Logistic Regression

Mona Maher

September 5, 2019

```r
logd<-read.csv(file.choose(), header = T)
attach(logd)
View(logd)
```

```r
tab_sex<-table(logd$SEX, logd$Treatment)
tab_sex
```

```
##
##          Newdrug Placebo
##   Female      46      45
##   Male         4       5
```

```r
chisq.test(tab_sex)
```

```
## Warning in chisq.test(tab_sex): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tab_sex
## X-squared = 0, df = 1, p-value = 1
```

```r
tab_sex1<-table(logd$SEX, logd$outcome)
chisq.test(tab_sex1)
```

```
## Warning in chisq.test(tab_sex1): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test with Yates' continuity correction
##
## data:  tab_sex1
## X-squared = 0.68114, df = 1, p-value = 0.4092
```

```r
x<-hist(tab_sex)
curve(dchisq(x,df = 1), col = "red", add = T)
```

Histogram of tab_sex
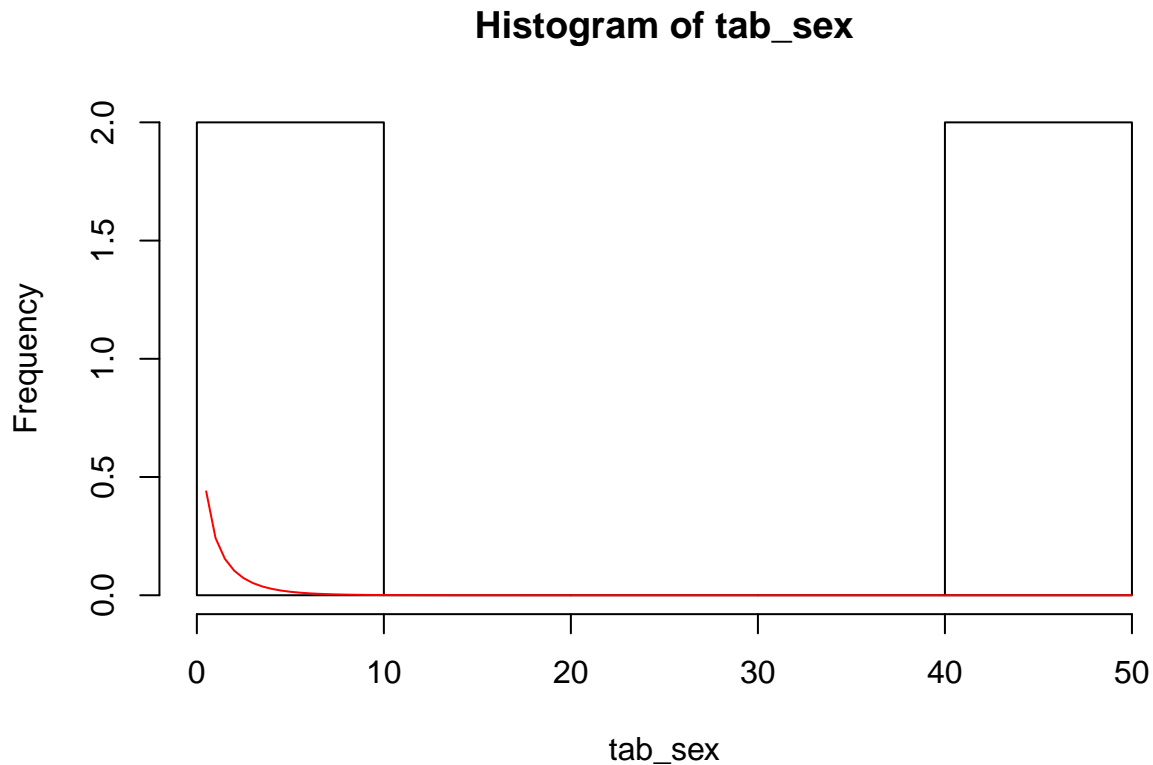
- p_value > 0.05 fail to reject null hypothesis there is no association between treatment and sex - no association between outcome and sex

```r
dummy_sex<- ifelse(logd$SEX == "Female", 0, 1)
dummy_ttt<-ifelse(logd$Treatment == "Placebo", 0, 1)
dummy_out<-ifelse(logd$outcome == "Failure", 0, 1)
logd1<- cbind(dummy_sex, dummy_ttt, dummy_out, logd)
View(logd1)
scatter.smooth(Treatment, outcome)
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : pseudoinverse used at 0.995

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : neighborhood radius 1.005

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : reciprocal condition number 0

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : There are other near singularities as well. 1.01

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : pseudoinverse used at 0.995

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : neighborhood radius 1.005

## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : reciprocal condition number 0
```
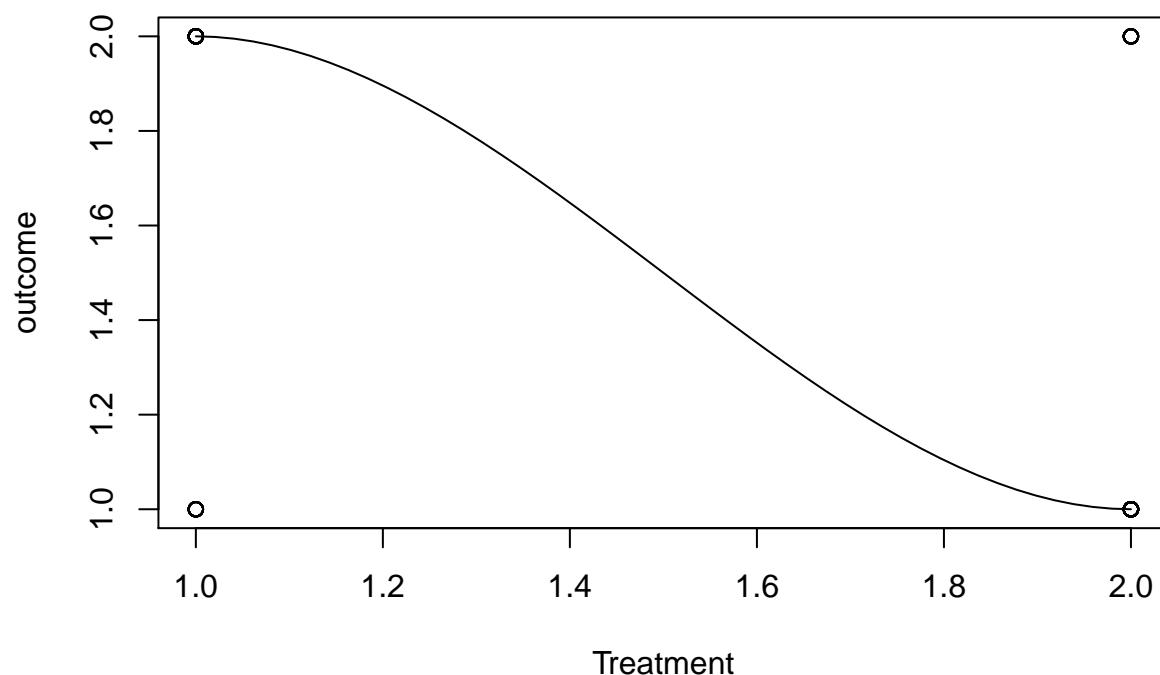
```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : There are other near singularities as well. 1.01
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : pseudoinverse used at 0.995
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : neighborhood radius 1.005
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : reciprocal condition number 0
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : There are other near singularities as well. 1.01
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : pseudoinverse used at 0.995
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : neighborhood radius 1.005
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : reciprocal condition number 0
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : There are other near singularities as well. 1.01
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : pseudoinverse used at 0.995
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : neighborhood radius 1.005
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : reciprocal condition number 0
```

```
## Warning in simpleLoess(y, x, w, span, degree = degree, parametric =
## FALSE, : There are other near singularities as well. 1.01
```

```r
cor(dummy_out, dummy_ttt, method = "spearman")
```

```
## [1] 0.5204165
```

- There is a moderate positive correlation between outcome and treatment

```r
logd2<- within(logd1, Treatment<- relevel(Treatment, ref = "Placebo"))
logmodel<- glm(formula = outcome~ Treatment, family = "binomial", data = logd2)
logmodel
```

```
##
## Call:  glm(formula = outcome ~ Treatment, family = "binomial", data = logd2)
##
## Coefficients:
##     (Intercept)   TreatmentNewdrug
##          -1.266              2.312
##
## Degrees of Freedom: 99 Total (i.e. Null);  98 Residual
## Null Deviance:       138.5
## Residual Deviance: 110    AIC: 114
```

```r
exp(logmodel$coefficients)
```

```
##     (Intercept) TreatmentNewdrug
##       0.2820513       10.0909091
```

- odds of successs of pt recieving placebo is 0.28
- odds of successs of pt recieving new drug is 10.09

```r
prob_placebo<-(exp(-1.266)/ (1+exp(-1.266)))
prob_placebo
```

```
## [1] 0.2199428
```

```r
prob_new<-(exp(2.312)/ (1+exp(2.312)))
prob_new
```

```
## [1] 0.909866
```

- probability of success for pt recieving placebo is 21.9%
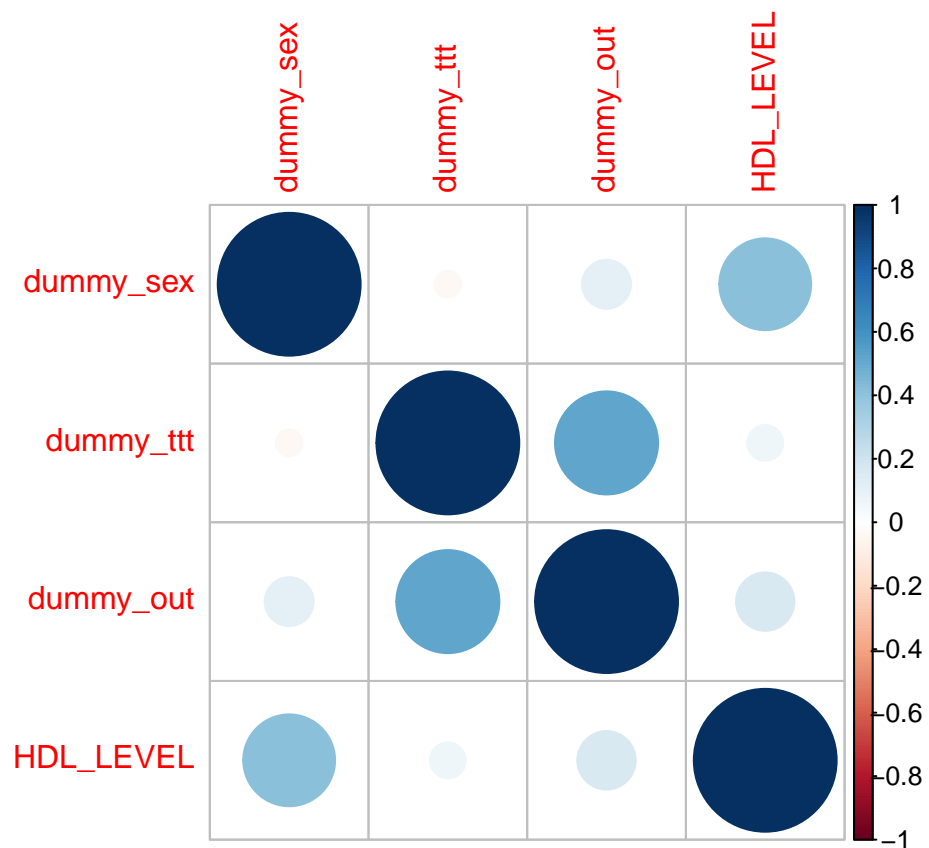- probability of success for pt recieving new drug is 90.98%

in case sex has sign difference between placebo and new drug

```r
library(corrplot)
```

```
## Warning: package 'corrplot' was built under R version 3.5.3
```

```
## corrplot 0.84 loaded
```

```r
cor1<-cor(logd1[,c(1:3,7)])
corrplot(cor1, method = "circle")
```



```r
cor1
```

```
##             dummy_sex   dummy_ttt dummy_out  HDL_LEVEL
## dummy_sex  1.00000000 -0.03494283 0.1175019 0.41327986
## dummy_ttt -0.03494283  1.00000000 0.5204165 0.06320816
## dummy_out  0.11750194  0.52041650 1.0000000 0.16738857
```

```
## HDL_LEVEL  0.41327986  0.06320816 0.1673886 1.00000000
```

```r
logmodel2<-glm(outcome~Treatment+ SEX+ HDL_LEVEL, family = "binomial", data = logd2)
logmodel2
```

```
##
## Call:  glm(formula = outcome ~ Treatment + SEX + HDL_LEVEL, family = "binomial",
##     data = logd2)
##
## Coefficients:
##     (Intercept)  TreatmentNewdrug          SEXMale         HDL_LEVEL
##        -4.00643           2.38664          0.90217           0.06643
##
## Degrees of Freedom: 99 Total (i.e. Null);  96 Residual
## Null Deviance:        138.5
## Residual Deviance: 106.6     AIC: 114.6
```

```r
exp(logmodel2$coefficients)
```

```
##     (Intercept) TreatmentNewdrug          SEXMale        HDL_LEVEL
##      0.01819817      10.87684799       2.46493495       1.06869133
```

- odds of successs of male pt recieving placebo in presence HDLis 0.018
- odds of successs of male pt recieving new drug is 10.87 in presence HDL

```r
prob_placebo1<-(exp(-4)/ (1+exp(-4)))
prob_placebo1
```

```
## [1] 0.01798621
```

```r
prob_new1<-(exp(2.386)/ (1+exp(2.386)))
prob_new1
```

```
## [1] 0.9157535
```

- probability of success for MALE pt recieving placebo is 1.7% on HDL level
- probability of success for MALE pt recieving new drug is 91.5% on HDL level

```r
library(Greg)
```

```
## Warning: package 'Greg' was built under R version 3.5.3
```

```
## Loading required package: forestplot
```

```
## Warning: package 'forestplot' was built under R version 3.5.3
```

```
## Loading required package: grid
```

```
## Loading required package: magrittr
```

```
## Warning: package 'magrittr' was built under R version 3.5.3
```

```
## Loading required package: checkmate
```

```
## Warning: package 'checkmate' was built under R version 3.5.3
```

```
## Loading required package: Gmisc
```

```
## Warning: package 'Gmisc' was built under R version 3.5.3
```

```
## Loading required package: Rcpp
```

```
## Warning: package 'Rcpp' was built under R version 3.5.3
```

```
## Loading required package: htmlTable
```

```
## Warning: package 'htmlTable' was built under R version 3.5.3
printCrudeAndAdjustedModel(logmodel2)[-1,]
```

Crude

Adjusted

Variable

OR

2.5 % to 97.5 %

OR

2.5 % to 97.5 %

Newdrug

10.09

4.15 to 26.41

10.88

4.35 to 29.76

Male

2.33

0.58 to 11.59

2.46

0.41 to 17.85

HDL_LEVEL

1.10

0.99 to 1.23

1.07

0.93 to 1.24

- The success of New drug is 10.09 times higher than the placebo, and 10.88 cosidering the gender and HDL level
- Being Male, the rate of success is 2.33 higher than being a female, and 2.46 cosidering recieving new drug and HDL level
- The success in control HDL level is 1.10 higher in this model, and 1.07 cosidering the gender and recieving New drug