the ESR**. To compare the two nested models (with fibrinogen and fibrinogen + gamma globulin) we can estimate the ANOVA of the models (Pr of 0.1716)

```r
anova(plasma_glm01, plasma_glm02, test = "Chisq")
```

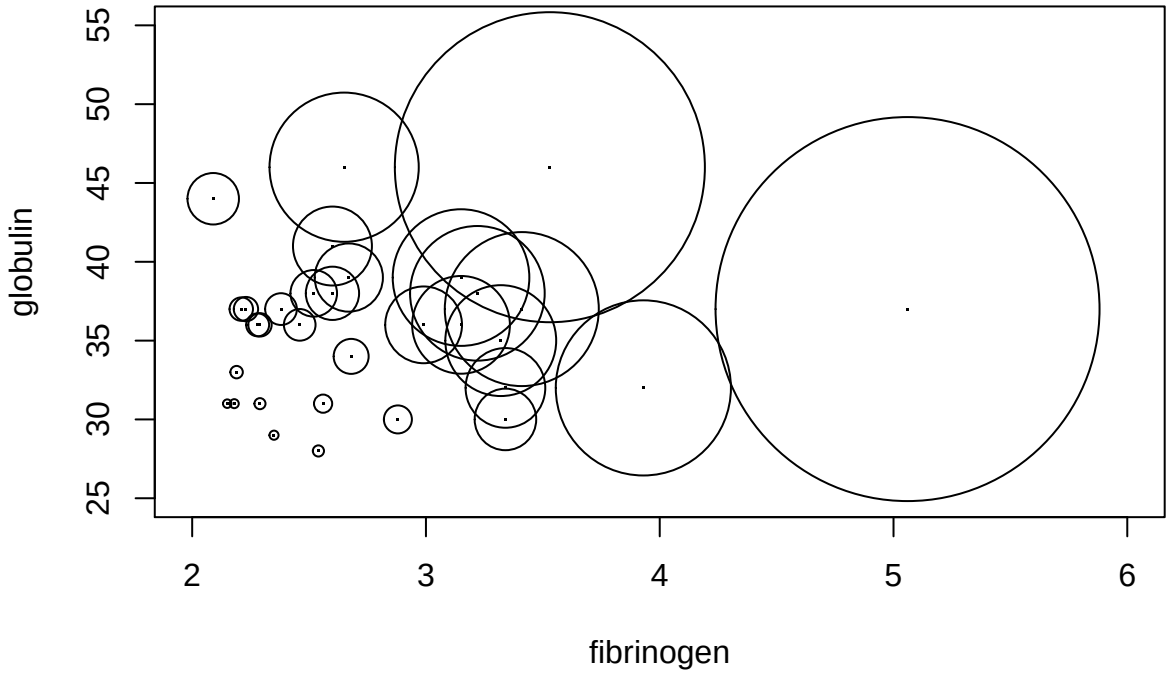
```
Analysis of Deviance Table
```

```
Model 1: ESR ~ fibrinogen
Model 2: ESR ~ fibrinogen + globulin
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1        30     24.840
2        29     22.971  1   1.8692   0.1716
```

```r
# Estimates conditional probability of a ESR > 20 for all observations

prob <- predict(plasma_glm02, type = "response")
layout(matrix(1:1, ncol = 1))

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



##

Single predictor models

In the linear model the "expected value" of the $Y|x$ is estimated with a simple linear model

$$E[y|x] = \beta_0 + \beta_1$$

And to model a function that has a binary outcome, in particular if we assign the expected value $E[y|x]$ to the observed proportion ($P(x)$) of a variable given x that take the fomr of a simple linear model in x

$$P(x) = E[y|x] = \beta_0 + \beta_1 x$$

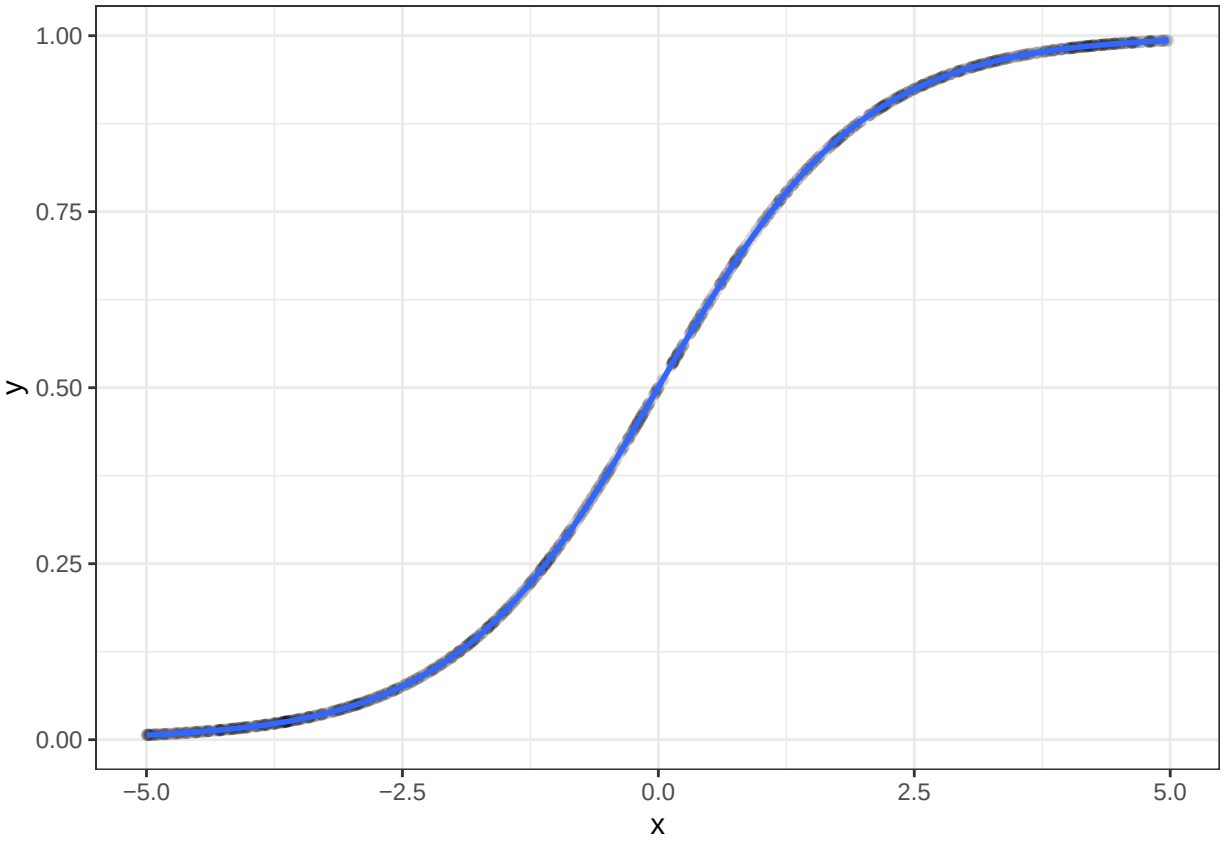
At this equation if x is a binary predictor taking on the values 0 or 1, $P(0) = \beta_0 + \beta_1(0)$ and $P(1) = \beta_0 + \beta_1(1)$, then $P(0) - P(1) = \beta_1$ therefore the effect of increasing x one unit is to add an increment β_1 to the outcome. This is the risk difference associated with a unit increase in x. Models with this property are often referred to as *additive risk models*.

The statistical machinery which allowed us to use this linear model to make inferences about the strength of relationship in expected value $E[y|x]$ linear model,required that the outcome variable follow an approximate normal distribution. For binary outcome, this assumption is incorret. And, the outcome in the model that we are studing now represents a probability or risk. Thus, any estimates of the regression coefficients must constrain the estimated probability to lie between zero and one for the model to make sense. $P(x) = E[y|x]$.

The smooth S-shaped curve in the following plot is known as the logistic model. The exponential model is also known as log linear because it specifies that the logarithm of the outcome risk is linear in x

```r
# generate fake data
set.seed(42)
n <- 1000
x <- (runif(n) * 10) - 5
y <- (exp(x) / (1 + exp(x)))
df <- data.frame(x = x, y = y)

# Logistic plot
p1 <- ggplot(df, aes(x, y)) +
    geom_point(alpha = 0.1) +
    geom_smooth(se = FALSE) +
    theme_bw()
p1
```



The logistic model allows for a smooth change in risk throughout the range of x, and has the property that risk increases slowly up to a "threshold" range of x. The mathematical model is the folowing for a simple linear model

$$P(x) = \frac{e^{(\beta_0+\beta_1 x)}}{1 + e^{(\beta_0+\beta_1 x)}}$$

in terms of the odds of the outcome associated with the predictor x, the model can also be expressed as

$$\frac{P(x)}{1 - P(x)} = e^{(\beta_0+\beta_1 x)}$$

If x takes the values 0 or 1 (binary predictor), the ratio of the odds for these two values are

$$\frac{\frac{P(1)}{1-P(1)}}{\frac{P(0)}{1-P(x)}} = \frac{e^{(\beta_0+\beta_1)}}{e^{\beta_0}} = e^{\beta_1}$$

Therefore the logit model ia a "multiplicative risk model". The most widely used model for binary outcomes in clinical and epidemiological applications, and forms the basis of logistic regression modeling. The random part of the model specifies the distribution of the outcome variable y_i, conditional on the observed value x_i of the predictor (where the subscript i denotes the value for a particular subject). For binary outcomes, this distribution is called the binomial distribution and is completely specified by the mean of yi conditional on the value x_i. To summarize, the logistic model makes the following assumptions about the outcome y_i:

1. y_i follows a Binomial distribution
2. The mean $E[y|x] = P(x)$ is given by the logistic function
3. Values of the outcome are statistically independent

Interpretation of Regression Coefficients

So, the estimated logistic-regression model is given by

$$log[\frac{\hat{\mu}(x)}{1-\hat{\mu}(x)}] = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_k x_k$$

If exponentiate both sides of the equation, we get

$$\frac{\hat{\mu}(x)}{1-\hat{\mu}(x)} = exp(\beta_0) \times exp(\beta_1 x_1) \times exp(\beta_2 x_2) \times \cdots \times exp(beta_k x_k)$$

where the left hadn of the equation, $\frac{\hat{\mu}(x)}{1-\hat{\mu}(x)}$, gives the *fitted odds* of success, **the fitted probability of success divided by the fitted probability of failure**. Exponentiating the model removes the logarithms and vhanges the model in the log-odds scale to one that is multiplicative, in this log odds scale.

For the WCGS data and the variable Corollary Heart Disease (CHD) and age, the β_1 is the age slope of the fitted logistic model. The outcome of the model is the log odds of CHD risk and the relationship with age is linear, the slope coefficient β_1 gives the change in the log odds of chd69 associated with

```
wcgs <- mutate(wcgs, chd69 = factor(chd69))
# For table 5.2
CHD_glm01 <- glm(chd69 ~ age, data = wcgs, family = binomial())
S(CHD_glm01)
```

```
Call: glm(formula = chd69 ~ age, family = binomial(), data = wcgs)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -5.93952    0.54932 -10.813  < 2e-16 ***
age          0.07442    0.01130   6.585 4.56e-11 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1781.2  on 3153  degrees of freedom
Residual deviance: 1738.4  on 3152  degrees of freedom
```

```
 logLik      df     AIC     BIC
-869.18       2 1742.36 1754.47

Number of Fisher Scoring iterations: 5

Exponentiated Coefficients and Confidence Bounds
               Estimate        2.5 %      97.5 %
(Intercept) 0.002633304 0.0008898193 0.007676359
age         1.077261913 1.0536638869 1.101432899
```

```
#confint(CHD_glm01, parm = "age")

exp(coef(CHD_glm01)["age"])
```

```
     age
1.077262
```

```
# To estimate the model

##################### From car
# carData Mroz
# lfp labor force participation
# k5 number of children ages 5 and younger
# k618 number of children ages 6 to 18
# age
# wc wife's college attendance
# hc husband's college attendance
# lwg log of estimated wife's wage
# inc family income excluding wife's income

summary(Mroz)
```

```
  lfp            k5              k618            age          wc        hc
 no :325   Min.   :0.0000   Min.   :0.000   Min.   :30.00   no :541   no :458
 yes:428   1st Qu.:0.0000   1st Qu.:0.000   1st Qu.:36.00   yes:212   yes:295
           Median :0.0000   Median :1.000   Median :43.00
           Mean   :0.2377   Mean   :1.353   Mean   :42.54
           3rd Qu.:0.0000   3rd Qu.:2.000   3rd Qu.:49.00
           Max.   :3.0000   Max.   :8.000   Max.   :60.00
      lwg               inc
 Min.   :-2.0541   Min.   :-0.029
 1st Qu.: 0.8181   1st Qu.:13.025
 Median : 1.0684   Median :17.700
 Mean   : 1.0971   Mean   :20.129
 3rd Qu.: 1.3997   3rd Qu.:24.466
 Max.   : 3.2189   Max.   :96.000
```

```
mroz.mod <- glm(lfp ~ k5 + k618 + age + wc + hc + lwg + inc, family=binomial, data=Mroz)
S(mroz.mod)
```

```
Call: glm(formula = lfp ~ k5 + k618 + age + wc + hc + lwg + inc, family =
          binomial, data = Mroz)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  3.182140   0.644375   4.938 7.88e-07 ***
```

```
k5          -1.462913   0.197001  -7.426 1.12e-13 ***
k618        -0.064571   0.068001  -0.950 0.342337
age         -0.062871   0.012783  -4.918 8.73e-07 ***
wcyes        0.807274   0.229980   3.510 0.000448 ***
hcyes        0.111734   0.206040   0.542 0.587618
lwg          0.604693   0.150818   4.009 6.09e-05 ***
inc         -0.034446   0.008208  -4.196 2.71e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1029.75  on 752  degrees of freedom
Residual deviance:  905.27  on 745  degrees of freedom

 logLik      df     AIC     BIC
-452.63       8  921.27  958.26

Number of Fisher Scoring iterations: 4

Exponentiated Coefficients and Confidence Bounds
              Estimate     2.5 %     97.5 %
(Intercept) 24.0982799 6.9377228 87.0347916
k5           0.2315607 0.1555331  0.3370675
k618         0.9374698 0.8200446  1.0710837
age          0.9390650 0.9154832  0.9625829
wcyes        2.2417880 1.4347543  3.5387571
hcyes        1.1182149 0.7467654  1.6766380
lwg          1.8306903 1.3689201  2.4768235
inc          0.9661401 0.9502809  0.9814042
```