

Enonce de TP:

```
coron=c(1,0,1,0,0,1,0,0,0,0,0,0,0,1,0,1,0,0,0,1,0,1,1,1,0,1,1,1,0,0,1,0,0,0,0,0,1,1,0,0,0,1,0,0,0,0,0,0,1,1,1,0,1,0,0,1,
0,1,0,0,0,1,1,0,1,1,0,1,1,0,0,0,1,0,1,1,1,0,0,0,0,0,1,1,0,0,0,0,1,1,1,0,0,0,0,0,1,0,0)
hta=c(0,0,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,1,1,0,0,0,1,0,1,1,1,1,1,0,1,1,1,
0,1,0,0,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,1,0,0,0,1,0,0,1,0,0,1,1,1,1,0,0,0,1,1,1,1)
sex=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,
1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)
y=data.frame(coron,sex,hta)
resu<-glm(coron~hta+sex,family=binomial(link=logit),data=y)
```

```
resu
summary(resu)
plot(resu)
```

Execution:

[illegible]

```
> summary(resu)

Call:
glm(formula = coron ~ hta + sex, family = binomial(link = logit),
     data = y)

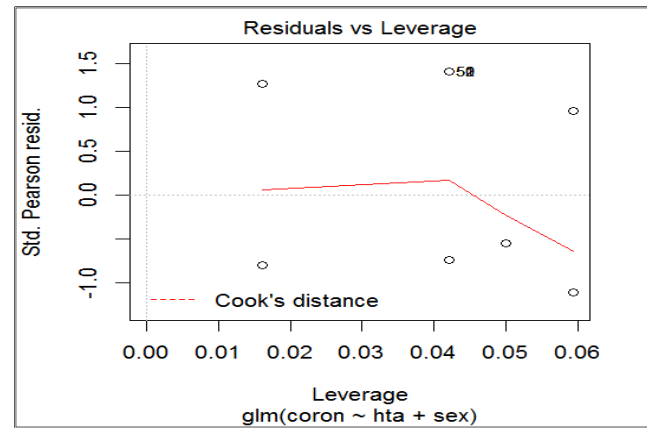
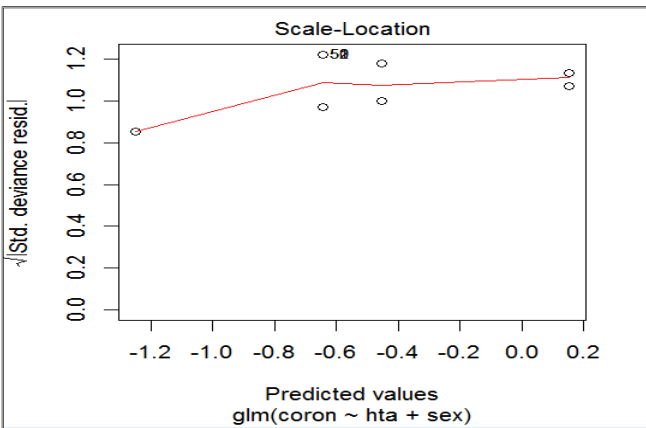
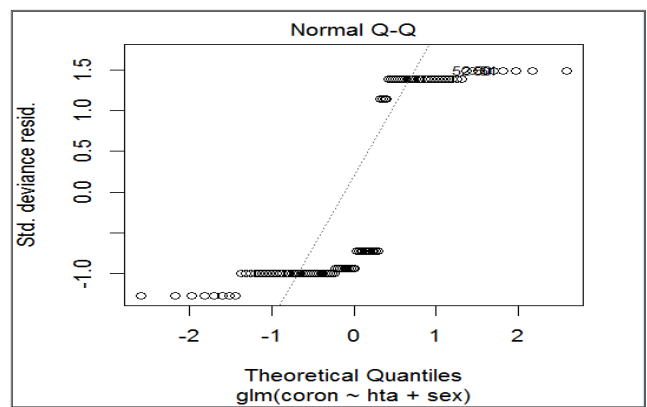
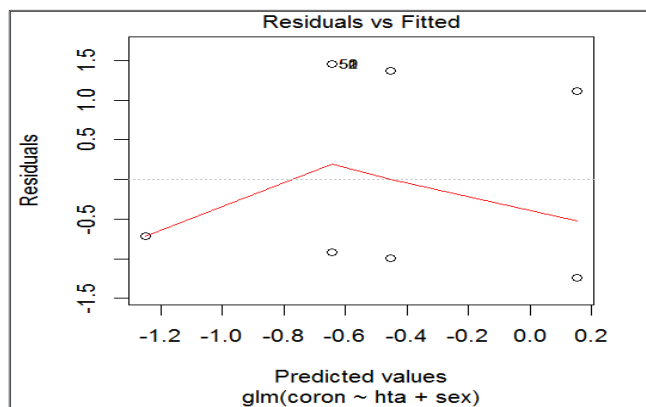
Deviance Residuals:
     Min       1Q   Median       3Q      Max
-1.2425  -0.9922  -0.9191   1.3747   1.4599

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.2476     0.5371  -2.323  0.0202 *
hta           0.6044     0.5149   1.174  0.2405
sex           0.7949     0.5396   1.473  0.1407
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 132.81  on 99  degrees of freedom
Residual deviance: 130.22  on 97  degrees of freedom
AIC: 136.22

Number of Fisher Scoring iterations: 4
```



Interpretation:

On a : $y = -1.2476 + 0.6044\text{hta} + 0.7949\text{sex}$

$$OR_{hta} = e^{0.6044} = 1.8267$$

$$OR_{sex} = e^{0.7949} = 2.2088$$

$$\text{On a aussi : } \pi(x_i) = \frac{\exp^{-1.2476 + 0.6044\text{hta} + 0.7949\text{sex}}}{1 + \exp^{-1.2476 + 0.6044\text{hta} + 0.7949\text{sex}}}$$

On a remarquer depuis summary (k) que le Test de Wald nous donne les résultats suivant :

$$\frac{\beta_{hta}}{\delta(\beta_{hta})} = 1.174 \quad , \quad \frac{\beta_{sex}}{\delta(\beta_{sex})} = 1.473$$

Et que la déviance égal : $D(m_0) = 132.81$ $D(m_1) = 130.22$ où :

$$m_0 = -0.4035 \quad m_1 = -1.2476 + 0.6044\text{hta} + 0.7949\text{sex}$$

$$\text{alors : } U = D(m_0) - D(m_1) = 132.81 - 130.22 = 2.59 \sim \chi_{97}^2$$

D'où : au niveau de signification $\alpha = 0.10$, on a remarquer que le **sex** et **hta** faisant une signification à la maladie du "coronarienne" à cause de ($OR_{hta} > 1$, $OR_{sex} > 1$)

D'après les 3ème partie on conclure que meilleure modèle est :

$$Y = -1.2476 + 0.6044\text{hta} + 0.7949\text{sex}$$