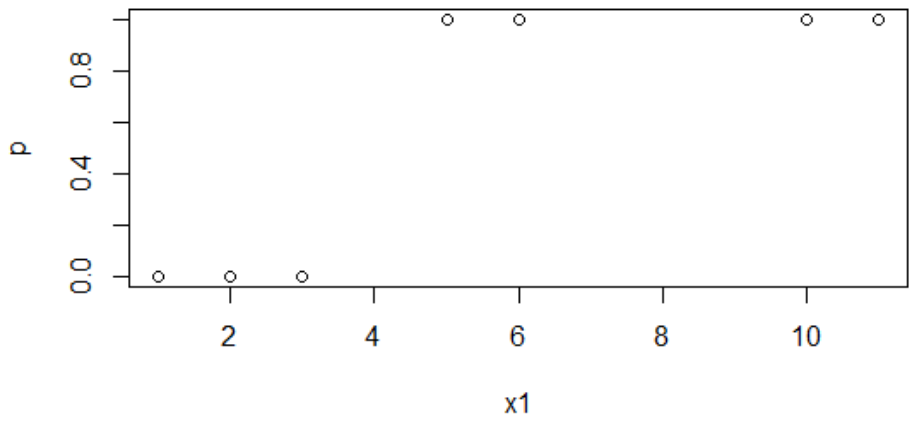
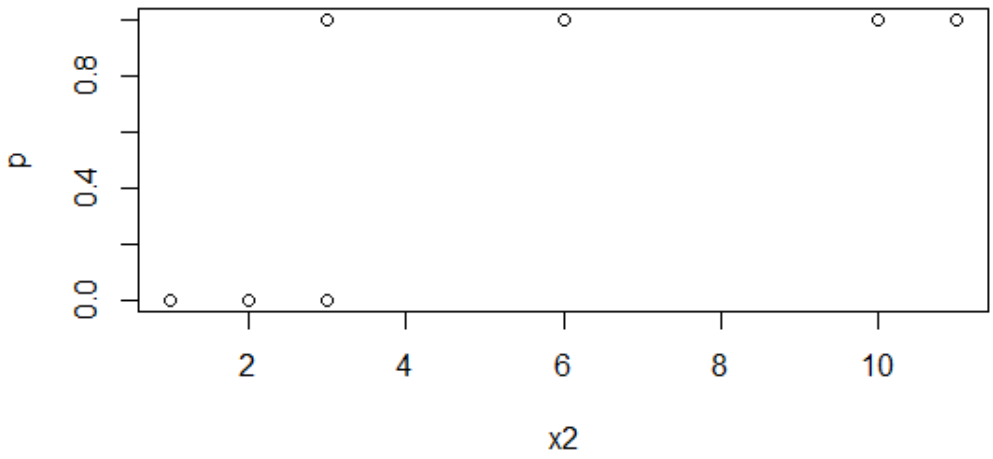
```
> rm(list = ls())
> setwd("E:/Data of R")
>
> #Question 1
> #(a)
>
> y=c(0,0,0,0,1,1,1,1)
> x1=c(1,2,3,3,5,6,10,11)
>
> data11=data.frame(cbind(y,x1))
>
> model11=glm(y~x1,data=data11,family = binomial(link = logit))
Warning message:
glm.fit:拟合機率算出来是数值零或一
> summary(model11)

Call:
glm(formula = y ~ x1, family = binomial(link = logit), data = data11)

Deviance Residuals:
      Min         1Q     Median         3Q        Max
-8.605e-06  -2.167e-06   0.000e+00   2.110e-08   1.288e-05

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  -94.87  202572.35       0        1
x1            23.62   48491.51       0        1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 1.109e+01  on 7  degrees of freedom
Residual deviance: 3.139e-10  on 6  degrees of freedom
AIC: 4

Number of Fisher Scoring iterations: 25

>
> #Coefficients and standard errors
> coef(summary(model11))
            Estimate Std. Error      z value  Pr(>|z|)
(Intercept) -94.86875  202572.35 -0.0004683203 0.9996263
x1           23.61643   48491.51  0.0004870218 0.9996114
>
> exp(model11$coefficients)
 (Intercept)          x1
6.295460e-42 1.805026e+10
>
> p=predict(model11,type = 'response')
> qqplot(x1,p)
```




```
>
> #As can be seen from the plot, warning message means that
> #When y=1,pi_hat=1. When y=0, pi_hat=0
> #Which is also an indication of complete seperation
> #Another signal is the unnaturally large standard errors
>
> #(b)
> y=c(0,0,0,0,1,1,1,1)
> x2=c(1,2,3,3,3,6,10,11)
>
> data12=data.frame(cbind(y,x2))
>
> model12=glm(y~x2,data=data12,family = binomial(link = logit))
Warning message:
glm.fit:拟合機率算出来是数值零或一
> summary(model12)

Call:
glm(formula = y ~ x2, family = binomial(link = logit), data = data12)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-0.9005  -0.2252   0.0000   0.0000   1.4823

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   -54.08   18834.18  -0.003    0.998
x2             17.80    6278.06   0.003    0.998

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 11.0904  on 7  degrees of freedom
Residual deviance:  3.8191  on 6  degrees of freedom
AIC: 7.8191
```

```
Number of Fisher Scoring iterations: 21

>
> #Coefficients and standard errors
> coef(summary(model12))
             Estimate Std. Error     z value  Pr(>|z|)
(Intercept) -54.08260  18834.176 -0.002871514 0.9977089
x2           17.79649   6278.059  0.002834711 0.9977382
>
> exp(model12$coefficients)
 (Intercept)          x2
3.252551e-24 5.356922e+07
>
> p=predict(model11,type = 'response')
> qqplot(x2,p)
```




```
>
> #As can be seen from the plot, warning message means that
> #Some observations have pi_hat=1 or 0, there is not  perfect discriminat
ion
> #which is  an indication of quasi-complete separation
> #Another signal is also the unnaturally large standard errors
```

```
> #Question 3
>
> data3=read.table("donner.txt",header = T)
>
> #(a)
> model3a=glm(survival~age,data=data3, family = binomial(link = logit))
> summary(model3a)

Call:
glm(formula = survival ~ age, family = binomial(link = logit),
    data = data3)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.5946  -1.2017   0.8436   0.9882   1.5765

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.97917    0.37460   2.614  0.00895 **
age         -0.03689    0.01493  -2.471  0.01346 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 120.86  on 87  degrees of freedom
Residual deviance: 114.02  on 86  degrees of freedom
AIC: 118.02

Number of Fisher Scoring iterations: 4

>
> #(b)
> model3a$coefficients[2]
        age
-0.03688823
> #Interpretation for
> #For every one year increase in age, the log odds of survial decreased b
y 0.03689
>
> 1/exp(model3a$coefficients[2])
     age
1.037577
> #Interpretation for
> #For every one year increase in age, a person is 1.0375770 times less li
kely to survive
>
> #(c)
> #H0:
```

```
> #Ha:
>
> #Z=         =0.03689/(0.01493)=2.471>1.96
>
> #P-value is 0.01346
> #Reject H0
>
> #(d)
> coef(summary(model3a))
             Estimate Std. Error   z value    Pr(>|z|)
(Intercept)  0.97917294 0.37459933  2.613921 0.008950982
age         -0.03688823 0.01492559 -2.471476 0.013455674
>
> #Confidence Interval for
> lb=coef(summary(model3a))[2,1]-qnorm(0.975)*coef(summary(model3a))[2,
2]
> ub=coef(summary(model3a))[2,1]+qnorm(0.975)*coef(summary(model3a))[2,
2]
> c(lb,ub)
[1] -0.066141852 -0.007634613
>
> #Confidence Interval for
> exp(c(lb,ub))
[1] 0.9359981 0.9923945
>
> #Effect of age on survial is statistically significant
> #because the CI for    does not contain 0 and the CI for    does not cont
ain 1
>
> #(e)
> age2=data3$age^2
> model3b=glm(survival~age+age2+sex+status, data = data3, family = binomi
al(link = logit))
> summary(model3b)

Call:
glm(formula = survival ~ age + age2 + sex + status, family = binomial(link
 = logit),
    data = data3)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.0431  -1.0391   0.5120   0.8664   2.0797

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  1.986e-01  6.172e-01   0.322   0.7476
age          1.675e-01  7.107e-02   2.357   0.0184 *
age2        -3.889e-03  1.525e-03  -2.550   0.0108 *
```

```
sex         -6.637e-01  5.588e-01  -1.188   0.2349
statusHired  -1.625e+00  7.481e-01  -2.173   0.0298 *
statusSingle -1.852e+01  1.760e+03  -0.011   0.9916
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 120.855  on 87  degrees of freedom
Residual deviance:  92.363  on 82  degrees of freedom
AIC: 104.36

Number of Fisher Scoring iterations: 16

>
> #(f)
> #H0:reduced model
> #Ha:full model
>
> #
>
> #Reject if
>
> diff.dev=deviance(model3a)-deviance(model3b)
> diff.dev
[1] 21.65525
> qchisq(0.95,4)
[1] 9.487729

>
> #21.65525 > 9.487729

> #Reject H0
>
> #(g)
> model3b$coefficients[4]
      sex
-0.663728
> #Interpretation for
> #A male decreases the log odds of survival by 0.663728050
>
> 1/exp(model3b$coefficients[4])
     sex
1.942019
> #Interpretation for
> #A male is 1.942019 times less likely to survive
>
> #Question 4
> #(a)
```

```
> H=rep(0,88)
> for (i in 1:88) {
+   if(data3$status[i]=='Hired'){
+     H[i]=1
+   }
+ }
> S=rep(0,88)
> for (i in 1:88) {
+   if(data3$status[i]=='Single'){
+     S[i]=1
+   }
+ }
> X=cbind(1,data3$age,age2,data3$sex,H,S)
> fv=X%*%model3b$coefficients
> summary(fv)
       V1
 Min.   :-17.8917
 1st Qu.: -0.3345
 Median :  0.3622
 Mean   : -0.7447
 3rd Qu.:  1.1821
 Max.   :  2.0004
```

```
> #(c)
> pi_hat=exp(fv)/(1+exp(fv))
> summary(pi_hat)
       V1
 Min.   :0.0000
 1st Qu.:0.4171
 Median :0.5896
 Mean   :0.5568
 3rd Qu.:0.7653
 Max.   :0.8808
>
> #(d)
> #(1)
> y_hat1=rep(0,88)
> for(i in 1:88){
+   if(pi_hat[i]>0.5){
+     y_hat1[i]=1
+   } else{
+     y_hat1[i]=0
+   }
+ }
>
> T1=table(data3$survival,y_hat1)
> T1
   y_hat1
     0  1
  0 23 16
  1  7 42
>
> #(2)
> y_hat2=rep(0,88)
> for(i in 1:88){
+   if(pi_hat[i]>(sum(data3$survival)/88)){
+     y_hat2[i]=1
+   } else{
+     y_hat2[i]=0
+   }
+ }
>
> T2=table(data3$survival,y_hat2)
> T2
   y_hat2
     0  1
  0 27 12
  1 10 39
>
> #(3)
> port1=T1[1,1]/88
> port1
```

```
[1] 0.2613636
> port2=(T2[1,2]+T2[2,1])/88
> port2
[1] 0.25
> #0.2613636 > 0.25
> #Second cutoff is better
>
> #(4)
> FPR1=T1[1,2]/(sum(T1[1,]))
> FNR1=T1[2,1]/(sum(T1[2,]))
> FPR2=T2[1,2]/(sum(T2[1,]))
> FNR2=T2[2,1]/(sum(T2[2,]))
>
> #(5)
> c(FPR1,FPR2)
[1] 0.4102564 0.3076923
> #0.4102564 > 0.3076923
> c(FNR1,FNR2)
[1] 0.1428571 0.2040816
> #0.1428571 < 0.2040816
> #It is hard to decide
>
> #(6)
> library(pROC)
> data4=data.frame(cbind(data3$survival,pi_hat,y_hat1,y_hat2))
> roc(data4$V1,data4$V2,plot = TRUE)

Call:
roc.default(response = data4$V1, predictor = data4$V2, plot = TRUE)

Data: data4$V2 in 39 controls (data4$V1 0) < 49 cases (data4$V1 1).
Area under the curve: 0.8004
> points(1-FPR1,1-FNR1,col='red', cex=2, pch=21)
> points(1-FPR2,1-FNR2,col='blue', cex=2, pch=24)
```