1

```
(a)
icu_data <- read.csv("/Users/CandiceDeng\ 1/Desktop/STATS500/HW#7/icu.csv")</pre>
icu data$race <- factor(icu data$race)</pre>
head(icu_data,5)
##
     sta age can cpr inf race
## 1
       0 27
               0
                   0
                        1
       0 59
                        0
                             1
## 2
               0
                    0
## 3
       0 77
               0
                        0
                             1
                        1
## 4
       0 54
               0
                    0
                             1
## 5
       0 87 0
                   0
                        1
                             1
icu_fit <- glm(sta~.,family=binomial,data=icu_data)</pre>
icu fit
##
         glm(formula = sta ~ ., family = binomial, data = icu_data)
## Call:
##
## Coefficients:
## (Intercept)
                                                     cpr
                                                                  inf
                         age
                                       can
                      0.0284
                                    0.2607
                                                 1.5394
                                                               0.8800
##
       -4.1075
##
         race2
                       race3
##
        0.9163
                      0.4227
##
## Degrees of Freedom: 199 Total (i.e. Null); 193 Residual
## Null Deviance:
                         200.2
## Residual Deviance: 176.3
                                 AIC: 190.3
icu reduce1 <- glm(sta~age+can+race,family=binomial,data=icu data)
anova(icu_reduce1,icu_fit)
## Analysis of Deviance Table
##
## Model 1: sta ~ age + can + race
## Model 2: sta ~ age + can + cpr + inf + race
     Resid. Df Resid. Dev Df Deviance
##
## 1
           195
                    189.13
## 2
           193
                    176.29 2
                                12.845
1-pchisq(12.845,2)
## [1] 0.00162459
beta <- coef(icu_fit)[4:5]</pre>
varb <- vcov(icu_fit)[4:5,4:5]</pre>
varbi <- solve(varb)</pre>
w <- t(beta) %*% varbi %*% beta
paste('w =',w)
## [1] "w = 12.3727100895835"
paste('p-value = ',1-pchisq(w,2))
```

```
## [1] "p-value = 0.00205731191322589"
```

For the likelihood ratio test, the chi-square test statistics is 12.845 with 2 degree of freedom. The null hypothesis should be rejected because p-value is 0.00162459 which is less than 0.05. For wald test, on the other hand, the test statistic is 12.3727100895835 with 2 degree of freedom. The null hypothesis should also be rejected because p-value is 0.00205731191322589 which is less than 0.05.

(b)

```
library(aod)
x <- model.matrix(icu_fit)[,-1]</pre>
new icu <- data.frame(sta=icu fit$y,x)</pre>
icu_reduce2 <- glm(sta~age+can+cpr+inf+I(race2+race3), family=binomial,data=new_icu)</pre>
anova(icu_reduce2,icu_fit)
## Analysis of Deviance Table
##
## Model 1: sta \sim age + can + cpr + inf + I(race2 + race3)
## Model 2: sta ~ age + can + cpr + inf + race
     Resid. Df Resid. Dev Df Deviance
##
## 1
           194
                   177.25
           193
## 2
                   176.29 1 0.96205
1-pchisq(0.96205, 1)
## [1] 0.3266709
wald.test(b=coef(icu_fit),Sigma=vcov(icu_fit),L=cbind(0,0,0,0,0,1,-1))
## Wald test:
## -----
##
## Chi-squared test:
## X2 = 0.95, df = 1, P(> X2) = 0.33
```

For the likelihood ratio test, the chi-square test statistics is 0.96205 with 1 degree of freedom. The null hypothesis should not be rejected because p-value is 0.3266709 which is greater than 0.05. For wald test, on the other hand, the test statistic is 0.95 with 2 degree of freedom. The null hypothesis should also not be rejected because p-value is 0.33 which is greater than 0.05.

(c)

```
beta <- summary(icu_fit)$coef
mean <- as.numeric(beta[6] - beta[7])
amatrix <- vcov(icu_fit)[6:7, 6:7]
var_beta <- amatrix[1, 1]+amatrix[2, 2]-2*amatrix[1, 2]
std <- sqrt(var_beta)
paste('95% CI = ', paste(mean-qnorm(0.975,0,1)*std,mean+qnorm(0.975,0,1)*std))
## [1] "95% CI = -0.501131458565487 1.48831148719703"</pre>
```

The 95% confidence interval for  $\beta_{race2}$ - $\beta_{race3}$  is to detect how the response sta varies between predictors race2 and race3 while holding other predictors constant. The interval is (-0.501131458565487, 1.48831148719703).

For the binary response model, unlike the usual form  $2[l(\beta_S)-l(\beta_\Omega)]$ , the likelihood under a saturated model is not feaible and the Residual Deviance is computed as  $-2l(\beta_\Omega)$ . Under this circumstance, the Residual Deviance does not follow chi-squared distribution. Therefore, this Residual Deviance cannot be appropriately considered as the sum of the squared deviance residuals, which means it should not be used as a Goodness-of-Fit statistic for this model.

2

(a)

Define 
$$f(p) = \frac{p}{1-p} \Rightarrow \frac{\partial f(p)}{\partial p} = \frac{1}{(1-p)^3}$$

Var  $(f(\hat{p}) - f(p)) = f'(p) \cdot \hat{p} - p)$ 

$$= [\frac{1}{(1-p)^3}]^2 \cdot Var(\hat{p} - p)$$

$$= [\frac{1}{(1-p)^3}]^2 \cdot P(1-p)$$

$$= \frac{p}{(1-p)^3}$$

$$\sqrt{n} \cdot (\frac{\hat{p}}{1-\hat{p}} - \frac{p}{1-p}) \xrightarrow{d} \mathcal{M}(0, \frac{p}{(1-p)^3})$$

(b)

$$Var\left(\frac{\hat{\rho}}{1-\hat{p}}\right) = Var\left(\frac{\hat{\rho}}{1-\hat{p}} - \frac{\hat{p}}{1-\hat{p}}\right) = \frac{\hat{p}}{(1-\hat{p})^3} \cdot \frac{1}{\sqrt{n}}$$

$$= \frac{\hat{p}}{n(1-\hat{p})^3}$$