Compupter Practical 3

Statistics 2

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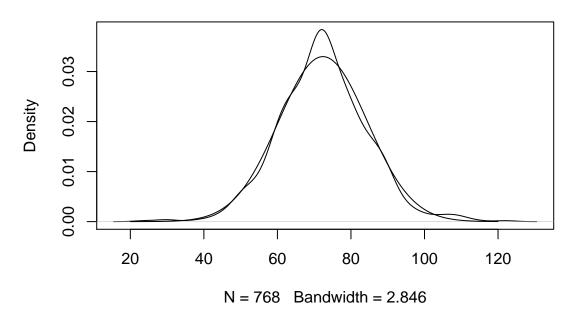
```
options(warn=-1)
diabetes<-read.csv("data/diabetes_data.csv",header=T)</pre>
head(diabetes)
     Pregnancies Glucose BloodPressure SkinThickness Insulin BMI
## 1
                       148
                                                                0 33.6
                6
## 2
                        85
                                       66
                                                      29
                1
                                                                0 26.6
## 3
                8
                       183
                                       64
                                                       0
                                                                0 23.3
                        89
                                       66
                                                       23
                                                               94 28.1
## 4
                1
## 5
                0
                       137
                                       40
                                                      35
                                                              168 43.1
                5
## 6
                       116
                                       74
                                                       0
                                                                0 25.6
##
     DiabetesPedigreeFunction Age Outcome
## 1
                          0.627
                                  50
## 2
                          0.351
                                 31
## 3
                          0.672
                                 32
## 4
                                           0
                          0.167
                                  21
## 5
                          2.288
## 6
                          0.201
                                 30
                                           0
missing<-function(var) { # Map missing values to median</pre>
  med<-median(var[var>0])
  var[var == 0] < -med
  return(var)
}
diabetes$Glucose<-missing(diabetes$Glucose)</pre>
diabetes$BloodPressure<-missing(diabetes$BloodPressure)</pre>
diabetes$Insulin<-missing(diabetes$Insulin)</pre>
diabetes$SkinThickness<-missing(diabetes$SkinThickness)</pre>
diabetes$BMI<-missing(diabetes$BMI)</pre>
head(diabetes)
##
     Pregnancies Glucose BloodPressure SkinThickness Insulin BMI
## 1
                6
                       148
                                       72
                                                      35
                                                              125 33.6
                                       66
## 2
                        85
                                                      29
                                                              125 26.6
                1
## 3
                8
                       183
                                       64
                                                      29
                                                              125 23.3
## 4
                1
                        89
                                       66
                                                      23
                                                               94 28.1
## 5
                0
                       137
                                       40
                                                      35
                                                              168 43.1
## 6
                5
                       116
                                       74
                                                      29
                                                              125 25.6
##
     DiabetesPedigreeFunction Age Outcome
## 1
                          0.627 50
## 2
                          0.351
                                 31
                                           0
## 3
                          0.672
                                  32
                                            1
## 4
                          0.167
                                  21
                                           0
## 5
                          2.288
                                  33
                                           1
## 6
                          0.201
                                 30
```

```
breaks<-c(-Inf,seq(45,95,by=5),Inf) # Quantise data
obs<-table(cut(diabetes$BloodPressure,breaks))

# Perform Pearson's Goodness of Fit Test
n<-length(diabetes$BloodPressure)
m<-length(breaks)-1-3
mu<-mean(diabetes$BloodPressure) # MLE
sigma<-sd(diabetes$BloodPressure) # MLE

x<-seq(20,120,0.1)
plot(density(diabetes$BloodPressure))
lines(x,dnorm(x,mu,sigma))</pre>
```

density.default(x = diabetes\$BloodPressure)



exp<-n*(pnorm(breaks[-1],mean=mu,sd=sigma)-pnorm(breaks[-length(breaks)],mean=mu,sd=sigma)) # calculate round(cbind(obs,exp),1) # Display observed & expected values

```
##
             obs
                   exp
## (-Inf,45]
               9
                   9.1
## (45,50]
              20
                  15.6
## (50,55]
              24
                  33.2
## (55,60]
                  59.6
              70
## (60,65]
                  90.5
              85
## (65,70]
             132 116.0
## (70,75]
             139 125.7
## (75,80]
             124 115.1
## (80,85]
              59
                  89.1
## (85,90]
              68 58.3
```

```
## (90,95] 15 32.2
## (95, Inf] 23 23.6

t_obs<-sum((obs-exp)^2/exp) # observered test statistic
p_val<-1-pchisq(t_obs,df=m) # p-value
cat("mu=",mu,"\nsigma=",sigma,"\ndf=",m,"\nt_obs=",t_obs,"\np-val=",p_val,sep="")

## mu=72.38672
## sigma=12.09664
## df=9
## t_obs=31.18803
## p-val=0.0002748274</pre>
```

Let $X_1, \ldots, X_n \stackrel{\text{iid}}{\sim} \text{Normal}(\mu, 12^2)$ model the blood pressume of members of the study. Here I shall test the hypotheses

$$H_0: \mu = 70 \text{ against } H_1: \mu > 70$$

I shall use Pearson's test statistic

$$T(\mathbf{X}) := \sum_{i=1}^{m} \frac{(o_i - e_i)^2}{e_i} = \sum_{i=1}^{m} \frac{(o_i - np_i)^2}{np_i} \to_{\mathcal{D}} \chi_{m-1}^2$$

where o_i is the number of observations in inteval i, e_i is the expected number of observations of interval i & p_i is the probability of an observation belonging to interval i given the null-hypothes is true. Due to the breaks chosen in Question 1 m = rlength(obs)'.

```
mu<-70; sigma<-12
exp<-n*(pnorm(breaks[-1],mean=mu,sd=sigma)-pnorm(breaks[-length(breaks)],mean=mu,sd=sigma))
round(cbind(obs,exp),1)</pre>
```

```
##
                   exp
## (-Inf,45]
                  14.3
               9
## (45,50]
                  22.4
              20
## (50,55]
              24 44.4
## (55,60]
              70 74.2
## (60,65]
              85 104.5
## (65,70]
             132 124.1
## (70,75]
             139 124.1
## (75,80]
             124 104.5
## (80,85]
              59 74.2
## (85,90]
              68 44.4
## (90,95]
              15 22.4
## (95, Inf] 23 14.3
t_obs<-sum((obs-exp)^2/exp) # observered test statistic
p_val<-1-pchisq(t_obs,df=m) # p-value</pre>
cat("mu=",mu,"\nsigma=",sigma,"\ndf=",m,"\nt_obs=",t_obs,"\np-val=",p_val,sep="")
```

```
## mu=70
## sigma=12
## df=9
## t_obs=44.82382
## p-val=9.945303e-07
```

Let $Y_i \stackrel{\text{ind}}{\sim} \text{Bernoulli}(\sigma(\theta^T x_i))$ for $i \in [1, n]$ $\pi_i = \mathbb{P}(Y_i = 1)$ where $\sigma(z) := \frac{1}{1 + e^{-z}}$. Then

$$\pi_{i} := \mathbb{P}(Y_{i} = 1)$$

$$= \sigma(\theta^{T}x_{i})$$

$$:= \frac{1}{1 + e^{-\theta^{T}x_{i}}}$$

$$= \frac{1}{1 + e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}}}$$

$$\Rightarrow \ln \pi_{i} = \ln \left(\frac{1}{1 + e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}}}\right)$$

$$= \ln 1 - \ln(1 + e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}})$$

$$= -\ln(1 + e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}})$$
and
$$\ln(1 - \pi_{i}) = \ln \left(1 - \frac{1}{1 + e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}}}\right)$$

$$= \ln \left(\frac{e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}}}{1 + e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}}}\right)$$

$$= \ln(e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}}) - \ln(1 + e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}})$$

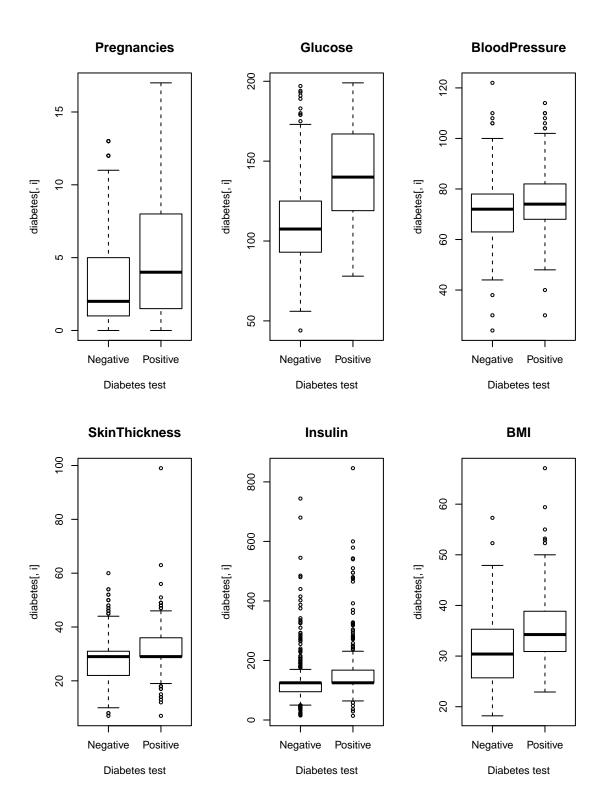
$$= -\left(\sum_{j=1}^{d} \theta_{j}x_{ij}\right) - \ln(1 + e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}})$$

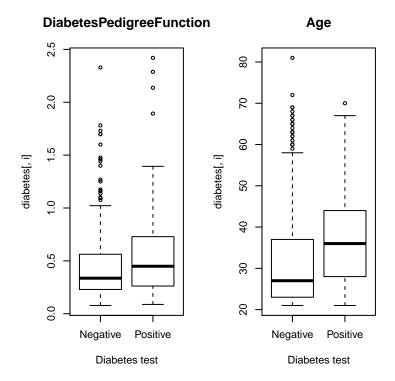
$$\Rightarrow \ln \frac{\pi_{i}}{1 - \pi_{i}} = \ln(\pi_{i}) - \ln(1 - \pi)$$

$$= -\ln(1 + e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}}) + \left(\sum_{j=1}^{d} \theta_{j}x_{ij}\right) + \ln(1 + e^{-\sum_{j=1}^{d} \theta_{j}x_{ij}})$$

$$= \sum_{j=1}^{d} \theta_{j}x_{ij}$$

```
Xnames <- colnames(diabetes[, -9]) #get names of explanatory variables
par(mfrow=c(1,3))
for (i in 1:8) {
boxplot(diabetes[,i]~diabetes$Outcome,main=paste(Xnames[i]),
names=c("Negative","Positive"),xlab="Diabetes test")
}</pre>
```





Here I shall test whether the variables *BloodPressure*, *SkinThichness*, *Insulin* and *Age* are statistically significant to the development of diabetes.

To do so I shall test the hypotheses

$$H_0: \theta := (\theta_3, \theta_4, \theta_5, \theta_8) = \mathbf{0} \text{ against } H_1: \theta \neq \mathbf{0}$$

Consider the likelihood ratio statistic

$$\Lambda_n := rac{L(\hat{m{ heta}}_0; m{x})}{L(\hat{m{ heta}}_{ ext{MLE}}; m{x})}$$

and define test statistic

$$T_n(\mathbf{X}) := -2\Lambda_n = -2[\ell(\hat{\boldsymbol{\theta}}_0; \mathbf{X}) - \ell(\hat{\boldsymbol{\theta}}_{\mathrm{MLE}}; \mathbf{X})] \sim \chi_r^2$$

where r=4 since we only have four restrictions under the null hypothesis.

```
X_rest<-cbind(1,as.matrix(diabetes[,c(1,2,6,7)])) # Variables we are not testing (ie assuming others=0)
X_full<-cbind(1,as.matrix(diabetes[,1:8])) # all variables
Y<-diabetes[,9] # outcomes

# sigmoid function
sigma<-function(z) {
    1/(1+exp(-z))
}
# Log likelihood
ell<-function(theta,X,y) {</pre>
```

```
p<-as.vector(sigma(X%*%theta))</pre>
   sum(y*log(p)+(1-y)*log(1-p))
}
# score function
score<-function(theta,X,y) {</pre>
   p<-as.vector(sigma(X%*%theta))</pre>
   as.vector(t(X)%*%(y-p))
}
# MLE
maximise.ell<-function(ell,score,X,y,theta0) {</pre>
   optim.out<-optim(theta0, fn=ell, gr=score, X=X, y=y, method="BFGS", control=list(fnscale=-1, maxit=1
   return(list(theta=optim.out$par, value=optim.out$value))
}
theta_hat_0.value<-maximise.ell(ell,score,X_rest,Y,rep(0,5))$value
theta_hat_mle.value<-maximise.ell(ell,score,X_full,Y,rep(0,9))$value
cat("ell(theta_hat_0): ",theta_hat_0.value,"\nell(theta_hat_mle): ",theta_hat_mle.value,sep="")
## ell(theta_hat_0): -358.1828
## ell(theta_hat_mle): -356.4209
```

Using these results we can calculate an observed test statistic

$$T_n(\mathbf{x}) = -2[\ell(\hat{\boldsymbol{\theta}}_0; \boldsymbol{x}) - \ell(\hat{\boldsymbol{\theta}}_{MLE}; \boldsymbol{x})] = -2[-358.182779 - -356.4209352] = 3.5236876$$

Since $T_n(\mathbf{X}) \sim \chi_4^2$ we have an observered p-value of

$$p(\mathbf{x}) := \mathbb{P}(T_n(\mathbf{X}) \ge T_n(\mathbf{x}); H_0) = \mathbb{P}(\chi_4^2 \ge 3.5236876) = 0.4742857$$

Using the code described in the epilogue we can confirm this value

```
model1<-glm(Y~X_full,family=binomial) #full model
model2<-glm(Y~X_rest,family=binomial) #restricted model
suppressMessages(library(lmtest))
lrtest(model1, model2)</pre>
```

```
## Likelihood ratio test
##
## Model 1: Y ~ X_full
## Model 2: Y ~ X_rest
## #Df LogLik Df Chisq Pr(>Chisq)
## 1 9 -356.42
## 2 5 -358.18 -4 3.5237 0.4743
```

This is not statistically significant enough to suggest rejecting H_0 .

Thus we accept that the variables BloodPressure, SkinThickness, Insulin and Age are <u>not</u> statistically significant for the development of diabetes.

Question 5

```
set.seed(16111998)
generate.ys<-function(X,theta) {
   n<-dim(X)[1]</pre>
```

x < -seq(0,20,0.1)

}

rbinom(n,size=1,prob=sigma(X%*%theta))

lines(density(simulation.raw),col="red",lty=2)

```
simulate<-function(theta_hat_mle) {
    new_Y<-generate.ys(X_rest,theta_hat_mle)

    theta_hat_0.value<-maximise.ell(ell,score,X_rest,new_Y,rep(0,5))$value
    theta_hat_mle.value<-maximise.ell(ell,score,X_full,new_Y,rep(0,9))$value

    t_obs<--2*(theta_hat_0.value-theta_hat_mle.value)
}

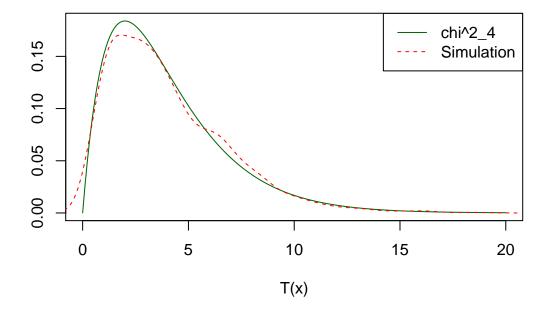
n_trials=2000; m<-4
theta_hat_mle<-maximise.ell(ell,score,X_rest,Y,rep(0,5))$theta
simulation.raw<-sapply(1:n_trials, function(i) simulate(theta_hat_mle))

a)</pre>
```

plot(x,dchisq(x,m),type="l",col="darkgreen",xlab="T(x)",ylab="",main="Comparision of density of observed of observed of the comparison of density of the comparison of density of observed of the comparison of density of the comparison of the compari

Comparision of density of observed statistics & chi^2_4 distribu

legend("topright",legend=c("chi^2_4","Simulation"),lty=1:2,col=c("darkgreen","red"))



```
b)
breaks<-c(-Inf,seq(1,13,by=1),Inf)
obs<-table(cut(simulation.raw,breaks))</pre>
```

```
exp<-n_trials*(pchisq(breaks[-1],4)-pchisq(breaks[-length(breaks)],4))</pre>
round(cbind(obs,exp),1)
##
            obs
                  exp
## (-Inf,1] 177 180.4
## (1,2]
            365 348.1
## (2,3]
            338 355.9
## (3,4] 298 303.6
## (4,5] 231 237.4
## (5,6] 157 176.3
## (6,7] 163 126.5
## (7,8]
          91 88.6
## (8,9]
           70 61.0
## (9,10] 40 41.3
## (10,11] 25 27.7
## (11,12] 15 18.4
## (12,13] 10 12.2
## (13, Inf] 20 22.6
t_obs<-sum((obs-exp)^2/exp) # observered test statistic
p_val<-1-pchisq(t_obs,df=m) # p-value</pre>
cat("df=",m,"\nt_obs=",t_obs,"\np-val=",p_val,sep="")
## df=4
## t_obs=17.71702
## p-val=0.001401555
```