**Enonce de TP:**

**coron=c(1,0,1,0,0,1,0,0,0,0,0,0,0,1,0,1,0,0,0,1,0,1,1,1,0,1,1,1,0,0,1,0,0,0,0,0,1,1,0,0,0,1,0,0,0,0,0,0,0,1,1,1,0,1,0,0,1,0,1,0,0,0,1,1,0,1,1,0,1,1,0,0,0,1,0,1,1,1,0,0,0,0,0,1,1,0,0,0,0,1,1,1,0,0,0,0,0,1,0,0)**

**hta=c(0,0,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,1,1,0,0,0,1,0,1,1,1,1,1,1,0,1,1,1,0,1,0,0,0,1,0,0,0,0,0,1,0,0,0,0,0,0,0,1,1,0,0,0,1,0,0,1,0,0,1,1,1,1,0,0,0,1,1,1,1)**

**sex=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0)**

**y=data.frame(coron,sex,hta)**

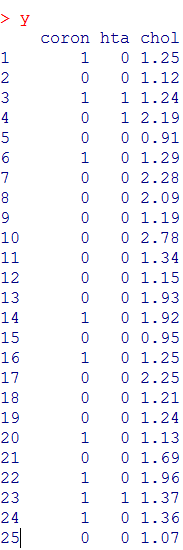
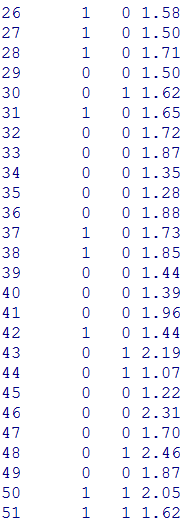
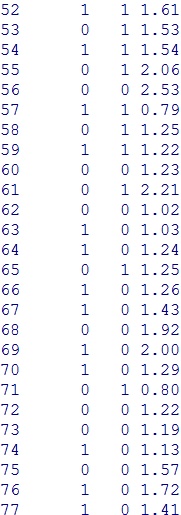
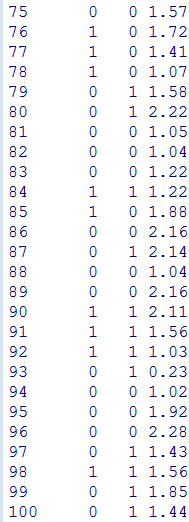
**resu<-glm(coron~hta+sex,family=binomial(link=logit),data=y)**

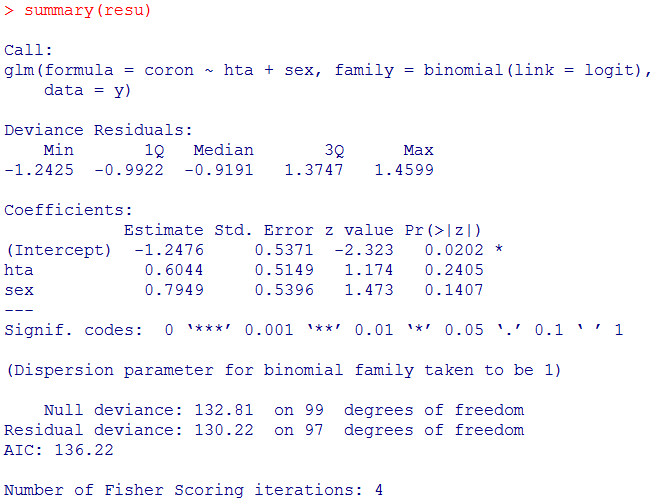
**resu**

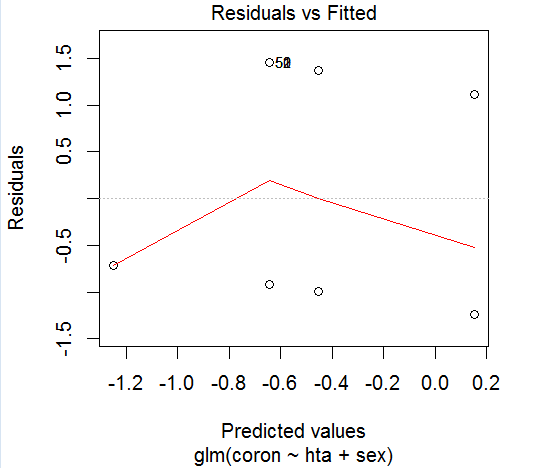
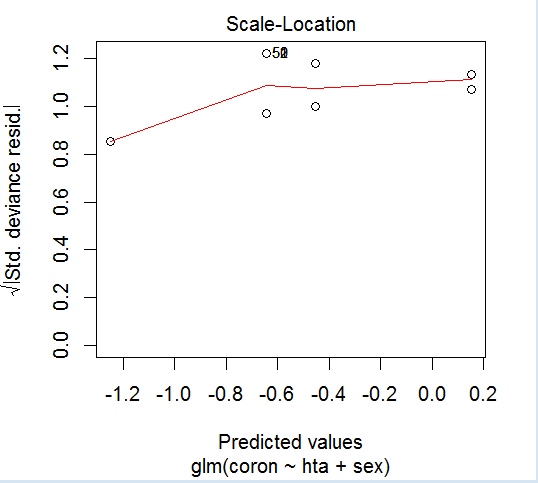
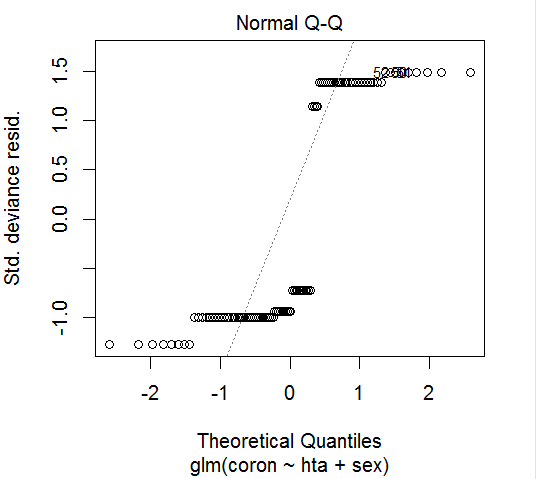
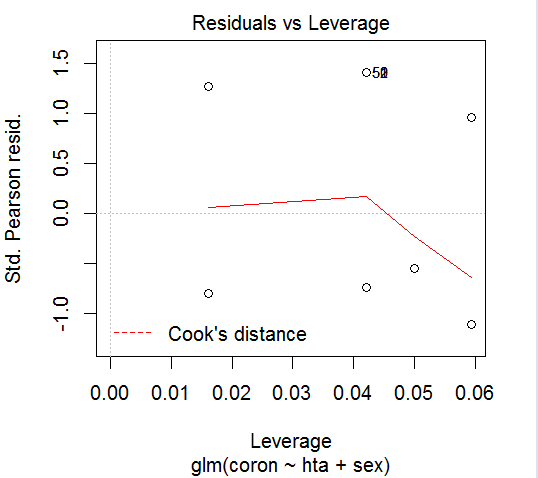
**summary(resu)**

**plot(resu)**

***Execution:***

**   **

****

***Interpretation:***

**On a : y=** -1.2476+0.6044**hta**+0.7949**sex**

**= = 1.8267**

**= = 2.2088**

On a aussi : π=

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

= 1.174 , =1.473

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

= -0.4035 =-1.2476+0.6044**hta**+0.7949**sex**

alors : U= D()- D( =132.81-130.22 = 2.59 ~

D’où : au niveau de signification α = 0.10 ,on a remarquer que le **sex** et **hta** faisant une signification à la maladie du "coronarienne" à cause de ( **> 1, > 1)**

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

**Y= -1.2476+0.6044hta+0.7949sex**