

Enonce de TP:

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

[illegible][illegible]

chol=c(1.25,1.12,1.24,2.19,0.91,1.29,2.28,2.09,1.19,2.78,1.34,1.15,1.93,1.92,0.95,1.25,2.25,1.21,1.24,1.13,1.69,1.96,1.37,1.36,1.07,1.58,1.5,1.71,1.5,1.62,1.65,1.72,1.87,1.35,1.28,1.88,1.73,1.85,1.44,1.39,1.96,1.44,2.19,1.07,1.22,2.31,1.7,2.46,1.87,2.05,1.62,1.61,1.53,1.54,2.06,2.53,0.79,1.25,1.22,1.23,2.21,1.02,1.03,1.24,1.25,1.26,1.43,1.92,2,1.29,0.8,1.22,1.19,1.13,1.57,1.72,1.41,1.07,1.58,2.22,1.05,1.04,1.22,1.22,1.88,2.16,2.14,1.04,2.16,2.11,1.56,1.03,0.23,1.02,1.92,2.28,1.43,1.56,1.85,1.44)

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y=data.frame(coron,sex,hta,chol)
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resu<-glm(coron~hta+sex+chol,family=binomial(link=logit),data=y)
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summary(resu)

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plot(resu)
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Execution:

[illegible]

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> summary(resu)

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

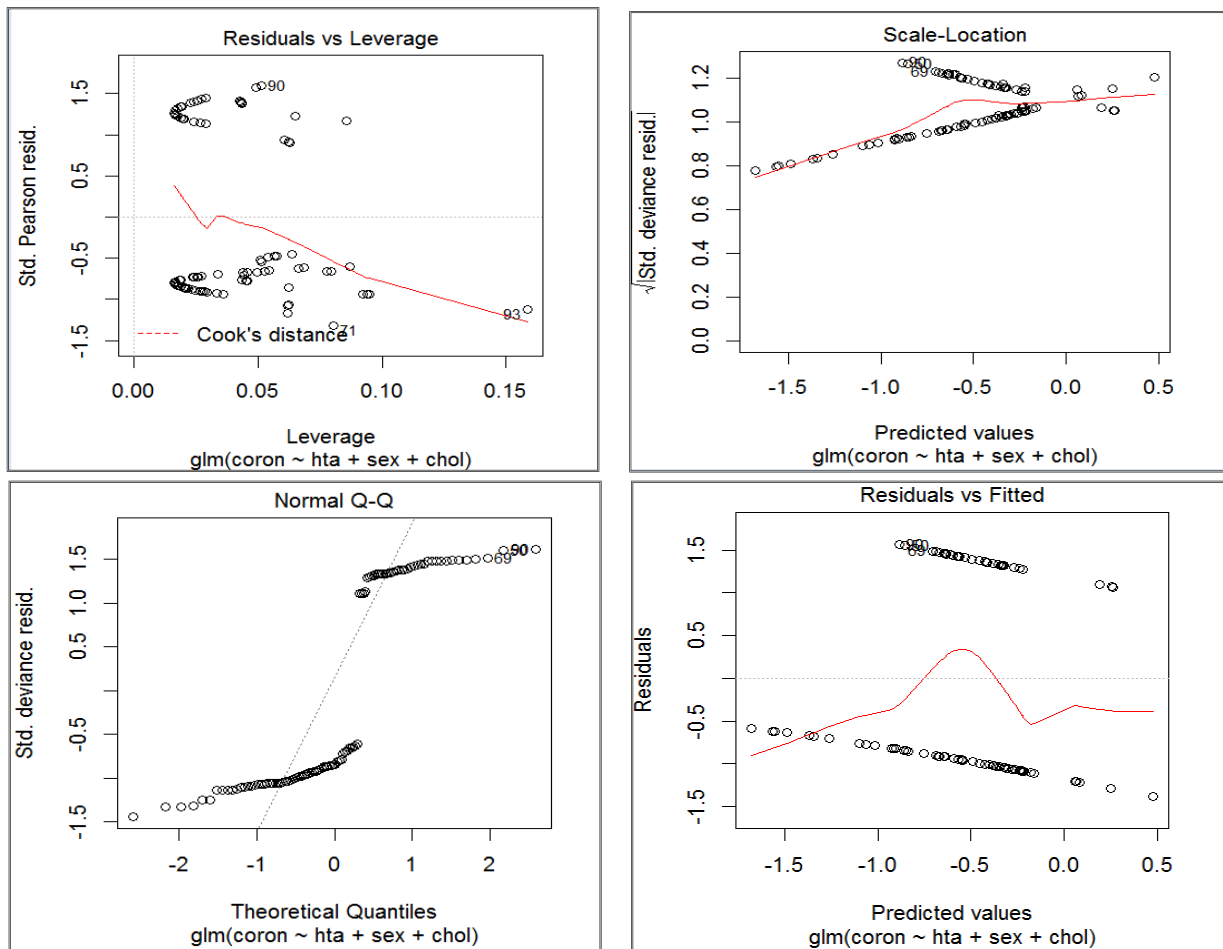
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.3839  -1.0293  -0.8168   1.3238   1.5693

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.4035     0.9656  -0.418   0.676
hta          0.5780     0.5199   1.112   0.266
sex          0.7010     0.5520   1.270   0.204
chol        -0.5027     0.4844  -1.038   0.299

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 132.81  on 99  degrees of freedom
Residual deviance: 129.13  on 96  degrees of freedom
AIC: 137.13

Number of Fisher Scoring iterations: 4
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Interpretation:

On a : $y = -0.4035 + 0.5780\text{hta} + 0.7010\text{sex} - 0.5027\text{chol}$

$$OR_{hta} = e^{0.578} = 1.7793 \quad OR_{chol} = e^{-0.5027} = 0.6058$$

$$OR_{sex} = e^{0.7010} = 2.0114$$

$$\text{On a aussi : } \pi(x_i) = \frac{\exp^{-0.4035 + 0.5780\text{hta} + 0.7010\text{sex} - 0.5027\text{chol}}}{1 + \exp^{-0.4035 + 0.5780\text{hta} + 0.7010\text{sex} - 0.5027\text{chol}}}$$

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

$$\frac{\beta_{hta}}{\delta(\beta_{hta})} = 1.112, \quad \frac{\beta_{sex}}{\delta(\beta_{sex})} = 1.270, \quad \frac{\beta_{chol}}{\delta(\beta_{chol})} = -1.038$$

Et que la déviance égal : $D(m_0) = 132.81$ $D(m_1) = 129.13$ où :

$$m_0 = -0.4035 \quad \text{et} \quad m_1 = -0.4035 + 0.5780\text{hta} + 0.7010\text{sex} - 0.5027\text{chol}$$

$$\text{alors : } U = D(m_0) - D(m_1) = 132.81 - 129.13 = 3.68 \sim \chi_{96}^2$$

D'où : au niveau de signification $\alpha = 0.2$, on a remarqué que le sex et hta font une signification à la maladie du "coronarienne" à cause de ($OR_{hta} > 1$, $OR_{sex} > 1$) et Chol n'est pas significatif car ($OR_{chol} \leq 1$) , alors le meilleur modèle qui représente la signification à la maladie de coronarienne est :

$$y = -0.4035 + 0.5780\text{hta} + 0.7010\text{sex} - 0.5027\text{chol}$$