

Enonce de TP:

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

[illegible]

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

```
age=c(47,58,44,67,60,72,54,56,67,49,69,64,73,49,68,58,81,49,69,38,75,82,75,51,66,43,33,85,51,83,47,81,61,60,34,33,58
,73,81,56,70,82,62,77,57,49,71,42,75,42,79,96,77,76,79,76,62,54,53,53,66,66,62,48,54,42,63,62,55,79,72,66,59,84,67,76
,82,71,70,66,52,46,30,60,58,70,63,60,57,77,83,29,28,29,75,40,56,31,73,70)
```

```
chol=c(1.25,1.12,1.24,2.19,0.91,1.29,2.28,2.09,1.19,2.78,1.34,1.15,1.93,1.92,0.95,1.25,2.25,1.21,1.24,1.13,1.69,1.96,1.3
7,1.36,1.07,1.58,1.5,1.71,1.5,1.62,1.65,1.72,1.87,1.35,1.28,1.88,1.73,1.85,1.44,1.39,1.96,1.44,2.19,1.07,1.22,2.31,1.7,2.
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.
19,1.13,1.57,1.72,1.41,1.07,1.58,2.22,1.05,1.04,1.22,1.22,1.88,2.16,2.14,1.04,2.16,2.11,1.56,1.03,0.23,1.02,1.92,2.28,1.4
3,1.56,1.85,1.44)
```

```
y=data.frame(coron,sex,hta,age,chol)
```

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

resu

summary(resu)

```
plot(resu)
```

exécution de modèle logistique :

codage R :

```
> coron=c(1,0,1,0,0,1,0,0,0,0,0,0,1,0,1,0,0,0,1,0,1,1,1,0,1,1,1,0,0,1,0,0,0,0,0,1,1,0,0,0,1,0,0,0,0,0,0,1,1,0,1,0,0,1,0,1,0,$
> hta=c(0,0,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,0,0,0,0,1,0,1,1,1,1,1,0,1,1,1,0,1,$
> sex=c(1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,1,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,1,1,1,1,$
> age=c(47,58,44,67,60,72,54,56,67,49,69,64,73,49,68,58,81,49,69,38,75,82,75,51,66,43,33,85,51,83,47,81,61,60,34,33,58,73,81,56,70,$
> 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,$
> y=data.frame(coron,sex,hta,age,chol)
> resu<-glm(coron~age+hta+sex+chol,family=binomial(link=logit),data=y)
> y|
```

```
> y
      coron sex hta age chol
1         1   1   0  47 1.25
2         0   1   0  58 1.12
3         1   1   1  44 1.24
4         0   1   1  67 2.19
5         0   1   0  60 0.91
6         1   1   0  72 1.29
7         0   1   0  54 2.28
8         0   1   0  56 2.09
9         0   1   0  67 1.19
10        0   1   0  49 2.78
11        0   1   0  69 1.34
12        0   1   0  64 1.15
13        0   1   0  73 1.93
14        1   1   0  49 1.92
15        0   1   0  68 0.95
16        1   1   0  58 1.25
17        0   1   0  81 2.25
18        0   1   0  49 1.21
19        0   1   0  69 1.24
20        1   1   0  38 1.13
21        0   1   0  75 1.69
22        1   1   0  82 1.96
23        1   1   1  75 1.37
```

```
24        1   1   0  51 1.36
25        0   1   0  66 1.07
26        1   1   0  43 1.58
27        1   1   0  33 1.50
28        1   1   0  85 1.71
29        0   1   0  51 1.50
30        0   1   1  83 1.62
31        1   1   0  47 1.65
32        0   1   0  81 1.72
33        0   1   0  61 1.87
34        0   1   0  60 1.35
35        0   1   0  34 1.28
36        0   1   0  33 1.88
37        1   1   0  58 1.73
38        1   1   0  73 1.85
39        0   1   0  81 1.44
40        0   1   0  56 1.39
41        0   1   0  70 1.96
42        1   1   0  82 1.44
43        0   0   1  62 2.19
44        0   0   1  77 1.07
45        0   0   0  57 1.22
46        0   0   0  49 2.31
47        0   0   0  71 1.70
48        0   0   1  42 2.46
```

```
49        0   0   0  75 1.87
50        1   0   1  42 2.05
51        1   0   1  79 1.62
52        1   0   1  96 1.61
53        0   0   1  77 1.53
54        1   0   1  76 1.54
55        0   0   1  79 2.06
56        0   0   0  76 2.53
57        1   0   1  62 0.79
58        0   1   1  54 1.25
59        1   1   1  53 1.22
60        0   1   0  53 1.23
61        0   1   1  66 2.21
62        0   1   0  66 1.02
63        1   1   0  62 1.03
64        1   1   0  48 1.24
65        0   1   1  54 1.25
66        1   1   0  42 1.26
67        1   1   0  63 1.43
68        0   1   0  62 1.92
69        1   1   0  55 2.00
70        1   1   0  79 1.29
71        0   1   1  72 0.80
72        0   1   0  66 1.22
73        0   1   0  59 1.19
```

```
74        1   1   0  84 1.13
75        0   1   0  67 1.57
76        1   1   0  76 1.72
77        1   1   0  82 1.41
78        1   1   0  71 1.07
79        0   1   1  70 1.58
80        0   1   1  66 2.22
81        0   1   0  52 1.05
82        0   1   0  46 1.04
83        0   1   0  30 1.22
84        1   1   1  60 1.22
85        1   1   0  58 1.88
86        0   0   0  70 2.16
87        0   0   1  63 2.14
88        0   0   0  60 1.04
89        0   0   0  57 2.16
90        1   0   1  77 2.11
91        1   0   1  83 1.56
92        1   0   1  29 1.03
93        0   0   1  28 0.23
94        0   0   0  29 1.02
95        0   0   0  75 1.92
96        0   0   0  40 2.28
97        0   0   1  56 1.43
98        1   0   1  31 1.56
99        0   0   1  73 1.85
100       0   0   1  70 1.44
```

```
> resu
```

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

```
Coefficients:
```

```
(Intercept)      age      hta      sex      chol
-0.566676    0.003327    0.566521    0.694565   -0.524564
```

```
Degrees of Freedom: 99 Total (i.e. Null); 95 Residual
```

```
Null Deviance: 132.8
```

```
Residual Deviance: 129.1 AIC: 139.1
```

```
> summary(resu)
```

Call:

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

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.4022	-1.0309	-0.8005	1.3260	1.5917

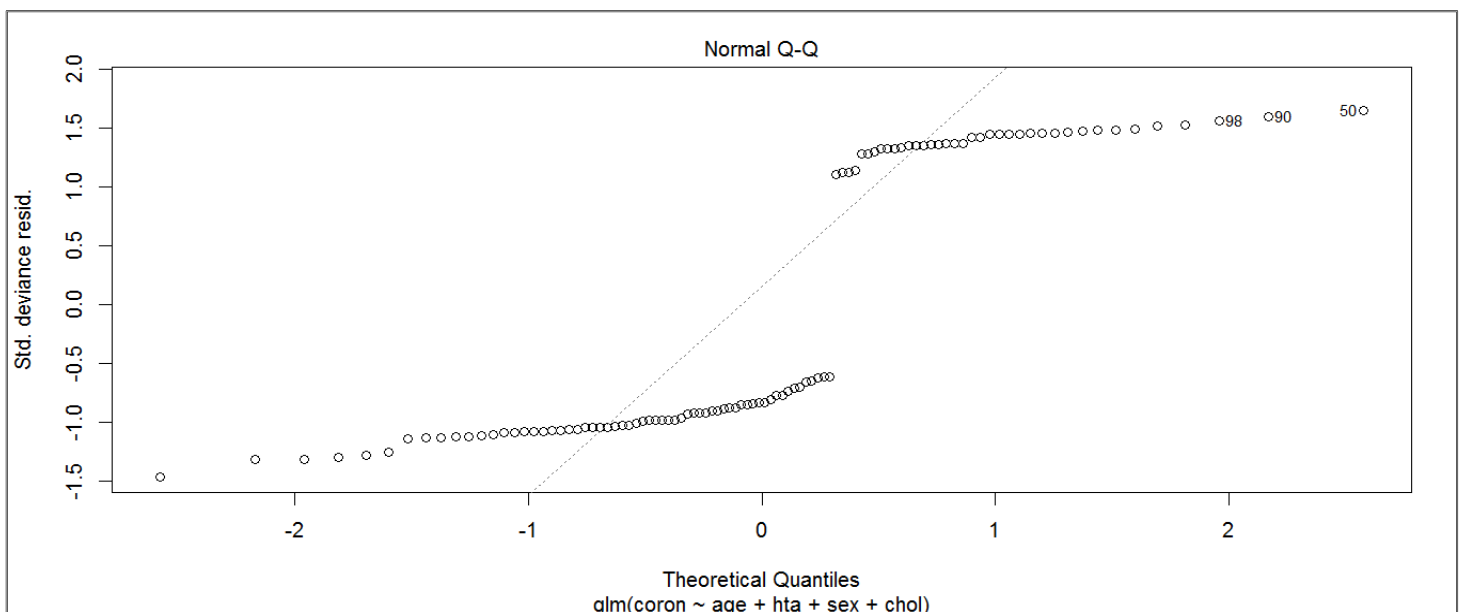
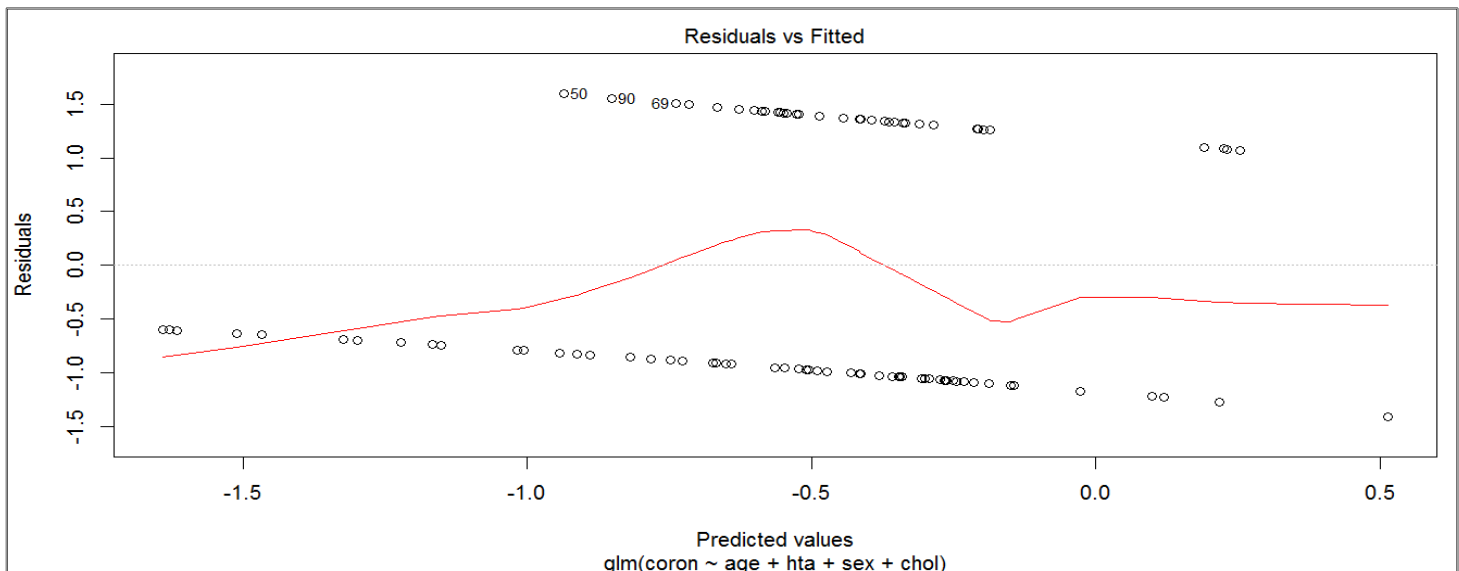
Coefficients:

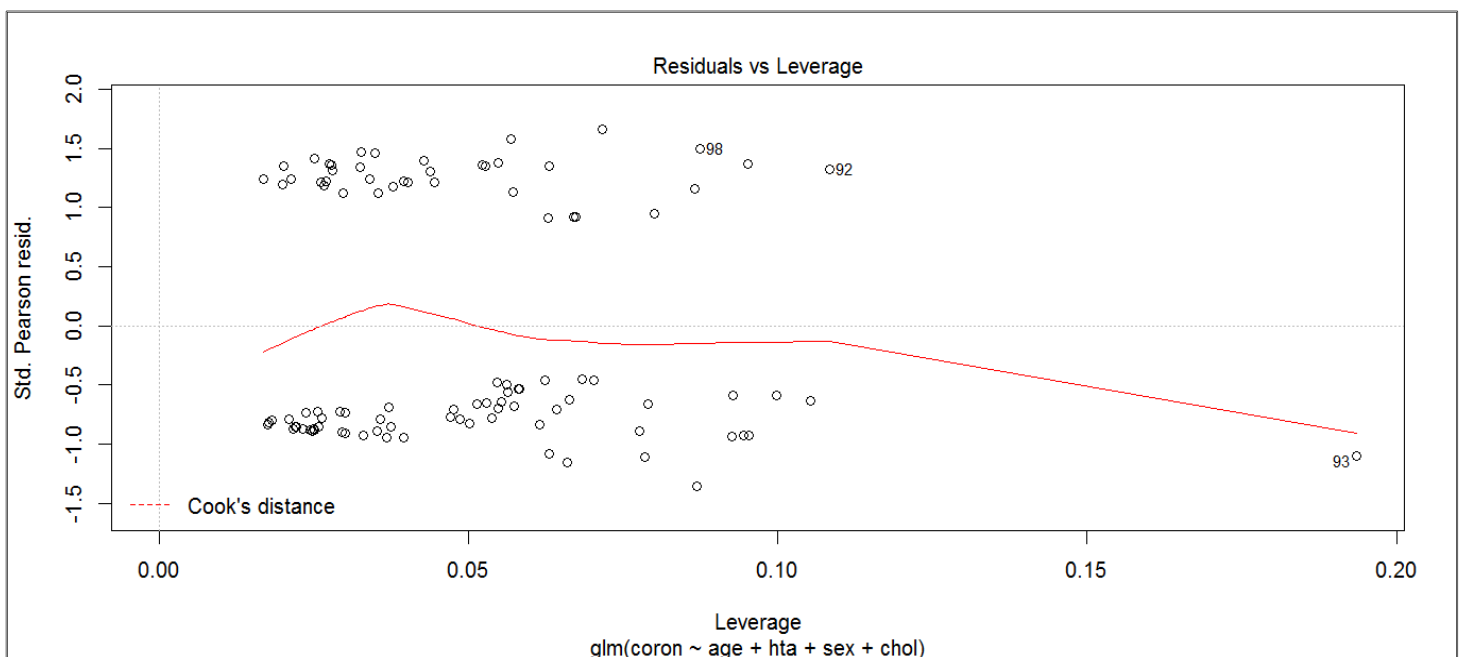
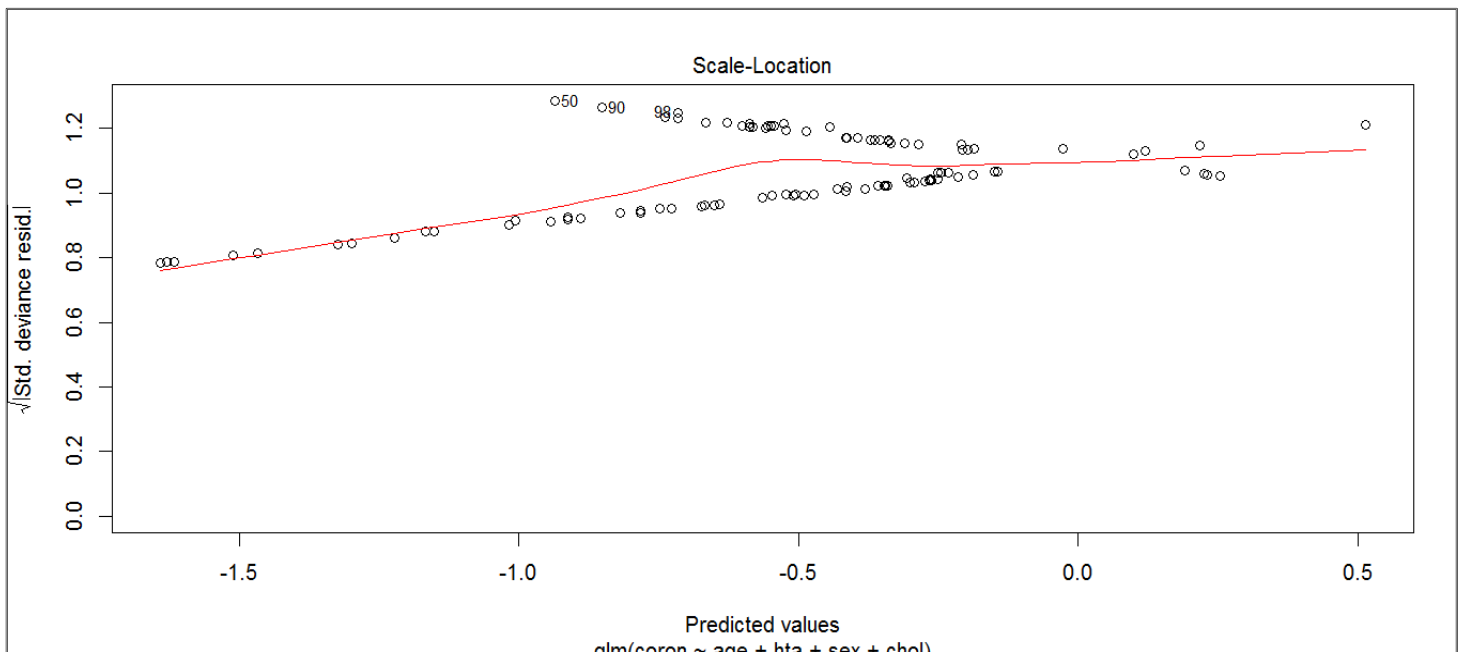
	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.566676	1.194639	-0.474	0.635
age	0.003327	0.014263	0.233	0.816
hta	0.566521	0.522273	1.085	0.278
sex	0.694565	0.552861	1.256	0.209
chol	-0.524564	0.494976	-1.060	0.289

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 132.81 on 99 degrees of freedom
Residual deviance: 129.07 on 95 degrees of freedom
AIC: 139.07

Number of Fisher Scoring iterations: 4





La forme du modèle logistique :

Coefficients:				
(Intercept)	age	hta	sex	chol
-0.566676	0.003327	0.566521	0.694565	-0.524564

Donc:

$$Y = \alpha + \beta_1 \text{age} + \beta_2 \text{hta} + \beta_3 \text{sex} - \beta_4 \text{chol} + \xi$$

$$Y = -0.566676 + 0.003327 \text{age} + 0.566521 \text{hta} + 0.694565 \text{sex} - 0.524564 \text{chol}$$

Test de signification du modèle :

$$1) OR_{\text{age}} = e^{0.003327} = 1.0033$$

$$3) OR_{\text{sex}} = e^{0.694565} = 2.0028$$

$$2) OR_{\text{hta}} = e^{0.566521} = 1.7621$$

$$4) OR_{\text{chol}} = e^{-0.524564} = 0.5918$$

Interprétation :

```
Coefficients:
      Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.566676    1.194639  -0.474    0.635
age          0.003327    0.014263   0.233    0.816
hta          0.566521    0.522273   1.085    0.278
sex          0.694565    0.552861   1.256    0.209
chol        -0.524564    0.494976  -1.060    0.289

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 132.81  on 99  degrees of freedom
Residual deviance: 129.07  on 95  degrees of freedom
AIC: 139.07
```

On a comme ($OR_{hta} > 1$) et ($OR_{sex} > 1$) alors (hta) et (sex) respectivement ont un effets positives a la maladie du "coronarienne " .

Nous savons que (OR) est un mesure de l'effet d'un facteur de risque , ce qui donne une idée générale du signification de ces facteurs de risque comme (hta, sex,.....) sur la malade du "coronarienne " dans cette étude .

Donc on trouve que les personnes qui sont malades et exposé de (hta) au même temps presque deux fois plus grand que les gens qui sont malade et ne sont pas exposé . De plus on remarque que la proportion ou la probabilité des femmes qui souffrent de la maladie du "coronarienne" sont deux fois plus grand que les hommes qui atteintes à cette maladie.

En revanche , nous voyons que ($OR_{age} \leq 1$) et ($OR_{chol} \leq 1$) .alors l'âge et le cholestérol n'ont aucun effet sur le risque de la maladie du "coronarienne".

Donc le modèle devient :

$$Y = -0.566676 + 0.566521 \text{hta} + 0.694565 \text{sex}$$

