

Devoir 1: Mise à niveau en statistiques

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1. Contexte

Certaines études d'observation suggèrent qu'un faible apport alimentaire ou une faible concentration en retinol, bêta-carotène ou d'autres carténoïdes pourraient être associé avec une augmentation du risque de développer certains types de cancer.

Cependant, relativement peu d'études ont enquêté sur le lien entre, d'une part les caractéristiques personnelles et les facteurs d'ordres alimentaires et d'autre part, la concentration plasmatique en retinol, bêta-carotène et d'autres carténoïdes.

Les sujets de l'étude, ($n = 315$) sont des patients ayant subit une intervention chirurgicale non urgente pendant une période de 3 ans et ayant pour but la biopsie ou l'ablation d'une lésion du poumon, du colon, du sein, de la peau, des ovaires ou de l'utérus s'étant avérée non cancéreuse.

2. Packages, données

2.1 Packages

```
library(tidyverse)

## -- Attaching packages ----

## v ggplot2 3.2.1     v purrr   0.3.3
## v tibble   2.1.3     v dplyr    0.8.3
## v tidyverse 1.0.0     v stringr  1.4.0
## v readr    1.3.1     v forcats 0.4.0

## -- Conflicts --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()   masks stats::lag()

library(ggplot2)
library(GGally)

## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2

##
## Attaching package: 'GGally'

## The following object is masked from 'package:dplyr':
## 
##   nasa

library(corrplot)

## corrplot 0.84 loaded

library(questionr)
library(RColorBrewer)
library(psy)
library(kableExtra)

##
## Attaching package: 'kableExtra'

## The following object is masked from 'package:dplyr':
## 
##   group_rows

library(tinytex)
library(xtable)
```

2.2 Importation des données

```
setwd(dir = "C:/Users/odeli/Desktop/Devoir1")
retinol = read.csv2("presentationTPretinol.csv", header = T, sep = ";")
```

2.3 Vérification des types des variables

Le jeu de données rétinol est composé de 315 sujets et de 14 variables:

- `age` : Age (en années)
- `sexe` : 1=Masculin, 2=Féminin
- `tabac` : 1 = jamais, 2 = autrefois, 3 = actuellement
- `bmi` : $\frac{\text{poids}}{(\text{taille}^2)}$
- `vitamines` : 1 = oui souvent, 2 = oui pas souvent, 3 = non
- `calories` : Nombre de calories par jour
- `graisses` : Grammes de graisse consommés par jour
- `fibres` : Grammes de fibre consommés par jour
- `alcool` : Nombre de verres d'alcool consommés par semaine
- `cholesterol` : Cholesterol consommé (mg par jour)
- `betadiet` : beta-carotene consommé (mcg par jour)
- `retdiet` : retinol consommé (mcg par jour)
- `betplasma` : beta-carotene plasmatique (ng/ml)
- `retplasma` : Retinol plasmatique (ng/ml)

On remarque que les variables catégorielles ont été considérées comme des entiers: sexe, vitamines, tabac.... Il faut y remédier:

```
retinol$sexe = as.factor(retinol$sexe)
levels(retinol$sexe) = c("Hommes", "Femmes")
retinol$sexe = relevel(retinol$sexe, ref = "Hommes")
retinol$tabac = as.factor(retinol$tabac)
levels(retinol$tabac) = c("Jamais", "Autrefois", "Fumeur")
retinol$tabac = relevel(retinol$tabac, ref = "Jamais")
retinol$vitamine = as.factor(retinol$vitamine)
levels(retinol$vitamine) = c("Souvent", "Pas-souvent", "Non" )
retinol$vitamine = relevel(retinol$vitamine, ref = "Non")
```

2.4 Vue globale et chiffrée des données

2.4.1 Variables quantitatives

```
names = c("Âge", "BMI", "Calories", "Graisses", "Fibres", "Alcool", "Cholesterol",
        "Bêta-carotène", "Rétinol", "Bêta-carotène plasmatique", "Rétinol plasmatique")
type_l = lapply(retinol[,c(1,4,6:14)], class)
min_l = lapply(retinol[,c(1,4,6:14)], min)
max_l = lapply(retinol[,c(1,4,6:14)], max)
sd_l = lapply(retinol[,c(1,4,6:14)], sd)
median_l = lapply(retinol[,c(1,4,6:14)], median)
mean_l = lapply(retinol[,c(1,4,6:14)], mean)

type = c()
min = c()
sd = c()
median = c()
mean = c()
max = c()

for(i in 1:11){
  type[i] = type_l[[i]]
```

Table 1: Tableau descriptif des variables quantitatives

Variables	Type	Mean	Standard Deviation	Median	Min	Max	NA
Âge	integer	50.15	14.58	48	19	83	0
BMI	numeric	26.16	6.01	24.74	16.33	50.4	0
Calories	numeric	1796.65	680.35	1666.8	445.2	6662.2	0
Graisses	numeric	77.03	33.83	72.9	14.4	235.9	0
Fibres	numeric	12.79	5.33	12.1	3.1	36.8	0
Alcool	numeric	3.28	12.32	0.3	0	203	0
Cholestérol	numeric	242.46	131.99	206.3	37.7	900.7	0
Bêta-carotène	integer	2185.6	1473.89	1802	214	9642	0
Rétinol	integer	832.71	589.29	707	30	6901	0
Bêta-carotène plasmatique	integer	189.89	183	140	0	1415	0
Rétinol plasmatique	integer	602.79	208.9	566	179	1727	0

```

min[i] = min_1[[i]]
max[i] = max_1[[i]]
sd[i] = sd_1[[i]]
median[i] = median_1[[i]]
mean[i] = mean_1[[i]]
}

na = c()
j = 1
for(i in c(1,4,6:14)){
  na[j] = length(which(is.na(retinol[,i])))
  j = j+1}

desc_var_quant = cbind(names, type, round(mean,2),
                      round(sd,2), round(median,2),
                      round(min,2), round(max,2), na )
colnames(desc_var_quant) = c("Variables","Type","Mean",
                            "Standard Deviation","Median","Min","Max", "NA")

kable(desc_var_quant,
      caption = "Tableau descriptif des variables quantitatives") %>% kable_styling(latex_options = "st

```

2.4.2 Variables qualitatives

```

tab_sexe = cbind( t(t(table(Sexe = retinol$sexes))) ,
                  round(t(t(prop.table(table(retinol$sexes))))*100 ,2) )
tab_tabac = cbind( t(t(table(tabac))) ,
                  round(t(t(prop.table(table(retinol$tabac))))*100 ,2) )
tab_vitamine = cbind( t(t(table(vitamine))) ,
                     round(t(t(prop.table(table(retinol$vitamine))))*100 ,2) )
desc_var_qual = rbind(tab_sexe,tab_tabac,tab_vitamine)

kable(desc_var_qual, caption = "Tableau descriptif des variables qualitatives",
      col.names = c("N","%")) %>%
  pack_rows("Sexe", 1, 2, bold = T) %>%
  pack_rows("Tabac", 3, 5, bold = T) %>%

```

Table 2: Tableau descriptif des variables qualitatives

	N	%
Sexe		
Hommes	42	13.33
Femmes	273	86.67
Tabac		
Jamais	157	49.84
Autrefois	115	36.51
Fumeur	43	13.65
Vitamins		
Non	111	35.24
Souvent	122	38.73
Pas-souvent	82	26.03

```
pack_rows("Vitamins", 6, 8, bold = T) %>%
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")
```

3. Question 1: Description des variables

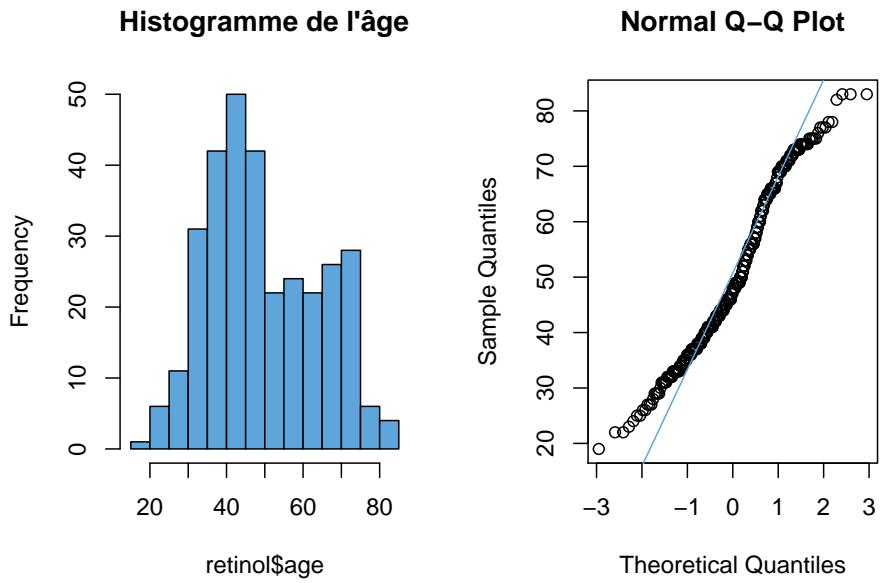
On peut distinguer deux groupes de variables :

- Celui des variables décrivant le style de vie des individus, composé de l'âge, du sexe, du bmi, du statut tabagique (tabac) et de la consommation d'alcool hebdomadaire (alcool).
- Celui des variables relatives à l'alimentation: les vitamines, les calories, les graisses, les fibres, le cholesterol, le bêta-carosène consommé (betadiet), le rétinol consommé (retddiet), le bêta-carosène plasmatique (betaplasma) et le rétinol plasmatique (retplasma).

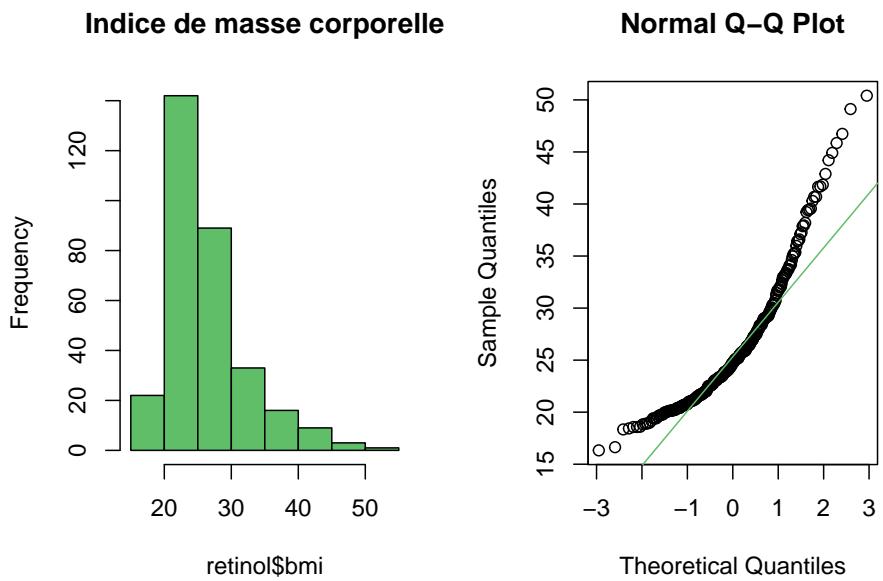
Pour les variables quantitatives, il est intéressant de regarder leur distribution ainsi que l'adéquation de ces dernières à des lois gaussiennes. Pour les variables qualitatives, on fait des barplot sur le pourcentage d'individus dans chacune des classes.

3.1 Variables de style de vie

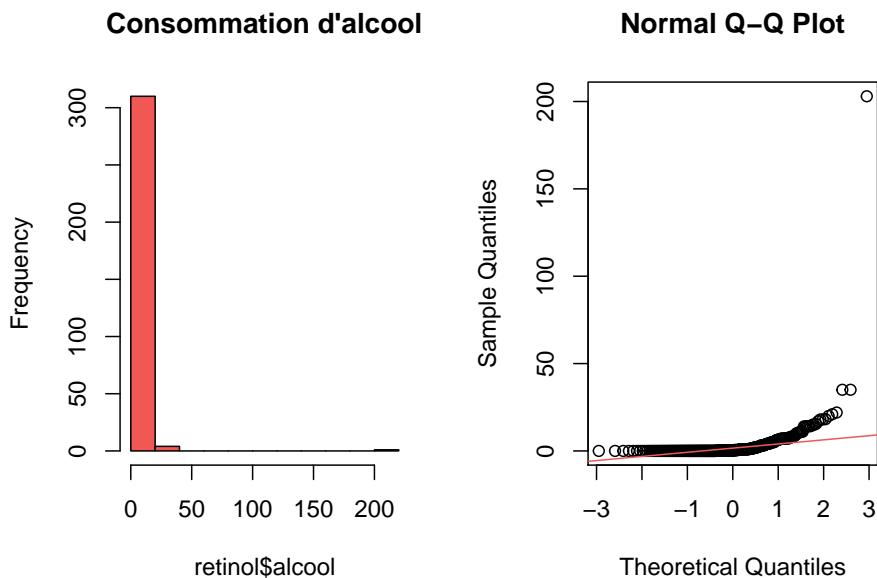
```
par(mfrow = c(1,2))
hist(retinol$age, main = "Histogramme de l'âge", col = "#5DA5DA" )
qqnorm(retinol$age); qqline(retinol$age, col = "#5DA5DA")
```



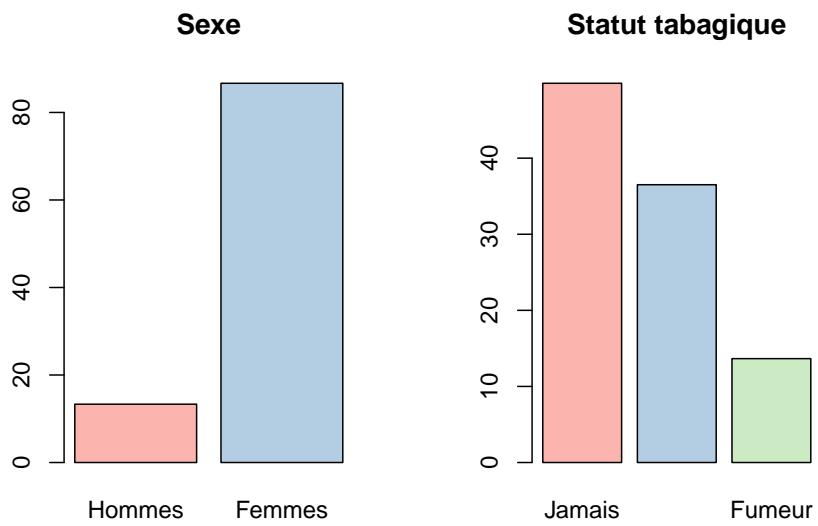
```
par(mfrow = c(1,2))
hist(retinol$bmi, main = "Indice de masse corporelle", col = "#60BD68" )
qqnorm(retinol$bmi); qqline(retinol$bmi, col = "#60BD68")
```



```
par(mfrow = c(1,2))
hist(retinol$alcool, main = "Consommation d'alcool", col = "#F15854" )
qqnorm(retinol$alcool); qqline(retinol$alcool, col = "#F15854")
```



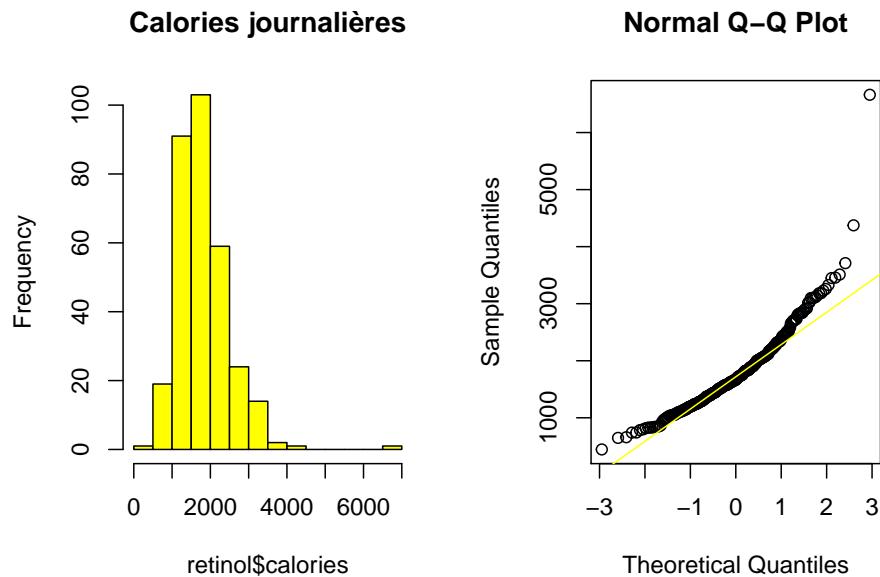
```
par(mfrow = c(1,2))
barplot(prop.table(table(retinol$sexe, useNA = "ifany"))*100, main = "Sexe",
       col = brewer.pal(n = 3, name = "Pastel1"))
barplot(prop.table(table(retinol$tabac, useNA = "ifany"))*100, main = "Statut tabagique",
       col = brewer.pal(n = 3, name = "Pastel1"))
```



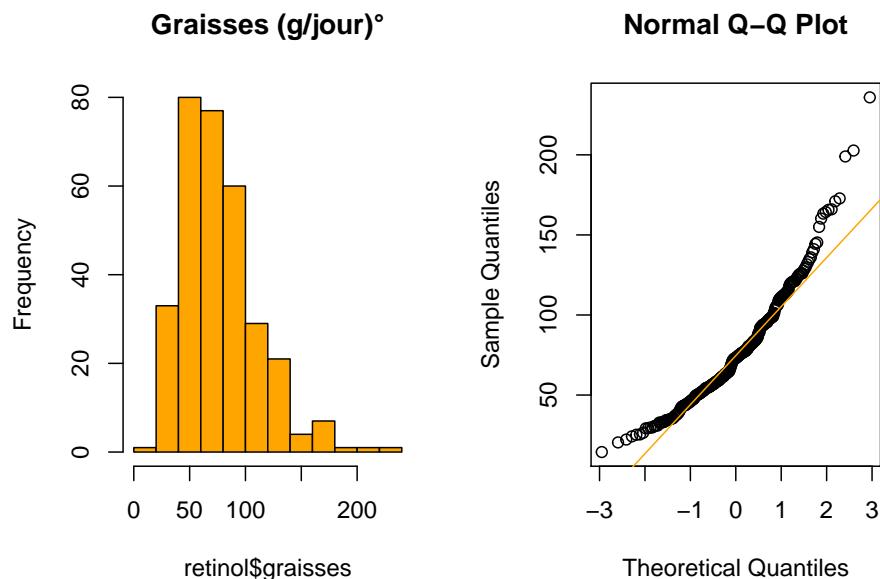
Variables d'habitudes alimentaires

```
par(mfrow = c(1,2))
hist(retinol$calories, main = "Calories journalières", col = "yellow")
```

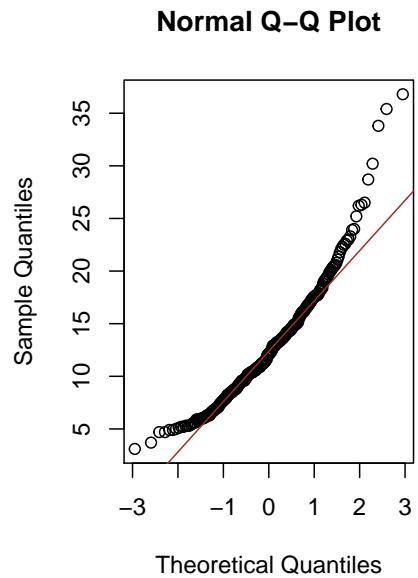
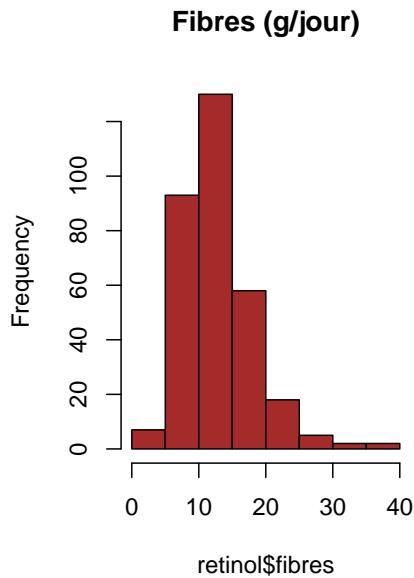
```
qqnorm(retinol$calories); qqline(retinol$calories, col = "yellow")
```



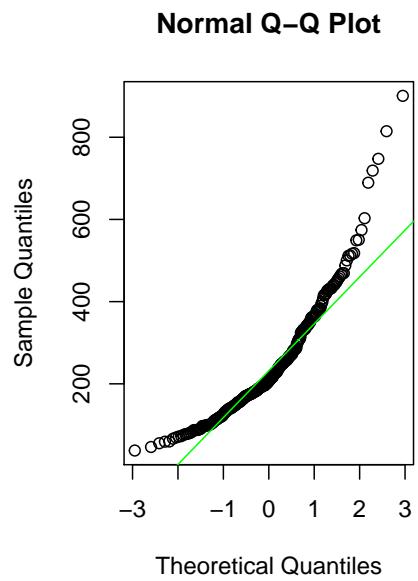
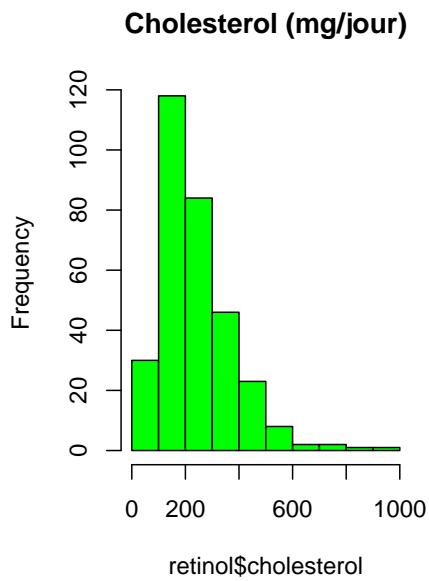
```
par(mfrow = c(1,2))
hist(retinol$graisses, main = "Graisses (g/jour)", col = "orange")
qqnorm(retinol$graisses); qqline(retinol$graisses, col = "orange")
```



```
par(mfrow = c(1,2))
hist(retinol$fibres, main = "Fibres (g/jour)", col = "brown")
qqnorm(retinol$fibres); qqline(retinol$fibres, col = "brown")
```

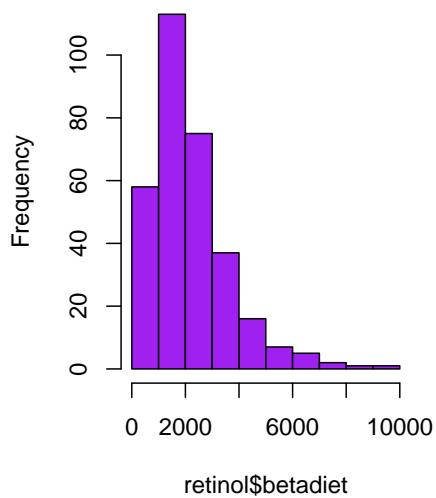


```
par(mfrow = c(1,2))
hist(retinol$cholesterol, main = "Cholesterol (mg/jour)", col = "green")
qqnorm(retinol$cholesterol); qqline(retinol$cholesterol, col = "green")
```

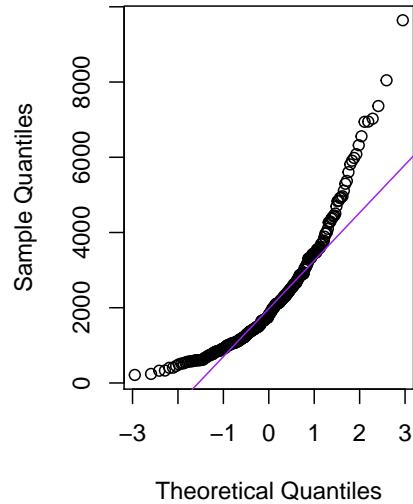


```
par(mfrow = c(1,2))
hist(retinol$betadiet, main = "Bêta-carotène consommé (mcg/jour)", col = "purple")
qqnorm(retinol$betadiet); qqline(retinol$betadiet, col = "purple")
```

Bêta-carotène consommé (mcg/jc)

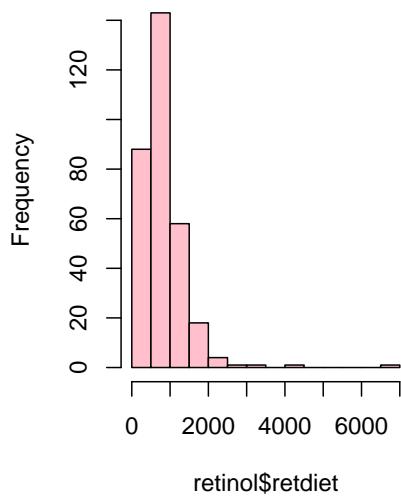


Normal Q–Q Plot

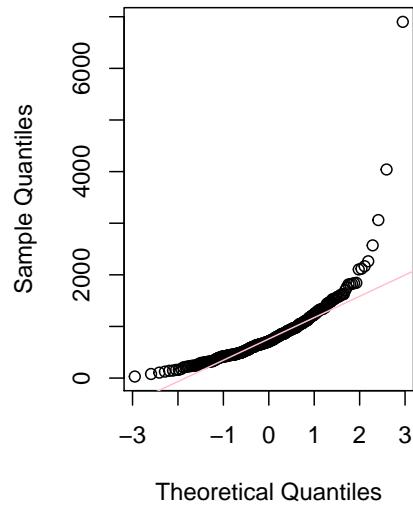


```
par(mfrow = c(1,2))
hist(retinol$retdiet, main = "Rétinol consommé (mcg/jour)", col = "pink")
qqnorm(retinol$retdiet); qqline(retinol$retdiet, col = "pink")
```

Rétinol consommé (mcg/jour)

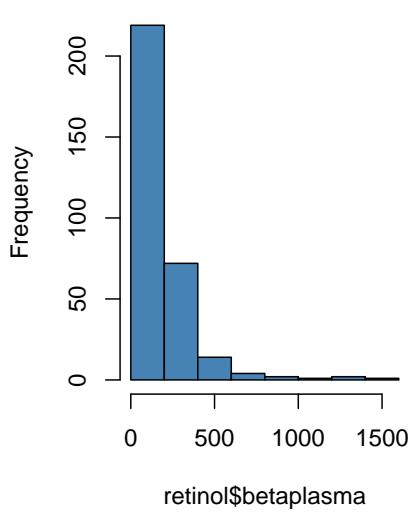


Normal Q–Q Plot

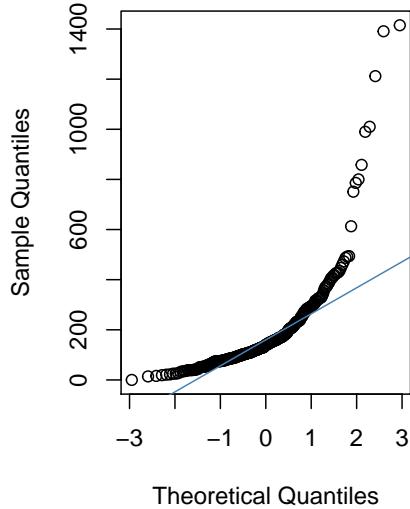


```
par(mfrow = c(1,2))
hist(retinol$betaplasma, main = "Bêta-carotène plasmatique (mcg/jour)", col = "steelblue")
qqnorm(retinol$betaplasma); qqline(retinol$betaplasma, col = "steelblue")
```

Bêta-carotène plasmatique (mcg/j)

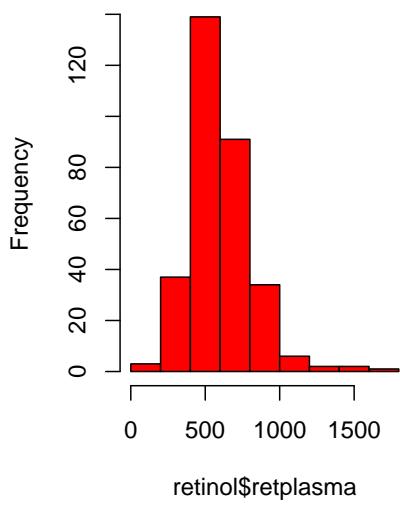


Normal Q–Q Plot

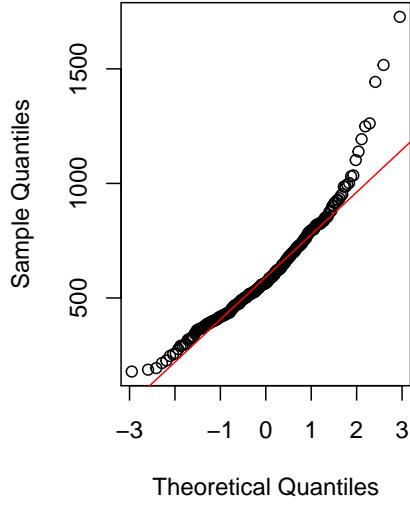


```
par(mfrow = c(1,2))
hist(retinol$retplasma, main = "Rétinol plasmatique (mcg/jour)", col = "red")
qqnorm(retinol$retplasma); qqline(retinol$retplasma, col = "red")
```

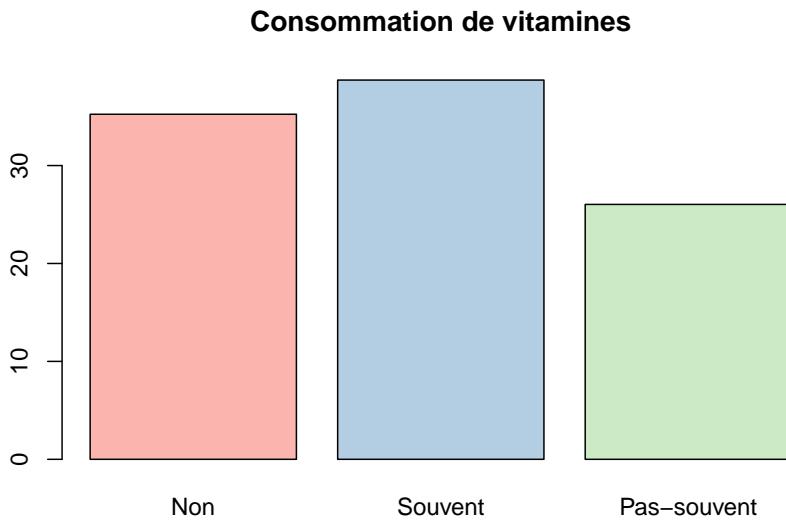
Rétinol plasmatique (mcg/jour)



Normal Q–Q Plot



```
barplot(prop.table(table(retinol$vitamine, useNA = "ifany"))*100, main = "Consommation de vitamines", c
```

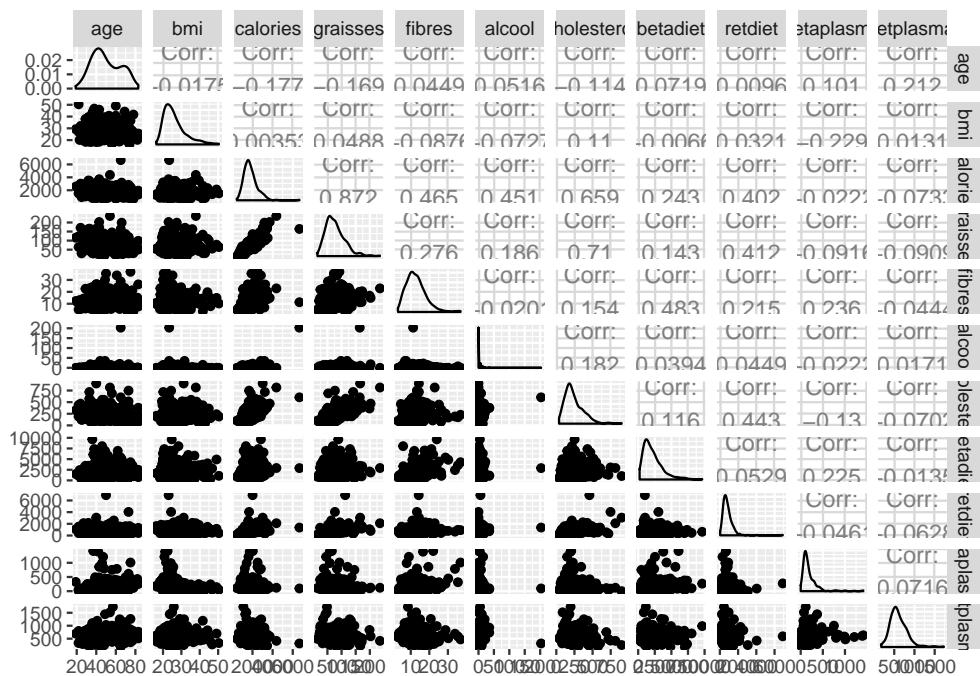


4. Question 2 : Etude des relations entre toutes les variables

4.1 Relations entre les variables quantitatives

En premier lieu, regardons la forme des nuages de points formés par les paires de variables quantitatives.

```
ggpairs(retinol[,c(1,4,6:14)], progress = F)
```



On remarque notamment une relation linéaire positive très marquée entre les calories et les graisses avec une

corrélation de de 0.872. De même on constate un lien entre les calories et le cholestérol comme en témoigne le nuage de points correspondant et la corrélation à 0.659. On observe encore un lien fort entre le cholestérol et les graisses.

Enfin, remarquons qu'une grande partie des corrélations entre variables quantitatives sont faibles.

Quelles sont les corrélations que l'on peut considérer comme nulles ? A l'aide d'une fonction assez simple, on peut afficher la matrice des valeurs du test de corrélation pour la corrélation de chaque paire de variables.

```
cor.test.matrix = function(m) {
  # On force le type de m en matrix
  m = as.matrix(m)
  # on définit une matrice de taille (nbr_var_m, nbr_var_m) que l'on remplit de NA
  m_pv = matrix(NA, ncol(m), ncol(m))
  # La diagonale de la matrice est 0
  diag(m_pv) = 0
  for (i in 1:(ncol(m) - 1)) {
    for (j in (i + 1):ncol(m)) {
      tmp = cor.test(m[, i], m[, j])
      m_pv[i, j] = m_pv[j, i] = tmp$p.value
    }
  }
  colnames(m_pv) = rownames(m_pv) = colnames(m)
  m_pv
}
```

On applique la fonction précédente à nos variables quantitatives puis on affiche un corrplot de toutes les corrélations possibles où les corrélations significativement nulles sont indiquées par une croix.

```
pv_m = cor.test.matrix(retinol[c(1,4,6:14)])
corr.res = cor(retinol[c(1,4,6:14)])
```

```
corrplot(corr = corr.res,
         type = "lower",
         diag=FALSE,
         p.mat = pv_m,
         tl.col = "steelblue", tl.srt = 30
         )
```

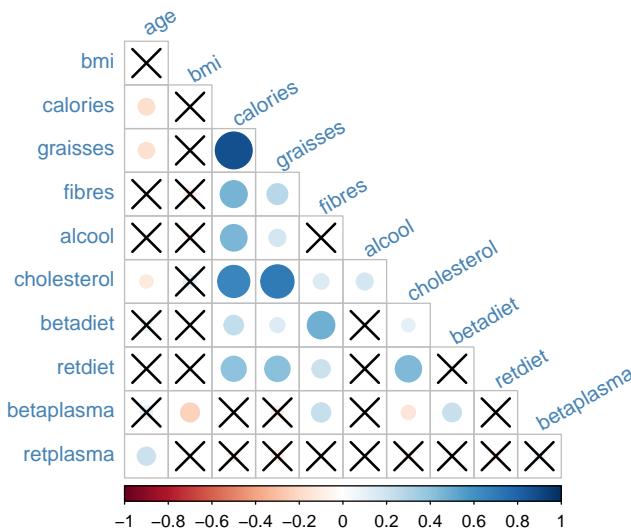


Table 3: Test du Chi 2 de Pearson

	Statistique	ddl	P-value
Tabac et Sexe	7.14	2	0.028
Sexe et Vitamines	11.07	2	0.004
Vitamines et Tabac	8.85	4	0.065

4.2 Liens entre variables qualitatives

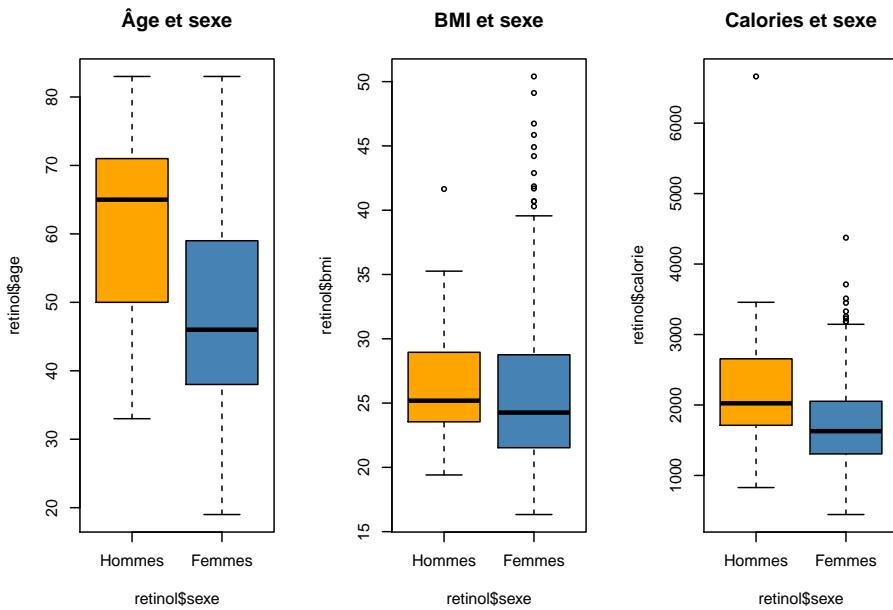
Pour montrer les liens entre deux variables qualitatives, on fait des tests du χ^2 de Pearson en vérifiant au préalable que lorsqu'on croise deux variables, chaque sous groupe contient au moins 5 individus.

```
tabac_sexe = chisq.test(retinol$tabac, retinol$sex)
sexe_vitamine = chisq.test(retinol$sex, retinol$vitamine)
vitamine_tabac = chisq.test(retinol$vitamine, retinol$tabac)
tab_chisq = matrix(c(round(tabac_sexe$statistic,2),
                     round(sexe_vitamine$statistic,2),
                     round(vitamine_tabac$statistic,2),
                     tabac_sexe$parameter,
                     sexe_vitamine$parameter,
                     vitamine_tabac$parameter,
                     round(tabac_sexe$p.value,3),
                     round(sexe_vitamine$p.value, 3),
                     round(vitamine_tabac$p.value, 3)),
                     ncol = 3)
rownames(tab_chisq) = c("Tabac et Sexe", "Sexe et Vitamines", "Vitamines et Tabac")
kable(tab_chisq,
      caption = "Test du Chi 2 de Pearson",
      col.names = c("Statistique", "ddl", "P-value")) %>%
  kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")
```

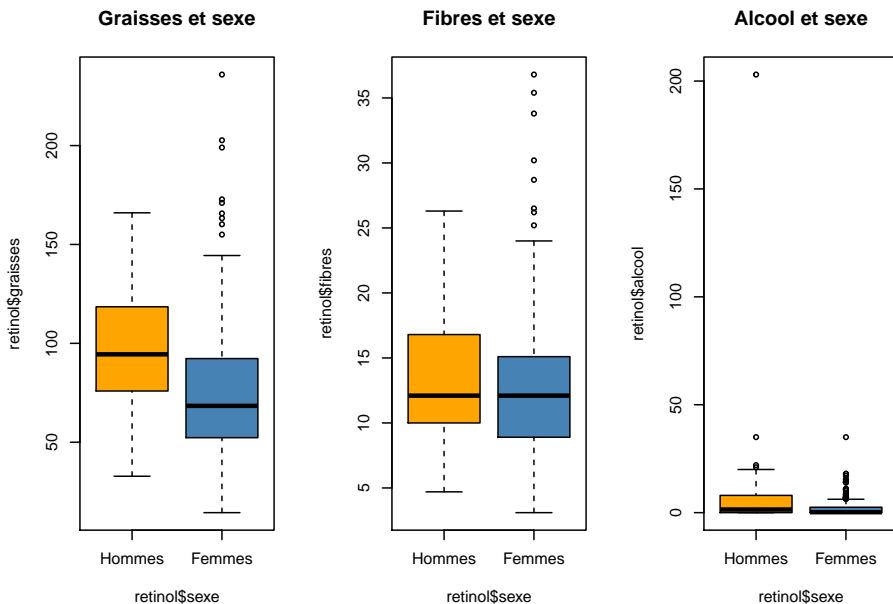
4.3 Lien variables qualitatives et quantitatives

4.3.1 Avec le sexe

```
par(mfrow=c(1,3))
boxplot(retinol$age ~ retinol$sex,
        col = c("orange", "steelblue"), main = "Âge et sexe")
boxplot(retinol$bmi ~ retinol$sex,
        col = c("orange", "steelblue"), main = "BMI et sexe")
boxplot(retinol$calorie ~ retinol$sex,
        col = c("orange", "steelblue"), main = "Calories et sexe")
```



```
par(mfrow=c(1,3))
boxplot(retinol$graisses ~ retinol$sexes,
        col = c("orange", "steelblue"), main = "Graisses et sexe")
boxplot(retinol$fibres ~ retinol$sexes,
        col = c("orange", "steelblue"), main = "Fibres et sexe")
boxplot(retinol$alcool ~ retinol$sexes,
        col = c("orange", "steelblue"), main = "Alcool et sexe")
```

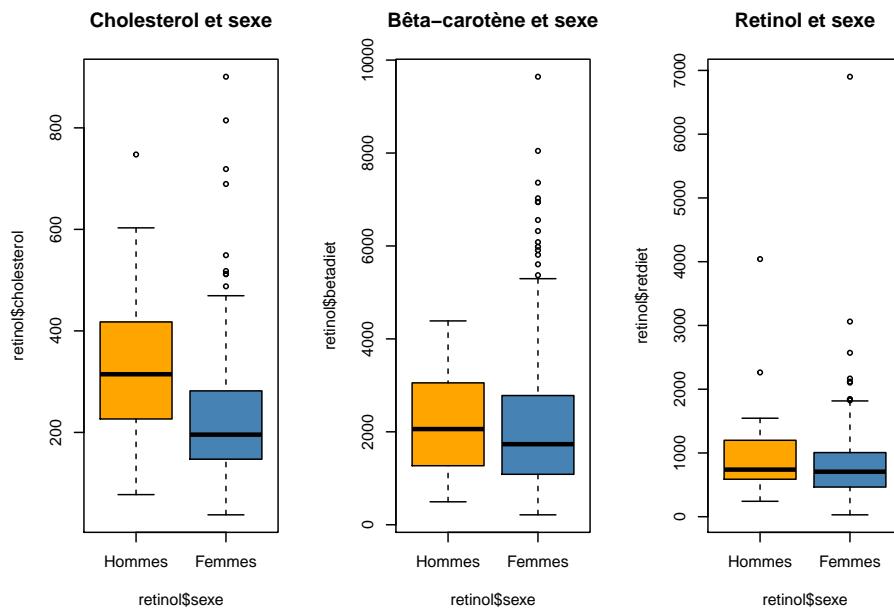


```
par(mfrow=c(1,3))
boxplot(retinol$cholesterol ~ retinol$sexes,
        col = c("orange", "steelblue"), main = "Cholesterol et sexe")
boxplot(retinol$betadiet ~ retinol$sexes,
```

```

    col = c("orange", "steelblue"), main = "Bêta-carotène et sexe")
boxplot(retinol$retidet ~ retinol$sex,
       col = c("orange", "steelblue"), main = "Retinol et sexe")

```



Les variables `âge`, `graisses` et `cholesterol` semblent dépendre du `sexe`. Pour vérifier que la différence entre les hommes et les femmes est significative pour ces 3 variables on fait des tests de student:

- Âge-sexe

Conditions de validité :

```

par(mfrow = c(1,2))
hist(retinol$age, main = "", xlab = "Âge")
qqnorm(retinol$age); qqline(retinol$age)

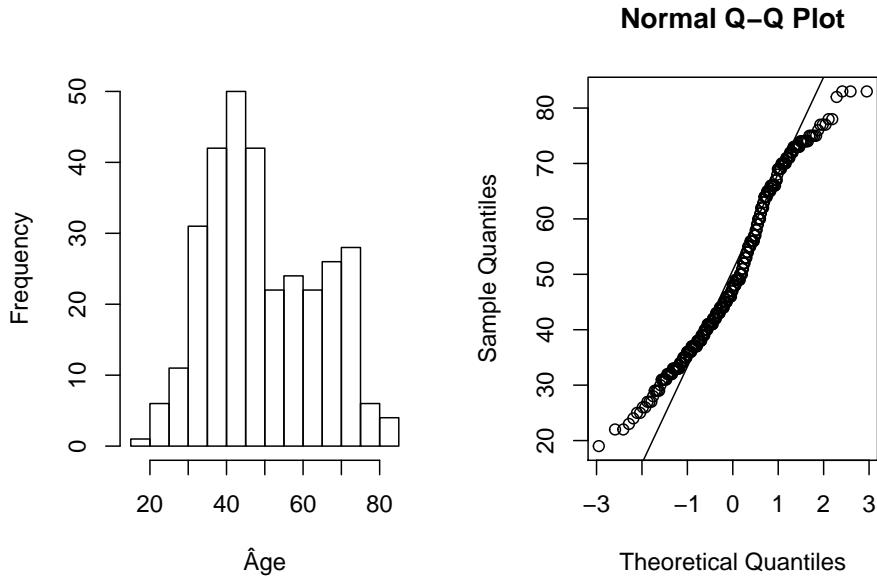
```

Table 4: Sexe

	n
Hommes	42
Femmes	273

Table 5: Egalité des variances

Sous-groupe	Variance
Hommes	181.4245
Femmes	198.6165



La variable `age` a une allure à peu près Gaussienne. On peut également vérifier que le nombre d'individus dans chaque sous groupe est supérieur à 5:

```
kable(table(retinol$sex), caption = "Sexe", col.names = c(" ", "n"))
```

Vérifions à présent l'égalité des variances de l'âge chez les hommes et chez les femmes:

```
kable(as.table(by(retinol$age, retinol$sex, FUN = function(x){var(x)})),
      col.names = c("Sous-groupe", "Variance"),
      caption = "Egalité des variances")
```

On peut considérer l'égalité des variances:

```
test_stu1 = matrix(c(round(t.test(retinol$age ~ retinol$sex, var.equal = T)$statistic,2),
                     t.test(retinol$age ~ retinol$sex, var.equal = T)$parameter,
                     t.test(retinol$age ~ retinol$sex, var.equal = T)$p.value),
                     ncol = 3)
kable(test_stu1, caption = "Test de student entre l'âge et le sexe",
      col.names = c("Statistique", "ddl","p-value"))
```

La p-valeur est très inférieure à 5%, il y a donc une différence significative entre la moyenne d'âge des hommes

Table 6: Test de student entre l'âge et le sexe

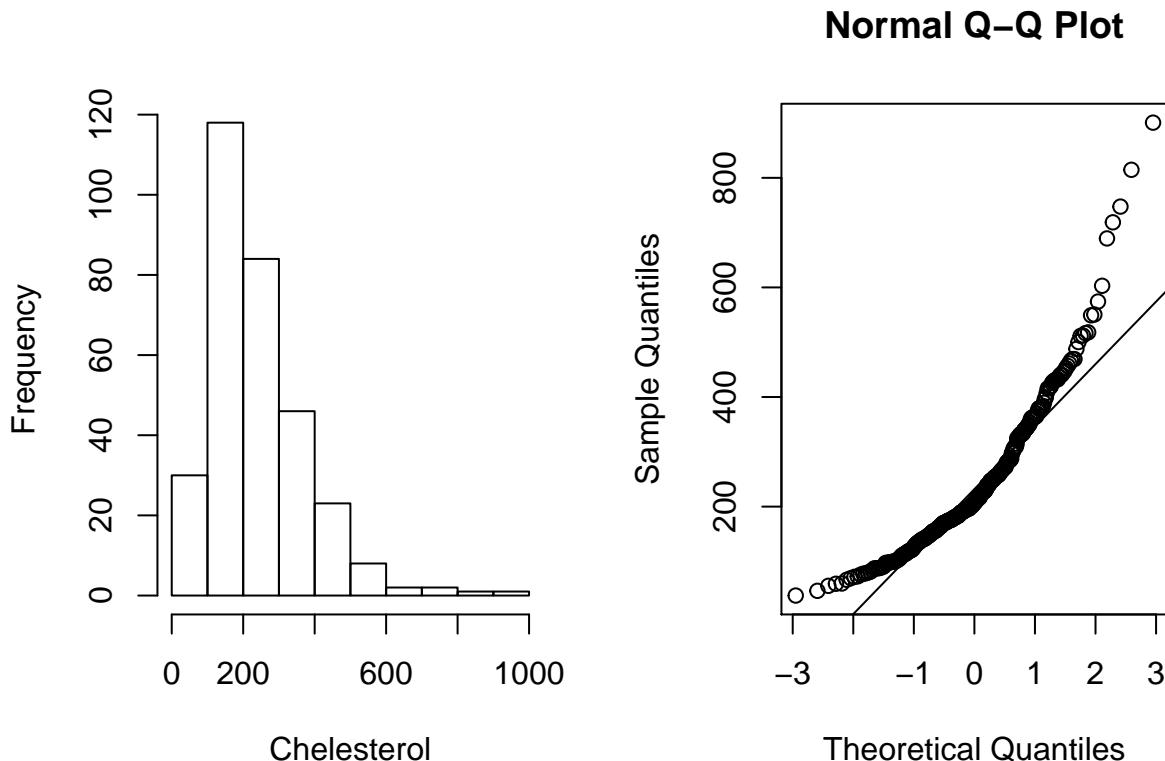
Statistique	ddl	p-value
5.17	313	4e-07

et celle des femmes.

- Cholesterol sexe

Conditions de validité :

```
par(mfrow = c(1,2))
hist(retinol$cholesterol, main = "",
      xlab = "Cholesterol")
qqnorm(retinol$cholesterol); qqline(retinol$cholesterol);
```



La variable `cholesterol` n'est clairement pas normale mais comme vu précédemment il y au moins 30 hommes et 30 femmes dans le jeu de données donc la première condition de validité est vérifiée. Contrôlons à présent l'égalité des variances:

```
kable(as.table(by(retinol$cholesterol, retinol$sex, FUN = function(x){var(x)})),
      col.names = c("Sous-groupe", "Variance"),
      caption = "Egalité des variances")

test_stu2 = matrix(c(
  round(t.test(retinol$cholesterol ~ retinol$sex, var.equal = T)$statistic,2),
  t.test(retinol$cholesterol ~ retinol$sex, var.equal = T)$parameter,
```

Table 7: Egalité des variances

Sous-groupe	Variance
Hommes	21150.83
Femmes	15616.31

Table 8: Test de student entre le cholesterol et le sexe

Statistique	ddl	p-value
4.66	313	4.6e-06

```
t.test(retinol$cholesterol ~ retinol$sexe, var.equal = T)$p.value),
      ncol = 3)
kable(test_stu2, caption = "Test de student entre le cholesterol et le sexe",
      col.names = c("Statistique", "ddl", "p-value"))
```

Cette fois encore le test de student non indique une différence significative entre la moyenne de cholesterol chez les femmes et chez les hommes.

- Graisse-sexe

Conditions de validité :

```
par(mfrow = c(1,2))
hist(retinol$graisses, xlab = "Graisses", main = "")
qqnorm(retinol$graisses); qqline(retinol$graisses);
```

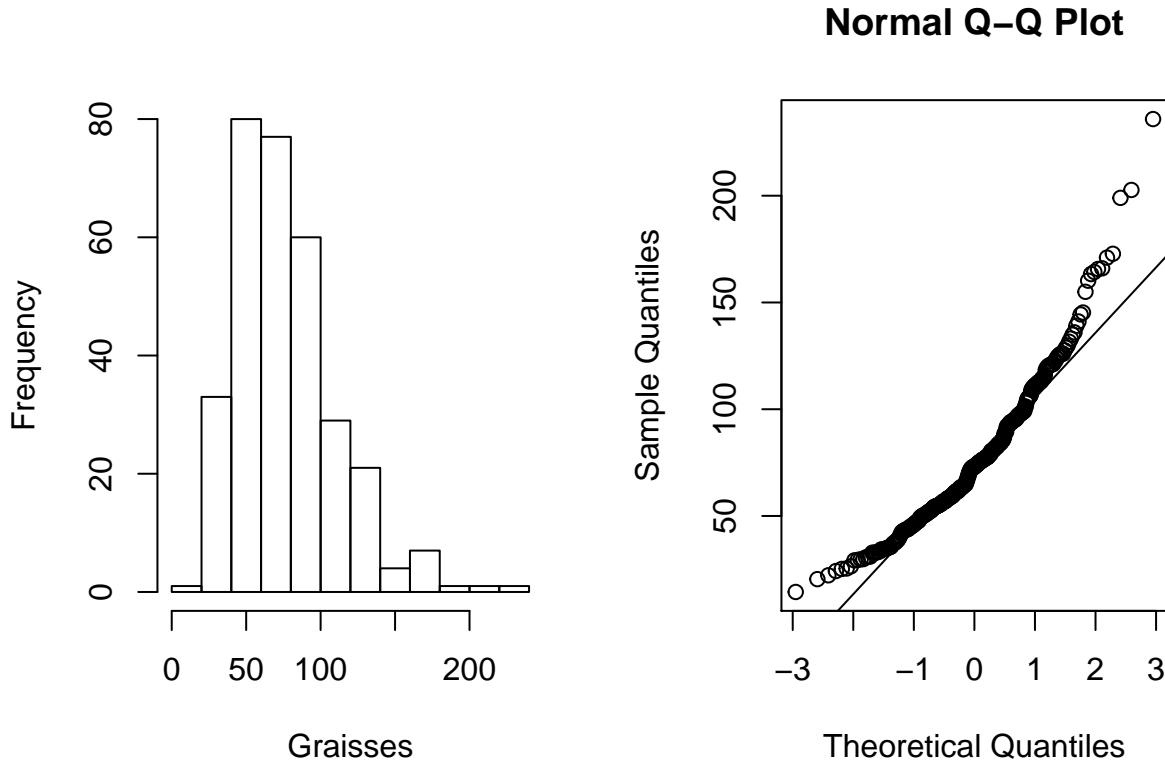


Table 9: Égalité des variances

Sous-groupe	Variance
Hommes	1132.643
Femmes	1099.787

Table 10: Test de student entre les graisses et le sexe

Statistique	ddl	p-value
3.53	313	0.0004751

La variable `graisses` a une allure normale. Vérifions l'égalité des variances dans les deux groupes:

```
kable(as.table(by(retinol$graisses, retinol$sex, FUN = function(x){var(x)})),
      col.names = c("Sous-groupe", "Variance"), caption = "Égalité des variances")
```

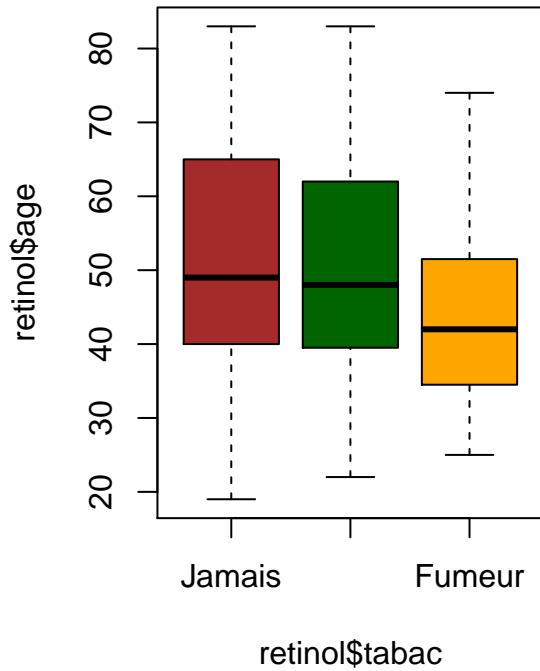
On peut considérer l'égalité:

```
test_stu3 = matrix(c(round(t.test(retinol$graisses ~ retinol$sex, var.equal = T)$statistic,2),
                     t.test(retinol$graisses ~ retinol$sex, var.equal = T)$parameter,
                     t.test(retinol$graisses ~ retinol$sex, var.equal = T)$p.value),
                     ncol = 3)
kable(test_stu3, caption = "Test de student entre les graisses et le sexe",
      col.names = c("Statistique", "ddl","p-value"))
```

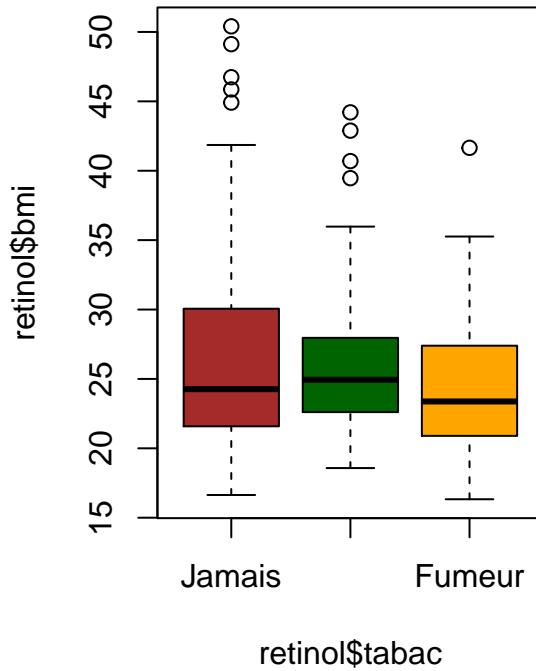
4.3.2 Avec le tabac

```
par(mfrow=c(1,2))
boxplot(retinol$age ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "Âge et tabac")
boxplot(retinol$bmi ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "BMI et tabac")
```

Âge et tabac

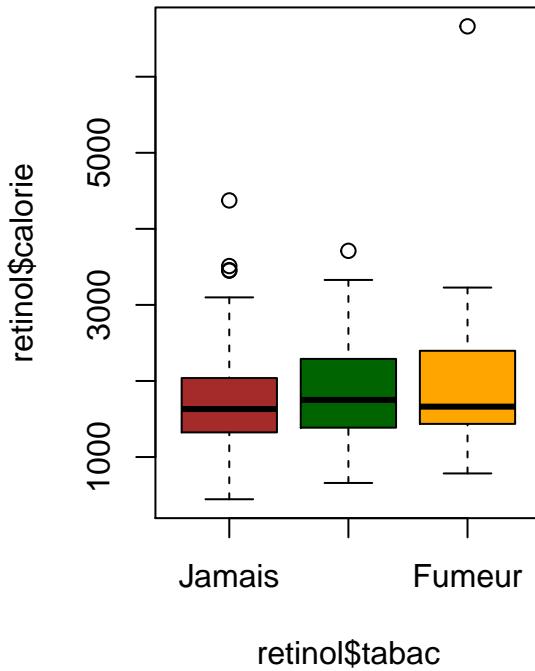


BMI et tabac

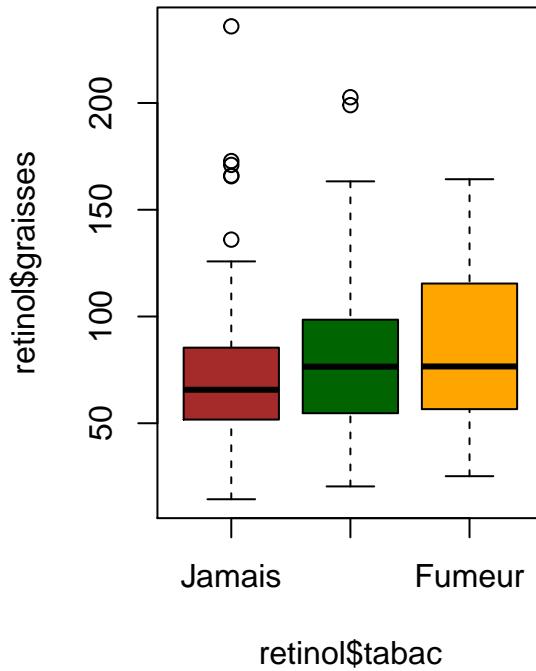


```
par(mfrow=c(1,2))
boxplot(retinol$calorie ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "Calories et tabac")
boxplot(retinol$graisses ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "Graisses et tabac")
```

Calories et tabac

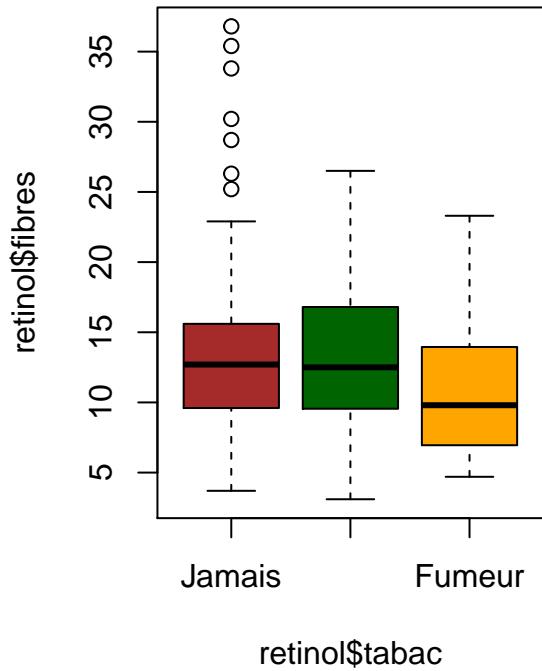


Graisses et tabac

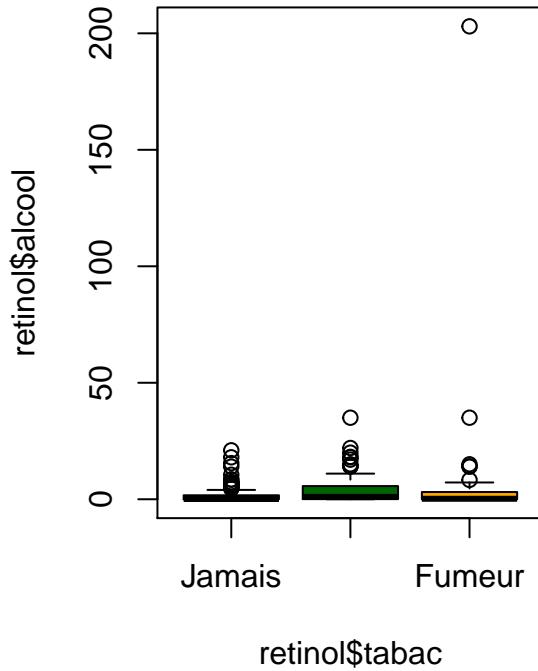


```
par(mfrow=c(1,2))
boxplot(retinol$fibres ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "Fibres et tabac")
boxplot(retinol$alcool ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "Alcool et tabac")
```

Fibres et tabac



Alcool et tabac

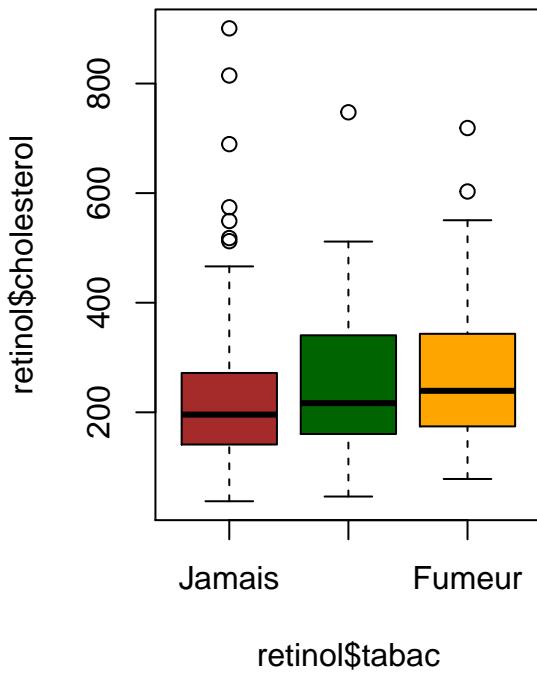


retinol\$tabac

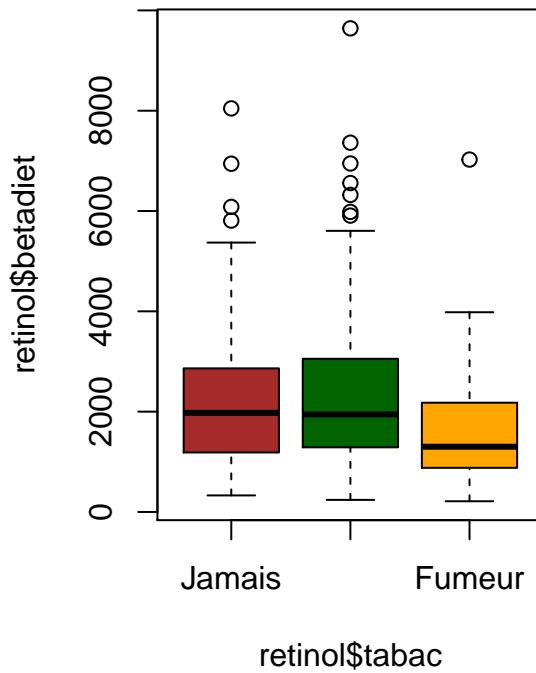
retinol\$tabac

```
par(mfrow = c(1,2))
boxplot(retinol$cholesterol ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "Cholesterol et tabac")
boxplot(retinol$betadiet ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "Bêta-carotène et tabac")
```

Cholesterol et tabac



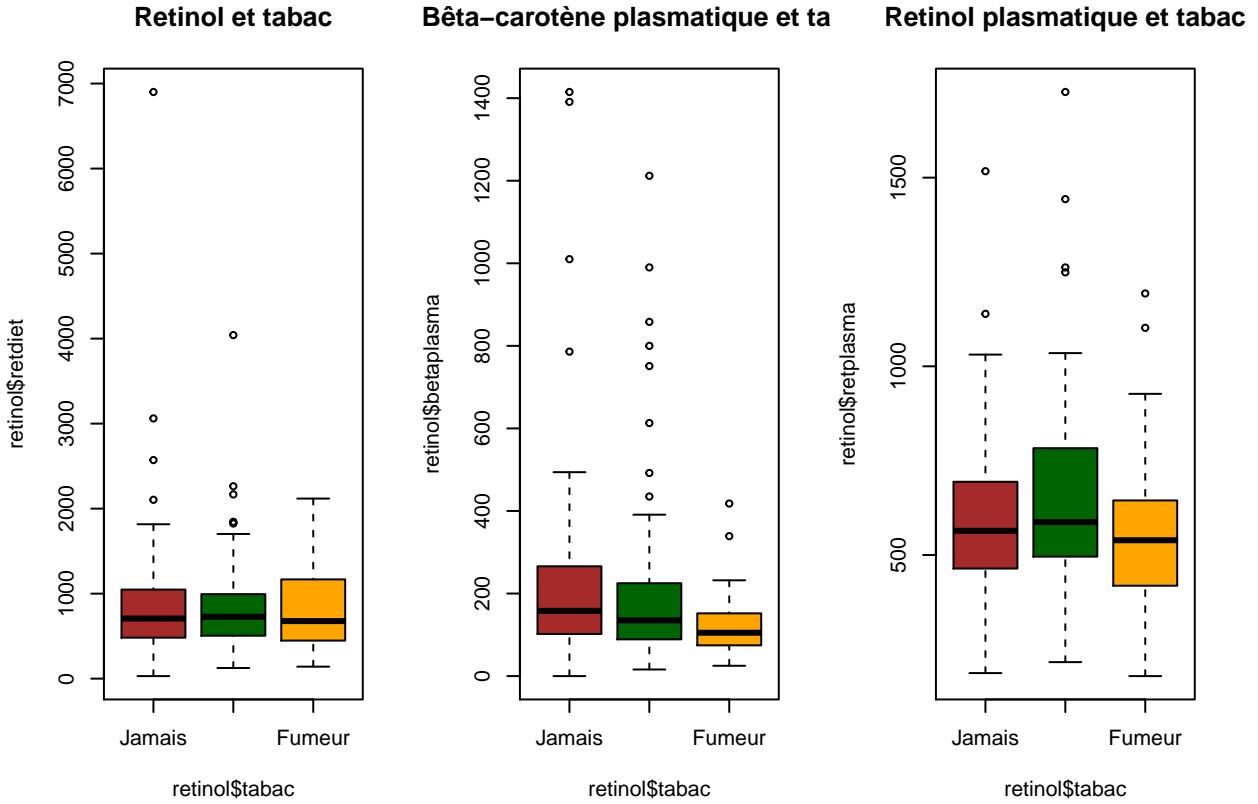
Bêta-carotène et tabac



```
par(mfrow=c(1,3))
boxplot(retinol$retrdiet ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "Retinol et tabac")
boxplot(retinol$betaplasma ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "Bêta-carotène plasmatique et tabac")
boxplot(retinol$retplasma ~ retinol$tabac,
        col = c("brown", "darkgreen","orange"),
        main = "Retinol plasmatique et tabac")
```

Table 11: Tabac

Jamais	157
Autrefois	115
Fumeur	43



Le tabac est une variable catégorielle à 3 classes, on ne peut donc pas faire de t-test pour comparer les moyennes des variables quantitatives dans chacune de ces 3 classes. Nous allons effectuer des ANOVA à un facteur pour chacune des variables quantitatives. La plupart des variables quantitatives ont une distribution normale. Cependant pour celles qui ne vérifient pas cette propriété on peut vérifier que dans chacune des trois classes de la variable tabac il y a plus de 30 individus:

```
kable(table(retinol$tabac), caption = "Tabac", col.names = c())
var = c("age", "bmi", "calories", "graisses", "fibres", "alcool", "cholesterol", "betadiet", "retdiet")
for(j in 1:length(var)){
  for(v in var[j]){
    cat("*Variable:", v, "\n")
    cat("→ Vérification homoscedasticité: \n")
    cat("\t", by(retinol[,v], retinol$tabac, function(x){var(x)}), "\n")
    cat("→ P-valeur de l'anova: \n")
    cat("\t", anova(lm(retinol[,v] ~ tabac, data = retinol))$`Pr(>F)`[1], "\n")
    if(anova(lm(retinol[,v] ~ tabac, data = retinol))$`Pr(>F)`[1] < 0.05){cat("\t -> SIGNIFICATIF \n \n")}
    else
      {cat("\t -> NON SIGNIFICATIF \n \n")}
  }
}
```

```

## *Variable: age
## -> Vérification homoscedaticité:
##    225.6743 195.2291 182.4452
## -> P-valeur de l'anova:
##    0.02369346
##    -> SIGNIFICATIF
##
## *Variable: bmi
## -> Vérification homoscedaticité:
##    47.11603 24.92469 24.15995
## -> P-valeur de l'anova:
##    0.1275941
##    -> NON SIGNIFICATIF
##
## *Variable: calories
## -> Vérification homoscedaticité:
##    350679.7 414135.7 978907.4
## -> P-valeur de l'anova:
##    0.0821071
##    -> NON SIGNIFICATIF
##
## *Variable: graisses
## -> Vérification homoscedaticité:
##    1023.585 1255.939 1161.556
## -> P-valeur de l'anova:
##    0.03393282
##    -> SIGNIFICATIF
##
## *Variable: fibres
## -> Vérification homoscedaticité:
##    32.48231 24.11279 20.59998
## -> P-valeur de l'anova:
##    0.01426937
##    -> SIGNIFICATIF
##
## *Variable: alcool
## -> Vérification homoscedaticité:
##    11.30632 33.81566 971.4905
## -> P-valeur de l'anova:
##    0.01530282
##    -> SIGNIFICATIF
##
## *Variable: cholesterol
## -> Vérification homoscedaticité:
##    18017.28 14808.84 21292.38
## -> P-valeur de l'anova:
##    0.1087336
##    -> NON SIGNIFICATIF
##
## *Variable: betadiet
## -> Vérification homoscedaticité:
##    1923273 2641437 1610707
## -> P-valeur de l'anova:
##    0.04622024

```

```

##      -> SIGNIFICATIF
##
## *Variable: retdiet
## -> Vérification homoscedasticité:
##    434446.8 280510.5 219384.3
## -> P-valeur de l'anova:
##    0.8993807
##      -> NON SIGNIFICATIF
##
## rm(v)
## rm(j)
## rm(var)

```

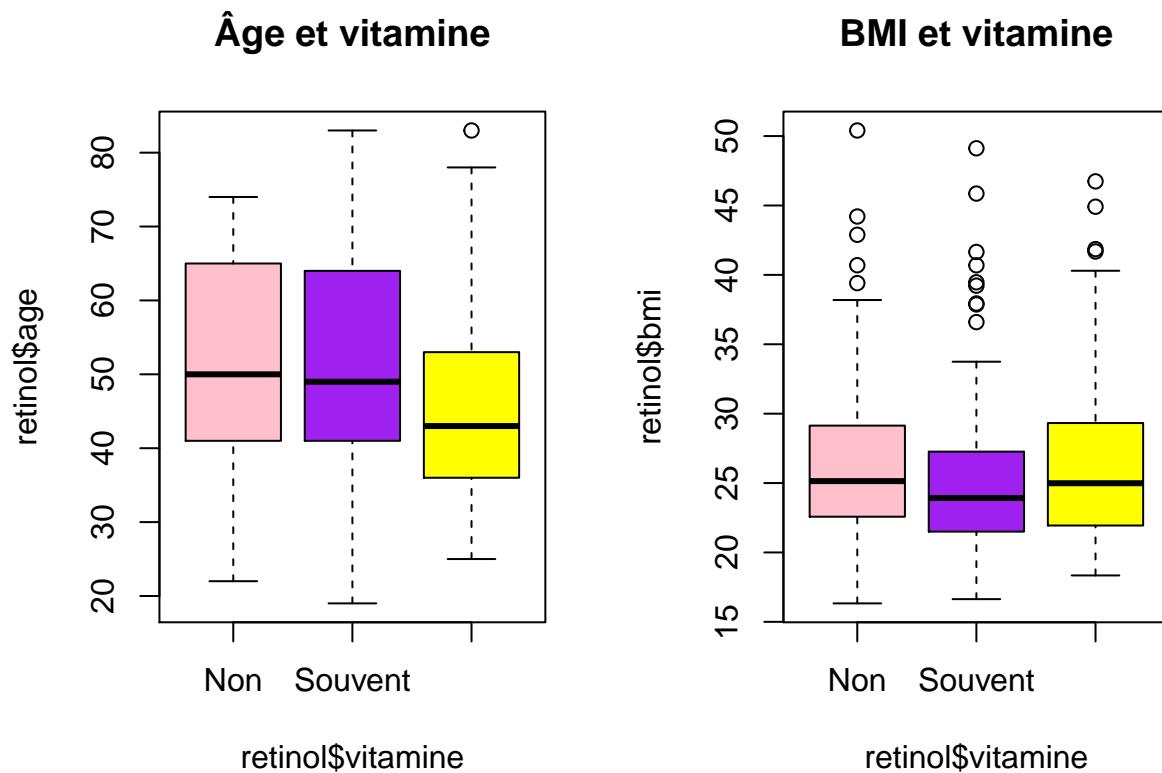
Petit bémol: l'égalité des variances n'est pas toujours respectée, notamment pour les variables `calories` et `alcool`. Il vaut mieux dans ce cas utiliser un autre test pour ces deux variables:

4.3.3 Avec les vitamines

```

par(mfrow=c(1,2))
boxplot(retinol$age ~ retinol$vitamine,
        col = c("pink", "purple", "yellow"),
        main = "Âge et vitamine")
boxplot(retinol$bmi ~ retinol$vitamine,
        col = c("pink", "purple", "yellow"),
        main = "BMI et vitamine")

```



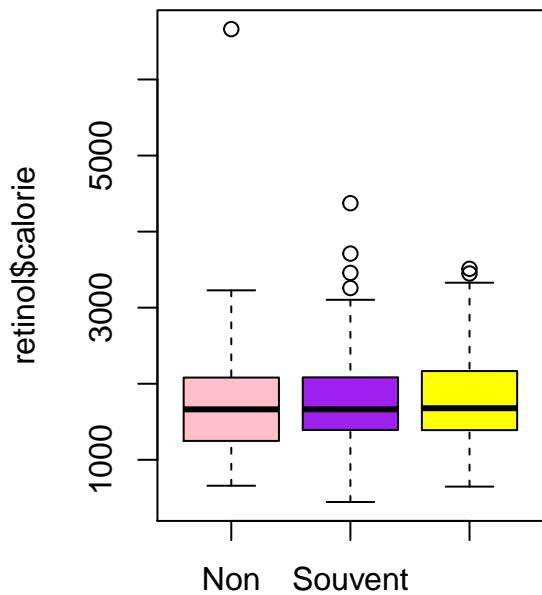
```

par(mfrow=c(1,2))
boxplot(retinol$calorie ~ retinol$vitamine,
        col = c("pink", "purple", "yellow"),
        main = "Calories et vitamine")

par(mfrow=c(1,2))

```

Calories et vitamine



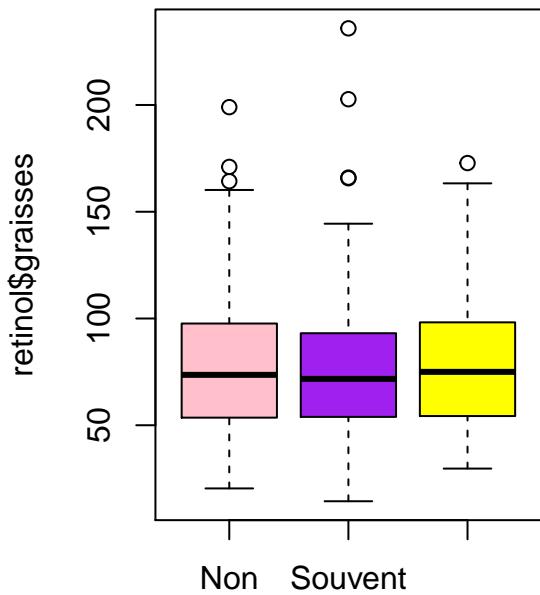
retinol\$vitamine

```

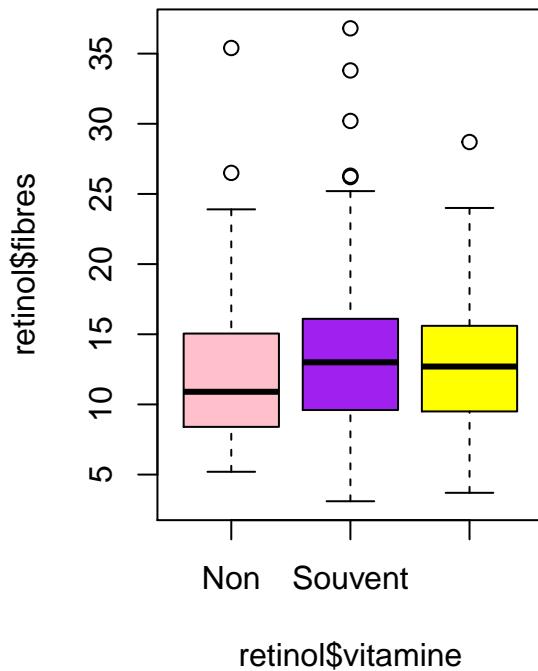
boxplot(retinol$graisses ~ retinol$vitamine,
        col = c("pink", "purple", "yellow"),
        main = "Graisses et vitamine")
boxplot(retinol$fibres ~ retinol$vitamine,
        col = c("pink", "purple", "yellow"),
        main = "Fibres et vitamine")

```

Graisses et vitamine



Fibres et vitamine



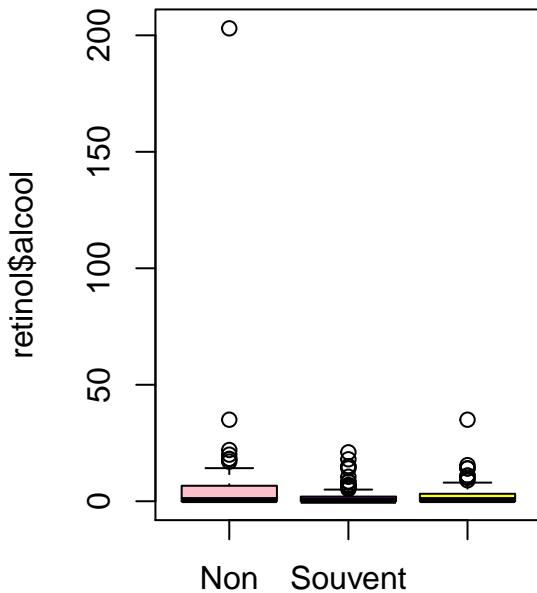
retinol\$vitamine

retinol\$vitamine

```
par(mfrow=c(1,2))
boxplot(retinol$alcool ~ retinol$vitamine,
        col = c("pink", "purple","yellow"),
        main = "Alcool et vitamine")

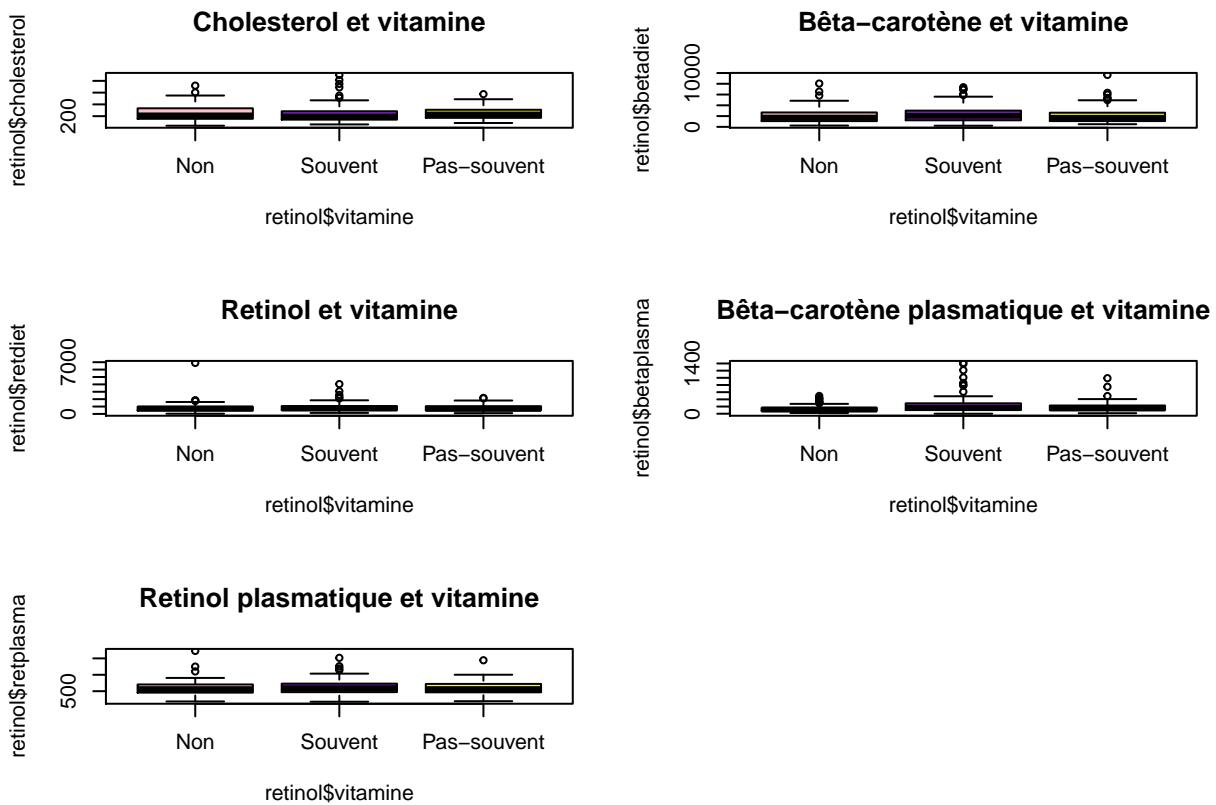
par(mfrow = c(3,2))
```

Alcool et vitamine



retinol\$vitamine

```
boxplot(retinol$cholesterol ~ retinol$vitamine,
       col = c("pink", "purple", "yellow"),
       main = "Cholesterol et vitamine")
boxplot(retinol$betadiet ~ retinol$vitamine,
       col = c("pink", "purple", "yellow"),
       main = "Bêta-carotène et vitamine")
boxplot(retinol$rettdiet ~ retinol$vitamine,
       col = c("pink", "purple", "yellow"),
       main = "Retinol et vitamine")
boxplot(retinol$betaplasma ~ retinol$vitamine,
       col = c("pink", "purple", "yellow"),
       main = "Bêta-carotène plasmatique et vitamine")
boxplot(retinol$retplasma ~ retinol$vitamine,
       col = c("pink", "purple", "yellow"),
       main = "Retinol plasmatique et vitamine")
```



On procède de la même manière qu'avec le tabac : analyse de la variance à 1 facteur.

```
table(Vitamines = retinol$vitamine)

## Vitamines
##      Non      Souvent Pas-souvent
##      111       122        82

var = c("age", "bmi", "calories", "graisses", "fibres", "alcool", "cholesterol", "betadiet", "retdiet")
for(j in 1:length(var)){
  for(v in var[j]){
    cat("*Variable:", v, "\n")
    cat("-> Vérification homoscedaticité: \n")
    cat("\t", by(retinol[,v], retinol$vitamine, function(x){var(x)}), "\n")
    cat("-> P-valeur de l'anova: \n")
    cat("\t", anova(lm(retinol[,v] ~ vitamine, data = retinol))$`Pr(>F)`[1], "\n")
    if(anova(lm(retinol[,v] ~ vitamine, data = retinol))$`Pr(>F)`[1] < 0.05){
      cat("\t -> SIGNIFICATIF \n \n")
    } else {
      {cat("\t -> NON SIGNIFICATIF \n \n")}
    }
  }
}

## *Variable: age
## -> Vérification homoscedaticité:
##   189.484 233.9914 193.8958
## -> P-valeur de l'anova:
##   0.01262553
## -> SIGNIFICATIF
```

```

## 
## *Variable: bmi
## -> Vérification homoscedaticité:
##    34.52593 33.80685 41.74802
## -> P-valeur de l'anova:
##    0.30951
##    -> NON SIGNIFICATIF
##
## *Variable: calories
## -> Vérification homoscedaticité:
##    571804.6 426647.1 379885.8
## -> P-valeur de l'anova:
##    0.9493215
##    -> NON SIGNIFICATIF
##
## *Variable: graisses
## -> Vérification homoscedaticité:
##    1167.466 1231.073 1007
## -> P-valeur de l'anova:
##    0.8393314
##    -> NON SIGNIFICATIF
##
## *Variable: fibres
## -> Vérification homoscedaticité:
##    25.99886 34.37984 22.29089
## -> P-valeur de l'anova:
##    0.1860997
##    -> NON SIGNIFICATIF
##
## *Variable: alcool
## -> Vérification homoscedaticité:
##    391.973 14.0931 25.99792
## -> P-valeur de l'anova:
##    0.08324381
##    -> NON SIGNIFICATIF
##
## *Variable: cholesterol
## -> Vérification homoscedaticité:
##    17247.7 22830.66 9925.836
## -> P-valeur de l'anova:
##    0.8261836
##    -> NON SIGNIFICATIF
##
## *Variable: betadiet
## -> Vérification homoscedaticité:
##    1742324 2363625 2427472
## -> P-valeur de l'anova:
##    0.1648997
##    -> NON SIGNIFICATIF
##
## *Variable: retdiet
## -> Vérification homoscedaticité:
##    492561.4 309716.3 214046.1
## -> P-valeur de l'anova:

```

```

##    0.9376647
##    -> NON SIGNIFICATIF
##
rm(v)
rm(j)
rm(var)

```

5. Question 3 : Régression linéaire

Effectuez ensuite une régression linéaire où la variable à expliquer sera la concentration en rétinol plasmatique, les autres variables étant explicatives. Recherchez des interactions entre les variables explicatives.

5.1 Analyse en Composantes Principales focalisée

La première chose que l'on peut faire pour y voir clair est une ACP focalisée pour visualiser les liens entre variables explicatives.

```

expliquer = "retplasma"
explicative = colnames(retinol)[1:13]
f pca(data = retinol, y = expliquer, x = explicative, partial = "NO")

```

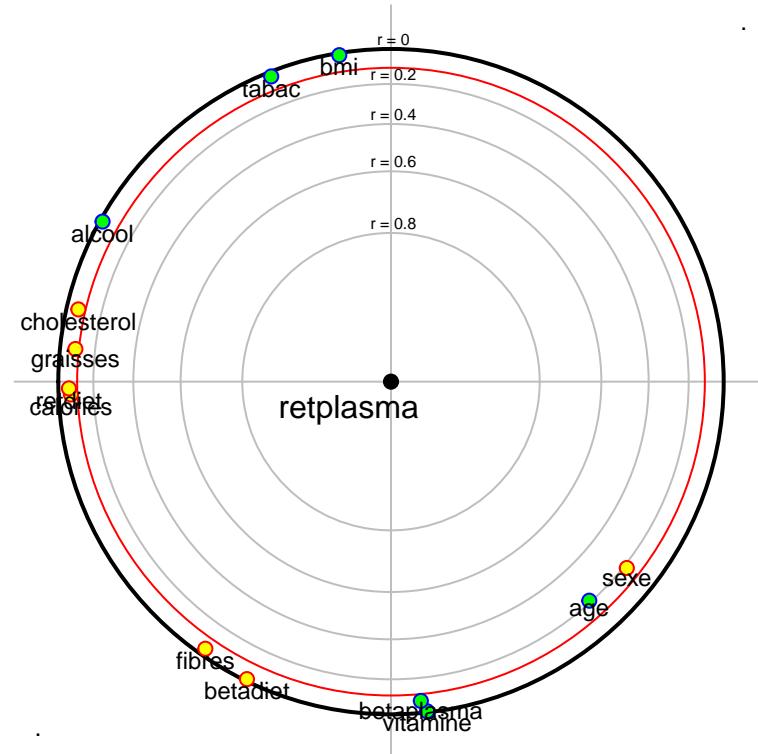


Table 12: Régression linéaire multiple

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	549.183	99.790	5.503	0.000
age	2.410	0.902	2.672	0.008
sexeFemmes	-101.733	38.243	-2.660	0.008
tabacAutrefois	60.522	25.555	2.368	0.019
tabacFumeur	0.378	37.395	0.010	0.992
bmi	1.318	2.009	0.656	0.512
vitamineSouvent	21.563	28.439	0.758	0.449
vitaminePas-souvent	23.280	30.641	0.760	0.448
calories	0.069	0.061	1.131	0.259
graisses	-1.229	0.969	-1.269	0.205
fibres	-4.369	3.428	-1.274	0.203
alcool	-1.340	1.494	-0.897	0.371
cholesterol	-0.086	0.132	-0.652	0.515
betadiet	-0.003	0.009	-0.318	0.751
retdiet	-0.010	0.022	-0.455	0.649
betaplasma	0.083	0.070	1.196	0.233

5.2 Modèle sans interactions

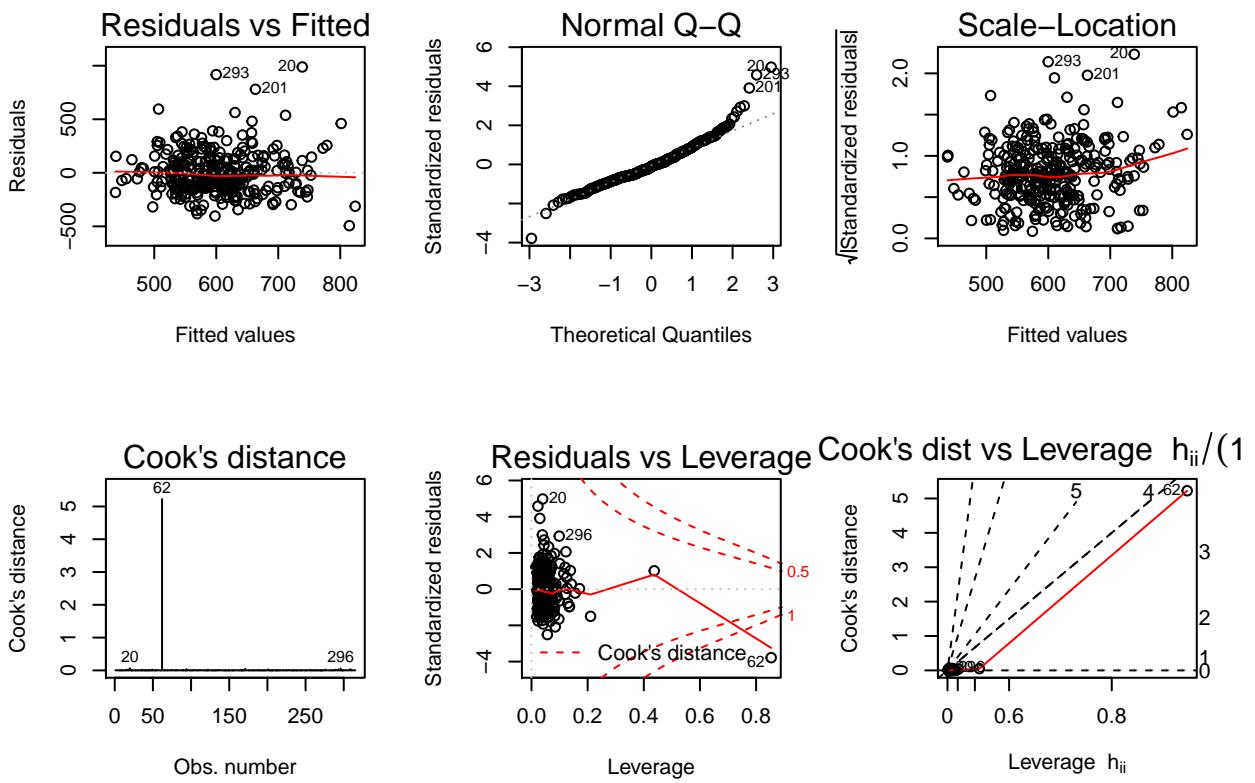
5.2.1 Modèle

On fait un premier modèle sans interactions pour comprendre ce qui se passe.

```
reg_lin = lm(retplasma ~ . -retplasma , data = retinol)
kable(round(xtable(reg_lin),3), caption = "Régression linéaire multiple") %>%
  kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")
```

5.2.2 Diagnostique

```
par(mfrow = c(2,3))
plot(reg_lin, which = 1:6)
```



```
hist(resid(reg_lin),
  main = "Histogramme des résidus de la regression linéaire sans interactions",
  xlab = "", col = "steelblue")
```

Histogramme des résidus de la regression linéaire sans interaction

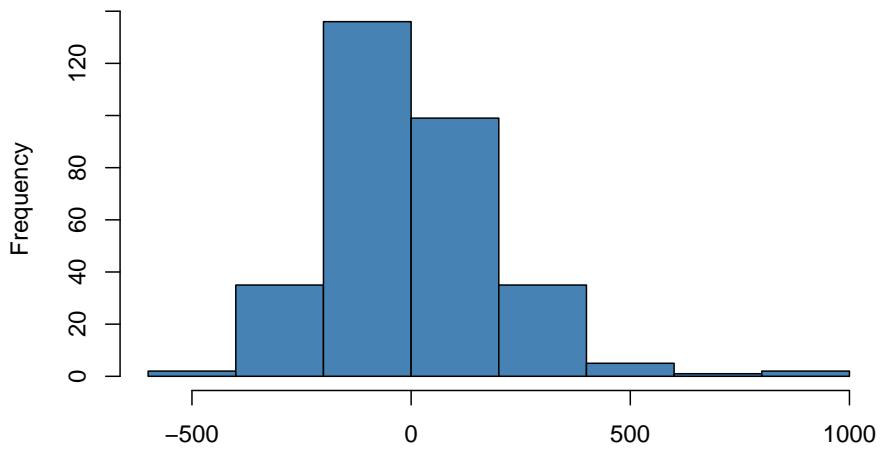


Table 13: Régression linéaire multiple avec interaction entre âge et sexe

	Bêta	IC	p
(Intercept)	703.429	[170.95;4.115]	1e-04
age	-0.092	[2.425;-0.038]	0.9698
sexeFemmes	-269.566	[155.82;-1.73]	0.0847
tabacAutrefois	62.142	[25.586;2.429]	0.0157
tabacFumeur	0.729	[37.381;0.02]	0.9844
bmi	1.212	[2.01;0.603]	0.5471
vitamineSouvent	18.421	[28.568;0.645]	0.5195
vitaminePas-souvent	21.819	[30.658;0.712]	0.4772
calories	0.073	[0.061;1.181]	0.2385
graisses	-1.31	[0.971;-1.349]	0.1784
fibres	-4.142	[3.433;-1.207]	0.2286
alcool	-1.399	[1.494;-0.936]	0.3499
cholesterol	-0.092	[0.132;-0.691]	0.4898
betadiet	-0.003	[0.009;-0.348]	0.7281
retdiet	-0.009	[0.022;-0.388]	0.6981
betaplasma	0.08	[0.07;1.153]	0.2499
age:retinol[, "sexe"]Femmes	2.839	[2.556;1.111]	0.2674

5.3 Tests de toutes les interactions possibles

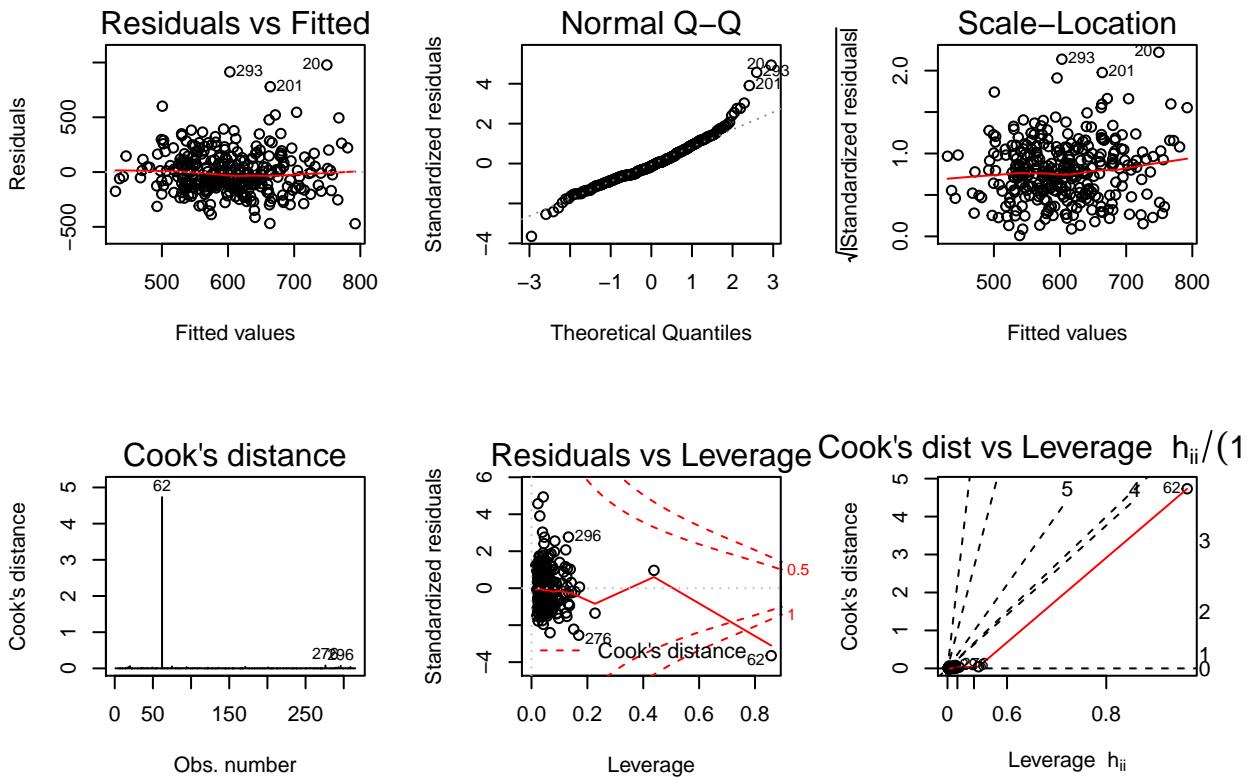
5.3.1 Interaction avec l'âge

```

mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "sexe"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et sexe",
      col.names = c("", "Bêta", "IC","p")) %>%
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp,which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

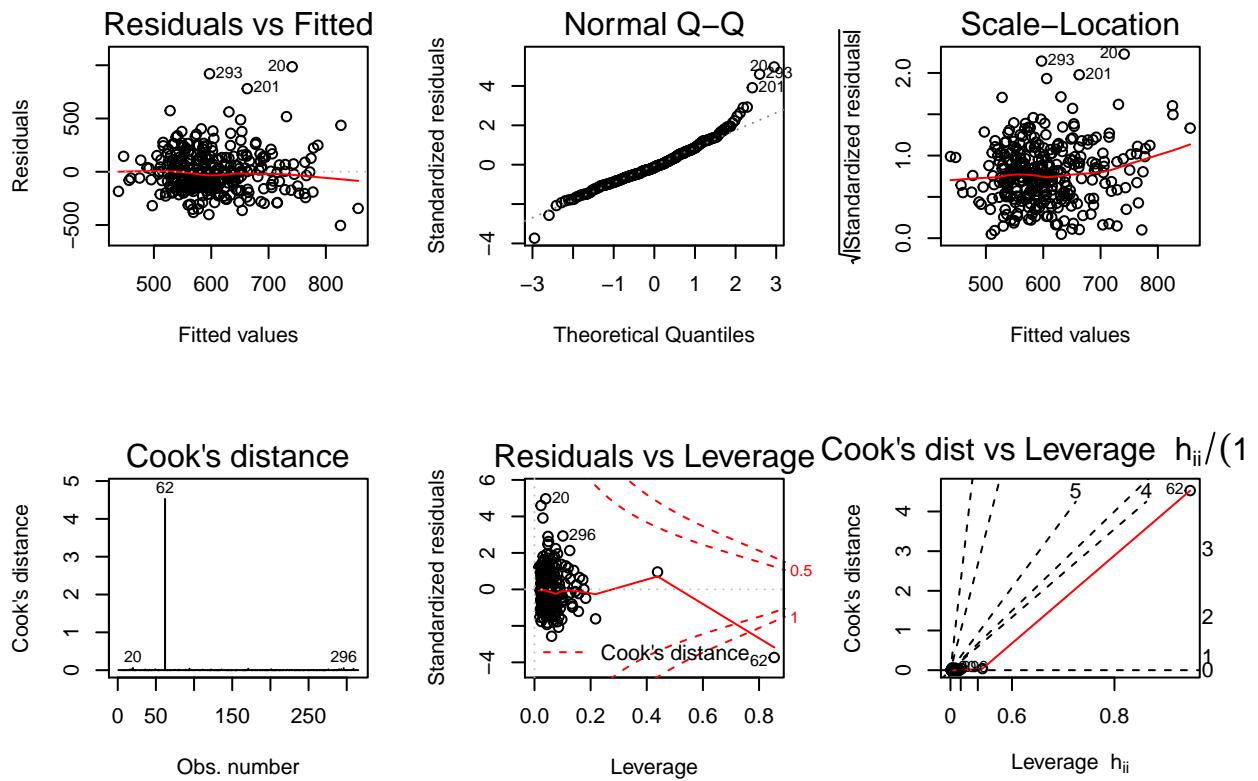
mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "tabac"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et tabac", col.names = c(" ",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 14: Régression linéaire multiple avec interaction entre âge et tabac

	Bêta	IC	p
(Intercept)	552.91	[103.862;5.324]	0
age	2.218	[1.141;1.944]	0.0529
sexeFemmes	-95.661	[38.705;-2.472]	0.014
tabacAutrefois	-14.668	[93.831;-0.156]	0.8759
tabacFumeur	100.623	[124.98;0.805]	0.4214
bmi	1.163	[2.012;0.578]	0.5636
vitamineSouvent	16.562	[28.69;0.577]	0.5642
vitaminePas-souvent	21.919	[30.676;0.715]	0.4754
calories	0.07	[0.062;1.142]	0.2543
graisses	-1.208	[0.971;-1.244]	0.2144
fibres	-4.064	[3.436;-1.183]	0.2378
alcool	-1.108	[1.517;-0.73]	0.4658
cholesterol	-0.091	[0.133;-0.685]	0.4938
betadiet	-0.003	[0.009;-0.306]	0.76
retdiet	-0.01	[0.022;-0.428]	0.6687
betaplasma	0.084	[0.07;1.201]	0.2308
age:retinol[, "tabac"]Autrefois	1.466	[1.783;0.822]	0.4117
age:retinol[, "tabac"]Fumeur	-2.317	[2.66;-0.871]	0.3846



```
rm(mod.tmp)
rm(res.tmp)
```

Table 15: Régression linéaire multiple avec interaction entre âge et bmi

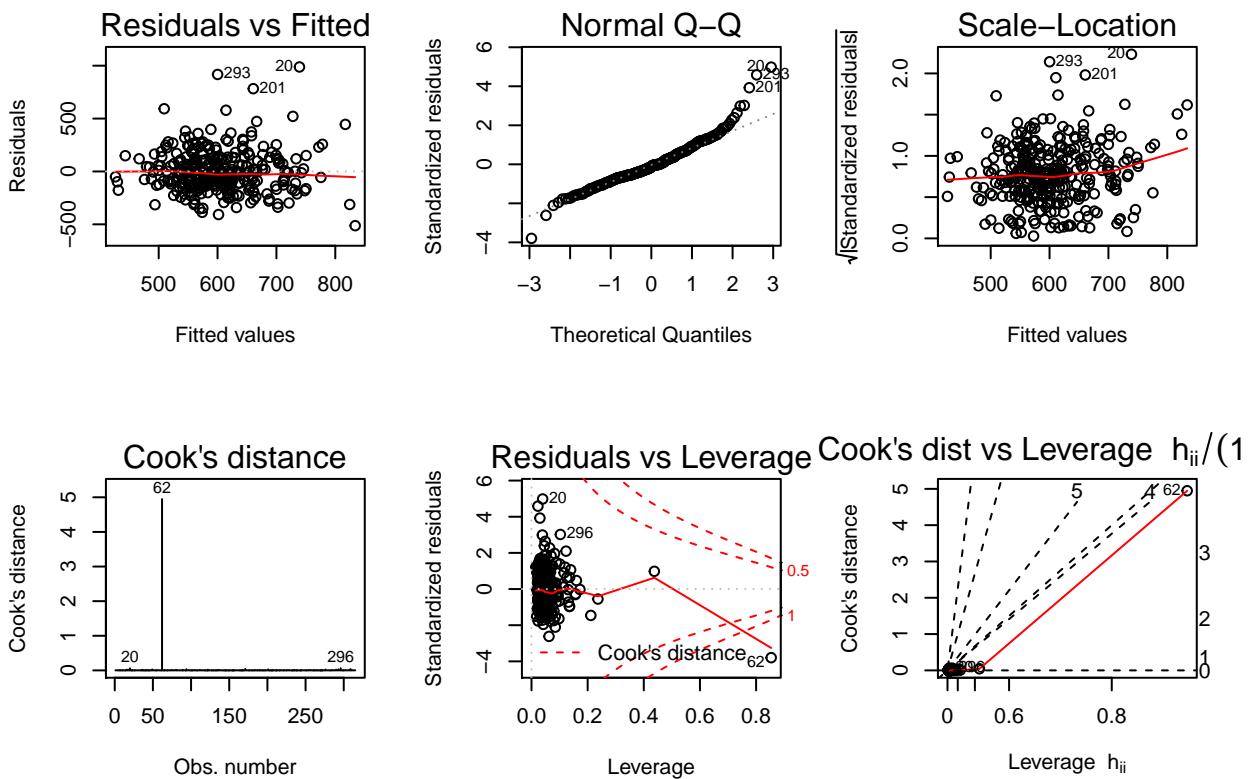
	Bêta	IC	p
(Intercept)	745.797	[186.946;3.989]	1e-04
age	-1.782	[3.49;-0.511]	0.6099
sexeFemmes	-102.331	[38.211;-2.678]	0.0078
tabacAutrefois	59.594	[25.542;2.333]	0.0203
tabacFumeur	1.8	[37.378;0.048]	0.9616
bmi	-6.311	[6.457;-0.977]	0.3291
vitamineSouvent	20.39	[28.428;0.717]	0.4738
vitaminePas-souvent	20.941	[30.671;0.683]	0.4953
calories	0.07	[0.061;1.135]	0.2575
graisses	-1.219	[0.968;-1.26]	0.2088
fibres	-4.16	[3.429;-1.213]	0.226
alcool	-1.312	[1.493;-0.879]	0.3802
cholesterol	-0.09	[0.132;-0.683]	0.495
betadiet	-0.004	[0.009;-0.436]	0.6633
retdiet	-0.01	[0.022;-0.43]	0.6678
betaplasma	0.089	[0.07;1.274]	0.2037
age:retinol[, "bmi"]	0.162	[0.131;1.243]	0.2147

```

mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "bmi"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et bmi", col.names = c(" ", "B",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

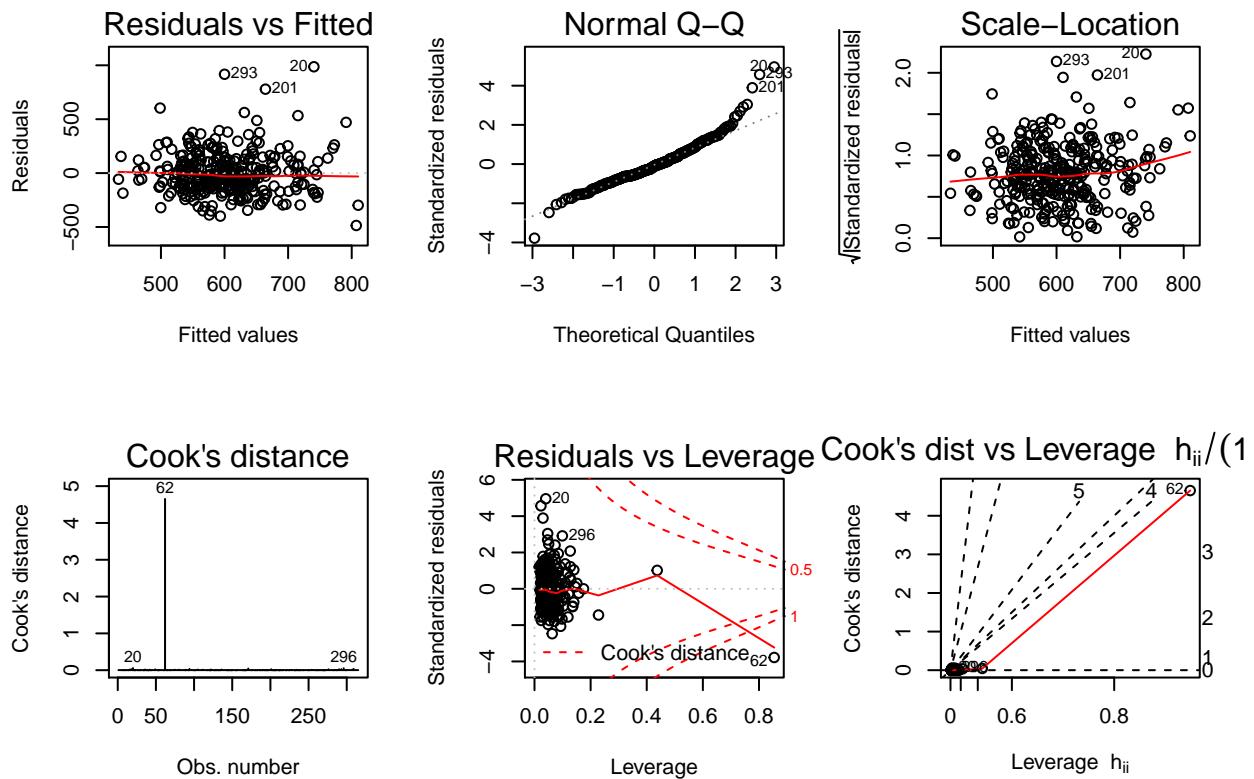
mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "vitamine"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et vitamine", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 16: Régression linéaire multiple avec interaction entre âge et vitamine

	Bêta	IC	p
(Intercept)	520.183	[122.028;4.263]	0
age	2.93	[1.517;1.932]	0.0544
sexeFemmes	-98.917	[38.991;-2.537]	0.0117
tabacAutrefois	61.049	[25.658;2.379]	0.018
tabacFumeur	0.035	[37.516;0.001]	0.9993
bmi	1.384	[2.024;0.684]	0.4945
vitamineSouvent	68.412	[102.551;0.667]	0.5052
vitaminePas-souvent	48.077	[110.252;0.436]	0.6631
calories	0.068	[0.062;1.095]	0.2742
graisses	-1.212	[0.973;-1.245]	0.214
fibres	-4.29	[3.443;-1.246]	0.2137
alcool	-1.317	[1.5;-0.878]	0.3806
cholesterol	-0.089	[0.133;-0.669]	0.5043
betadiet	-0.003	[0.009;-0.344]	0.7308
retdiet	-0.01	[0.022;-0.458]	0.6471
betaplasma	0.084	[0.07;1.199]	0.2316
age:retinol[, "vitamine"]Souvent	-0.912	[1.918;-0.476]	0.6348
age:retinol[, "vitamine"]Pas-souvent	-0.485	[2.198;-0.221]	0.8255



```
rm(mod.tmp)
rm(res.tmp)
```

Table 17: Régression linéaire multiple avec interaction entre âge et calories

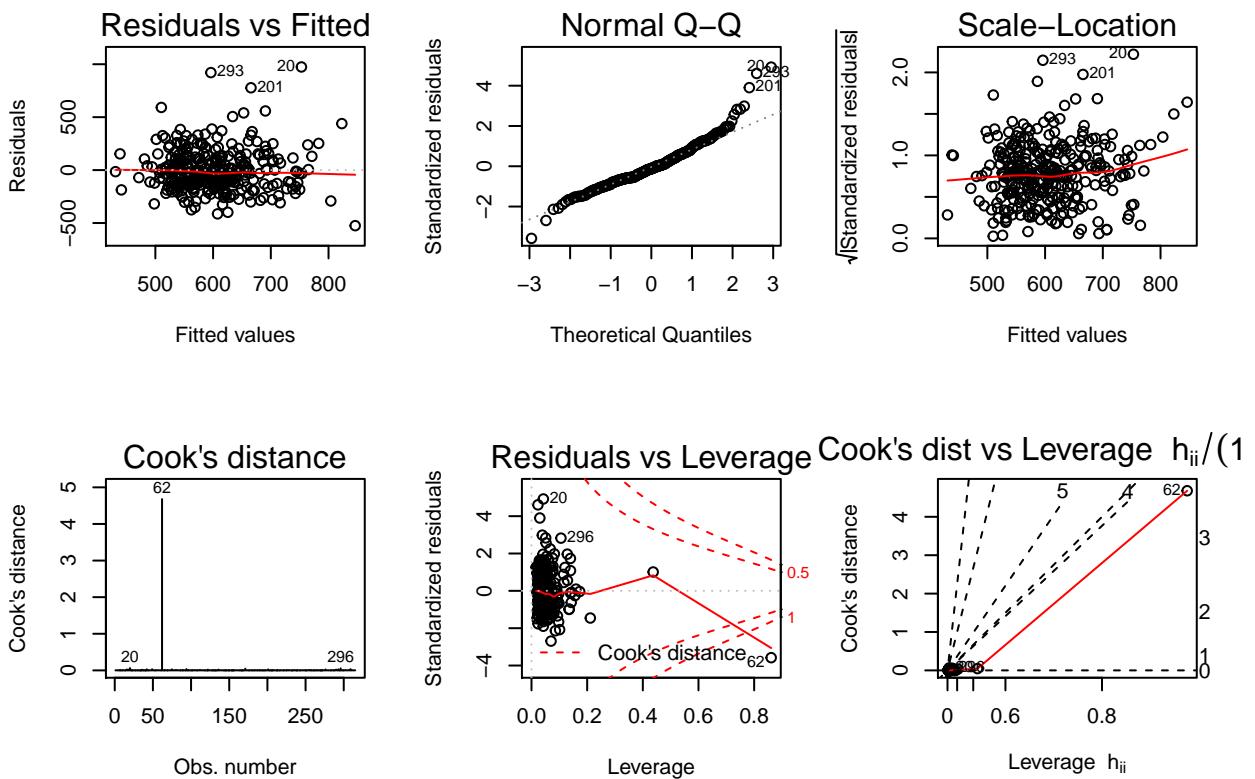
	Bêta	IC	p
(Intercept)	404.174	[147.441;2.741]	0.0065
age	5.428	[2.435;2.23]	0.0265
sexeFemmes	-107.935	[38.475;-2.805]	0.0054
tabacAutrefois	58.357	[25.573;2.282]	0.0232
tabacFumeur	3.708	[37.429;0.099]	0.9211
bmi	1.449	[2.009;0.721]	0.4712
vitamineSouvent	16.975	[28.609;0.593]	0.5534
vitaminePas-souvent	20.305	[30.683;0.662]	0.5086
calories	0.147	[0.085;1.74]	0.0829
graisses	-1.127	[0.97;-1.162]	0.2463
fibres	-3.665	[3.464;-1.058]	0.2908
alcool	-0.528	[1.611;-0.328]	0.7435
cholesterol	-0.095	[0.132;-0.72]	0.4721
betadiet	-0.003	[0.009;-0.315]	0.7532
retdiet	-0.01	[0.022;-0.464]	0.6427
betaplasma	0.091	[0.07;1.298]	0.1952
age:retinol[, "calories"]	-0.002	[0.001;-1.335]	0.183

```

mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "calories"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et calories", col.names = c("",
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

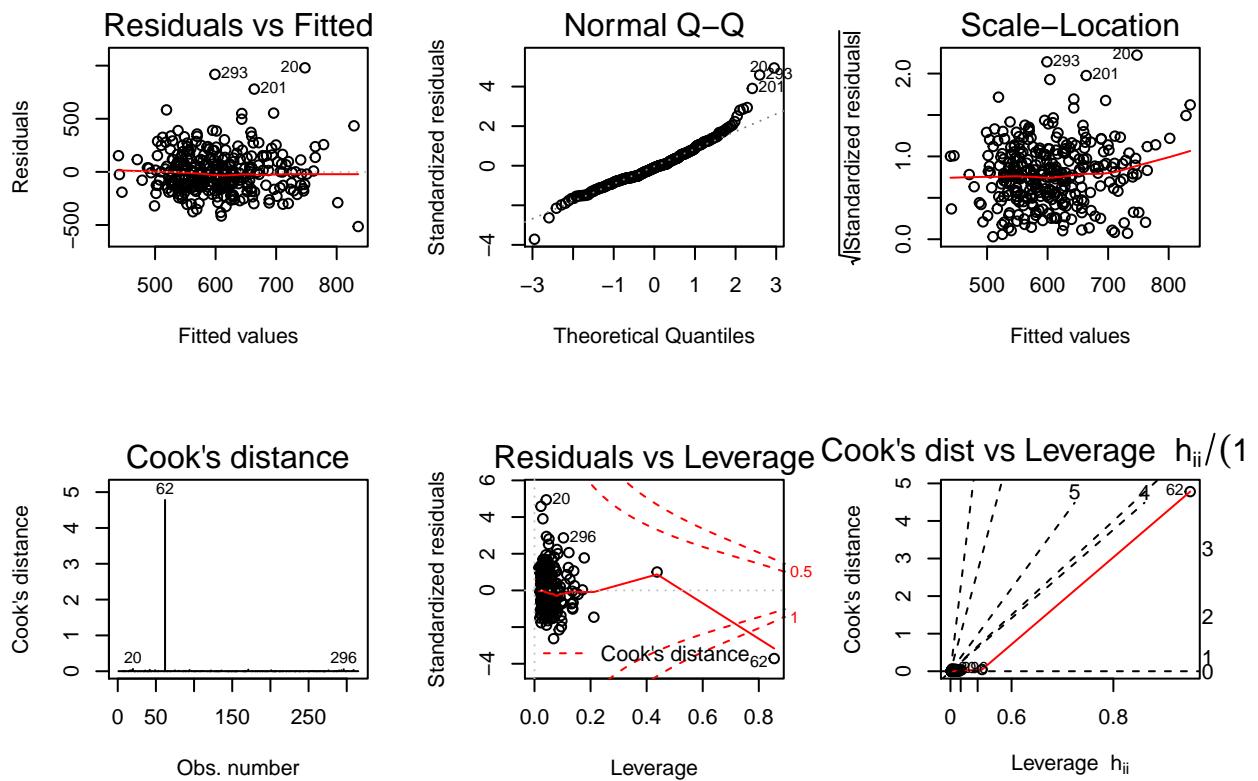
mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "graisses"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et graisses", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 18: Régression linéaire multiple avec interaction entre âge et graisses

	Bêta	IC	p
(Intercept)	467.256	[131.544;3.552]	4e-04
age	4.154	[2.035;2.041]	0.0421
sexeFemmes	-105.712	[38.474;-2.748]	0.0064
tabacAutrefois	60.6	[25.558;2.371]	0.0184
tabacFumeur	2.655	[37.476;0.071]	0.9436
bmi	1.372	[2.01;0.683]	0.4953
vitamineSouvent	18.131	[28.668;0.632]	0.5276
vitaminePas-souvent	21.617	[30.695;0.704]	0.4818
calories	0.063	[0.062;1.027]	0.3053
graisses	0.028	[1.634;0.017]	0.9861
fibres	-4.089	[3.441;-1.188]	0.2357
alcool	-1.081	[1.519;-0.712]	0.4773
cholesterol	-0.097	[0.133;-0.73]	0.466
betadiet	-0.003	[0.009;-0.313]	0.7543
rettdiet	-0.01	[0.022;-0.434]	0.6647
betaplasma	0.088	[0.07;1.267]	0.2062
age:retinol[, "graisses"]	-0.024	[0.025;-0.956]	0.3398



```
rm(mod.tmp)
rm(res.tmp)
```

Table 19: Régression linéaire multiple avec interaction entre âge et fibres

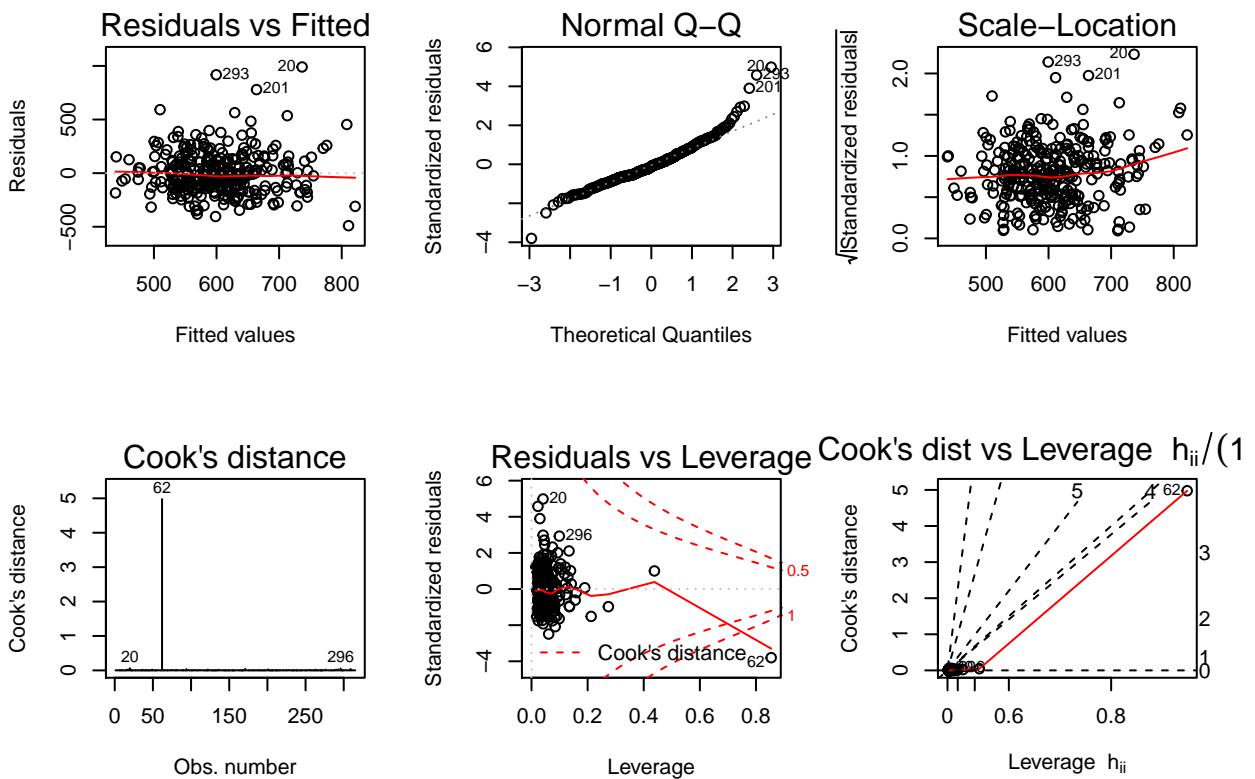
	Bêta	IC	p
(Intercept)	572.965	[132.069;4.338]	0
age	1.909	[2.03;0.94]	0.3479
sexeFemmes	-99.933	[38.856;-2.572]	0.0106
tabacAutrefois	61.449	[25.814;2.38]	0.0179
tabacFumeur	-0.474	[37.58;-0.013]	0.99
bmi	1.306	[2.012;0.649]	0.5169
vitamineSouvent	21.815	[28.497;0.766]	0.4446
vitaminePas-souvent	23.507	[30.7;0.766]	0.4445
calories	0.07	[0.062;1.137]	0.2564
graisses	-1.236	[0.971;-1.274]	0.2038
fibres	-6.591	[8.768;-0.752]	0.4528
alcool	-1.335	[1.497;-0.892]	0.3732
cholesterol	-0.084	[0.133;-0.631]	0.5285
betadiet	-0.003	[0.009;-0.294]	0.769
retdiet	-0.01	[0.022;-0.439]	0.6612
betaplasma	0.082	[0.07;1.172]	0.2421
age:retinol[, "fibres"]	0.041	[0.15;0.275]	0.7831

```

mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "fibres"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et fibres", col.names = c(" " ,
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

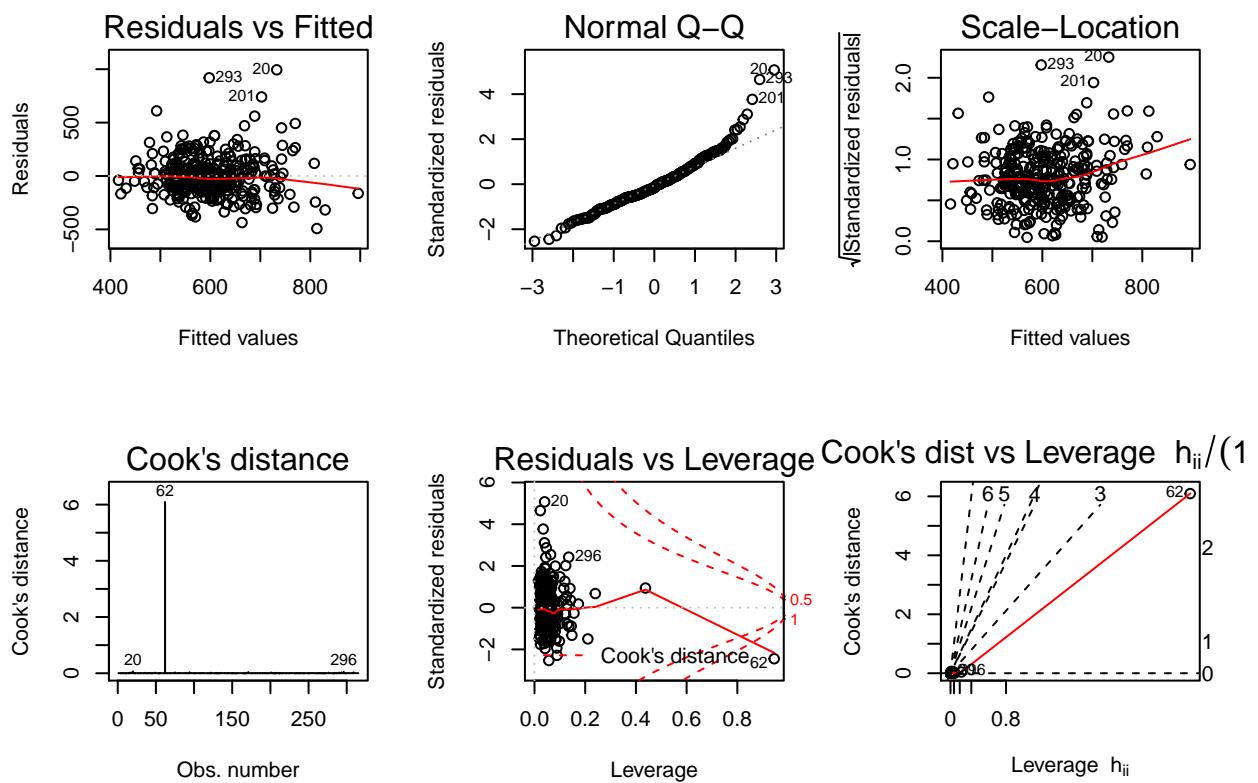
mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "alcool"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et alcool", col.names = c(" " ,
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 20: Régression linéaire multiple avec interaction entre âge et alcool

	Bêta	IC	p
(Intercept)	478.147	[101.426;4.714]	0
age	3.271	[0.937;3.491]	6e-04
sexeFemmes	-93.743	[37.856;-2.476]	0.0138
tabacAutrefois	55.796	[25.282;2.207]	0.0281
tabacFumeur	5.934	[36.97;0.161]	0.8726
bmi	1.799	[1.99;0.904]	0.3669
vitamineSouvent	24.431	[28.096;0.87]	0.3852
vitaminePas-souvent	22.93	[30.254;0.758]	0.4491
calories	0.076	[0.061;1.248]	0.2129
graisses	-1.361	[0.958;-1.421]	0.1562
fibres	-4.468	[3.385;-1.32]	0.1878
alcool	22.837	[8.324;2.744]	0.0064
cholesterol	-0.085	[0.131;-0.652]	0.5148
betadiet	-0.004	[0.009;-0.416]	0.6774
rettdiet	-0.011	[0.022;-0.484]	0.629
betaplasma	0.074	[0.069;1.081]	0.2807
age:retinol[, "alcool"]	-0.387	[0.131;-2.951]	0.0034



```
rm(mod.tmp)
rm(res.tmp)
```

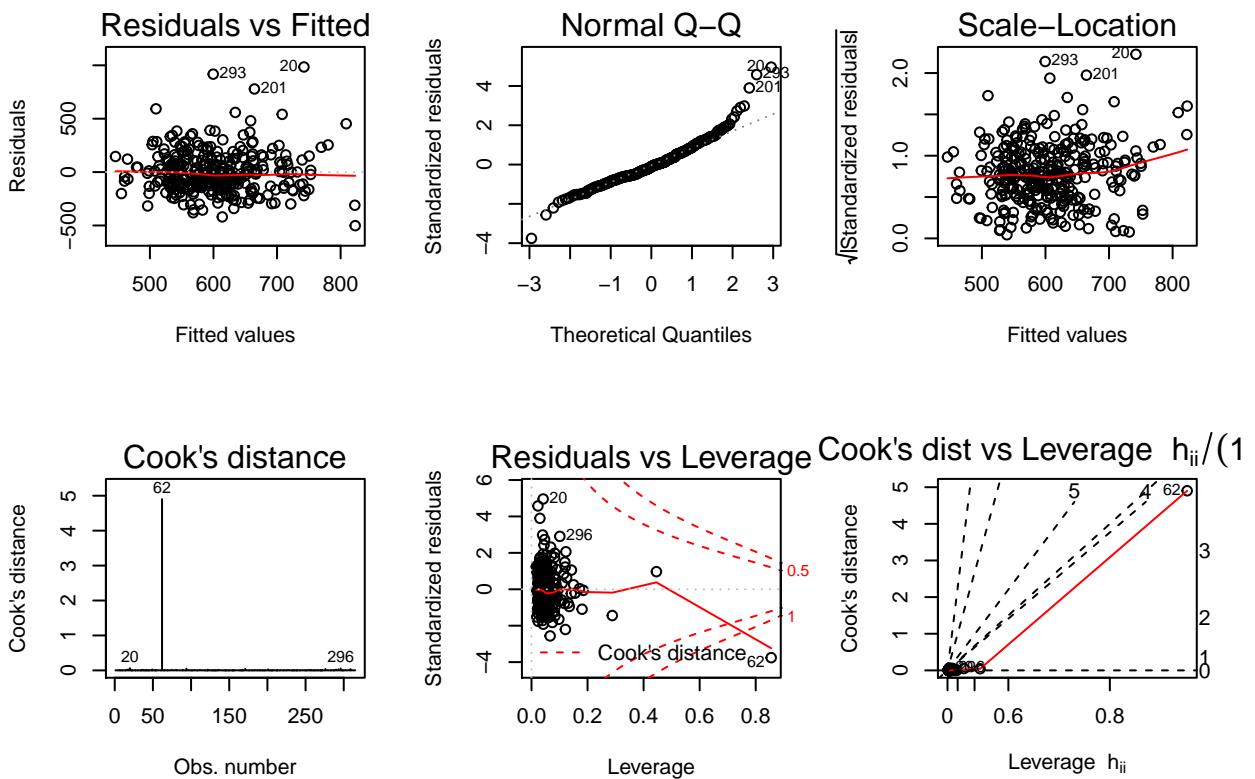
Table 21: Régression linéaire multiple avec interaction entre âge et cholesterol

	Bêta	IC	p
(Intercept)	523.666	[117.706;4.449]	0
age	2.986	[1.671;1.787]	0.0749
sexeFemmes	-103.478	[38.532;-2.686]	0.0076
tabacAutrefois	61.184	[25.641;2.386]	0.0176
tabacFumeur	0.963	[37.474;0.026]	0.9795
bmi	1.31	[2.012;0.651]	0.5156
vitamineSouvent	20.01	[28.729;0.697]	0.4867
vitaminePas-souvent	22.768	[30.71;0.741]	0.459
calories	0.068	[0.062;1.098]	0.2729
graisses	-1.265	[0.974;-1.299]	0.1951
fibres	-4.336	[3.434;-1.263]	0.2077
alcool	-1.25	[1.512;-0.827]	0.4092
cholesterol	0.052	[0.362;0.143]	0.8862
betadiet	-0.003	[0.009;-0.296]	0.7674
retdiet	-0.009	[0.023;-0.392]	0.6951
retplasma	0.084	[0.07;1.202]	0.2304
age:retinol[, "cholesterol"]	-0.003	[0.006;-0.41]	0.6819

```

mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "cholesterol"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et cholesterol", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")
      )
par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

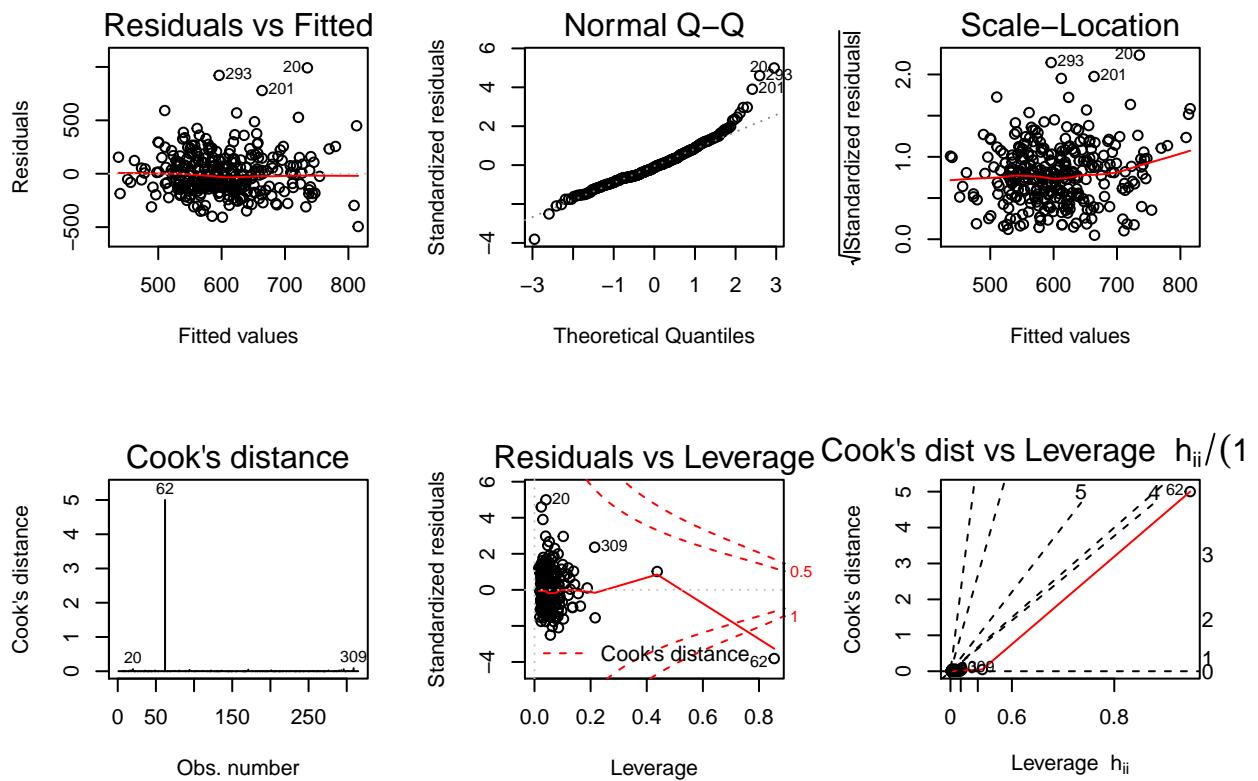
mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "betadiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et betadiet", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 22: Régression linéaire multiple avec interaction entre âge et betadiet

	Bêta	IC	p
(Intercept)	583.664	[119.044;4.903]	0
age	1.708	[1.597;1.07]	0.2855
sexeFemmes	-100.977	[38.315;-2.635]	0.0088
tabacAutrefois	61.177	[25.615;2.388]	0.0175
tabacFumeur	-0.573	[37.482;-0.015]	0.9878
bmi	1.245	[2.016;0.617]	0.5374
vitamineSouvent	21.89	[28.479;0.769]	0.4427
vitaminePas-souvent	23.549	[30.682;0.767]	0.4434
calories	0.068	[0.062;1.107]	0.2693
graisses	-1.197	[0.972;-1.232]	0.2189
fibres	-4.473	[3.438;-1.301]	0.1942
alcool	-1.325	[1.496;-0.886]	0.3764
cholesterol	-0.086	[0.133;-0.648]	0.5178
betadiet	-0.019	[0.032;-0.6]	0.5487
retdiet	-0.01	[0.022;-0.458]	0.6471
betaplasma	0.086	[0.07;1.227]	0.2208
age:retinol[, "betadiet"]	0	[0.001;0.533]	0.5946



```
rm(mod.tmp)
rm(res.tmp)
```

Table 23: Régression linéaire multiple avec interaction entre âge et retdiet

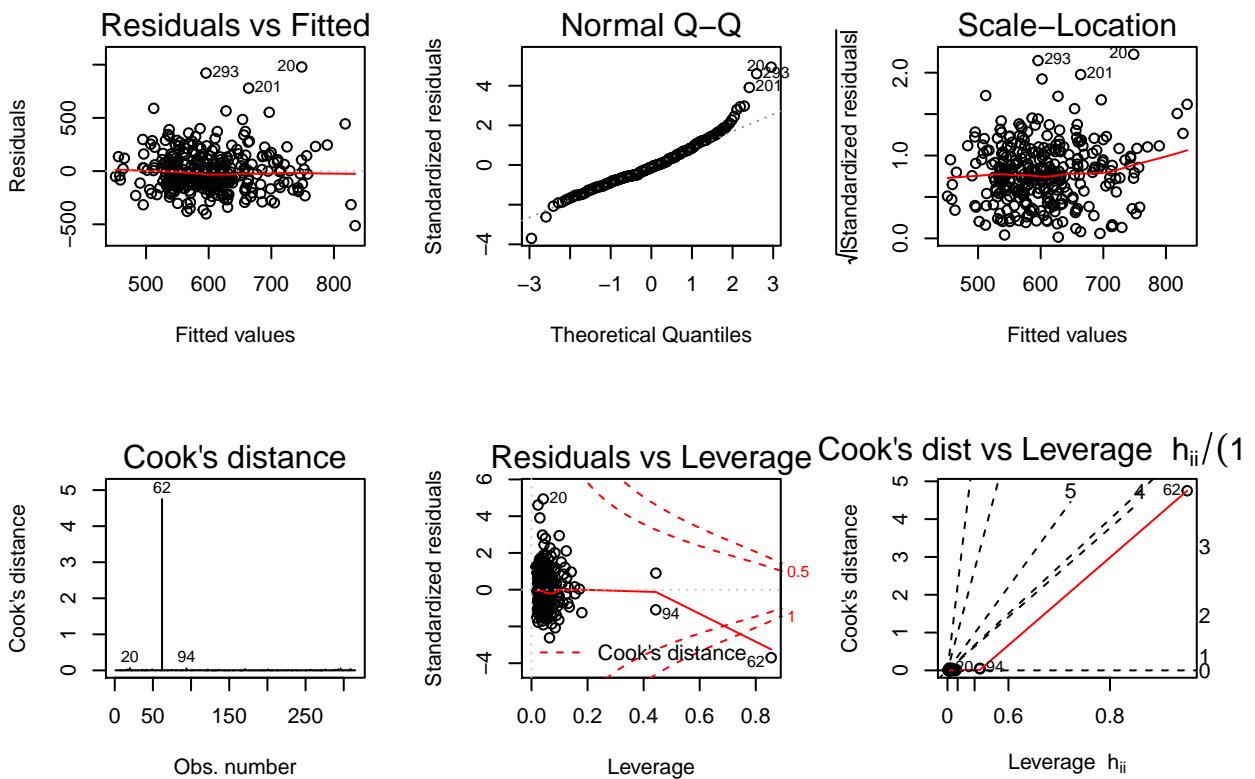
	Bêta	IC	p
(Intercept)	490.43	[113.828;4.309]	0
age	3.777	[1.562;2.418]	0.0162
sexeFemmes	-105.118	[38.364;-2.74]	0.0065
tabacAutrefois	59.62	[25.562;2.332]	0.0203
tabacFumeur	1.979	[37.415;0.053]	0.9579
bmi	1.211	[2.011;0.602]	0.5475
vitamineSouvent	19.527	[28.495;0.685]	0.4937
vitaminePas-souvent	22.359	[30.646;0.73]	0.4662
calories	0.063	[0.062;1.021]	0.3079
graisses	-1.25	[0.969;-1.291]	0.1977
fibres	-4.344	[3.427;-1.268]	0.206
alcool	-1.222	[1.498;-0.816]	0.4152
cholesterol	-0.062	[0.134;-0.46]	0.646
betadiet	-0.002	[0.009;-0.26]	0.7951
retdiet	0.077	[0.084;0.912]	0.3624
betaplasma	0.087	[0.07;1.246]	0.2138
age:retinol[, "retdiet"]	-0.002	[0.002;-1.072]	0.2846

```

mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et retdiet", col.names = c(" "
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

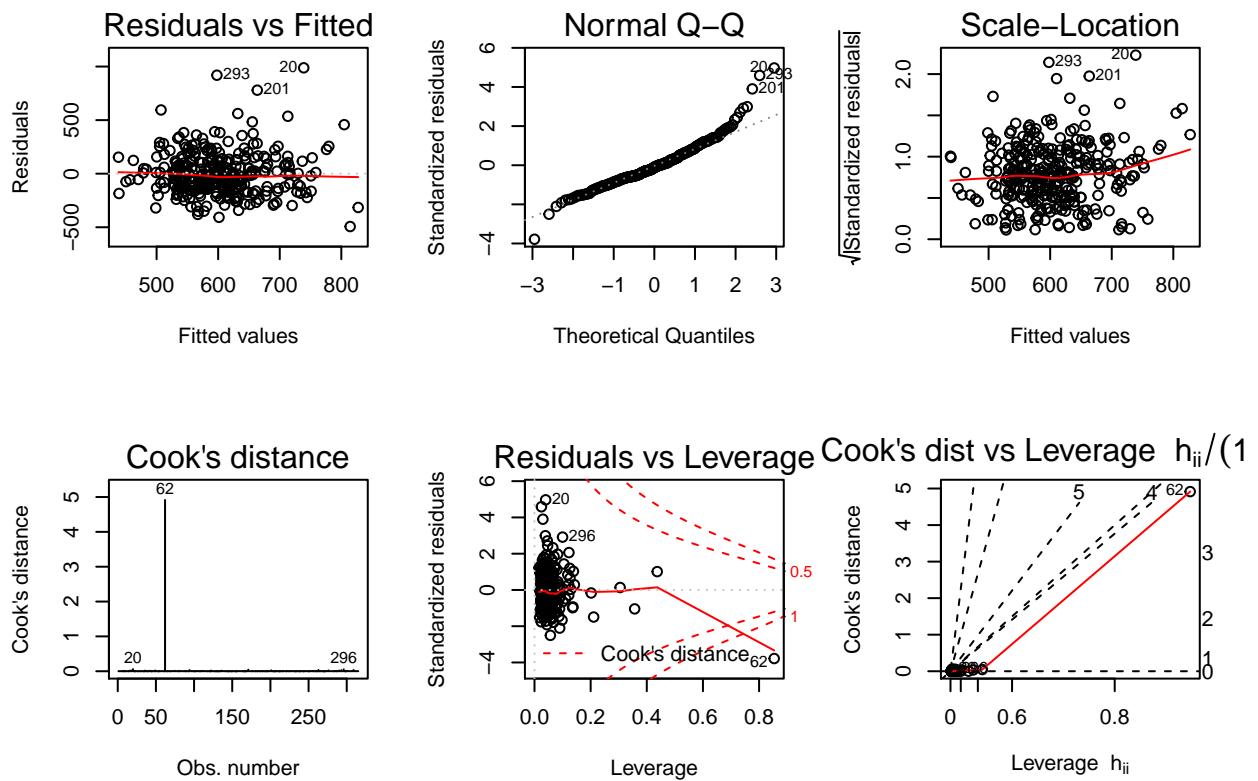
mod.tmp = lm(retplasma ~ . -retplasma + age*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre âge et betaplasma", col.names = c(
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 24: Régression linéaire multiple avec interaction entre âge et betaplasma

	Bêta	IC	p
(Intercept)	561.333	[112.71;4.98]	0
age	2.182	[1.33;1.641]	0.1019
sexeFemmes	-102.417	[38.416;-2.666]	0.0081
tabacAutrefois	60.846	[25.633;2.374]	0.0182
tabacFumeur	0.17	[37.464;0.005]	0.9964
bmi	1.32	[2.012;0.656]	0.5123
vitamineSouvent	21.135	[28.543;0.74]	0.4596
vitaminePas-souvent	23.085	[30.701;0.752]	0.4527
calories	0.069	[0.062;1.126]	0.2612
graisses	-1.238	[0.971;-1.275]	0.2033
fibres	-4.455	[3.453;-1.29]	0.198
alcool	-1.328	[1.497;-0.887]	0.3759
cholesterol	-0.084	[0.133;-0.631]	0.5283
betadiet	-0.003	[0.009;-0.274]	0.7844
retdiet	-0.01	[0.022;-0.451]	0.6525
betaplasma	0.026	[0.256;0.101]	0.9196
age:retinol[, "betaplasma"]	0.001	[0.005;0.233]	0.8157



```
rm(mod.tmp)
rm(res.tmp)
```

La seule interaction observée est celle entre l'âge et l'alcool

Table 25: Régression linéaire multiple avec interaction entre sexe et tabac

	Bêta	IC	p
(Intercept)	461.746	[106.389;4.34]	0
age	2.364	[0.897;2.635]	0.0089
sexeFemmes	-8.989	[60.236;-0.149]	0.8815
tabacAutrefois	208.811	[70.98;2.942]	0.0035
tabacFumeur	41.668	[100.586;0.414]	0.679
bmi	1.309	[2.011;0.651]	0.5156
vitamineSouvent	17.687	[28.338;0.624]	0.533
vitaminePas-souvent	23.697	[30.499;0.777]	0.4378
calories	0.074	[0.061;1.212]	0.2266
graisses	-1.25	[0.963;-1.298]	0.1954
fibres	-4.268	[3.41;-1.252]	0.2117
alcool	-1.366	[1.501;-0.91]	0.3635
cholesterol	-0.094	[0.132;-0.713]	0.4765
betadiet	-0.002	[0.009;-0.245]	0.8065
retdiet	-0.012	[0.022;-0.519]	0.6042
betaplasma	0.085	[0.069;1.219]	0.2238
sexeFemmes:retinol[, "tabac"]Autrefois	-171.878	[76.081;-2.259]	0.0246
sexeFemmes:retinol[, "tabac"]Fumeur	-41.425	[107.561;-0.385]	0.7004

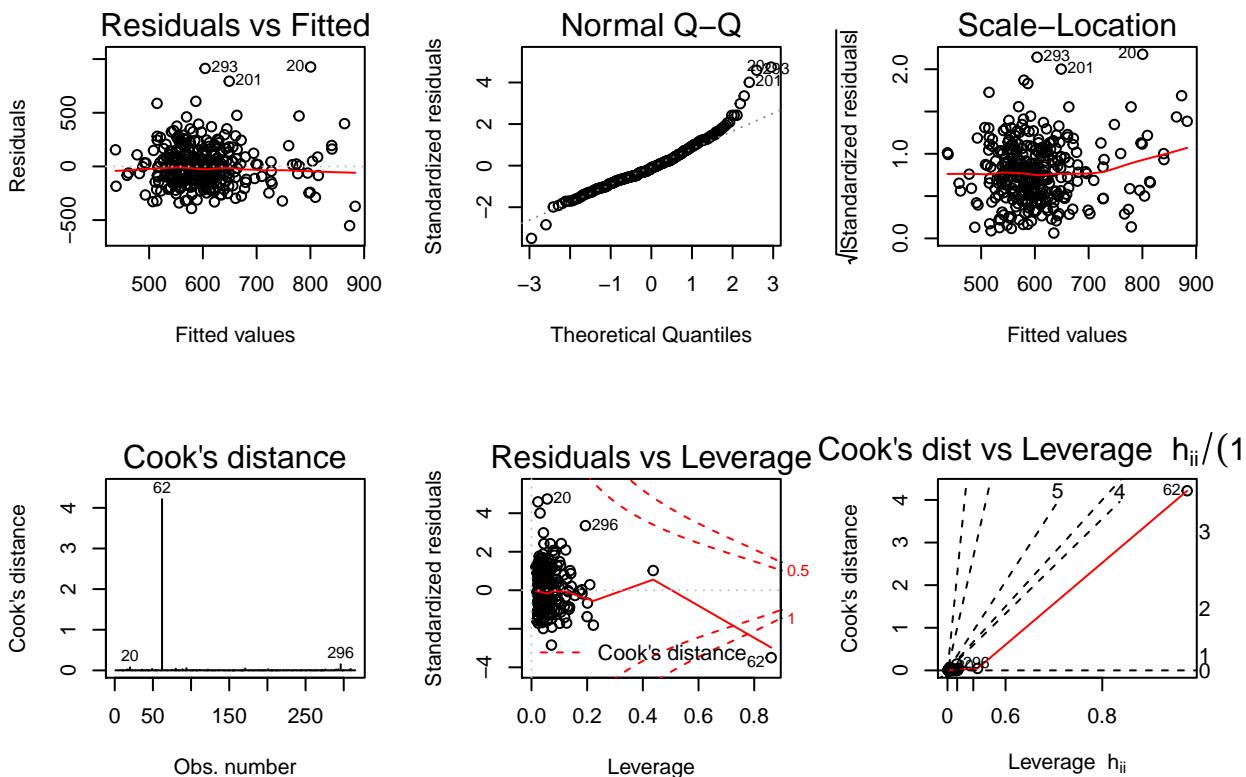
5.3.2 Avec le sexe

```

mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "tabac"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(summary(mod.tmp)$coefficient[,1],3),
                  paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                         round(summary(mod.tmp)$coefficient[,3],3), "]"),
                  round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et tabac", col.names = c(" " ,
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

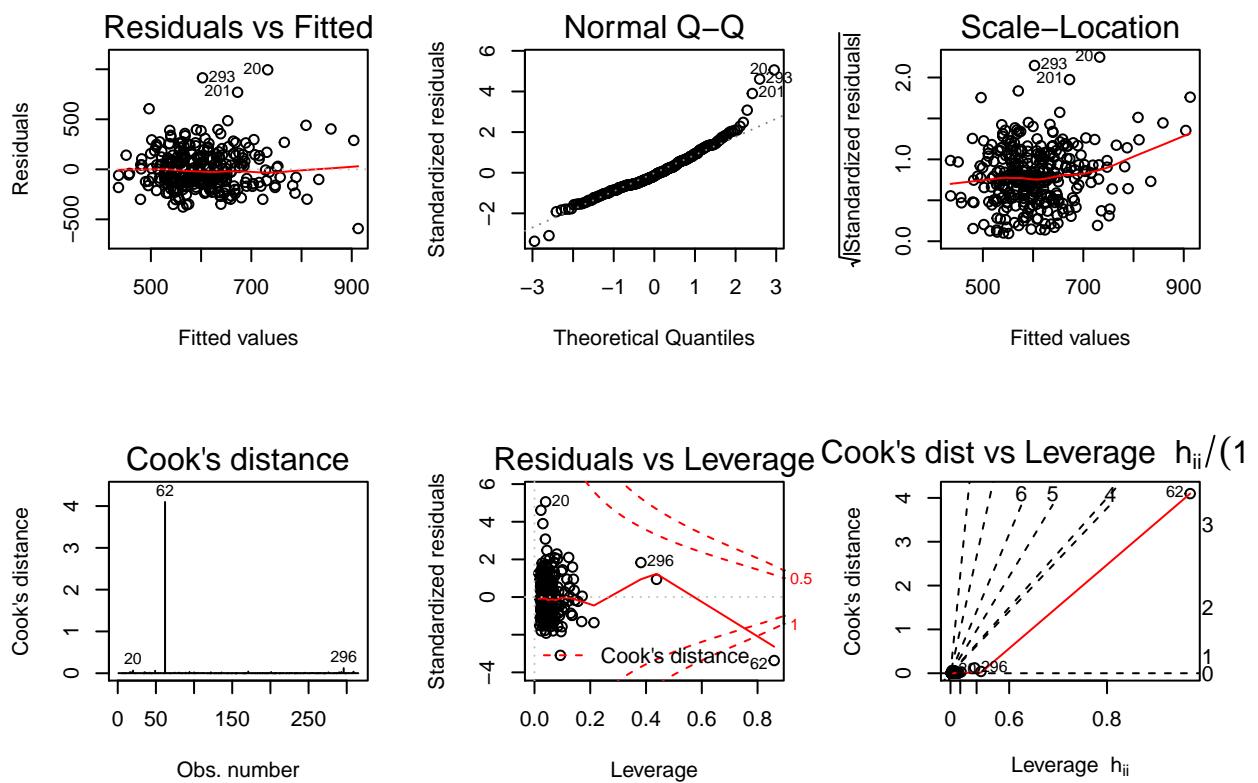
mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "bmi"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et bmi", col.names = c(" ", " ",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 26: Régression linéaire multiple avec interaction entre sexe et bmi

	Bêta	IC	p
(Intercept)	42.637	[220.825;0.193]	0.847
age	2.564	[0.895;2.863]	0.0045
sexeFemmes	432.397	[211.625;2.043]	0.0419
tabacAutrefois	60.039	[25.32;2.371]	0.0184
tabacFumeur	-7.576	[37.18;-0.204]	0.8387
bmi	20.229	[7.635;2.649]	0.0085
vitamineSouvent	18.258	[28.206;0.647]	0.5179
vitaminePas-souvent	27.349	[30.401;0.9]	0.369
calories	0.07	[0.061;1.151]	0.2507
graisses	-1.314	[0.96;-1.369]	0.1721
fibres	-3.876	[3.402;-1.139]	0.2554
alcool	-1.23	[1.481;-0.83]	0.4071
cholesterol	-0.07	[0.131;-0.534]	0.594
betadiet	-0.005	[0.009;-0.525]	0.5997
retdiet	-0.01	[0.022;-0.437]	0.6624
betaplasma	0.082	[0.069;1.187]	0.2361
sexeFemmes:retinol[, "bmi"]	-20.236	[7.888;-2.565]	0.0108



```
rm(mod.tmp)
rm(res.tmp)
```

Table 27: Régression linéaire multiple avec interaction entre sexe et vitamine

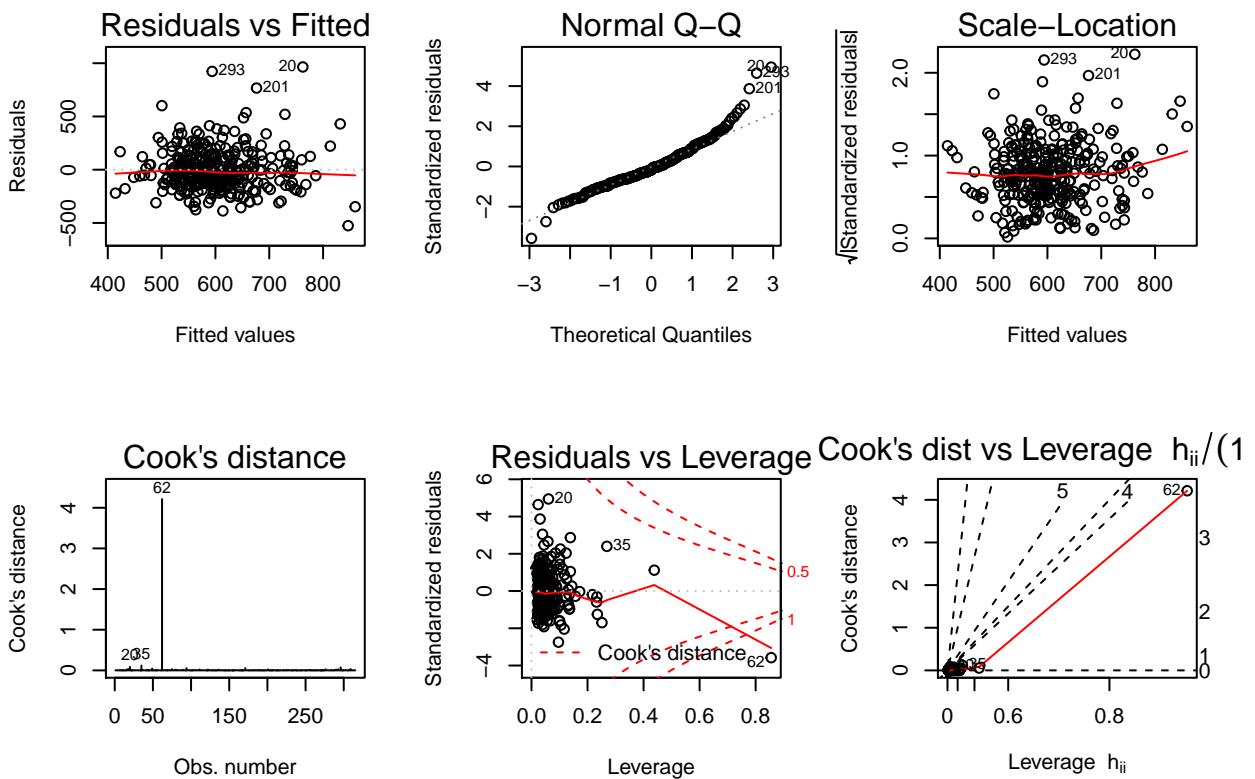
	Bêta	IC	p
(Intercept)	591.23	[105.386;5.61]	0
age	2.333	[0.904;2.58]	0.0103
sexeFemmes	-132.473	[51.654;-2.565]	0.0108
tabacAutrefois	55.818	[25.553;2.184]	0.0297
tabacFumeur	-7.529	[37.379;-0.201]	0.8405
bmi	0.952	[2.007;0.474]	0.6357
vitamineSouvent	32.432	[70.639;0.459]	0.6465
vitaminePas-souvent	-193.872	[101.319;-1.913]	0.0566
calories	0.063	[0.062;1.014]	0.3113
graisses	-1.098	[0.971;-1.13]	0.2593
fibres	-4.285	[3.428;-1.25]	0.2123
alcool	-1.426	[1.488;-0.959]	0.3384
cholesterol	-0.081	[0.132;-0.612]	0.5409
betadiet	-0.003	[0.009;-0.326]	0.7445
retdiet	-0.013	[0.022;-0.598]	0.5502
betaplasma	0.094	[0.069;1.361]	0.1745
sexeFemmes:retinol[, "vitamine"]Souvent	-11.164	[77.29;-0.144]	0.8852
sexeFemmes:retinol[, "vitamine"]Pas-souvent	234.928	[106.115;2.214]	0.0276

```

mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "vitamine"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(summary(mod.tmp)$coefficient[,1],3),
                  paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                         round(summary(mod.tmp)$coefficient[,3],3), "]"),
                  round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et vitamine", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

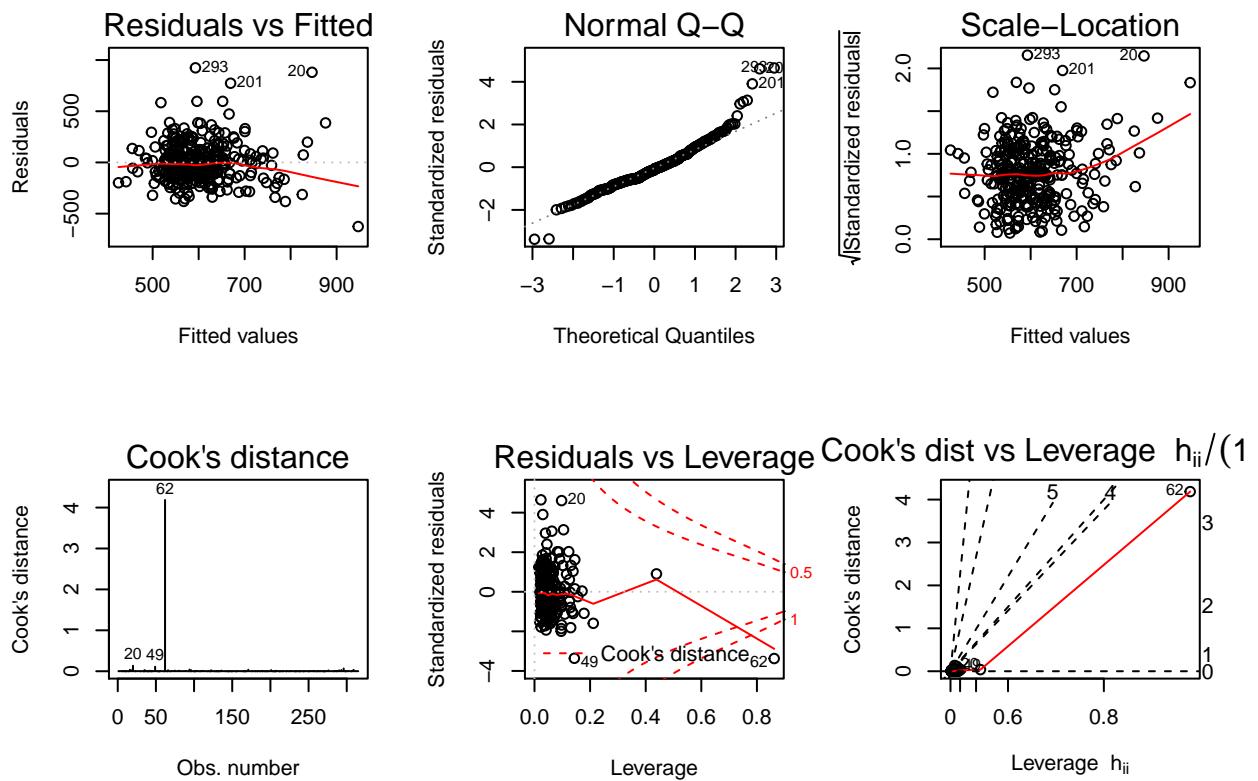
mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "calories"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et calories", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 28: Régression linéaire multiple avec interaction entre sexe et calories

	Bêta	IC	p
(Intercept)	770.927	[140.412;5.49]	0
age	2.43	[0.896;2.713]	0.0071
sexeFemmes	-361.86	[122.681;-2.95]	0.0034
tabacAutrefois	54.726	[25.519;2.145]	0.0328
tabacFumeur	8.536	[37.328;0.229]	0.8193
bmi	1.794	[2.007;0.894]	0.3721
vitamineSouvent	21.204	[28.252;0.751]	0.4535
vitaminePas-souvent	20.167	[30.472;0.662]	0.5086
calories	-0.046	[0.08;-0.575]	0.5658
graisses	-1.167	[0.963;-1.212]	0.2263
fibres	-4.811	[3.411;-1.41]	0.1595
alcool	1.121	[1.849;0.606]	0.545
cholesterol	-0.12	[0.132;-0.906]	0.3656
betadiet	-0.003	[0.009;-0.339]	0.7352
retdiet	-0.009	[0.022;-0.402]	0.6876
betaplasma	0.085	[0.069;1.232]	0.2189
sexeFemmes:retinol[, "calories"]	0.132	[0.059;2.23]	0.0265



```
rm(mod.tmp)
rm(res.tmp)
```

Table 29: Régression linéaire multiple avec interaction entre sexe et graisses

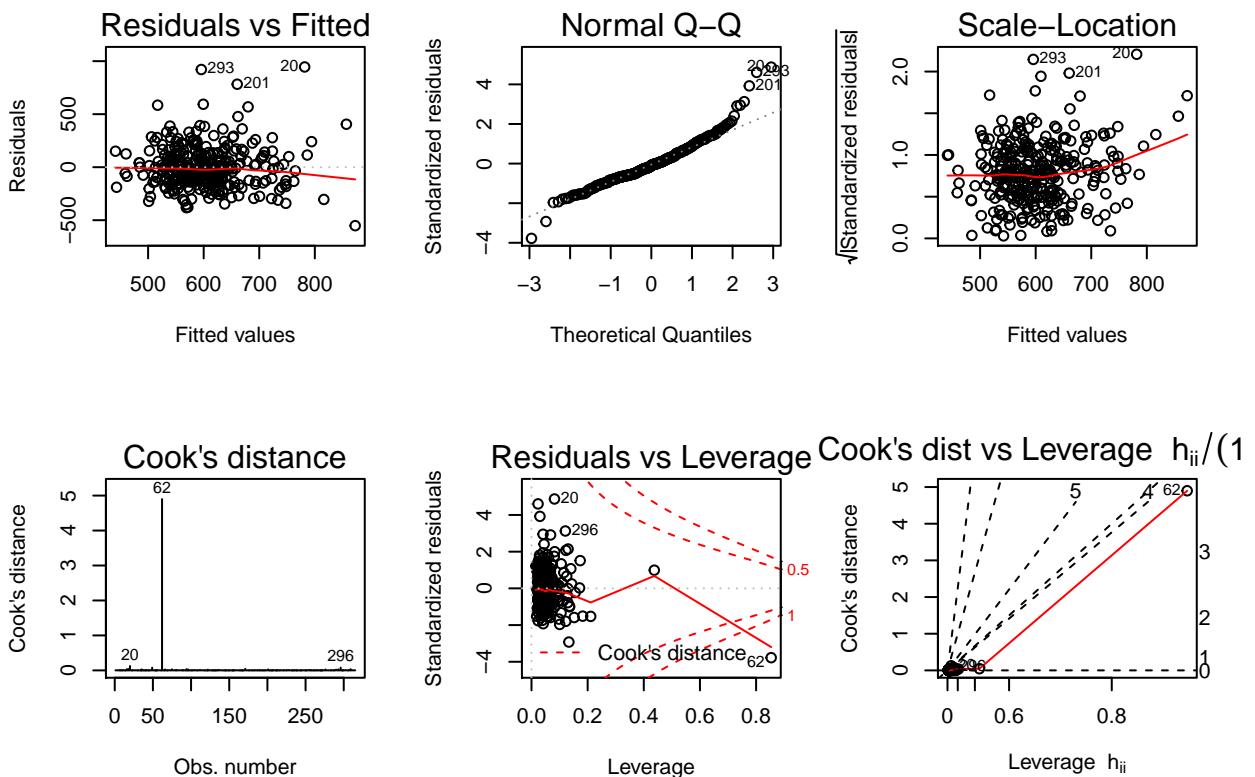
	Bêta	IC	p
(Intercept)	639.676	[132.681;4.821]	0
age	2.385	[0.902;2.645]	0.0086
sexeFemmes	-203.824	[105.817;-1.926]	0.055
tabacAutrefois	59.258	[25.581;2.317]	0.0212
tabacFumeur	4.664	[37.619;0.124]	0.9014
bmi	1.462	[2.013;0.726]	0.4683
vitamineSouvent	21.177	[28.438;0.745]	0.457
vitaminePas-souvent	22.563	[30.646;0.736]	0.4621
calories	0.072	[0.061;1.168]	0.2438
graisses	-2.223	[1.364;-1.63]	0.1042
fibres	-4.617	[3.436;-1.344]	0.1801
alcool	-1.036	[1.522;-0.681]	0.4967
cholesterol	-0.099	[0.133;-0.744]	0.4574
betadiet	-0.003	[0.009;-0.34]	0.7337
rettdiet	-0.01	[0.022;-0.464]	0.643
betaplasma	0.088	[0.07;1.257]	0.2098
sexeFemmes:retinol[, "graisses"]	1.133	[1.095;1.035]	0.3016

```

mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "graisses"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et graisses", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

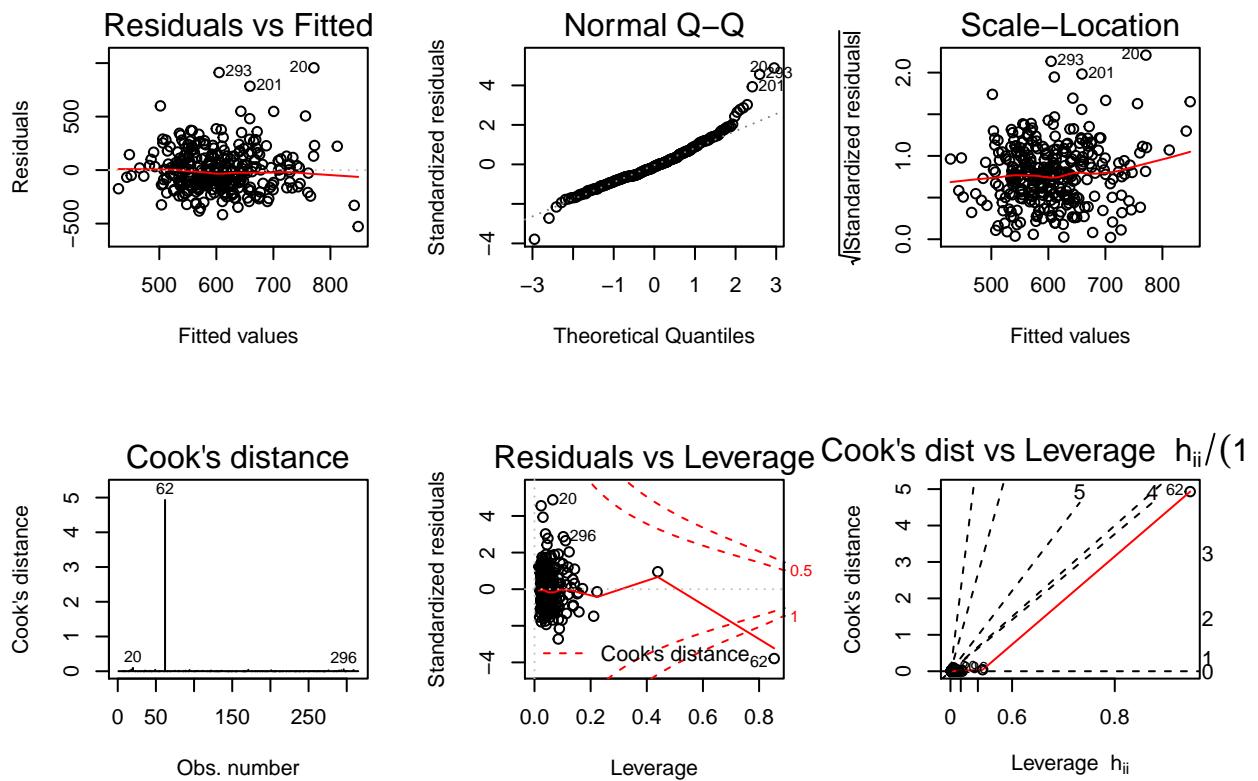
mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "fibres"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et fibres", col.names = c(" " ))
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 30: Régression linéaire multiple avec interaction entre sexe et fibres

	Bêta	IC	p
(Intercept)	638.516	[133.848;4.77]	0
age	2.469	[0.904;2.732]	0.0067
sexeFemmes	-199.574	[104.919;-1.902]	0.0581
tabacAutrefois	59.273	[25.585;2.317]	0.0212
tabacFumeur	1.887	[37.425;0.05]	0.9598
bmi	1.289	[2.009;0.641]	0.5218
vitamineSouvent	21.673	[28.439;0.762]	0.4466
vitaminePas-souvent	24.231	[30.656;0.79]	0.4299
calories	0.067	[0.061;1.094]	0.2749
graisses	-1.169	[0.971;-1.204]	0.2295
fibres	-10.66	[7.156;-1.49]	0.1374
alcool	-1.354	[1.494;-0.906]	0.3656
cholesterol	-0.114	[0.135;-0.844]	0.3991
betadiet	-0.003	[0.009;-0.326]	0.7447
retdiet	-0.008	[0.023;-0.359]	0.7195
betaplasma	0.077	[0.07;1.103]	0.2709
sexeFemmes:retinol[, "fibres"]	7.218	[7.207;1.001]	0.3174



```
rm(mod.tmp)
rm(res.tmp)
```

Table 31: Régression linéaire multiple avec interaction entre sexe et alcool

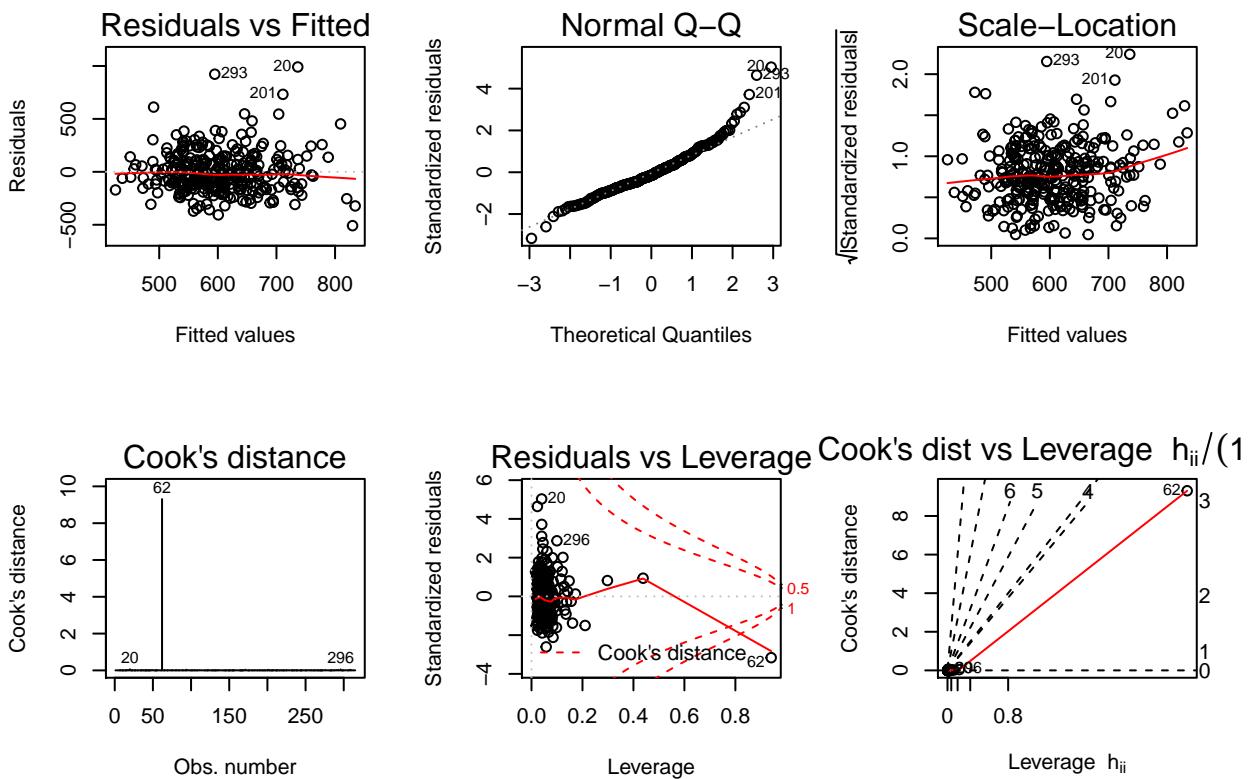
	Bêta	IC	p
(Intercept)	533.05	[99.302;5.368]	0
age	2.474	[0.896;2.763]	0.0061
sexeFemmes	-125.584	[39.32;-3.194]	0.0016
tabacAutrefois	54.021	[25.521;2.117]	0.0351
tabacFumeur	-1.735	[37.132;-0.047]	0.9628
bmi	2.155	[2.026;1.064]	0.2884
vitamineSouvent	28.514	[28.388;1.004]	0.316
vitaminePas-souvent	21.557	[30.426;0.709]	0.4792
calories	0.082	[0.061;1.335]	0.1828
graisses	-1.374	[0.964;-1.426]	0.155
fibres	-4.631	[3.405;-1.36]	0.1748
alcool	-2.26	[1.535;-1.472]	0.142
cholesterol	-0.101	[0.132;-0.768]	0.4431
betadiet	-0.003	[0.009;-0.323]	0.747
retdiet	-0.011	[0.022;-0.513]	0.6086
betaplasma	0.072	[0.069;1.039]	0.2997
sexeFemmes:retinol[, "alcool"]	7.592	[3.259;2.33]	0.0205

```

mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "alcool"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et alcool", col.names = c(" "
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

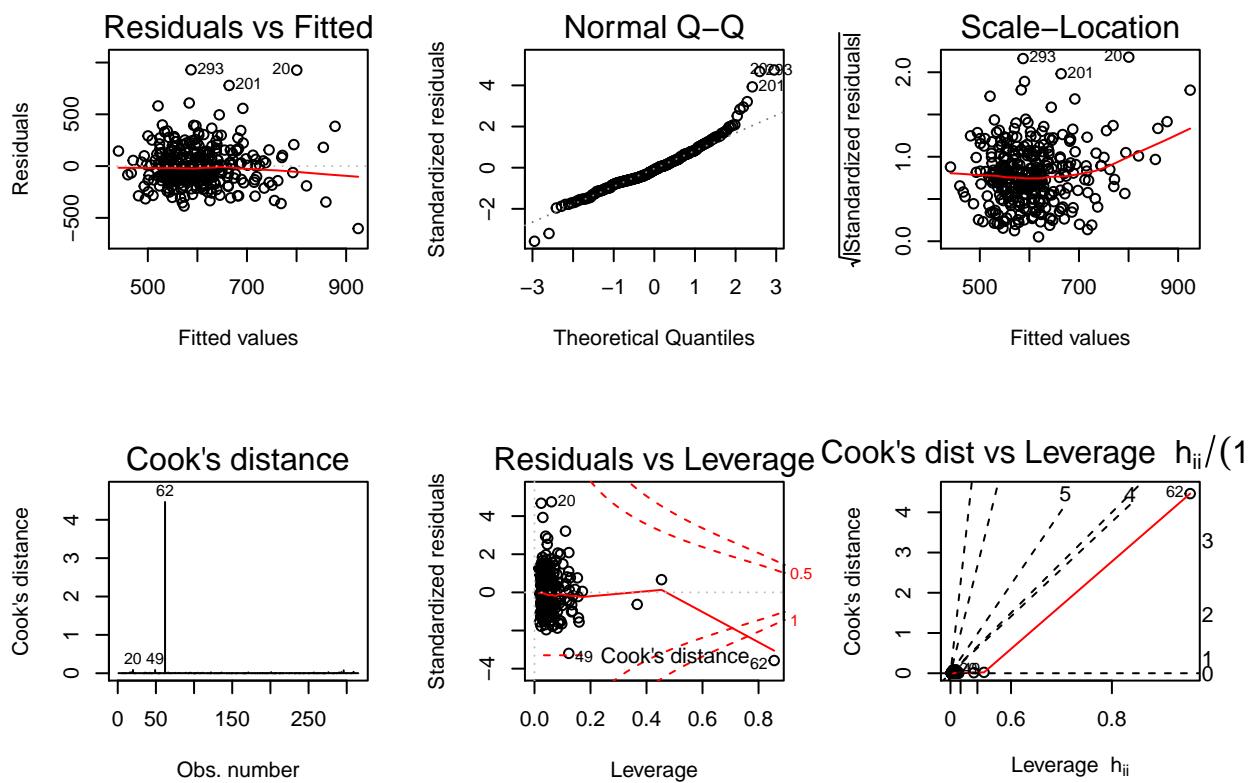
mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "cholesterol"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(summary(mod.tmp)$coefficient[,1],3),
                  paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                         round(summary(mod.tmp)$coefficient[,3],3), "]"),
                  round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et cholesterol", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 32: Régression linéaire multiple avec interaction entre sexe et cholesterol

	Bêta	IC	p
(Intercept)	714.317	[126.123;5.664]	0
age	2.34	[0.897;2.609]	0.0095
sexeFemmes	-268.364	[87.293;-3.074]	0.0023
tabacAutrefois	59.788	[25.409;2.353]	0.0193
tabacFumeur	4.028	[37.218;0.108]	0.9139
bmi	1.184	[1.998;0.593]	0.5538
vitamineSouvent	19.755	[28.287;0.698]	0.4855
vitaminePas-souvent	20.487	[30.492;0.672]	0.5022
calories	0.075	[0.061;1.224]	0.222
graisses	-1.467	[0.97;-1.513]	0.1312
fibres	-5.49	[3.449;-1.592]	0.1125
alcool	-0.908	[1.499;-0.605]	0.5453
cholesterol	-0.524	[0.245;-2.141]	0.0331
betadiet	-0.002	[0.009;-0.209]	0.8349
retdiet	-0.004	[0.022;-0.174]	0.8618
betaplasma	0.085	[0.069;1.227]	0.2208
sexeFemmes:retinol[, "cholesterol"]	0.542	[0.255;2.121]	0.0348



```
rm(mod.tmp)
rm(res.tmp)
```

Table 33: Régression linéaire multiple avec interaction entre sexe et betadiet

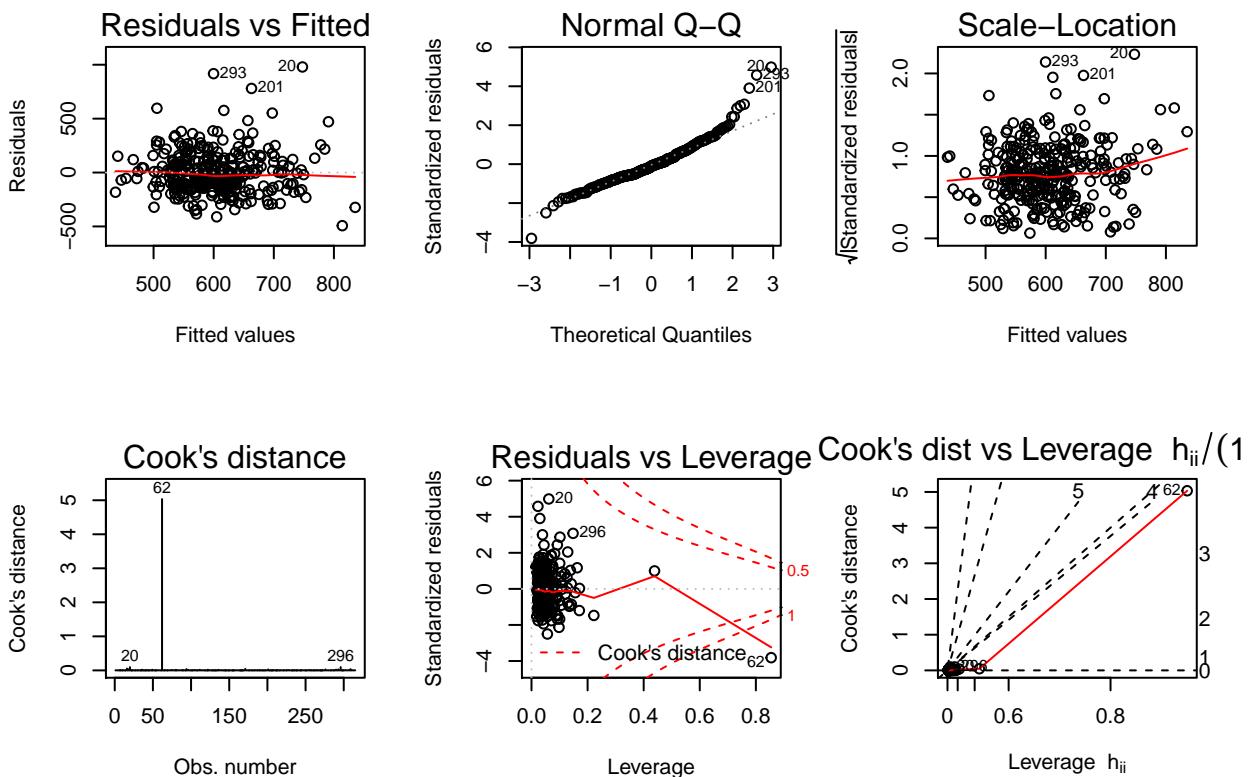
	Bêta	IC	p
(Intercept)	567.973	[118.39;4.797]	0
age	2.41	[0.903;2.668]	0.008
sexeFemmes	-121.978	[78.373;-1.556]	0.1207
tabacAutrefois	60.208	[25.616;2.35]	0.0194
tabacFumeur	0.323	[37.452;0.009]	0.9931
bmi	1.34	[2.013;0.665]	0.5063
vitamineSouvent	21.423	[28.486;0.752]	0.4526
vitaminePas-souvent	23.261	[30.688;0.758]	0.4491
calories	0.069	[0.062;1.127]	0.2606
graisses	-1.238	[0.971;-1.276]	0.2031
fibres	-4.316	[3.438;-1.255]	0.2103
alcool	-1.293	[1.505;-0.859]	0.3909
cholesterol	-0.088	[0.133;-0.661]	0.5093
betadiet	-0.012	[0.031;-0.377]	0.7064
rettdiet	-0.01	[0.023;-0.427]	0.6697
betaplasma	0.081	[0.07;1.157]	0.2484
sexeFemmes:retinol[, "betadiet"]	0.009	[0.031;0.296]	0.7674

```

mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "betadiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et betadiet", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

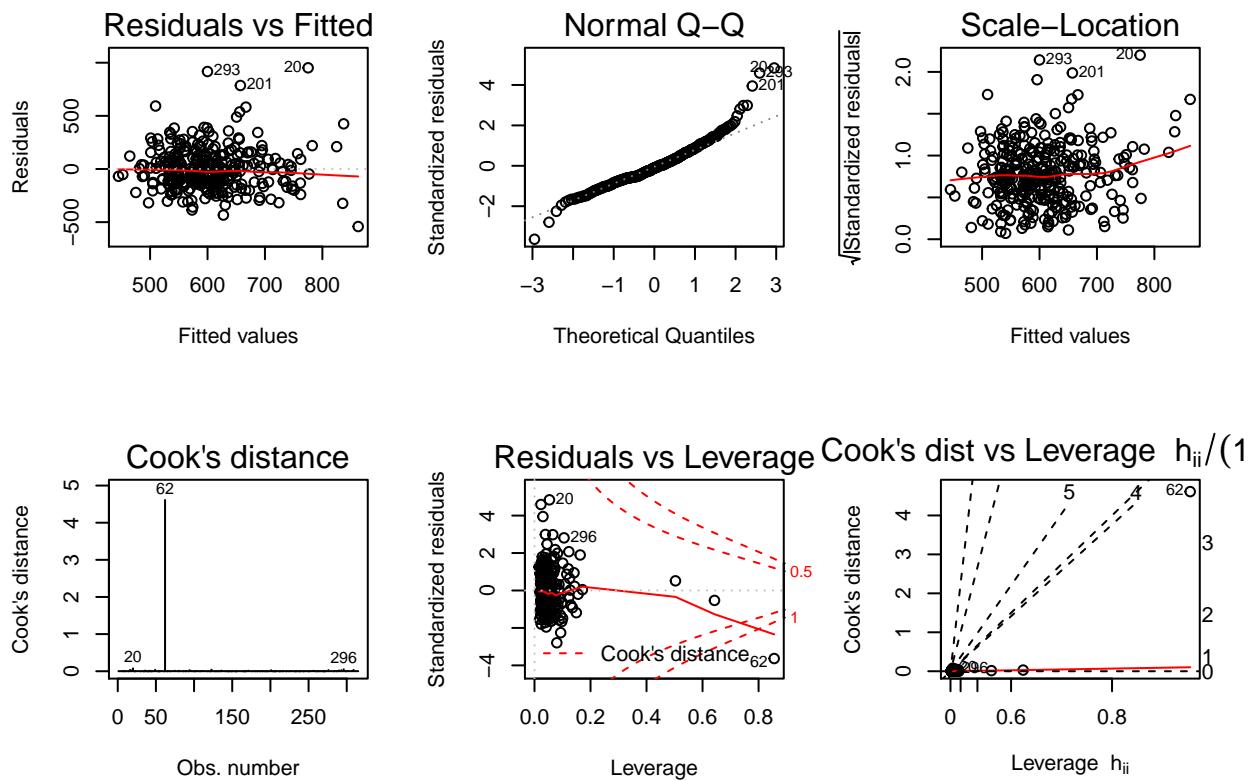
mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et retdiet", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 34: Régression linéaire multiple avec interaction entre sexe et retdiet

	Bêta	IC	p
(Intercept)	614.947	[108.217;5.683]	0
age	2.461	[0.9;2.734]	0.0066
sexeFemmes	-177.699	[62.102;-2.861]	0.0045
tabacAutrefois	61.602	[25.504;2.415]	0.0163
tabacFumeur	4.518	[37.403;0.121]	0.9039
bmi	1.231	[2.005;0.614]	0.5396
vitamineSouvent	21.219	[28.373;0.748]	0.4551
vitaminePas-souvent	21.451	[30.592;0.701]	0.4837
calories	0.071	[0.061;1.158]	0.2476
graisses	-1.385	[0.972;-1.425]	0.1551
fibres	-4.411	[3.42;-1.29]	0.1982
alcool	-1.306	[1.491;-0.876]	0.3816
cholesterol	-0.053	[0.134;-0.394]	0.6942
betadiet	-0.002	[0.009;-0.257]	0.797
retdiet	-0.082	[0.052;-1.595]	0.1118
betaplasma	0.081	[0.069;1.165]	0.2452
sexeFemmes:retinol[, "retdiet"]	0.085	[0.055;1.55]	0.1221



```
rm(mod.tmp)
rm(res.tmp)
```

Table 35: Régression linéaire multiple avec interaction entre sexe et betaplasma

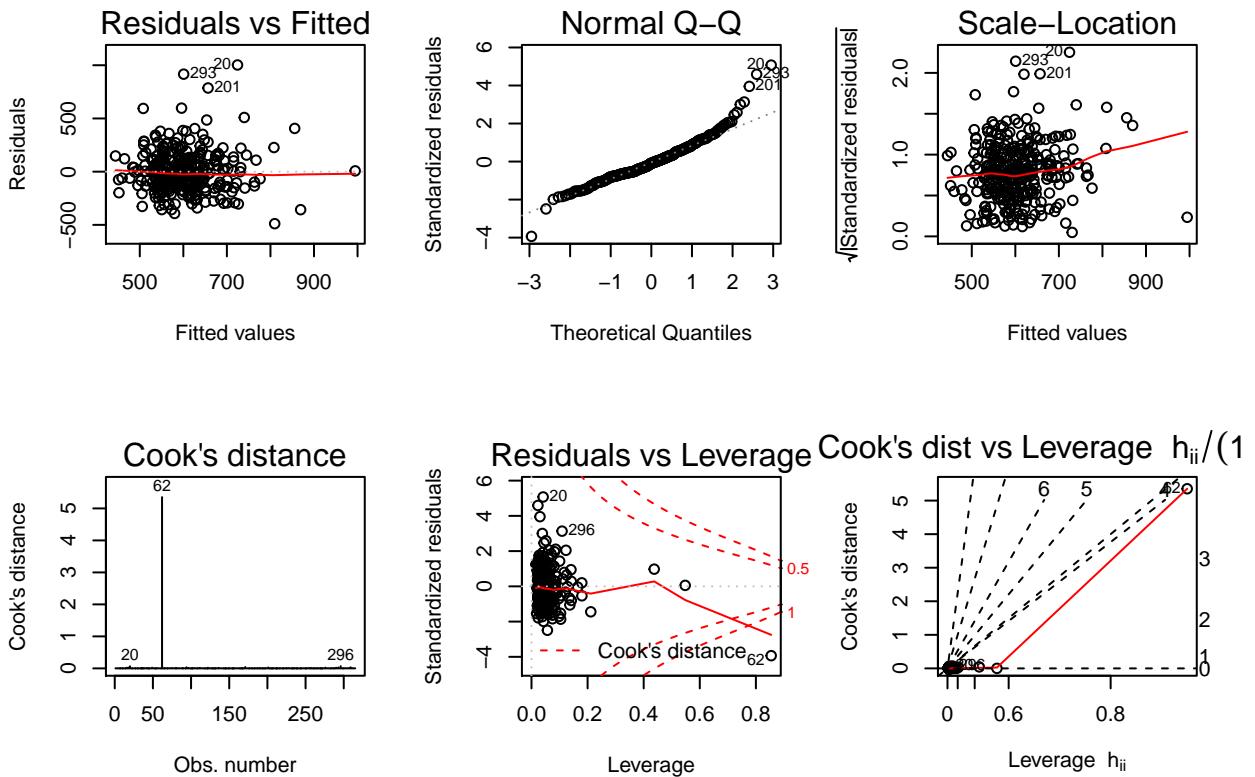
	Bêta	IC	p
(Intercept)	490.034	[105.516;4.644]	0
age	2.385	[0.899;2.653]	0.0084
sexeFemmes	-34.737	[55.131;-0.63]	0.5291
tabacAutrefois	60.12	[25.478;2.36]	0.0189
tabacFumeur	-1.259	[37.293;-0.034]	0.9731
bmi	1.276	[2.003;0.637]	0.5245
vitamineSouvent	18.787	[28.4;0.662]	0.5088
vitaminePas-souvent	17.272	[30.756;0.562]	0.5748
calories	0.07	[0.061;1.148]	0.252
graisses	-1.323	[0.967;-1.367]	0.1726
fibres	-4.382	[3.418;-1.282]	0.2008
alcool	-1.21	[1.492;-0.811]	0.4179
cholesterol	-0.062	[0.133;-0.468]	0.64
betadiet	-0.002	[0.009;-0.173]	0.8626
rettdiet	-0.01	[0.022;-0.427]	0.6699
betaplasma	0.474	[0.243;1.955]	0.0515
sexeFemmes:retinol[, "betaplasma"]	-0.422	[0.251;-1.682]	0.0935

```

mod.tmp = lm(retplasma ~ . -retplasma + sexe*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(summary(mod.tmp)$coefficient[,1],3),
                  paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                         round(summary(mod.tmp)$coefficient[,3],3), "]"),
                  round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et betaplasma", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

Interration avec :tabac, calories, vitamines, alcool, cholesterol et betaplasma.

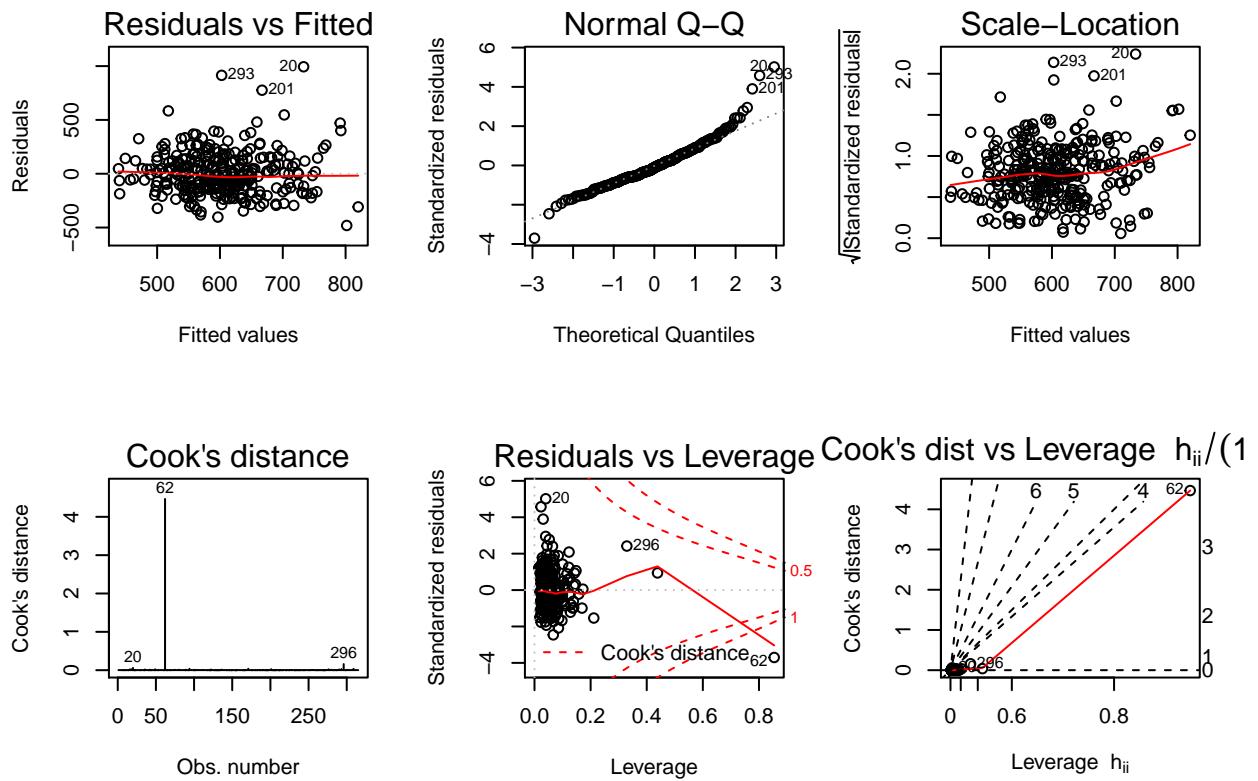
5.3.3 Avec le tabac

```
mod.tmp = lm(retplasma ~ . -retplasma + tabac*retinol[, "bmi"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interraction entre tabac et bmi", col.names = c(" ",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)
```

Table 36: Régression linéaire multiple avec interaction entre tabac et bmi

	Bêta	IC	p
(Intercept)	564.424	[105.848;5.332]	0
age	2.59	[0.908;2.854]	0.0046
sexeFemmes	-91.617	[38.67;-2.369]	0.0185
tabacAutrefois	48.551	[120.009;0.405]	0.6861
tabacFumeur	-286.576	[177.03;-1.619]	0.1066
bmi	0.094	[2.453;0.038]	0.9694
vitamineSouvent	19.177	[28.459;0.674]	0.5009
vitaminePas-souvent	23.2	[30.629;0.757]	0.4494
calories	0.076	[0.062;1.243]	0.215
graisses	-1.374	[0.972;-1.413]	0.1586
fibres	-4.648	[3.431;-1.355]	0.1765
alcool	-1.422	[1.493;-0.953]	0.3416
cholesterol	-0.068	[0.133;-0.511]	0.6094
betadiet	-0.004	[0.009;-0.421]	0.6741
retdiet	-0.009	[0.022;-0.423]	0.6723
betaplasma	0.081	[0.07;1.166]	0.2445
tabacAutrefois:retinol[, "bmi"]	0.465	[4.49;0.104]	0.9176
tabacFumeur:retinol[, "bmi"]	11.523	[6.936;1.661]	0.0977



```
rm(mod.tmp)
rm(res.tmp)
```

Table 37: Régression linéaire multiple avec interaction entre tabac et vitamine

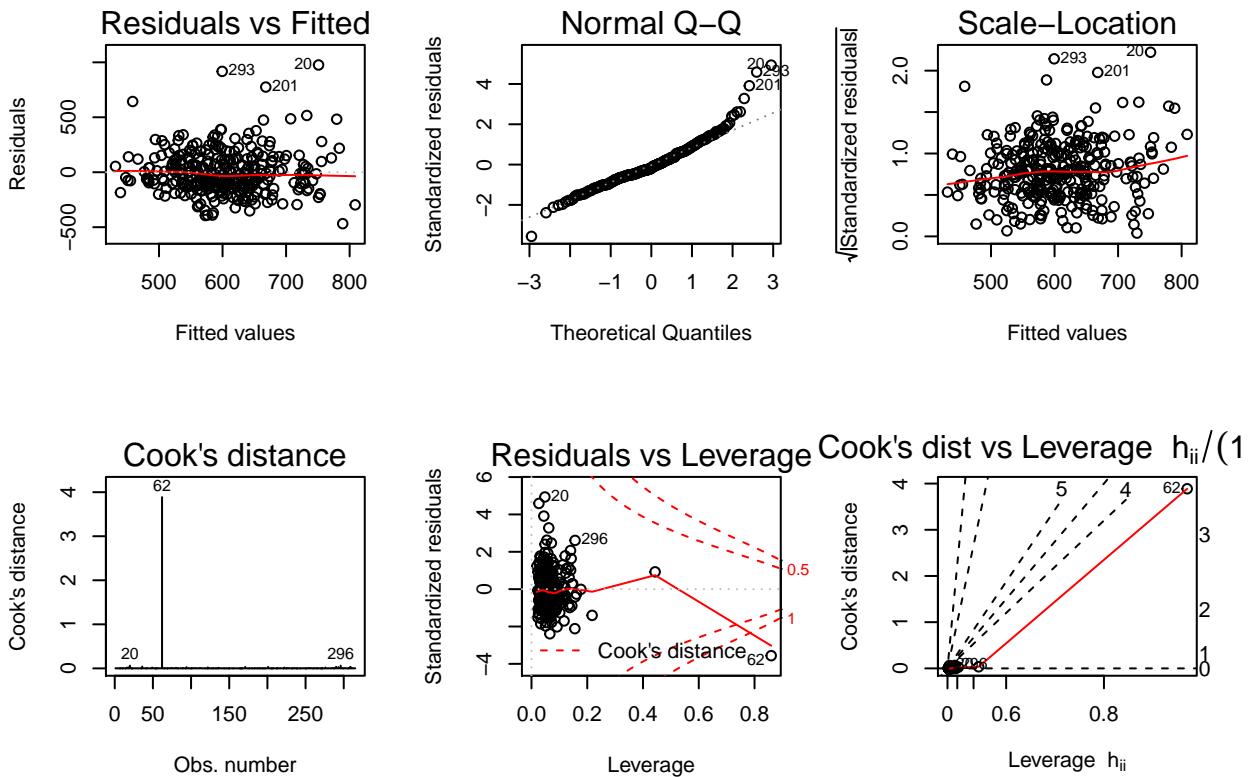
	Bêta	IC	p
(Intercept)	533.375	[101.655;5.247]	0
age	2.663	[0.916;2.907]	0.0039
sexeFemmes	-97.789	[38.726;-2.525]	0.0121
tabacAutrefois	71.676	[43.322;1.655]	0.0991
tabacFumeur	-51.872	[55.017;-0.943]	0.3465
bmi	1.26	[2.012;0.626]	0.5315
vitamineSouvent	14.996	[39.575;0.379]	0.705
vitaminePas-souvent	10.261	[44.62;0.23]	0.8183
calories	0.077	[0.062;1.245]	0.2142
graisses	-1.29	[0.973;-1.325]	0.1861
fibres	-4.617	[3.448;-1.339]	0.1815
alcool	-1.379	[1.5;-0.919]	0.3587
cholesterol	-0.086	[0.133;-0.648]	0.5173
betadiet	-0.003	[0.009;-0.368]	0.7129
retdiet	-0.009	[0.023;-0.404]	0.6862
betaplasma	0.093	[0.07;1.325]	0.1861
tabacAutrefois:retinol[, "vitamine"]Souvent	-32.698	[58.78;-0.556]	0.5784
tabacFumeur:retinol[, "vitamine"]Souvent	135.361	[88.982;1.521]	0.1293
tabacAutrefois:retinol[, "vitamine"]Pas-souvent	0.559	[65.962;0.008]	0.9932
tabacFumeur:retinol[, "vitamine"]Pas-souvent	74.93	[86.476;0.866]	0.3869

```

mod.tmp = lm(retplasma ~ . -retplasma + tabac*retinol[, "vitamine"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et vitamine", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

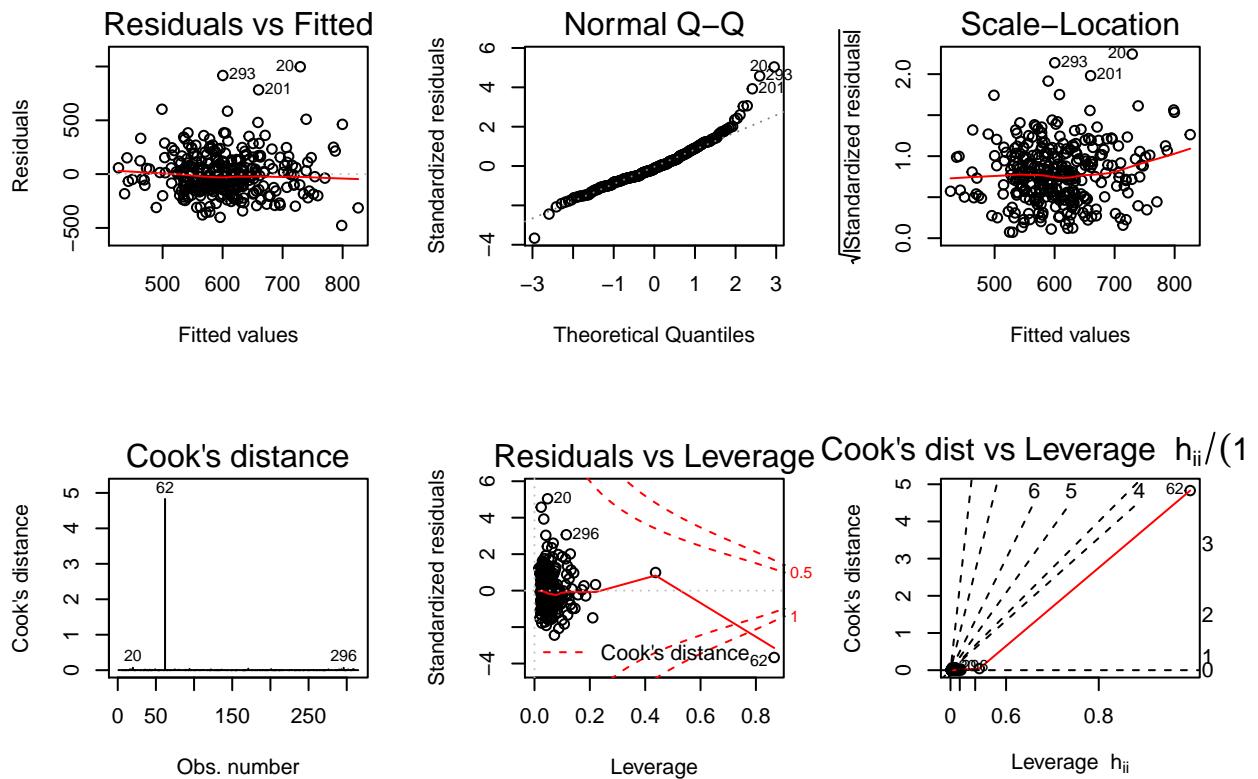
mod.tmp = lm(retplasma ~ . -retplasma + tabac*retinol[, "calories"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et calories", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 38: Régression linéaire multiple avec interaction entre tabac et calories

	Bêta	IC	p
(Intercept)	542.699	[105.881;5.126]	0
age	2.495	[0.909;2.744]	0.0064
sexeFemmes	-102.149	[38.332;-2.665]	0.0081
tabacAutrefois	30.143	[77.503;0.389]	0.6976
tabacFumeur	64.198	[105.143;0.611]	0.5419
bmi	1.429	[2.016;0.709]	0.479
vitamineSouvent	21.796	[28.494;0.765]	0.4449
vitaminePas-souvent	23.026	[30.709;0.75]	0.454
calories	0.075	[0.066;1.128]	0.26
graisses	-1.347	[0.979;-1.376]	0.1698
fibres	-4.547	[3.463;-1.313]	0.1902
alcool	-0.694	[1.698;-0.409]	0.6829
cholesterol	-0.081	[0.133;-0.606]	0.5452
betadiet	-0.004	[0.009;-0.399]	0.6899
retldiet	-0.01	[0.022;-0.447]	0.6554
betaplasma	0.085	[0.07;1.21]	0.2274
tabacAutrefois:retinol[, "calories"]	0.016	[0.041;0.383]	0.7024
tabacFumeur:retinol[, "calories"]	-0.035	[0.055;-0.632]	0.5279



```
rm(mod.tmp)
rm(res.tmp)
```

Table 39: Régression linéaire multiple avec interaction entre tabac et graisses

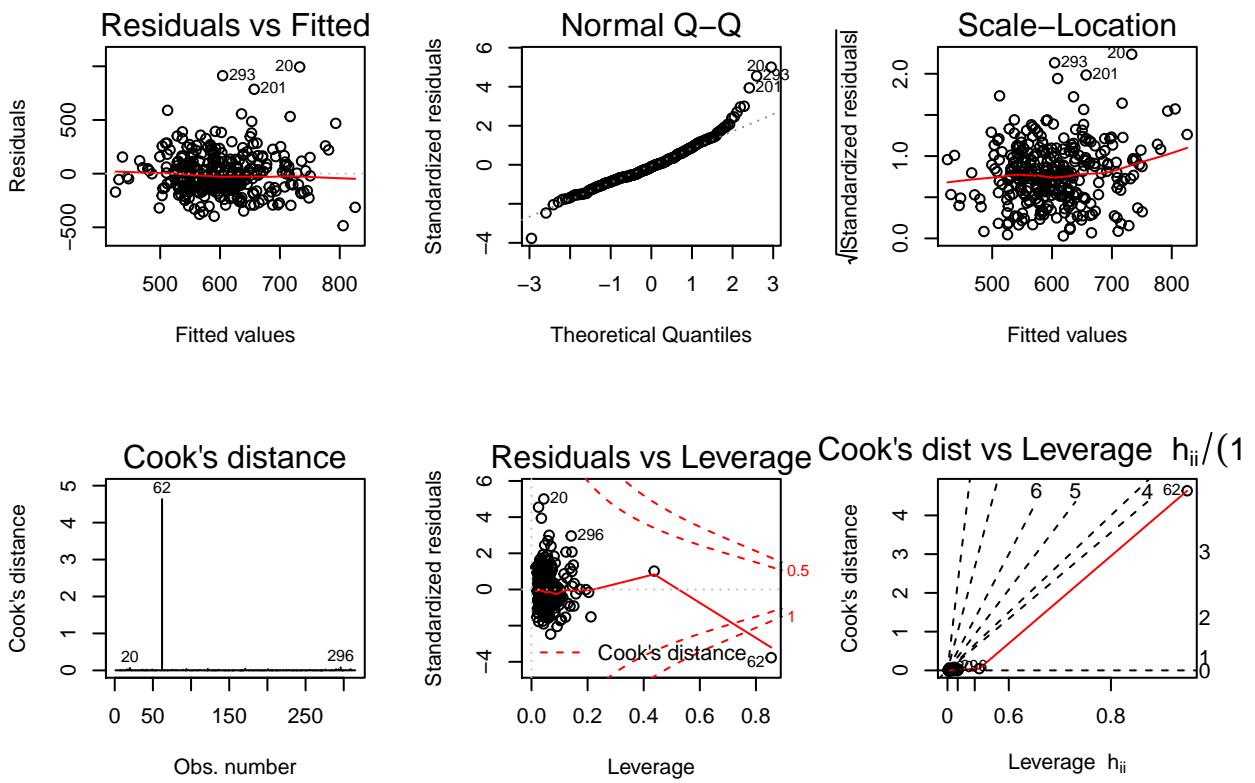
	Bêta	IC	p
(Intercept)	562.195	[103.917;5.41]	0
age	2.381	[0.909;2.621]	0.0092
sexeFemmes	-100.639	[38.571;-2.609]	0.0095
tabacAutrefois	35.321	[62.87;0.562]	0.5747
tabacFumeur	-24.837	[99.128;-0.251]	0.8023
bmi	1.323	[2.016;0.656]	0.5123
vitamineSouvent	21.636	[28.543;0.758]	0.449
vitaminePas-souvent	22.692	[30.761;0.738]	0.4613
calories	0.067	[0.062;1.082]	0.2803
graisses	-1.399	[1.046;-1.337]	0.1824
fibres	-4.248	[3.457;-1.229]	0.2202
alcool	-1.363	[1.509;-0.904]	0.3668
cholesterol	-0.08	[0.134;-0.6]	0.5489
betadiet	-0.003	[0.009;-0.356]	0.7217
retdiet	-0.01	[0.023;-0.423]	0.6728
betaplasma	0.085	[0.07;1.22]	0.2233
tabacAutrefois:retinol[, "graisses"]	0.335	[0.753;0.445]	0.6566
tabacFumeur:retinol[, "graisses"]	0.33	[1.147;0.288]	0.7735

```

mod.tmp = lm(retplasma ~ . -retplasma + tabac*retinol[, "graisses"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et graisses", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

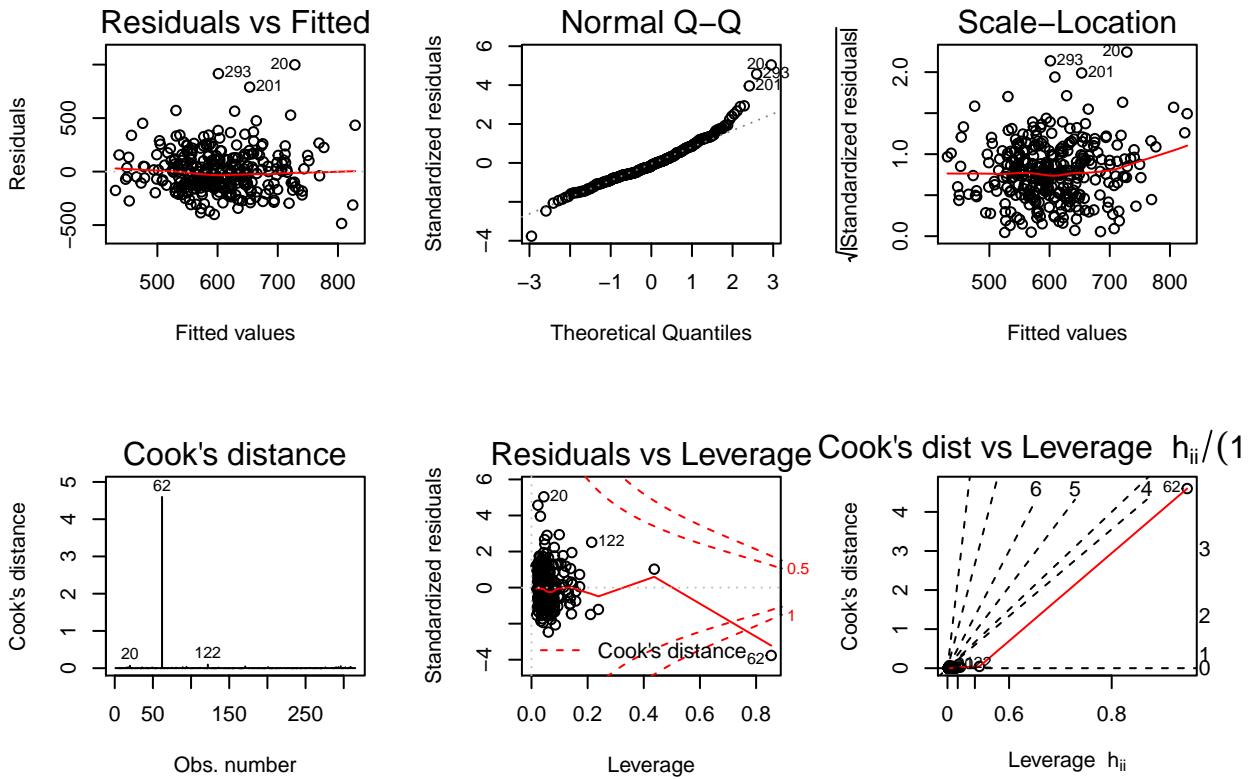
mod.tmp = lm(retplasma ~ . -retplasma + tabac*retinol[, "fibres"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et fibres", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 40: Régression linéaire multiple avec interaction entre tabac et fibres

	Bêta	IC	p
(Intercept)	553.395	[102.203;5.415]	0
age	2.507	[0.908;2.761]	0.0061
sexeFemmes	-103.873	[38.328;-2.71]	0.0071
tabacAutrefois	14.595	[69.788;0.209]	0.8345
tabacFumeur	58.817	[91.103;0.646]	0.519
bmi	1.38	[2.012;0.686]	0.4933
vitamineSouvent	20.464	[28.485;0.718]	0.4731
vitaminePas-souvent	19.981	[30.805;0.649]	0.5171
calories	0.071	[0.062;1.153]	0.2497
graisses	-1.227	[0.971;-1.263]	0.2074
fibres	-4.957	[3.97;-1.248]	0.2128
alcool	-1.367	[1.498;-0.913]	0.3621
cholesterol	-0.098	[0.133;-0.734]	0.4633
betadiet	-0.003	[0.009;-0.346]	0.7299
rettdiet	-0.01	[0.022;-0.456]	0.6486
betaplasma	0.086	[0.071;1.207]	0.2286
tabacAutrefois:retinol[, "fibres"]	3.495	[4.97;0.703]	0.4825
tabacFumeur:retinol[, "fibres"]	-5.58	[7.6;-0.734]	0.4634



```
rm(mod.tmp)
rm(res.tmp)
```

Table 41: Régression linéaire multiple avec interaction entre tabac et alcool

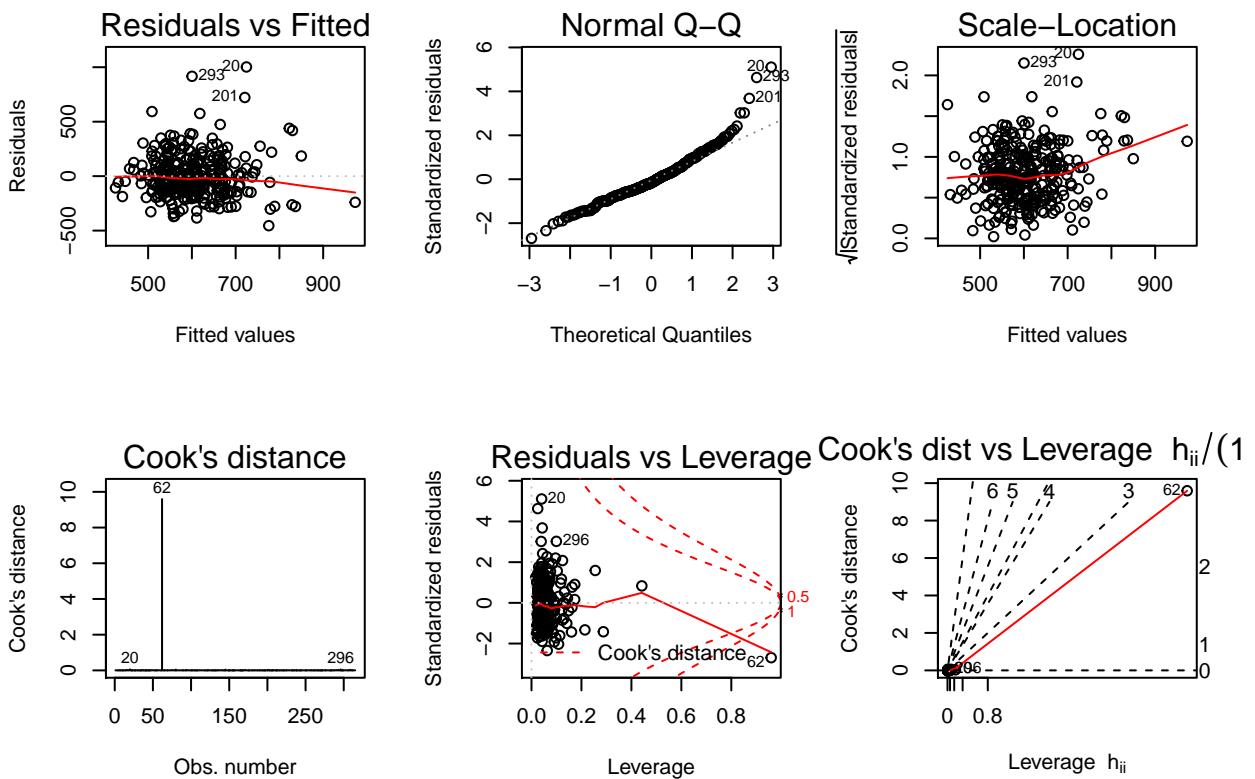
	Bêta	IC	p
(Intercept)	472.668	[104.661;4.516]	0
age	2.752	[0.908;3.03]	0.0027
sexeFemmes	-78.403	[38.75;-2.023]	0.0439
tabacAutrefois	43.007	[29.146;1.476]	0.1411
tabacFumeur	23.711	[38.941;0.609]	0.5431
bmi	1.997	[2.018;0.989]	0.3233
vitamineSouvent	32.428	[28.434;1.14]	0.255
vitaminePas-souvent	29.342	[30.411;0.965]	0.3354
calories	0.081	[0.062;1.299]	0.1949
graisses	-1.384	[0.969;-1.428]	0.1544
fibres	-4.398	[3.433;-1.281]	0.2012
alcool	4.53	[4.92;0.921]	0.3579
cholesterol	-0.087	[0.131;-0.658]	0.5108
betadiet	-0.004	[0.009;-0.484]	0.6285
rettdiet	-0.009	[0.022;-0.384]	0.7015
betaplasma	0.07	[0.069;1.016]	0.3106
tabacAutrefois:retinol[, "alcool"]	2.275	[5.99;0.38]	0.7044
tabacFumeur:retinol[, "alcool"]	-6.932	[5.12;-1.354]	0.1768

```

mod.tmp = lm(retplasma ~ . -retplasma + tabac*retinol[, "alcool"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et alcool", col.names = c("",
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

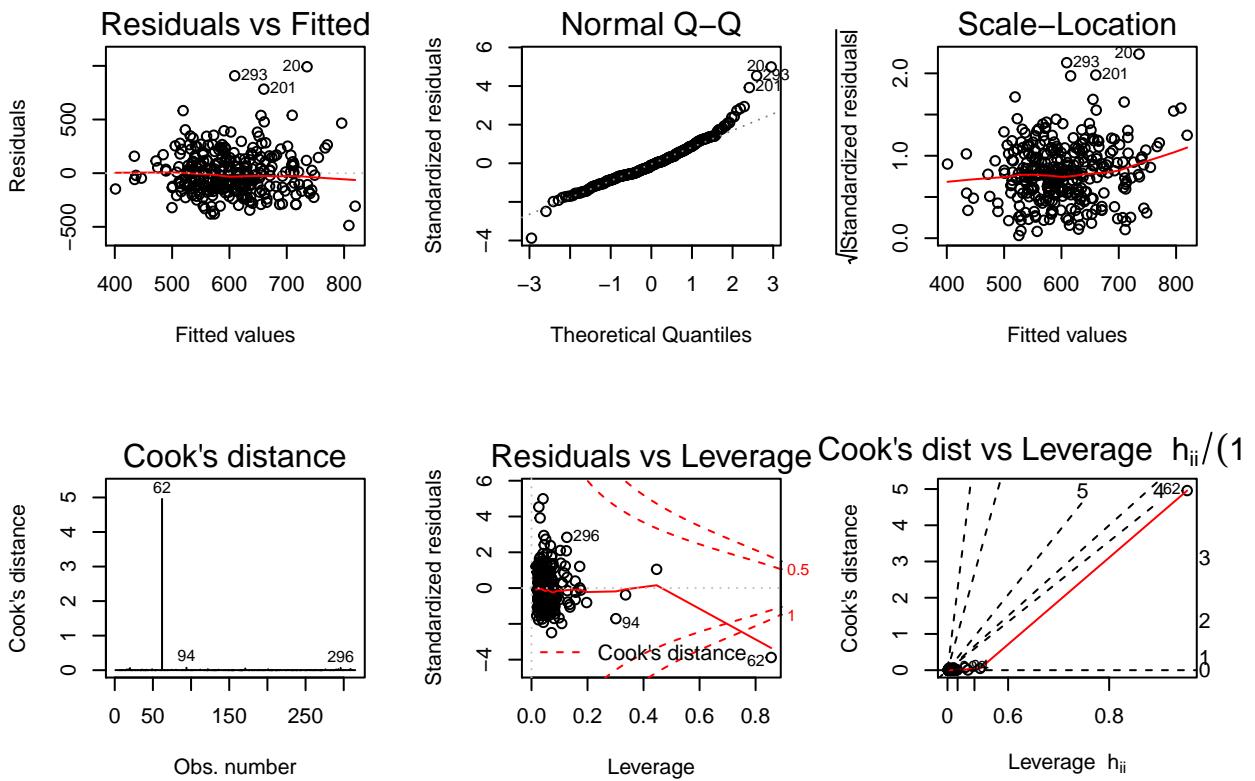
mod.tmp = lm(retplasma ~ . -retplasma + tabac*retinol[, "cholesterol"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et cholesterol", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 42: Régression linéaire multiple avec interaction entre tabac et cholesterol

	Bêta	IC	p
(Intercept)	564.819	[101.877;5.544]	0
age	2.319	[0.909;2.55]	0.0113
sexeFemmes	-99.051	[38.5;-2.573]	0.0106
tabacAutrefois	39.32	[54.796;0.718]	0.4736
tabacFumeur	-57.177	[77.074;-0.742]	0.4588
bmi	1.407	[2.016;0.698]	0.4858
vitamineSouvent	22.368	[28.512;0.785]	0.4334
vitaminePas-souvent	22.808	[30.715;0.743]	0.4583
calories	0.061	[0.062;0.977]	0.3294
graisses	-1.137	[0.976;-1.165]	0.2451
fibres	-4.05	[3.455;-1.172]	0.2419
alcool	-1.409	[1.507;-0.935]	0.3503
cholesterol	-0.145	[0.152;-0.951]	0.3426
betadiet	-0.003	[0.009;-0.316]	0.7521
retdiet	-0.009	[0.023;-0.391]	0.6964
betaplasma	0.084	[0.07;1.197]	0.2325
tabacAutrefois:retinol[, "cholesterol"]	0.094	[0.202;0.464]	0.6427
tabacFumeur:retinol[, "cholesterol"]	0.228	[0.265;0.862]	0.3896



```
rm(mod.tmp)
rm(res.tmp)
```

Table 43: Régression linéaire multiple avec interaction entre tabac et betadiet

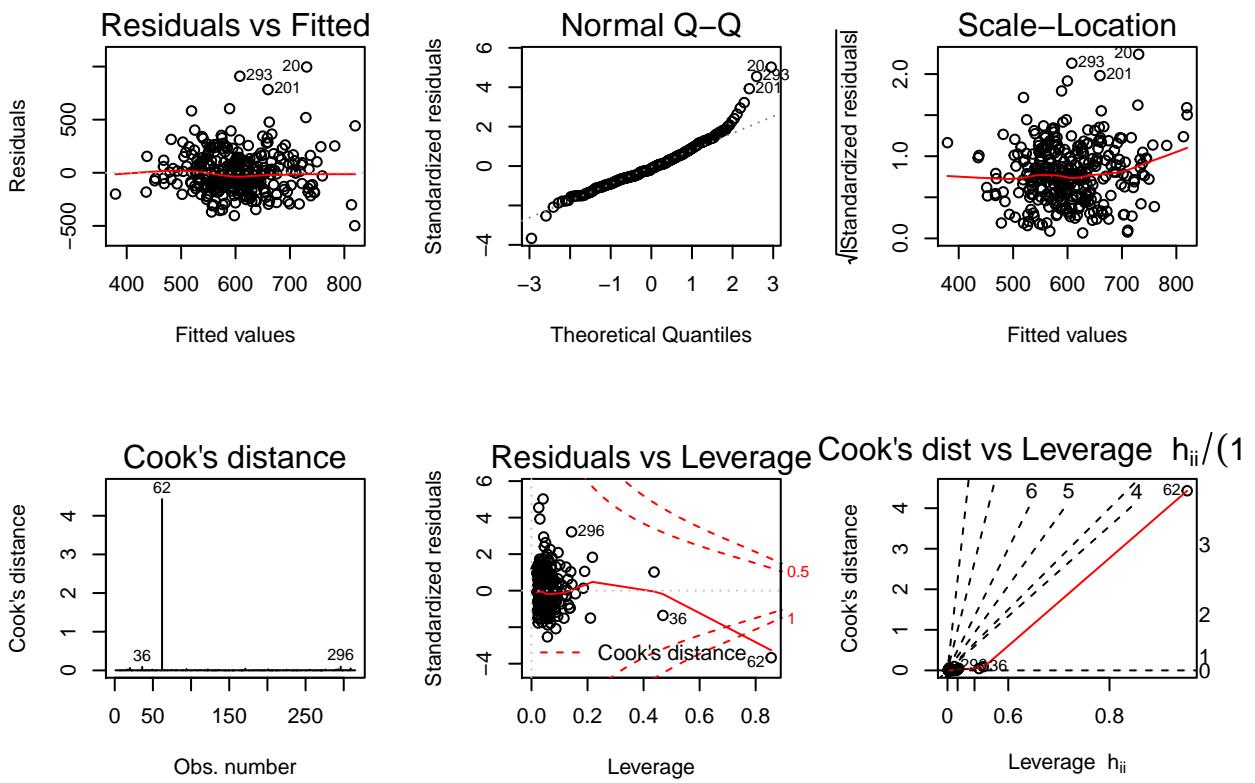
	Bêta	IC	p
(Intercept)	558.138	[101.985;5.473]	0
age	2.427	[0.903;2.689]	0.0076
sexeFemmes	-104.264	[38.34;-2.719]	0.0069
tabacAutrefois	28.27	[45.954;0.615]	0.5389
tabacFumeur	30.202	[62.821;0.481]	0.631
bmi	1.445	[2.016;0.717]	0.4741
vitamineSouvent	22.442	[28.538;0.786]	0.4323
vitaminePas-souvent	21.37	[30.702;0.696]	0.4869
calories	0.064	[0.062;1.027]	0.3052
graisses	-1.135	[0.978;-1.161]	0.2467
fibres	-3.863	[3.459;-1.117]	0.2649
alcool	-1.141	[1.521;-0.75]	0.4536
cholesterol	-0.098	[0.133;-0.736]	0.4621
betadiet	-0.008	[0.013;-0.598]	0.5502
retdiet	-0.011	[0.022;-0.505]	0.6137
betaplasma	0.081	[0.071;1.156]	0.2488
tabacAutrefois:retinol[, "betadiet"]	0.014	[0.017;0.829]	0.4077
tabacFumeur:retinol[, "betadiet"]	-0.018	[0.028;-0.648]	0.5174

```

mod.tmp = lm(retplasma ~ . -retplasma + tabac*retinol[, "betadiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et betadiet", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

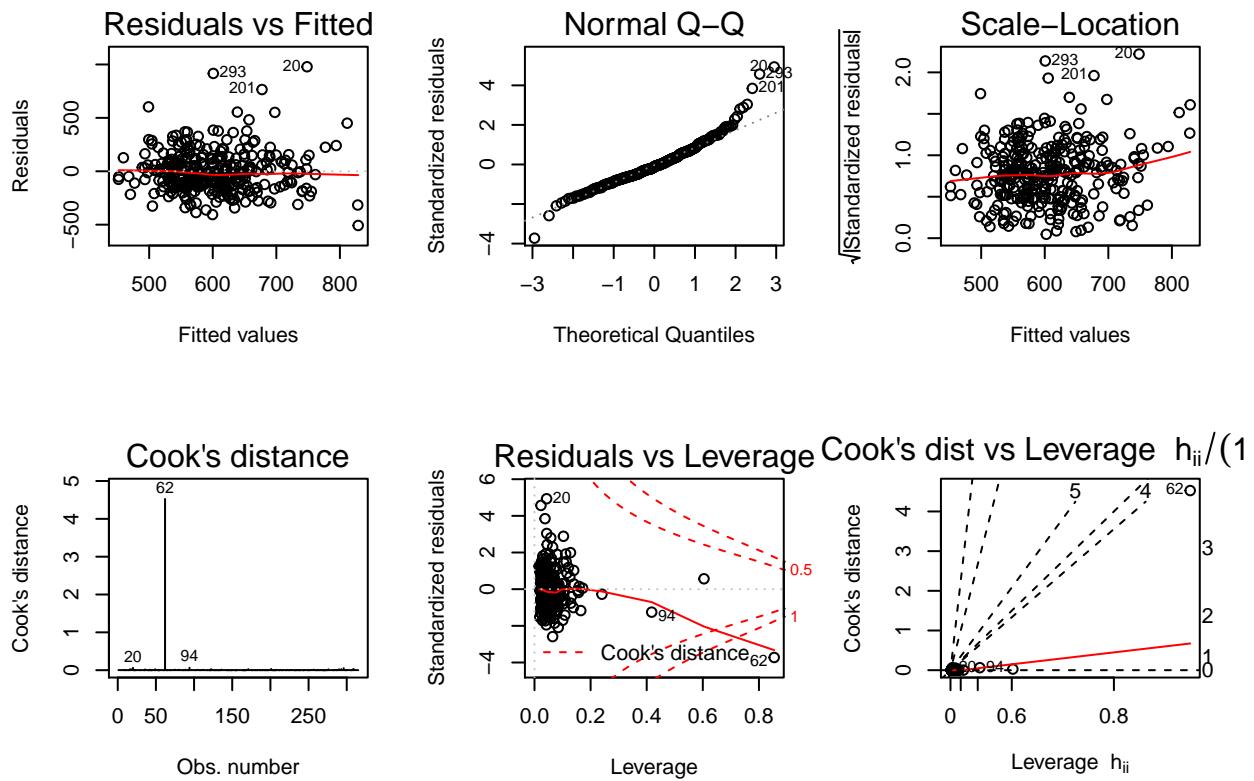
mod.tmp = lm(retplasma ~ . -retplasma + tabac*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et retdiet", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 44: Régression linéaire multiple avec interaction entre tabac et retdiet

	Bêta	IC	p
(Intercept)	535.966	[100.867;5.314]	0
age	2.445	[0.907;2.695]	0.0074
sexeFemmes	-104.404	[38.442;-2.716]	0.007
tabacAutrefois	92.95	[45.04;2.064]	0.0399
tabacFumeur	35.811	[69.131;0.518]	0.6048
bmi	1.23	[2.015;0.61]	0.5421
vitamineSouvent	21.487	[28.579;0.752]	0.4527
vitaminePas-souvent	24.7	[30.736;0.804]	0.4223
calories	0.079	[0.063;1.264]	0.2073
graisses	-1.366	[0.981;-1.392]	0.165
fibres	-4.703	[3.463;-1.358]	0.1754
alcool	-1.482	[1.504;-0.986]	0.325
cholesterol	-0.082	[0.134;-0.611]	0.5416
betadiet	-0.002	[0.009;-0.247]	0.8052
retdiet	0.004	[0.027;0.146]	0.884
betaplasma	0.079	[0.07;1.129]	0.2598
tabacAutrefois:retinol[, "retdiet"]	-0.039	[0.044;-0.885]	0.3767
tabacFumeur:retinol[, "retdiet"]	-0.045	[0.075;-0.602]	0.5474



```
rm(mod.tmp)
rm(res.tmp)
```

Table 45: Régression linéaire multiple avec interaction entre tabac et betaplasma

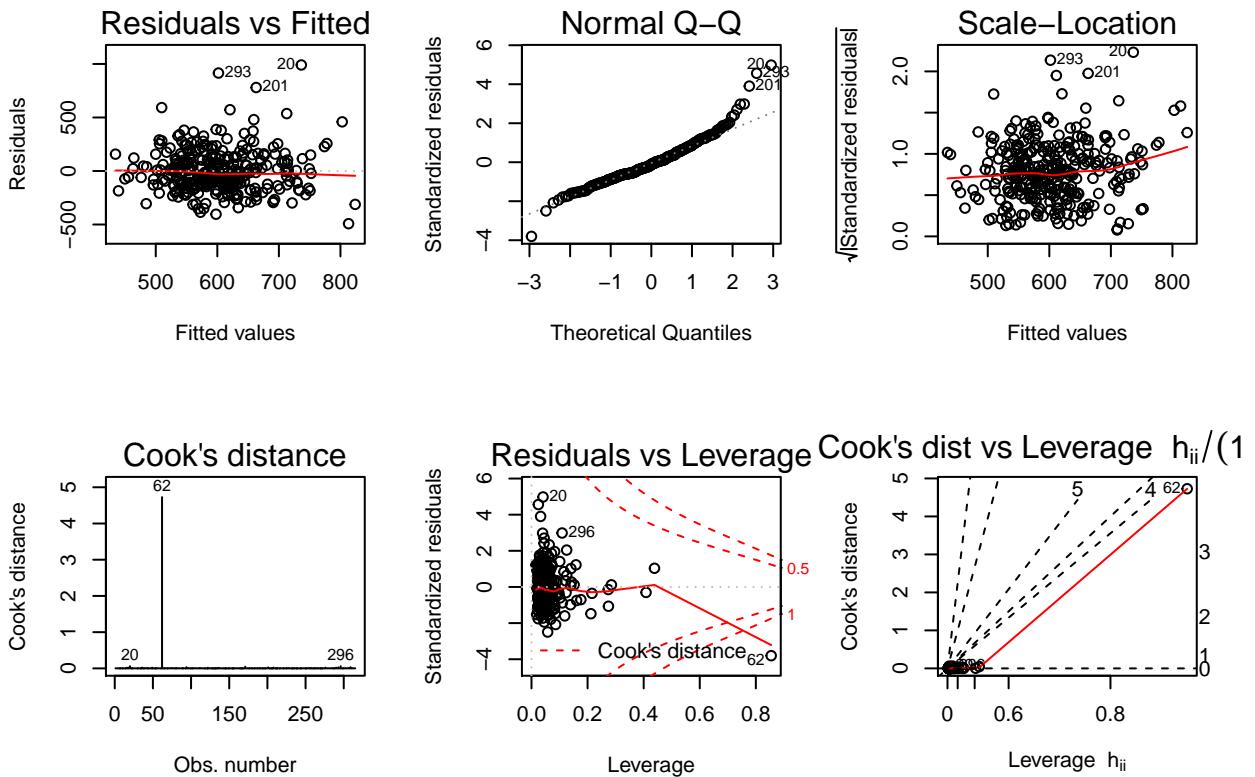
	Bêta	IC	p
(Intercept)	546.945	[100.532;5.441]	0
age	2.422	[0.906;2.673]	0.0079
sexeFemmes	-100.755	[38.414;-2.623]	0.0092
tabacAutrefois	56.582	[37.128;1.524]	0.1286
tabacFumeur	-23.863	[63.725;-0.374]	0.7083
bmi	1.353	[2.02;0.67]	0.5036
vitamineSouvent	21.546	[28.631;0.753]	0.4523
vitaminePas-souvent	22.275	[31.03;0.718]	0.4734
calories	0.072	[0.062;1.162]	0.246
graisses	-1.253	[0.973;-1.287]	0.1991
fibres	-4.314	[3.459;-1.247]	0.2133
alcool	-1.355	[1.501;-0.902]	0.3677
cholesterol	-0.088	[0.133;-0.664]	0.5074
betadiet	-0.003	[0.009;-0.293]	0.7699
retdiet	-0.011	[0.022;-0.468]	0.6404
betaplasma	0.069	[0.092;0.75]	0.4541
tabacAutrefois:retinol[, "betaplasma"]	0.02	[0.135;0.146]	0.8843
tabacFumeur:retinol[, "betaplasma"]	0.193	[0.415;0.466]	0.6414

```

mod.tmp = lm(retplasma ~ . -retplasma + tabac*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et betaplasma", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

Pas d'interactions avec le tabac (sauf bmi limite).

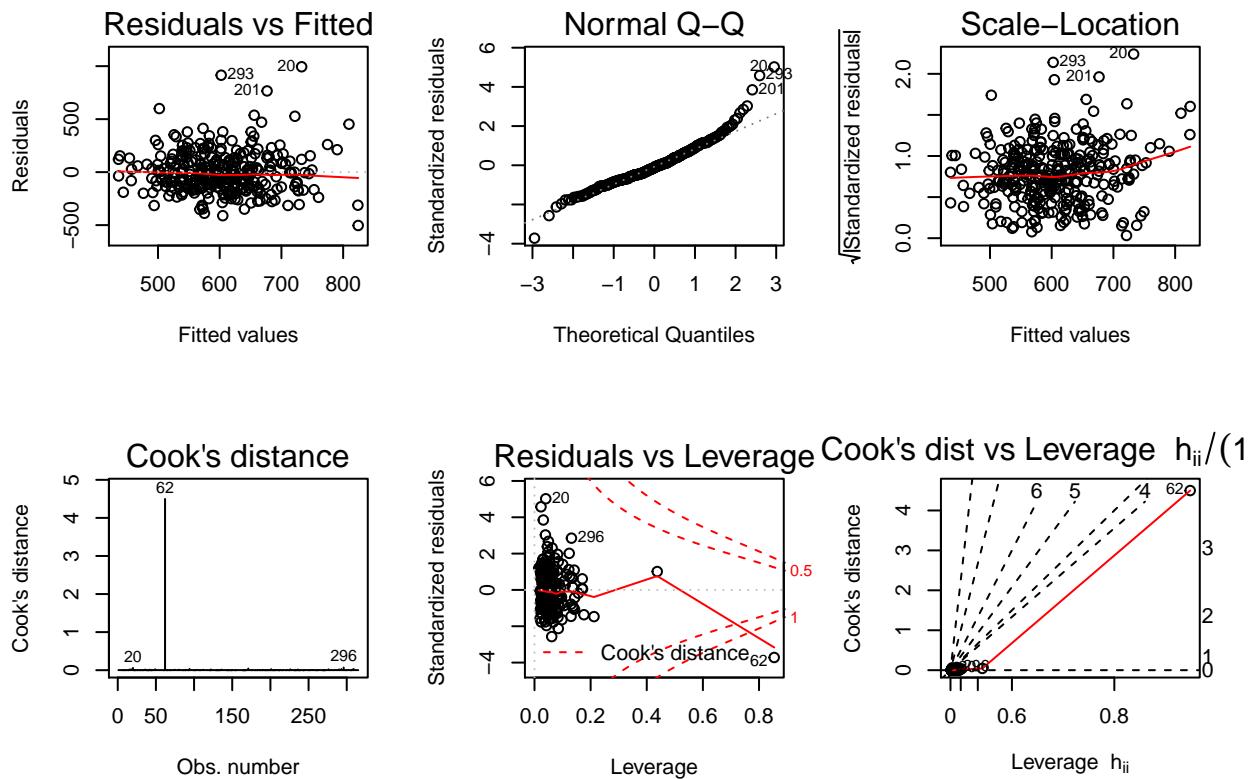
5.3.4 Avec le bmi

```
mod.tmp = lm(retplasma ~ . -retplasma + bmi*retinol[, "vitamine"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et vitamine", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)
```

Table 46: Régression linéaire multiple avec interaction entre bmi et vitamine

	Bêta	IC	p
(Intercept)	475.745	[125.495;3.791]	2e-04
age	2.532	[0.904;2.8]	0.0054
sexeFemmes	-98.207	[38.241;-2.568]	0.0107
tabacAutrefois	59.476	[25.526;2.33]	0.0205
tabacFumeur	0.417	[37.379;0.011]	0.9911
bmi	3.665	[3.361;1.09]	0.2764
vitamineSouvent	28.187	[123.684;0.228]	0.8199
vitaminePas-souvent	219.216	[132.21;1.658]	0.0984
calories	0.076	[0.061;1.241]	0.2156
graisses	-1.319	[0.968;-1.362]	0.1743
fibres	-4.324	[3.423;-1.263]	0.2075
alcool	-1.434	[1.493;-0.96]	0.3377
cholesterol	-0.101	[0.132;-0.763]	0.4461
betadiet	-0.003	[0.009;-0.361]	0.7184
rettdiet	-0.008	[0.022;-0.371]	0.7109
betaplasma	0.085	[0.07;1.221]	0.223
bmi:retinol[, "vitamine"]Souvent	-0.221	[4.595;-0.048]	0.9616
bmi:retinol[, "vitamine"]Pas-souvent	-7.389	[4.837;-1.528]	0.1277



```
rm(mod.tmp)
rm(res.tmp)
```

Table 47: Régression linéaire multiple avec interaction entre bmi et calories

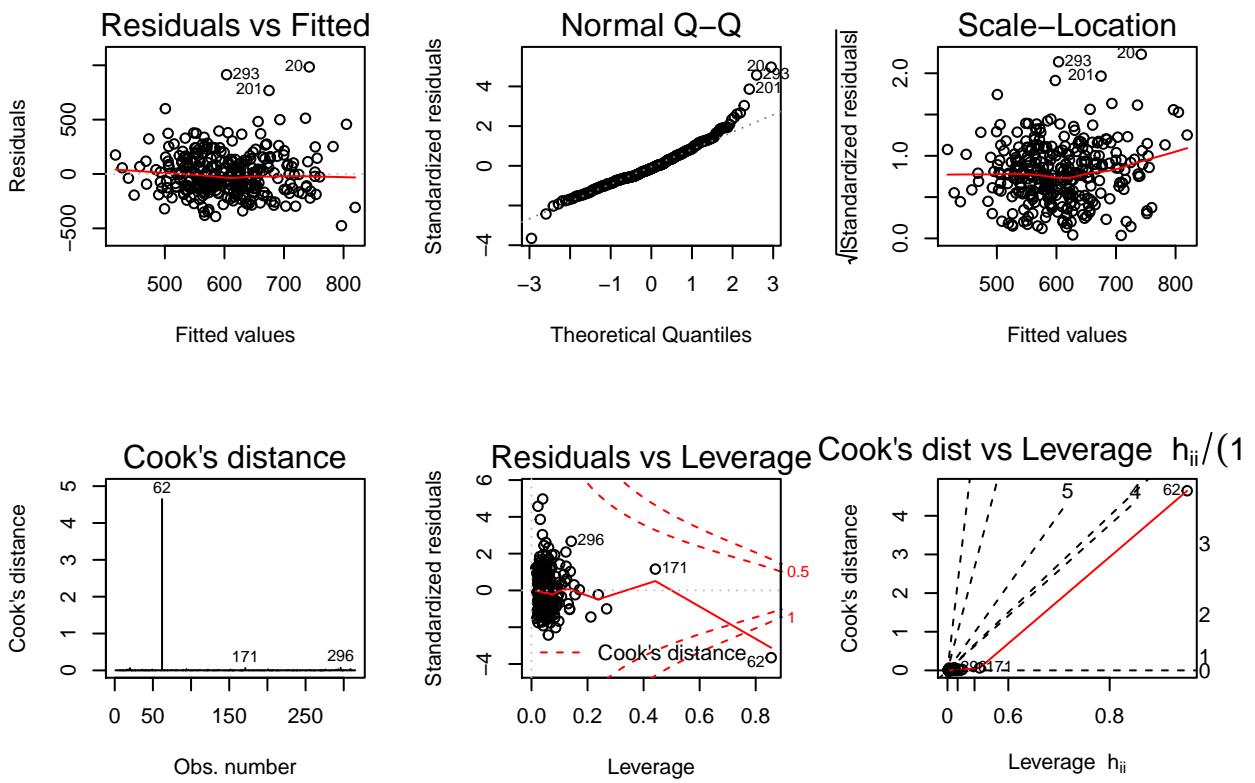
	Bêta	IC	p
(Intercept)	758.364	[171.453;4.423]	0
age	2.376	[0.9;2.639]	0.0087
sexeFemmes	-101.549	[38.164;-2.661]	0.0082
tabacAutrefois	60.789	[25.502;2.384]	0.0178
tabacFumeur	0.748	[37.318;0.02]	0.984
bmi	-6.388	[5.519;-1.158]	0.248
vitamineSouvent	22.005	[28.381;0.775]	0.4387
vitaminePas-souvent	23.512	[30.578;0.769]	0.4426
calories	-0.048	[0.1;-0.485]	0.6284
graisses	-1.282	[0.967;-1.325]	0.1862
fibres	-4.059	[3.427;-1.184]	0.2372
alcool	-0.994	[1.509;-0.659]	0.5103
cholesterol	-0.093	[0.132;-0.7]	0.4843
betadiet	-0.003	[0.009;-0.293]	0.77
retdiet	-0.013	[0.022;-0.562]	0.5746
betaplasma	0.082	[0.069;1.182]	0.2383
bmi:retinol[, "calories"]	0.004	[0.003;1.499]	0.135

```

mod.tmp = lm(retplasma ~ . -retplasma + bmi*retinol[, "calories"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et calories", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

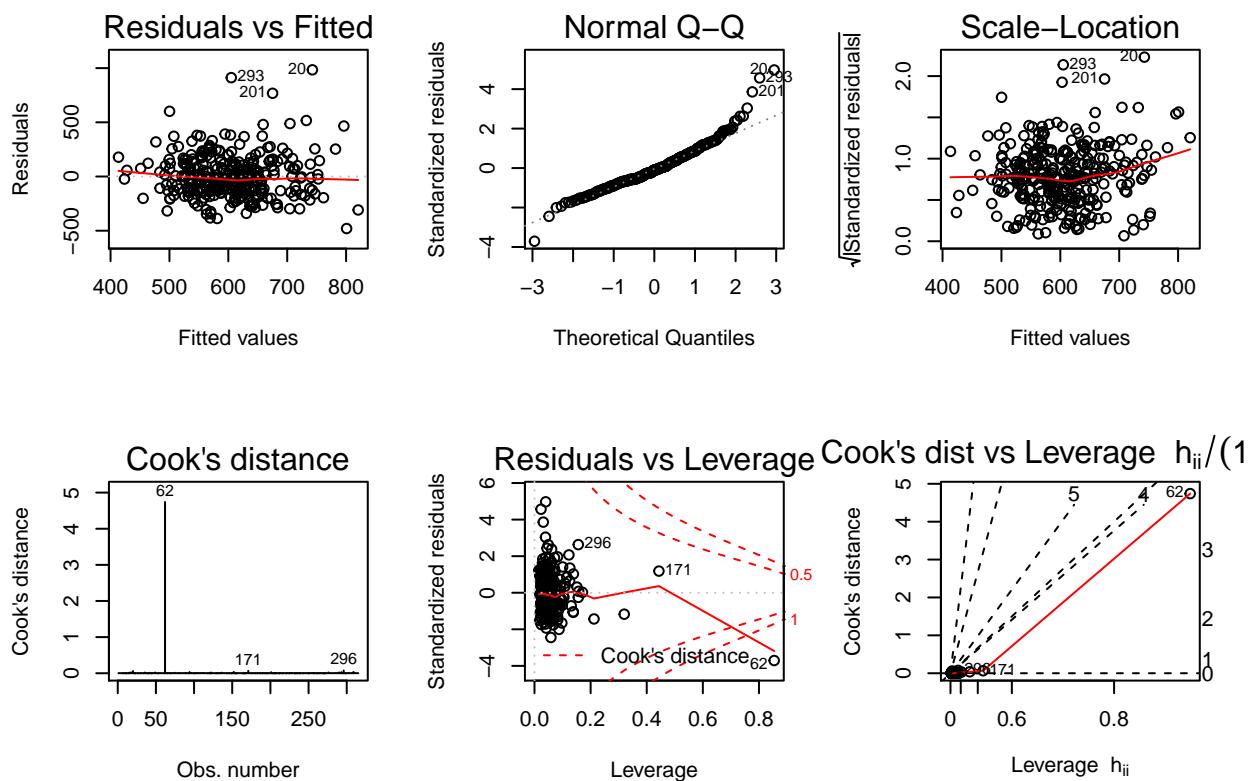
mod.tmp = lm(retplasma ~ . -retplasma + bmi*retinol[, "graisses"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et graisses", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 48: Régression linéaire multiple avec interaction entre bmi et graisses

	Bêta	IC	p
(Intercept)	730.4	[154.171;4.738]	0
age	2.387	[0.9;2.653]	0.0084
sexeFemmes	-103.271	[38.169;-2.706]	0.0072
tabacAutrefois	60.936	[25.498;2.39]	0.0175
tabacFumeur	0.837	[37.31;0.022]	0.9821
bmi	-5.18	[4.673;-1.109]	0.2685
vitamineSouvent	21.728	[28.374;0.766]	0.4444
vitaminePas-souvent	24.851	[30.588;0.812]	0.4172
calories	0.07	[0.061;1.136]	0.2569
graisses	-3.57	[1.801;-1.982]	0.0484
fibres	-4.44	[3.421;-1.298]	0.1953
alcool	-1.207	[1.493;-0.808]	0.4195
cholesterol	-0.105	[0.133;-0.788]	0.4311
betadiet	-0.003	[0.009;-0.277]	0.7821
retdiет	-0.011	[0.022;-0.501]	0.6167
betaplasma	0.082	[0.069;1.174]	0.2412
bmi:retinol[, "graisses"]	0.087	[0.056;1.54]	0.1247



```
rm(mod.tmp)
rm(res.tmp)
```

Table 49: Régression linéaire multiple avec interaction entre bmi et fibres

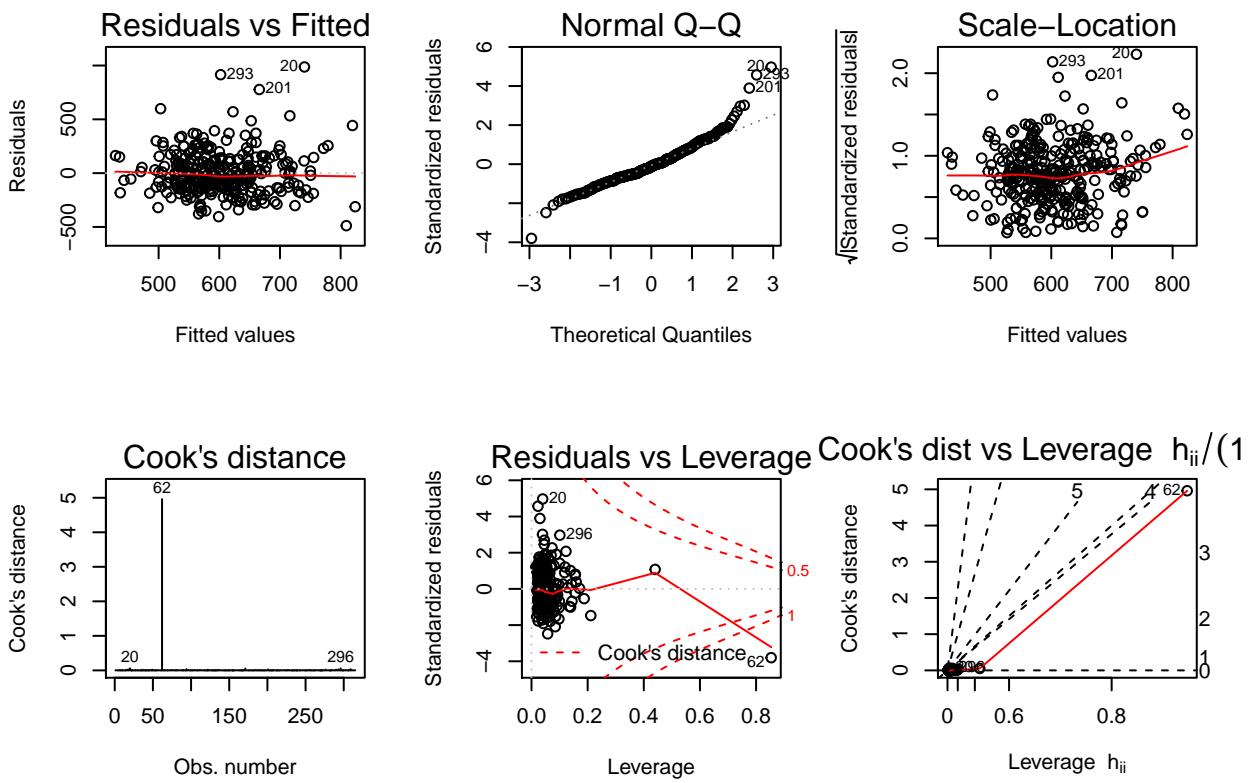
	Bêta	IC	p
(Intercept)	662.751	[174.331;3.802]	2e-04
age	2.368	[0.904;2.619]	0.0093
sexeFemmes	-103.15	[38.308;-2.693]	0.0075
tabacAutrefois	59.365	[25.612;2.318]	0.0211
tabacFumeur	-0.907	[37.453;-0.024]	0.9807
bmi	-2.947	[5.731;-0.514]	0.6075
vitamineSouvent	21.63	[28.456;0.76]	0.4478
vitaminePas-souvent	21.694	[30.725;0.706]	0.4807
calories	0.067	[0.062;1.097]	0.2735
graisses	-1.248	[0.97;-1.287]	0.1991
fibres	-12.749	[11.088;-1.15]	0.2512
alcool	-1.276	[1.497;-0.853]	0.3946
cholesterol	-0.086	[0.132;-0.647]	0.5182
betadiet	-0.003	[0.009;-0.352]	0.7254
rettdiet	-0.012	[0.023;-0.525]	0.5999
betaplasma	0.087	[0.07;1.249]	0.2125
bmi:retinol[, "fibres"]	0.348	[0.438;0.795]	0.4274

```

mod.tmp = lm(retplasma ~ . -retplasma + bmi*retinol[, "fibres"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et fibres", col.names = c(" " ,
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

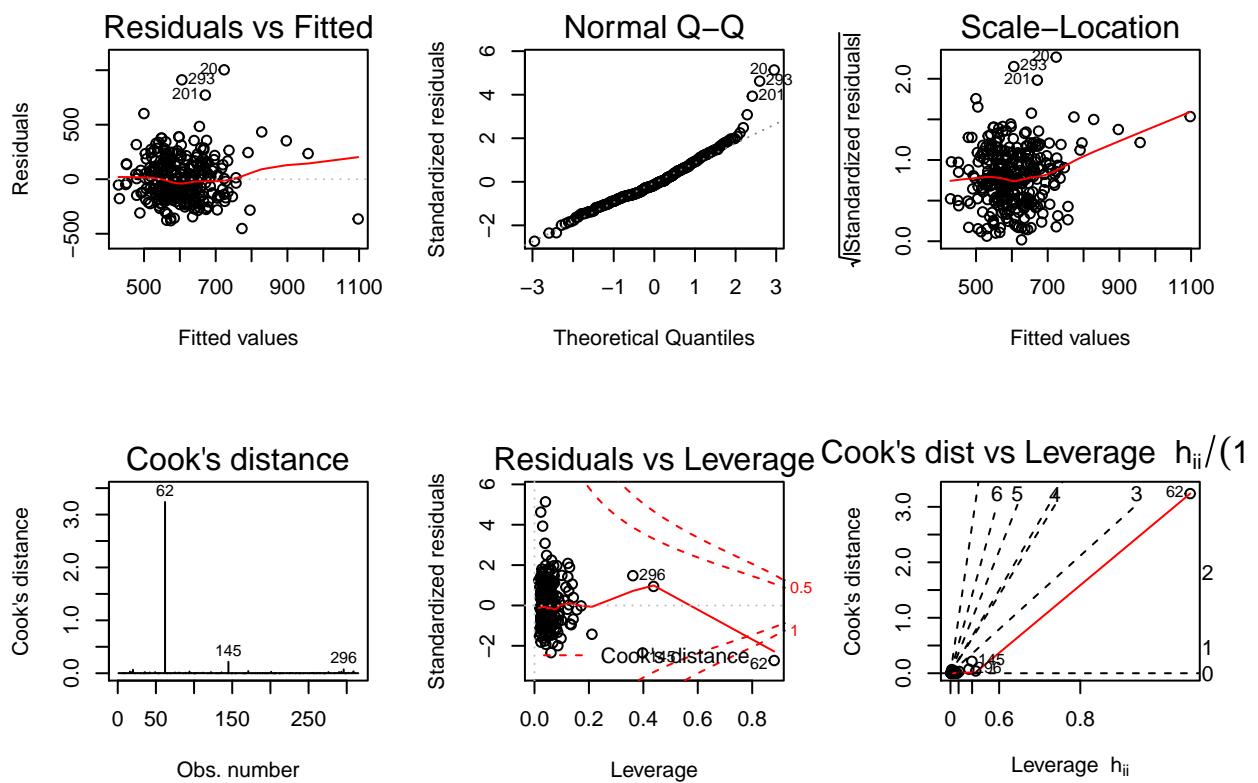
mod.tmp = lm(retplasma ~ . -retplasma + bmi*retinol[, "alcool"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et alcool", col.names = c(" " ,
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 50: Régression linéaire multiple avec interaction entre bmi et alcool

	Bêta	IC	p
(Intercept)	557.789	[98.315;5.673]	0
age	2.586	[0.89;2.906]	0.0039
sexeFemmes	-71.402	[38.835;-1.839]	0.067
tabacAutrefois	55.789	[25.211;2.213]	0.0277
tabacFumeur	-3.396	[36.847;-0.092]	0.9266
bmi	-0.503	[2.058;-0.245]	0.807
vitamineSouvent	21.696	[28.008;0.775]	0.4392
vitaminePas-souvent	28.212	[30.216;0.934]	0.3512
calories	0.067	[0.06;1.108]	0.2688
graisses	-1.292	[0.954;-1.354]	0.1769
fibres	-3.826	[3.38;-1.132]	0.2586
alcool	-36.004	[10.916;-3.298]	0.0011
cholesterol	-0.074	[0.13;-0.567]	0.571
betadiet	-0.004	[0.009;-0.453]	0.6511
rettdiet	-0.009	[0.022;-0.394]	0.6939
betaplasma	0.088	[0.069;1.284]	0.2002
bmi:retinol[, "alcool"]	1.469	[0.458;3.205]	0.0015



```
rm(mod.tmp)
rm(res.tmp)
```

Table 51: Régression linéaire multiple avec interaction entre bmi et cholesterol

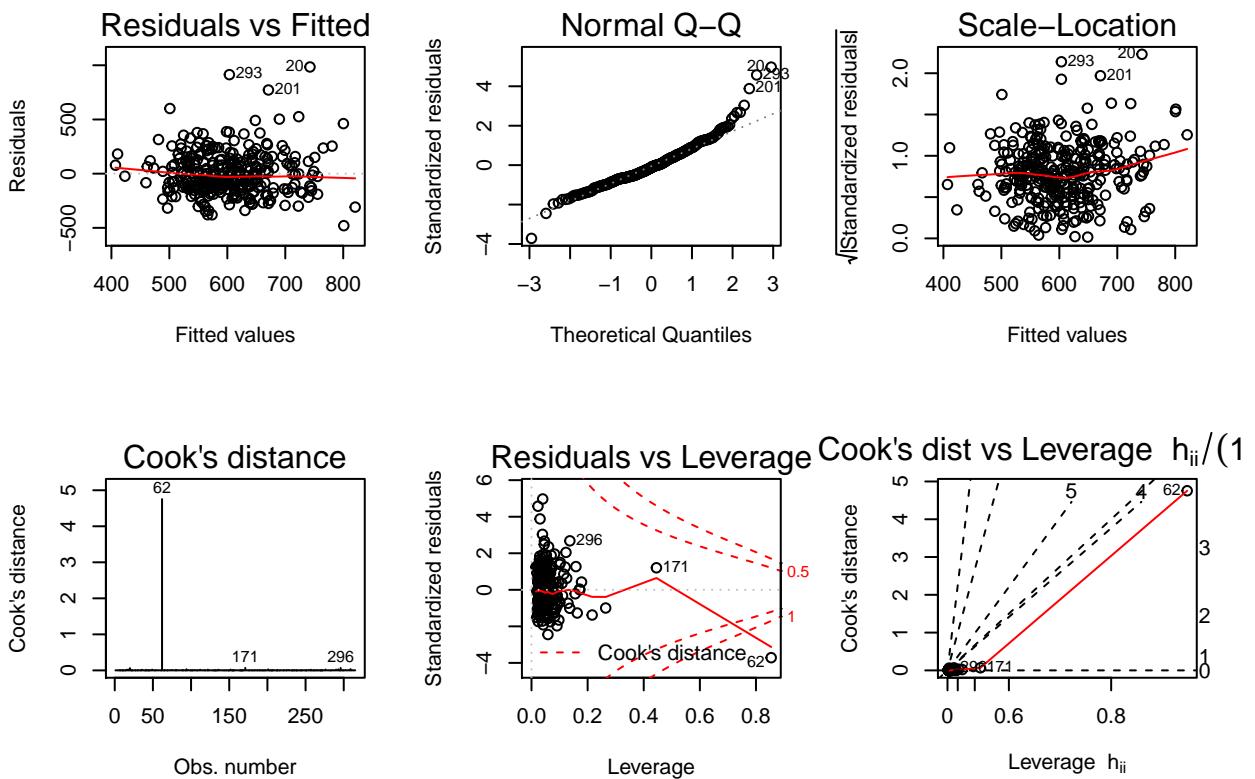
	Bêta	IC	p
(Intercept)	695.963	[139.027;5.006]	0
age	2.388	[0.9;2.654]	0.0084
sexeFemmes	-104.941	[38.22;-2.746]	0.0064
tabacAutrefois	62.041	[25.519;2.431]	0.0156
tabacFumeur	3.781	[37.382;0.101]	0.9195
bmi	-3.929	[4.006;-0.981]	0.3275
vitamineSouvent	21.408	[28.378;0.754]	0.4512
vitaminePas-souvent	25.702	[30.617;0.839]	0.4019
calories	0.073	[0.061;1.19]	0.2348
graisses	-1.382	[0.972;-1.422]	0.156
fibres	-4.546	[3.423;-1.328]	0.1852
alcool	-1.288	[1.491;-0.864]	0.3883
cholesterol	-0.651	[0.396;-1.644]	0.1012
betadiet	-0.002	[0.009;-0.251]	0.8019
retdiet	-0.011	[0.022;-0.473]	0.6368
betaplasma	0.079	[0.069;1.143]	0.2538
bmi:retinol[, "cholesterol"]	0.021	[0.014;1.513]	0.1314

```

mod.tmp = lm(retplasma ~ . -retplasma + bmi*retinol[, "cholesterol"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et cholesterol", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

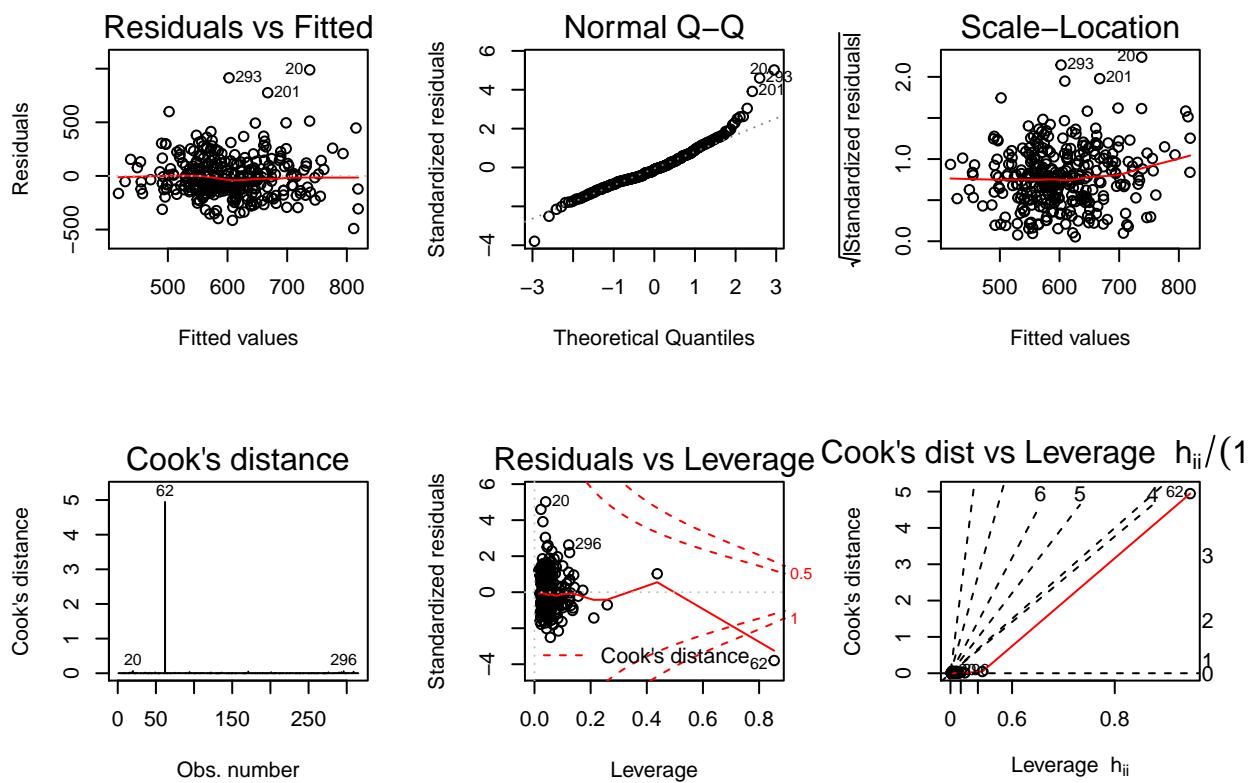
mod.tmp = lm(retplasma ~ . -retplasma + bmi*retinol[, "betadiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et betadiet", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 52: Régression linéaire multiple avec interaction entre bmi et betadiet

	Bêta	IC	p
(Intercept)	725.484	[127.121;5.707]	0
age	2.227	[0.9;2.475]	0.0139
sexeFemmes	-101.688	[37.995;-2.676]	0.0079
tabacAutrefois	58.233	[25.41;2.292]	0.0226
tabacFumeur	-6.603	[37.286;-0.177]	0.8596
bmi	-5.178	[3.547;-1.46]	0.1453
vitamineSouvent	20.144	[28.262;0.713]	0.4766
vitaminePas-souvent	21.125	[30.459;0.694]	0.4885
calories	0.069	[0.061;1.137]	0.2564
graisses	-1.272	[0.963;-1.322]	0.1873
fibres	-3.966	[3.411;-1.163]	0.2459
alcool	-1.263	[1.485;-0.851]	0.3956
cholesterol	-0.076	[0.132;-0.58]	0.5626
betadiet	-0.081	[0.036;-2.226]	0.0268
retdiet	-0.013	[0.022;-0.581]	0.5615
betaplasma	0.099	[0.069;1.42]	0.1568
bmi:retinol[, "betadiet"]	0.003	[0.001;2.216]	0.0275



```
rm(mod.tmp)
rm(res.tmp)
```

Table 53: Régression linéaire multiple avec interaction entre bmi et retdiet

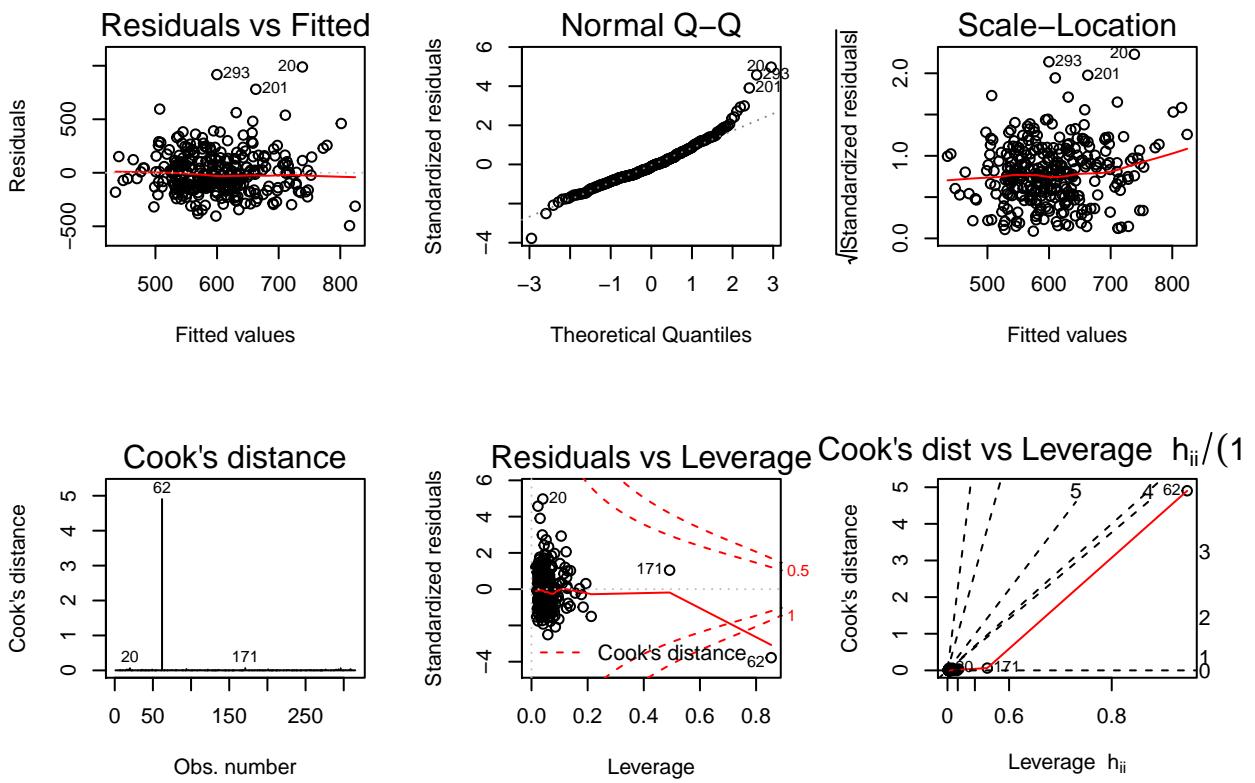
	Bêta	IC	p
(Intercept)	544.166	[140.231;3.88]	1e-04
age	2.412	[0.904;2.667]	0.0081
sexeFemmes	-101.62	[38.371;-2.648]	0.0085
tabacAutrefois	60.489	[25.606;2.362]	0.0188
tabacFumeur	0.269	[37.518;0.007]	0.9943
bmi	1.49	[3.922;0.38]	0.7043
vitamineSouvent	21.587	[28.49;0.758]	0.4492
vitaminePas-souvent	23.337	[30.713;0.76]	0.4479
calories	0.07	[0.062;1.127]	0.2607
graisses	-1.231	[0.971;-1.268]	0.2058
fibres	-4.375	[3.436;-1.273]	0.2039
alcool	-1.349	[1.508;-0.895]	0.3717
cholesterol	-0.086	[0.133;-0.644]	0.5201
betadiet	-0.003	[0.009;-0.318]	0.7509
retdiet	-0.005	[0.106;-0.047]	0.9627
betaplasma	0.083	[0.07;1.194]	0.2332
bmi:retinol[, "retdiet"]	0	[0.004;-0.051]	0.9593

```

mod.tmp = lm(retplasma ~ . -retplasma + bmi*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et retdiet", col.names = c(" "
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

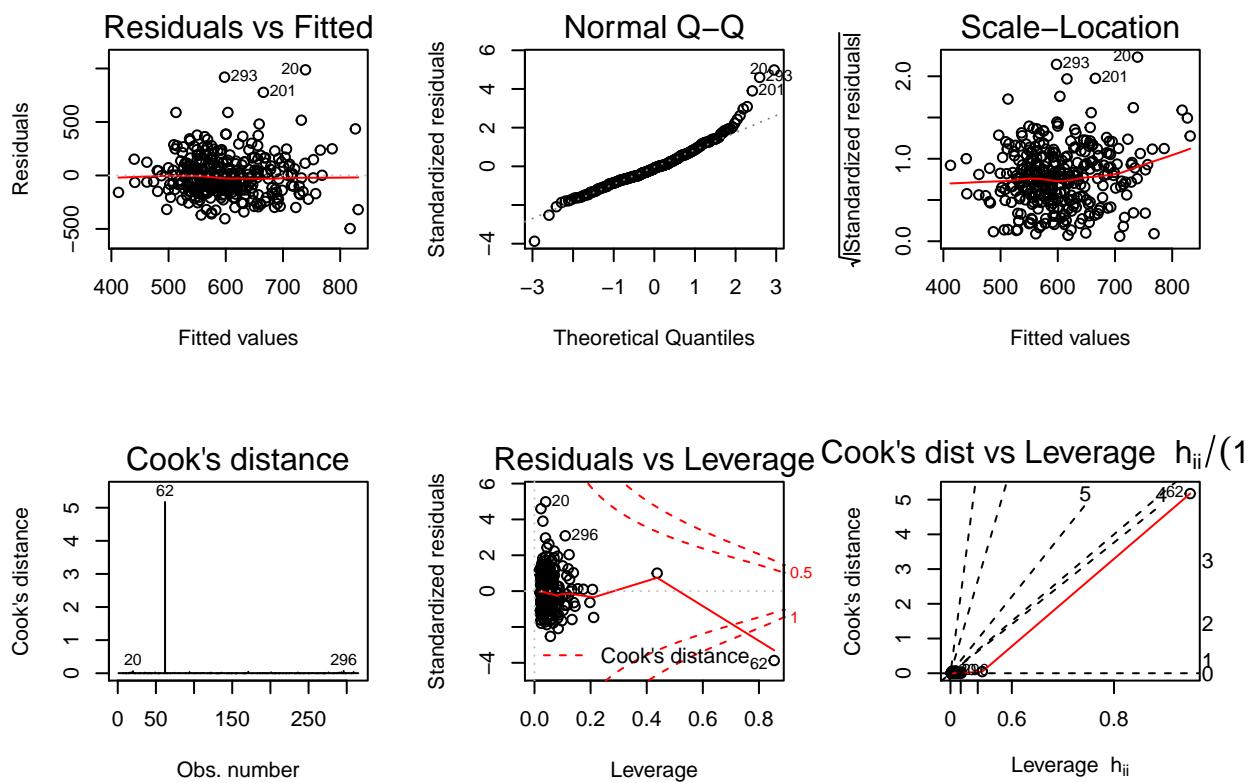
mod.tmp = lm(retplasma ~ . -retplasma + bmi*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et betaplasma", col.names = c(
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 54: Régression linéaire multiple avec interaction entre bmi et betaplasma

	Bêta	IC	p
(Intercept)	631.791	[119.431;5.29]	0
age	2.303	[0.905;2.545]	0.0114
sexeFemmes	-101.825	[38.206;-2.665]	0.0081
tabacAutrefois	59.16	[25.553;2.315]	0.0213
tabacFumeur	0.928	[37.361;0.025]	0.9802
bmi	-1.95	[3.286;-0.593]	0.5534
vitamineSouvent	19.291	[28.469;0.678]	0.4985
vitaminePas-souvent	19.22	[30.782;0.624]	0.5329
calories	0.065	[0.061;1.064]	0.2883
graisses	-1.158	[0.969;-1.194]	0.2334
fibres	-4.031	[3.435;-1.173]	0.2416
alcool	-1.248	[1.494;-0.835]	0.4044
cholesterol	-0.088	[0.132;-0.662]	0.5082
betadiet	-0.003	[0.009;-0.316]	0.7525
retdiet	-0.011	[0.022;-0.487]	0.6268
betaplasma	-0.512	[0.479;-1.069]	0.2859
bmi:retinol[, "betaplasma"]	0.026	[0.021;1.256]	0.2101



```
rm(mod.tmp)
rm(res.tmp)
```

Interactions avec alcool et betadiet.

Table 55: Régression linéaire multiple avec interaction entre vitamine et calories

	Bêta	IC	p
(Intercept)	583.618	[108.203;5.394]	0
age	2.455	[0.91;2.697]	0.0074
sexeFemmes	-104.486	[38.458;-2.717]	0.007
tabacAutrefois	59.297	[25.642;2.313]	0.0214
tabacFumeur	1.66	[37.562;0.044]	0.9648
bmi	1.384	[2.014;0.687]	0.4925
vitamineSouvent	-17.448	[80.795;-0.216]	0.8292
vitaminePas-souvent	-56.786	[91.666;-0.619]	0.5361
calories	0.042	[0.069;0.606]	0.5448
graisses	-1.147	[0.975;-1.177]	0.2403
fibres	-4.107	[3.453;-1.189]	0.2352
alcool	-0.789	[1.63;-0.484]	0.6288
cholesterol	-0.081	[0.134;-0.607]	0.5446
betadiet	-0.003	[0.009;-0.33]	0.7413
retdiet	-0.011	[0.023;-0.482]	0.6305
betaplasma	0.082	[0.07;1.178]	0.2397
vitamineSouvent:retinol[, "calories"]	0.023	[0.044;0.532]	0.5955
vitaminePas-souvent:retinol[, "calories"]	0.046	[0.049;0.93]	0.3532

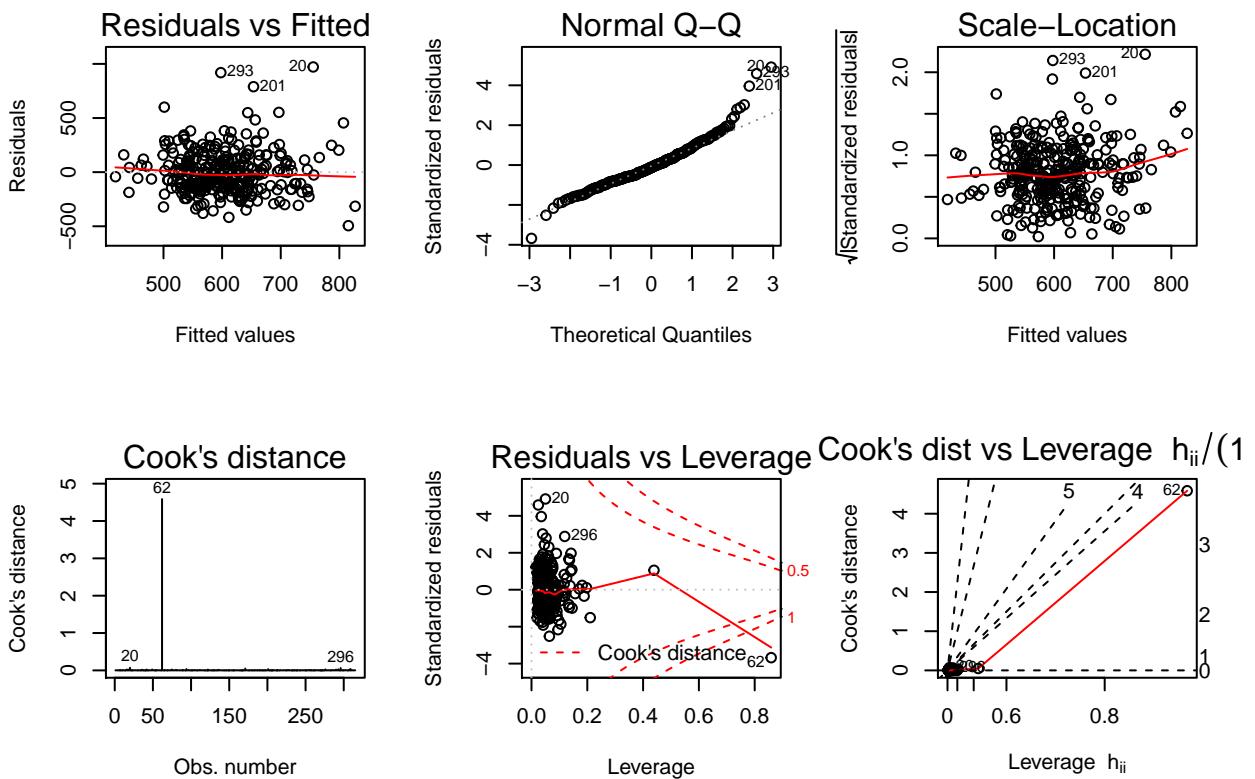
5.3.5 Avec vitamines

```

mod.tmp = lm(retplasma ~ . -retplasma + vitamine*retinol[, "calories"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(summary(mod.tmp)$coefficient[,1],3),
                  paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                         round(summary(mod.tmp)$coefficient[,3],3), "]"),
                  round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et calories", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

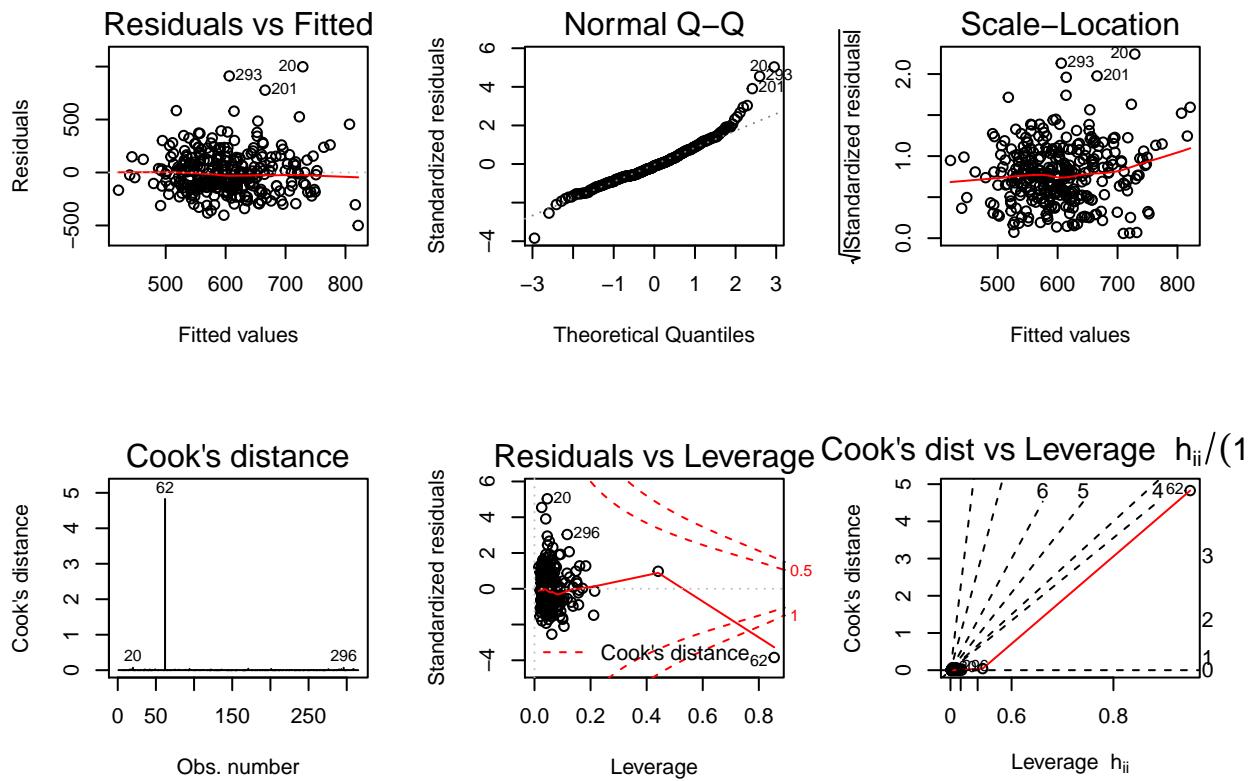
mod.tmp = lm(retplasma ~ . -retplasma + vitamine*retinol[, "graisses"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et graisses", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 56: Régression linéaire multiple avec interaction entre vitamine et graisses

	Bêta	IC	p
(Intercept)	528.721	[105.203;5.026]	0
age	2.347	[0.91;2.58]	0.0104
sexeFemmes	-99.843	[38.452;-2.597]	0.0099
tabacAutrefois	60.898	[25.663;2.373]	0.0183
tabacFumeur	-1.569	[37.656;-0.042]	0.9668
bmi	1.278	[2.015;0.634]	0.5264
vitamineSouvent	61.326	[67.545;0.908]	0.3647
vitaminePas-souvent	52.856	[77.409;0.683]	0.4953
calories	0.07	[0.062;1.132]	0.2585
graisses	-0.934	[1.071;-0.872]	0.3841
fibres	-4.339	[3.441;-1.261]	0.2083
alcool	-1.444	[1.511;-0.956]	0.3398
cholesterol	-0.08	[0.134;-0.595]	0.552
betadiet	-0.003	[0.009;-0.354]	0.7237
rettdiet	-0.011	[0.023;-0.503]	0.6154
betaplasma	0.082	[0.07;1.172]	0.2423
vitamineSouvent:retinol[, "graisses"]	-0.521	[0.802;-0.65]	0.5165
vitaminePas-souvent:retinol[, "graisses"]	-0.39	[0.929;-0.42]	0.6745



```
rm(mod.tmp)
rm(res.tmp)
```

Table 57: Régression linéaire multiple avec interaction entre vitamine et fibres

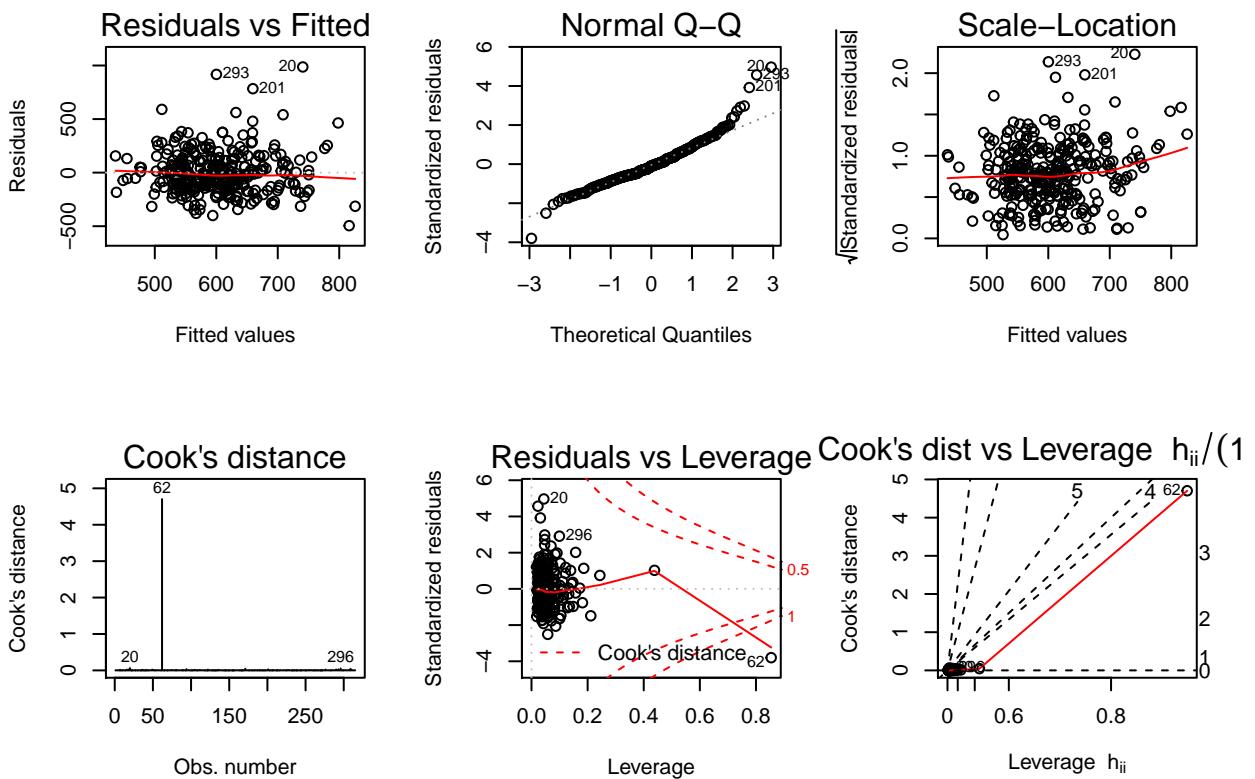
	Bêta	IC	p
(Intercept)	555.971	[107.743;5.16]	0
age	2.411	[0.905;2.665]	0.0081
sexeFemmes	-101.803	[38.384;-2.652]	0.0084
tabacAutrefois	59.866	[25.69;2.33]	0.0205
tabacFumeur	1.899	[37.674;0.05]	0.9598
bmi	1.311	[2.015;0.651]	0.5157
vitamineSouvent	21.503	[68.798;0.313]	0.7548
vitaminePas-souvent	-7.181	[83.571;-0.086]	0.9316
calories	0.067	[0.062;1.078]	0.282
graisses	-1.195	[0.979;-1.222]	0.2229
fibres	-4.717	[4.471;-1.055]	0.2922
alcool	-1.292	[1.505;-0.858]	0.3914
cholesterol	-0.084	[0.133;-0.627]	0.5312
betadiet	-0.004	[0.009;-0.384]	0.7013
retdiet	-0.011	[0.023;-0.477]	0.6335
betaplasma	0.086	[0.071;1.216]	0.225
vitamineSouvent:retinol[, "fibres"]	0.065	[5.068;0.013]	0.9898
vitaminePas-souvent:retinol[, "fibres"]	2.43	[6.286;0.387]	0.6993

```

mod.tmp = lm(retplasma ~ . -retplasma + vitamine*retinol[, "fibres"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et fibres", col.names = c
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

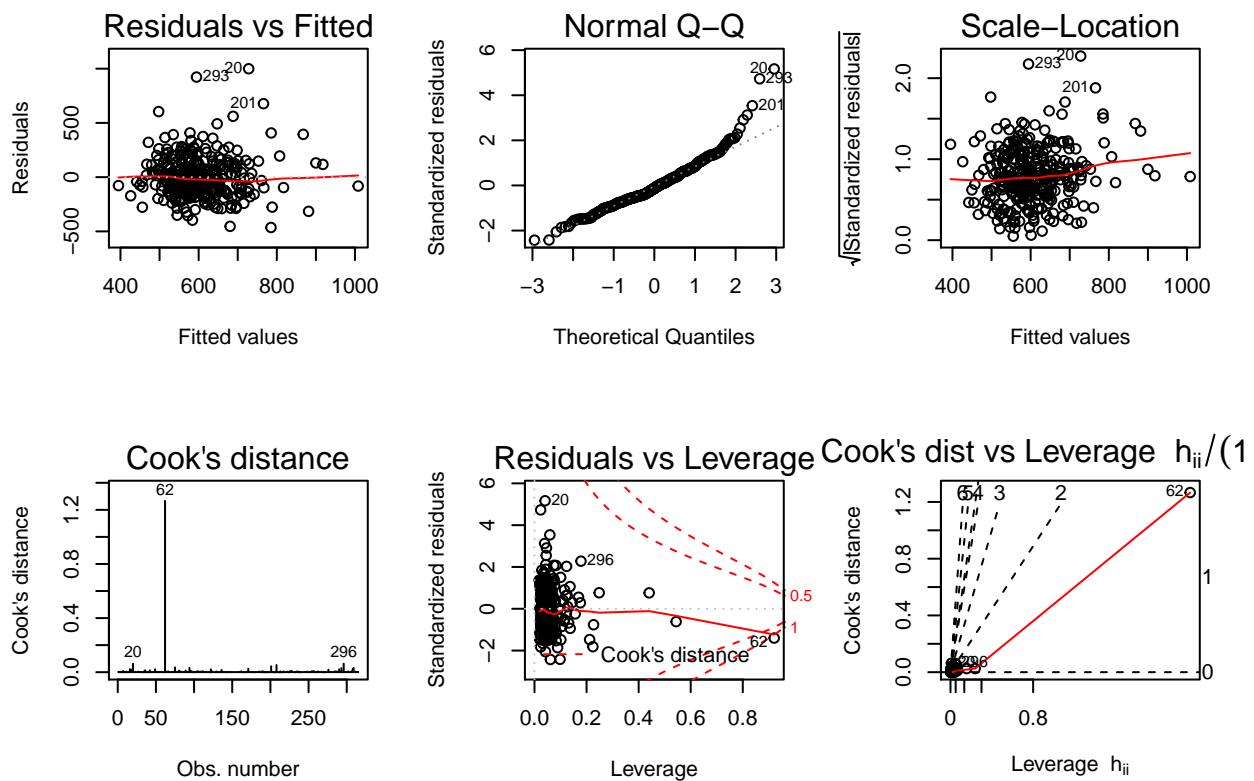
mod.tmp = lm(retplasma ~ . -retplasma + vitamine*retinol[, "alcool"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et alcool", col.names = c
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 58: Régression linéaire multiple avec interaction entre vitamine et alcool

	Bêta	IC	p
(Intercept)	523.48	[97.936;5.345]	0
age	2.618	[0.887;2.951]	0.0034
sexeFemmes	-92.777	[37.949;-2.445]	0.0151
tabacAutrefois	52.306	[25.031;2.09]	0.0375
tabacFumeur	-8.831	[36.565;-0.242]	0.8093
bmi	2.068	[1.968;1.05]	0.2944
vitamineSouvent	-9.019	[29.707;-0.304]	0.7617
vitaminePas-souvent	-19.629	[32.255;-0.609]	0.5433
calories	0.086	[0.06;1.426]	0.1548
graisses	-1.599	[0.954;-1.676]	0.0948
fibres	-4.142	[3.349;-1.237]	0.2172
alcool	-2.619	[1.491;-1.756]	0.08
cholesterol	-0.1	[0.129;-0.775]	0.4388
betadiet	-0.005	[0.009;-0.521]	0.6026
retdiet	-0.002	[0.022;-0.072]	0.9428
betaplasma	0.056	[0.068;0.816]	0.4153
vitamineSouvent:retinol[, "alcool"]	14.097	[5.099;2.765]	0.0061
vitaminePas-souvent:retinol[, "alcool"]	14.837	[4.492;3.303]	0.0011



```
rm(mod.tmp)
rm(res.tmp)
```

Table 59: Régression linéaire multiple avec interaction entre vitamine et cholesterol

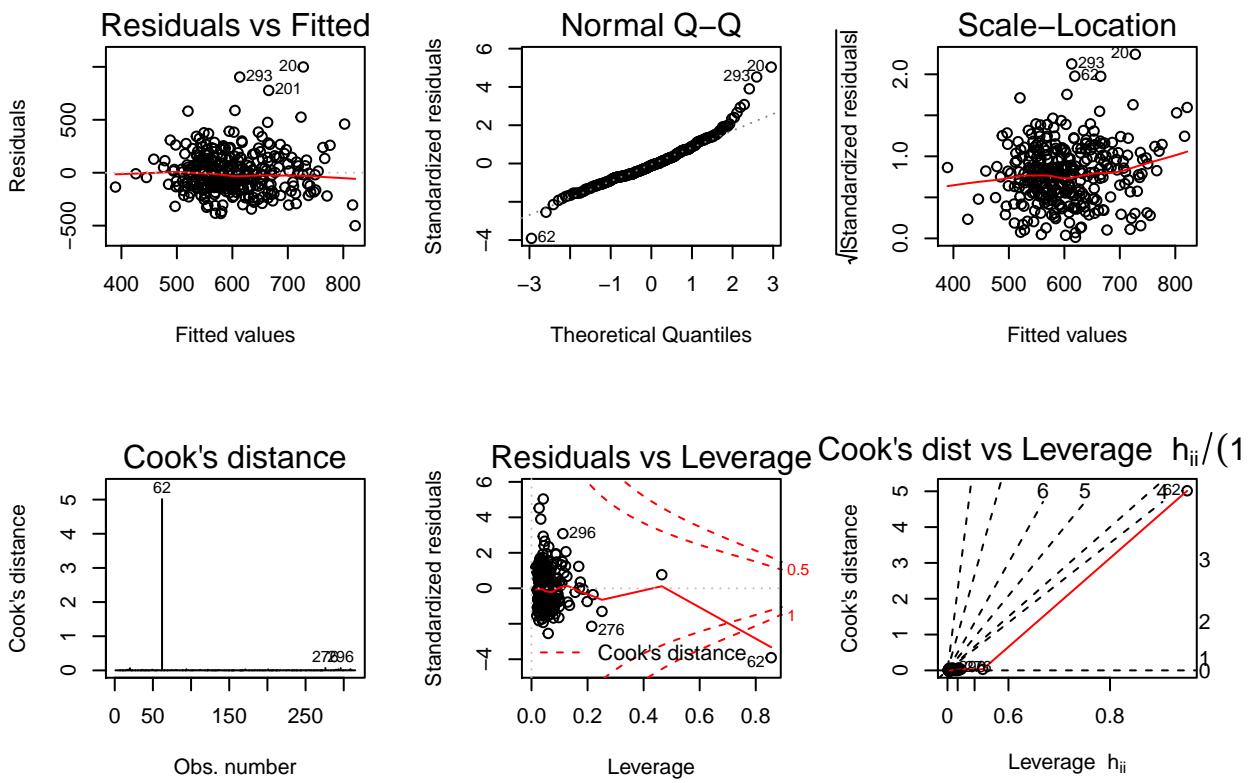
	Bêta	IC	p
(Intercept)	517.428	[103.785;4.986]	0
age	2.287	[0.912;2.508]	0.0127
sexeFemmes	-96.628	[38.521;-2.508]	0.0127
tabacAutrefois	61.042	[25.604;2.384]	0.0177
tabacFumeur	-1.903	[37.563;-0.051]	0.9596
bmi	1.244	[2.013;0.618]	0.537
vitamineSouvent	77.014	[55.431;1.389]	0.1658
vitaminePas-souvent	71.418	[73.508;0.972]	0.3321
calories	0.066	[0.062;1.069]	0.286
graisses	-1.213	[0.971;-1.25]	0.2122
fibres	-4.163	[3.442;-1.21]	0.2274
alcool	-1.469	[1.509;-0.974]	0.331
cholesterol	0.07	[0.186;0.377]	0.7062
betadiet	-0.003	[0.009;-0.323]	0.7473
retdiet	-0.009	[0.022;-0.412]	0.6805
betaplasma	0.08	[0.07;1.155]	0.2492
vitamineSouvent:retinol[, "cholesterol"]	-0.233	[0.199;-1.167]	0.2441
vitaminePas-souvent:retinol[, "cholesterol"]	-0.202	[0.276;-0.734]	0.4636

```

mod.tmp = lm(retplasma ~ . -retplasma + vitamine*retinol[, "cholesterol"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et cholesterol", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

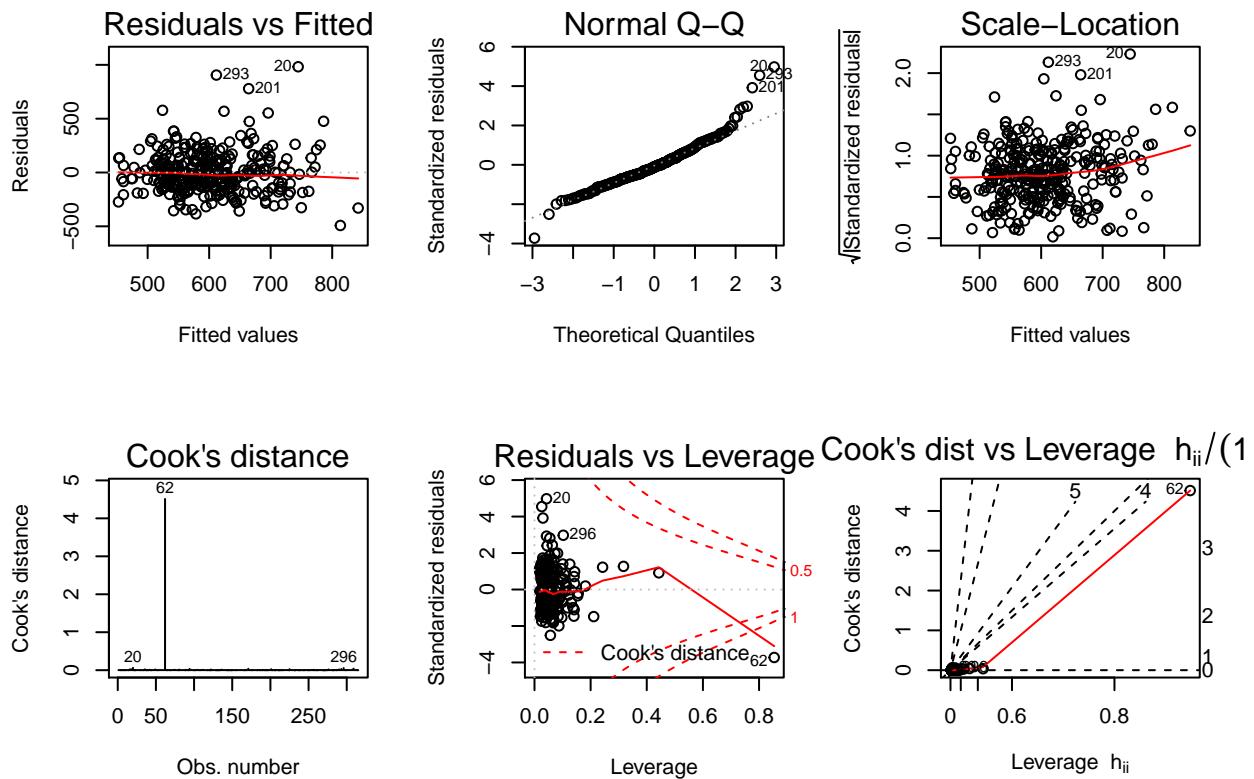
mod.tmp = lm(retplasma ~ . -retplasma + vitamine*retinol[, "betadiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et betadiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 60: Régression linéaire multiple avec interaction entre vitamine et betadiet

	Bêta	IC	p
(Intercept)	563.214	[102.644;5.487]	0
age	2.378	[0.901;2.638]	0.0088
sexeFemmes	-101.258	[38.145;-2.655]	0.0084
tabacAutrefois	59.897	[25.484;2.35]	0.0194
tabacFumeur	6.785	[37.482;0.181]	0.8565
bmi	1.382	[2.003;0.69]	0.4906
vitamineSouvent	31.378	[49.985;0.628]	0.5307
vitaminePas-souvent	-46.98	[52.114;-0.901]	0.3681
calories	0.058	[0.062;0.947]	0.3445
graisses	-1.052	[0.97;-1.085]	0.2788
fibres	-4.195	[3.433;-1.222]	0.2226
alcool	-1.173	[1.491;-0.786]	0.4322
cholesterol	-0.073	[0.133;-0.55]	0.5828
betadiet	-0.012	[0.015;-0.76]	0.4476
retdiet	-0.01	[0.022;-0.459]	0.6466
betaplasma	0.097	[0.07;1.375]	0.1703
vitamineSouvent:retinol[, "betadiet"]	-0.003	[0.019;-0.137]	0.891
vitaminePas-souvent:retinol[, "betadiet"]	0.034	[0.021;1.62]	0.1063



```
rm(mod.tmp)
rm(res.tmp)
```

Table 61: Régression linéaire multiple avec interaction entre vitamine et retdiet

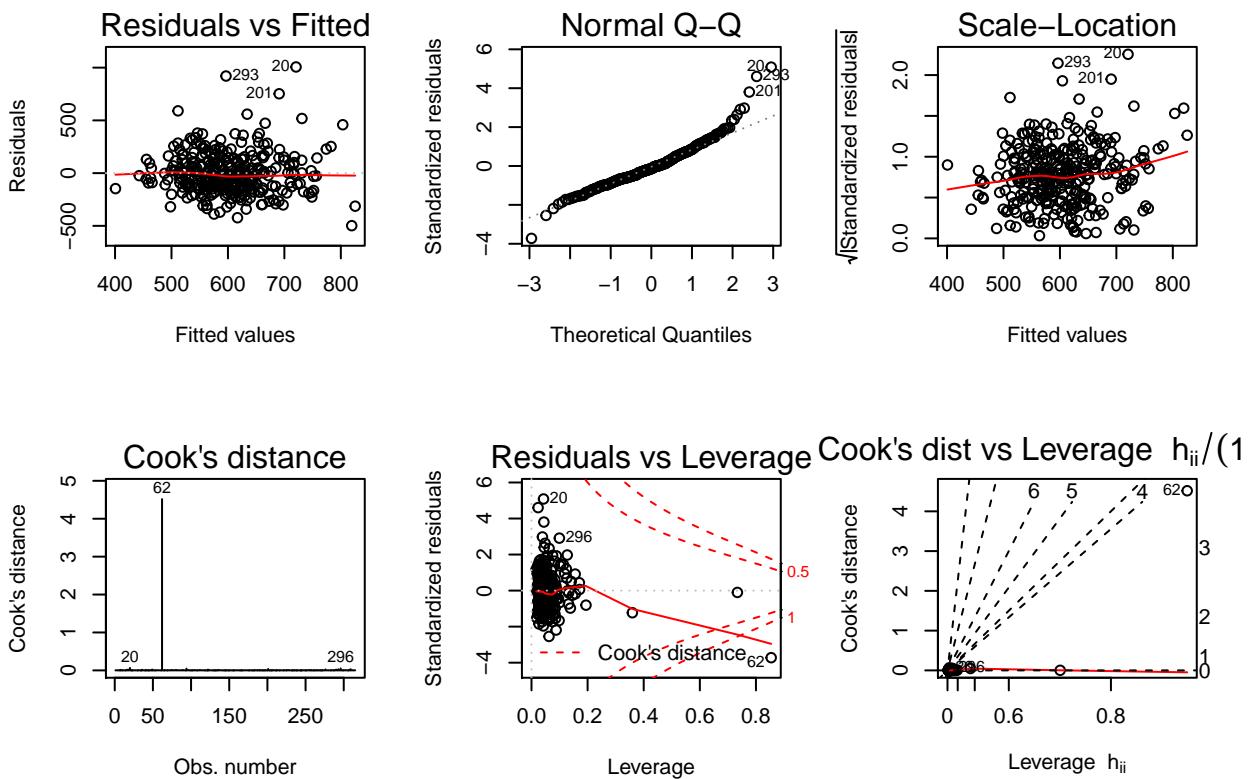
	Bêta	IC	p
(Intercept)	502.756	[103.879;4.84]	0
age	2.492	[0.905;2.753]	0.0063
sexeFemmes	-96.222	[38.373;-2.508]	0.0127
tabacAutrefois	62.96	[25.572;2.462]	0.0144
tabacFumeur	1.102	[37.576;0.029]	0.9766
bmi	1.421	[2.011;0.707]	0.4804
vitamineSouvent	64.007	[47.106;1.359]	0.1753
vitaminePas-souvent	91.416	[56.011;1.632]	0.1037
calories	0.092	[0.063;1.457]	0.1461
graisses	-1.521	[0.985;-1.544]	0.1237
fibres	-4.821	[3.436;-1.403]	0.1616
alcool	-1.887	[1.53;-1.233]	0.2186
cholesterol	-0.065	[0.136;-0.476]	0.6345
betadiet	-0.004	[0.009;-0.398]	0.6912
retdiet	0.017	[0.029;0.602]	0.5475
betaplasma	0.075	[0.07;1.071]	0.2851
vitamineSouvent:retinol[, "retdiet"]	-0.052	[0.045;-1.157]	0.2483
vitaminePas-souvent:retinol[, "retdiet"]	-0.086	[0.059;-1.459]	0.1456

```

mod.tmp = lm(retplasma ~ . -retplasma + vitamine*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et retdiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

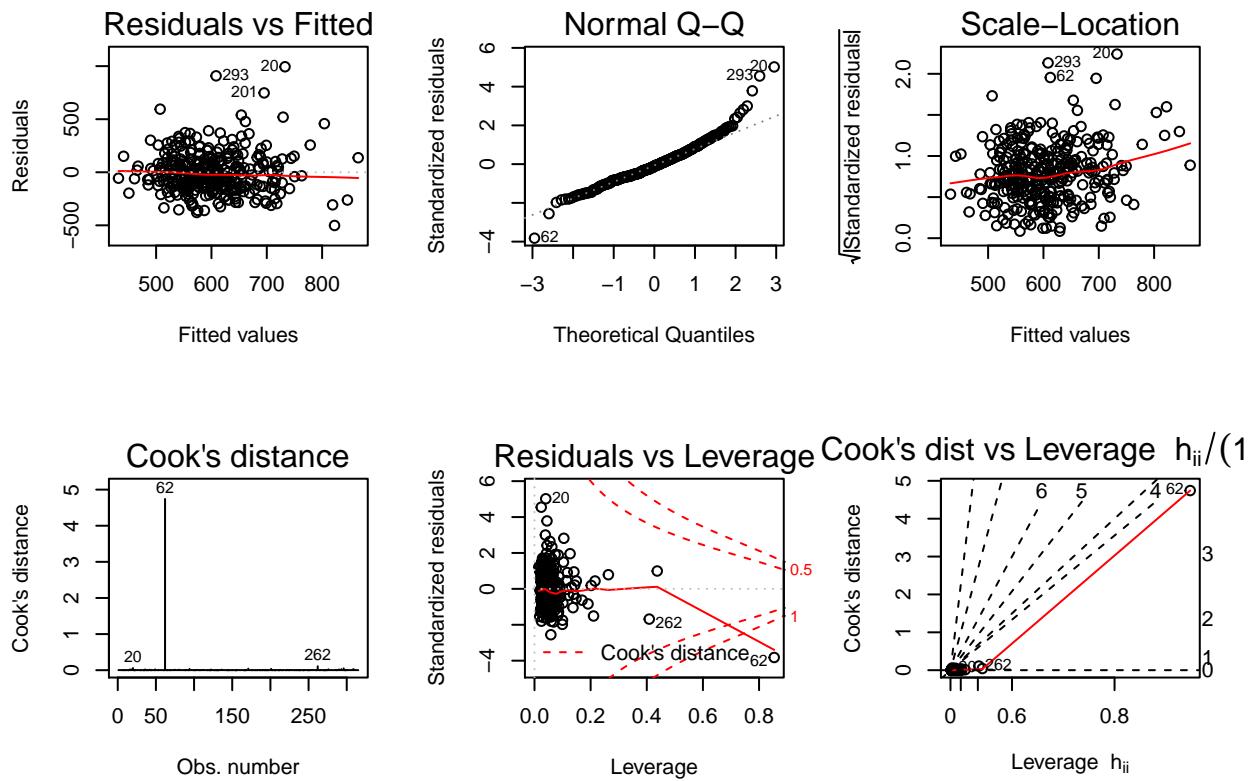
mod.tmp = lm(retplasma ~ . -retplasma + vitamine*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et betaplasma", col.names =
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 62: Régression linéaire multiple avec interaction entre vitamine et betaplasma

	Bêta	IC	p
(Intercept)	505.318	[105.651;4.783]	0
age	2.359	[0.901;2.618]	0.0093
sexeFemmes	-102.501	[38.365;-2.672]	0.008
tabacAutrefois	61.977	[25.947;2.389]	0.0175
tabacFumeur	4.758	[37.458;0.127]	0.899
bmi	1.751	[2.027;0.864]	0.3883
vitamineSouvent	68.398	[45.277;1.511]	0.1319
vitaminePas-souvent	21.669	[52.445;0.413]	0.6798
calories	0.077	[0.062;1.251]	0.2119
graisses	-1.372	[0.973;-1.409]	0.1598
fibres	-4.213	[3.432;-1.228]	0.2206
alcool	-1.426	[1.493;-0.955]	0.3405
cholesterol	-0.075	[0.133;-0.565]	0.5725
betadiet	-0.003	[0.009;-0.322]	0.7477
retdiet	-0.014	[0.023;-0.627]	0.5314
betaplasma	0.309	[0.223;1.381]	0.1682
vitamineSouvent:retinol[, "betaplasma"]	-0.29	[0.234;-1.244]	0.2146
vitaminePas-souvent:retinol[, "betaplasma"]	-0.055	[0.273;-0.2]	0.8417



```
rm(mod.tmp)
rm(res.tmp)
```

Table 63: Régression linéaire multiple avec interaction entre calories et graisses

	Bêta	IC	p
(Intercept)	457.148	[124.913;3.66]	3e-04
age	2.481	[0.903;2.747]	0.0064
sexeFemmes	-94.824	[38.627;-2.455]	0.0147
tabacAutrefois	59.535	[25.546;2.33]	0.0204
tabacFumeur	-0.605	[37.372;-0.016]	0.9871
bmi	1.63	[2.023;0.806]	0.4211
vitamineSouvent	24.578	[28.522;0.862]	0.3895
vitaminePas-souvent	23.119	[30.616;0.755]	0.4508
calories	0.105	[0.068;1.544]	0.1237
graisses	-0.151	[1.309;-0.115]	0.9084
fibres	-4.302	[3.426;-1.256]	0.2101
alcool	-0.58	[1.617;-0.359]	0.7201
cholesterol	-0.082	[0.132;-0.621]	0.5353
betadiet	-0.004	[0.009;-0.435]	0.6641
retdiet	-0.012	[0.022;-0.535]	0.593
betaplasma	0.079	[0.07;1.132]	0.2584
calories:retinol[, "graisses"]	0	[0;-1.223]	0.2222

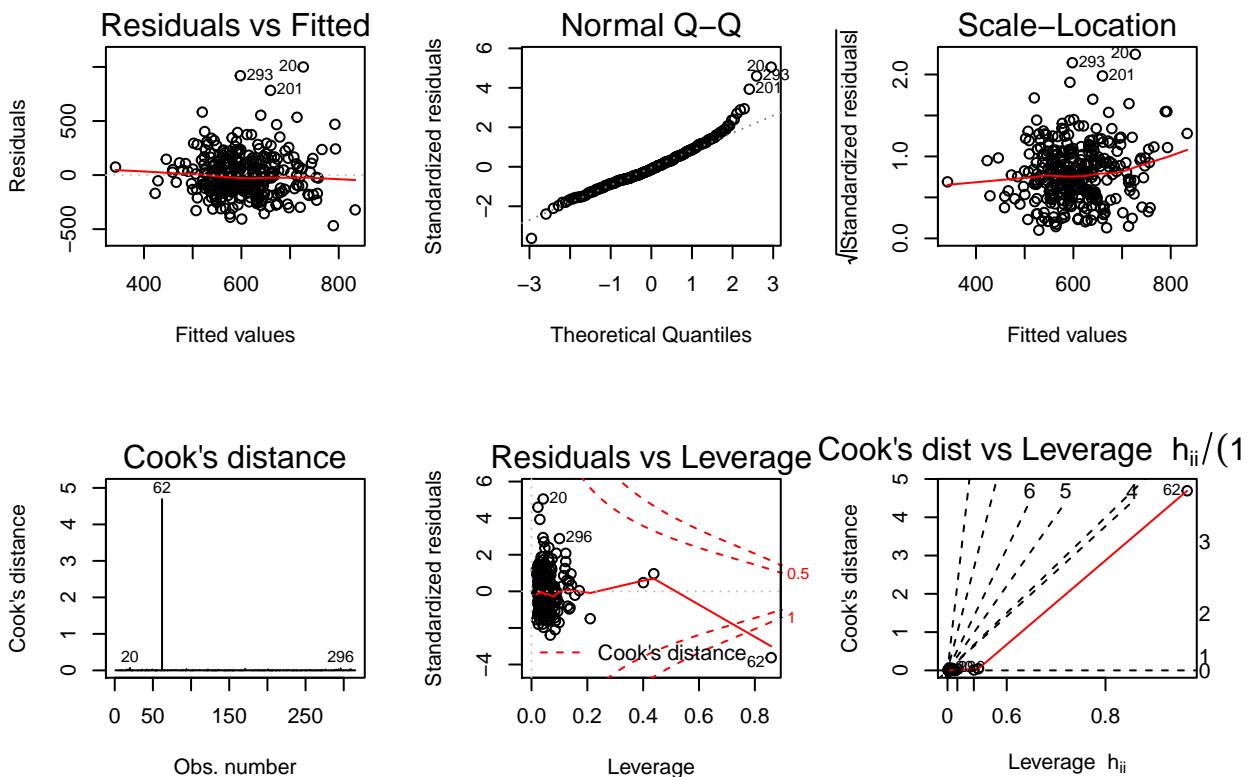
5.3.6 Avec les calories

```

mod.tmp = lm(retplasma ~ . -retplasma + calories*retinol[, "graisses"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficients),
                  round(summary(mod.tmp)$coefficients[,1],3),
                  paste0("[",round(summary(mod.tmp)$coefficients[,2],3),";",
                         round(summary(mod.tmp)$coefficients[,3],3), "]"),
                  round(summary(mod.tmp)$coefficients[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et graisses", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

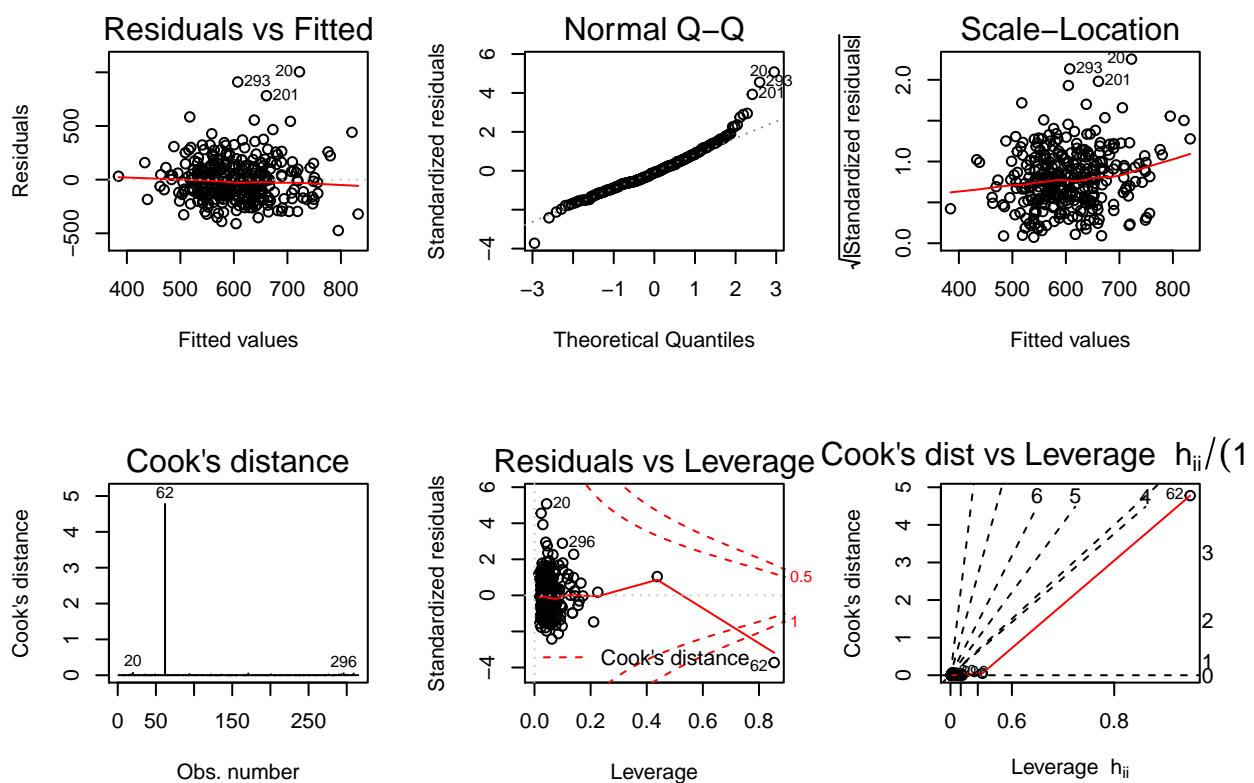
mod.tmp = lm(retplasma ~ . -retplasma + calories*retinol[, "fibres"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et fibres", col.names = c
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 64: Régression linéaire multiple avec interaction entre calories et fibres

	Bêta	IC	p
(Intercept)	429.649	[133.6;3.216]	0.0014
age	2.493	[0.903;2.762]	0.0061
sexeFemmes	-95.271	[38.493;-2.475]	0.0139
tabacAutrefois	60.469	[25.52;2.369]	0.0185
tabacFumeur	-0.128	[37.346;-0.003]	0.9973
bmi	1.384	[2.007;0.69]	0.491
vitamineSouvent	20.408	[28.413;0.718]	0.4732
vitaminePas-souvent	21.029	[30.646;0.686]	0.4931
calories	0.133	[0.077;1.716]	0.0872
graisses	-1.229	[0.967;-1.271]	0.2048
fibres	4.076	[7.158;0.569]	0.5695
alcool	-1.688	[1.514;-1.115]	0.2659
cholesterol	-0.09	[0.132;-0.678]	0.4981
betadiet	-0.003	[0.009;-0.355]	0.7226
retdiet	-0.012	[0.022;-0.556]	0.5788
betaplasma	0.09	[0.07;1.285]	0.1996
calories:retinol[, "fibres"]	-0.004	[0.003;-1.343]	0.1802



```
rm(mod.tmp)
rm(res.tmp)
```

Table 65: Régression linéaire multiple avec interaction entre calories et alcool

	Bêta	IC	p
(Intercept)	456.381	[100.311;4.55]	0
age	2.698	[0.884;3.052]	0.0025
sexeFemmes	-80.666	[37.741;-2.137]	0.0334
tabacAutrefois	45.84	[25.241;1.816]	0.0704
tabacFumeur	5.202	[36.548;0.142]	0.8869
bmi	2.279	[1.977;1.153]	0.25
vitamineSouvent	33.216	[27.938;1.189]	0.2354
vitaminePas-souvent	26.578	[29.943;0.888]	0.3755
calories	0.089	[0.06;1.471]	0.1425
graisses	-1.457	[0.948;-1.537]	0.1254
fibres	-4.536	[3.349;-1.355]	0.1766
alcool	12.492	[3.819;3.271]	0.0012
cholesterol	-0.089	[0.129;-0.689]	0.4916
betadiet	-0.004	[0.009;-0.429]	0.6679
retdiet	-0.008	[0.022;-0.349]	0.7277
betaplasma	0.069	[0.068;1.015]	0.3107
calories:retinol[, "alcool"]	-0.002	[0.001;-3.92]	1e-04

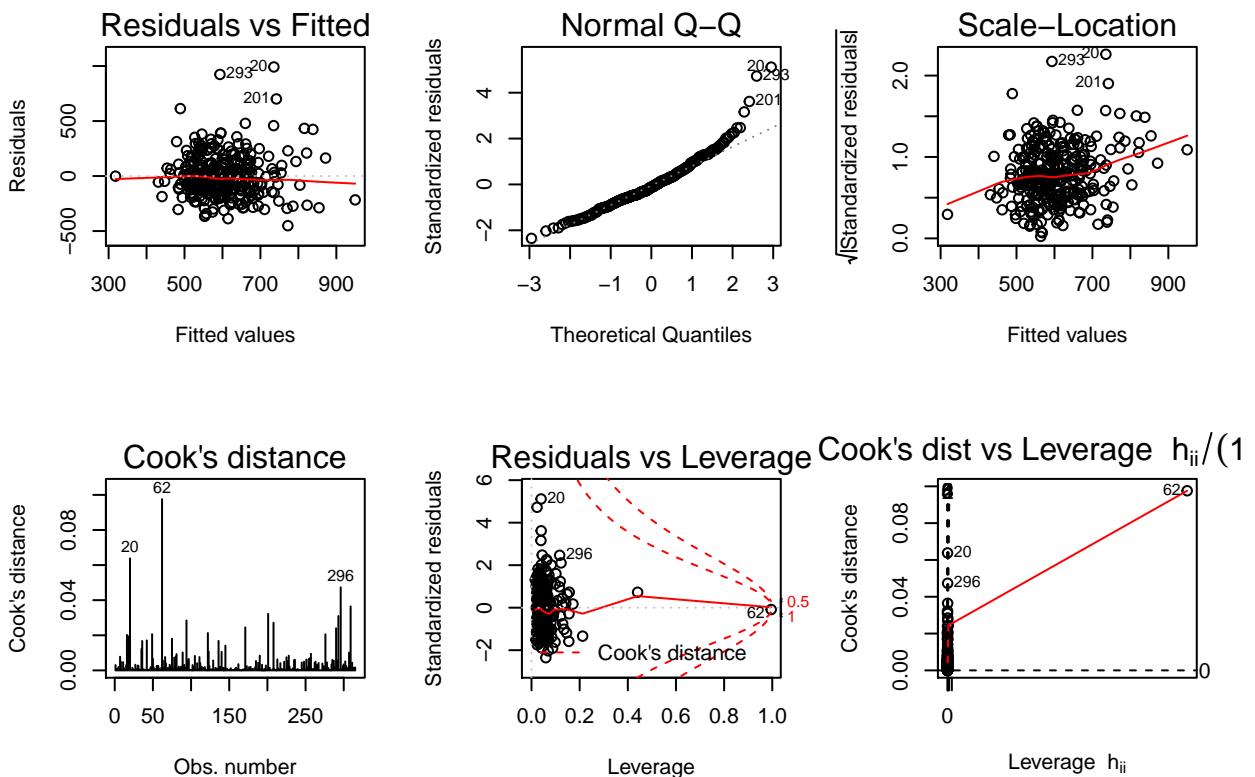
```

mod.tmp = lm(retplasma ~ . -retplasma + calories*retinol[, "alcool"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et alcool", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

## Warning in sqrt(crit * p * (1 - hh)/hh): production de NaN
## Warning in sqrt(crit * p * (1 - hh)/hh): production de NaN

```



```

rm(mod.tmp)
rm(res.tmp)

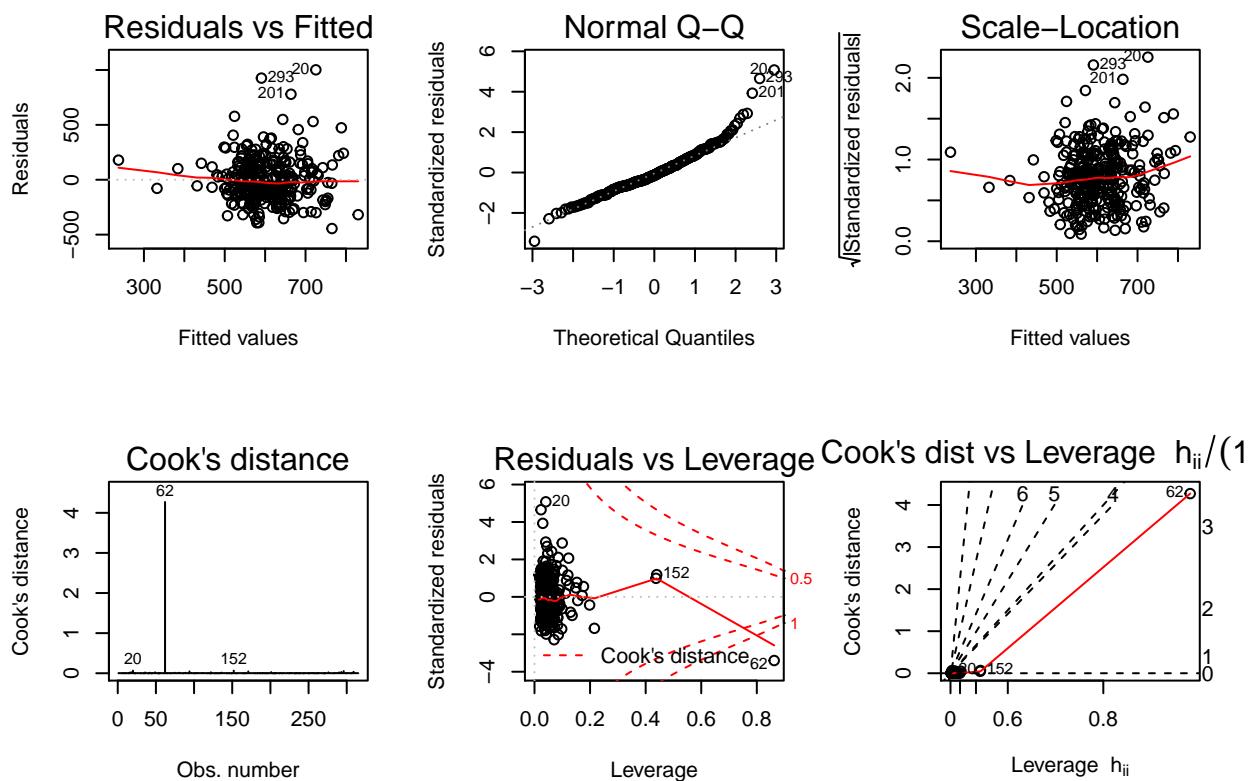
mod.tmp = lm(retplasma ~ . -retplasma + calories*retinol[, "cholesterol"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et cholesterol", col.names =
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 66: Régression linéaire multiple avec interaction entre calories et cholestérol

	Bêta	IC	p
(Intercept)	409.491	[120.057;3.411]	7e-04
age	2.526	[0.899;2.811]	0.0053
sexeFemmes	-87.457	[38.657;-2.262]	0.0244
tabacAutrefois	57.416	[25.46;2.255]	0.0249
tabacFumeur	-0.141	[37.192;-0.004]	0.997
bmi	1.759	[2.009;0.876]	0.382
vitamineSouvent	27.328	[28.421;0.962]	0.3371
vitaminePas-souvent	20.67	[30.501;0.678]	0.4985
calories	0.132	[0.068;1.939]	0.0534
graisses	-1.177	[0.964;-1.222]	0.2228
fibres	-4.665	[3.412;-1.367]	0.1726
alcool	-0.024	[1.616;-0.015]	0.9881
cholesterol	0.355	[0.251;1.417]	0.1577
betadiet	-0.005	[0.009;-0.503]	0.615
retdiet	-0.013	[0.022;-0.602]	0.5474
betaplasma	0.071	[0.069;1.028]	0.305
calories:retinol[, "cholesterol"]	0	[0;-2.068]	0.0395



```
rm(mod.tmp)
rm(res.tmp)
```

Table 67: Régression linéaire multiple avec interaction entre calories et betadiet

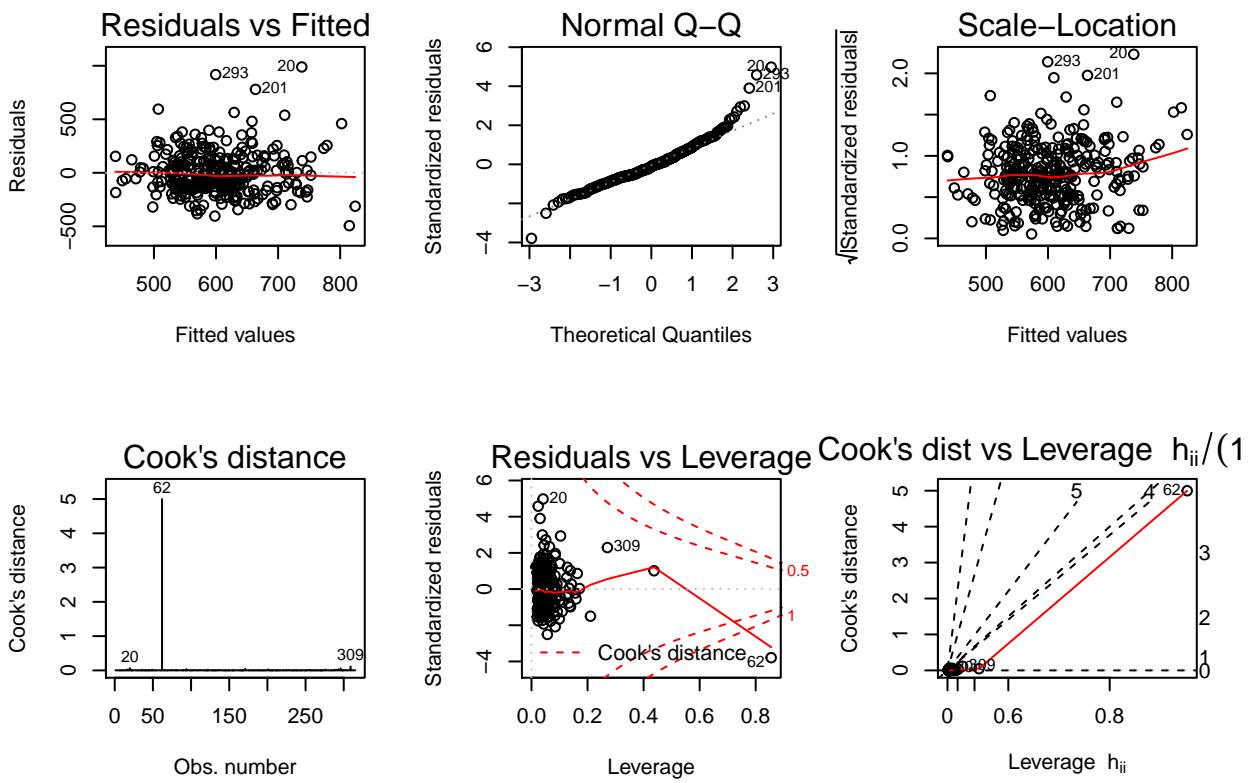
	Bêta	IC	p
(Intercept)	545.492	[113.03;4.826]	0
age	2.41	[0.903;2.668]	0.008
sexeFemmes	-101.533	[38.413;-2.643]	0.0086
tabacAutrefois	60.654	[25.666;2.363]	0.0188
tabacFumeur	0.37	[37.457;0.01]	0.9921
bmi	1.318	[2.012;0.655]	0.5131
vitamineSouvent	21.488	[28.507;0.754]	0.4516
vitaminePas-souvent	23.239	[30.698;0.757]	0.4496
calories	0.072	[0.068;1.047]	0.2959
graisses	-1.232	[0.971;-1.269]	0.2055
fibres	-4.366	[3.434;-1.271]	0.2046
alcool	-1.331	[1.502;-0.886]	0.3765
cholesterol	-0.086	[0.133;-0.652]	0.5149
betadiet	-0.001	[0.026;-0.047]	0.9623
retdiet	-0.01	[0.022;-0.457]	0.6481
betaplasma	0.083	[0.07;1.193]	0.2338
calories:retinol[, "betadiet"]	0	[0;-0.07]	0.9443

```

mod.tmp = lm(retplasma ~ . -retplasma + calories*retinol[, "betadiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et betadiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

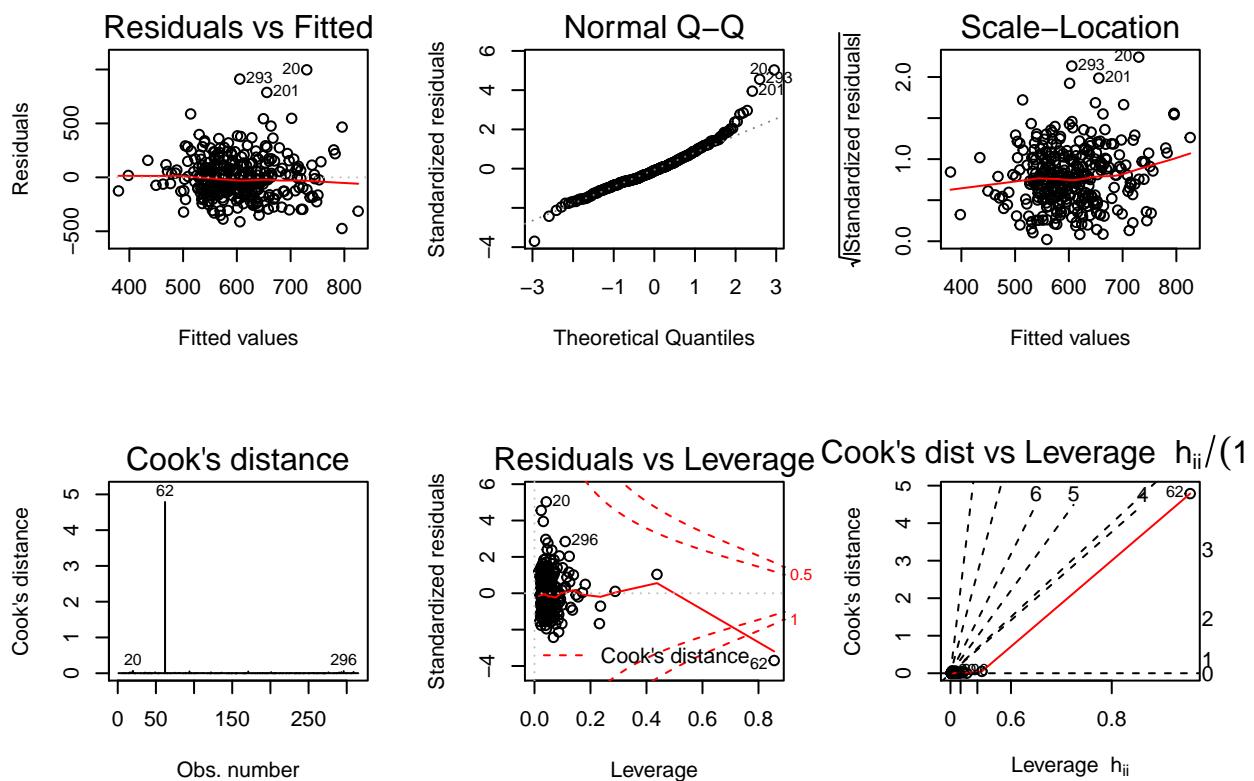
mod.tmp = lm(retplasma ~ . -retplasma + calories*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et retdiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 68: Régression linéaire multiple avec interaction entre calories et retdiet

	Bêta	IC	p
(Intercept)	494.205	[117.159;4.218]	0
age	2.383	[0.902;2.641]	0.0087
sexeFemmes	-98.901	[38.386;-2.577]	0.0105
tabacAutrefois	59.724	[25.578;2.335]	0.0202
tabacFumeur	0.236	[37.407;0.006]	0.995
bmi	1.586	[2.032;0.781]	0.4356
vitamineSouvent	22.252	[28.458;0.782]	0.4349
vitaminePas-souvent	24.294	[30.672;0.792]	0.429
calories	0.093	[0.067;1.389]	0.1659
graisses	-1.148	[0.973;-1.18]	0.2391
fibres	-4.324	[3.43;-1.261]	0.2084
alcool	-1.013	[1.538;-0.658]	0.5109
cholesterol	-0.086	[0.132;-0.65]	0.516
betadiet	-0.003	[0.009;-0.365]	0.7151
retdiet	0.047	[0.068;0.696]	0.4867
betaplasma	0.079	[0.07;1.14]	0.2554
calories:retinol[, "retdiet"]	0	[0;-0.896]	0.3708



```
rm(mod.tmp)
rm(res.tmp)
```

Table 69: Régression linéaire multiple avec interaction entre calories et betaplasma

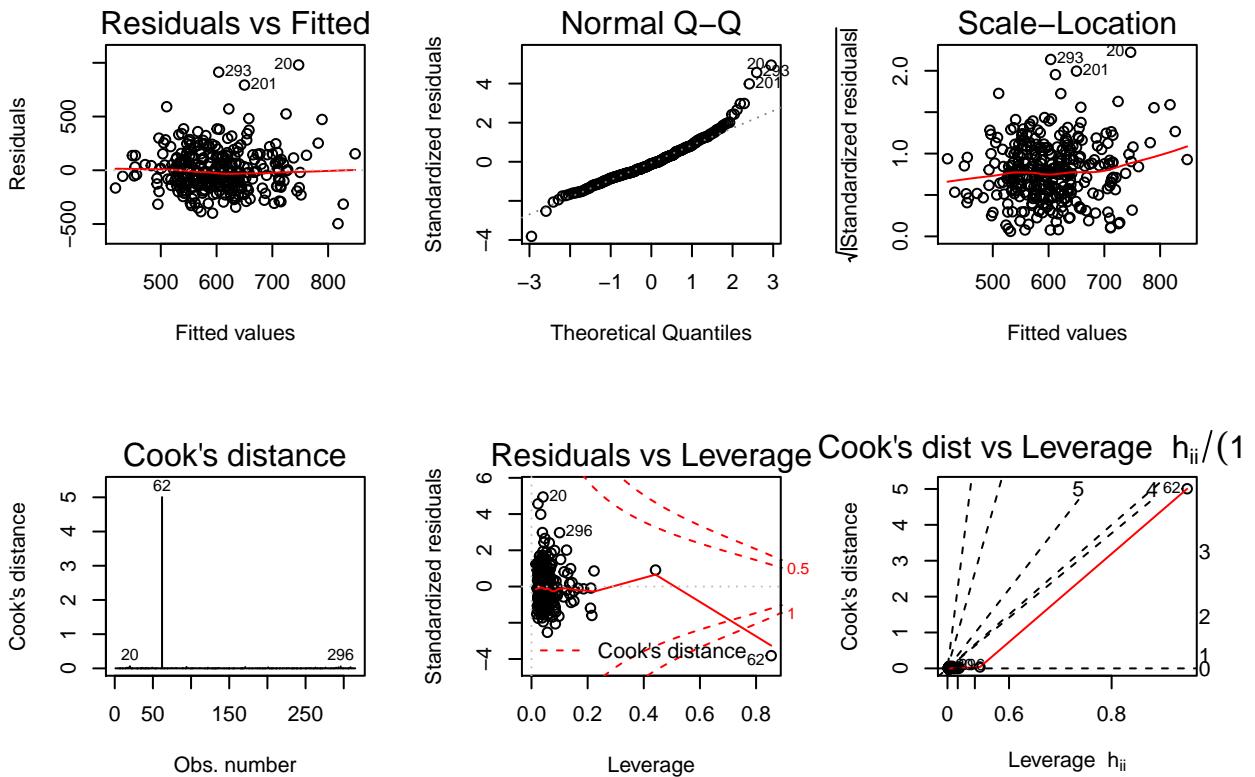
	Bêta	IC	p
(Intercept)	596.801	[107.704;5.541]	0
age	2.425	[0.901;2.69]	0.0075
sexeFemmes	-100.859	[38.227;-2.638]	0.0088
tabacAutrefois	62.861	[25.617;2.454]	0.0147
tabacFumeur	1.167	[37.377;0.031]	0.9751
bmi	1.261	[2.008;0.628]	0.5306
vitamineSouvent	22.454	[28.431;0.79]	0.4303
vitaminePas-souvent	23.998	[30.629;0.784]	0.4339
calories	0.046	[0.065;0.716]	0.4743
graisses	-1.26	[0.968;-1.301]	0.1944
fibres	-5.1	[3.482;-1.465]	0.1441
alcool	-1.133	[1.504;-0.754]	0.4515
cholesterol	-0.073	[0.133;-0.548]	0.5841
betadiet	-0.003	[0.009;-0.297]	0.7665
retdiet	-0.008	[0.022;-0.361]	0.7181
betaplasma	-0.191	[0.245;-0.782]	0.4346
calories:retinol[, "betaplasma"]	0	[0;1.171]	0.2426

```

mod.tmp = lm(retplasma ~ . -retplasma + calories*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et betaplasma",col.names
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



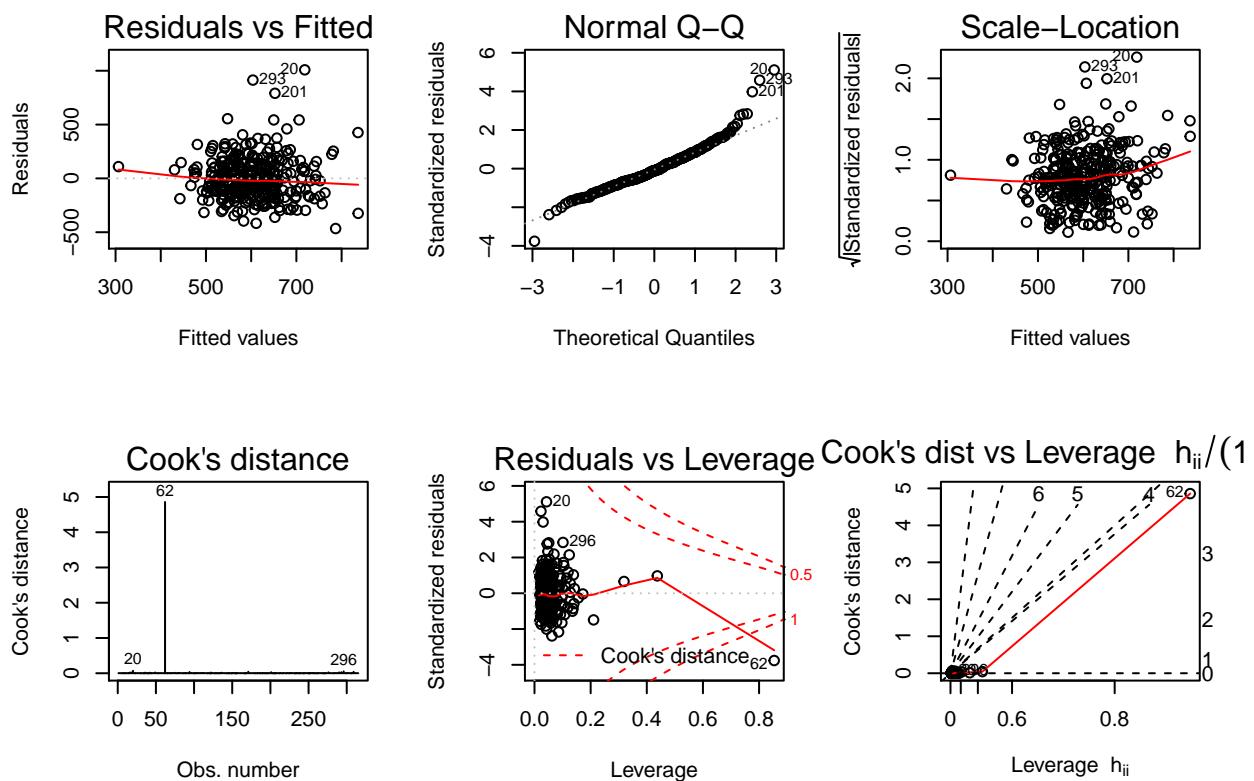
```
rm(mod.tmp)
rm(res.tmp)
```

5.3.7 Avec les graisses

```
mod.tmp = lm(retplasma ~ . -retplasma + graisses*retinol[, "fibres"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et fibres", col.names = c("Variable", "B", "S.E.", "t", "P"))
par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)
```

Table 70: Régression linéaire multiple avec interaction entre graisses et fibres

	Bêta	IC	p
(Intercept)	400.502	[127.924;3.131]	0.0019
age	2.495	[0.899;2.774]	0.0059
sexeFemmes	-92.02	[38.452;-2.393]	0.0173
tabacAutrefois	61.358	[25.456;2.41]	0.0165
tabacFumeur	-2.671	[37.281;-0.072]	0.9429
bmi	1.538	[2.004;0.767]	0.4436
vitamineSouvent	21.19	[28.325;0.748]	0.455
vitaminePas-souvent	21.548	[30.533;0.706]	0.4809
calories	0.066	[0.061;1.074]	0.2838
graisses	0.688	[1.417;0.485]	0.6279
fibres	5.47	[6.329;0.864]	0.3882
alcool	-1.436	[1.489;-0.964]	0.3358
cholesterol	-0.094	[0.132;-0.715]	0.4749
betadiet	-0.003	[0.009;-0.332]	0.7401
retdiet	-0.01	[0.022;-0.463]	0.6439
betaplasma	0.081	[0.069;1.173]	0.2419
graisses:retinol[, "fibres"]	-0.128	[0.07;-1.846]	0.0659



```
rm(mod.tmp)
rm(res.tmp)
```

Table 71: Régression linéaire multiple avec interaction entre graisses et alcool

	Bêta	IC	p
(Intercept)	455.735	[101.877;4.473]	0
age	2.666	[0.889;2.997]	0.003
sexeFemmes	-89.039	[37.774;-2.357]	0.0191
tabacAutrefois	47.419	[25.412;1.866]	0.063
tabacFumeur	6.476	[36.798;0.176]	0.8604
bmi	2.269	[1.994;1.138]	0.2562
vitamineSouvent	35.11	[28.235;1.243]	0.2147
vitaminePas-souvent	27.639	[30.144;0.917]	0.3599
calories	0.081	[0.06;1.338]	0.1821
graisses	-1.054	[0.954;-1.106]	0.2697
fibres	-4.554	[3.37;-1.352]	0.1775
alcool	15.896	[5.289;3.006]	0.0029
cholesterol	-0.108	[0.13;-0.828]	0.4082
betadiet	-0.004	[0.009;-0.412]	0.6806
retdiet	-0.008	[0.022;-0.361]	0.7187
retplasma	0.065	[0.069;0.945]	0.3455
graisses:retinol[, "alcool"]	-0.113	[0.033;-3.392]	8e-04

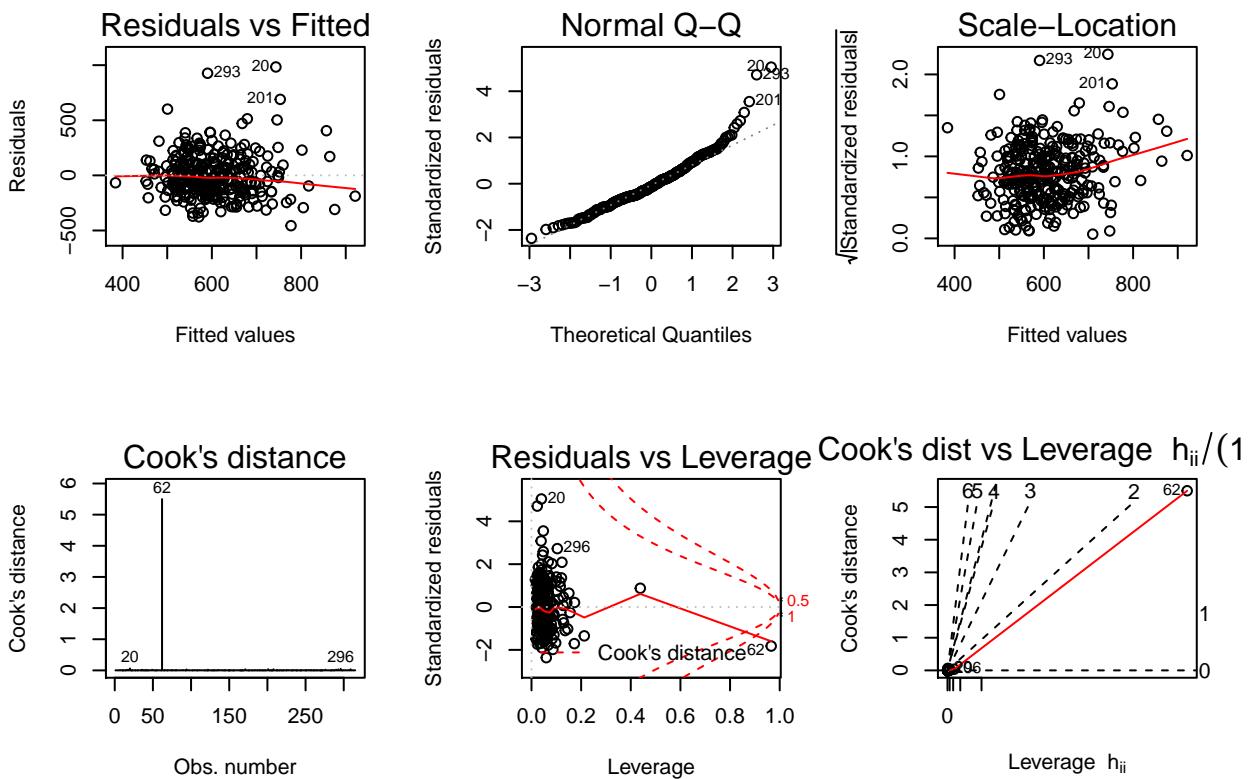
```

mod.tmp = lm(retplasma ~ . -retplasma + graisses*retinol[, "alcool"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et alcool", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

## Warning in sqrt(crit * p * (1 - hh)/hh): production de NaN
## Warning in sqrt(crit * p * (1 - hh)/hh): production de NaN

```



```

rm(mod.tmp)
rm(res.tmp)

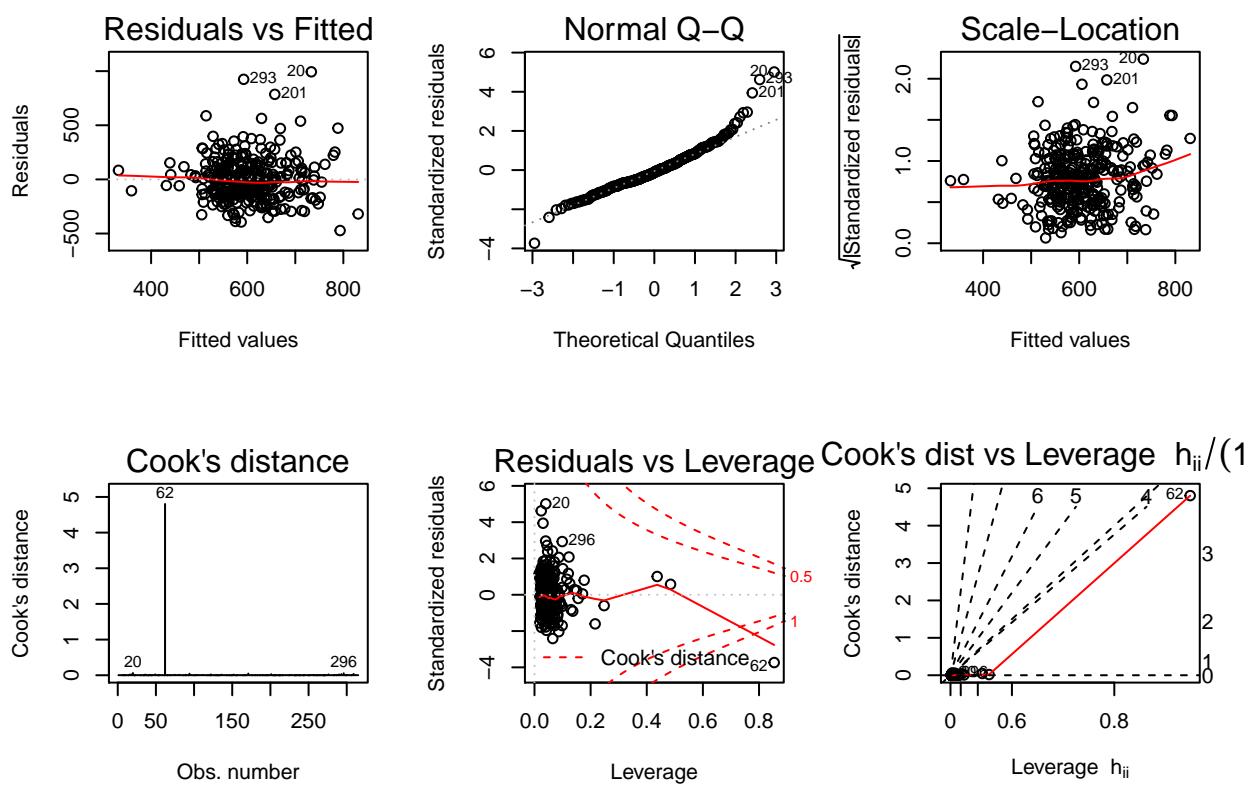
mod.tmp = lm(retplasma ~ . -retplasma + graisses*retinol[, "cholesterol"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et cholesterol", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 72: Régression linéaire multiple avec interaction entre graisses et cholestérol

	Bêta	IC	p
(Intercept)	490.093	[112.233;4.367]	0
age	2.424	[0.901;2.689]	0.0076
sexeFemmes	-96.199	[38.525;-2.497]	0.0131
tabacAutrefois	59.001	[25.575;2.307]	0.0217
tabacFumeur	-0.527	[37.383;-0.014]	0.9888
bmi	1.551	[2.018;0.768]	0.4428
vitamineSouvent	24.319	[28.525;0.853]	0.3946
vitaminePas-souvent	21.533	[30.663;0.702]	0.4831
calories	0.067	[0.061;1.096]	0.2738
graisses	-0.569	[1.126;-0.506]	0.6135
fibres	-4.236	[3.428;-1.236]	0.2176
alcool	-1.105	[1.507;-0.733]	0.4642
cholesterol	0.108	[0.215;0.504]	0.6146
betadiet	-0.004	[0.009;-0.423]	0.6725
retdiet	-0.011	[0.022;-0.481]	0.6307
betaplasma	0.079	[0.07;1.137]	0.2563
graisses:retinol[, "cholesterol"]	-0.002	[0.002;-1.148]	0.2518



```
rm(mod.tmp)
rm(res.tmp)
```

Table 73: Régression linéaire multiple avec interaction entre graisses et betadiet

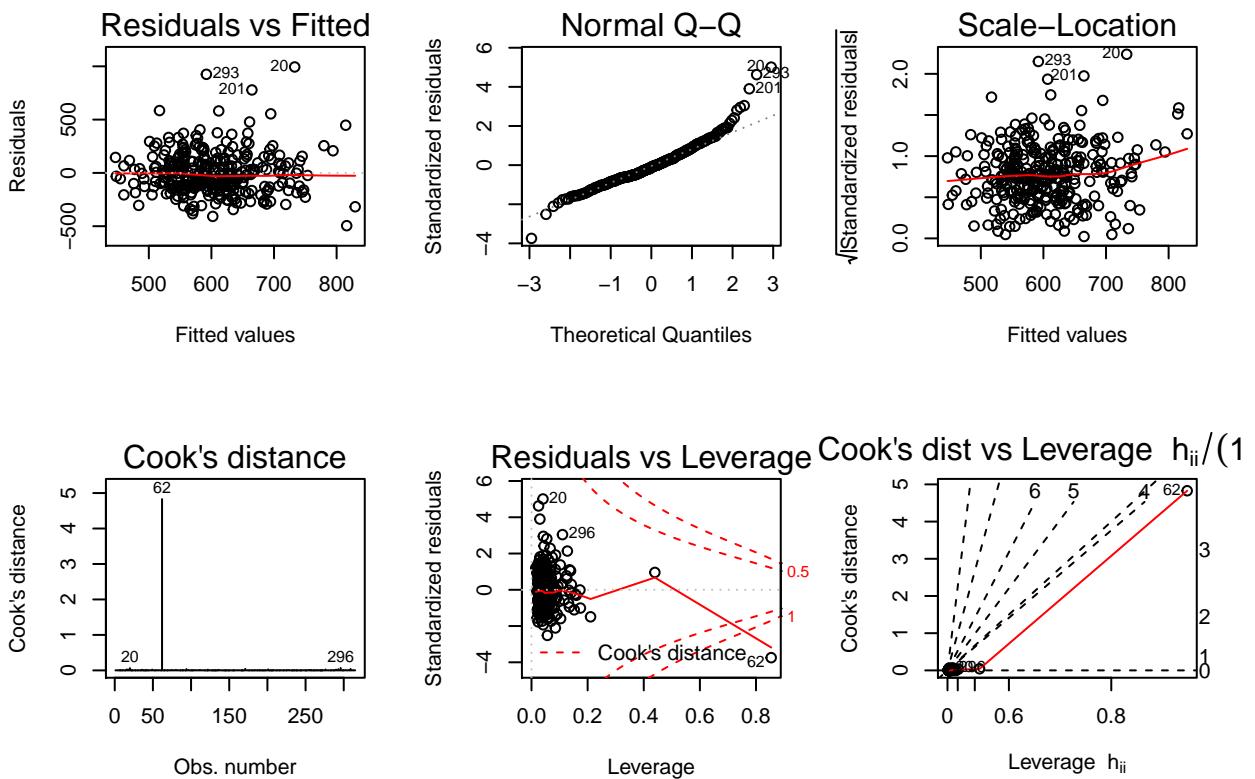
	Bêta	IC	p
(Intercept)	509.89	[110.045;4.633]	0
age	2.403	[0.902;2.663]	0.0082
sexeFemmes	-98.508	[38.449;-2.562]	0.0109
tabacAutrefois	62.598	[25.683;2.437]	0.0154
tabacFumeur	0.198	[37.413;0.005]	0.9958
bmi	1.335	[2.01;0.664]	0.5072
vitamineSouvent	20.818	[28.465;0.731]	0.4651
vitaminePas-souvent	21.521	[30.726;0.7]	0.4842
calories	0.068	[0.061;1.102]	0.2712
graisses	-0.702	[1.151;-0.61]	0.5425
fibres	-4.312	[3.43;-1.257]	0.2097
alcool	-1.251	[1.498;-0.835]	0.4044
cholesterol	-0.09	[0.133;-0.676]	0.4993
betadiet	0.015	[0.023;0.656]	0.5121
retdiet	-0.011	[0.022;-0.471]	0.6382
betaplasma	0.078	[0.07;1.109]	0.2684
graisses:retinol[, "betadiet"]	0	[0;-0.849]	0.3966

```

mod.tmp = lm(retplasma ~ . -retplasma + graisses*retinol[, "betadiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et betadiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

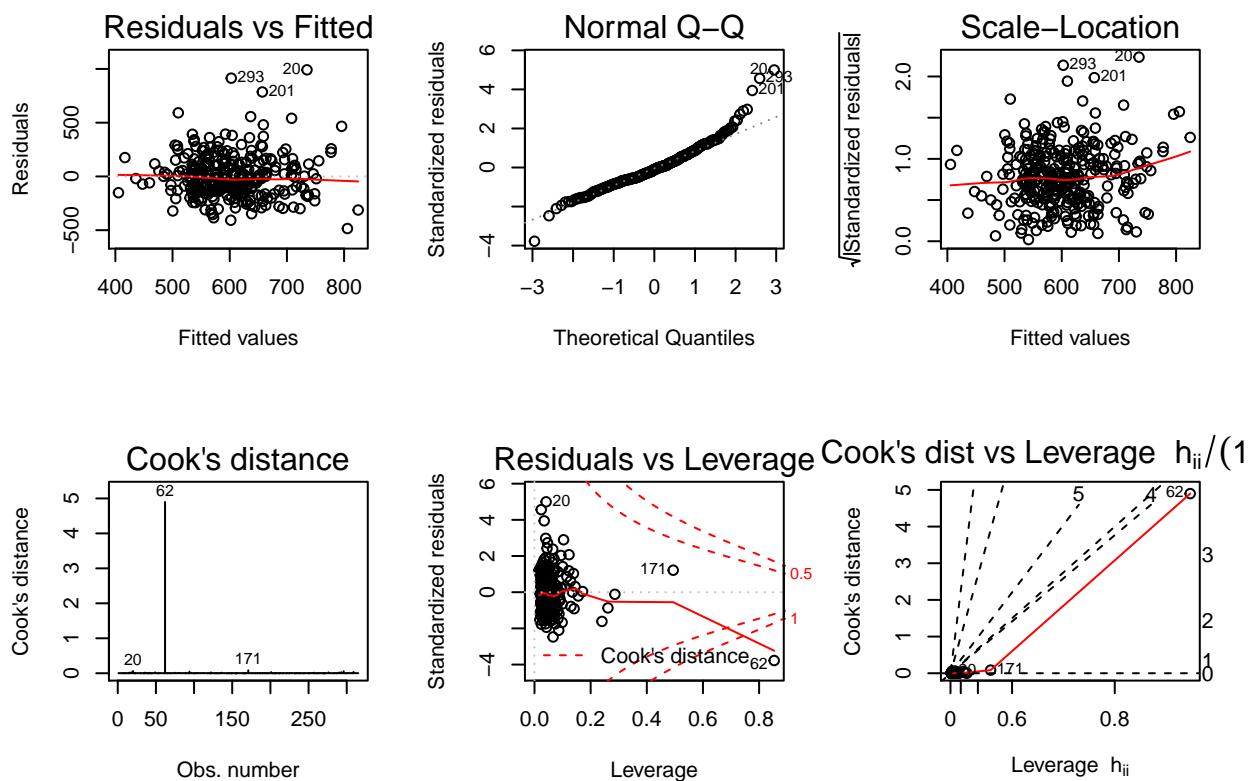
mod.tmp = lm(retplasma ~ . -retplasma + graisses*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et retdiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 74: Régression linéaire multiple avec interaction entre graisses et retdiet

	Bêta	IC	p
(Intercept)	528.901	[109.907;4.812]	0
age	2.39	[0.904;2.644]	0.0086
sexeFemmes	-100.22	[38.446;-2.607]	0.0096
tabacAutrefois	59.948	[25.622;2.34]	0.02
tabacFumeur	-0.2	[37.468;-0.005]	0.9957
bmi	1.409	[2.022;0.697]	0.4864
vitamineSouvent	21.428	[28.479;0.752]	0.4524
vitaminePas-souvent	23.243	[30.683;0.758]	0.4493
calories	0.065	[0.062;1.045]	0.2969
graisses	-0.944	[1.165;-0.81]	0.4185
fibres	-4.237	[3.445;-1.23]	0.2197
alcool	-1.227	[1.518;-0.809]	0.4193
cholesterol	-0.084	[0.133;-0.631]	0.5284
betadiet	-0.003	[0.009;-0.338]	0.7359
retdiet	0.013	[0.057;0.229]	0.8191
betaplasma	0.083	[0.07;1.185]	0.2369
graisses:retinol[, "retdiet"]	0	[0.001;-0.443]	0.658



```
rm(mod.tmp)
rm(res.tmp)
```

Table 75: Régression linéaire multiple avec interaction entre graisses et betaplasma

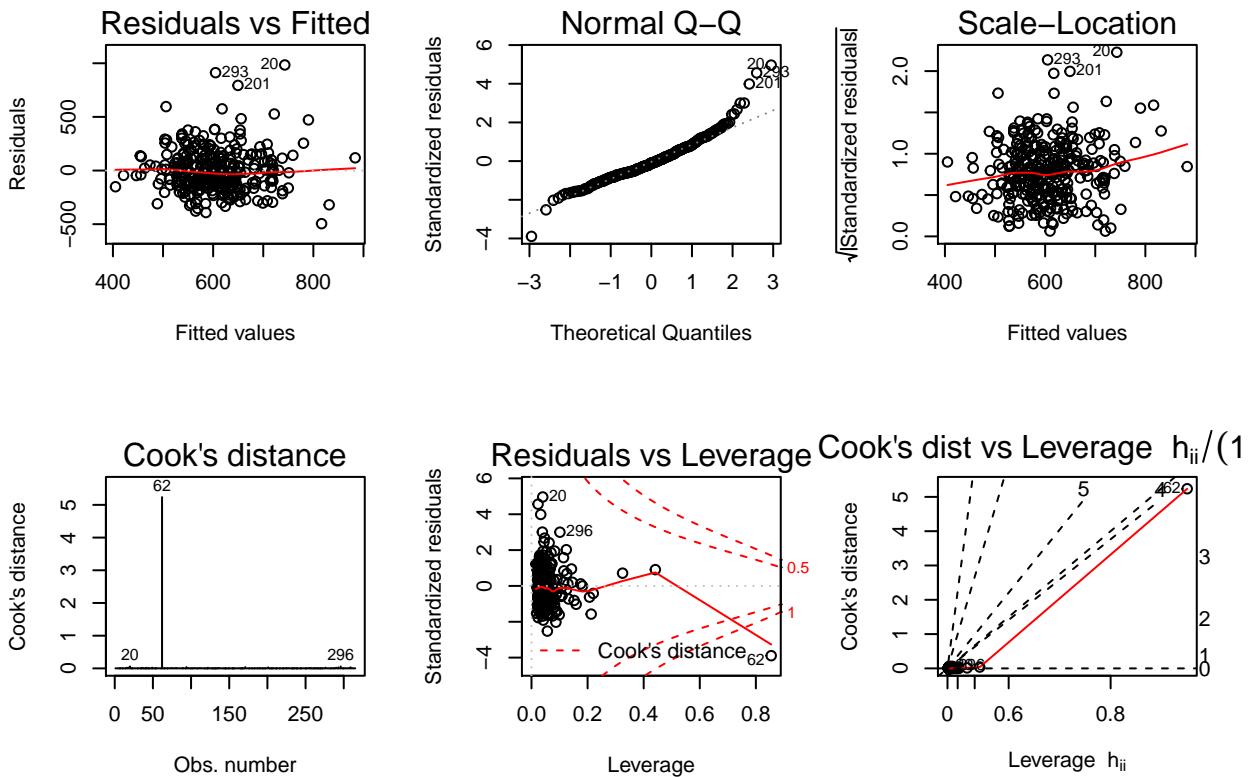
	Bêta	IC	p
(Intercept)	578.509	[102.602;5.638]	0
age	2.39	[0.901;2.652]	0.0084
sexeFemmes	-101.039	[38.217;-2.644]	0.0086
tabacAutrefois	62.136	[25.569;2.43]	0.0157
tabacFumeur	2.26	[37.397;0.06]	0.9519
bmi	1.376	[2.008;0.686]	0.4936
vitamineSouvent	21.886	[28.417;0.77]	0.4418
vitaminePas-souvent	22.053	[30.634;0.72]	0.4722
calories	0.077	[0.062;1.245]	0.214
graisses	-1.839	[1.091;-1.686]	0.0928
fibres	-4.766	[3.441;-1.385]	0.1671
alcool	-1.372	[1.493;-0.919]	0.359
cholesterol	-0.066	[0.133;-0.496]	0.6203
betadiet	-0.003	[0.009;-0.288]	0.7738
rettdiet	-0.009	[0.022;-0.42]	0.6748
betaplasma	-0.106	[0.171;-0.622]	0.5347
graisses:retinol[, "betaplasma"]	0.003	[0.002;1.213]	0.2261

```

mod.tmp = lm(retplasma ~ . -retplasma + graisses*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et betaplasma",col.names
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

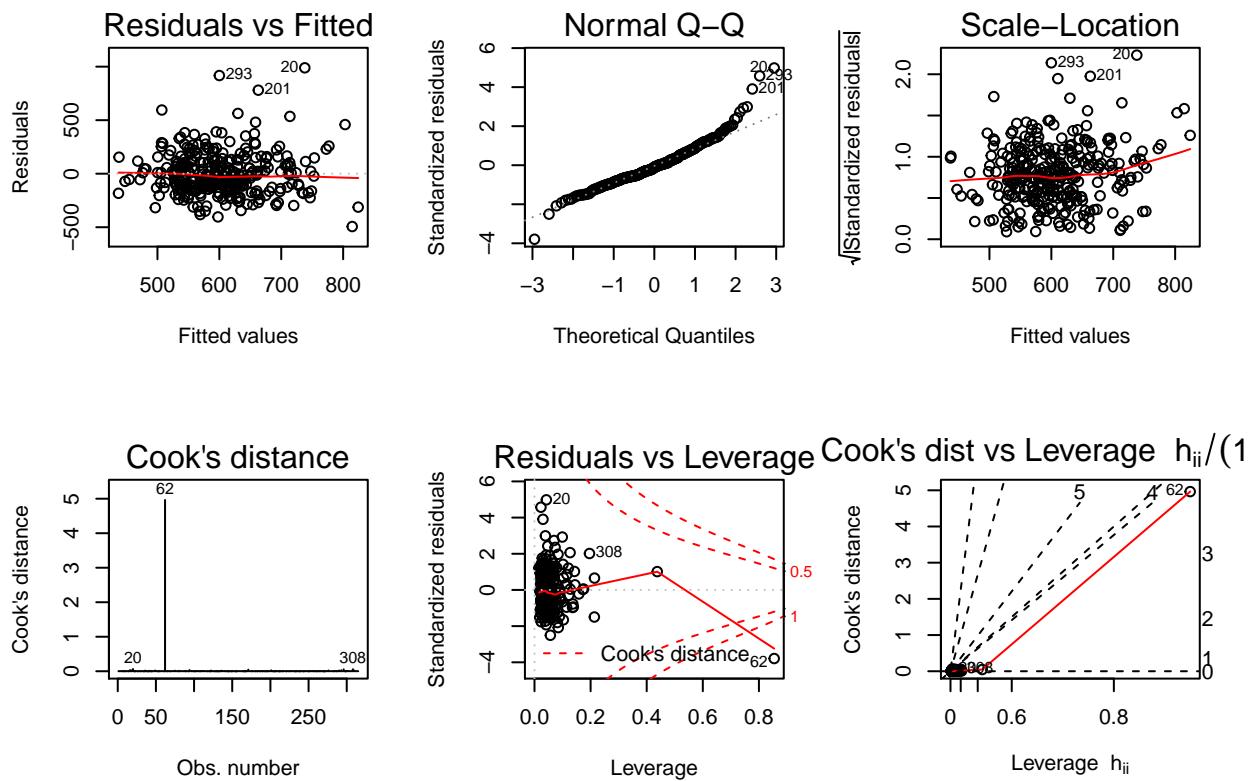
5.3.8 Avec les fibres

```
mod.tmp = lm(retplasma ~ . -retplasma + fibres*retinol[, "alcool"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre fibres et alcool", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)
```

Table 76: Régression linéaire multiple avec interaction entre fibres et alcool

	Bêta	IC	p
(Intercept)	548.978	[100;5.49]	0
age	2.42	[0.914;2.646]	0.0086
sexeFemmes	-101.471	[38.491;-2.636]	0.0088
tabacAutrefois	60.424	[25.636;2.357]	0.0191
tabacFumeur	0.436	[37.466;0.012]	0.9907
bmi	1.327	[2.016;0.658]	0.5109
vitamineSouvent	21.63	[28.502;0.759]	0.4485
vitaminePas-souvent	23.362	[30.715;0.761]	0.4475
calories	0.07	[0.063;1.123]	0.2623
graisses	-1.239	[0.98;-1.264]	0.2071
fibres	-4.472	[3.738;-1.196]	0.2325
alcool	-1.782	[6.518;-0.273]	0.7848
cholesterol	-0.086	[0.133;-0.651]	0.5153
betadiet	-0.003	[0.009;-0.323]	0.7469
rettdiet	-0.01	[0.022;-0.458]	0.6472
betaplasma	0.084	[0.07;1.196]	0.2325
fibres:retinol[, "alcool"]	0.038	[0.546;0.07]	0.9445



```
rm(mod.tmp)
rm(res.tmp)
```

Table 77: Régression linéaire multiple avec interaction entre fibres et cholesterol

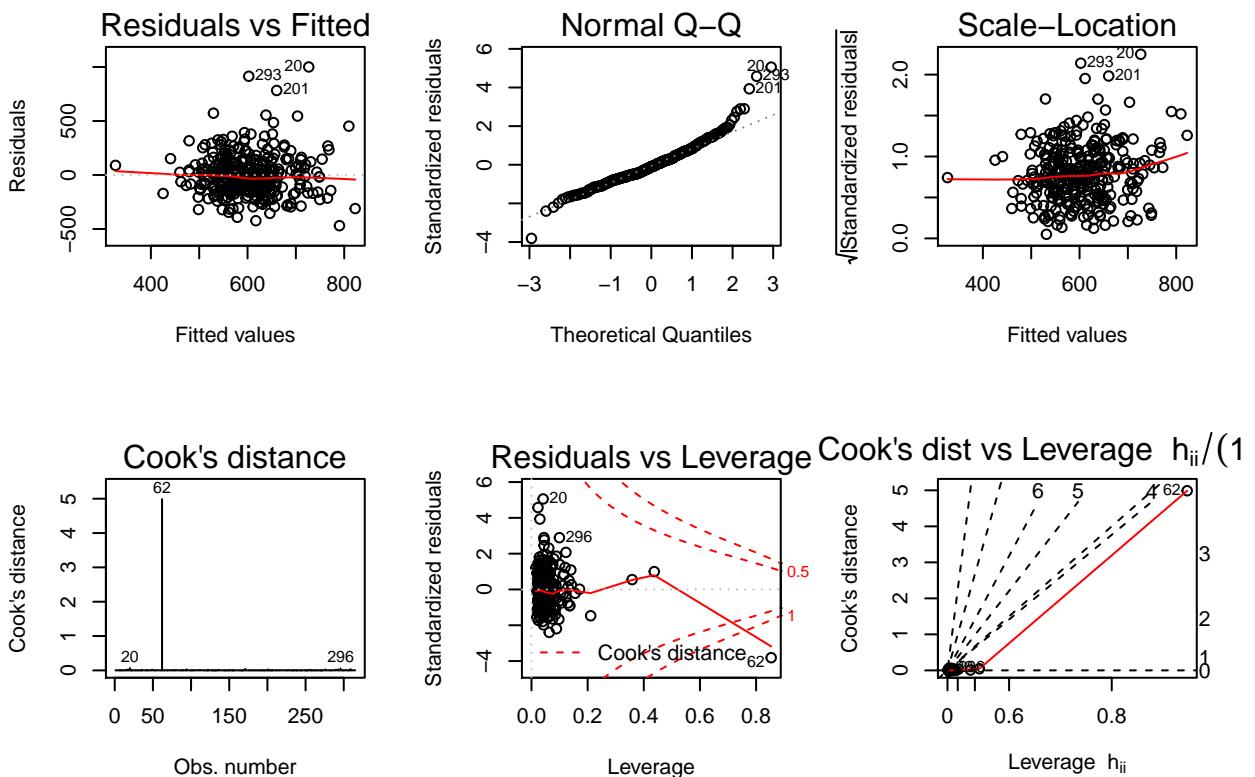
	Bêta	IC	p
(Intercept)	446.175	[121.593;3.669]	3e-04
age	2.438	[0.9;2.708]	0.0072
sexeFemmes	-89.394	[39.072;-2.288]	0.0228
tabacAutrefois	63.525	[25.585;2.483]	0.0136
tabacFumeur	-3.747	[37.425;-0.1]	0.9203
bmi	1.436	[2.006;0.716]	0.4747
vitamineSouvent	23.143	[28.403;0.815]	0.4158
vitaminePas-souvent	22.42	[30.587;0.733]	0.4641
calories	0.071	[0.061;1.16]	0.2469
graisses	-1.138	[0.969;-1.174]	0.2412
fibres	1.788	[5.394;0.332]	0.7405
alcool	-1.443	[1.493;-0.967]	0.3345
cholesterol	0.282	[0.282;1]	0.3183
betadiet	-0.002	[0.009;-0.255]	0.7992
retdiet	-0.009	[0.022;-0.403]	0.6873
betaplasma	0.078	[0.07;1.127]	0.2609
fibres:retinol[, "cholesterol"]	-0.029	[0.019;-1.477]	0.1408

```

mod.tmp = lm(retplasma ~ . -retplasma + fibres*retinol[, "cholesterol"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre fibres et cholesterol",col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

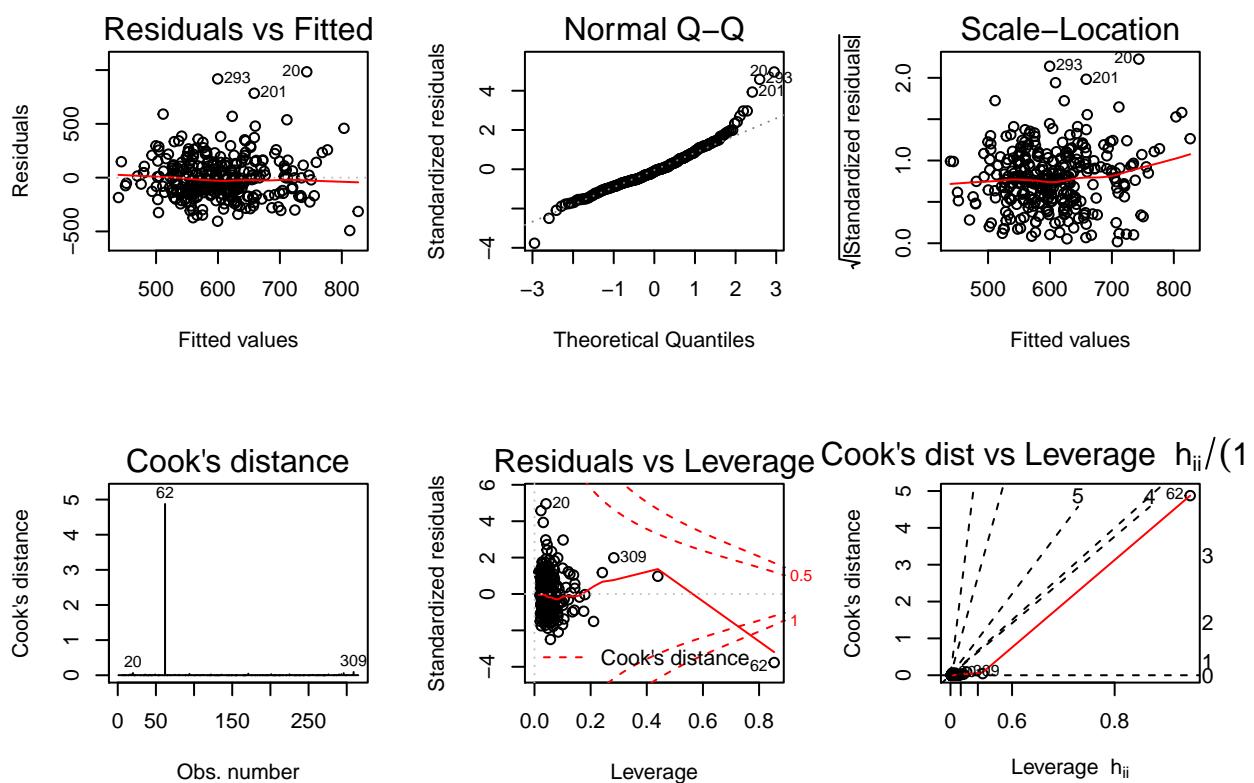
mod.tmp = lm(retplasma ~ . -retplasma + fibres*retinol[, "betadiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre fibres et betadiet", col.names = c
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 78: Régression linéaire multiple avec interaction entre fibres et betadiet

	Bêta	IC	p
(Intercept)	575.91	[108.722;5.297]	0
age	2.419	[0.903;2.68]	0.0078
sexeFemmes	-102.375	[38.296;-2.673]	0.0079
tabacAutrefois	60.404	[25.581;2.361]	0.0189
tabacFumeur	-1.967	[37.622;-0.052]	0.9583
bmi	1.358	[2.012;0.675]	0.5003
vitamineSouvent	21.362	[28.47;0.75]	0.4536
vitaminePas-souvent	22.41	[30.705;0.73]	0.466
calories	0.067	[0.062;1.087]	0.278
graisses	-1.188	[0.972;-1.223]	0.2225
fibres	-6.368	[4.699;-1.355]	0.1764
alcool	-1.278	[1.499;-0.853]	0.3944
cholesterol	-0.086	[0.133;-0.648]	0.5174
betadiet	-0.015	[0.022;-0.698]	0.4856
retdiet	-0.009	[0.023;-0.398]	0.691
betaplasma	0.078	[0.07;1.106]	0.2695
fibres:retinol[, "betadiet"]	0.001	[0.001;0.623]	0.5339



```
rm(mod.tmp)
rm(res.tmp)
```

Table 79: Régression linéaire multiple avec interraction entre fibres et retdiet

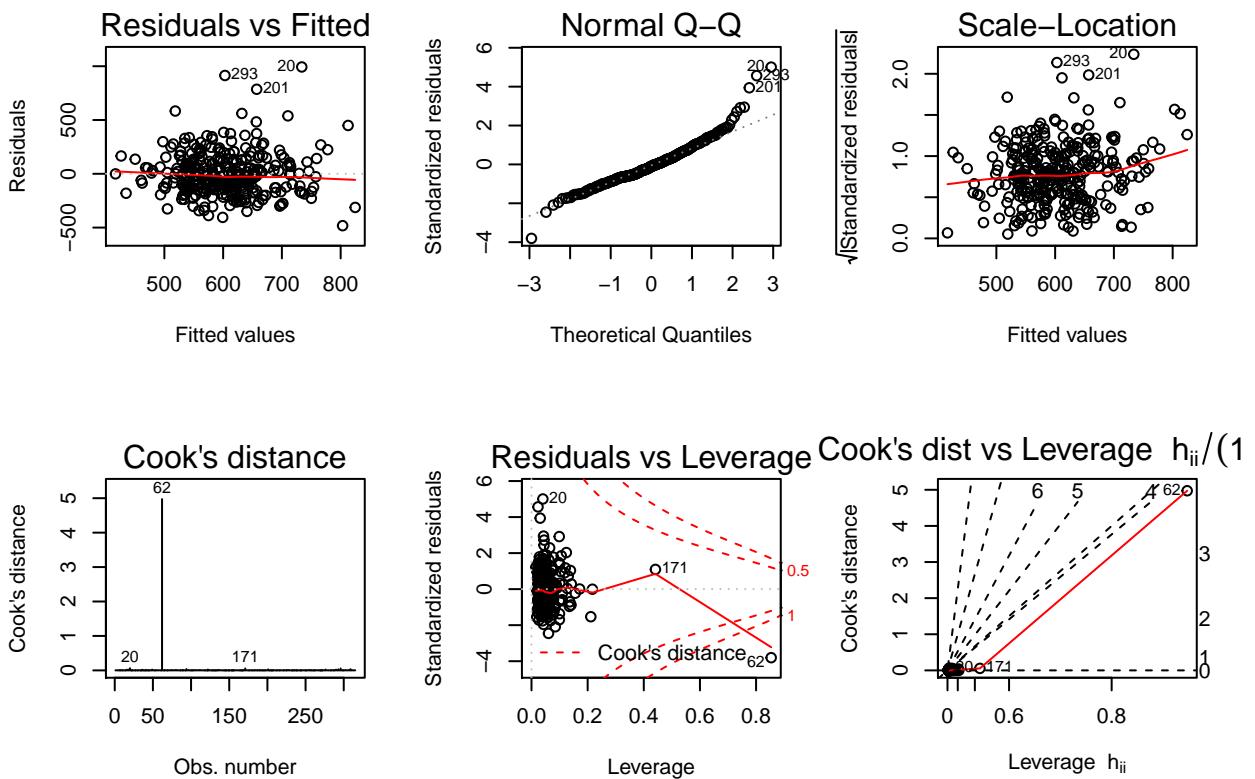
	Bêta	IC	p
(Intercept)	499.965	[114.311;4.374]	0
age	2.328	[0.907;2.568]	0.0107
sexeFemmes	-101.889	[38.257;-2.663]	0.0082
tabacAutrefois	60.179	[25.567;2.354]	0.0192
tabacFumeur	-1.572	[37.473;-0.042]	0.9666
bmi	1.455	[2.015;0.722]	0.4711
vitamineSouvent	20.191	[28.491;0.709]	0.4791
vitaminePas-souvent	23.322	[30.653;0.761]	0.4474
calories	0.063	[0.062;1.022]	0.3075
graisses	-1.109	[0.979;-1.134]	0.2578
fibres	-0.135	[5.892;-0.023]	0.9818
alcool	-1.262	[1.497;-0.843]	0.4
cholesterol	-0.09	[0.133;-0.682]	0.4958
betadiet	-0.003	[0.009;-0.363]	0.7168
retdiet	0.06	[0.083;0.727]	0.4678
betaplasma	0.082	[0.07;1.177]	0.2403
fibres:retinol[, "retdiet"]	-0.005	[0.006;-0.884]	0.3775

```

mod.tmp = lm(retplasma ~ . -retplasma + fibres*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interraction entre fibres et retdiet", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

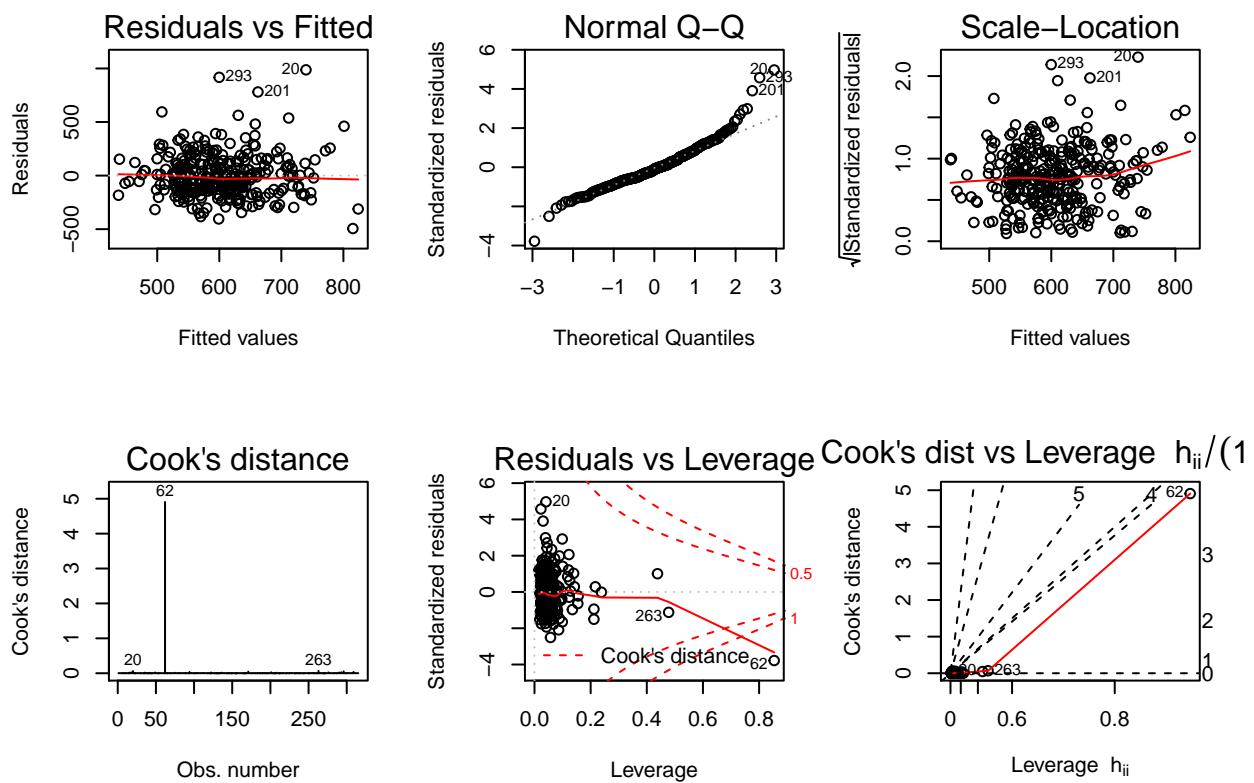
mod.tmp = lm(retplasma ~ . -retplasma + fibres*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre fibres et betaplasma", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 80: Régression linéaire multiple avec interaction entre fibres et betaplasma

	Bêta	IC	p
(Intercept)	553.661	[104.739;5.286]	0
age	2.41	[0.903;2.668]	0.008
sexeFemmes	-101.855	[38.315;-2.658]	0.0083
tabacAutrefois	60.939	[25.762;2.365]	0.0186
tabacFumeur	0.196	[37.477;0.005]	0.9958
bmi	1.306	[2.014;0.648]	0.5172
vitamineSouvent	21.6	[28.486;0.758]	0.4489
vitaminePas-souvent	23.621	[30.784;0.767]	0.4435
calories	0.069	[0.062;1.125]	0.2615
graisses	-1.223	[0.971;-1.259]	0.209
fibres	-4.698	[4.131;-1.137]	0.2564
alcool	-1.337	[1.497;-0.893]	0.3724
cholesterol	-0.087	[0.133;-0.654]	0.5133
betadiet	-0.003	[0.009;-0.31]	0.7565
retdiet	-0.01	[0.023;-0.44]	0.66
betaplasma	0.065	[0.147;0.439]	0.6609
fibres:retinol[, "betaplasma"]	0.001	[0.008;0.143]	0.8863



```
rm(mod.tmp)
rm(res.tmp)
```

Table 81: Régression linéaire multiple avec interaction entre alcool et cholesterol

	Bêta	IC	p
(Intercept)	460.654	[101.266;4.549]	0
age	2.661	[0.888;2.995]	0.003
sexeFemmes	-84.946	[37.867;-2.243]	0.0256
tabacAutrefois	46.533	[25.417;1.831]	0.0681
tabacFumeur	3.976	[36.738;0.108]	0.9139
bmi	2.22	[1.99;1.115]	0.2655
vitamineSouvent	34.034	[28.158;1.209]	0.2277
vitaminePas-souvent	26.37	[30.104;0.876]	0.3818
calories	0.083	[0.06;1.379]	0.1689
graisses	-1.428	[0.953;-1.498]	0.1352
fibres	-4.478	[3.367;-1.33]	0.1845
alcool	14.104	[4.687;3.009]	0.0028
cholesterol	-0.037	[0.131;-0.285]	0.7759
betadiet	-0.004	[0.009;-0.404]	0.6863
retdiet	-0.008	[0.022;-0.38]	0.7042
betaplasma	0.064	[0.069;0.939]	0.3486
alcool:retinol[, "cholesterol"]	-0.028	[0.008;-3.469]	6e-04

5.3.9 Avec l'alcool

```

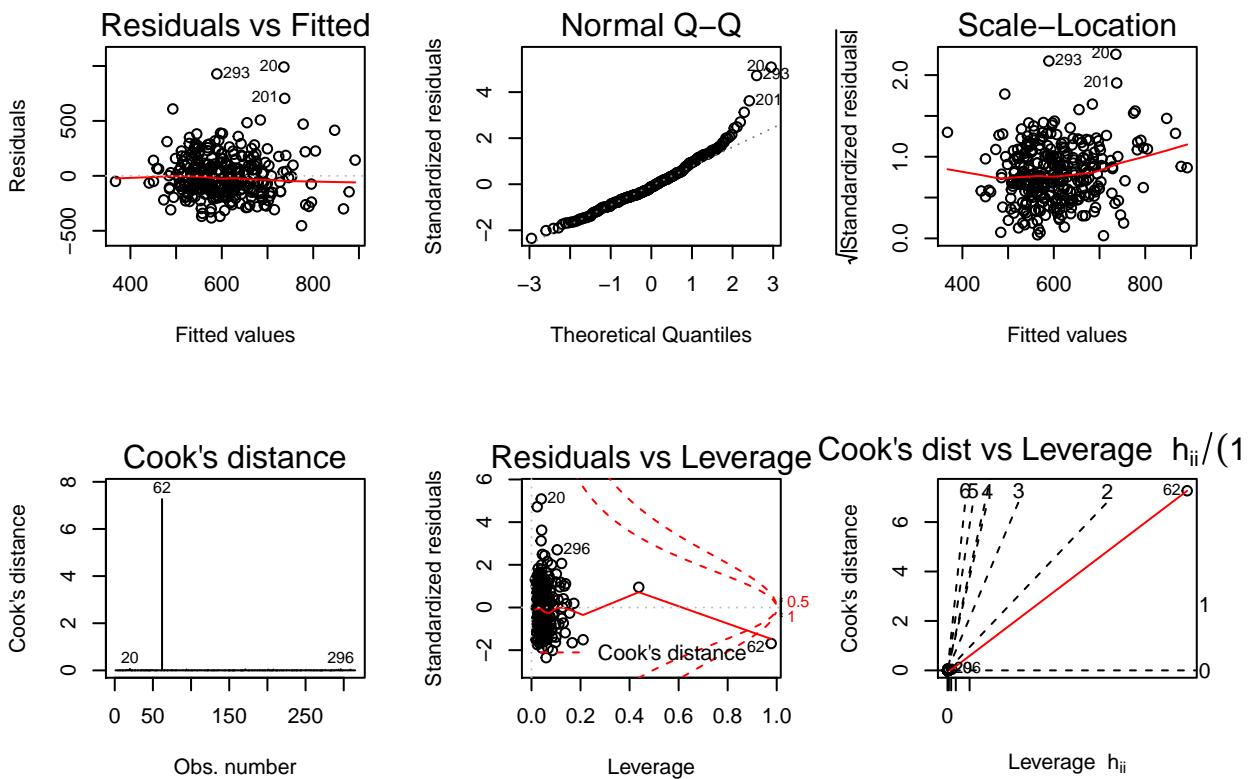
mod.tmp = lm(retplasma ~ . -retplasma + alcool*retinol[, "cholesterol"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficients),
                  round(summary(mod.tmp)$coefficients[,1],3),
                  paste0("[",round(summary(mod.tmp)$coefficients[,2],3),";",
                         round(summary(mod.tmp)$coefficients[,3],3), "]"),
                  round(summary(mod.tmp)$coefficients[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre alcool et cholesterol", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

## Warning in sqrt(crit * p * (1 - hh)/hh): production de NaN

## Warning in sqrt(crit * p * (1 - hh)/hh): production de NaN

```



```

rm(mod.tmp)
rm(res.tmp)

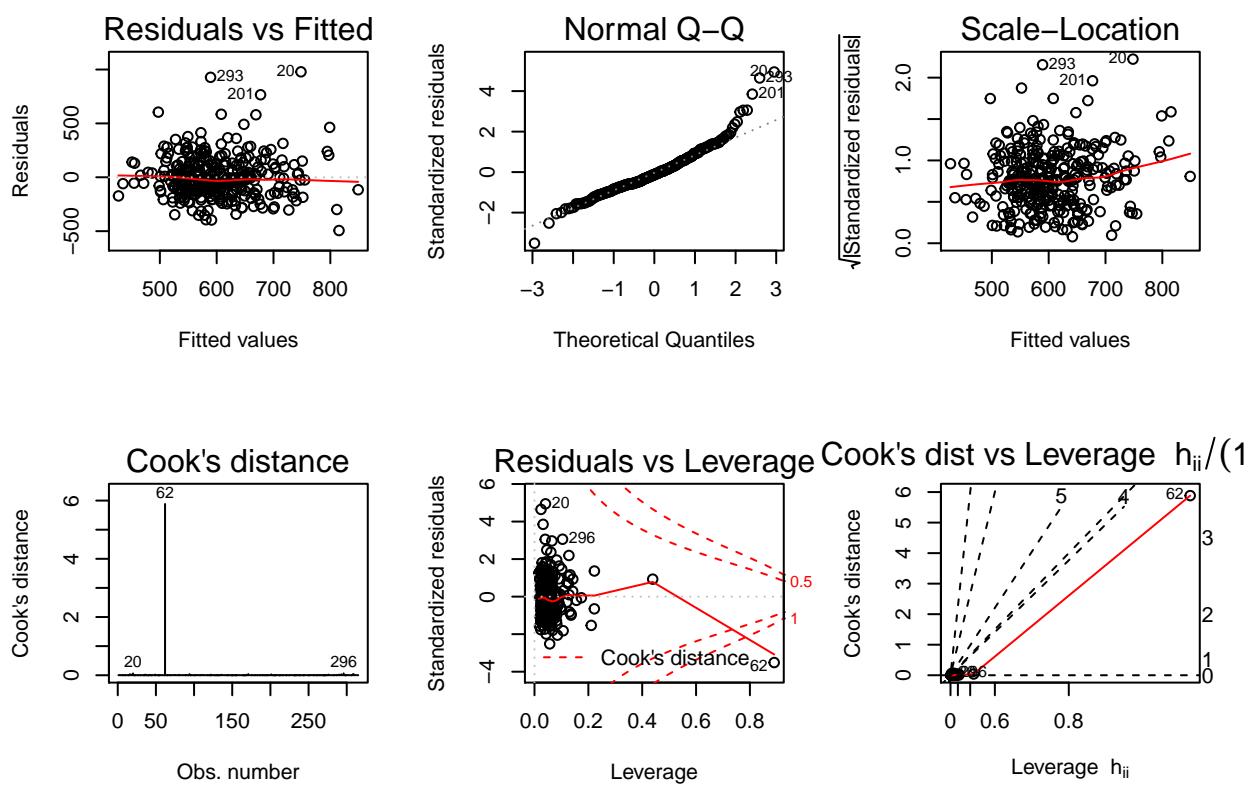
mod.tmp = lm(retplasma ~ . -retplasma + alcool*retinol[, "betadiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre alcool et betadiet", col.names = c
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 82: Régression linéaire multiple avec interaction entre alcool et betadiet

	Bêta	IC	p
(Intercept)	533.802	[100.11;5.332]	0
age	2.351	[0.901;2.61]	0.0095
sexeFemmes	-103.103	[38.175;-2.701]	0.0073
tabacAutrefois	61.427	[25.509;2.408]	0.0166
tabacFumeur	0.931	[37.319;0.025]	0.9801
bmi	1.442	[2.006;0.719]	0.4727
vitamineSouvent	23.169	[28.4;0.816]	0.4153
vitaminePas-souvent	25.027	[30.6;0.818]	0.4141
calories	0.07	[0.061;1.143]	0.254
graisses	-1.278	[0.967;-1.321]	0.1875
fibres	-4.343	[3.421;-1.27]	0.2052
alcool	4.806	[4.363;1.102]	0.2716
cholesterol	-0.084	[0.132;-0.635]	0.526
betadiet	0.004	[0.01;0.352]	0.7252
retdiet	-0.01	[0.022;-0.449]	0.6535
betaplasma	0.082	[0.069;1.18]	0.2388
alcool:retinol[, "betadiet"]	-0.002	[0.001;-1.499]	0.135



```
rm(mod.tmp)
rm(res.tmp)
```

Table 83: Régression linéaire multiple avec interaction entre alcool et retdiet

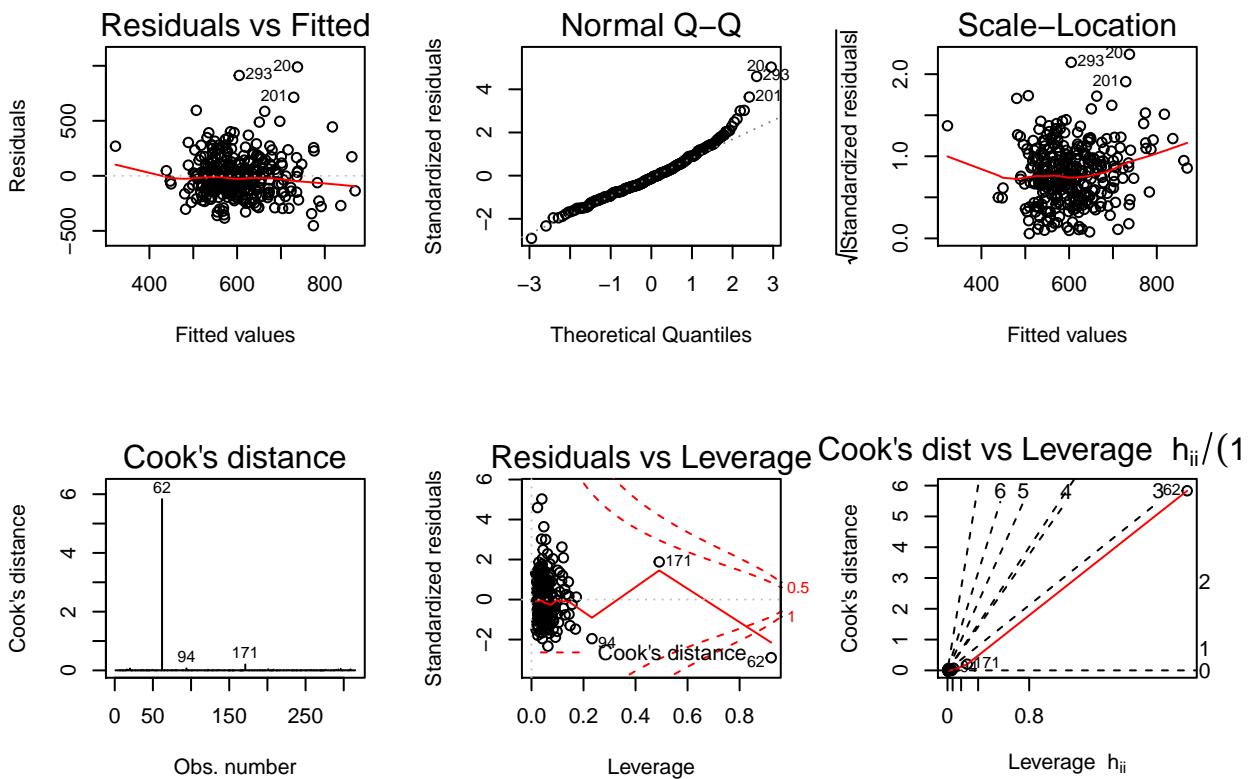
	Bêta	IC	p
(Intercept)	497.446	[101.121;4.919]	0
age	2.431	[0.894;2.719]	0.0069
sexeFemmes	-87.271	[38.365;-2.275]	0.0236
tabacAutrefois	52.408	[25.548;2.051]	0.0411
tabacFumeur	3.134	[37.094;0.084]	0.9327
bmi	1.719	[1.998;0.86]	0.3905
vitamineSouvent	20.71	[28.199;0.734]	0.4633
vitaminePas-souvent	19.981	[30.41;0.657]	0.5117
calories	0.068	[0.061;1.11]	0.268
graisses	-1.235	[0.96;-1.285]	0.1997
fibres	-4.112	[3.401;-1.209]	0.2276
alcool	10.147	[4.865;2.086]	0.0379
cholesterol	-0.113	[0.132;-0.856]	0.3924
betadiet	-0.003	[0.009;-0.366]	0.7147
retdiet	0.026	[0.027;0.969]	0.3333
betaplasma	0.076	[0.069;1.098]	0.2731
alcool:retinol[, "retdiet"]	-0.009	[0.004;-2.479]	0.0137

```

mod.tmp = lm(retplasma ~ . -retplasma + alcool*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre alcool et retdiet", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

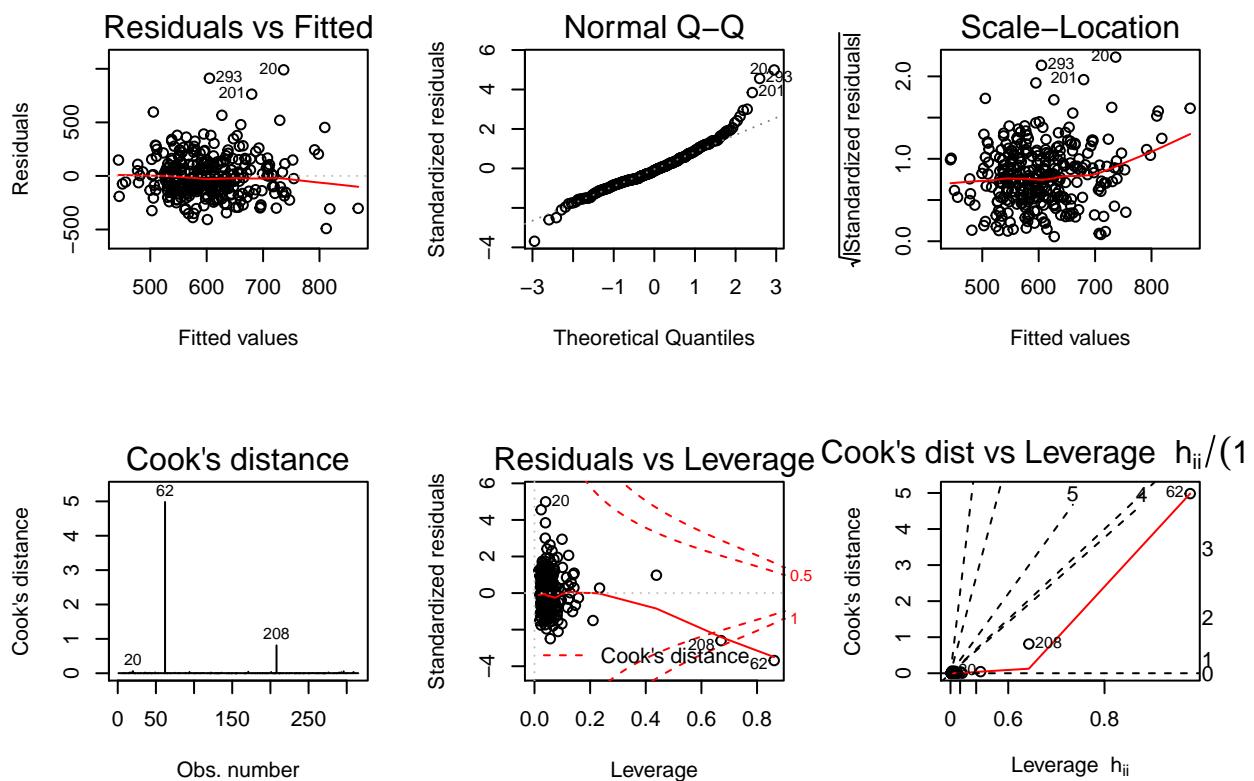
mod.tmp = lm(retplasma ~ . -retplasma + alcool*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre alcool et betaplasma", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 84: Régression linéaire multiple avec interaction entre alcool et betaplasma

	Bêta	IC	p
(Intercept)	548.474	[99.844;5.493]	0
age	2.484	[0.907;2.74]	0.0065
sexeFemmes	-101.302	[38.266;-2.647]	0.0085
tabacAutrefois	57.057	[25.901;2.203]	0.0284
tabacFumeur	-0.095	[37.418;-0.003]	0.998
bmi	1.308	[2.01;0.651]	0.5157
vitamineSouvent	22.349	[28.468;0.785]	0.4331
vitaminePas-souvent	22.709	[30.664;0.741]	0.4595
calories	0.071	[0.061;1.156]	0.2487
graisses	-1.238	[0.969;-1.277]	0.2026
fibres	-4.175	[3.438;-1.215]	0.2255
alcool	-2.459	[2.006;-1.226]	0.2212
cholesterol	-0.088	[0.132;-0.661]	0.5094
betadiet	-0.003	[0.009;-0.334]	0.7385
retdiet	-0.01	[0.022;-0.465]	0.6422
betaplasma	0.04	[0.086;0.466]	0.6417
alcool:retinol[, "betaplasma"]	0.01	[0.012;0.837]	0.4034



```
rm(mod.tmp)
rm(res.tmp)
```

Table 85: Régression linéaire multiple avec interaction entre cholesterol et betadiet

	Bêta	IC	p
(Intercept)	504.287	[105.929;4.761]	0
age	2.393	[0.901;2.656]	0.0083
sexeFemmes	-99.091	[38.265;-2.59]	0.0101
tabacAutrefois	63.979	[25.679;2.492]	0.0133
tabacFumeur	-2.028	[37.408;-0.054]	0.9568
bmi	1.347	[2.007;0.671]	0.5025
vitamineSouvent	22.886	[28.431;0.805]	0.4215
vitaminePas-souvent	21.91	[30.632;0.715]	0.475
calories	0.069	[0.061;1.123]	0.2623
graisses	-1.184	[0.968;-1.223]	0.2223
fibres	-4.502	[3.426;-1.314]	0.1899
alcool	-1.207	[1.496;-0.807]	0.4205
cholesterol	0.086	[0.19;0.449]	0.6536
betadiet	0.019	[0.02;0.968]	0.3336
retdiet	-0.011	[0.022;-0.475]	0.6351
betaplasma	0.077	[0.07;1.107]	0.2691
cholesterol:retinol[, "betadiet"]	0	[0;-1.254]	0.2108

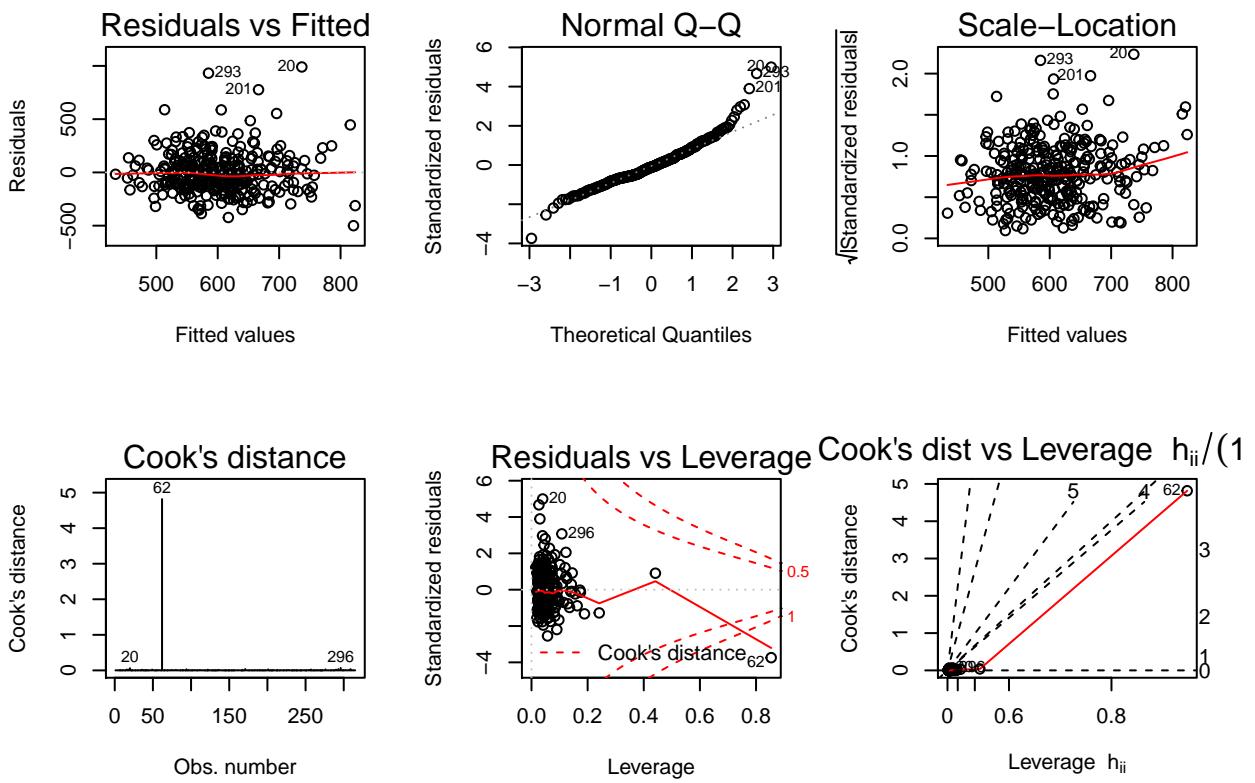
5.3.10 Avec le cholesterol

```

mod.tmp = lm(retplasma ~ . -retplasma + cholesterol*retinol[, "betadiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficients),
                  round(summary(mod.tmp)$coefficients[,1],3),
                  paste0("[",round(summary(mod.tmp)$coefficients[,2],3),";",
                         round(summary(mod.tmp)$coefficients[,3],3), "]"),
                  round(summary(mod.tmp)$coefficients[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre cholesterol et betadiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

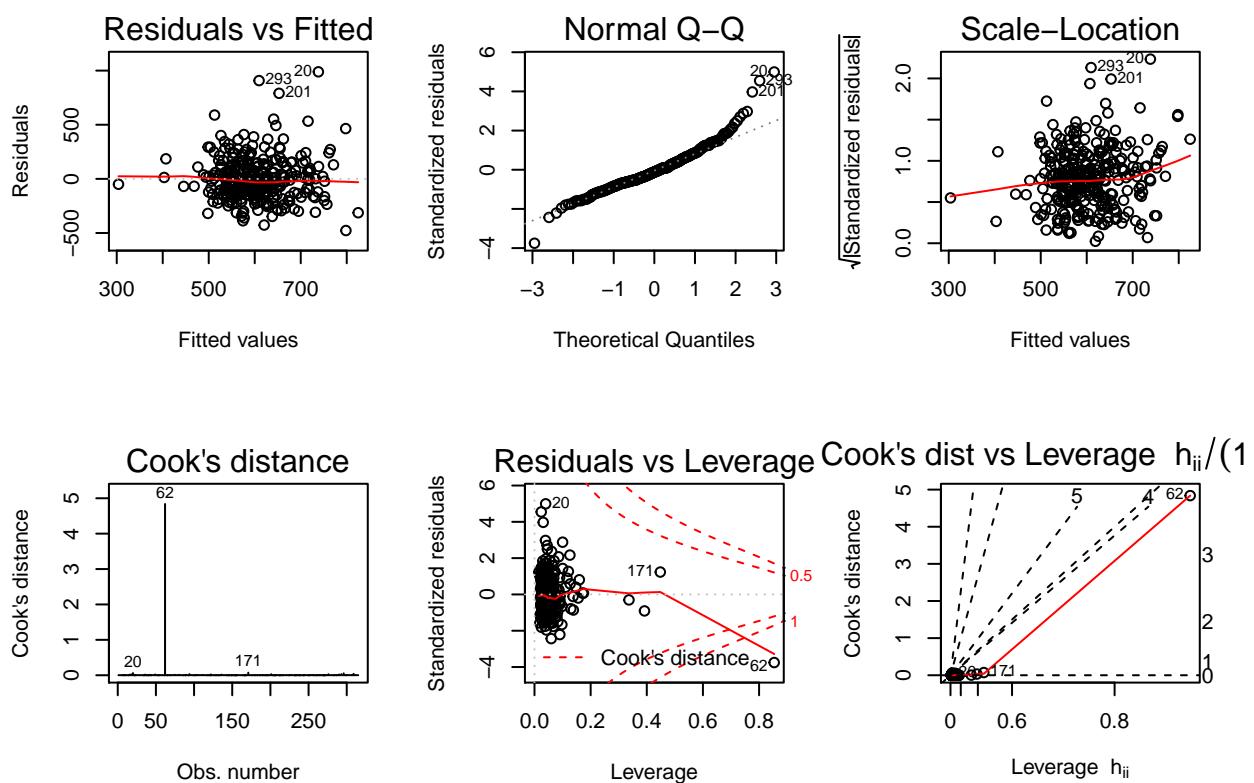
mod.tmp = lm(retplasma ~ . -retplasma + cholesterol*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre cholesterol et retdiet", col.names =
kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```

Table 86: Régression linéaire multiple avec interaction entre cholesterol et retdiet

	Bêta	IC	p
(Intercept)	511.366	[102.856;4.972]	0
age	2.373	[0.9;2.636]	0.0088
sexeFemmes	-101.501	[38.169;-2.659]	0.0083
tabacAutrefois	61.319	[25.511;2.404]	0.0168
tabacFumeur	-0.728	[37.329;-0.019]	0.9845
bmi	1.406	[2.006;0.701]	0.4839
vitamineSouvent	26.07	[28.548;0.913]	0.3619
vitaminePas-souvent	24.411	[30.591;0.798]	0.4255
calories	0.048	[0.063;0.765]	0.4446
graisses	-1.108	[0.97;-1.142]	0.2543
fibres	-3.87	[3.438;-1.126]	0.2613
alcool	-0.911	[1.519;-0.6]	0.549
cholesterol	0.091	[0.179;0.511]	0.6098
betadiet	-0.003	[0.009;-0.379]	0.7052
retdiet	0.049	[0.046;1.067]	0.2869
betaplasma	0.08	[0.069;1.157]	0.248
cholesterol:retinol[, "retdiet"]	0	[0;-1.472]	0.1421



```
rm(mod.tmp)
rm(res.tmp)
```

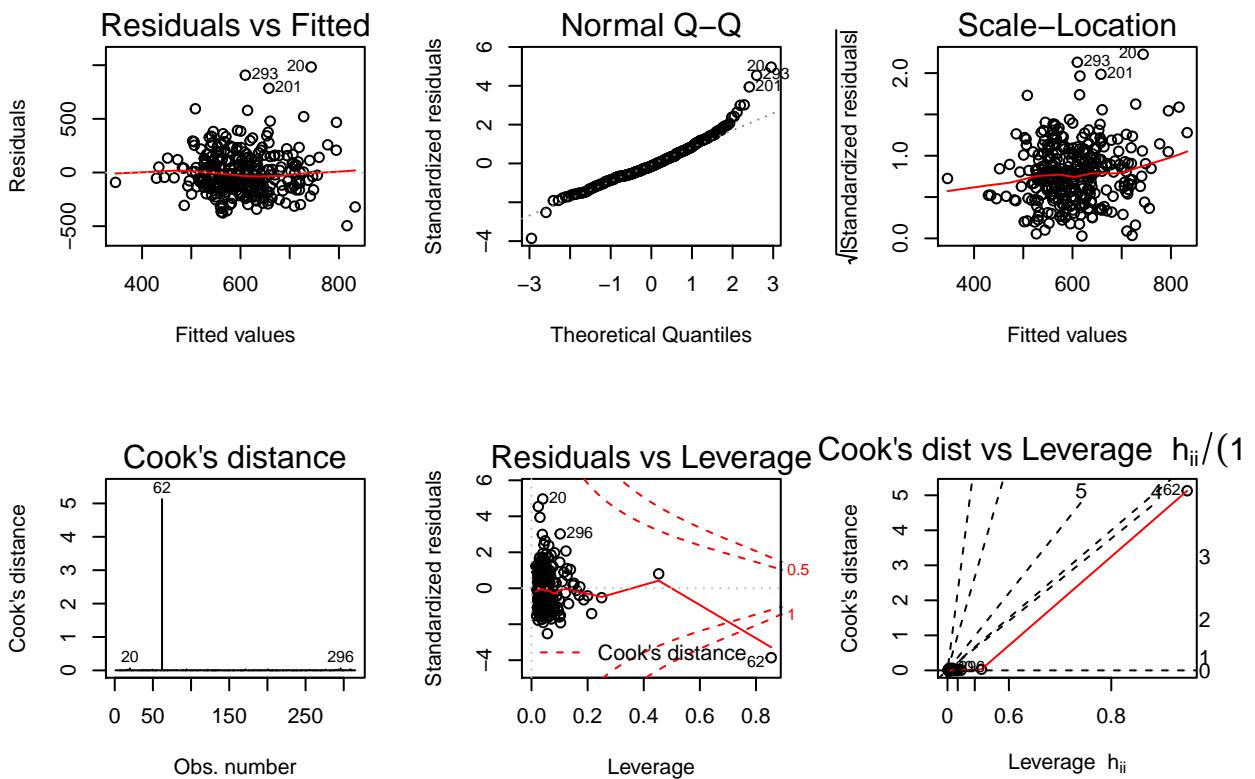
Table 87: Régression linéaire multiple avec interaction entre cholesterol et betaplasma

	Bêta	IC	p
(Intercept)	575.631	[101.619;5.665]	0
age	2.499	[0.903;2.768]	0.006
sexeFemmes	-102.036	[38.194;-2.672]	0.008
tabacAutrefois	62.546	[25.567;2.446]	0.015
tabacFumeur	1.072	[37.35;0.029]	0.9771
bmi	1.33	[2.006;0.663]	0.5079
vitamineSouvent	21.547	[28.402;0.759]	0.4487
vitaminePas-souvent	21.319	[30.637;0.696]	0.4871
calories	0.076	[0.062;1.24]	0.216
graisses	-1.353	[0.972;-1.393]	0.1648
fibres	-4.613	[3.429;-1.345]	0.1795
alcool	-1.379	[1.492;-0.924]	0.3561
cholesterol	-0.215	[0.164;-1.313]	0.1902
betadiet	-0.004	[0.009;-0.446]	0.6562
retdiet	-0.011	[0.022;-0.471]	0.638
betaplasma	-0.131	[0.175;-0.749]	0.4546
cholesterol:retinol[, "betaplasma"]	0.001	[0.001;1.332]	0.1837

```

mod.tmp = lm(retplasma ~ . -retplasma + cholesterol*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre cholesterol et betaplasma", col.names = c("Variable", "Bêta", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")
)
par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

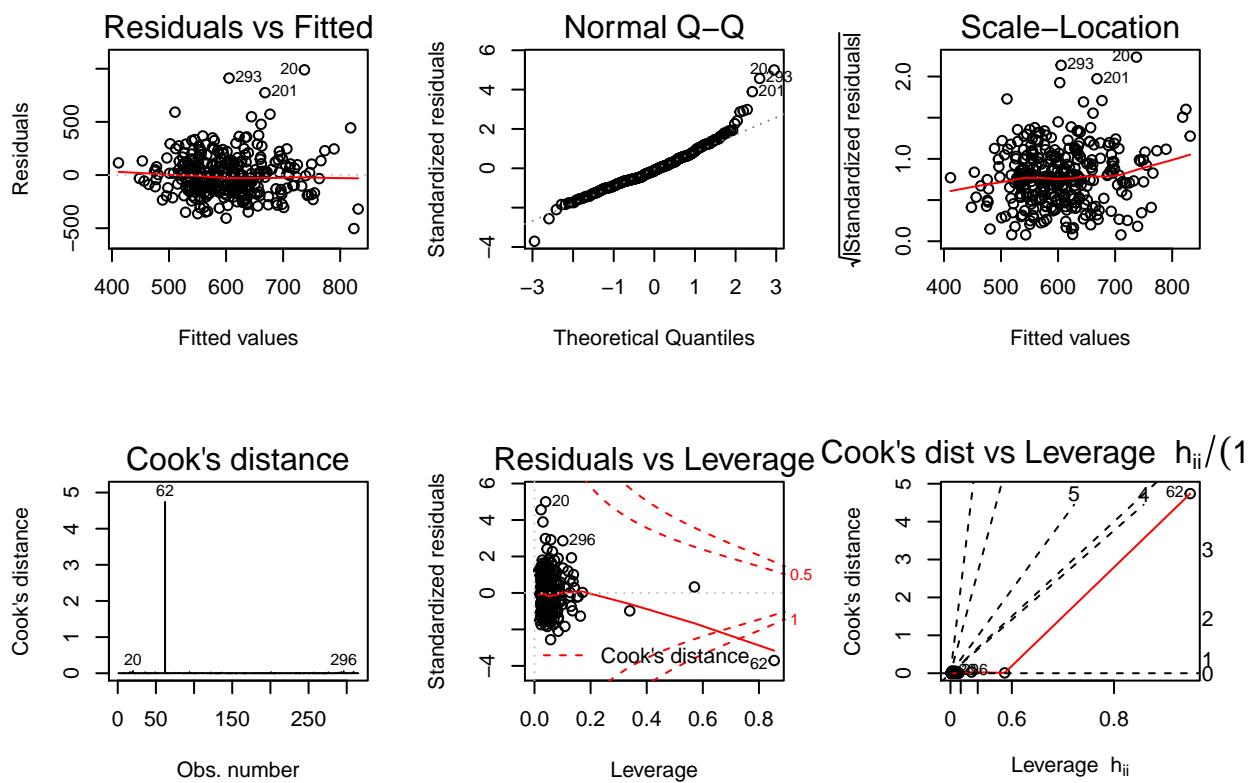
5.3.11 Avec le béta-carotène

```
mod.tmp = lm(retplasma ~ . -retplasma + betadiet*retinol[, "retdiet"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre betadiet et retdiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)
```

Table 88: Régression linéaire multiple avec interaction entre betadiet et retdiet

	Bêta	IC	p
(Intercept)	503.152	[104.242;4.827]	0
age	2.473	[0.901;2.745]	0.0064
sexeFemmes	-102.133	[38.165;-2.676]	0.0079
tabacAutrefois	64.278	[25.626;2.508]	0.0127
tabacFumeur	-1.178	[37.332;-0.032]	0.9749
bmi	1.46	[2.007;0.728]	0.4674
vitamineSouvent	21.549	[28.38;0.759]	0.4483
vitaminePas-souvent	22.232	[30.586;0.727]	0.4679
calories	0.076	[0.061;1.232]	0.2191
graisses	-1.252	[0.967;-1.295]	0.1964
fibres	-4.33	[3.421;-1.266]	0.2066
alcool	-1.432	[1.492;-0.96]	0.3379
cholesterol	-0.082	[0.132;-0.623]	0.534
betadiet	0.016	[0.016;1.029]	0.3044
retdiet	0.033	[0.037;0.909]	0.3642
betaplasma	0.077	[0.07;1.1]	0.2724
betadiet:retinol[, "retdiet"]	0	[0;-1.494]	0.1362



```
rm(mod.tmp)
rm(res.tmp)
```

Table 89: Régression linéaire multiple avec interaction entre betadiet et betaplasma

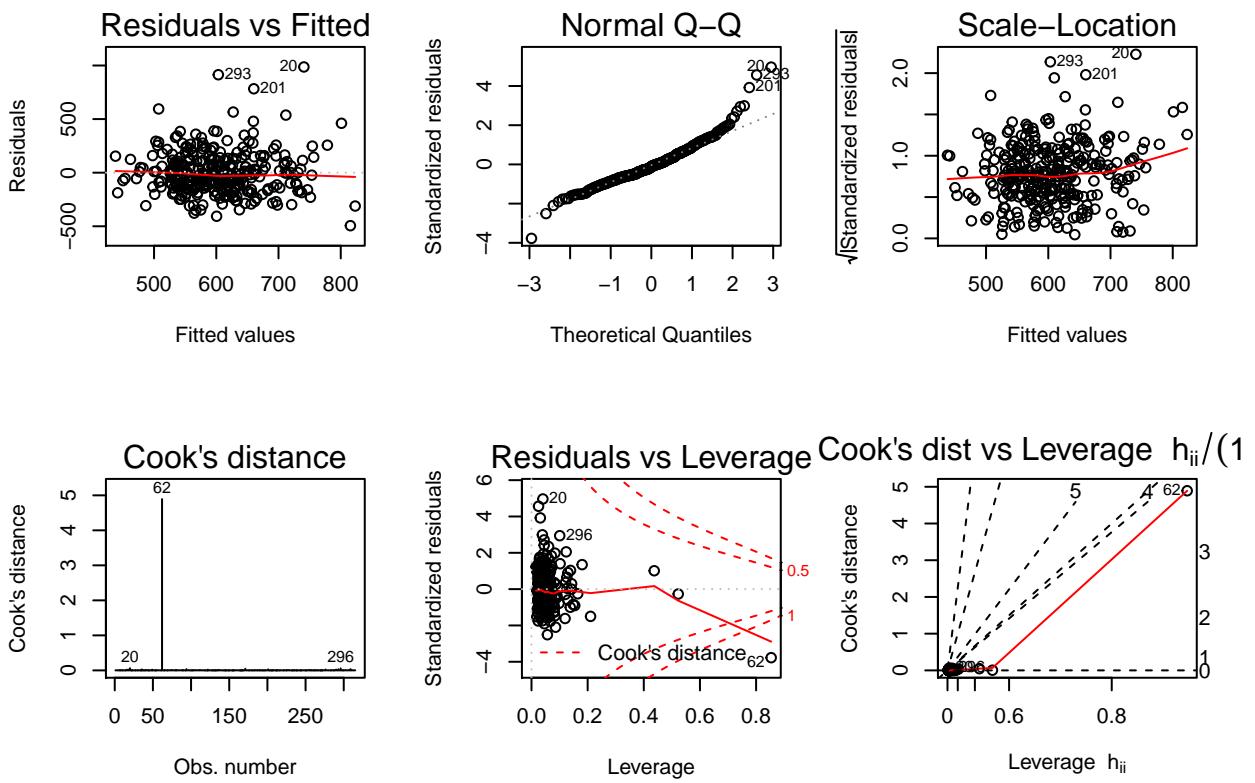
	Bêta	IC	p
(Intercept)	555.282	[101.381;5.477]	0
age	2.458	[0.913;-2.692]	0.0075
sexeFemmes	-101.873	[38.301;-2.66]	0.0082
tabacAutrefois	60.995	[25.626;2.38]	0.0179
tabacFumeur	0.214	[37.452;0.006]	0.9954
bmi	1.298	[2.013;0.645]	0.5195
vitamineSouvent	21.751	[28.485;0.764]	0.4457
vitaminePas-souvent	24.128	[30.778;0.784]	0.4337
calories	0.069	[0.062;1.116]	0.2651
graisses	-1.202	[0.973;-1.236]	0.2176
fibres	-4.415	[3.435;-1.285]	0.1997
alcool	-1.328	[1.497;-0.887]	0.3756
cholesterol	-0.09	[0.133;-0.679]	0.4979
betadiet	-0.006	[0.012;-0.474]	0.6356
retdiet	-0.01	[0.022;-0.43]	0.6673
betaplasma	0.041	[0.137;0.297]	0.7663
betadiet:retinol[, "betaplasma"]	0	[0;0.358]	0.7209

```

mod.tmp = lm(retplasma ~ . -retplasma + betadiet*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3), "]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre betadiet et betaplasma",col.names
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

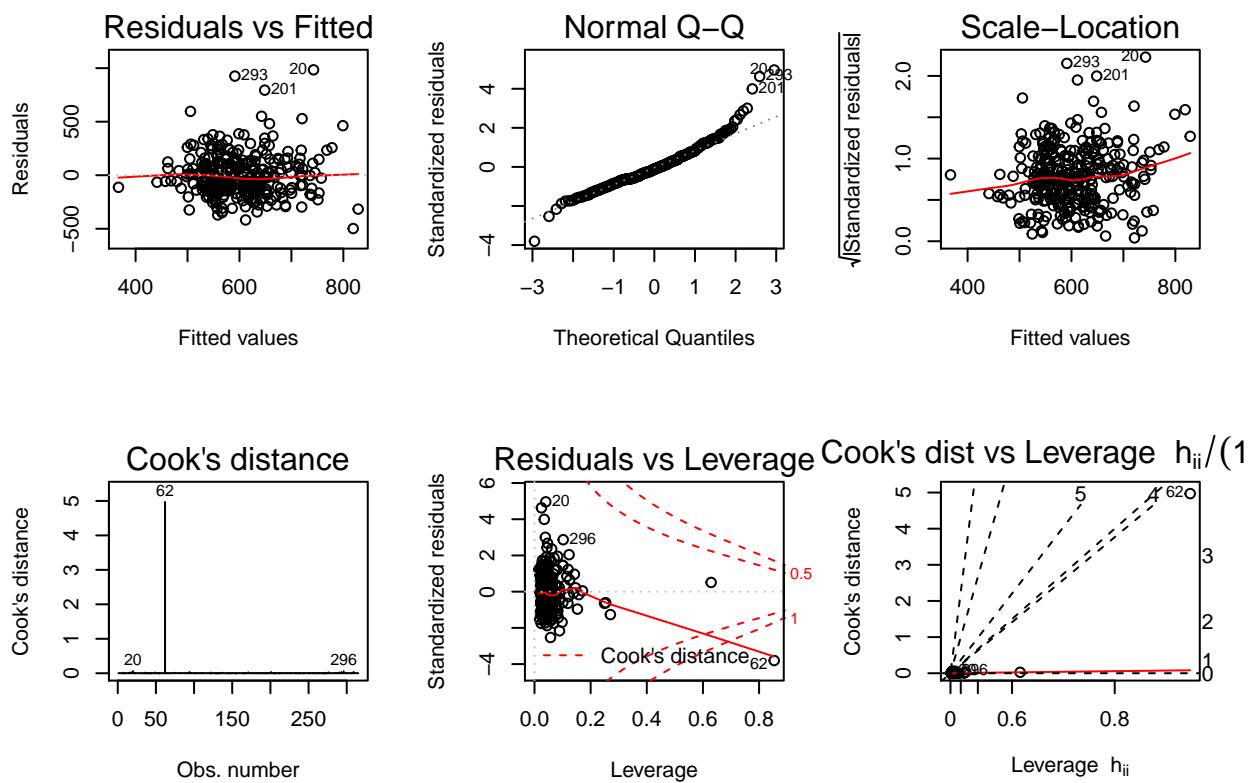
5.3.12 Avec retdiet

```
mod.tmp = lm(retplasma ~ . -retplasma + retdiet*retinol[, "betaplasma"], data = retinol)
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                 round(summary(mod.tmp)$coefficient[,1],3),
                 paste0("[",round(summary(mod.tmp)$coefficient[,2],3),";",
                        round(summary(mod.tmp)$coefficient[,3],3),"]"),
                 round(summary(mod.tmp)$coefficient[,4],4)), ncol = 4 )
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre retdiet et betaplasma", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)
```

Table 90: Régression linéaire multiple avec interaction entre retdiet et betaplasma

	Bêta	IC	p
(Intercept)	566.11	[101.136;5.598]	0
age	2.397	[0.902;2.658]	0.0083
sexeFemmes	-103.547	[38.281;-2.705]	0.0072
tabacAutrefois	62.546	[25.628;2.441]	0.0152
tabacFumeur	1.28	[37.402;0.034]	0.9727
bmi	1.407	[2.011;0.7]	0.4845
vitamineSouvent	23.944	[28.531;0.839]	0.402
vitaminePas-souvent	25.142	[30.692;0.819]	0.4134
calories	0.075	[0.062;1.212]	0.2265
graisses	-1.288	[0.97;-1.327]	0.1854
fibres	-4.613	[3.436;-1.342]	0.1805
alcool	-1.414	[1.496;-0.945]	0.3454
cholesterol	-0.067	[0.134;-0.5]	0.6172
betadiet	-0.003	[0.009;-0.307]	0.7594
retdiet	-0.046	[0.042;-1.11]	0.2679
betaplasma	-0.043	[0.142;-0.306]	0.7601
retdiet:retinol[, "betaplasma"]	0	[0;1.026]	0.3057



```
rm(mod.tmp)
rm(res.tmp)
```

6. Question 4 : Regression logistique

6.1 Binarisation

Transformez la variable “rétinol plasmatique” en une variable binaire (en la coupant en deux au niveau de la médiane). Refaites les calculs précédents en ayant recours cette fois à une régression logistique.

```
retinol$retplasmaBin = retplasmaBin = ifelse(retinol$retplasma <= median(retinol$retplasma), 0, 1)
table(retinol$retplasmaBin)
```

```
##  
##   0   1  
## 159 156
```

6.2.2 Conditions de validité

On vérifie qu'il y a assez d'événement dans la variable à expliquer pour le nombre de variables du dataset:

```
table("Rétinol plasmatique binarisé" = retinol$retplasmaB)
```

```
## Rétinol plasmatique binarisé
##   0   1
## 159 156
```

Il y a 156 événements.

Liste des variables: * age : quantitative donc compte pour 1 * sexe : catégorielle à 2 classes donc compte pour 2-1 = 1 * tabac : catégorielle à 3 classes donc compte pour 3-1 = 2 * bmi : quantitative donc compte pour 1 * vitamine : catégorielle à 3 classes donc compte pour 3-1 = 2 * calories : quantitative donc compte pour 1 * graisses : quantitative donc compte pour 1 * fibres : quantitative donc compte pour 1 * alcool : quantitative donc compte pour 1 * cholesterol : quantitative donc compte pour 1 * betadiet : quantitative donc compte pour 1 * retdiet : quantitative donc compte pour 1 * betaplasma : quantitative donc compte pour 1

On a $10(1 + 1 + 2 + 1 + 2 + 1 + 1 + 1 + 1 + 1) = 150 < 156$

6.3 Tests de toutes les interactions possibles

6.3.1 Interaction avec l'âge

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "sexe"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 91: Régression linéaire multiple avec interaction entre age et sexe

	OR	IC	p
(Intercept)	0.993	[0.944;1.043]	0.7782
age	0.061	[0.002;1.4]	0.0852
sexeFemmes	1.249	[0.747;2.097]	0.3979
tabacAutrefois	0.984	[0.457;2.094]	0.9675
tabacFumeur	1.016	[0.975;1.058]	0.4542
bmi	1.054	[0.593;1.874]	0.8574
vitamineSouvent	1.098	[0.593;2.039]	0.7652
vitaminePas-souvent	1.001	[0.999;1.002]	0.4045
calories	0.993	[0.974;1.013]	0.4804
graisses	0.964	[0.898;1.034]	0.313
fibres	0.989	[0.959;1.02]	0.4738
alcool	1	[0.997;1.002]	0.8286
cholesterol	1	[1;1]	0.8395
betadiet	1	[1;1.001]	0.8137
rettdiet	1.001	[1;1.003]	0.0554
betaplasma	NA	[NA;NA]	0.1179
age:retinol[, "sexe"]Femmes	1.042	[0.99;1.1]	0.8349
1.446	[0.047;52.921]	0.8349	(Intercept)

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

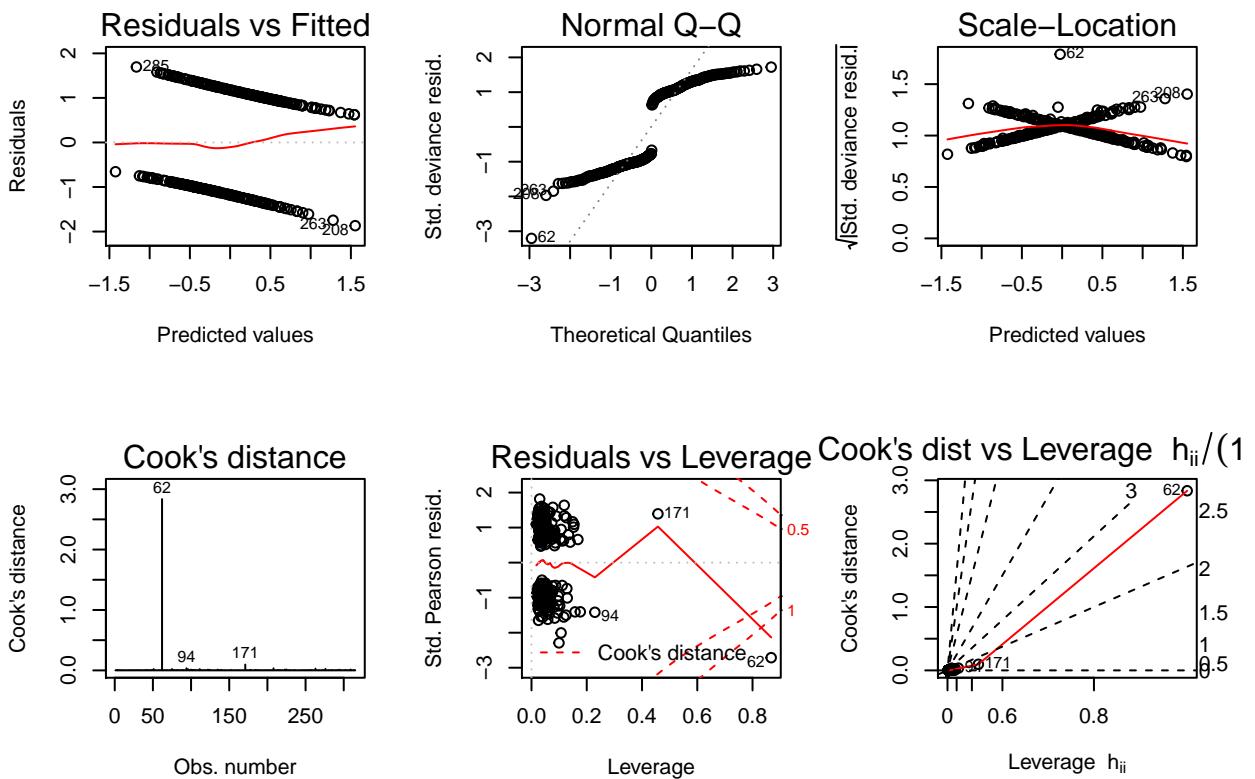
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et sexe",
      col.names = c(" ", "OR", "IC","p")) %>%
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "tabac"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 92: Régression linéaire multiple avec interaction entre age et tabac

	OR	IC	p
(Intercept)	0.735	[0.331;1.603]	0.4415
age	0.548	[0.076;3.784]	0.5447
sexeFemmes	1.349	[0.104;16.224]	0.8143
tabacAutrefois	1.016	[0.976;1.058]	0.4385
tabacFumeur	1.077	[0.605;1.918]	0.8009
bmi	1.116	[0.604;2.067]	0.7268
vitamineSouvent	1.001	[0.999;1.002]	0.4225
vitaminePas-souvent	0.994	[0.975;1.014]	0.5483
calories	0.963	[0.897;1.033]	0.2956
graisses	0.991	[0.96;1.022]	0.5415
fibres	1	[0.997;1.002]	0.8313
alcool	1	[1;1]	0.8739
cholesterol	1	[1;1.001]	0.8733
betadiet	1.002	[1;1.003]	0.0491
rettdiet	NA	[NA;NA]	0.4068
betaplasma	NA	[NA;NA]	0.7734
age:retinol[, "tabac"]Autrefois	1.016	[0.979;1.055]	0.1082
age:retinol[, "tabac"]Fumeur	0.992	[0.941;1.048]	0.032
0.18	[0.021;1.433]	0.1082	(Intercept)
1.026	[1.003;1.05]	0.032	age

```

## Waiting for profiling to be done...

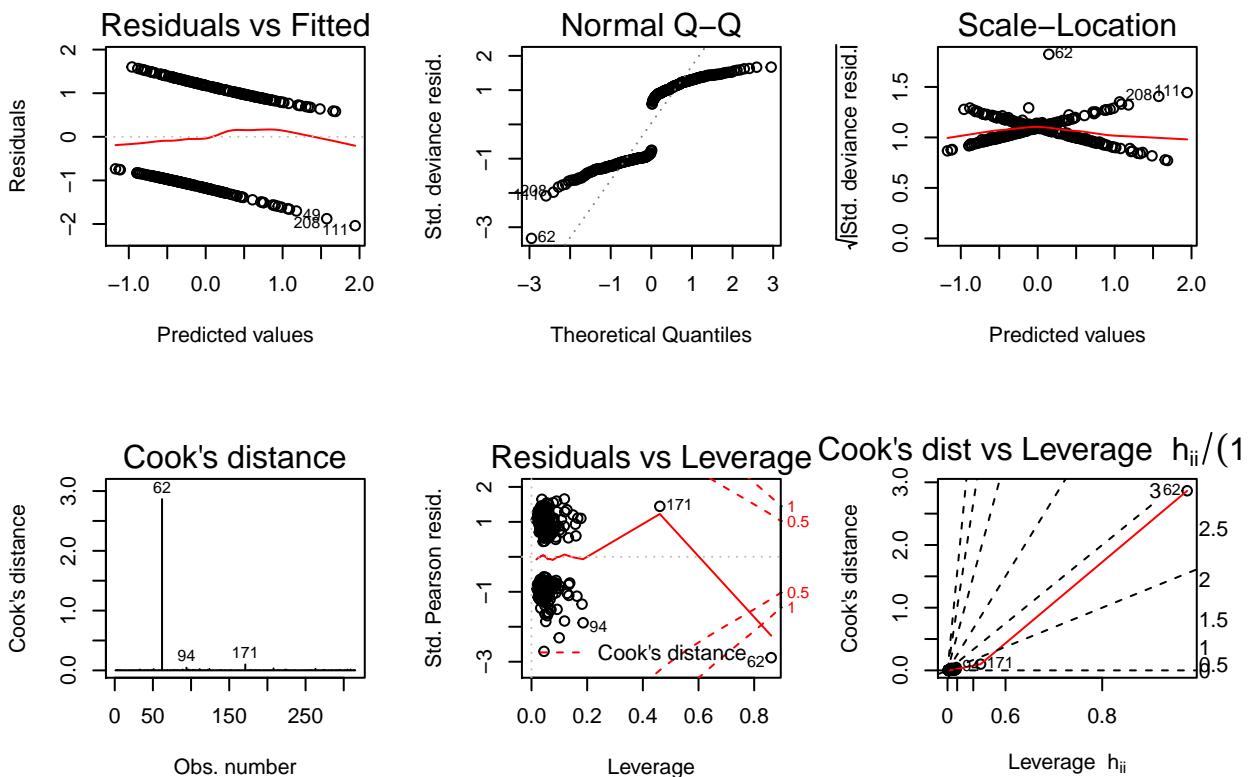
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [78] n'est pas un
## diviseur ni un multiple du nombre de lignes [20]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et tabac", col.names = c(" ",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "bmi"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 93: Régression linéaire multiple avec interaction entre age et bmi

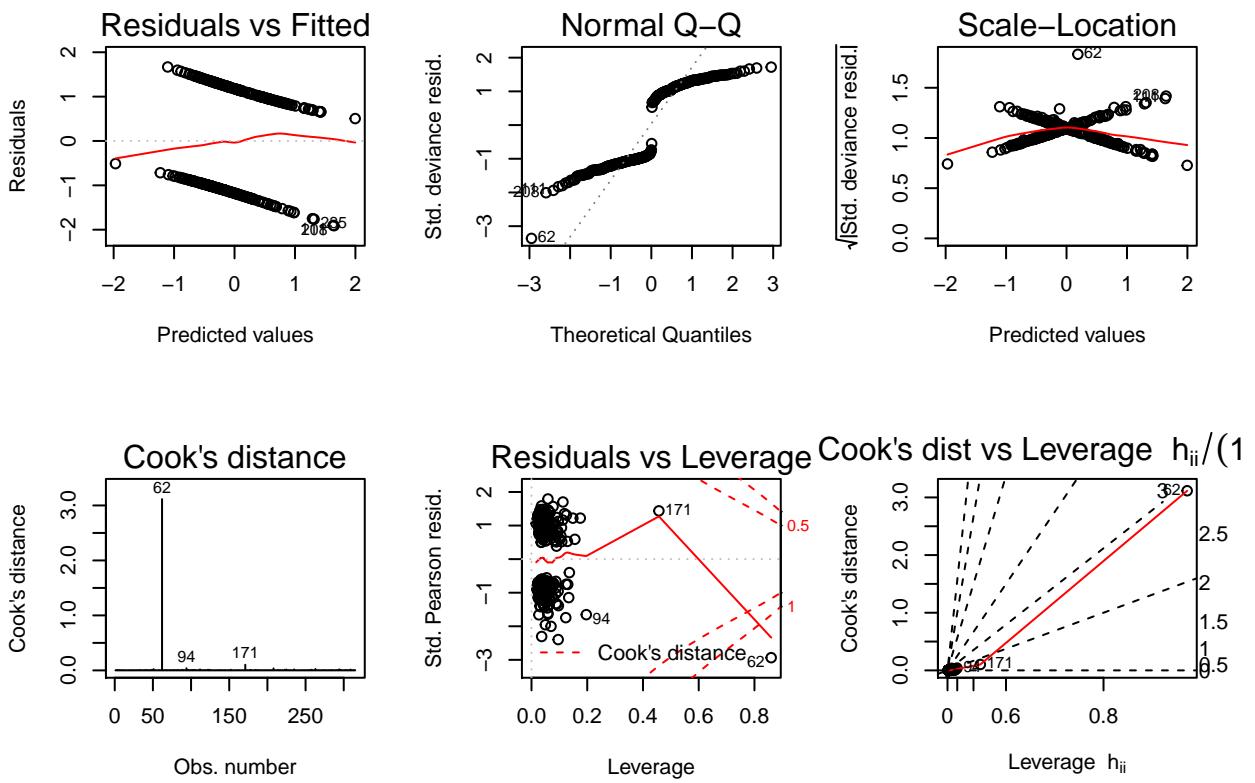
	OR	IC	p
(Intercept)	0.979	[0.903;1.054]	0.5824
age	0.695	[0.315;1.5]	0.3574
sexeFemmes	1.206	[0.721;2.022]	0.4761
tabacAutrefois	0.998	[0.467;2.106]	0.9964
tabacFumeur	0.926	[0.795;1.063]	0.2995
bmi	1.094	[0.618;1.941]	0.7571
vitamineSouvent	1.102	[0.594;2.048]	0.7584
vitaminePas-souvent	1	[0.999;1.002]	0.4372
calories	0.994	[0.975;1.014]	0.5563
graisses	0.963	[0.897;1.033]	0.2953
fibres	0.99	[0.96;1.022]	0.5151
alcool	1	[0.997;1.002]	0.8389
cholesterol	1	[1;1]	0.7749
betadiet	1	[1;1.001]	0.8662
retdiet	1.002	[1;1.003]	0.0427
betaplasma	NA	[NA;NA]	0.1867
age:retinol[, "bmi"]	1.002	[0.999;1.005]	0.7978
1.692	[0.033;105.702]	0.7978	(Intercept)

```

## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats:::coef(x)), exp(stats:::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et bmi", col.names = c(" ", "O",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "vitamine"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 94: Régression linéaire multiple avec interaction entre age et vitamine

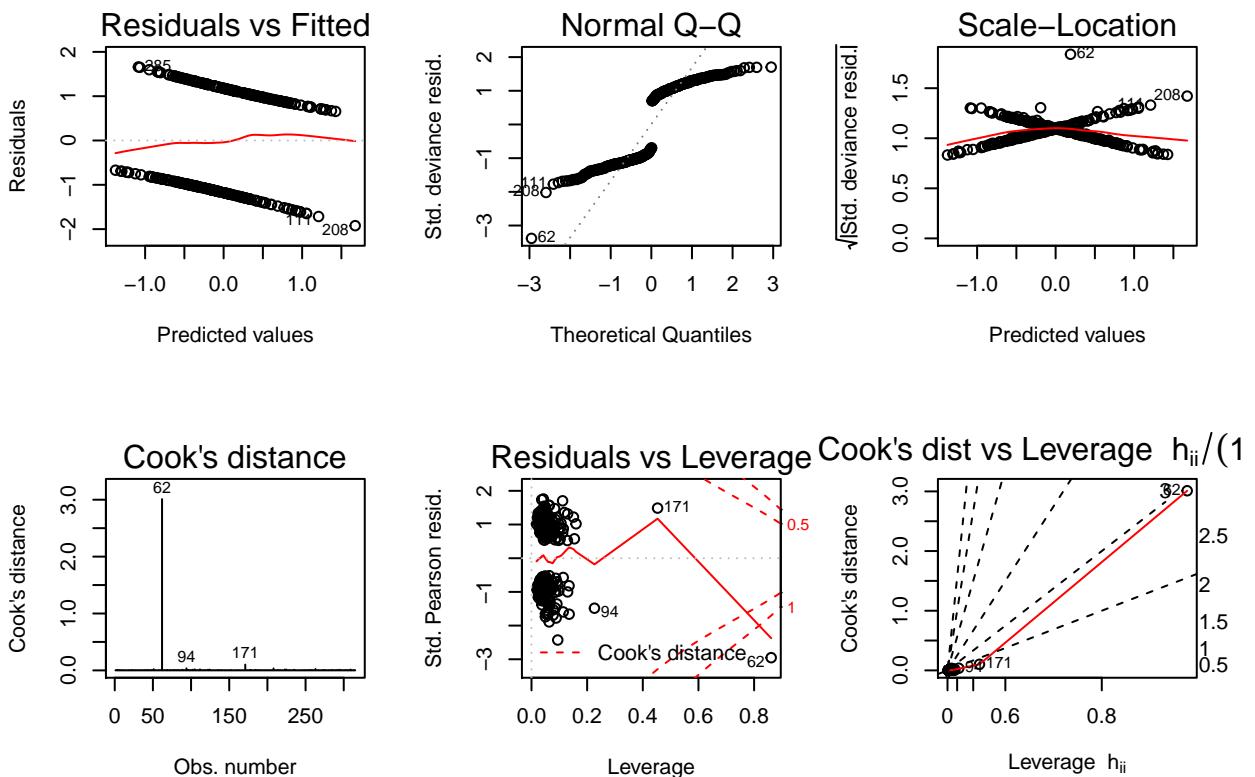
	OR	IC	p
(Intercept)	0.755	[0.339;1.651]	0.4843
age	1.234	[0.738;2.07]	0.4238
sexeFemmes	0.967	[0.45;2.054]	0.9304
tabacAutrefois	1.019	[0.978;1.061]	0.3705
tabacFumeur	4.223	[0.516;36.502]	0.1833
bmi	2.305	[0.231;23.188]	0.4757
vitamineSouvent	1	[0.999;1.002]	0.494
vitaminePas-souvent	0.995	[0.975;1.014]	0.5856
calories	0.963	[0.897;1.032]	0.2941
graisses	0.991	[0.961;1.022]	0.5344
fibres	1	[0.997;1.002]	0.8349
alcool	1	[1;1]	0.829
cholesterol	1	[1;1]	0.8963
betadiet	1.002	[1;1.003]	0.0494
retdiet	NA	[NA;NA]	0.1978
betaplasma	NA	[NA;NA]	0.5475
age:retinol[, "vitamine"]Souvent	0.974	[0.936;1.013]	0.0351
age:retinol[, "vitamine"]Pas-souvent	0.986	[0.942;1.033]	0.0065
0.068	[0.005;0.801]	0.0351	(Intercept)
1.045	[1.013;1.08]	0.0065	age

```

## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [78] n'est pas un
## diviseur ni un multiple du nombre de lignes [20]
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et vitamine", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "calories"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[" ,round(odds.ratio(mod.tmp)[,2],3), ";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 95: Régression linéaire multiple avec interaction entre age et calories

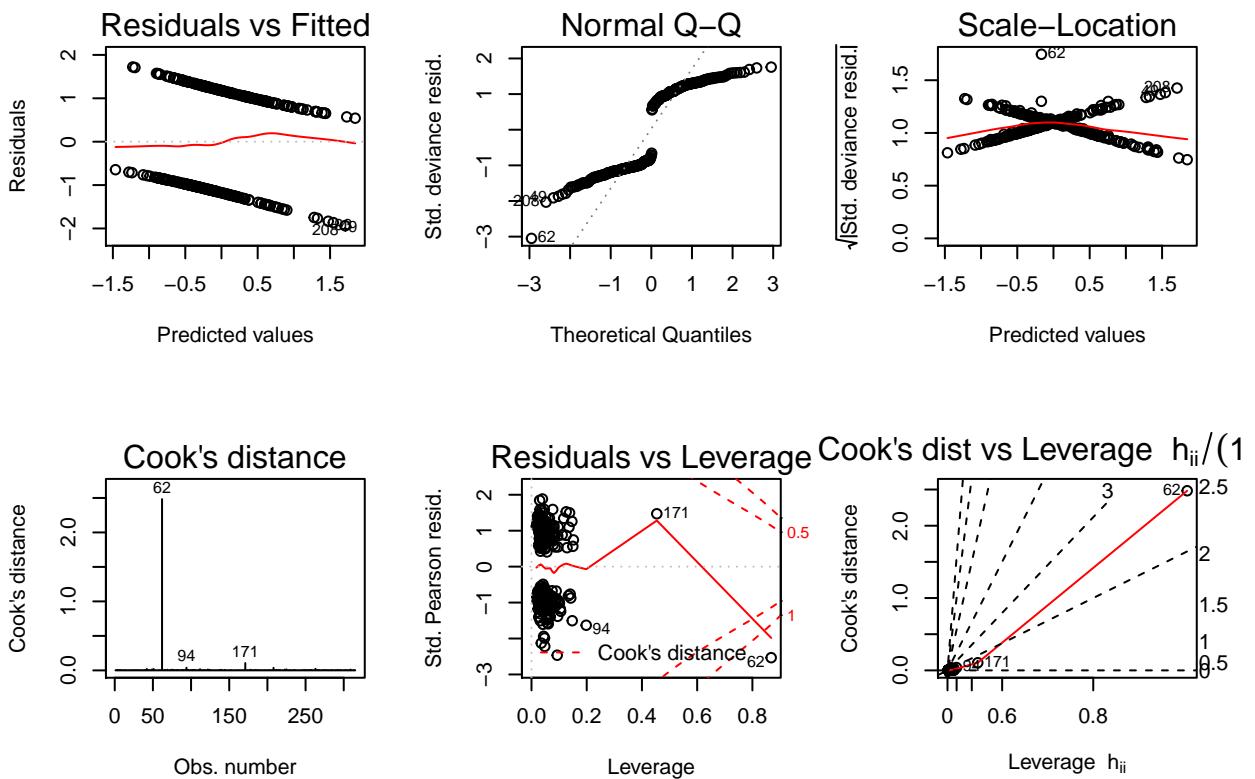
	OR	IC	p
(Intercept)	1.079	[1.026;1.138]	0.0038
age	0.64	[0.288;1.388]	0.2631
sexeFemmes	1.181	[0.705;1.986]	0.5274
tabacAutrefois	1.029	[0.479;2.186]	0.9405
tabacFumeur	1.02	[0.979;1.062]	0.3451
bmi	1.035	[0.58;1.846]	0.9076
vitamineSouvent	1.074	[0.578;1.998]	0.82
vitaminePas-souvent	1.002	[1;1.003]	0.0586
calories	0.996	[0.976;1.015]	0.6636
graisses	0.972	[0.904;1.042]	0.4235
fibres	1.002	[0.97;1.036]	0.8797
alcool	1	[0.997;1.002]	0.7958
cholesterol	1	[1;1]	0.878
betadiet	1	[1;1]	0.906
retdiet	1.002	[1;1.003]	0.0362
betaplasma	NA	[NA;NA]	0.0531
age:retinol[, "calories"]	1	[1;1]	0.009
0.016	[0.001;0.338]	0.009	(Intercept)

```

## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats:::coef(x)), exp(stats:::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et calories", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "graisses"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 96: Régression linéaire multiple avec interaction entre age et graisses

	OR	IC	p
(Intercept)	1.06	[1.017;1.107]	0.0073
age	0.657	[0.296;1.424]	0.292
sexeFemmes	1.222	[0.731;2.051]	0.4448
tabacAutrefois	1.016	[0.474;2.155]	0.9662
tabacFumeur	1.018	[0.978;1.06]	0.3791
bmi	1.047	[0.588;1.866]	0.8755
vitamineSouvent	1.093	[0.59;2.029]	0.7762
vitaminePas-souvent	1	[0.999;1.002]	0.5497
calories	1.015	[0.982;1.049]	0.3804
graisses	0.966	[0.899;1.036]	0.3333
fibres	0.994	[0.964;1.026]	0.7084
alcool	1	[0.997;1.002]	0.7788
cholesterol	1	[1;1]	0.8851
betadiet	1	[1;1.001]	0.8664
retdiet	1.002	[1;1.003]	0.0387
betaplasma	NA	[NA;NA]	0.1331
age:retinol[, "graisses"]	1	[0.999;1]	0.0199
0.04	[0.002;0.579]	0.0199	(Intercept)

```

## Waiting for profiling to be done...

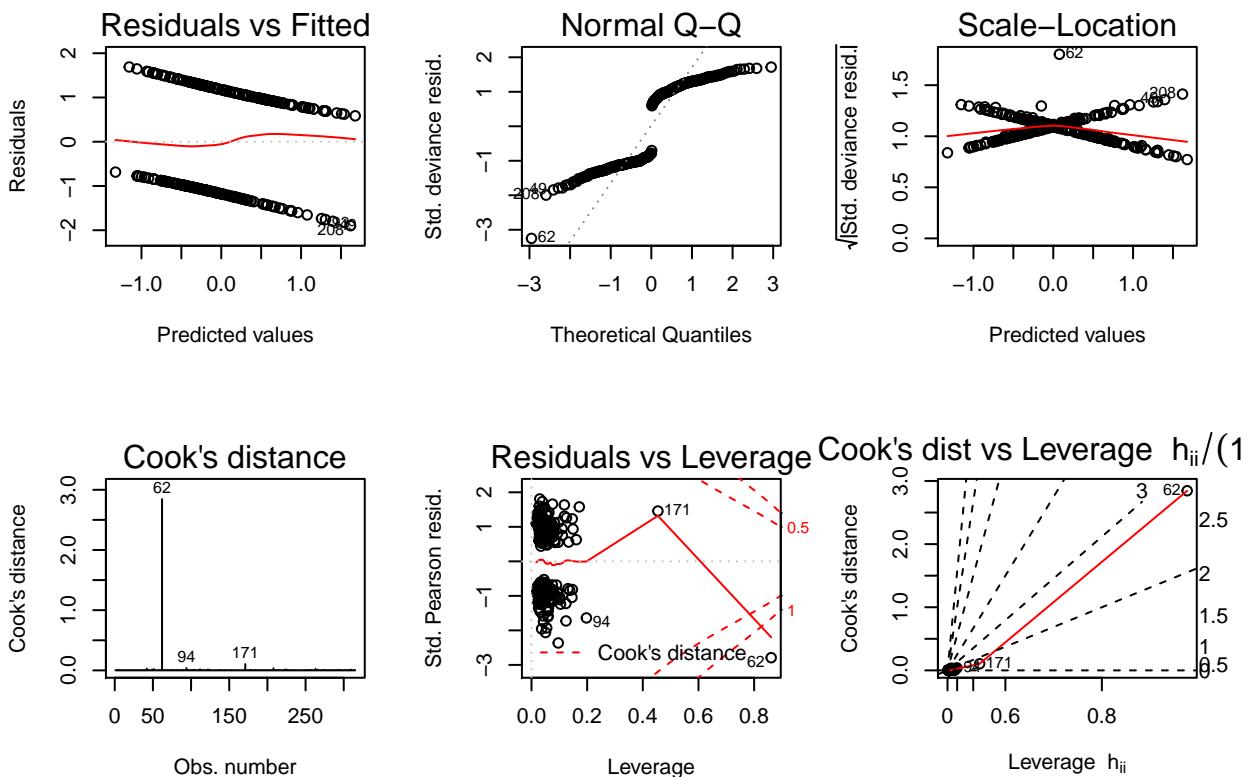
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et graisses", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "fibres"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 97: Régression linéaire multiple avec interaction entre age et fibres

	OR	IC	p
(Intercept)	1.031	[0.988;1.076]	0.1569
age	0.696	[0.313;1.516]	0.3647
sexeFemmes	1.216	[0.725;2.045]	0.4591
tabacAutrefois	0.98	[0.457;2.075]	0.9579
tabacFumeur	1.017	[0.977;1.059]	0.4102
bmi	1.104	[0.624;1.957]	0.7339
vitamineSouvent	1.12	[0.606;2.075]	0.7166
vitaminePas-souvent	1	[0.999;1.002]	0.4483
calories	0.994	[0.975;1.014]	0.5572
graisses	0.966	[0.804;1.156]	0.71
fibres	0.99	[0.96;1.021]	0.5062
alcool	1	[0.997;1.002]	0.8706
cholesterol	1	[1;1]	0.8737
betadiet	1	[1;1]	0.8948
retdiet	1.002	[1;1.003]	0.0502
betaplasma	NA	[NA;NA]	0.9514
age:retinol[, "fibres"]	1	[0.997;1.003]	0.1657
0.148	[0.01;2.166]	0.1657	(Intercept)

```

## Waiting for profiling to be done...

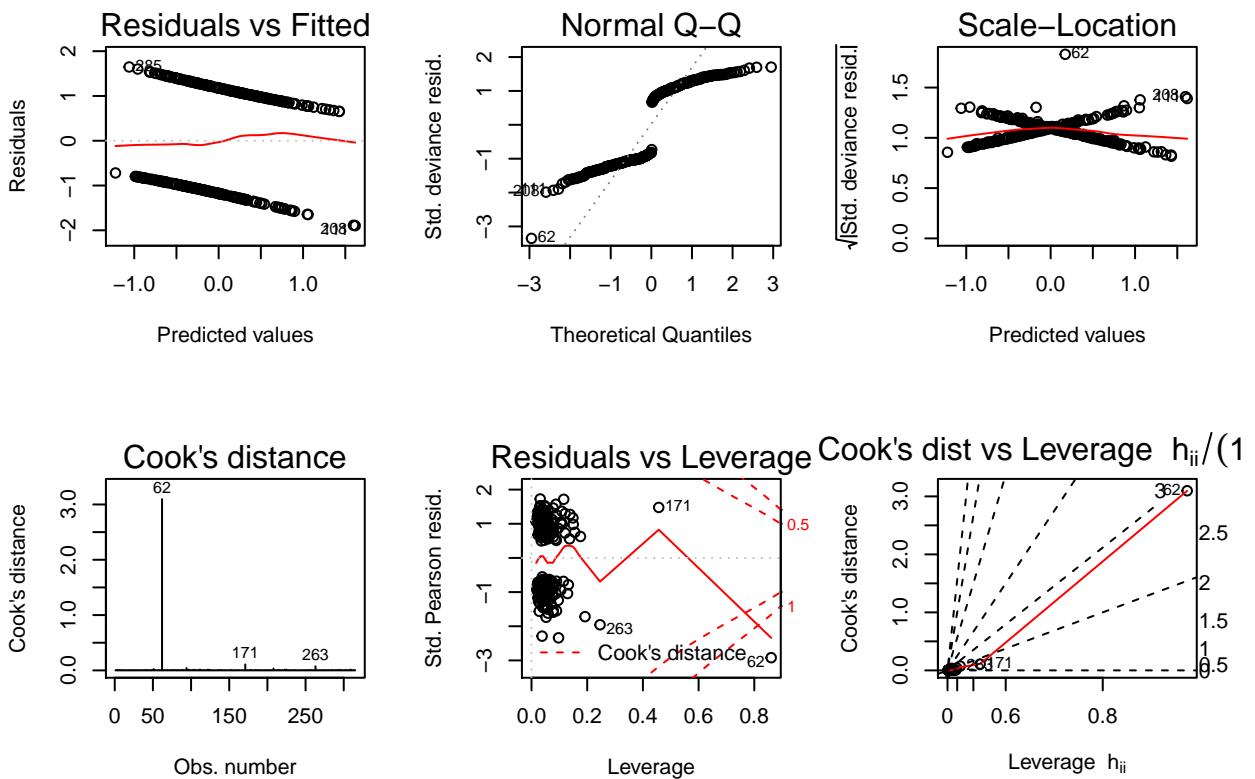
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et fibres", col.names = c(" "),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "alcool"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 98: Régression linéaire multiple avec interaction entre age et alcool

	OR	IC	p
(Intercept)	1.041	[1.021;1.063]	1e-04
age	0.76	[0.341;1.661]	0.4946
sexeFemmes	1.168	[0.694;1.971]	0.5591
tabacAutrefois	1.062	[0.487;2.289]	0.8789
tabacFumeur	1.024	[0.982;1.067]	0.2638
bmi	1.141	[0.639;2.043]	0.6556
vitamineSouvent	1.127	[0.603;2.111]	0.7074
vitaminePas-souvent	1.001	[0.999;1.002]	0.3317
calories	0.992	[0.972;1.012]	0.4127
graisses	0.956	[0.888;1.026]	0.2162
fibres	1.328	[1.098;1.658]	0.0064
alcool	1	[0.997;1.002]	0.8767
cholesterol	1	[1;1]	0.7777
betadiet	1	[1;1]	0.9211
retdiet	1.002	[1;1.003]	0.0594
betaplasma	NA	[NA;NA]	0.0048
age:retinol[, "alcool"]	0.995	[0.992;0.998]	0.0114
0.063	[0.007;0.52]	0.0114	(Intercept)

```

## Waiting for profiling to be done...

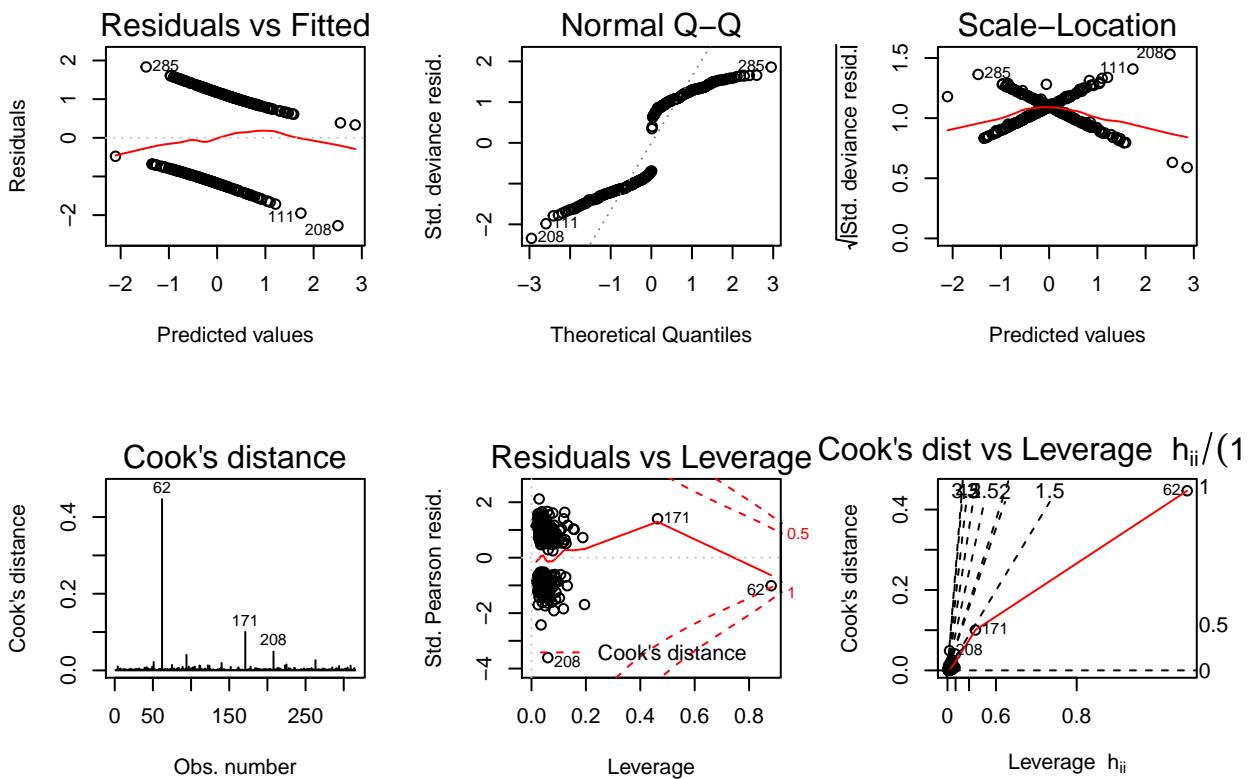
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et alcool", col.names = c(" ", ),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "cholesterol"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 99: Régression linéaire multiple avec interaction entre age et cholesterol

	OR	IC	p
(Intercept)	1.043	[1.008;1.08]	0.0171
age	0.675	[0.305;1.458]	0.3217
sexeFemmes	1.238	[0.74;2.078]	0.4171
tabacAutrefois	0.991	[0.462;2.096]	0.9803
tabacFumeur	1.017	[0.977;1.059]	0.4109
bmi	1.071	[0.602;1.907]	0.8147
vitamineSouvent	1.109	[0.6;2.054]	0.7411
vitaminePas-souvent	1	[0.999;1.002]	0.4857
calories	0.994	[0.974;1.013]	0.5108
graisses	0.962	[0.896;1.032]	0.2814
fibres	0.992	[0.962;1.023]	0.5979
alcool	1.003	[0.995;1.01]	0.459
cholesterol	1	[1;1]	0.9098
betadiet	1	[1;1.001]	0.8015
rettdiet	1.002	[1;1.003]	0.0481
betaplasma	NA	[NA;NA]	0.3919
age:retinol[, "cholesterol"]	1	[1;1]	0.0483
0.089	[0.008;0.964]	0.0483	(Intercept)

```

## Waiting for profiling to be done...

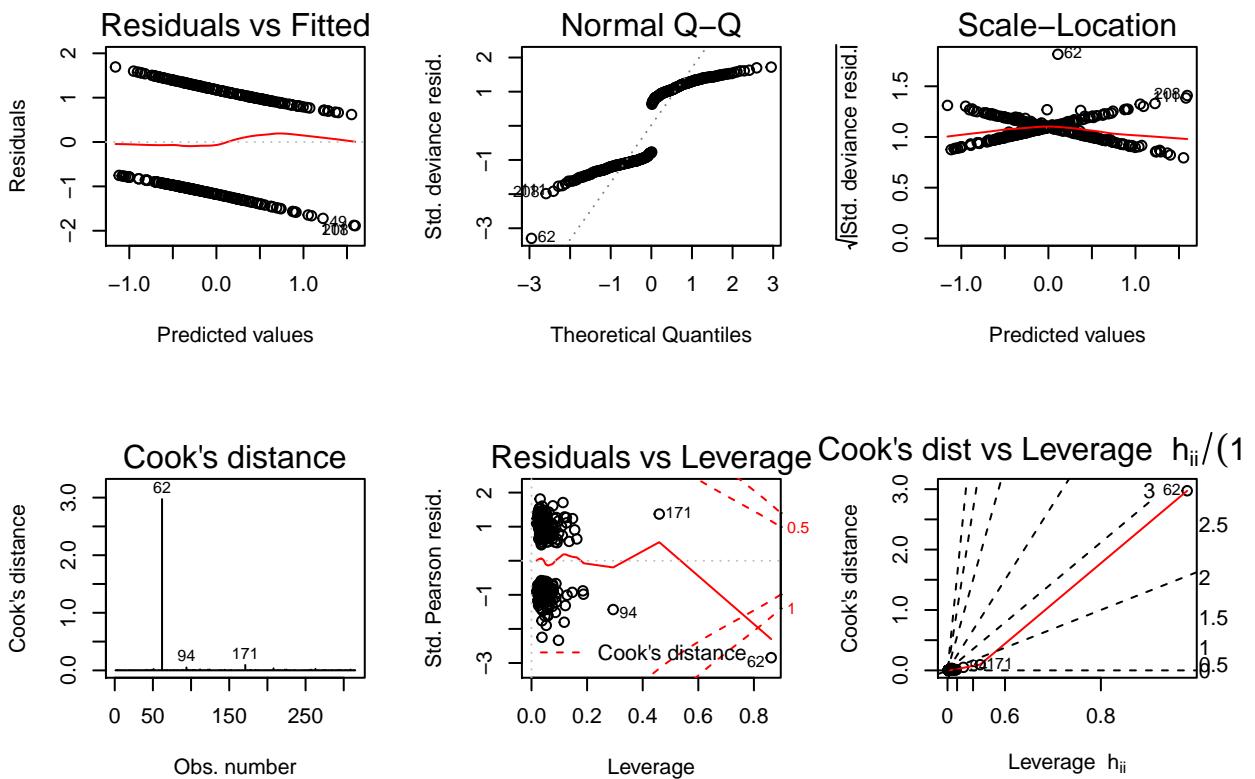
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et cholesterol", col.names = c(
        "Variable", "OR", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "betadiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 100: Régression linéaire multiple avec interaction entre age et betadiet

	OR	IC	p
(Intercept)	1.036	[1.003;1.071]	0.0356
age	0.694	[0.316;1.496]	0.3552
sexeFemmes	1.212	[0.726;2.031]	0.4625
tabacAutrefois	0.986	[0.46;2.086]	0.9705
tabacFumeur	1.018	[0.977;1.06]	0.3942
bmi	1.103	[0.623;1.954]	0.7369
vitamineSouvent	1.119	[0.606;2.074]	0.7191
vitaminePas-souvent	1	[0.999;1.002]	0.4374
calories	0.994	[0.975;1.013]	0.5408
graisses	0.962	[0.896;1.032]	0.281
fibres	0.99	[0.96;1.021]	0.5016
alcool	1	[0.997;1.002]	0.8697
cholesterol	1	[0.999;1.001]	0.7087
betadiet	1	[1;1]	0.8915
retdiet	1.002	[1;1.003]	0.0535
betaplasma	NA	[NA;NA]	0.6648
age:retinol[, "betadiet"]	1	[1;1]	0.0819
0.117	[0.01;1.284]	0.0819	(Intercept)

```

## Waiting for profiling to be done...

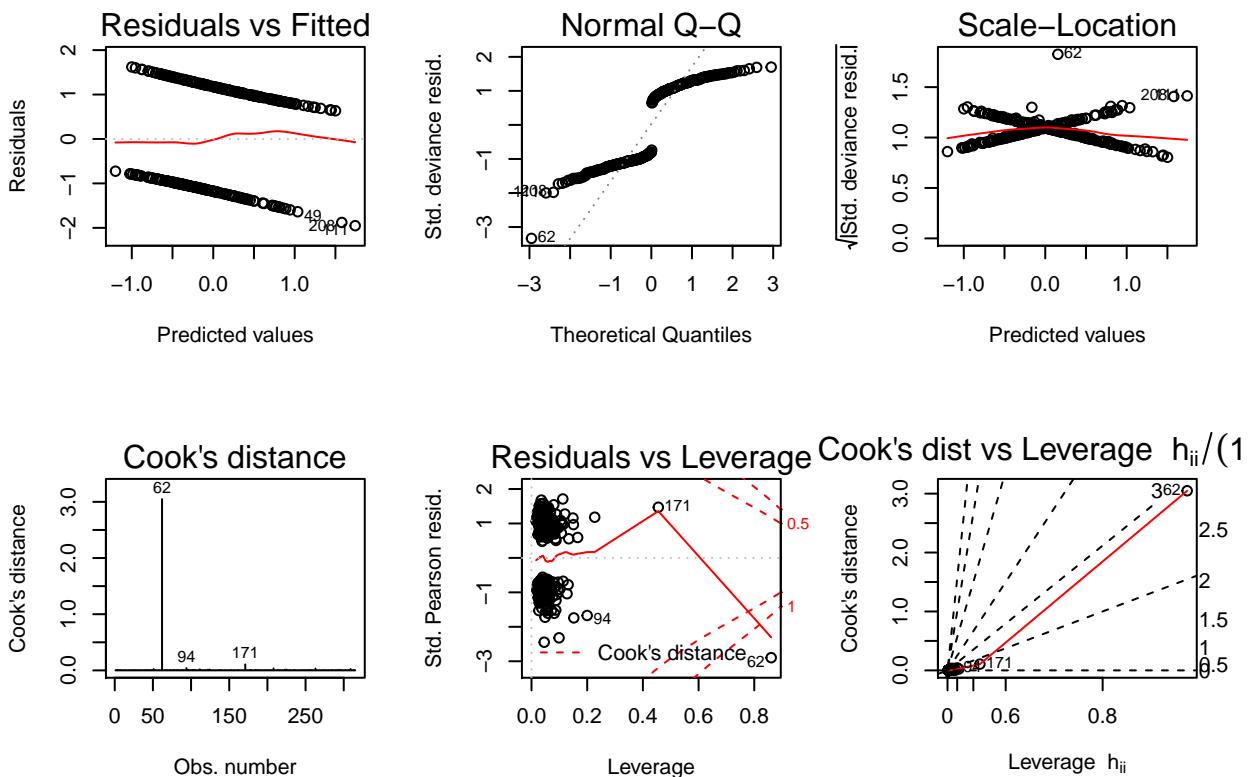
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et betadiet", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 101: Régression linéaire multiple avec interaction entre age et retdiet

	OR	IC	p
(Intercept)	1.039	[1.006;1.073]	0.0183
age	0.682	[0.309;1.475]	0.3356
sexeFemmes	1.212	[0.726;2.031]	0.4632
tabacAutrefois	0.988	[0.462;2.089]	0.975
tabacFumeur	1.016	[0.976;1.058]	0.4285
bmi	1.092	[0.616;1.937]	0.7637
vitamineSouvent	1.115	[0.603;2.067]	0.7279
vitaminePas-souvent	1	[0.999;1.002]	0.4922
calories	0.994	[0.975;1.014]	0.55
graisses	0.962	[0.895;1.031]	0.2744
fibres	0.991	[0.961;1.022]	0.5433
alcool	1	[0.997;1.003]	0.963
cholesterol	1	[1;1]	0.9045
betadiet	1.001	[0.999;1.002]	0.4854
retdiet	1.002	[1;1.003]	0.0468
betaplasma	NA	[NA;NA]	0.4921
age:retinol[, "retdiet"]	1	[1;1]	0.0563
0.106	[0.01;1.049]	0.0563	(Intercept)

```

## Waiting for profiling to be done...

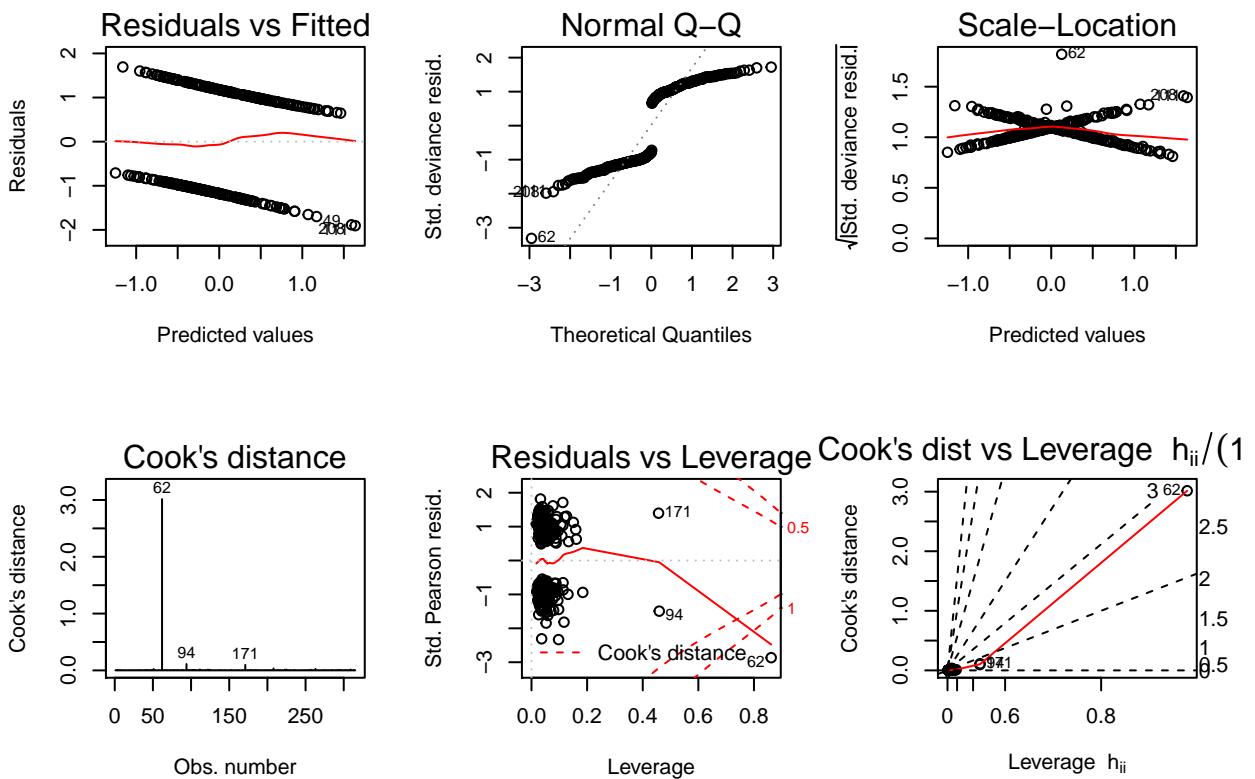
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et retdiet", col.names = c(" "
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + age*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 102: Régression linéaire multiple avec interaction entre age et betaplasma

	OR	IC	p
(Intercept)	1.033	[1.005;1.062]	0.0208
age	0.704	[0.32;1.52]	0.3755
sexeFemmes	1.213	[0.726;2.033]	0.4624
tabacAutrefois	0.98	[0.458;2.073]	0.9589
tabacFumeur	1.017	[0.977;1.059]	0.4106
bmi	1.11	[0.626;1.968]	0.7214
vitamineSouvent	1.123	[0.608;2.081]	0.7118
vitaminePas-souvent	1	[0.999;1.002]	0.4438
calories	0.994	[0.975;1.014]	0.5613
graisses	0.962	[0.896;1.032]	0.2844
fibres	0.99	[0.96;1.021]	0.5005
alcool	1	[0.997;1.002]	0.8577
cholesterol	1	[1;1]	0.844
betadiet	1	[1;1]	0.8954
rettdiet	1.002	[0.997;1.008]	0.4166
betaplasma	NA	[NA;NA]	0.7727
age:retinol[, "betaplasma"]	1	[1;1]	0.085
0.134	[0.013;1.288]	0.085	(Intercept)

```

## Waiting for profiling to be done...

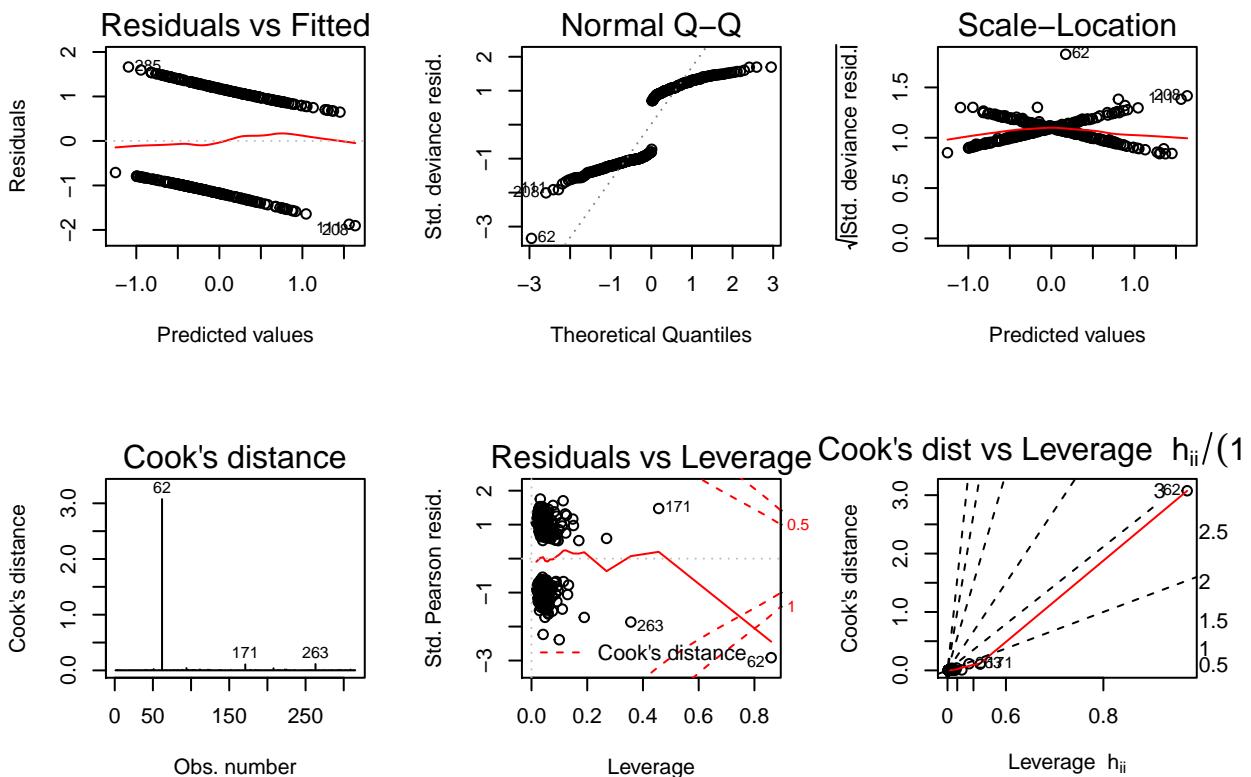
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre age et betaplasma", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.2 Interaction avec le sexe

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "tabac"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4)

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 103: Régression linéaire multiple avec interaction entre sexe et tabac

	OR	IC	p
(Intercept)	0.628	[0.172;2.118]	0.4584
age	1.241	[0.275;5.475]	0.7746
sexeFemmes	0.462	[0.055;3.456]	0.4543
tabacAutrefois	1.019	[0.979;1.062]	0.3564
tabacFumeur	1.11	[0.626;1.971]	0.7203
bmi	1.107	[0.598;2.053]	0.7465
vitamineSouvent	1.001	[0.999;1.002]	0.418
vitaminePas-souvent	0.994	[0.975;1.014]	0.5617
calories	0.96	[0.894;1.03]	0.2613
graisses	0.992	[0.961;1.023]	0.5895
fibres	1	[0.997;1.002]	0.8547
alcool	1	[1;1]	0.8723
cholesterol	1	[1;1]	0.8915
betadiet	1.002	[1;1.003]	0.0444
retdiet	NA	[NA;NA]	0.9597
betaplasma	NA	[NA;NA]	0.4253
sexeFemmes:retinol[, "tabac"]Autrefois	0.96	[0.197;4.776]	0.0885
sexeFemmes:retinol[, "tabac"]Fumeur	2.41	[0.28;23.041]	0.0018
0.153	[0.017;1.325]	0.0885	(Intercept)
1.03	[1.011;1.05]	0.0018	age

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

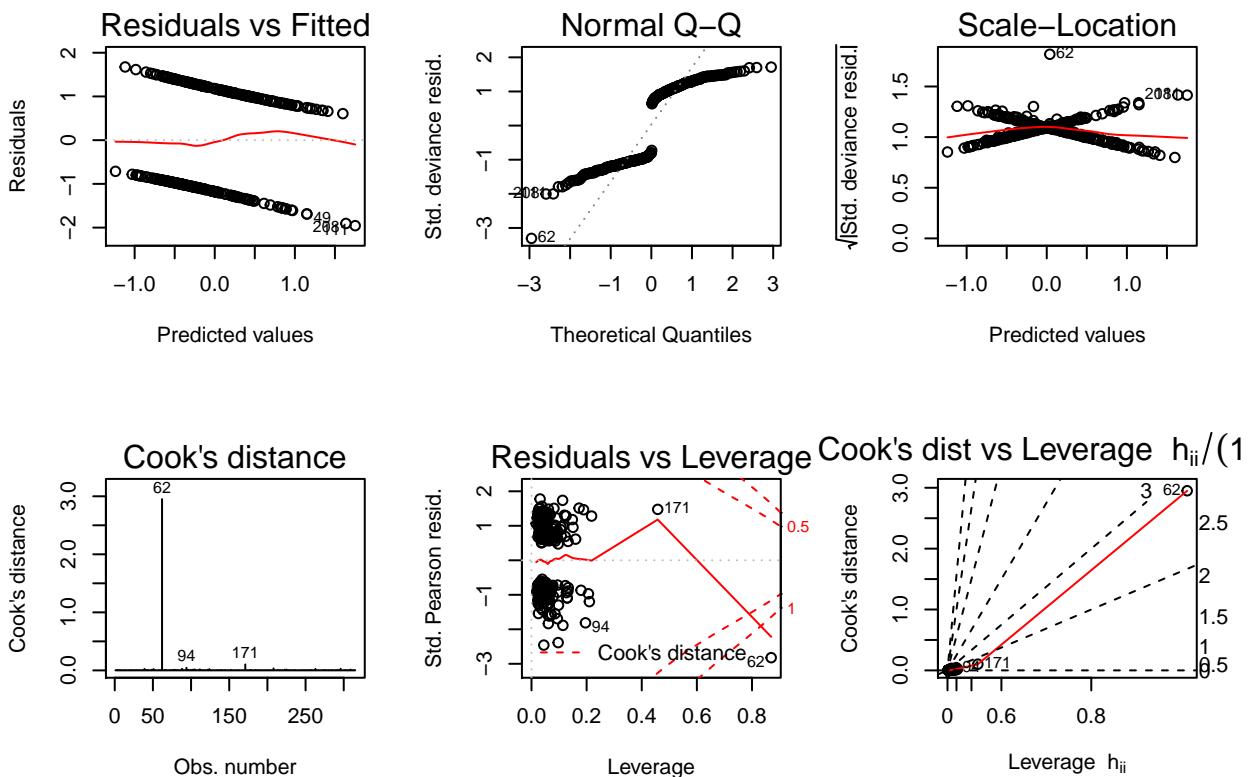
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [78] n'est pas un
## diviseur ni un multiple du nombre de lignes [20]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et tabac", col.names = c(" " ,
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "bmi"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 104: Régression linéaire multiple avec interaction entre sexe et bmi

	OR	IC	p
(Intercept)	1.031	[1.012;1.05]	0.0015
age	12.118	[0.146;1966.308]	0.2907
sexeFemmes	1.216	[0.728;2.039]	0.4562
tabacAutrefois	0.941	[0.436;2]	0.8741
tabacFumeur	1.126	[0.96;1.367]	0.173
bmi	1.088	[0.613;1.935]	0.7722
vitamineSouvent	1.144	[0.618;2.121]	0.6687
vitaminePas-souvent	1	[0.999;1.002]	0.4442
calories	0.994	[0.974;1.013]	0.5236
graisses	0.964	[0.897;1.033]	0.3029
fibres	0.991	[0.96;1.022]	0.5348
alcool	1	[0.997;1.003]	0.9253
cholesterol	1	[1;1]	0.8036
betadiet	1	[1;1]	0.8857
retdiet	1.002	[1;1.003]	0.0507
betaplasma	NA	[NA;NA]	0.2245
sexeFemmes:retinol[, "bmi"]	0.897	[0.737;1.058]	0.0633
0.01	[0;1.031]	0.0633	(Intercept)

```

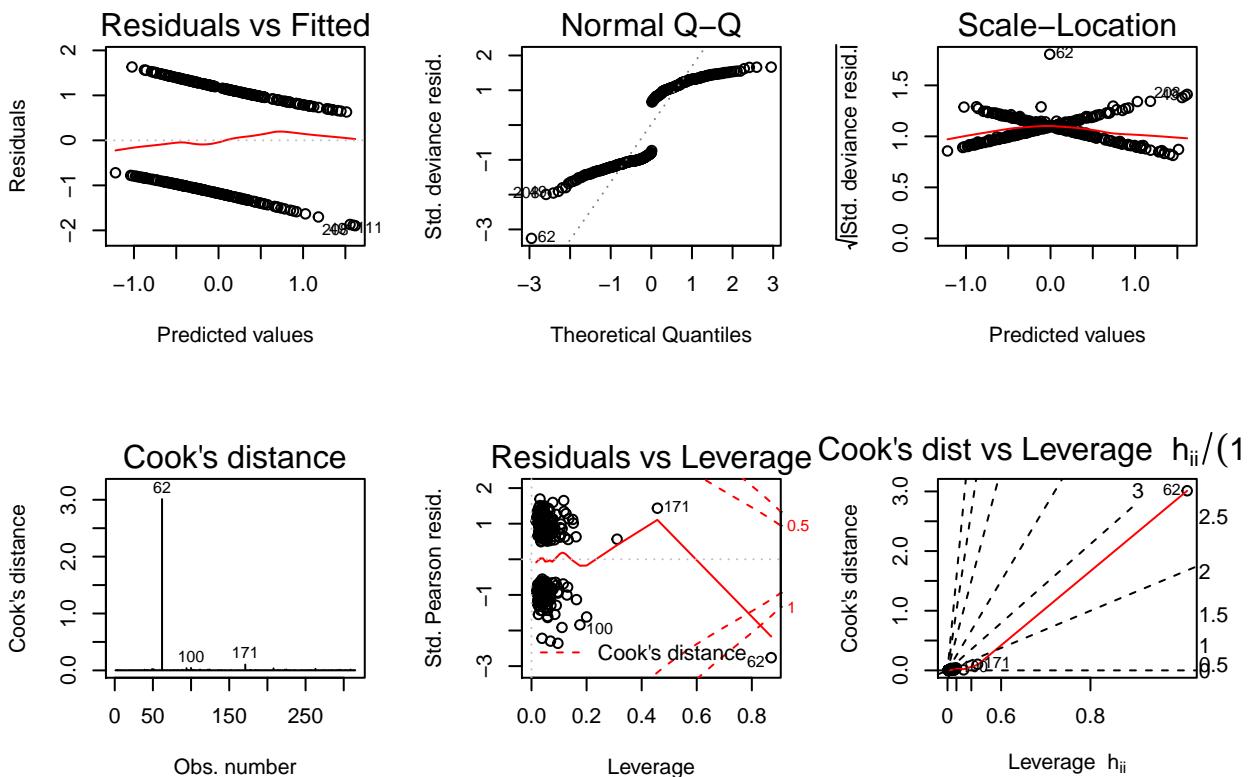
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats:::coef(x)), exp(stats:::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et bmi", col.names = c(" ", " ",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "vitamine"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 105: Régression linéaire multiple avec interaction entre sexe et vitamine

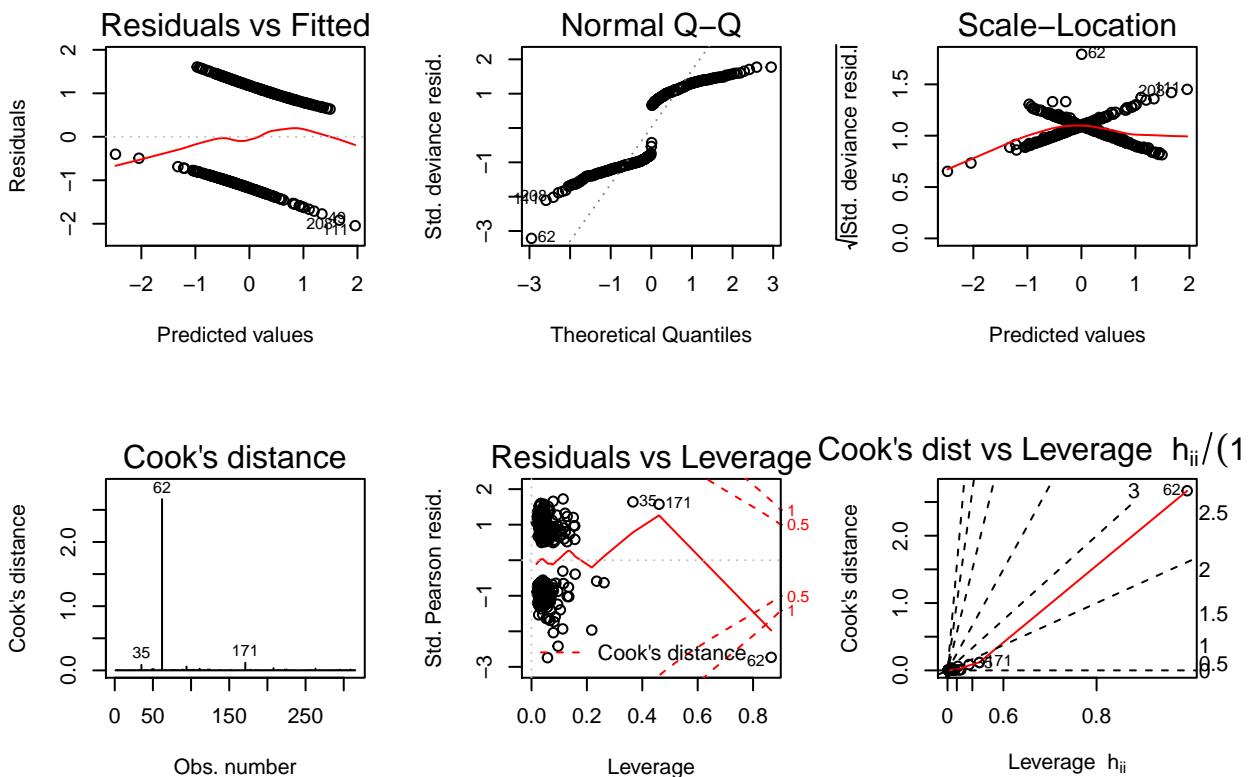
	OR	IC	p
(Intercept)	0.502	[0.165;1.43]	0.206
age	1.177	[0.7;1.983]	0.5388
sexeFemmes	0.913	[0.422;1.947]	0.8151
tabacAutrefois	1.014	[0.974;1.056]	0.5025
tabacFumeur	1.16	[0.259;5.652]	0.8474
bmi	0.107	[0.005;0.998]	0.077
vitamineSouvent	1	[0.999;1.002]	0.518
vitaminePas-souvent	0.996	[0.976;1.015]	0.655
calories	0.962	[0.895;1.033]	0.2877
graisses	0.989	[0.959;1.02]	0.4722
fibres	1	[0.997;1.002]	0.8755
alcool	1	[1;1]	0.8592
cholesterol	1	[1;1]	0.9761
betadiet	1.002	[1;1.003]	0.0354
retdiet	NA	[NA;NA]	0.9604
betaplasma	NA	[NA;NA]	0.053
sexeFemmes:retinol[, "vitamine"]Souvent	0.959	[0.175;4.863]	0.1856
sexeFemmes:retinol[, "vitamine"]Pas-souvent	12.44	[1.219;302.358]	0.0026
0.232	[0.026;2.013]	0.1856	(Intercept)
1.029	[1.01;1.049]	0.0026	age

```

## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [78] n'est pas un
## diviseur ni un multiple du nombre de lignes [20]
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et vitamine", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "calories"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 106: Régression linéaire multiple avec interaction entre sexe et calories

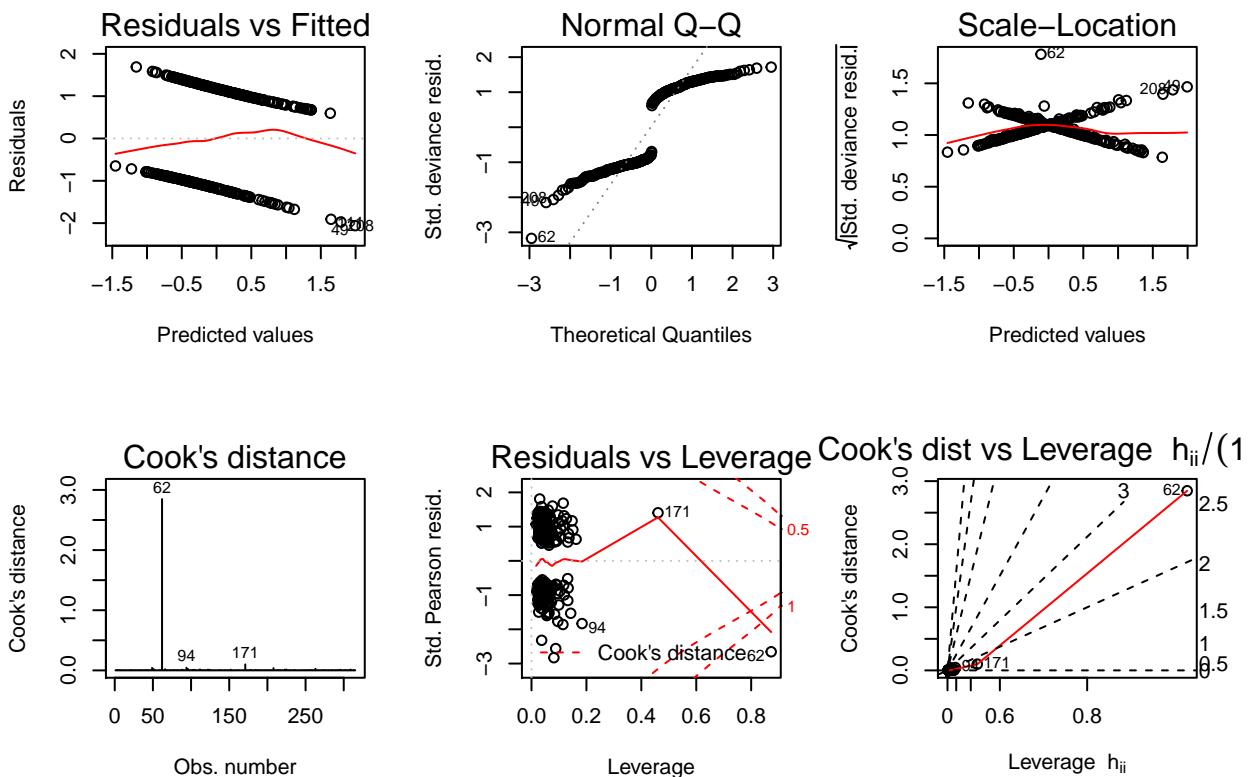
	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0018
age	0.114	[0.006;1.533]	0.118
sexeFemmes	1.179	[0.703;1.982]	0.5334
tabacAutrefois	1.04	[0.484;2.213]	0.9189
tabacFumeur	1.021	[0.98;1.063]	0.3212
bmi	1.107	[0.623;1.967]	0.7294
vitamineSouvent	1.094	[0.591;2.03]	0.7741
vitaminePas-souvent	1	[0.998;1.001]	0.7079
calories	0.994	[0.975;1.014]	0.5741
graisses	0.959	[0.892;1.028]	0.2427
fibres	1.007	[0.969;1.047]	0.7231
alcool	1	[0.997;1.002]	0.7461
cholesterol	1	[1;1]	0.8678
betadiet	1	[1;1.001]	0.8642
retdiet	1.002	[1;1.003]	0.048
betaplasma	NA	[NA;NA]	0.1687
sexeFemmes:retinol[, "calories"]	1.001	[1;1.002]	0.8411
0.735	[0.039;16.845]	0.8411	(Intercept)

```

## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats:::coef(x)), exp(stats:::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et calories", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "graisses"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 107: Régression linéaire multiple avec interaction entre sexe et graisses

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.002
age	0.52	[0.051;4.441]	0.5592
sexeFemmes	1.214	[0.727;2.035]	0.4593
tabacAutrefois	0.991	[0.461;2.103]	0.9812
tabacFumeur	1.017	[0.977;1.06]	0.3998
bmi	1.104	[0.624;1.957]	0.7337
vitamineSouvent	1.118	[0.605;2.07]	0.7223
vitaminePas-souvent	1	[0.999;1.002]	0.4414
calories	0.991	[0.964;1.019]	0.54
graisses	0.961	[0.894;1.03]	0.2651
fibres	0.991	[0.96;1.023]	0.5522
alcool	1	[0.997;1.002]	0.8542
cholesterol	1	[1;1]	0.8737
betadiet	1	[1;1]	0.8935
retdiet	1.002	[1;1.003]	0.0485
betaplasma	NA	[NA;NA]	0.7774
sexeFemmes:retinol[, "graisses"]	1.003	[0.981;1.027]	0.2509
0.204	[0.014;3.26]	0.2509	(Intercept)

```

## Waiting for profiling to be done...

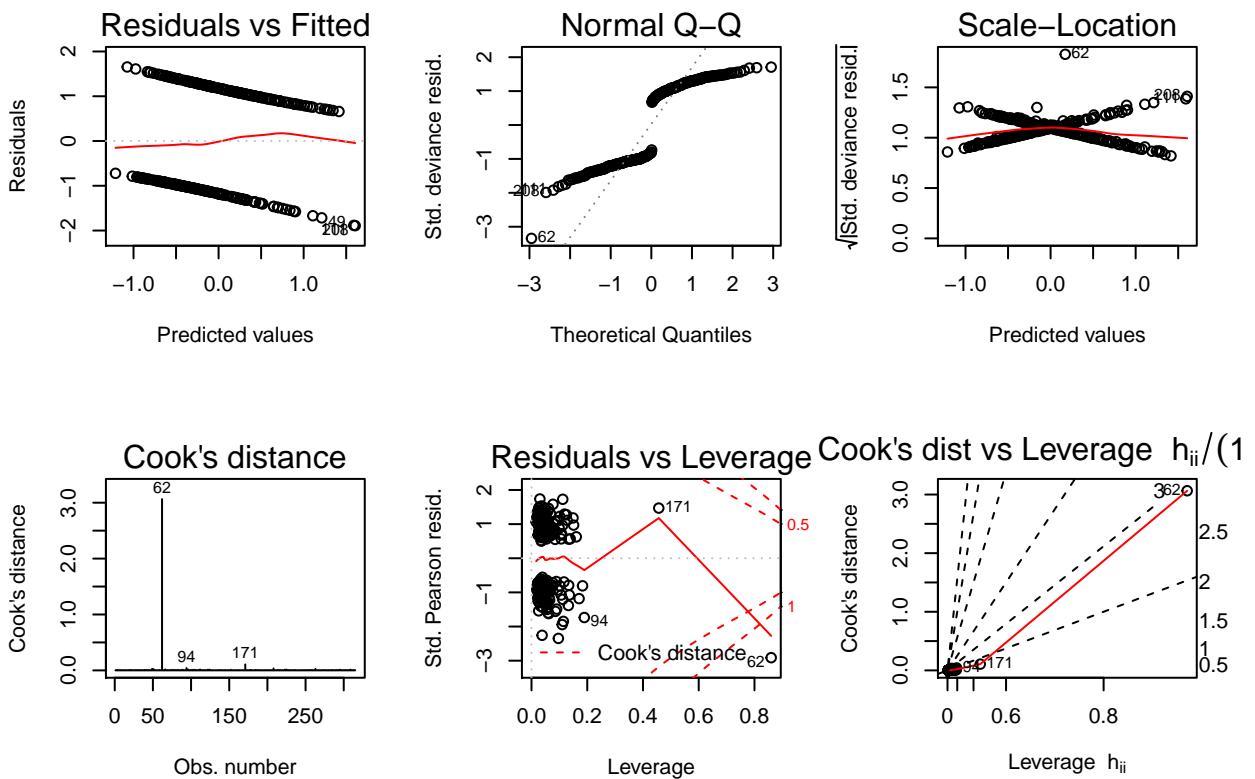
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et graisses", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "fibres"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[" ,round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 108: Régression linéaire multiple avec interaction entre sexe et fibres

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0019
age	0.568	[0.063;4.803]	0.604
sexeFemmes	1.215	[0.728;2.037]	0.4569
tabacAutrefois	0.981	[0.458;2.075]	0.9608
tabacFumeur	1.017	[0.977;1.059]	0.4127
bmi	1.105	[0.624;1.958]	0.7315
vitamineSouvent	1.123	[0.608;2.08]	0.7112
vitaminePas-souvent	1	[0.999;1.002]	0.4528
calories	0.994	[0.975;1.014]	0.5672
graisses	0.949	[0.82;1.101]	0.4771
fibres	0.99	[0.96;1.021]	0.5059
alcool	1	[0.997;1.002]	0.8427
cholesterol	1	[1;1]	0.875
betadiet	1	[1;1.001]	0.8772
retdiet	1.002	[1;1.003]	0.053
betaplasma	NA	[NA;NA]	0.8379
sexeFemmes:retinol[, "fibres"]	1.015	[0.874;1.177]	0.2302
0.19	[0.012;2.921]	0.2302	(Intercept)

```

## Waiting for profiling to be done...

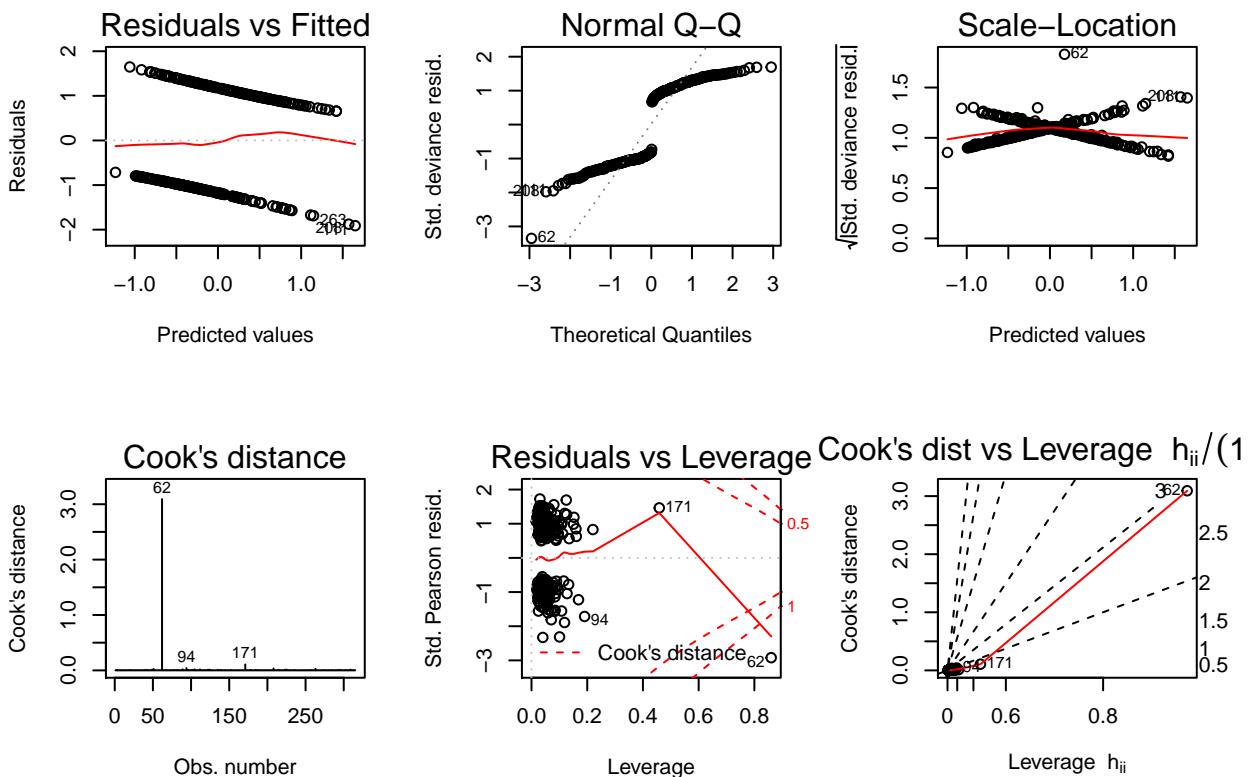
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et fibres", col.names = c(" "
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "alcool"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 109: Régression linéaire multiple avec interaction entre sexe et alcool

	OR	IC	p
(Intercept)	1.031	[1.012;1.051]	0.0014
age	0.532	[0.231;1.186]	0.1273
sexeFemmes	1.14	[0.678;1.92]	0.6224
tabacAutrefois	0.968	[0.446;2.072]	0.9327
tabacFumeur	1.027	[0.986;1.071]	0.2029
bmi	1.201	[0.674;2.15]	0.5351
vitamineSouvent	1.11	[0.596;2.075]	0.7417
vitaminePas-souvent	1.001	[0.999;1.002]	0.3073
calories	0.992	[0.973;1.012]	0.4305
graisses	0.956	[0.889;1.026]	0.2153
fibres	0.979	[0.934;1.011]	0.2208
alcool	1	[0.997;1.002]	0.7707
cholesterol	1	[1;1]	0.8639
betadiet	1	[1;1]	0.9411
rettdiet	1.001	[1;1.003]	0.0657
betaplasma	NA	[NA;NA]	0.0224
sexeFemmes:retinol[, "alcool"]	1.092	[1.017;1.184]	0.0459
0.125	[0.016;0.946]	0.0459	(Intercept)

```

## Waiting for profiling to be done...

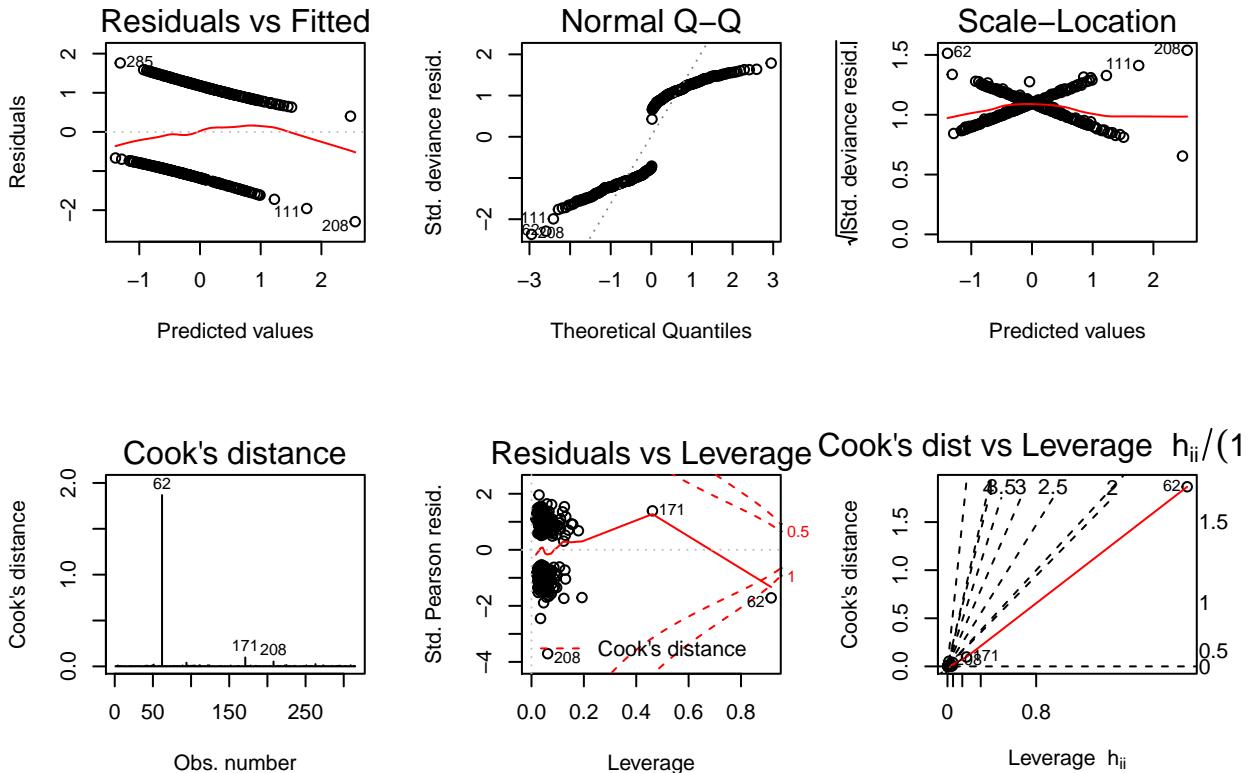
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et alcool", col.names = c(" "
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "cholesterol"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 110: Régression linéaire multiple avec interaction entre sexe et cholesterol

	OR	IC	p
(Intercept)	1.029	[1.011;1.049]	0.0022
age	0.103	[0.011;0.71]	0.0297
sexeFemmes	1.222	[0.728;2.06]	0.4486
tabacAutrefois	1.026	[0.478;2.18]	0.9463
tabacFumeur	1.016	[0.976;1.058]	0.4363
bmi	1.1	[0.617;1.961]	0.7472
vitamineSouvent	1.094	[0.589;2.036]	0.7757
vitaminePas-souvent	1.001	[0.999;1.002]	0.3925
calories	0.992	[0.972;1.011]	0.3975
graisses	0.95	[0.882;1.02]	0.1617
fibres	0.995	[0.964;1.026]	0.7239
alcool	0.995	[0.989;1]	0.0694
cholesterol	1	[1;1]	0.9666
betadiet	1	[1;1.001]	0.6763
retdiet	1.002	[1;1.003]	0.0466
betaplasma	NA	[NA;NA]	0.0426
sexeFemmes:retinol[, "cholesterol"]	1.006	[1;1.012]	0.9967
1.006	[0.069;16.857]	0.9967	(Intercept)

```

## Waiting for profiling to be done...

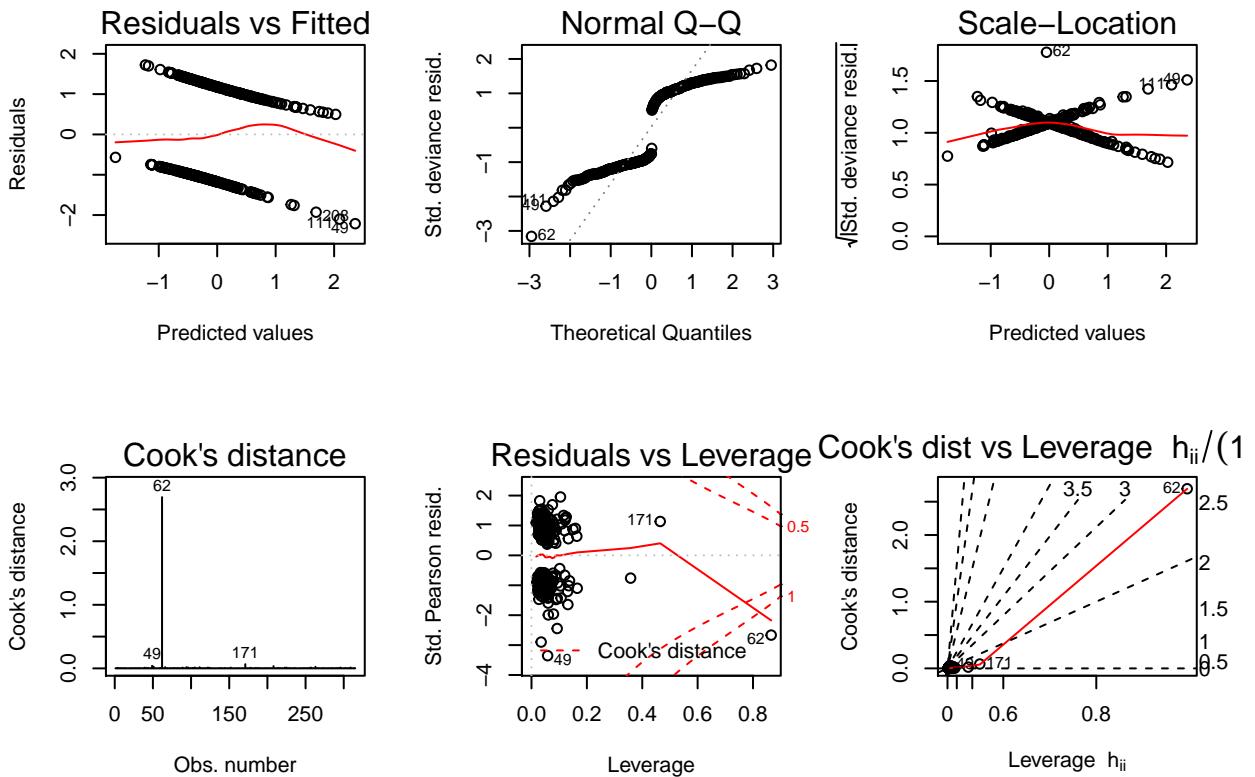
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et cholesterol", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "betadiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[" ,round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 111: Régression linéaire multiple avec interaction entre sexe et betadiet

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0019
age	0.346	[0.061;1.737]	0.2106
sexeFemmes	1.208	[0.723;2.024]	0.471
tabacAutrefois	0.977	[0.456;2.068]	0.9522
tabacFumeur	1.018	[0.978;1.06]	0.3918
bmi	1.1	[0.621;1.95]	0.7433
vitamineSouvent	1.124	[0.608;2.084]	0.7094
vitaminePas-souvent	1	[0.999;1.002]	0.4528
calories	0.994	[0.975;1.014]	0.5468
graisses	0.963	[0.897;1.033]	0.2933
fibres	0.991	[0.961;1.023]	0.575
alcool	1	[0.997;1.002]	0.8375
cholesterol	1	[0.999;1]	0.342
betadiet	1	[1;1.001]	0.8299
retdiet	1.001	[1;1.003]	0.0614
betaplasma	NA	[NA;NA]	0.3432
sexeFemmes:retinol[, "betadiet"]	1	[1;1.001]	0.3285
0.299	[0.026;3.454]	0.3285	(Intercept)

```

## Waiting for profiling to be done...

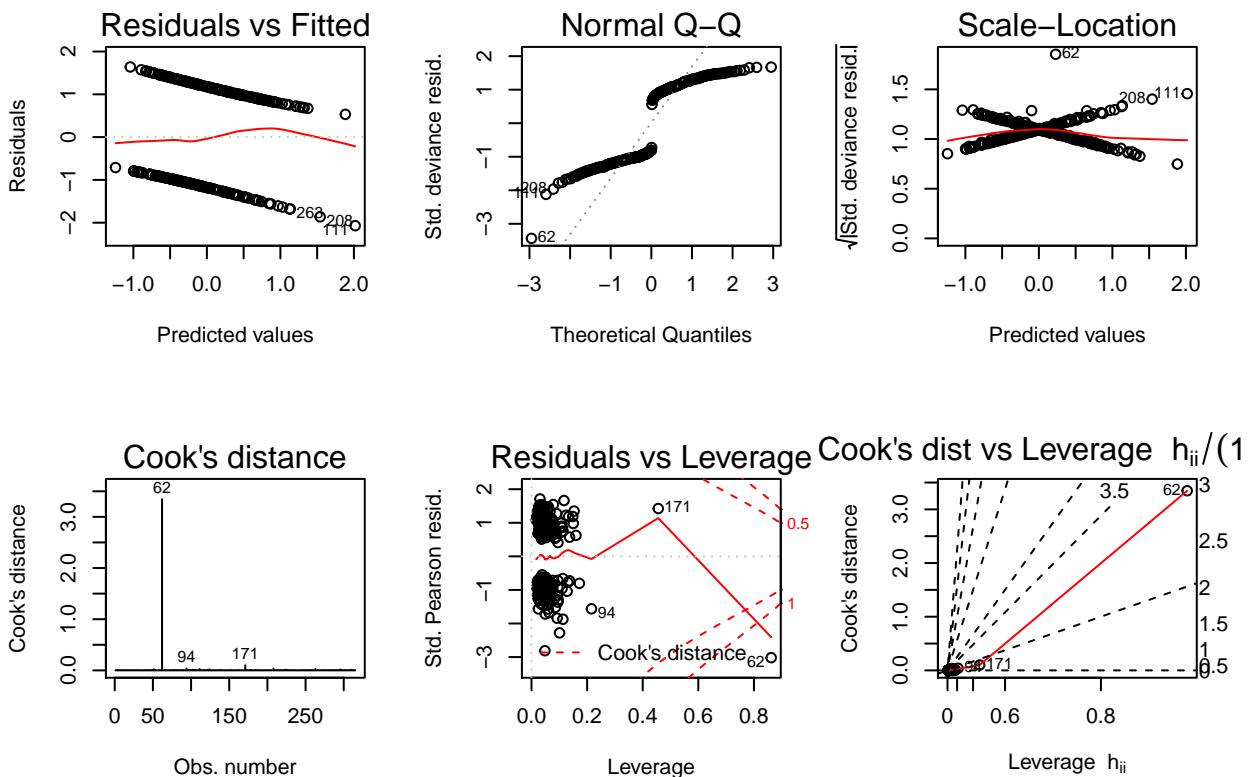
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et betadiet", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 112: Régression linéaire multiple avec interaction entre sexe et retdiet

	OR	IC	p
(Intercept)	1.03	[1.012;1.05]	0.0016
age	0.329	[0.076;1.173]	0.1003
sexeFemmes	1.236	[0.739;2.075]	0.421
tabacAutrefois	1.021	[0.476;2.164]	0.9577
tabacFumeur	1.016	[0.976;1.058]	0.4308
bmi	1.105	[0.622;1.965]	0.7325
vitamineSouvent	1.104	[0.596;2.048]	0.7533
vitaminePas-souvent	1	[0.999;1.002]	0.4333
calories	0.993	[0.973;1.012]	0.4642
graisses	0.961	[0.894;1.031]	0.2693
fibres	0.99	[0.96;1.021]	0.5191
alcool	1	[0.997;1.003]	0.9509
cholesterol	1	[1;1]	0.9186
betadiet	0.999	[0.998;1]	0.2355
retdiet	1.001	[1;1.003]	0.0533
betaplasma	NA	[NA;NA]	0.1677
sexeFemmes:retinol[, "retdiet"]	1.001	[1;1.002]	0.2859
0.299	[0.032;2.817]	0.2859	(Intercept)

```

## Waiting for profiling to be done...

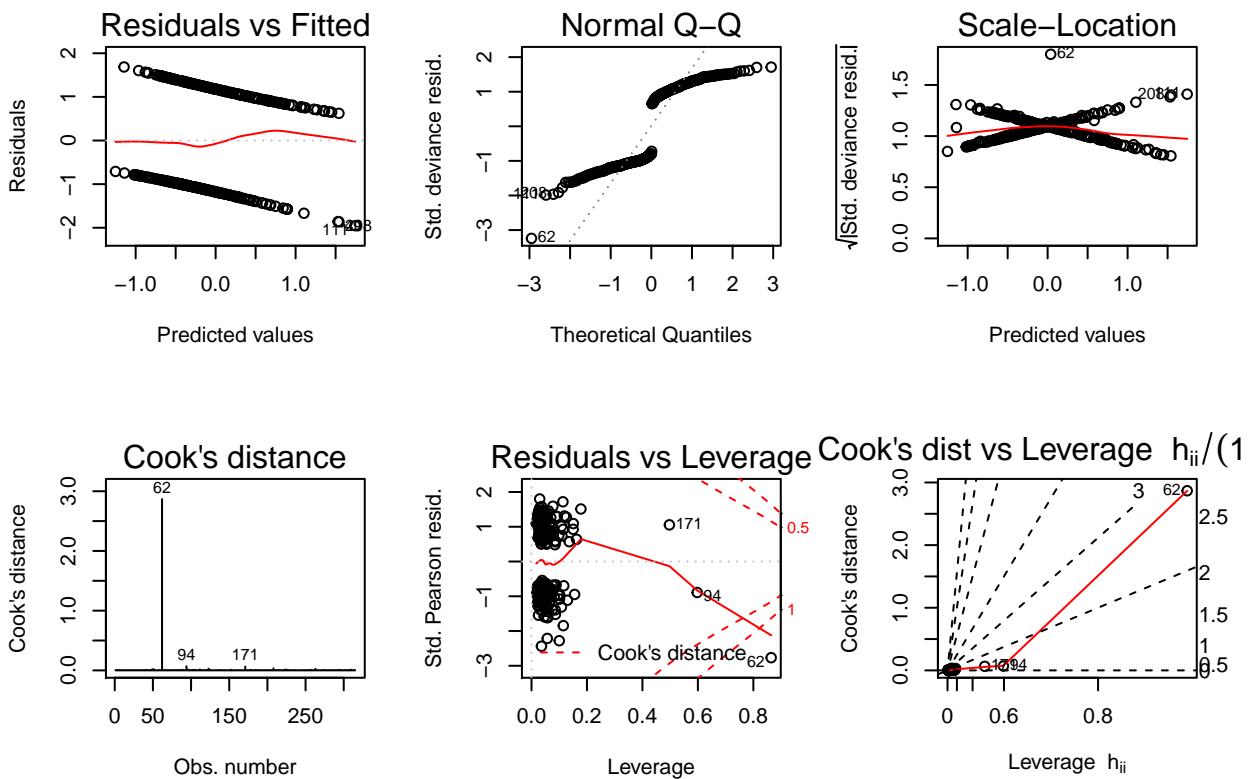
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et retdiet", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + sexe*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 113: Régression linéaire multiple avec interaction entre sexe et betaplasma

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.002
age	1.034	[0.316;3.685]	0.9573
sexeFemmes	1.22	[0.731;2.045]	0.4475
tabacAutrefois	0.967	[0.451;2.046]	0.9314
tabacFumeur	1.017	[0.977;1.059]	0.4147
bmi	1.086	[0.612;1.929]	0.7776
vitamineSouvent	1.094	[0.59;2.031]	0.7763
vitaminePas-souvent	1	[0.999;1.002]	0.4464
calories	0.994	[0.975;1.014]	0.5513
graisses	0.961	[0.895;1.031]	0.2696
fibres	0.991	[0.961;1.022]	0.5387
alcool	1	[0.997;1.003]	0.9201
cholesterol	1	[1;1]	0.912
betadiet	1	[1;1]	0.8935
rettdiet	1.004	[0.998;1.012]	0.2317
betaplasma	NA	[NA;NA]	0.4324
sexeFemmes:retinol[, "betaplasma"]	0.997	[0.989;1.003]	0.0484
0.109	[0.012;0.954]	0.0484	(Intercept)

```

## Waiting for profiling to be done...

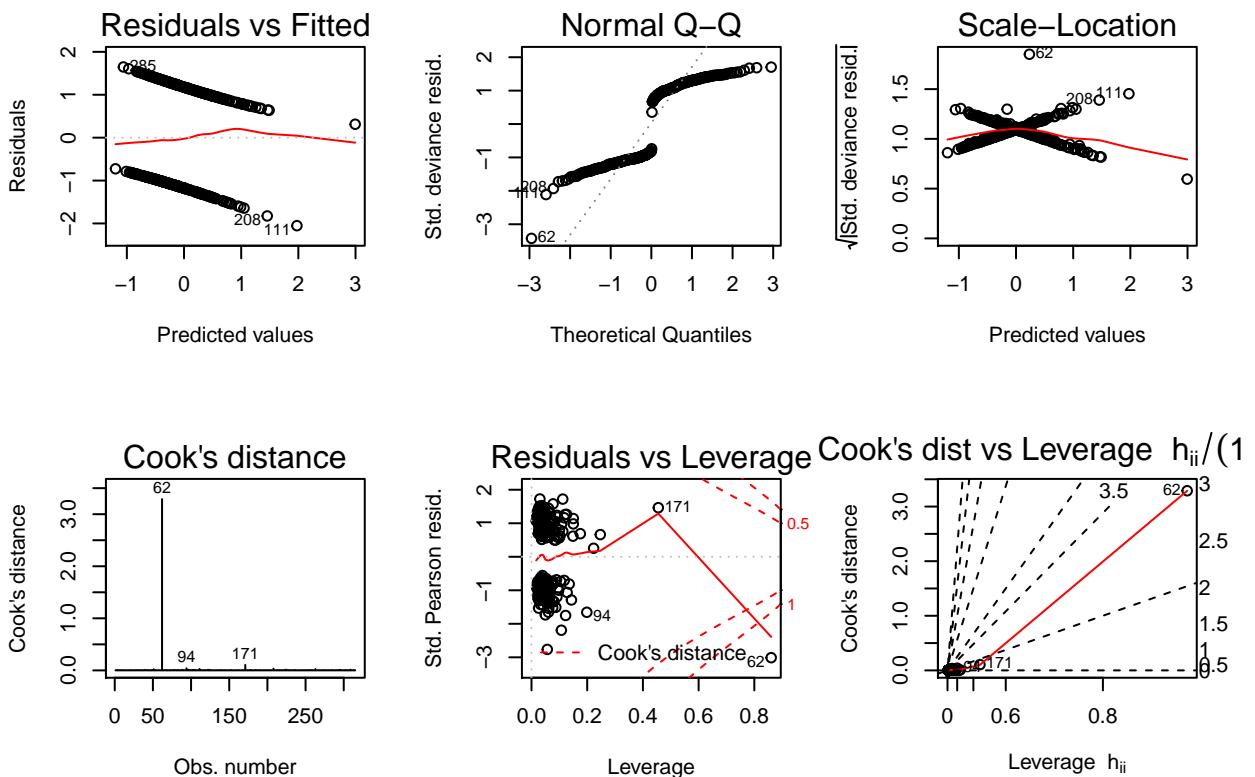
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre sexe et betaplasma", col.names = c(
        "Variable", "OR", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.3 Interaction avec le tabac

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + tabac*retinol[, "bmi"],
               data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 114: Régression linéaire multiple avec interaction entre tabac et bmi

	OR	IC	p
(Intercept)	1.031	[1.012;1.05]	0.0015
age	0.73	[0.329;1.589]	0.4312
sexeFemmes	2.476	[0.224;27.973]	0.4591
tabacAutrefois	0.377	[0.009;13.073]	0.5933
tabacFumeur	1.02	[0.971;1.072]	0.4254
bmi	1.087	[0.613;1.929]	0.7755
vitamineSouvent	1.112	[0.601;2.061]	0.7352
vitaminePas-souvent	1	[0.999;1.002]	0.4387
calories	0.994	[0.975;1.014]	0.5388
graisses	0.961	[0.895;1.031]	0.269
fibres	0.99	[0.96;1.021]	0.5036
alcool	1	[0.997;1.003]	0.9155
cholesterol	1	[1;1]	0.8546
betadiet	1	[1;1.001]	0.8805
retdiet	1.002	[1;1.003]	0.0523
betaplasma	NA	[NA;NA]	0.5538
tabacAutrefois:retinol[, "bmi"]	0.973	[0.889;1.065]	0.5862
tabacFumeur:retinol[, "bmi"]	1.04	[0.905;1.204]	0.0641
0.132	[0.015;1.104]	0.0641	(Intercept)

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

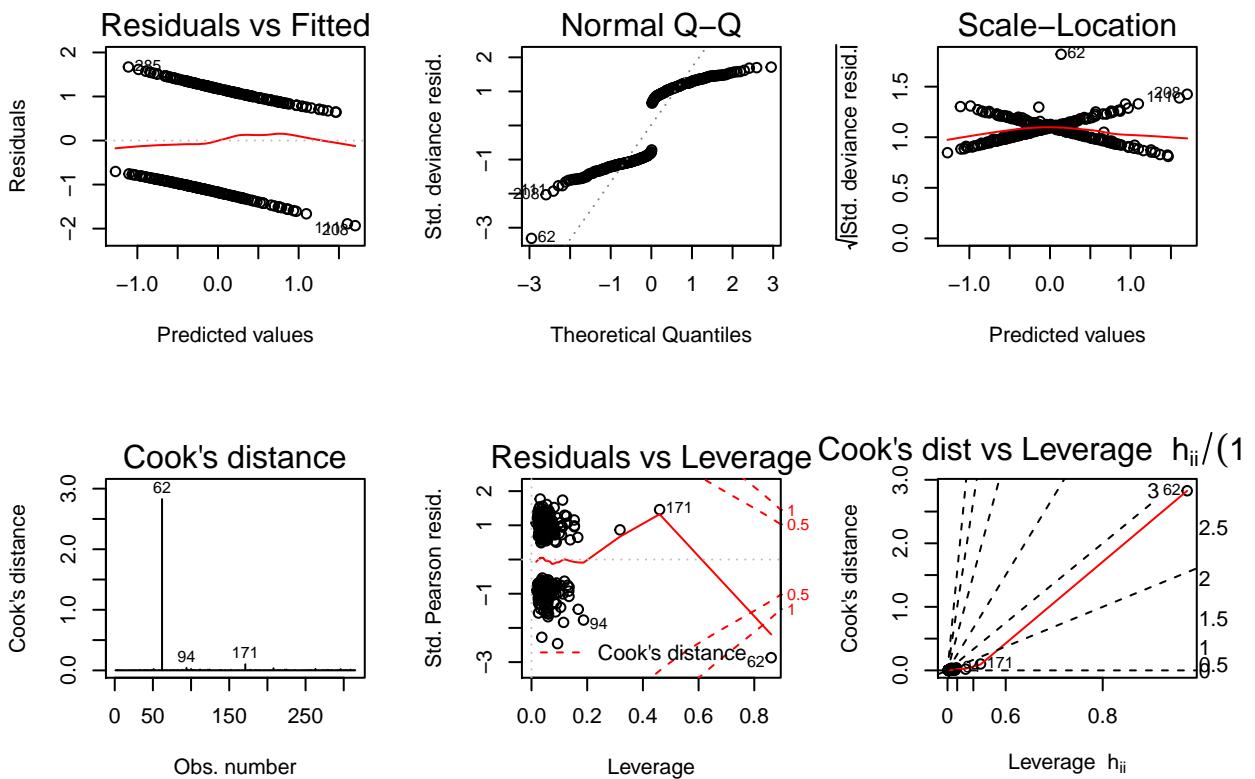
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [75] n'est pas un
## diviseur ni un multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et bmi", col.names = c(" ", ),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + tabac*retinol[, "vitamine"],
              data = retinol, family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4)

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 115: Régression linéaire multiple avec interaction entre tabac et vitamine

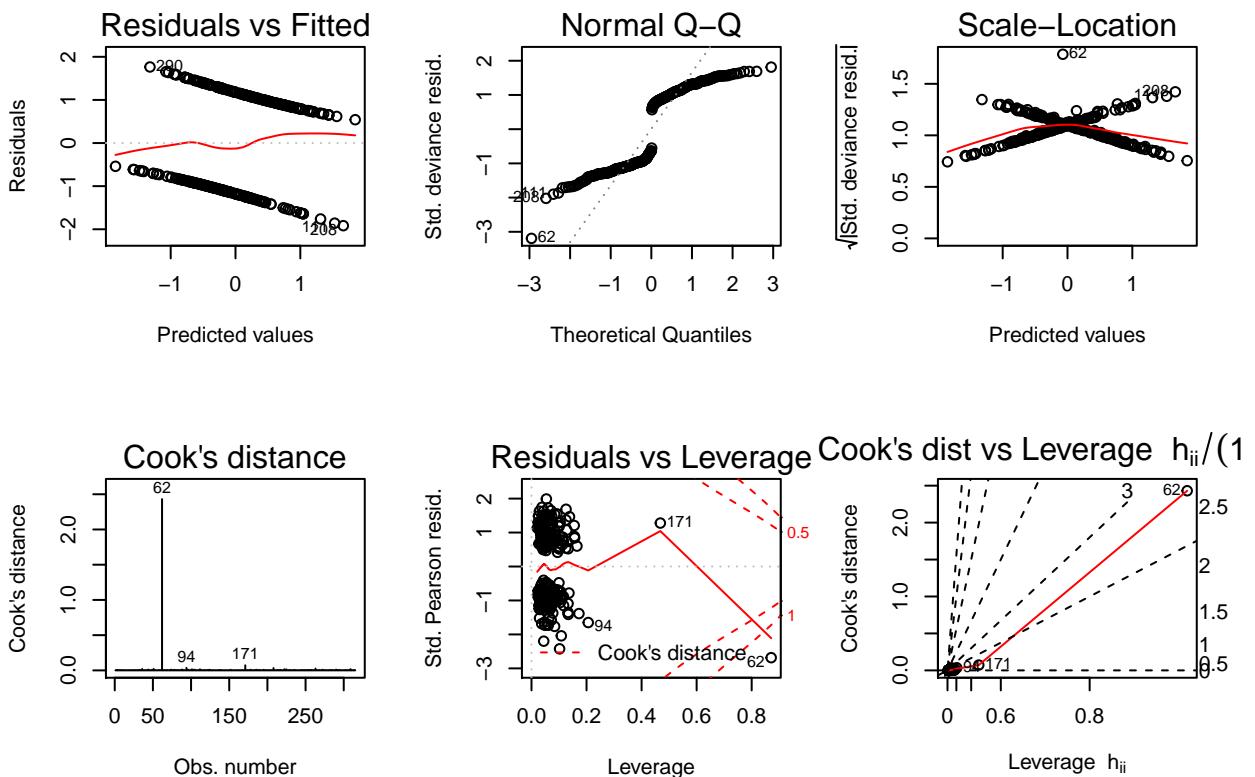
	OR	IC	p
(Intercept)	0.778	[0.346;1.718]	0.5362
age	1.553	[0.651;3.744]	0.3224
sexeFemmes	0.451	[0.129;1.426]	0.1891
tabacAutrefois	1.016	[0.975;1.058]	0.4569
tabacFumeur	0.926	[0.416;2.057]	0.8497
bmi	1.236	[0.502;3.057]	0.6438
vitamineSouvent	1.001	[0.999;1.002]	0.3961
vitaminePas-souvent	0.994	[0.975;1.014]	0.5618
calories	0.96	[0.893;1.03]	0.2583
graisses	0.991	[0.96;1.022]	0.5484
fibres	1	[0.997;1.003]	0.9186
alcool	1	[1;1]	0.7451
cholesterol	1	[1;1.001]	0.7995
betadiet	1.002	[1;1.004]	0.0255
retdiet	NA	[NA;NA]	0.6078
betaplasma	NA	[NA;NA]	0.0144
tabacAutrefois:retinol[, "vitamine"]Souvent	0.732	[0.222;2.402]	0.4126
tabacFumeur:retinol[, "vitamine"]Souvent	10.871	[1.712;82.433]	0.4893
tabacAutrefois:retinol[, "vitamine"]Pas-souvent	0.575	[0.152;2.159]	0.0342
tabacFumeur:retinol[, "vitamine"]Pas-souvent	1.879	[0.312;11.479]	5e-04
0.106	[0.013;0.828]	0.0342	(Intercept)
1.034	[1.015;1.055]	5e-04	age

```

## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [86] n'est pas un
## diviseur ni un multiple du nombre de lignes [22]
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et vitamine", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + tabac*retinol[, "calories"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

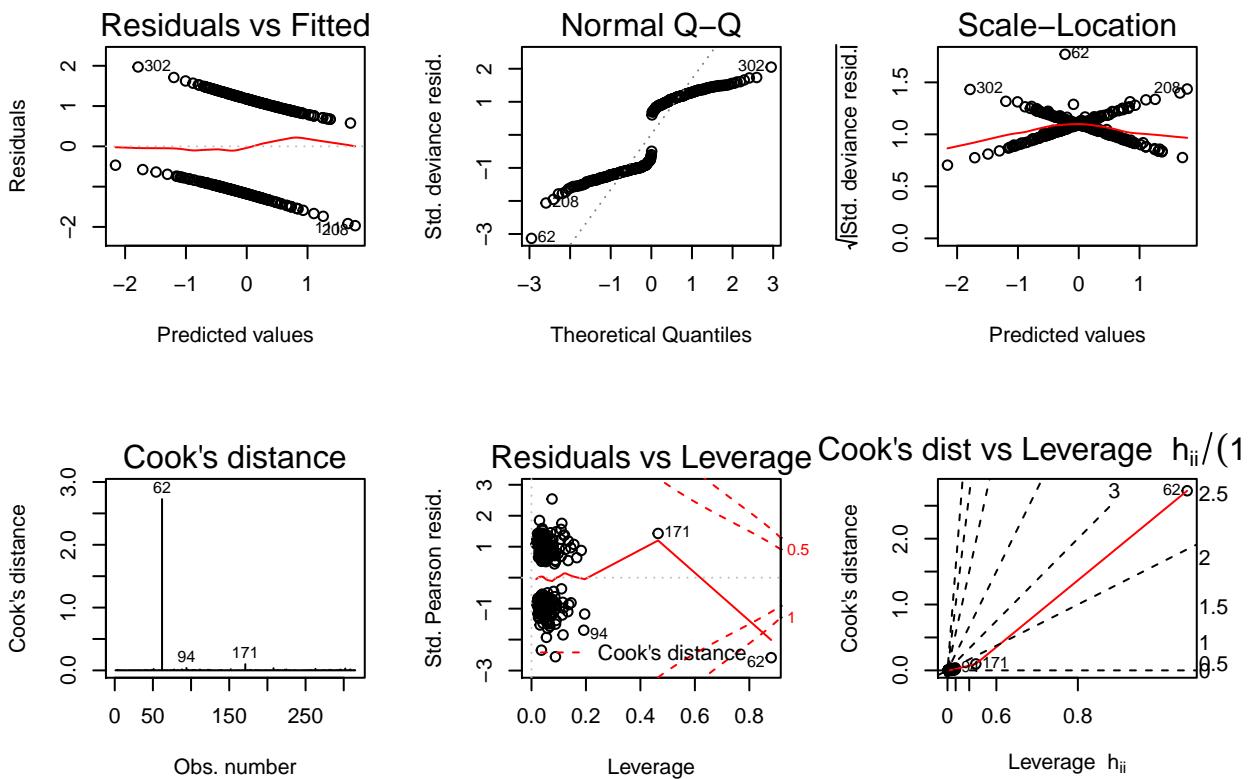
Table 116: Régression linéaire multiple avec interaction entre tabac et calories

	OR	IC	p
(Intercept)	1.032	[1.013;1.052]	0.001
age	0.674	[0.303;1.468]	0.3251
sexeFemmes	0.897	[0.19;4.248]	0.8906
tabacAutrefois	5.108	[0.59;48.639]	0.1447
tabacFumeur	1.02	[0.979;1.063]	0.3368
bmi	1.108	[0.624;1.97]	0.7257
vitamineSouvent	1.12	[0.604;2.084]	0.7192
vitaminePas-souvent	1.001	[0.999;1.002]	0.3116
calories	0.992	[0.972;1.012]	0.4231
graisses	0.956	[0.889;1.025]	0.212
fibres	1.006	[0.971;1.043]	0.7349
alcool	1	[0.997;1.003]	0.8797
cholesterol	1	[1;1]	0.7889
betadiet	1	[1;1.001]	0.87
retdiet	1.002	[1;1.003]	0.0499
betaplasma	NA	[NA;NA]	0.7352
tabacAutrefois:retinol[, "calories"]	1	[0.999;1.001]	0.1241
tabacFumeur:retinol[, "calories"]	0.999	[0.998;1]	0.0491
0.117	[0.013;0.973]	0.0491	(Intercept)

```

## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level))), : number of rows of result is not a multiple of vector length (arg
## 3)
## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [75] n'est pas un
## diviseur ni un multiple du nombre de lignes [19]
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et calories", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")
par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + tabac*retinol[, "graisses"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 117: Régression linéaire multiple avec interaction entre tabac et graisses

	OR	IC	p
(Intercept)	1.03	[1.012;1.05]	0.0016
age	0.669	[0.3;1.457]	0.3159
sexeFemmes	0.73	[0.205;2.573]	0.6244
tabacAutrefois	1.947	[0.264;14.515]	0.5107
tabacFumeur	1.018	[0.978;1.06]	0.3805
bmi	1.089	[0.614;1.932]	0.7699
vitamineSouvent	1.112	[0.6;2.065]	0.7366
vitaminePas-souvent	1.001	[0.999;1.002]	0.3775
calories	0.991	[0.97;1.012]	0.3869
graisses	0.959	[0.893;1.029]	0.2484
fibres	0.992	[0.962;1.024]	0.5963
alcool	1	[0.997;1.003]	0.9684
cholesterol	1	[1;1]	0.8035
betadiet	1	[1;1.001]	0.87
retdiet	1.002	[1;1.003]	0.0418
betaplasma	NA	[NA;NA]	0.404
tabacAutrefois:retinol[, "graisses"]	1.006	[0.991;1.022]	0.4889
tabacFumeur:retinol[, "graisses"]	0.992	[0.968;1.015]	0.0954
0.169	[0.02;1.353]	0.0954	(Intercept)

```

## Waiting for profiling to be done...

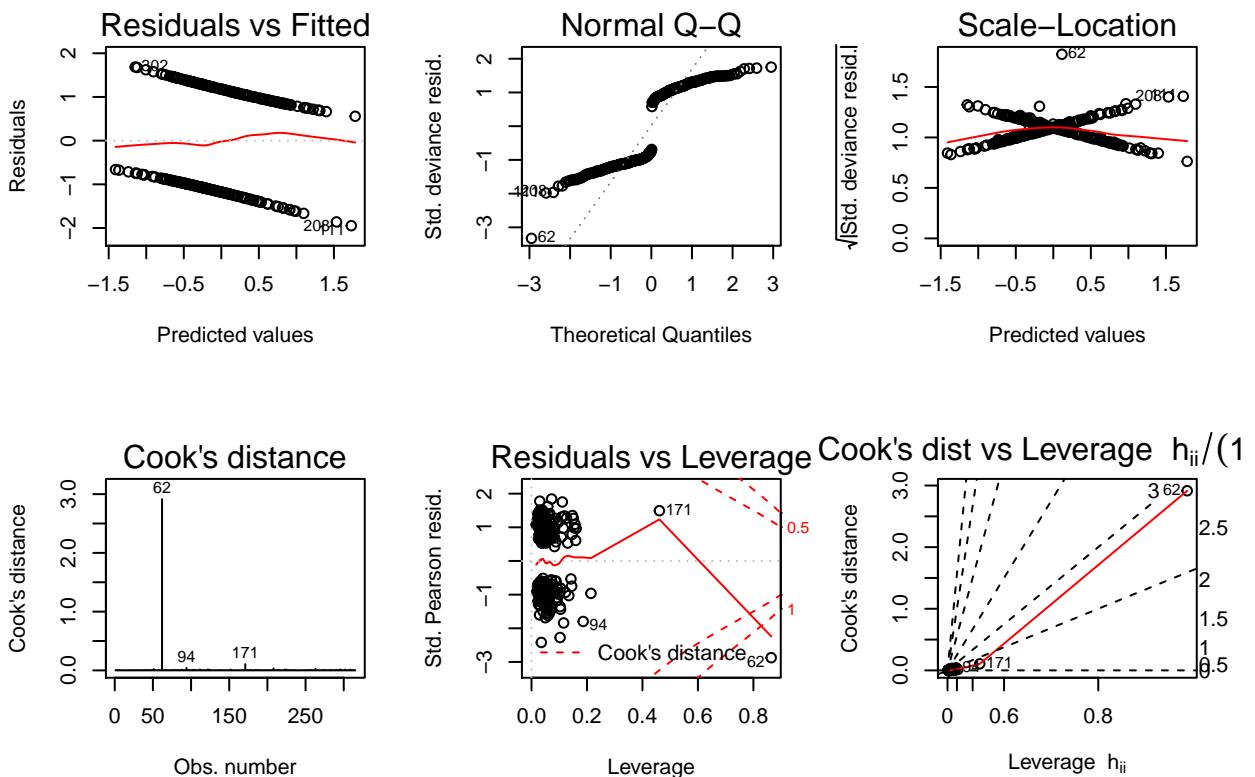
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et graisses", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + tabac*retinol[, "fibres"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[" ,round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 118: Régression linéaire multiple avec interaction entre tabac et fibres

	OR	IC	p
(Intercept)	1.03	[1.012;1.05]	0.0016
age	0.682	[0.308;1.476]	0.3355
sexeFemmes	0.966	[0.237;3.95]	0.9618
tabacAutrefois	1.947	[0.307;13.058]	0.4819
tabacFumeur	1.018	[0.977;1.06]	0.3935
bmi	1.091	[0.615;1.937]	0.7662
vitamineSouvent	1.089	[0.588;2.023]	0.7855
vitaminePas-souvent	1	[0.999;1.002]	0.4446
calories	0.994	[0.975;1.014]	0.571
graisses	0.962	[0.885;1.044]	0.353
fibres	0.99	[0.96;1.021]	0.5064
alcool	1	[0.997;1.002]	0.8125
cholesterol	1	[1;1]	0.8804
betadiet	1	[1;1]	0.8873
retdiet	1.002	[1;1.003]	0.0572
betaplasma	NA	[NA;NA]	0.7331
tabacAutrefois:retinol[, "fibres"]	1.018	[0.92;1.125]	0.4192
tabacFumeur:retinol[, "fibres"]	0.936	[0.79;1.094]	0.0741
0.153	[0.019;1.18]	0.0741	(Intercept)

```

## Waiting for profiling to be done...

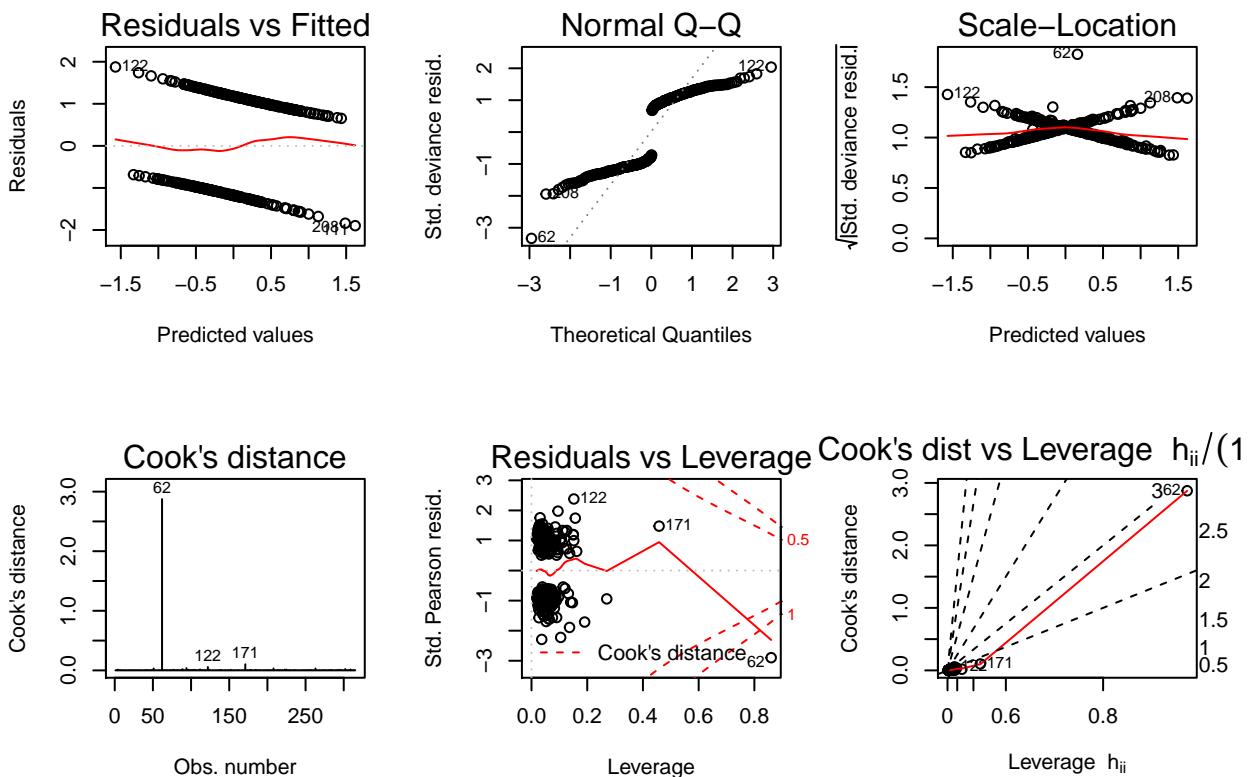
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et fibres", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + tabac*retinol[, "alcool"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[" ,round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 119: Régression linéaire multiple avec interaction entre tabac et alcool

	OR	IC	p
(Intercept)	1.033	[1.014;1.054]	7e-04
age	0.836	[0.374;1.844]	0.658
sexeFemmes	1.085	[0.594;1.981]	0.791
tabacAutrefois	1.235	[0.555;2.73]	0.6017
tabacFumeur	1.025	[0.984;1.069]	0.2418
bmi	1.211	[0.678;2.169]	0.5182
vitamineSouvent	1.18	[0.635;2.2]	0.6016
vitaminePas-souvent	1.001	[0.999;1.002]	0.3152
calories	0.992	[0.972;1.012]	0.4262
graisses	0.957	[0.89;1.028]	0.2307
fibres	1.054	[0.954;1.174]	0.3058
alcool	1	[0.997;1.002]	0.8466
cholesterol	1	[1;1]	0.7734
betadiet	1	[1;1.001]	0.8625
retdiet	1.001	[1;1.003]	0.062
betaplasma	NA	[NA;NA]	0.9035
tabacAutrefois:retinol[, "alcool"]	1.008	[0.884;1.149]	0.1734
tabacFumeur:retinol[, "alcool"]	0.929	[0.829;1.031]	0.018
0.073	[0.008;0.624]	0.018	(Intercept)

```

## Waiting for profiling to be done...

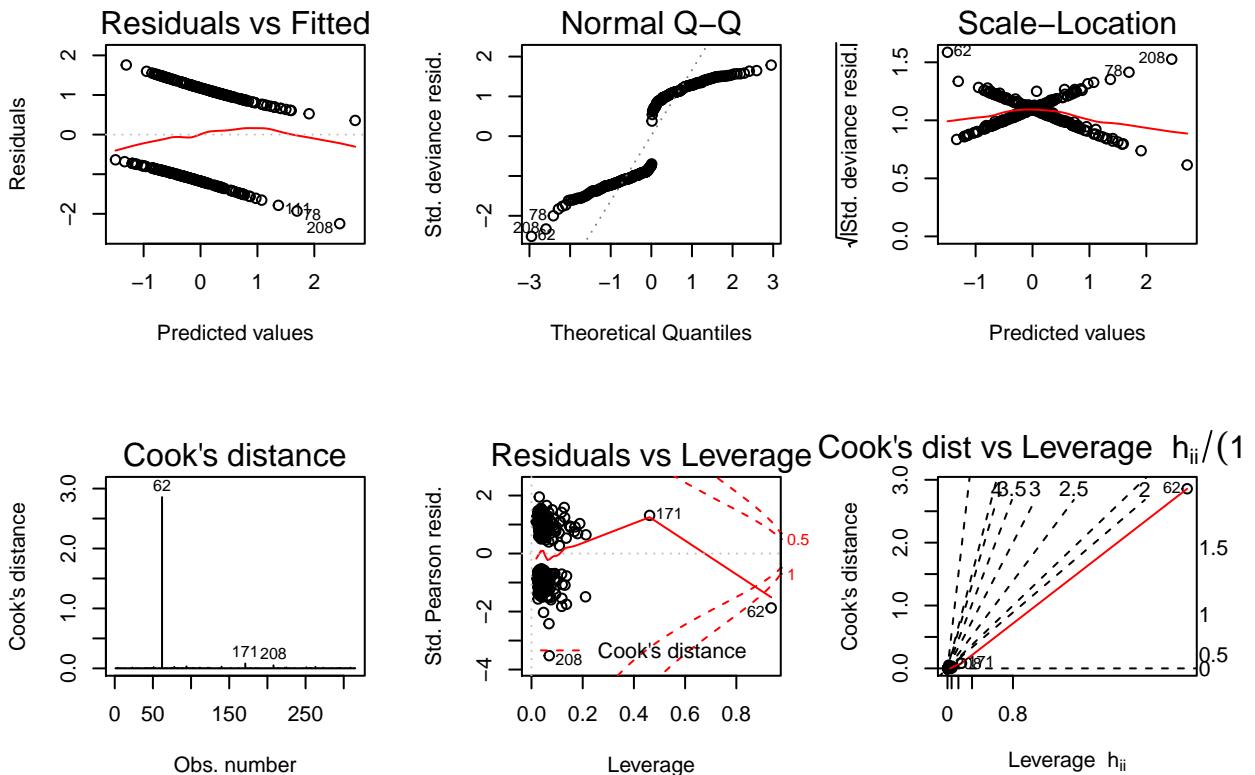
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et alcool", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + tabac*retinol[, "cholesterol"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 120: Régression linéaire multiple avec interaction entre tabac et cholesterol

	OR	IC	p
(Intercept)	1.03	[1.012;1.05]	0.0017
age	0.691	[0.312;1.498]	0.3526
sexeFemmes	1.096	[0.361;3.31]	0.8704
tabacAutrefois	1.559	[0.325;7.745]	0.5801
tabacFumeur	1.017	[0.977;1.059]	0.4137
bmi	1.099	[0.621;1.949]	0.7457
vitamineSouvent	1.123	[0.607;2.084]	0.7115
vitaminePas-souvent	1.001	[0.999;1.002]	0.406
calories	0.994	[0.974;1.013]	0.519
graisses	0.959	[0.892;1.029]	0.2457
fibres	0.991	[0.961;1.023]	0.5766
alcool	1	[0.997;1.003]	0.9632
cholesterol	1	[1;1]	0.8264
betadiet	1	[1;1]	0.9511
retdiet	1.002	[1;1.003]	0.0454
betaplasma	NA	[NA;NA]	0.8518
tabacAutrefois:retinol[, "cholesterol"]	1	[0.996;1.005]	0.5183
tabacFumeur:retinol[, "cholesterol"]	0.998	[0.992;1.004]	0.0698
0.15	[0.019;1.148]	0.0698	(Intercept)

```

## Waiting for profiling to be done...

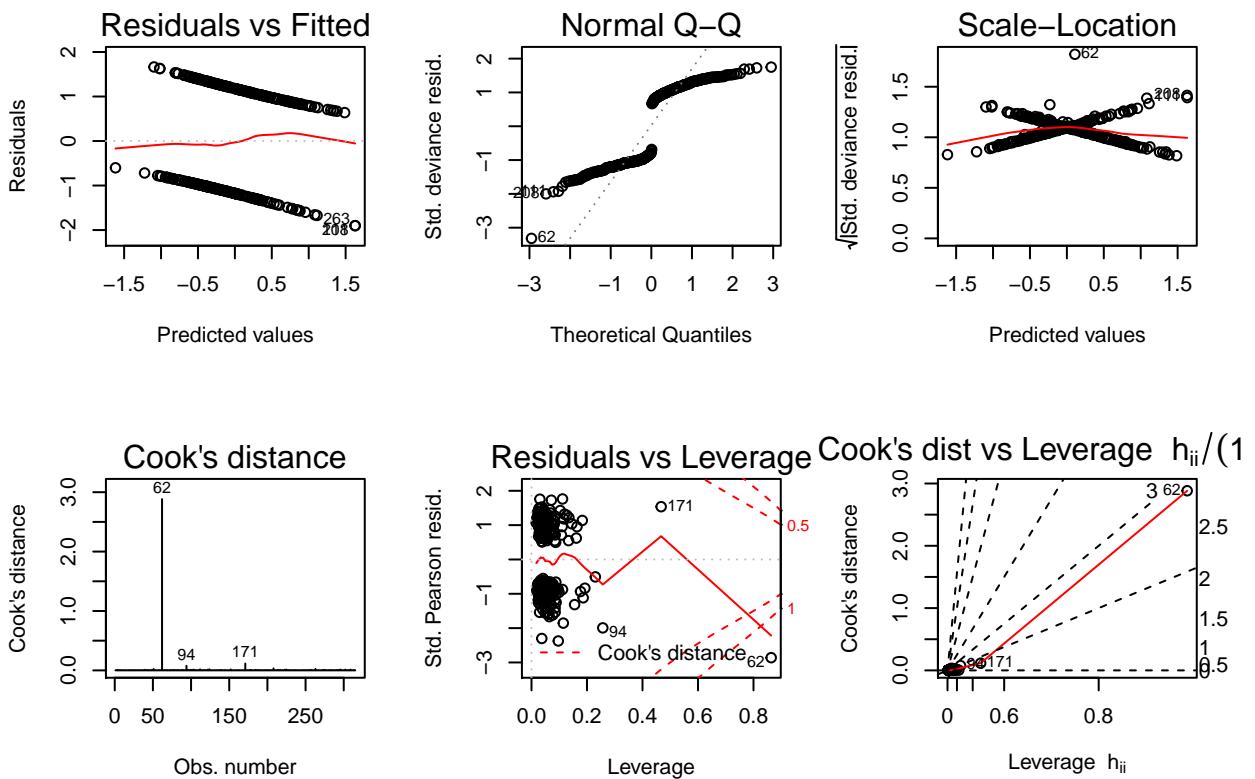
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et cholesterol", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + tabac*retinol[, "betadiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 121: Régression linéaire multiple avec interaction entre tabac et betadiet

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0018
age	0.685	[0.31;1.479]	0.3387
sexeFemmes	1.02	[0.406;2.555]	0.9669
tabacAutrefois	1.428	[0.389;5.579]	0.5975
tabacFumeur	1.018	[0.978;1.061]	0.3739
bmi	1.113	[0.627;1.977]	0.7143
vitamineSouvent	1.099	[0.594;2.038]	0.7642
vitaminePas-souvent	1	[0.999;1.002]	0.4997
calories	0.995	[0.976;1.015]	0.6173
graisses	0.966	[0.898;1.036]	0.3318
fibres	0.992	[0.962;1.024]	0.6093
alcool	1	[0.997;1.002]	0.8112
cholesterol	1	[1;1]	0.8072
betadiet	1	[1;1]	0.9113
retdiet	1.001	[1;1.003]	0.0579
betaplasma	NA	[NA;NA]	0.6582
tabacAutrefois:retinol[, "betadiet"]	1	[1;1]	0.482
tabacFumeur:retinol[, "betadiet"]	1	[0.999;1]	0.0798
0.159	[0.02;1.223]	0.0798	(Intercept)

```

## Waiting for profiling to be done...

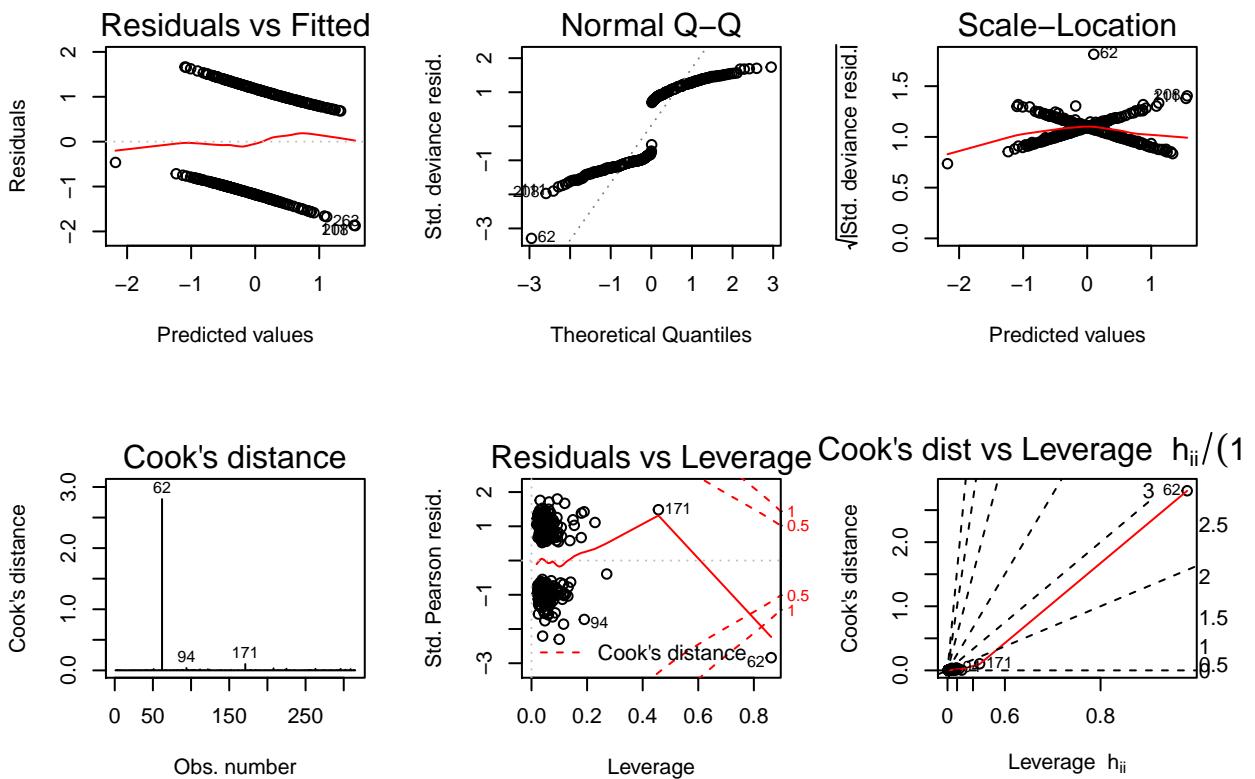
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et betadiet", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + tabac*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[" ,round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 122: Régression linéaire multiple avec interaction entre tabac et retdiet

	OR	IC	p
(Intercept)	1.031	[1.012;1.051]	0.0014
age	0.663	[0.299;1.438]	0.3028
sexeFemmes	1.605	[0.649;4.018]	0.305
tabacAutrefois	2.149	[0.527;8.956]	0.286
tabacFumeur	1.016	[0.975;1.058]	0.4502
bmi	1.082	[0.61;1.923]	0.7871
vitamineSouvent	1.141	[0.616;2.122]	0.6755
vitaminePas-souvent	1.001	[0.999;1.002]	0.3063
calories	0.992	[0.973;1.012]	0.4322
graisses	0.955	[0.888;1.025]	0.2046
fibres	0.988	[0.958;1.02]	0.4449
alcool	1	[0.997;1.002]	0.8348
cholesterol	1	[1;1]	0.9101
betadiet	1	[1;1.001]	0.4807
retdiet	1.002	[1;1.003]	0.0533
betaplasma	NA	[NA;NA]	0.4501
tabacAutrefois:retinol[, "retdiet"]	1	[0.999;1.001]	0.2045
tabacFumeur:retinol[, "retdiet"]	0.999	[0.997;1.001]	0.051
0.132	[0.017;0.991]	0.051	(Intercept)

```

## Waiting for profiling to be done...

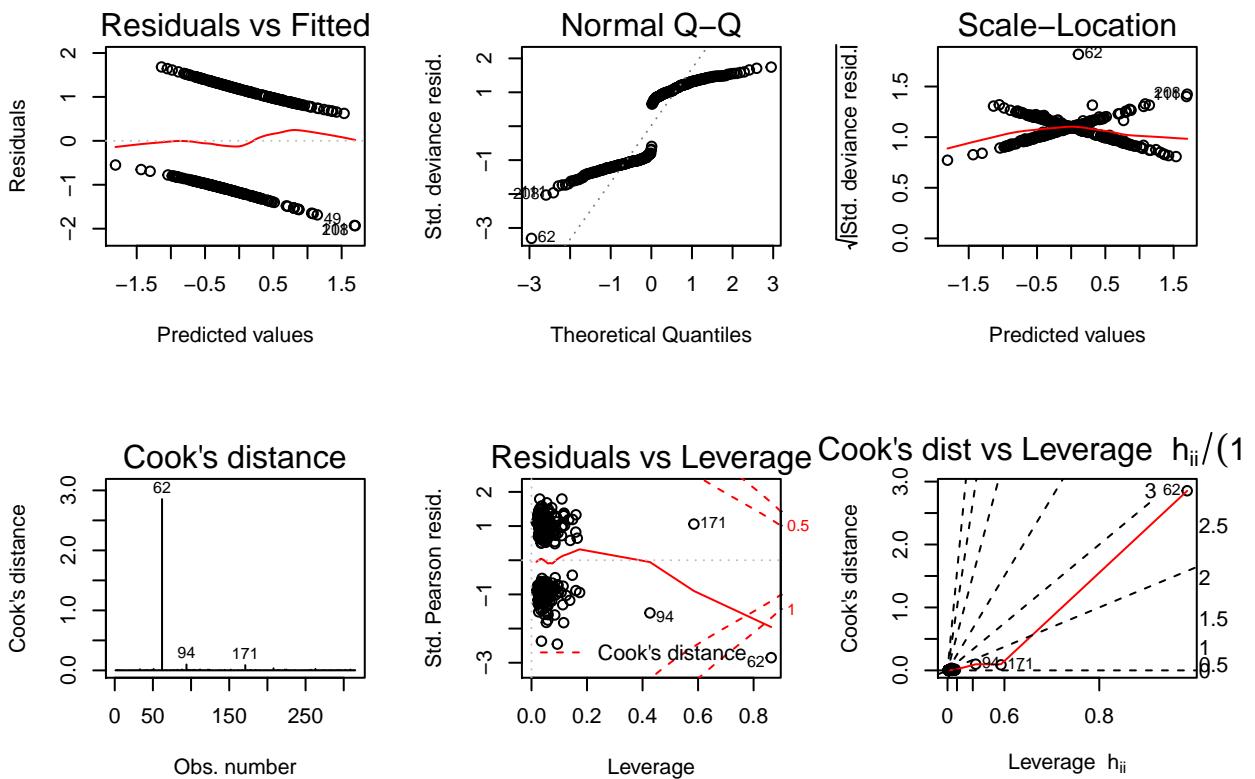
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et retdiet", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + tabac*retinol[, "betaplasma"] ,
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[" ,round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 123: Régression linéaire multiple avec interaction entre tabac et betaplasma

	OR	IC	p
(Intercept)	1.029	[1.011;1.049]	0.0022
age	0.701	[0.318;1.512]	0.368
sexeFemmes	1.409	[0.659;3.052]	0.3787
tabacAutrefois	0.859	[0.22;3.103]	0.8191
tabacFumeur	1.018	[0.978;1.06]	0.3862
bmi	1.121	[0.632;1.994]	0.6954
vitamineSouvent	1.141	[0.614;2.125]	0.6762
vitaminePas-souvent	1	[0.999;1.002]	0.4511
calories	0.994	[0.975;1.014]	0.5652
graisses	0.96	[0.893;1.029]	0.2537
fibres	0.991	[0.961;1.022]	0.531
alcool	1	[0.997;1.002]	0.8513
cholesterol	1	[1;1]	0.9051
betadiet	1	[1;1]	0.8914
retdiet	1.002	[1;1.004]	0.0895
betaplasma	NA	[NA;NA]	0.6119
tabacAutrefois:retinol[, "betaplasma"]	0.999	[0.996;1.002]	0.7777
tabacFumeur:retinol[, "betaplasma"]	1.001	[0.993;1.01]	0.0636
0.147	[0.019;1.096]	0.0636	(Intercept)

```

## Waiting for profiling to be done...

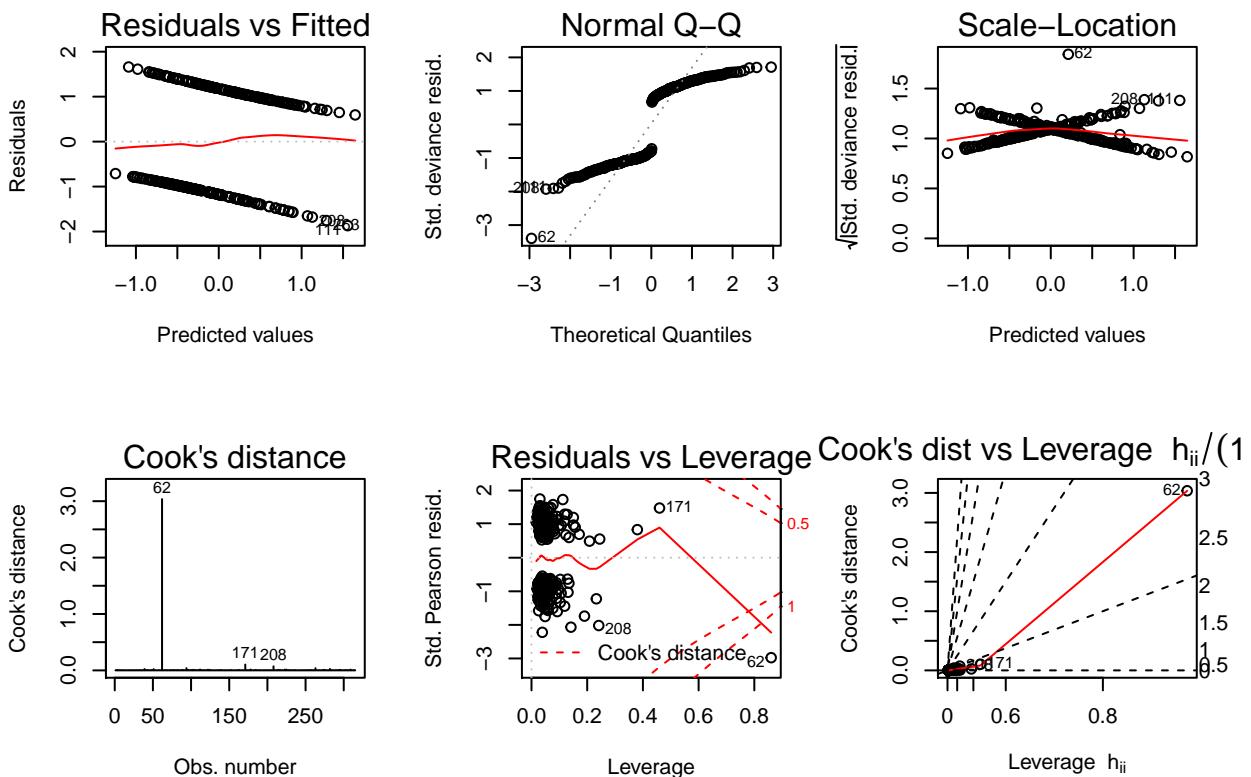
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre tabac et betaplasma", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.4 Interaction avec le bmi

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + bmi*retinol[, "vitamine"],
               data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4)

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 124: Régression linéaire multiple avec interaction entre bmi et vitamine

	OR	IC	p
(Intercept)	0.719	[0.325;1.557]	0.4063
age	1.205	[0.72;2.024]	0.4792
sexeFemmes	0.992	[0.462;2.105]	0.9843
tabacAutrefois	1.06	[0.991;1.139]	0.0942
tabacFumeur	2.833	[0.23;35.684]	0.4158
bmi	14.246	[0.968;234.378]	0.0566
vitamineSouvent	1.001	[0.999;1.002]	0.3799
vitaminePas-souvent	0.993	[0.974;1.013]	0.4948
calories	0.961	[0.894;1.031]	0.2672
graisses	0.989	[0.959;1.021]	0.4695
fibres	1	[0.997;1.002]	0.7733
alcool	1	[1;1]	0.8465
cholesterol	1	[1;1.001]	0.7911
betadiet	1.002	[1;1.003]	0.0505
retdiet	NA	[NA;NA]	0.4536
betaplasma	NA	[NA;NA]	0.0617
bmi:retinol[, "vitamine"]Souvent	0.965	[0.879;1.059]	0.0184
bmi:retinol[, "vitamine"]Pas-souvent	0.909	[0.819;1.003]	0.0011
0.045	[0.003;0.567]	0.0184	(Intercept)
1.032	[1.013;1.052]	0.0011	age

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

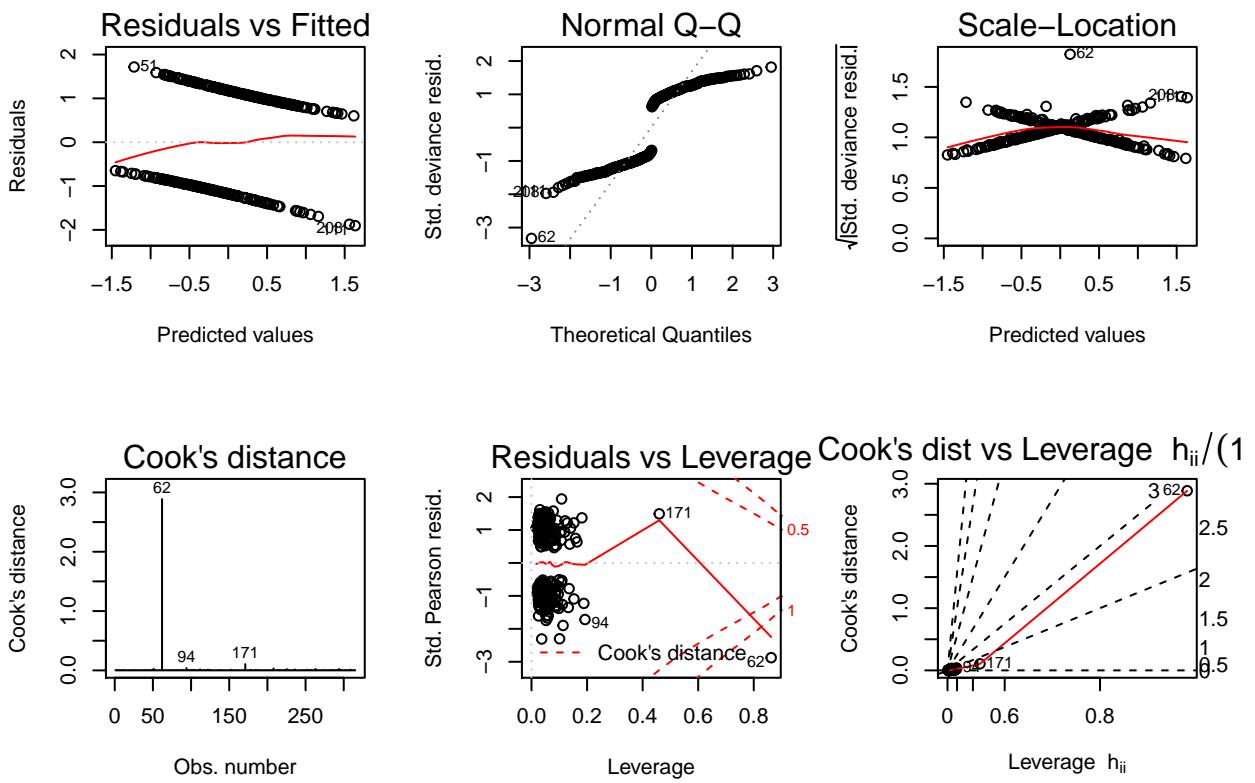
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [78] n'est pas un
## diviseur ni un multiple du nombre de lignes [20]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et vitamine", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + bmi*retinol[, "calories"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 125: Régression linéaire multiple avec interaction entre bmi et calories

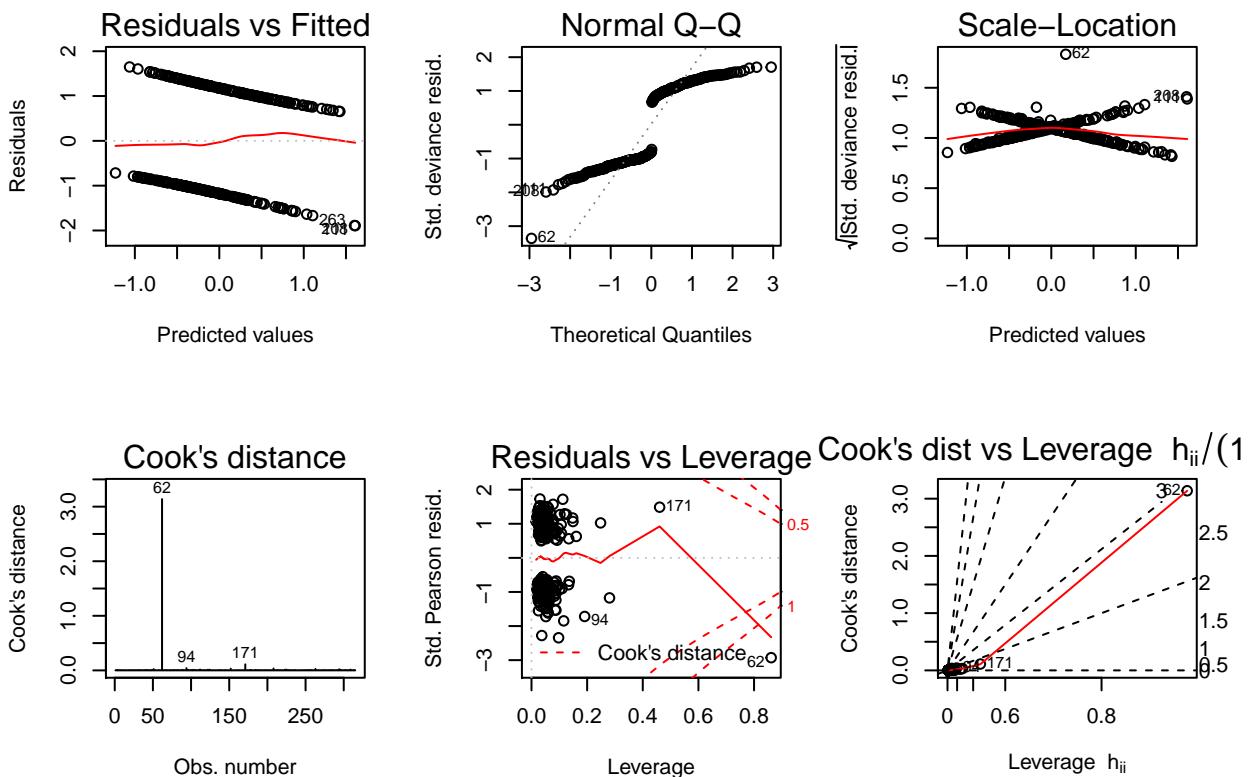
	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0019
age	0.699	[0.318;1.505]	0.3637
sexeFemmes	1.219	[0.73;2.041]	0.4502
tabacAutrefois	0.978	[0.457;2.066]	0.9538
tabacFumeur	1.014	[0.907;1.134]	0.8041
bmi	1.105	[0.624;1.958]	0.7321
vitamineSouvent	1.121	[0.607;2.076]	0.7153
vitaminePas-souvent	1	[0.998;1.002]	0.6707
calories	0.994	[0.975;1.014]	0.5551
graisses	0.961	[0.895;1.031]	0.2734
fibres	0.99	[0.96;1.022]	0.5183
alcool	1	[0.997;1.002]	0.8723
cholesterol	1	[1;1]	0.8779
betadiet	1	[1;1]	0.895
retdiet	1.002	[1;1.003]	0.0501
betaplasma	NA	[NA;NA]	0.9564
bmi:retinol[, "calories"]	1	[1;1]	0.3132
0.17	[0.005;5.281]	0.3132	(Intercept)

```

## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats:::coef(x)), exp(stats:::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]
kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et calories", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + bmi*retinol[, "graisses"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 126: Régression linéaire multiple avec interaction entre bmi et graisses

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0019
age	0.699	[0.318;1.507]	0.3651
sexeFemmes	1.218	[0.729;2.04]	0.4521
tabacAutrefois	0.978	[0.457;2.065]	0.9534
tabacFumeur	1.023	[0.932;1.125]	0.6282
bmi	1.105	[0.624;1.957]	0.7324
vitamineSouvent	1.12	[0.606;2.074]	0.7184
vitaminePas-souvent	1	[0.999;1.002]	0.4472
calories	0.996	[0.961;1.033]	0.8464
graisses	0.961	[0.895;1.031]	0.2721
fibres	0.99	[0.96;1.021]	0.5019
alcool	1	[0.997;1.002]	0.8848
cholesterol	1	[1;1]	0.874
betadiet	1	[1;1]	0.8894
retdiet	1.002	[1;1.003]	0.0497
betaplasma	NA	[NA;NA]	0.8846
bmi:retinol[, "graisses"]	1	[0.999;1.001]	0.2007
0.132	[0.006;2.893]	0.2007	(Intercept)

```

## Waiting for profiling to be done...

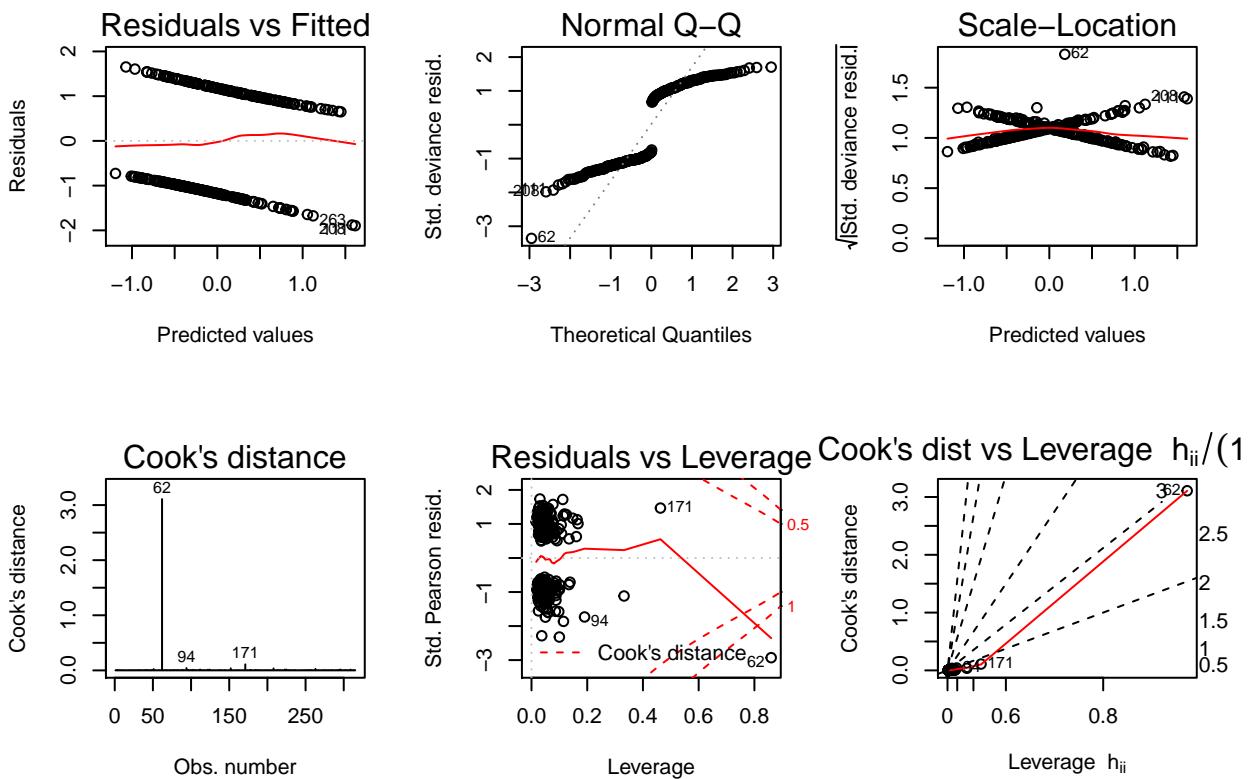
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et graisses", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + bmi*retinol[, "fibres"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 127: Régression linéaire multiple avec interaction entre bmi et fibres

	OR	IC	p
(Intercept)	1.03	[1.011;1.05]	0.0017
age	0.708	[0.322;1.527]	0.3818
sexeFemmes	1.229	[0.735;2.06]	0.4323
tabacAutrefois	0.988	[0.461;2.09]	0.9751
tabacFumeur	1.053	[0.938;1.187]	0.3831
bmi	1.104	[0.624;1.957]	0.7335
vitamineSouvent	1.137	[0.614;2.111]	0.6831
vitaminePas-souvent	1	[0.999;1.002]	0.4339
calories	0.994	[0.975;1.014]	0.5694
graisses	1.03	[0.822;1.295]	0.7964
fibres	0.99	[0.96;1.021]	0.4866
alcool	1	[0.997;1.002]	0.871
cholesterol	1	[1;1]	0.8973
betadiet	1	[1;1.001]	0.8474
retdiet	1.001	[1;1.003]	0.0557
betaplasma	NA	[NA;NA]	0.5289
bmi:retinol[, "fibres"]	0.997	[0.988;1.006]	0.1251
0.061	[0.002;2.058]	0.1251	(Intercept)

```

## Waiting for profiling to be done...

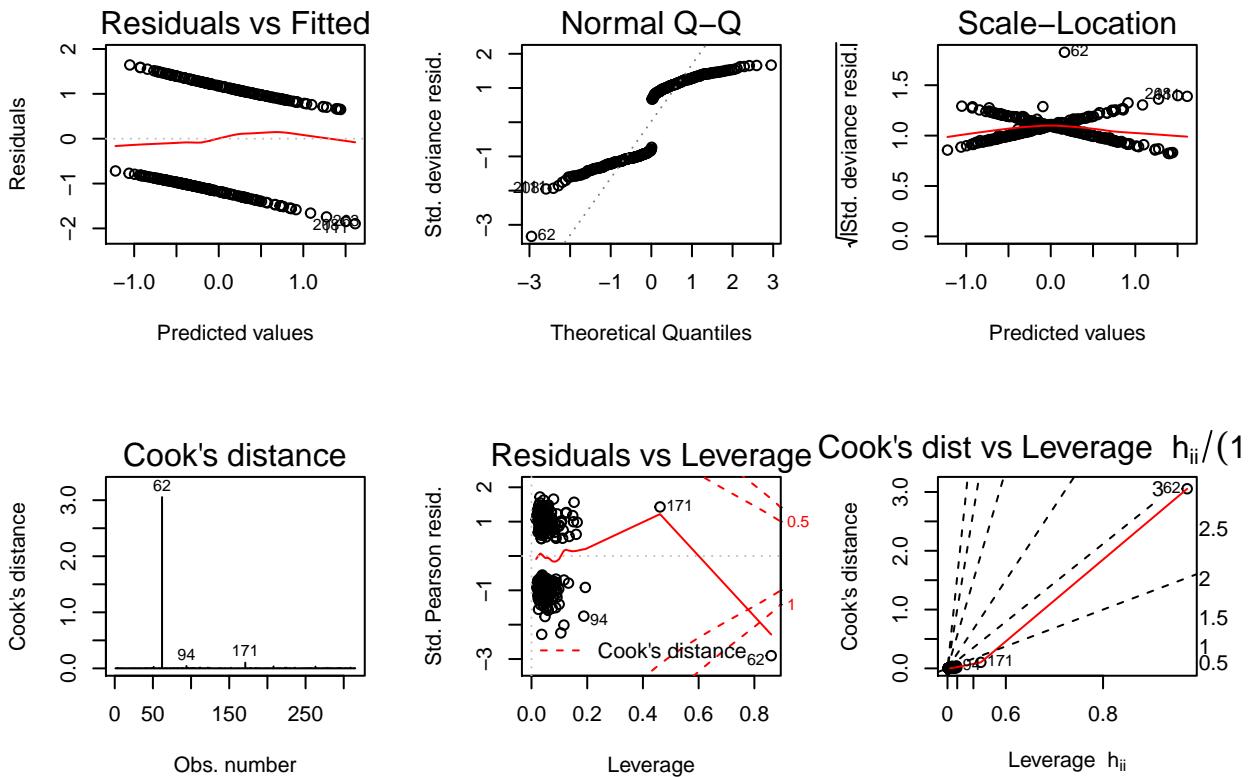
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et fibres", col.names = c(" "),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + bmi*retinol[, "alcool"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 128: Régression linéaire multiple avec interaction entre bmi et alcool

	OR	IC	p
(Intercept)	1.031	[1.012;1.051]	0.0013
age	0.836	[0.373;1.845]	0.6586
sexeFemmes	1.185	[0.709;1.989]	0.5178
tabacAutrefois	0.959	[0.445;2.042]	0.915
tabacFumeur	1.005	[0.963;1.048]	0.8331
bmi	1.108	[0.622;1.974]	0.7277
vitamineSouvent	1.156	[0.624;2.146]	0.6457
vitaminePas-souvent	1	[0.999;1.002]	0.4315
calories	0.993	[0.974;1.013]	0.4984
graisses	0.963	[0.896;1.033]	0.297
fibres	0.746	[0.49;0.997]	0.1075
alcool	1	[0.997;1.003]	0.9215
cholesterol	1	[1;1]	0.8237
betadiet	1	[1;1.001]	0.8685
retdiet	1.002	[1;1.003]	0.0426
betaplasma	NA	[NA;NA]	0.1194
bmi:retinol[, "alcool"]	1.012	[1;1.03]	0.0834
0.169	[0.022;1.247]	0.0834	(Intercept)

```

## Waiting for profiling to be done...

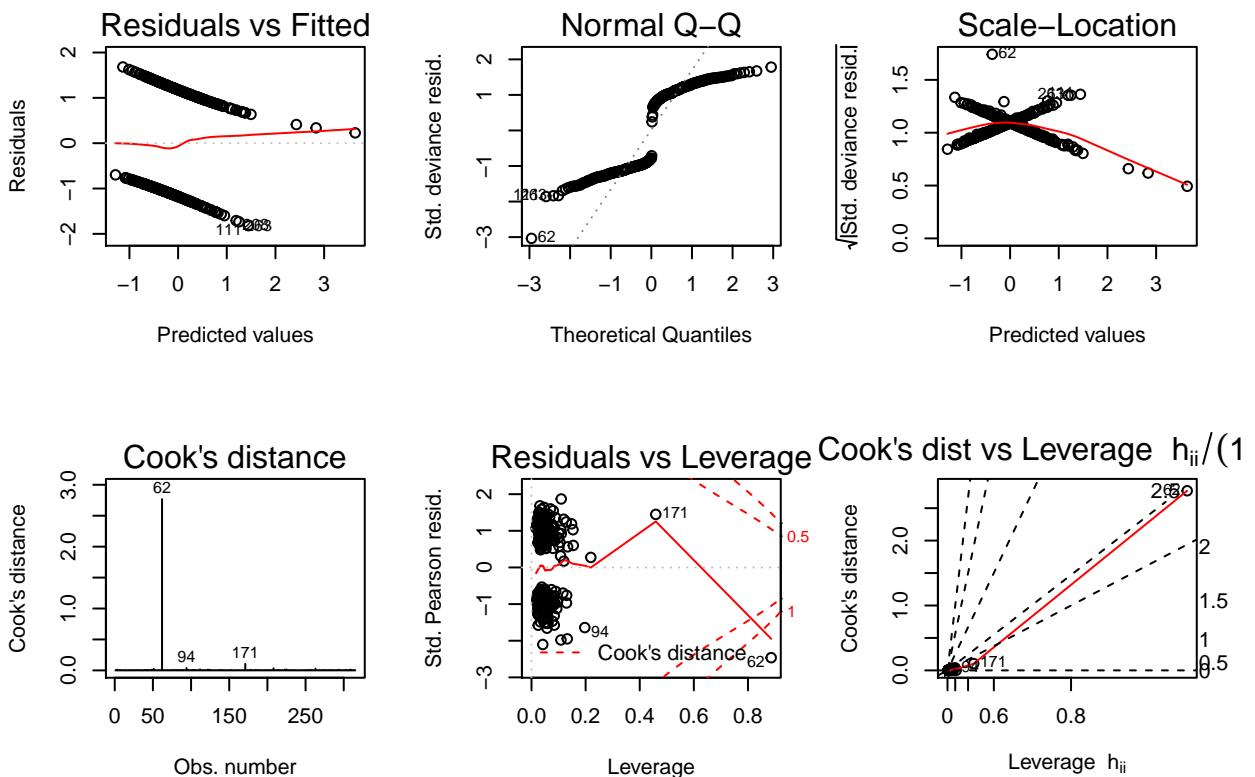
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et alcool", col.names = c(" ", ),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + bmi*retinol[, "cholesterol"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 129: Régression linéaire multiple avec interaction entre bmi et cholesterol

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0019
age	0.698	[0.317;1.505]	0.3626
sexeFemmes	1.219	[0.73;2.043]	0.4496
tabacAutrefois	0.979	[0.457;2.071]	0.9562
tabacFumeur	1.015	[0.936;1.1]	0.7153
bmi	1.105	[0.624;1.957]	0.7326
vitamineSouvent	1.122	[0.607;2.079]	0.7136
vitaminePas-souvent	1	[0.999;1.002]	0.4463
calories	0.994	[0.975;1.014]	0.5545
graisses	0.961	[0.895;1.031]	0.2705
fibres	0.99	[0.96;1.021]	0.5081
alcool	1	[0.992;1.008]	0.9169
cholesterol	1	[1;1]	0.8791
betadiet	1	[1;1]	0.8921
rettdiet	1.002	[1;1.003]	0.0503
betaplasma	NA	[NA;NA]	0.9568
bmi:retinol[, "cholesterol"]	1	[1;1]	0.2088
0.166	[0.01;2.701]	0.2088	(Intercept)

```

## Waiting for profiling to be done...

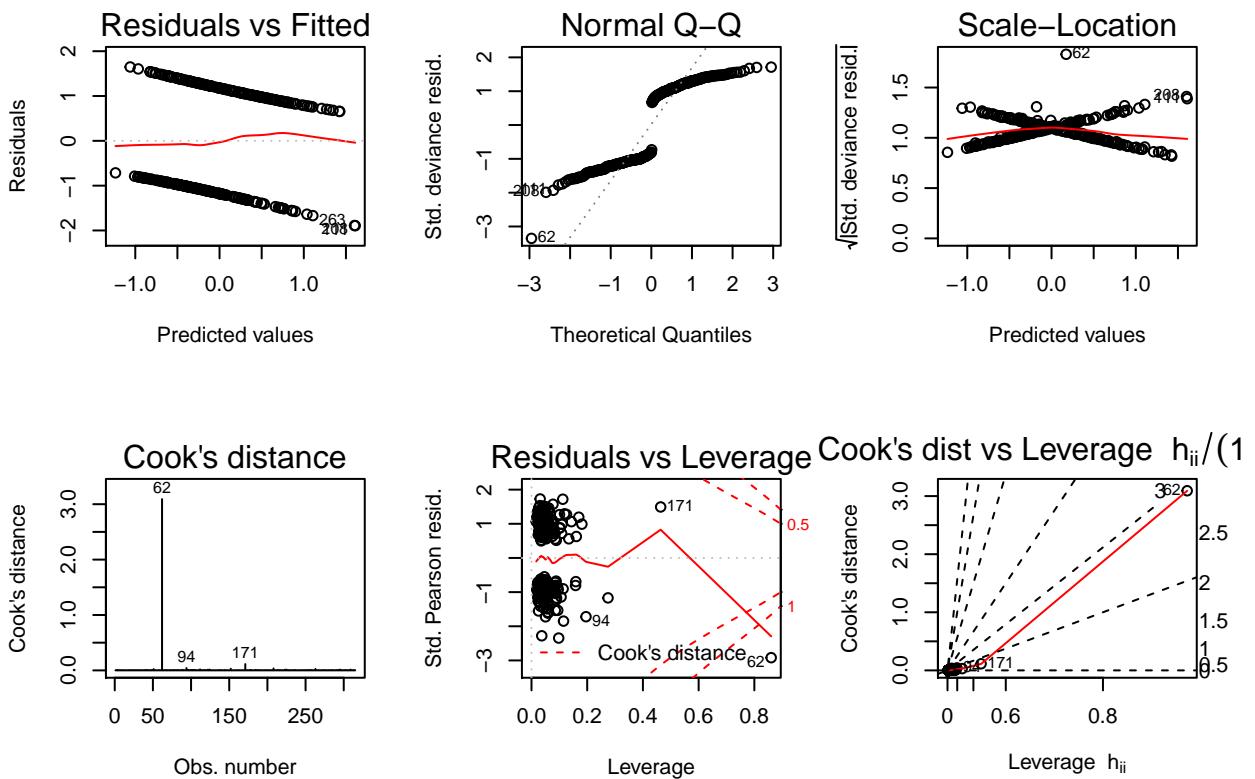
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et cholesterol", col.names = c(
        "Variable", "B", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + bmi*retinol[, "betadiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 130: Régression linéaire multiple avec interaction entre bmi et betadiet

	OR	IC	p
(Intercept)	1.028	[1.01;1.048]	0.0032
age	0.699	[0.317;1.51]	0.3656
sexeFemmes	1.195	[0.714;2.008]	0.4982
tabacAutrefois	0.923	[0.429;1.957]	0.8347
tabacFumeur	0.96	[0.888;1.033]	0.2858
bmi	1.096	[0.617;1.949]	0.7532
vitamineSouvent	1.102	[0.595;2.047]	0.7571
vitaminePas-souvent	1	[0.999;1.002]	0.4335
calories	0.994	[0.974;1.013]	0.5192
graisses	0.964	[0.897;1.034]	0.3099
fibres	0.99	[0.96;1.022]	0.5266
alcool	1	[0.997;1.003]	0.9069
cholesterol	0.999	[0.998;1]	0.0793
betadiet	1	[1;1]	0.9714
rettdiet	1.002	[1;1.003]	0.0332
betaplasma	NA	[NA;NA]	0.0788
bmi:retinol[, "betadiet"]	1	[1;1]	0.8141
0.732	[0.054;10.032]	0.8141	(Intercept)

```

## Waiting for profiling to be done...

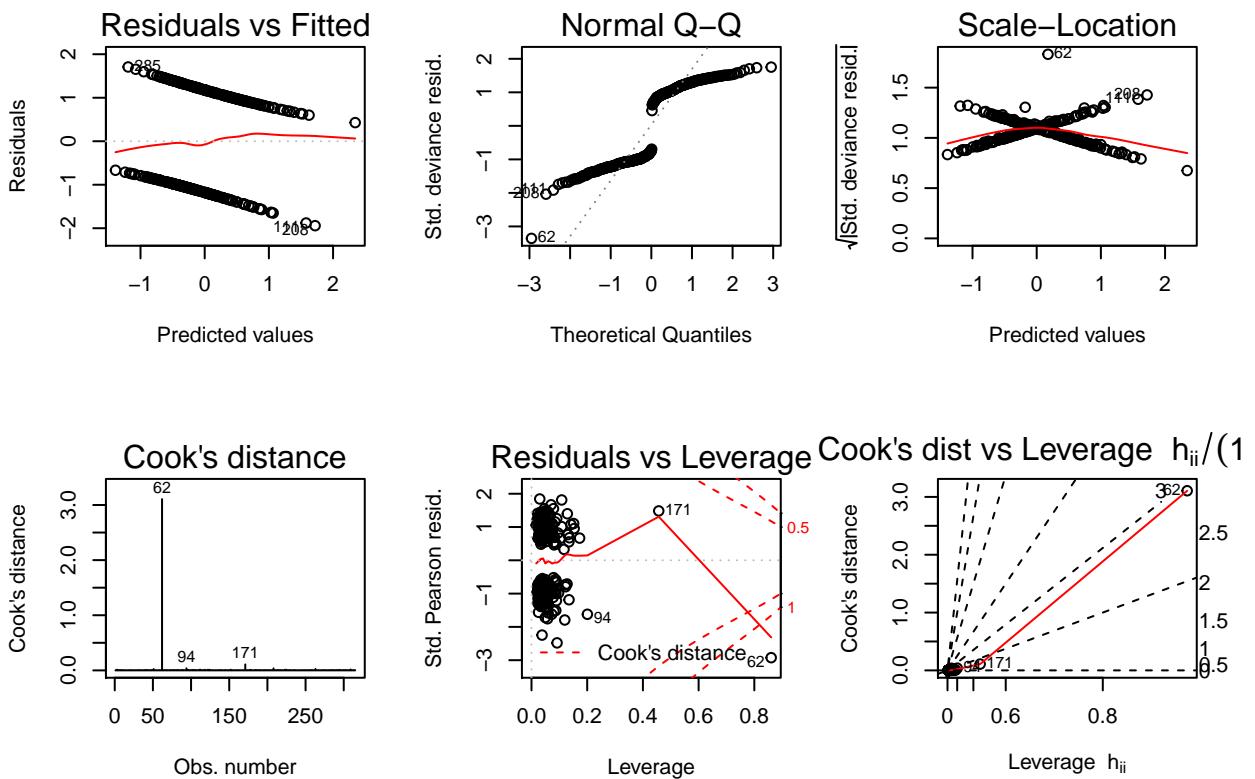
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et betadiet", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + bmi*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 131: Régression linéaire multiple avec interaction entre bmi et retdiet

	OR	IC	p
(Intercept)	1.03	[1.011;1.05]	0.0017
age	0.709	[0.322;1.529]	0.3835
sexeFemmes	1.212	[0.726;2.03]	0.4631
tabacAutrefois	0.964	[0.45;2.041]	0.9247
tabacFumeur	1.04	[0.962;1.126]	0.3198
bmi	1.108	[0.626;1.964]	0.7252
vitamineSouvent	1.129	[0.611;2.093]	0.6985
vitaminePas-souvent	1.001	[0.999;1.002]	0.4029
calories	0.994	[0.975;1.014]	0.5421
graisses	0.96	[0.894;1.03]	0.261
fibres	0.989	[0.959;1.02]	0.4565
alcool	1	[0.997;1.003]	0.9167
cholesterol	1	[1;1]	0.8715
betadiet	1.001	[0.999;1.003]	0.4962
retdiet	1.002	[1;1.003]	0.0495
betaplasma	NA	[NA;NA]	0.5051
bmi:retinol[, "retdiet"]	1	[1;1]	0.0797
0.08	[0.005;1.319]	0.0797	(Intercept)

```

## Waiting for profiling to be done...

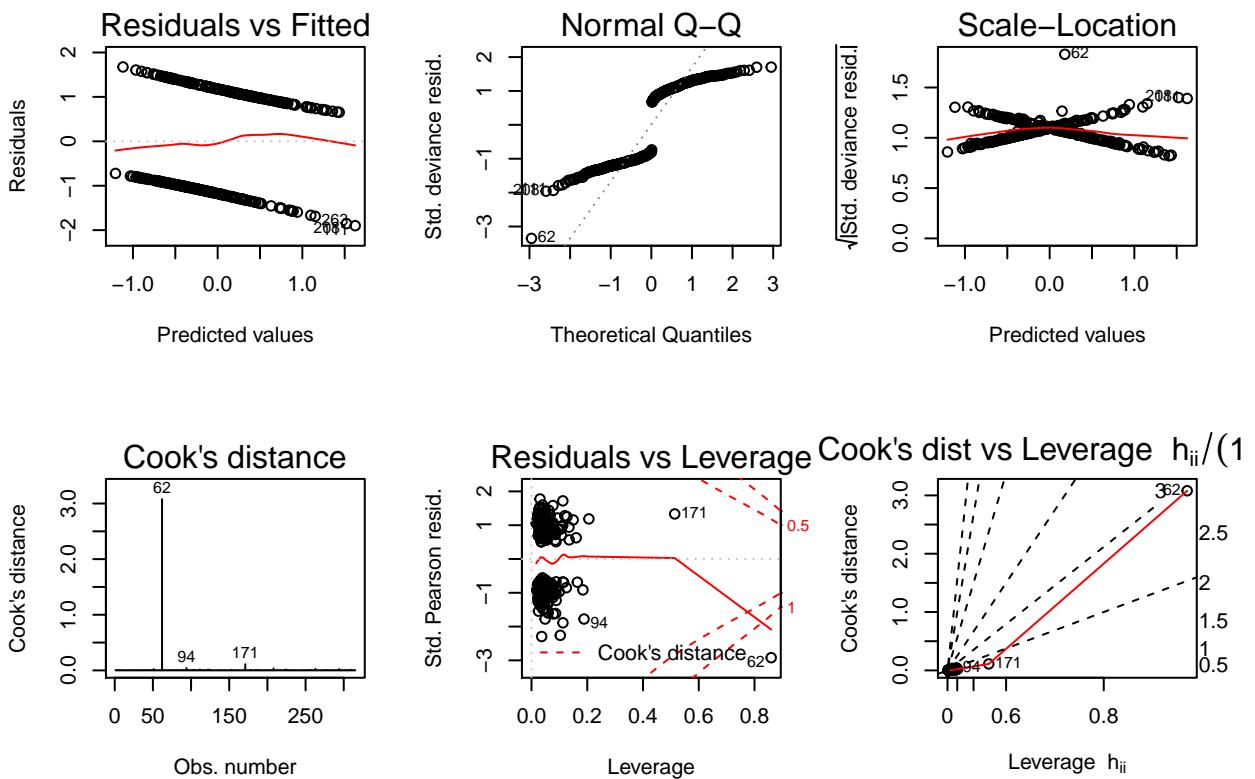
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et retdiet", col.names = c(" "
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + bmi*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 132: Régression linéaire multiple avec interaction entre bmi et betaplasma

	OR	IC	p
(Intercept)	1.029	[1.01;1.048]	0.0029
age	0.697	[0.316;1.504]	0.3609
sexeFemmes	1.203	[0.719;2.02]	0.4813
tabacAutrefois	0.988	[0.462;2.088]	0.9756
tabacFumeur	0.977	[0.911;1.045]	0.4985
bmi	1.077	[0.607;1.913]	0.799
vitamineSouvent	1.068	[0.574;1.989]	0.835
vitaminePas-souvent	1	[0.999;1.002]	0.4953
calories	0.995	[0.976;1.015]	0.6163
graisses	0.965	[0.899;1.035]	0.327
fibres	0.991	[0.961;1.023]	0.5506
alcool	1	[0.997;1.002]	0.863
cholesterol	1	[1;1]	0.88
betadiet	1	[1;1]	0.9249
retdiet	0.994	[0.984;1.004]	0.2534
betaplasma	NA	[NA;NA]	0.1481
bmi:retinol[, "betaplasma"]	1	[1;1.001]	0.4948
0.43	[0.037;4.857]	0.4948	(Intercept)

```

## Waiting for profiling to be done...

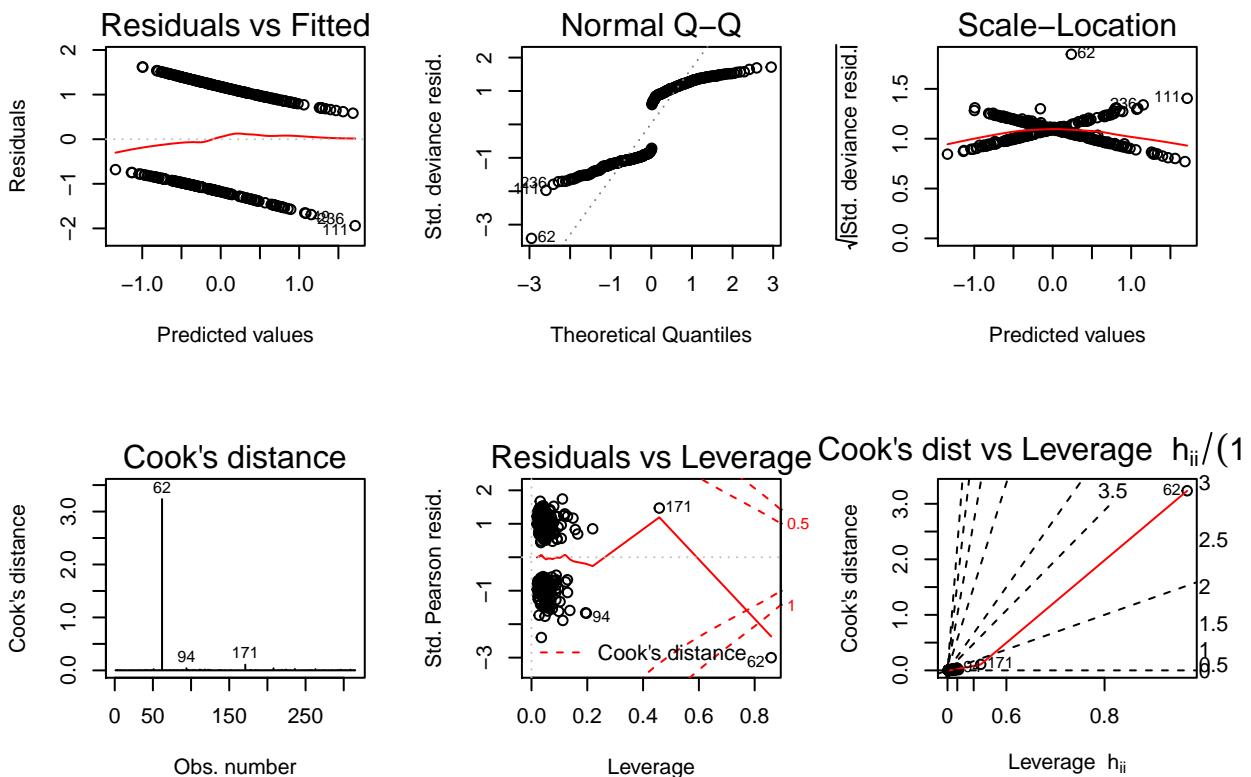
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre bmi et betaplasma", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.5 Interaction avec les vitamines

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + vitamine*retinol[, "calories"],
               data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4)

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 133: Régression linéaire multiple avec interaction entre vitamine et calories

	OR	IC	p
(Intercept)	1.031	[1.012;1.05]	0.0016
age	0.688	[0.311;1.486]	0.3453
sexeFemmes	1.22	[0.73;2.044]	0.4491
tabacAutrefois	0.996	[0.464;2.109]	0.9907
tabacFumeur	1.017	[0.977;1.059]	0.4003
bmi	0.667	[0.13;3.339]	0.6234
vitamineSouvent	1.035	[0.163;6.62]	0.9706
vitaminePas-souvent	1	[0.999;1.002]	0.6292
calories	0.994	[0.975;1.014]	0.5652
graisses	0.96	[0.894;1.03]	0.263
fibres	0.993	[0.96;1.027]	0.6672
alcool	1	[0.997;1.002]	0.8094
cholesterol	1	[1;1]	0.909
betadiet	1	[1;1.001]	0.8346
retdiet	1.001	[1;1.003]	0.0539
betaplasma	NA	[NA;NA]	0.517
vitamineSouvent:retinol[, "calories"]	1	[0.999;1.001]	0.9111
vitaminePas-souvent:retinol[, "calories"]	1	[0.999;1.001]	0.1361
0.19	[0.021;1.673]	0.1361	(Intercept)

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

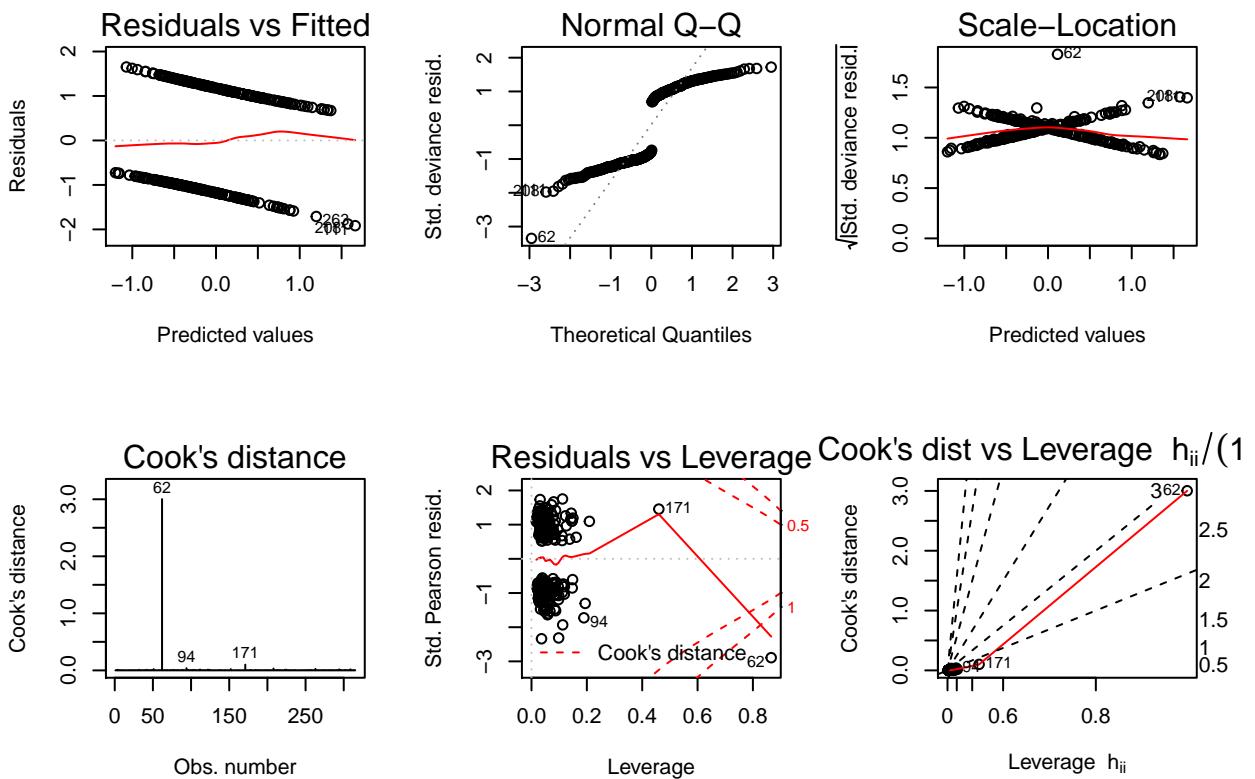
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [75] n'est pas un
## diviseur ni un multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et calories", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + vitamine*retinol[, "graisses"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 134: Régression linéaire multiple avec interaction entre vitamine et graisses

	OR	IC	p
(Intercept)	1.03	[1.011;1.05]	0.0019
age	0.711	[0.323;1.534]	0.3886
sexeFemmes	1.233	[0.738;2.069]	0.4249
tabacAutrefois	0.984	[0.458;2.09]	0.9674
tabacFumeur	1.016	[0.976;1.059]	0.4255
bmi	1.166	[0.303;4.486]	0.823
vitamineSouvent	2.079	[0.439;10.144]	0.3587
vitaminePas-souvent	1.001	[0.999;1.002]	0.4081
calories	0.996	[0.975;1.018]	0.7094
graisses	0.96	[0.893;1.029]	0.2516
fibres	0.988	[0.958;1.02]	0.4488
alcool	1	[0.997;1.002]	0.8144
cholesterol	1	[1;1]	0.8529
betadiet	1	[1;1.001]	0.859
retdiet	1.002	[1;1.003]	0.0488
betaplasma	NA	[NA;NA]	0.9287
vitamineSouvent:retinol[, "graisses"]	0.999	[0.983;1.015]	0.4019
vitaminePas-souvent:retinol[, "graisses"]	0.992	[0.973;1.011]	0.0602
0.131	[0.015;1.073]	0.0602	(Intercept)

```

## Waiting for profiling to be done...

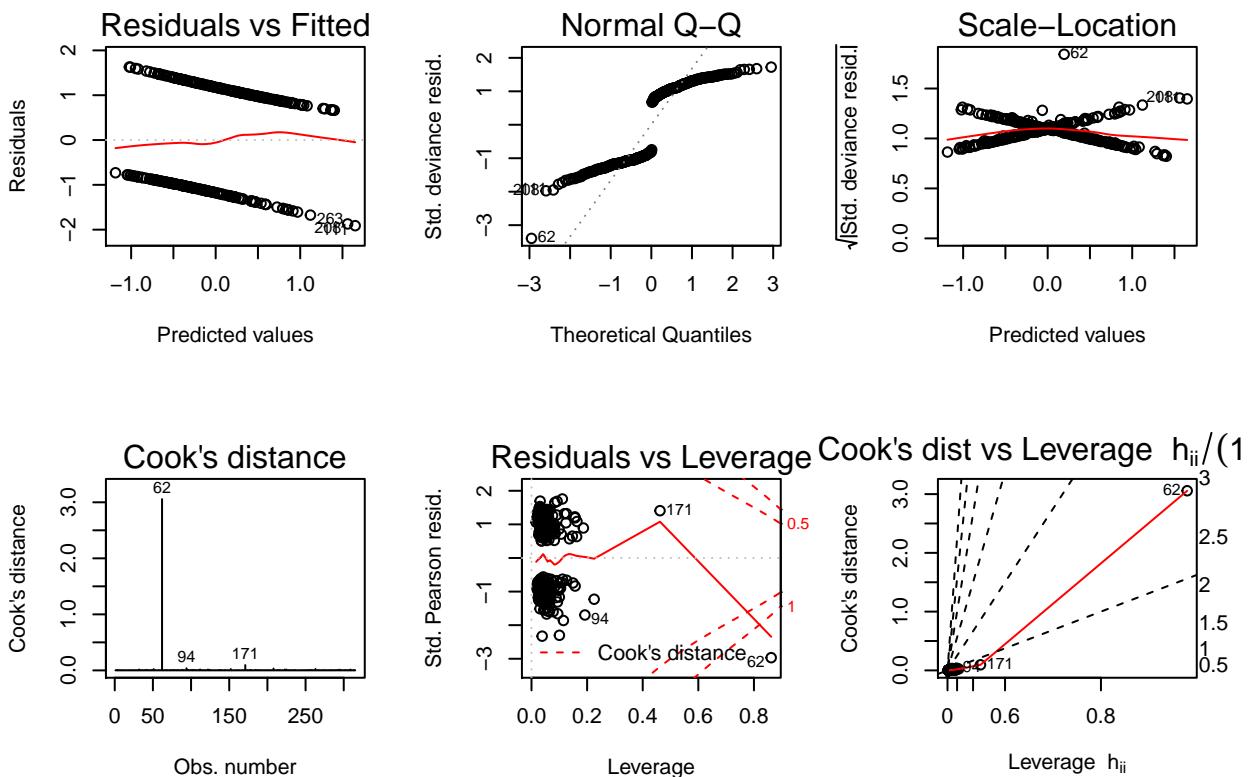
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et graisses", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + vitamine*retinol[, "fibres"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 135: Régression linéaire multiple avec interaction entre vitamine et fibres

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0021
age	0.712	[0.324;1.535]	0.3894
sexeFemmes	1.226	[0.732;2.06]	0.4386
tabacAutrefois	0.94	[0.436;2.001]	0.8731
tabacFumeur	1.017	[0.977;1.06]	0.4049
bmi	2.297	[0.577;9.242]	0.2377
vitamineSouvent	3.296	[0.614;18.419]	0.1671
vitaminePas-souvent	1.001	[0.999;1.002]	0.3442
calories	0.992	[0.973;1.012]	0.4353
graisses	0.999	[0.913;1.094]	0.9892
fibres	0.988	[0.958;1.019]	0.4192
alcool	1	[0.997;1.003]	0.9213
cholesterol	1	[1;1]	0.955
betadiet	1	[1;1]	0.9309
retdiet	1.002	[1;1.003]	0.0454
betaplasma	NA	[NA;NA]	0.2417
vitamineSouvent:retinol[, "fibres"]	0.941	[0.849;1.042]	0.1737
vitaminePas-souvent:retinol[, "fibres"]	0.916	[0.804;1.039]	0.0279
0.086	[0.009;0.748]	0.0279	(Intercept)

```

## Waiting for profiling to be done...

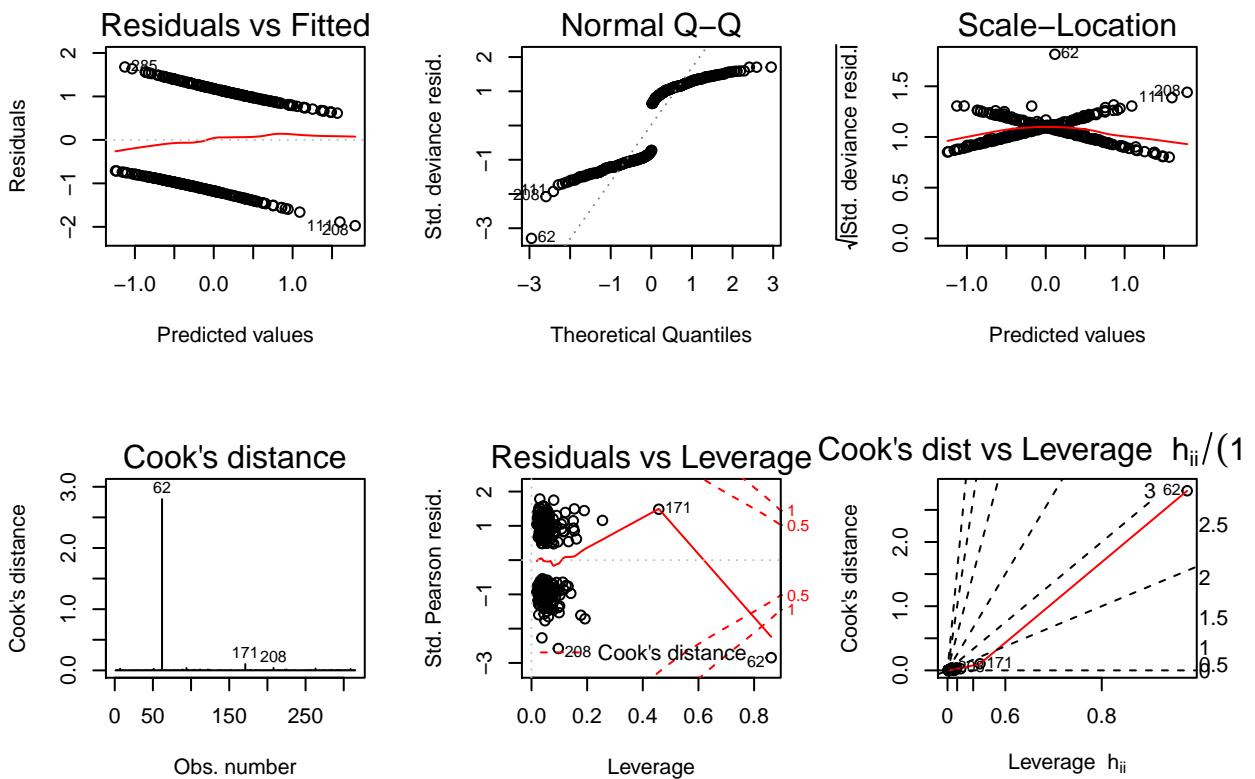
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et fibres", col.names = c(
        "Variable", "OR", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + vitamine*retinol[, "alcool"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 136: Régression linéaire multiple avec interaction entre vitamine et alcool

	OR	IC	p
(Intercept)	1.032	[1.013;1.052]	0.0012
age	0.706	[0.313;1.566]	0.3947
sexeFemmes	1.103	[0.651;1.871]	0.7151
tabacAutrefois	0.939	[0.428;2.028]	0.873
tabacFumeur	1.026	[0.985;1.07]	0.2125
bmi	0.921	[0.494;1.709]	0.7936
vitamineSouvent	0.679	[0.333;1.366]	0.2807
vitaminePas-souvent	1.001	[0.999;1.002]	0.2991
calories	0.991	[0.971;1.011]	0.3773
graisses	0.959	[0.891;1.029]	0.2456
fibres	0.978	[0.935;1.01]	0.2105
alcool	1	[0.997;1.002]	0.7921
cholesterol	1	[1;1]	0.6556
betadiet	1	[1;1.001]	0.6841
retdiet	1.001	[1;1.003]	0.0817
betaplasma	NA	[NA;NA]	0.1557
vitamineSouvent:retinol[, "alcool"]	1.089	[0.975;1.241]	0.0155
vitaminePas-souvent:retinol[, "alcool"]	1.245	[1.069;1.532]	0.0451
0.121	[0.015;0.936]	0.0451	(Intercept)

```

## Waiting for profiling to be done...

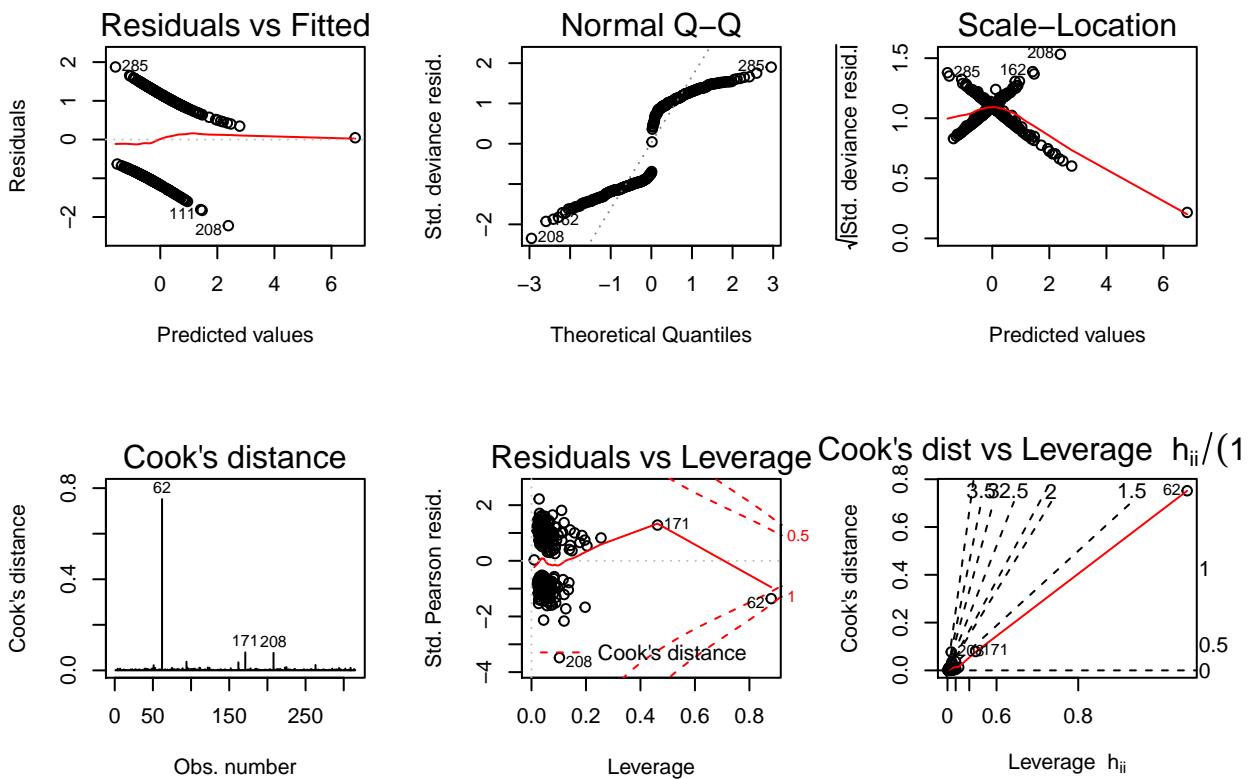
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et alcool", col.names = c(
        "Variable", "OR", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + vitamine*retinol[, "cholesterol"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]",
                         round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 137: Régression linéaire multiple avec interaction entre vitamine et cholesterol

	OR	IC	p
(Intercept)	1.029	[1.011;1.049]	0.0023
age	0.725	[0.328;1.573]	0.4181
sexeFemmes	1.23	[0.736;2.064]	0.4302
tabacAutrefois	0.979	[0.456;2.077]	0.9571
tabacFumeur	1.016	[0.976;1.058]	0.435
bmi	1.468	[0.485;4.465]	0.4962
vitamineSouvent	2.087	[0.479;9.354]	0.3296
vitaminePas-souvent	1.001	[0.999;1.002]	0.4235
calories	0.994	[0.975;1.014]	0.5425
graisses	0.961	[0.895;1.031]	0.2706
fibres	0.988	[0.958;1.02]	0.4329
alcool	1.001	[0.997;1.005]	0.6896
cholesterol	1	[1;1]	0.8541
betadiet	1	[1;1.001]	0.8749
retdiet	1.002	[1;1.003]	0.052
betaplasma	NA	[NA;NA]	0.5526
vitamineSouvent:retinol[, "cholesterol"]	0.999	[0.995;1.003]	0.3638
vitaminePas-souvent:retinol[, "cholesterol"]	0.997	[0.992;1.003]	0.0485
0.121	[0.014;0.966]	0.0485	(Intercept)

```

## Waiting for profiling to be done...

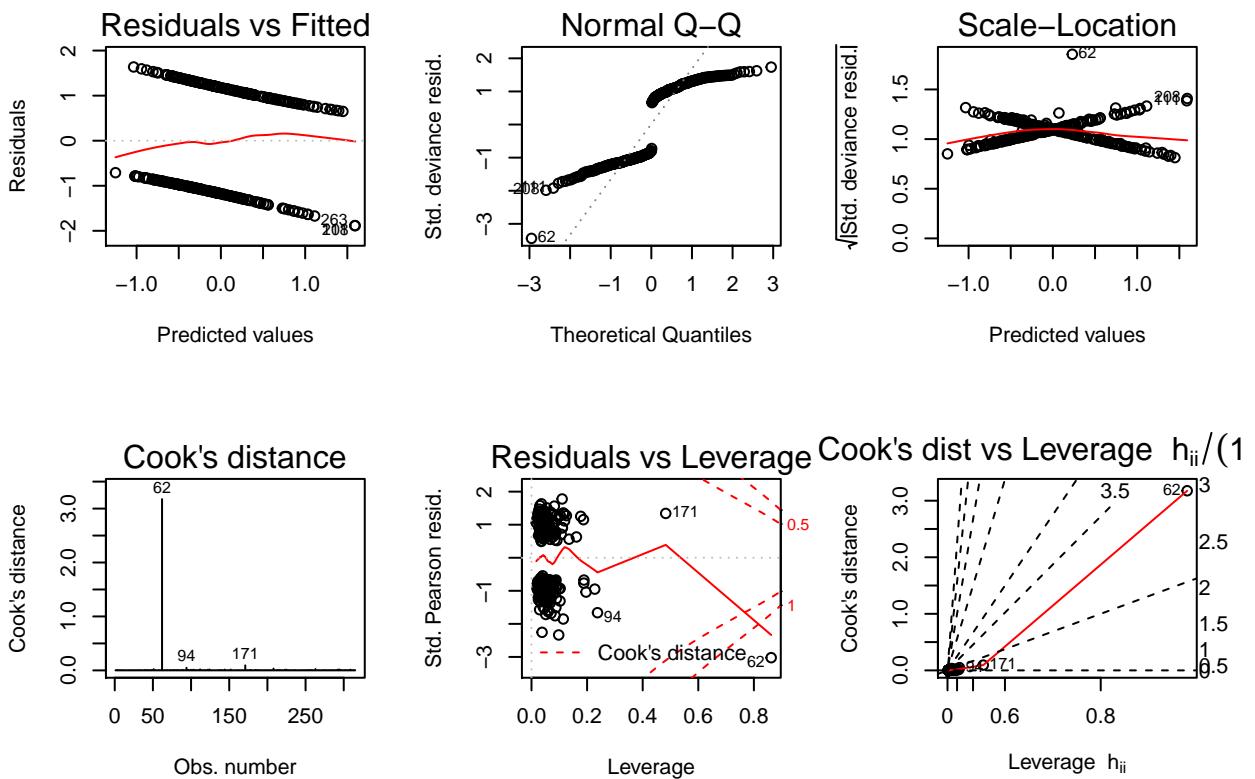
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et cholesterol", col.names = 
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + vitamine*retinol[, "betadiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 138: Régression linéaire multiple avec interaction entre vitamine et betadiet

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0019
age	0.699	[0.317;1.507]	0.3651
sexeFemmes	1.213	[0.725;2.036]	0.4618
tabacAutrefois	1.006	[0.468;2.139]	0.9868
tabacFumeur	1.017	[0.977;1.059]	0.4033
bmi	1.043	[0.378;2.863]	0.9346
vitamineSouvent	0.726	[0.249;2.073]	0.5522
vitaminePas-souvent	1	[0.999;1.002]	0.4987
calories	0.995	[0.976;1.015]	0.6258
graisses	0.961	[0.894;1.031]	0.2736
fibres	0.991	[0.961;1.022]	0.5418
alcool	1	[0.997;1.003]	0.8945
cholesterol	1	[1;1]	0.5647
betadiet	1	[1;1.001]	0.8865
retdiet	1.002	[1;1.003]	0.0467
betaplasma	NA	[NA;NA]	0.8501
vitamineSouvent:retinol[, "betadiet"]	1	[1;1]	0.3308
vitaminePas-souvent:retinol[, "betadiet"]	1	[1;1.001]	0.1044
0.179	[0.022;1.41]	0.1044	(Intercept)

```

## Waiting for profiling to be done...

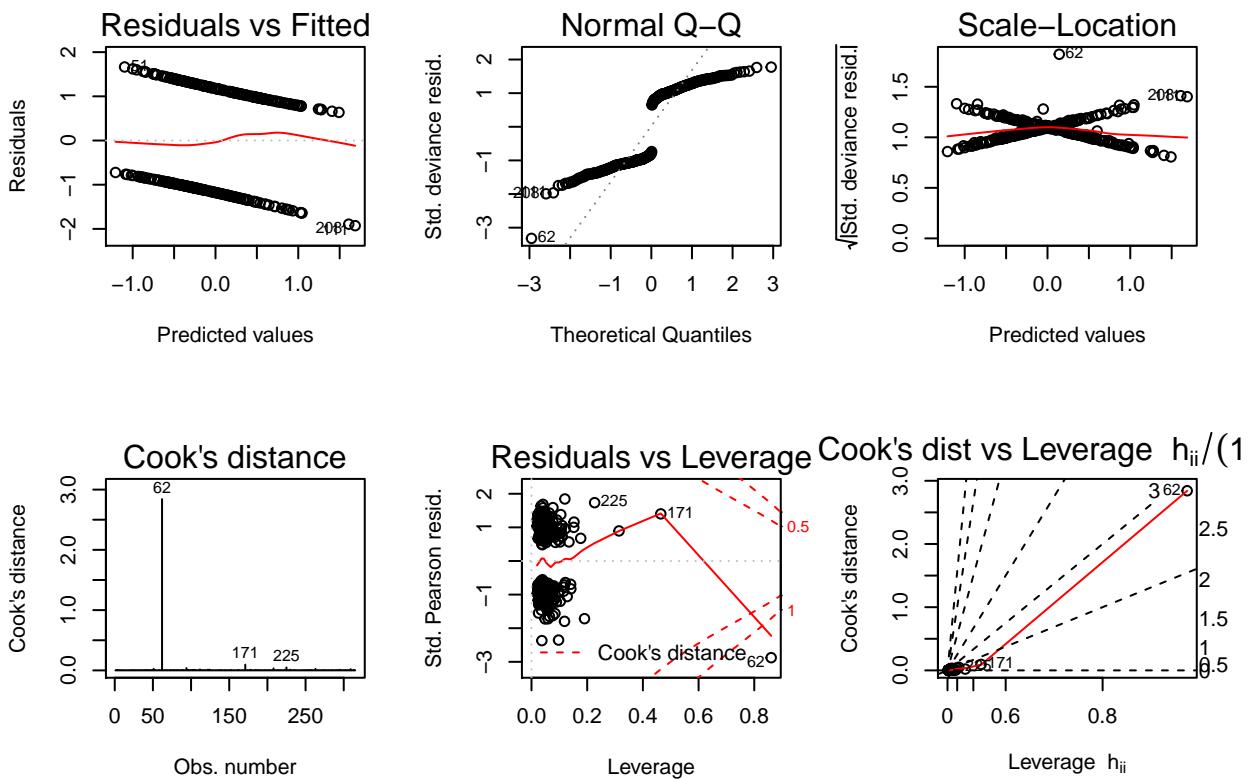
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et betadiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + vitamine*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 139: Régression linéaire multiple avec interaction entre vitamine et retdiet

	OR	IC	p
(Intercept)	1.031	[1.012;1.051]	0.0013
age	0.76	[0.344;1.65]	0.4908
sexeFemmes	1.259	[0.751;2.118]	0.3827
tabacAutrefois	0.987	[0.456;2.113]	0.9734
tabacFumeur	1.019	[0.978;1.061]	0.3749
bmi	1.919	[0.717;5.689]	0.2122
vitamineSouvent	3.262	[1.01;11.485]	0.055
vitaminePas-souvent	1.001	[1;1.002]	0.2248
calories	0.99	[0.971;1.01]	0.3318
graisses	0.955	[0.889;1.025]	0.2021
fibres	0.982	[0.952;1.014]	0.2594
alcool	1	[0.997;1.003]	0.9926
cholesterol	1	[1;1]	0.7755
betadiet	1	[1;1.001]	0.2592
retdiet	1.001	[1;1.003]	0.0669
betaplasma	NA	[NA;NA]	0.1952
vitamineSouvent:retinol[, "retdiet"]	0.999	[0.998;1]	0.0463
vitaminePas-souvent:retinol[, "retdiet"]	0.999	[0.997;1]	0.0187
0.078	[0.009;0.639]	0.0187	(Intercept)

```

## Waiting for profiling to be done...

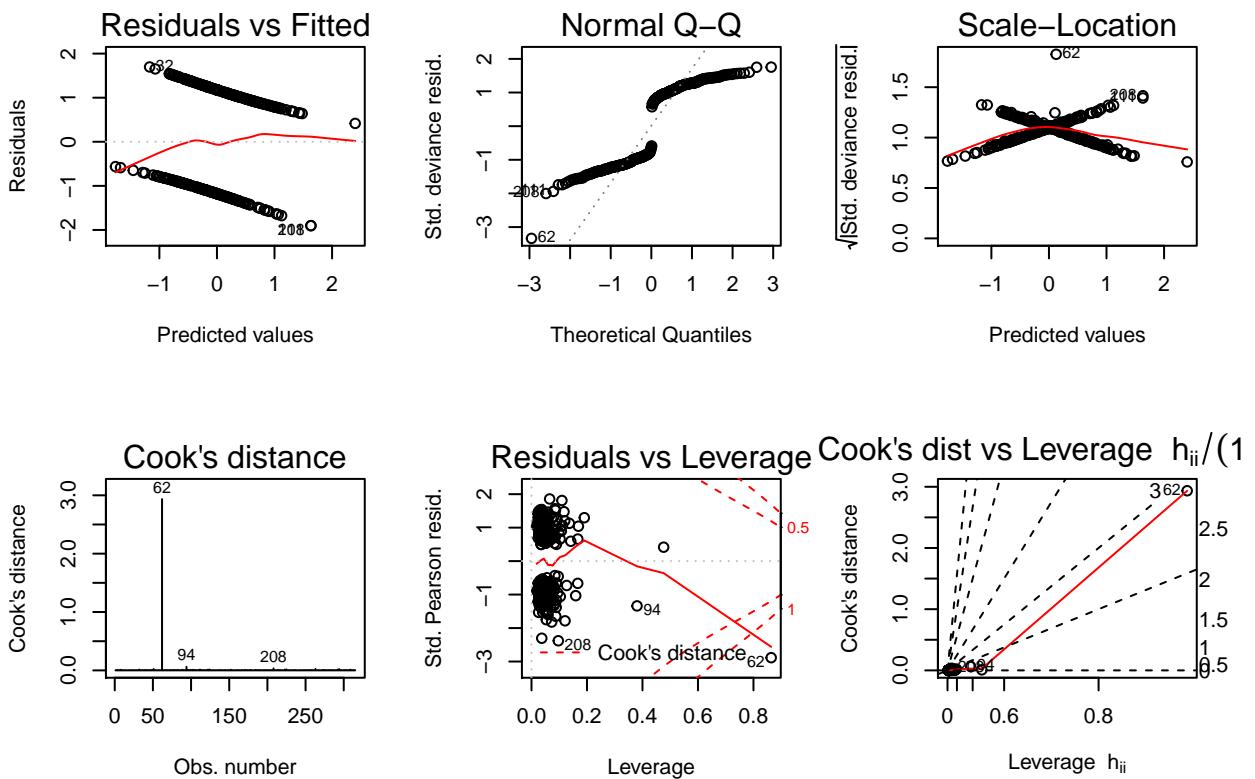
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et retdiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + vitamine*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 140: Régression linéaire multiple avec interaction entre vitamine et betaplasma

	OR	IC	p
(Intercept)	1.029	[1.011;1.049]	0.0021
age	0.678	[0.305;1.474]	0.3314
sexeFemmes	1.253	[0.744;2.119]	0.398
tabacAutrefois	1.018	[0.475;2.161]	0.9622
tabacFumeur	1.021	[0.98;1.064]	0.3122
bmi	1.75	[0.699;4.482]	0.2361
vitamineSouvent	1.238	[0.388;3.8]	0.7118
vitaminePas-souvent	1.001	[0.999;1.002]	0.3841
calories	0.993	[0.974;1.013]	0.4873
graisses	0.962	[0.896;1.031]	0.2696
fibres	0.989	[0.959;1.021]	0.4713
alcool	1	[0.997;1.003]	0.9219
cholesterol	1	[1;1]	0.8703
betadiet	1	[1;1]	0.9639
retdiet	1.004	[0.999;1.009]	0.1009
betaplasma	NA	[NA;NA]	0.2385
vitamineSouvent:retinol[, "betaplasma"]	0.997	[0.992;1.002]	0.7128
vitaminePas-souvent:retinol[, "betaplasma"]	0.999	[0.993;1.005]	0.0361
0.1	[0.011;0.843]	0.0361	(Intercept)

```

## Waiting for profiling to be done...

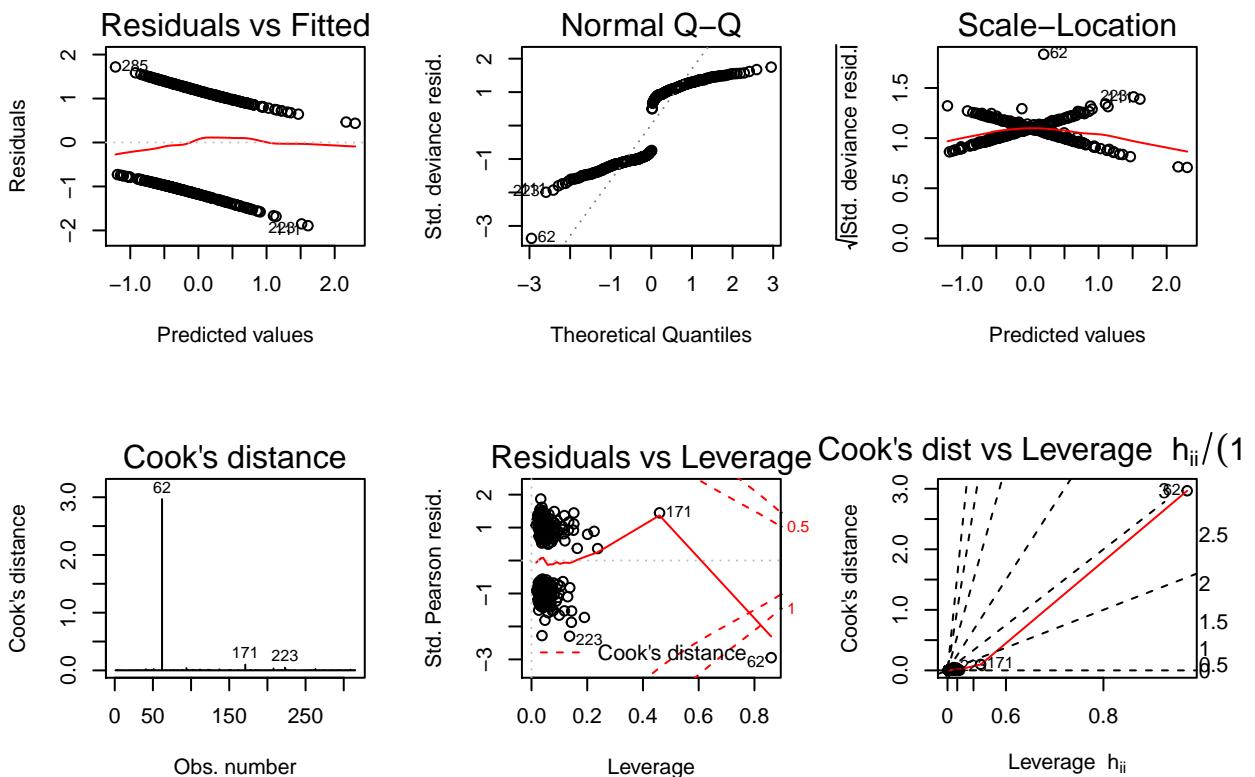
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [75] n'est pas un diviseur ni un
## multiple du nombre de lignes [19]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre vitamine et betaplasma", col.names
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.6 Interaction avec les calories

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + calories*retinol[, "graisses"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 141: Régression linéaire multiple avec interaction entre calories et graisses

	OR	IC	p
(Intercept)	1.031	[1.012;1.051]	0.0013
age	0.778	[0.349;1.705]	0.5328
sexeFemmes	1.203	[0.718;2.021]	0.4829
tabacAutrefois	0.964	[0.448;2.046]	0.9239
tabacFumeur	1.022	[0.981;1.065]	0.2933
bmi	1.159	[0.651;2.068]	0.6156
vitamineSouvent	1.114	[0.601;2.07]	0.7312
vitaminePas-souvent	1.001	[1;1.003]	0.1225
calories	1.013	[0.986;1.042]	0.3486
graisses	0.962	[0.895;1.031]	0.2754
fibres	1.004	[0.97;1.038]	0.83
alcool	1	[0.997;1.003]	0.8809
cholesterol	1	[1;1]	0.7349
betadiet	1	[1;1]	0.9934
rettdiet	1.001	[1;1.003]	0.062
betaplasma	NA	[NA;NA]	0.0647
calories:retinol[, "graisses"]	1	[1;1]	0.0094
0.032	[0.002;0.41]	0.0094	(Intercept)

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

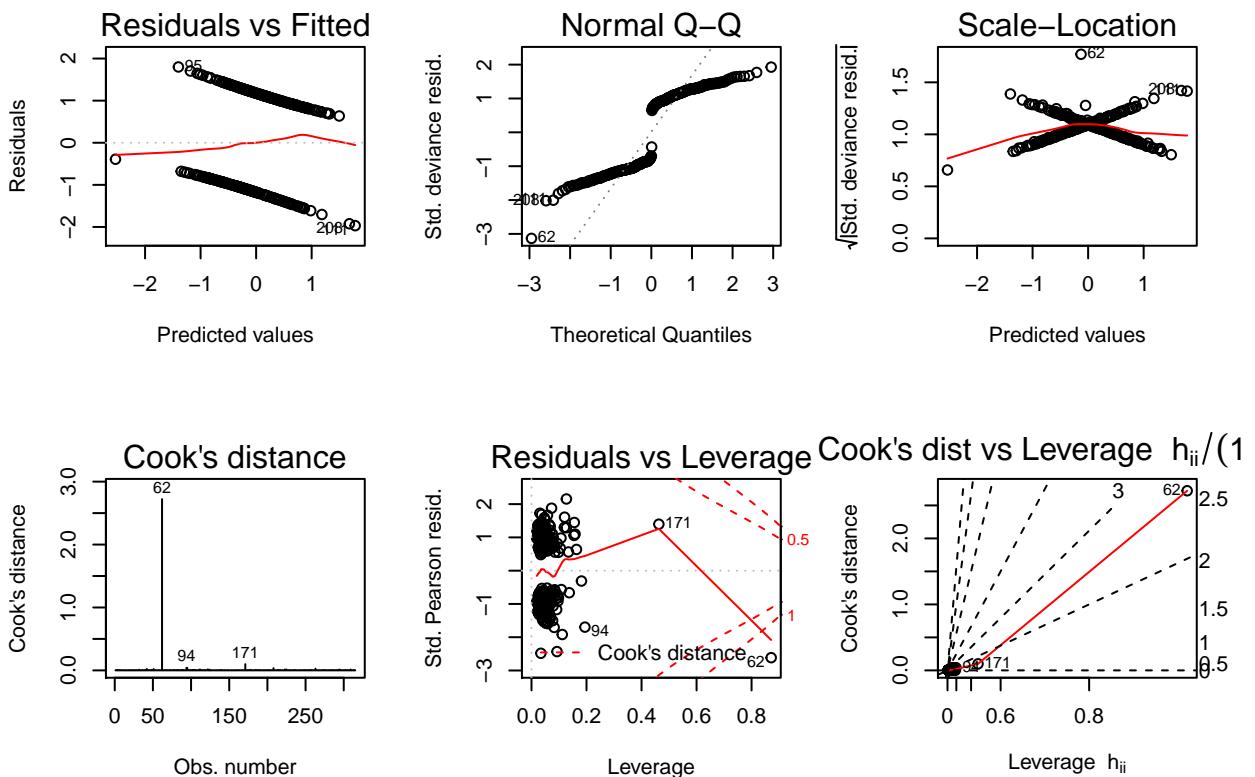
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et graisses", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + calories*retinol[, "fibres"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 142: Régression linéaire multiple avec interaction entre calories et fibres

	OR	IC	p
(Intercept)	1.031	[1.012;1.051]	0.0013
age	0.756	[0.341;1.646]	0.4831
sexeFemmes	1.218	[0.728;2.045]	0.4542
tabacAutrefois	0.972	[0.453;2.06]	0.942
tabacFumeur	1.018	[0.978;1.06]	0.3875
bmi	1.087	[0.613;1.932]	0.7744
vitamineSouvent	1.084	[0.585;2.013]	0.798
vitaminePas-souvent	1.001	[1;1.003]	0.0987
calories	0.994	[0.975;1.014]	0.5641
graisses	1.077	[0.931;1.252]	0.3233
fibres	0.985	[0.955;1.017]	0.3413
alcool	1	[0.997;1.002]	0.8394
cholesterol	1	[1;1]	0.8379
betadiet	1	[1;1]	0.9996
rettdiet	1.002	[1;1.003]	0.039
betaplasma	NA	[NA;NA]	0.0867
calories:retinol[, "fibres"]	1	[1;1]	0.0133
0.031	[0.002;0.469]	0.0133	(Intercept)

```

## Waiting for profiling to be done...

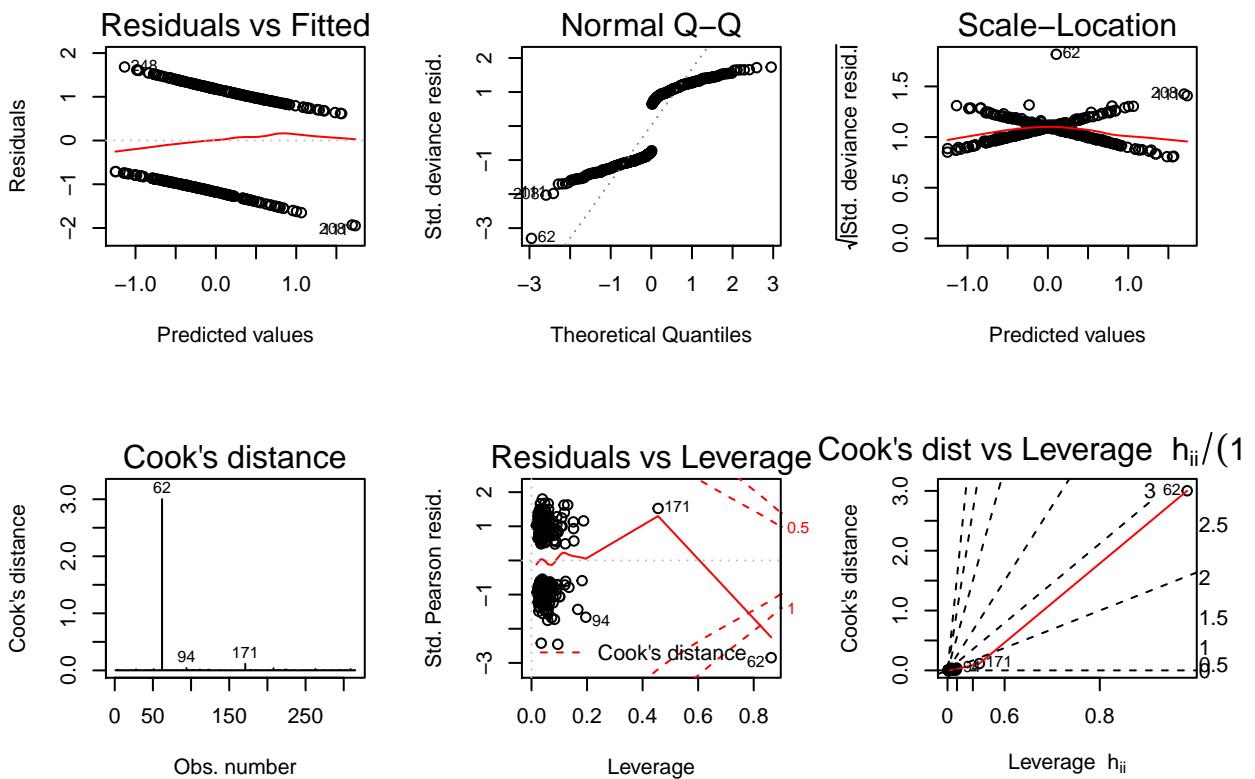
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et fibres", col.names = c(
        "Variable", "OR", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + calories*retinol[, "alcool"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```


Table 143: Régression linéaire multiple avec interaction entre calories et alcool

	OR	IC	p
(Intercept)	1.032	[1.013;1.052]	9e-04
age	0.809	[0.363;1.779]	0.6001
sexeFemmes	1.098	[0.651;1.855]	0.7252
tabacAutrefois	1.021	[0.471;2.188]	0.9577
tabacFumeur	1.026	[0.985;1.069]	0.2234
bmi	1.216	[0.681;2.179]	0.5097
vitamineSouvent	1.155	[0.62;2.162]	0.6502
vitaminePas-souvent	1.001	[0.999;1.002]	0.2923
calories	0.992	[0.972;1.012]	0.4195
graisses	0.957	[0.89;1.027]	0.2259
fibres	1.111	[1.02;1.253]	0.0209
alcool	1	[0.997;1.002]	0.8466
cholesterol	1	[1;1]	0.8085
betadiet	1	[1;1.001]	0.8381
retdiet	1.001	[1;1.003]	0.0623
betaplasma	NA	[NA;NA]	0.0225
calories:retinol[, "alcool"]	1	[NA;1]	0.0147
0.072	[0.008;0.58]	0.0147	(Intercept)

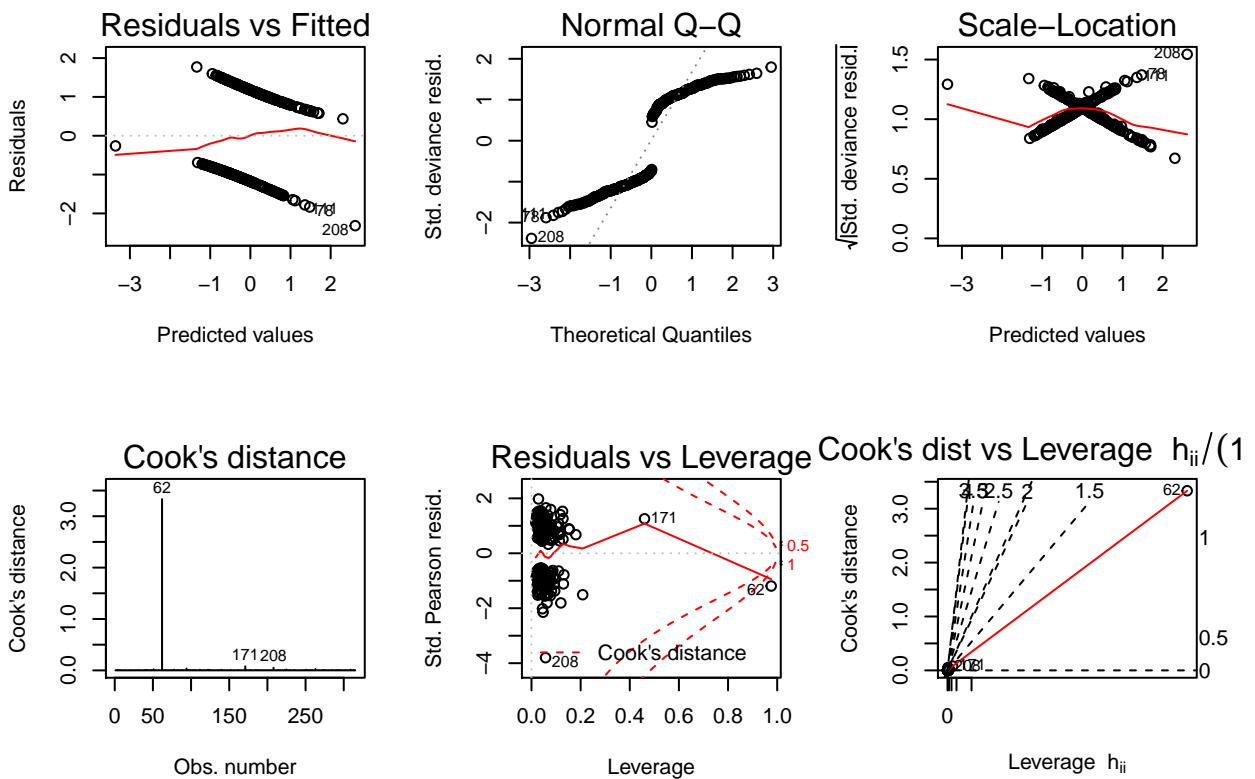
```

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et alcool", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

## Warning in sqrt(crit * p * (1 - hh)/hh): production de NaN
## Warning in sqrt(crit * p * (1 - hh)/hh): production de NaN

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + calories*retinol[, "cholesterol"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]",
                         round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 144: Régression linéaire multiple avec interaction entre calories et cholestérol

	OR	IC	p
(Intercept)	1.031	[1.013;1.051]	0.0012
age	0.834	[0.371;1.849]	0.6559
sexeFemmes	1.183	[0.704;1.995]	0.5257
tabacAutrefois	0.972	[0.45;2.078]	0.9427
tabacFumeur	1.024	[0.983;1.067]	0.2632
bmi	1.205	[0.673;2.165]	0.5312
vitamineSouvent	1.087	[0.583;2.031]	0.793
vitaminePas-souvent	1.002	[1;1.003]	0.0347
calories	0.994	[0.974;1.014]	0.5458
graisses	0.952	[0.884;1.022]	0.1786
fibres	1.015	[0.979;1.053]	0.4111
alcool	1.008	[1.002;1.014]	0.0166
cholestérol	1	[1;1]	0.7161
betadiet	1	[1;1]	0.9599
rettdiet	1.001	[1;1.003]	0.0867
betaplasma	NA	[NA;NA]	0.009
calories:retinol[, "cholestérol"]	1	[1;1]	0.0018
0.015	[0.001;0.197]	0.0018	(Intercept)

```

## Waiting for profiling to be done...

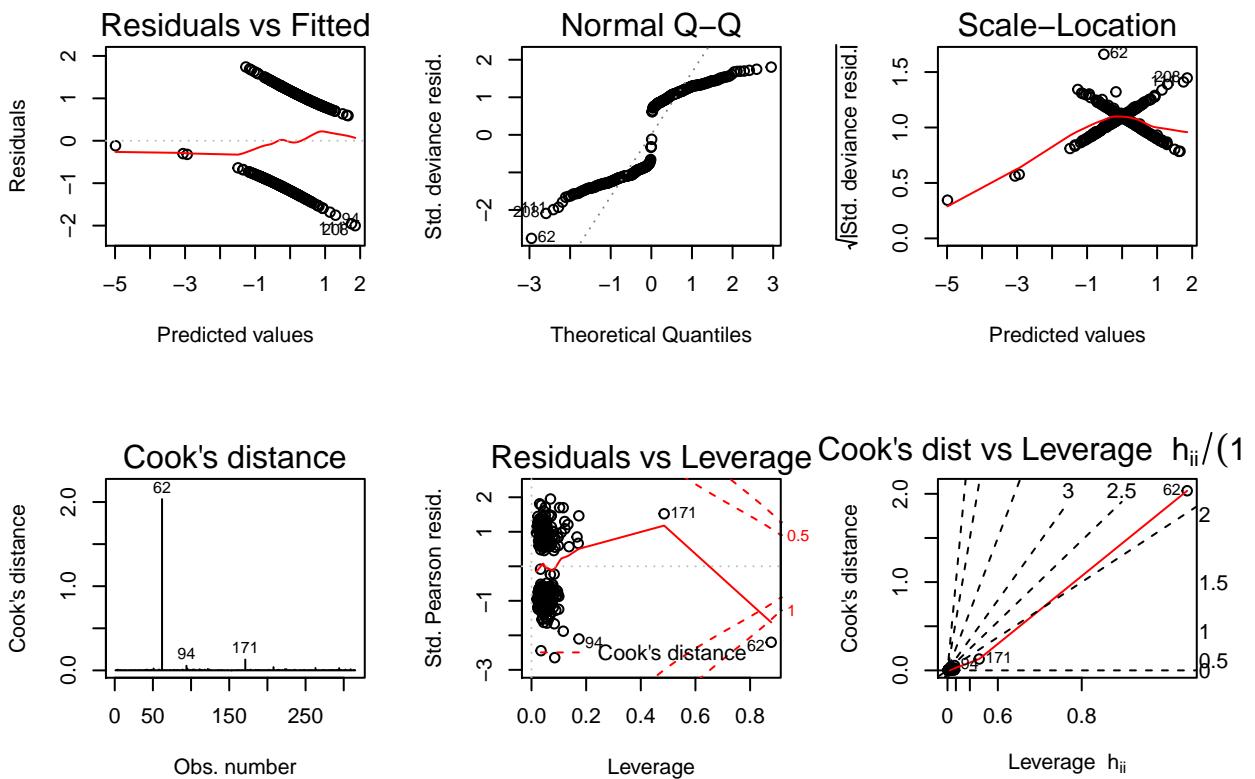
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et cholestérol", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + calories*retinol[, "betadiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 145: Régression linéaire multiple avec interaction entre calories et betadiet

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0019
age	0.715	[0.324;1.544]	0.3964
sexeFemmes	1.239	[0.741;2.079]	0.4148
tabacAutrefois	0.978	[0.457;2.066]	0.9535
tabacFumeur	1.017	[0.977;1.059]	0.4107
bmi	1.096	[0.619;1.943]	0.7538
vitamineSouvent	1.115	[0.603;2.067]	0.7282
vitaminePas-souvent	1.001	[0.999;1.002]	0.292
calories	0.994	[0.975;1.013]	0.539
graisses	0.962	[0.896;1.031]	0.2773
fibres	0.991	[0.961;1.023]	0.5614
alcool	1	[0.997;1.002]	0.8564
cholesterol	1	[1;1.001]	0.4604
betadiet	1	[1;1]	0.9173
rettdiet	1.002	[1;1.003]	0.0508
betaplasma	NA	[NA;NA]	0.3995
calories:retinol[, "betadiet"]	1	[1;1]	0.0471
0.098	[0.01;0.948]	0.0471	(Intercept)

```

## Waiting for profiling to be done...

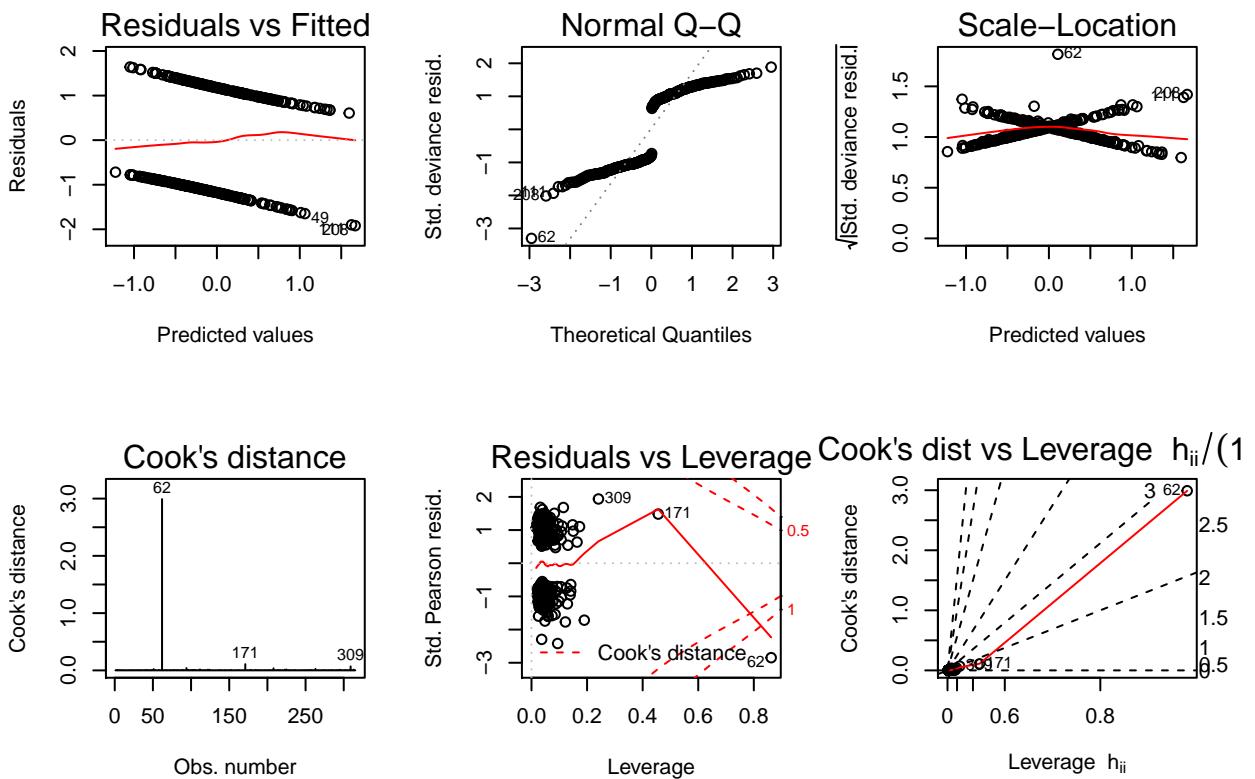
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et betadiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + calories*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 146: Régression linéaire multiple avec interaction entre calories et retdiet

	OR	IC	p
(Intercept)	1.029	[1.011;1.049]	0.0022
age	0.729	[0.33;1.58]	0.426
sexeFemmes	1.202	[0.719;2.017]	0.4832
tabacAutrefois	0.974	[0.453;2.065]	0.9446
tabacFumeur	1.021	[0.981;1.064]	0.3048
bmi	1.113	[0.628;1.976]	0.7145
vitamineSouvent	1.14	[0.616;2.115]	0.6768
vitaminePas-souvent	1.001	[1;1.002]	0.1943
calories	0.995	[0.976;1.015]	0.6452
graisses	0.961	[0.895;1.031]	0.2738
fibres	0.996	[0.965;1.028]	0.7829
alcool	1	[0.997;1.002]	0.8613
cholesterol	1	[1;1]	0.8179
betadiet	1.001	[1;1.003]	0.1483
retdiet	1.001	[1;1.003]	0.0601
betaplasma	NA	[NA;NA]	0.1403
calories:retinol[, "retdiet"]	1	[1;1]	0.0203
0.059	[0.005;0.627]	0.0203	(Intercept)

```

## Waiting for profiling to be done...

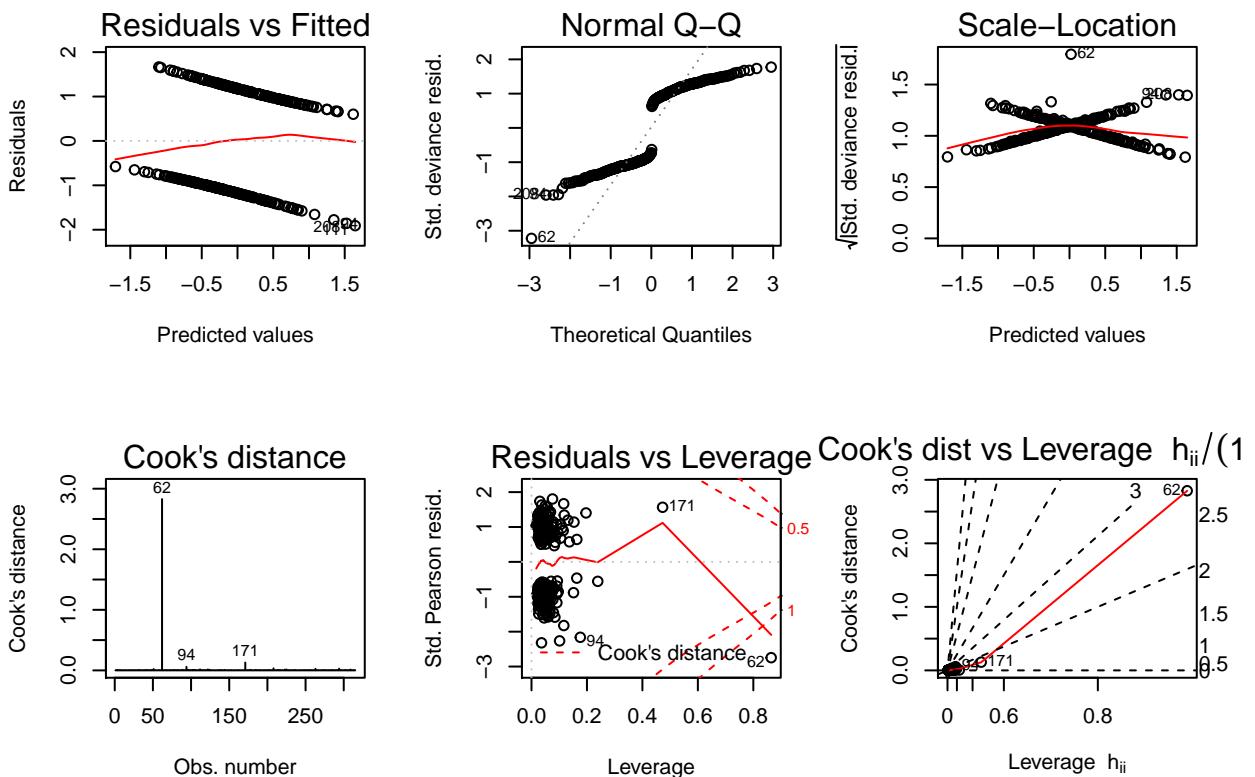
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et retdiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + calories*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 147: Régression linéaire multiple avec interaction entre calories et betaplasma

	OR	IC	p
(Intercept)	1.03	[1.011;1.05]	0.0018
age	0.694	[0.314;1.506]	0.3594
sexeFemmes	1.25	[0.747;2.1]	0.3958
tabacAutrefois	0.989	[0.462;2.092]	0.978
tabacFumeur	1.017	[0.977;1.059]	0.4186
bmi	1.115	[0.629;1.979]	0.709
vitamineSouvent	1.136	[0.614;2.11]	0.6846
vitaminePas-souvent	1	[0.999;1.002]	0.7601
calories	0.994	[0.975;1.014]	0.5589
graisses	0.955	[0.887;1.025]	0.2075
fibres	0.992	[0.962;1.024]	0.6157
alcool	1	[0.997;1.003]	0.9413
cholesterol	1	[1;1]	0.8714
betadiet	1	[1;1.001]	0.8258
retdiet	0.998	[0.993;1.004]	0.5711
betaplasma	NA	[NA;NA]	0.2515
calories:retinol[, "betaplasma"]	1	[1;1]	0.2322
0.263	[0.029;2.336]	0.2322	(Intercept)

```

## Waiting for profiling to be done...

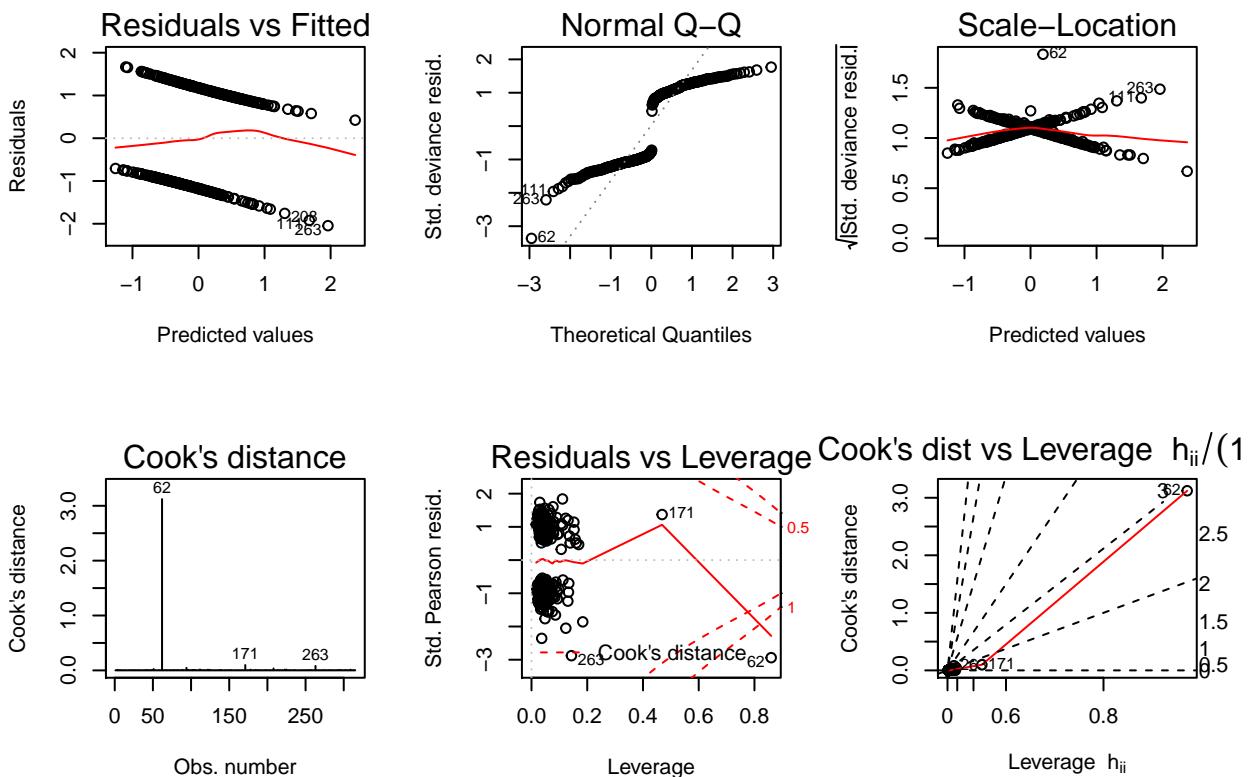
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre calories et betaplasma", col.names
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.7 Interaction avec les graisses

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + graisses*retinol[, "fibres"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4)

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 148: Régression linéaire multiple avec interaction entre graisses et fibres

	OR	IC	p
(Intercept)	1.031	[1.012;1.05]	0.0015
age	0.759	[0.342;1.659]	0.4926
sexeFemmes	1.228	[0.734;2.062]	0.4341
tabacAutrefois	0.949	[0.441;2.014]	0.8928
tabacFumeur	1.019	[0.979;1.061]	0.3626
bmi	1.098	[0.618;1.952]	0.7495
vitamineSouvent	1.098	[0.593;2.038]	0.7668
vitaminePas-souvent	1	[0.999;1.002]	0.4876
calories	1.013	[0.984;1.044]	0.3878
graisses	1.059	[0.928;1.215]	0.4013
fibres	0.989	[0.959;1.021]	0.4705
alcool	1	[0.997;1.002]	0.8119
cholesterol	1	[1;1]	0.8687
betadiet	1	[1;1]	0.8956
rettdiet	1.002	[1;1.003]	0.0522
betaplasma	NA	[NA;NA]	0.099
graisses:retinol[, "fibres"]	0.999	[0.997;1]	0.0145
0.037	[0.003;0.501]	0.0145	(Intercept)

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

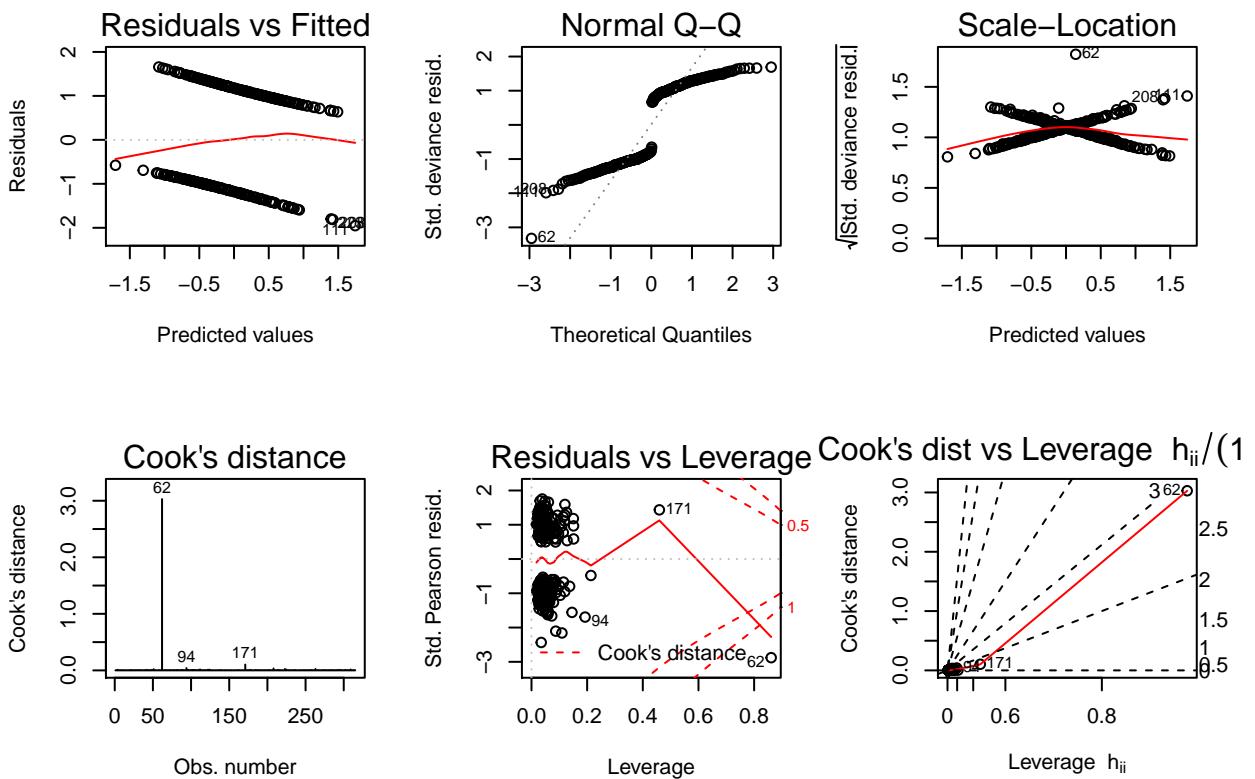
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et fibres", col.names = c
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + graisses*retinol[, "alcool"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 149: Régression linéaire multiple avec interaction entre graisses et alcool

	OR	IC	p
(Intercept)	1.031	[1.013;1.051]	0.0011
age	0.753	[0.34;1.638]	0.4769
sexeFemmes	1.13	[0.671;1.906]	0.6456
tabacAutrefois	1.018	[0.473;2.168]	0.9627
tabacFumeur	1.024	[0.983;1.067]	0.2594
bmi	1.208	[0.677;2.164]	0.5234
vitamineSouvent	1.152	[0.621;2.146]	0.6541
vitaminePas-souvent	1.001	[0.999;1.002]	0.3689
calories	0.995	[0.976;1.015]	0.6197
graisses	0.959	[0.892;1.028]	0.2427
fibres	1.107	[0.991;1.247]	0.0802
alcool	1	[0.997;1.002]	0.7911
cholesterol	1	[1;1]	0.8257
betadiet	1	[1;1.001]	0.8534
retdiet	1.001	[1;1.003]	0.0641
betaplasma	NA	[NA;NA]	0.0487
graisses:retinol[, "alcool"]	0.999	[0.998;1]	0.0221
0.084	[0.01;0.684]	0.0221	(Intercept)

```

## Waiting for profiling to be done...

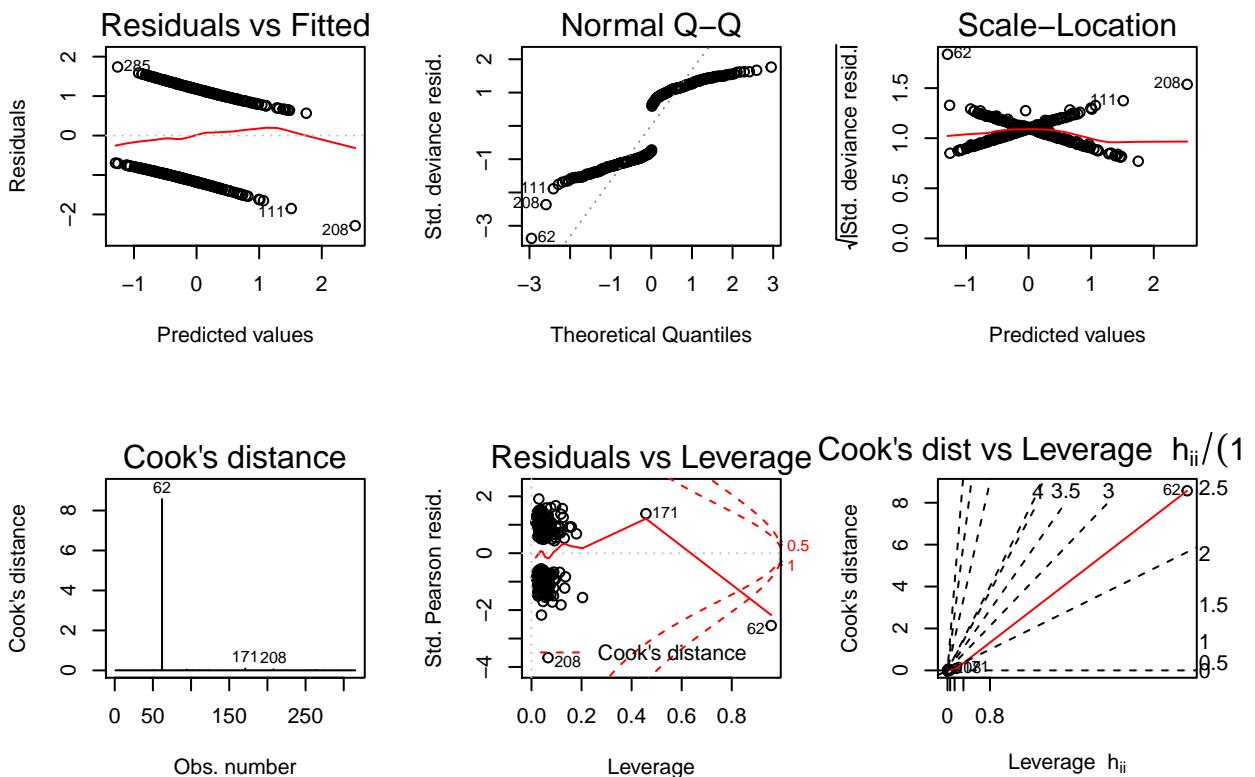
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et alcool", col.names = c(
        "Variable", "OR", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + graisses*retinol[, "cholesterol"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 150: Régression linéaire multiple avec interaction entre graisses et cholestérol

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.002
age	0.757	[0.34;1.656]	0.4884
sexeFemmes	1.193	[0.712;2.006]	0.5025
tabacAutrefois	0.967	[0.45;2.053]	0.9311
tabacFumeur	1.021	[0.981;1.064]	0.312
bmi	1.155	[0.649;2.062]	0.6242
vitamineSouvent	1.083	[0.583;2.013]	0.8012
vitaminePas-souvent	1	[0.999;1.002]	0.4677
calories	1.009	[0.985;1.035]	0.4699
graisses	0.962	[0.895;1.032]	0.281
fibres	0.995	[0.965;1.027]	0.7666
alcool	1.004	[0.999;1.01]	0.1164
cholestérol	1	[1;1]	0.7483
betadiet	1	[1;1]	0.9265
rettdiet	1.001	[1;1.003]	0.0628
betaplasma	NA	[NA;NA]	0.0668
graisses:retinol[, "cholestérol"]	1	[1;1]	0.0102
0.045	[0.004;0.461]	0.0102	(Intercept)

```

## Waiting for profiling to be done...

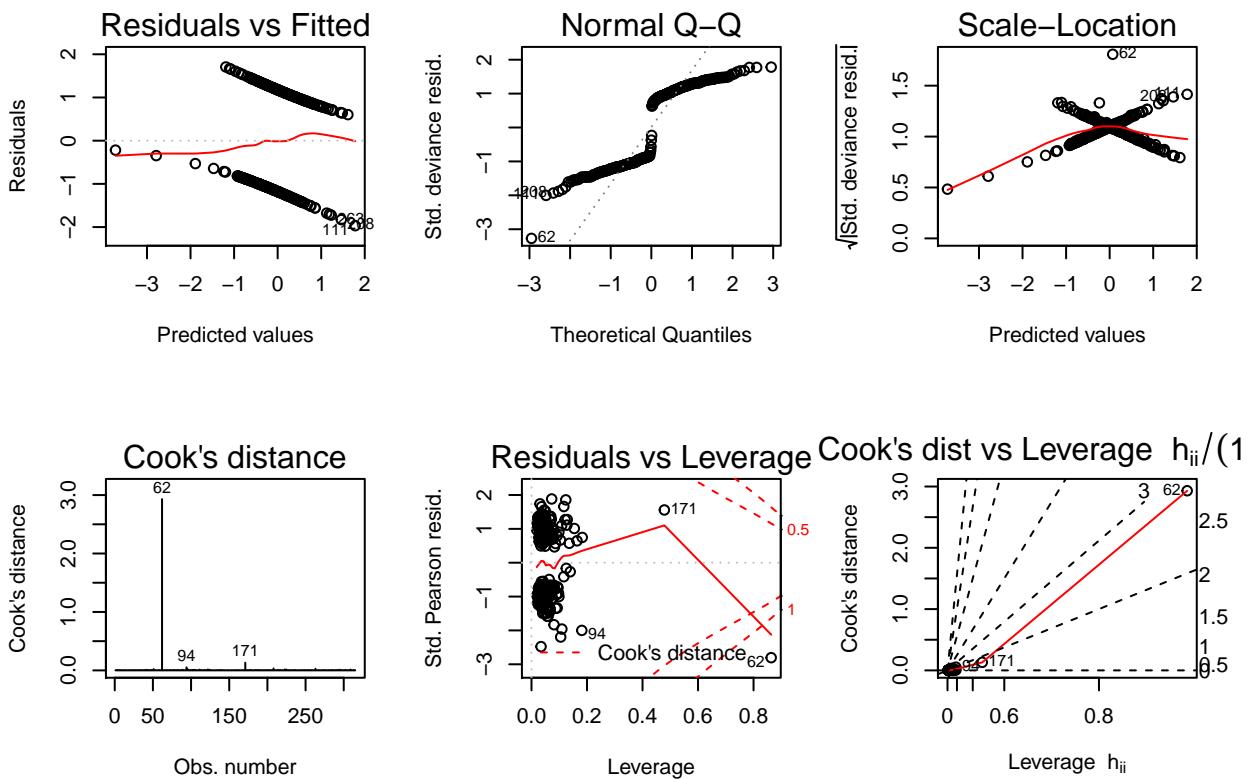
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et cholestérol", col.names = c("Variable", "OR", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + graisses*retinol[, "betadiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 151: Régression linéaire multiple avec interaction entre graisses et betadiet

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.002
age	0.729	[0.33;1.577]	0.4254
sexeFemmes	1.258	[0.751;2.115]	0.3839
tabacAutrefois	0.976	[0.455;2.065]	0.9486
tabacFumeur	1.018	[0.977;1.06]	0.3982
bmi	1.093	[0.617;1.941]	0.7596
vitamineSouvent	1.093	[0.59;2.028]	0.7783
vitaminePas-souvent	1	[0.999;1.002]	0.47
calories	1.002	[0.979;1.026]	0.8492
graisses	0.962	[0.896;1.031]	0.2807
fibres	0.991	[0.961;1.023]	0.5648
alcool	1	[0.997;1.002]	0.836
cholesterol	1	[1;1.001]	0.2791
betadiet	1	[1;1]	0.9136
retdiet	1.001	[1;1.003]	0.0636
betaplasma	NA	[NA;NA]	0.2178
graisses:retinol[, "betadiet"]	1	[1;1]	0.0314
0.085	[0.009;0.783]	0.0314	(Intercept)

```

## Waiting for profiling to be done...

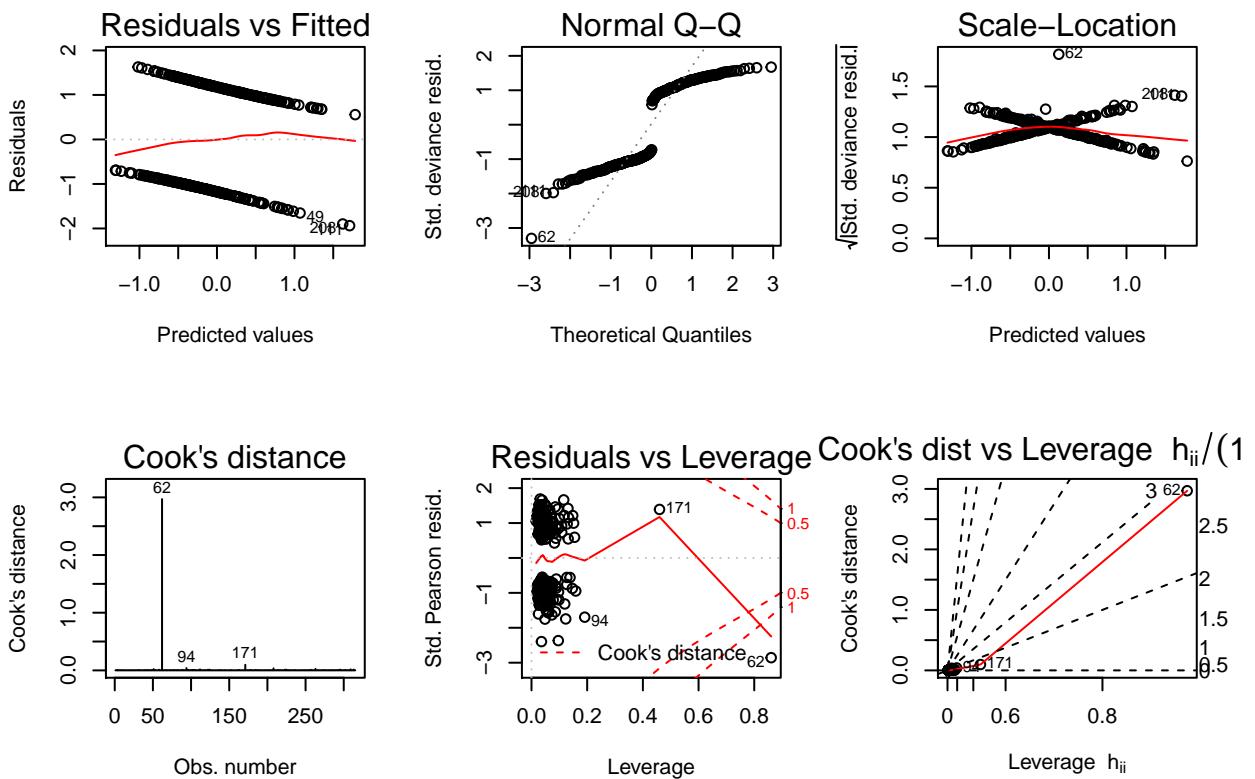
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et betadiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + graisses*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 152: Régression linéaire multiple avec interaction entre graisses et retdiet

	OR	IC	p
(Intercept)	1.029	[1.011;1.049]	0.0024
age	0.73	[0.331;1.581]	0.4273
sexeFemmes	1.195	[0.714;2.004]	0.4985
tabacAutrefois	0.958	[0.446;2.03]	0.9105
tabacFumeur	1.02	[0.979;1.062]	0.3447
bmi	1.094	[0.617;1.942]	0.7581
vitamineSouvent	1.12	[0.606;2.077]	0.7172
vitaminePas-souvent	1	[0.999;1.002]	0.5928
calories	1.004	[0.98;1.028]	0.7667
graisses	0.965	[0.899;1.035]	0.3234
fibres	0.994	[0.963;1.025]	0.6735
alcool	1	[0.997;1.003]	0.9109
cholesterol	1	[1;1]	0.8337
betadiet	1.001	[1;1.002]	0.1931
retdiet	1.001	[1;1.003]	0.0524
betaplasma	NA	[NA;NA]	0.1789
graisses:retinol[, "retdiet"]	1	[1;1]	0.0273
0.081	[0.008;0.736]	0.0273	(Intercept)

```

## Waiting for profiling to be done...

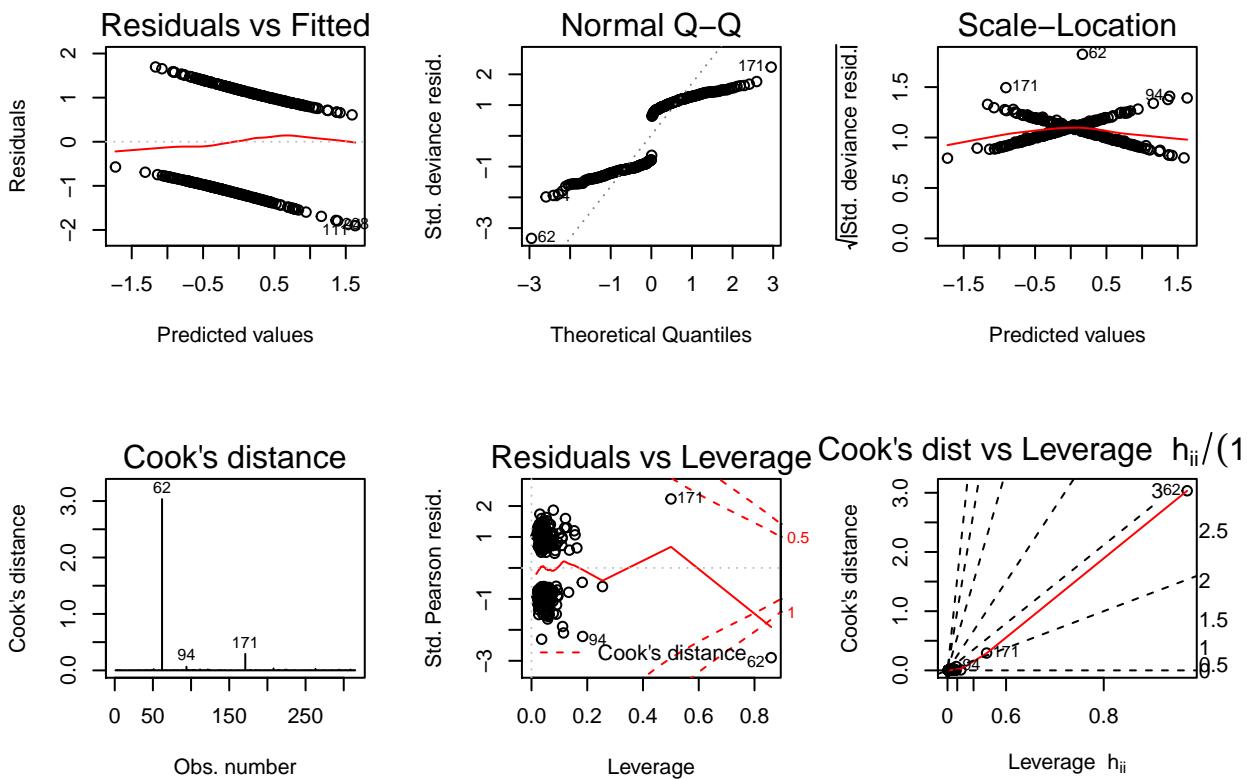
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et retdiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + graisses*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 153: Régression linéaire multiple avec interaction entre graisses et betaplasma

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.002
age	0.682	[0.306;1.488]	0.3406
sexeFemmes	1.252	[0.748;2.105]	0.3937
tabacAutrefois	1.006	[0.469;2.132]	0.9875
tabacFumeur	1.018	[0.978;1.06]	0.384
bmi	1.108	[0.625;1.968]	0.7258
vitamineSouvent	1.119	[0.604;2.077]	0.7213
vitaminePas-souvent	1.001	[0.999;1.002]	0.3775
calories	0.987	[0.964;1.009]	0.2378
graisses	0.957	[0.89;1.027]	0.2234
fibres	0.99	[0.96;1.021]	0.4934
alcool	1	[0.997;1.003]	0.9818
cholesterol	1	[1;1]	0.8807
betadiet	1	[1;1.001]	0.8711
rettdiet	0.999	[0.995;1.003]	0.5966
betaplasma	NA	[NA;NA]	0.1777
graisses:retinol[, "betaplasma"]	1	[1;1]	0.1743
0.233	[0.028;1.892]	0.1743	(Intercept)

```

## Waiting for profiling to be done...

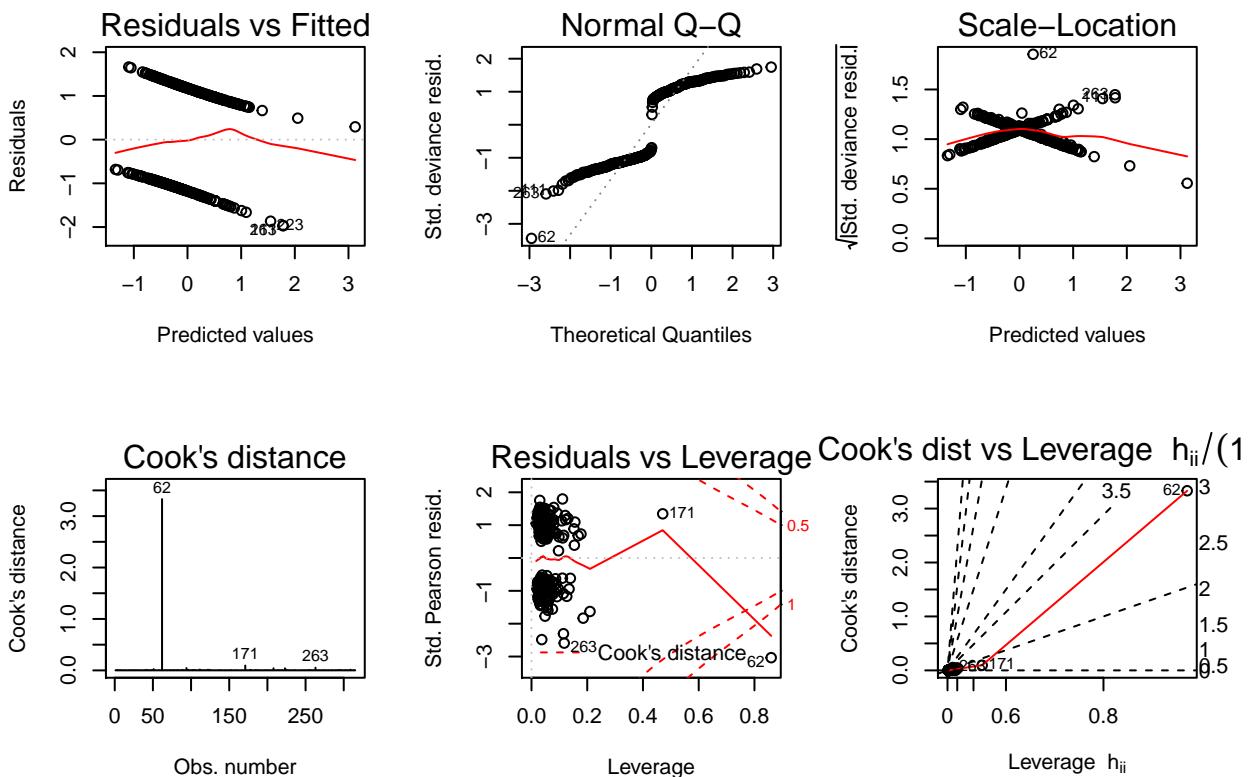
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre graisses et betaplasma", col.names
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.8 Interaction avec les fibres

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + fibres*retinol[, "alcool"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 154: Régression linéaire multiple avec interaction entre fibres et alcool

	OR	IC	p
(Intercept)	1.031	[1.012;1.051]	0.0016
age	0.714	[0.324;1.544]	0.3957
sexeFemmes	1.208	[0.723;2.025]	0.4711
tabacAutrefois	0.983	[0.46;2.078]	0.9647
tabacFumeur	1.018	[0.978;1.06]	0.3908
bmi	1.111	[0.627;1.97]	0.7182
vitamineSouvent	1.129	[0.611;2.092]	0.6983
vitaminePas-souvent	1.001	[0.999;1.002]	0.3922
calories	0.993	[0.974;1.013]	0.5058
graisses	0.953	[0.882;1.028]	0.2123
fibres	0.953	[0.834;1.086]	0.4683
alcool	1	[0.997;1.002]	0.8653
cholesterol	1	[1;1]	0.8236
betadiet	1	[1;1]	0.9207
retdiet	1.002	[1;1.003]	0.0463
betaplasma	NA	[NA;NA]	0.5552
fibres:retinol[, "alcool"]	1.003	[0.992;1.015]	0.0679
0.153	[0.02;1.13]	0.0679	(Intercept)

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

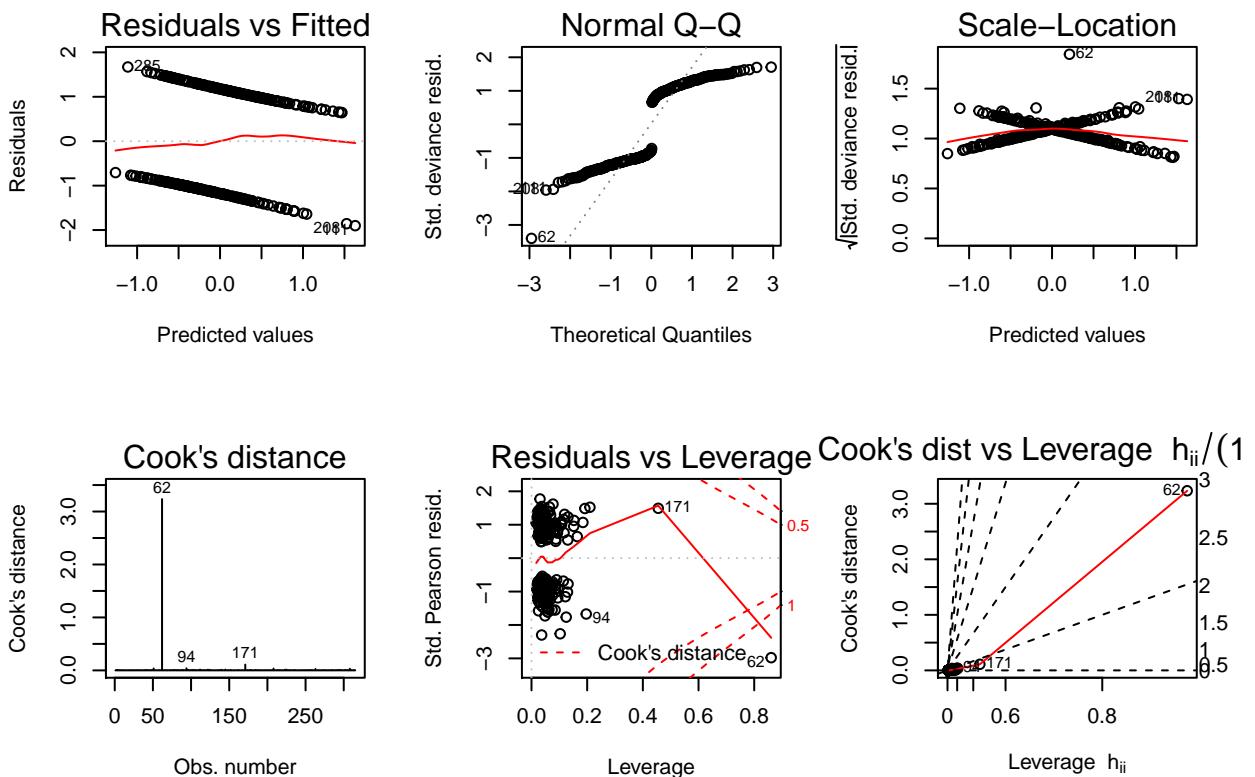
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre fibres et alcool", col.names = c("",
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + fibres*retinol[, "cholesterol"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 155: Régression linéaire multiple avec interaction entre fibres et cholesterol

	OR	IC	p
(Intercept)	1.03	[1.011;1.05]	0.0018
age	0.834	[0.372;1.847]	0.6565
sexeFemmes	1.281	[0.763;2.16]	0.3504
tabacAutrefois	0.915	[0.423;1.95]	0.8186
tabacFumeur	1.018	[0.978;1.061]	0.3778
bmi	1.127	[0.634;2.007]	0.6842
vitamineSouvent	1.108	[0.598;2.059]	0.7446
vitaminePas-souvent	1.001	[0.999;1.002]	0.432
calories	0.995	[0.976;1.015]	0.6498
graisses	1.063	[0.947;1.2]	0.3123
fibres	0.988	[0.958;1.02]	0.4493
alcool	1.006	[1;1.012]	0.0725
cholesterol	1	[1;1]	0.9683
betadiet	1	[1;1.001]	0.8143
retldiet	1.001	[1;1.003]	0.063
betaplasma	NA	[NA;NA]	0.042
fibres:retinol[, "cholesterol"]	1	[0.999;1]	0.0072
0.031	[0.002;0.377]	0.0072	(Intercept)

```

## Waiting for profiling to be done...

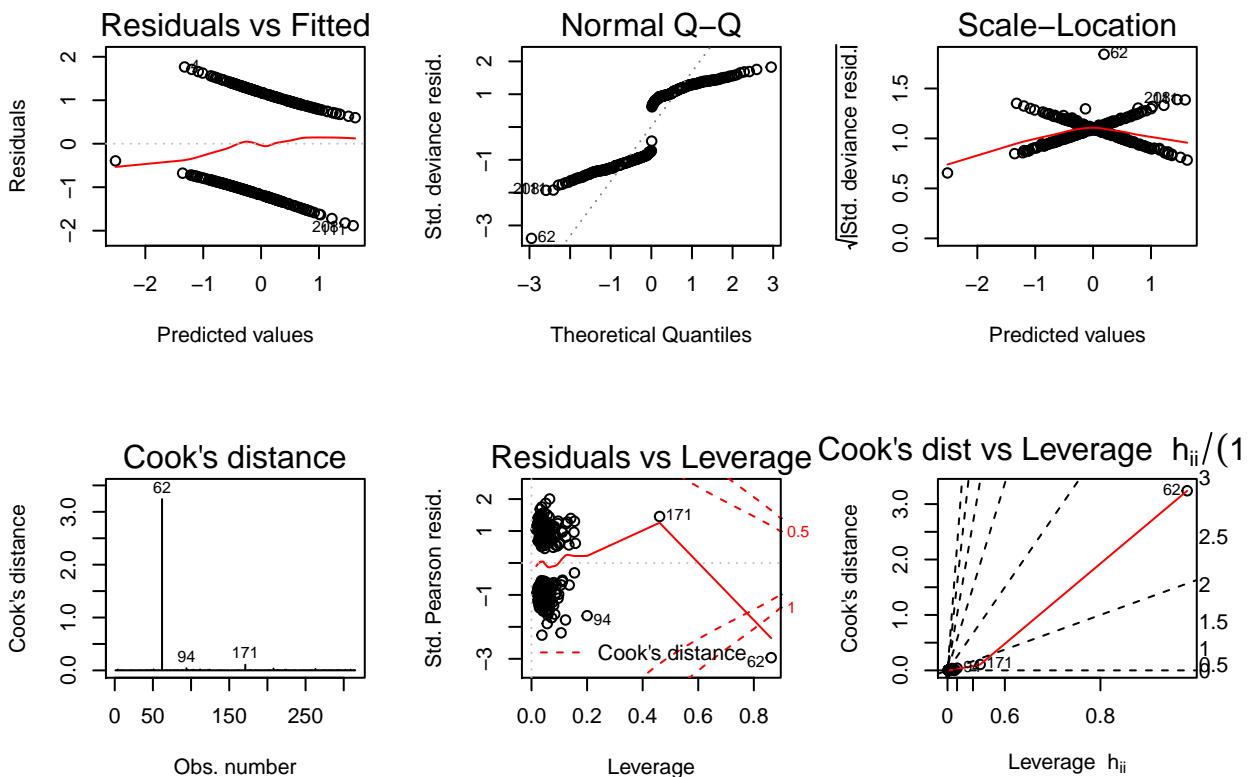
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre fibres et cholesterol", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + fibres*retinol[, "betadiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[" ,round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 156: Régression linéaire multiple avec interaction entre fibres et betadiet

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0019
age	0.701	[0.319;1.51]	0.3677
sexeFemmes	1.22	[0.731;2.043]	0.4481
tabacAutrefois	0.989	[0.461;2.099]	0.9781
tabacFumeur	1.017	[0.977;1.059]	0.4165
bmi	1.106	[0.625;1.96]	0.7296
vitamineSouvent	1.126	[0.609;2.086]	0.7052
vitaminePas-souvent	1	[0.999;1.002]	0.4357
calories	0.994	[0.975;1.014]	0.5421
graisses	0.971	[0.883;1.068]	0.5384
fibres	0.99	[0.96;1.021]	0.4945
alcool	1	[0.997;1.002]	0.873
cholesterol	1	[1;1]	0.8341
betadiet	1	[1;1]	0.914
rettdiet	1.002	[1;1.003]	0.0478
betaplasma	NA	[NA;NA]	0.7647
fibres:retinol[, "betadiet"]	1	[1;1]	0.0757
0.138	[0.015;1.206]	0.0757	(Intercept)

```

## Waiting for profiling to be done...

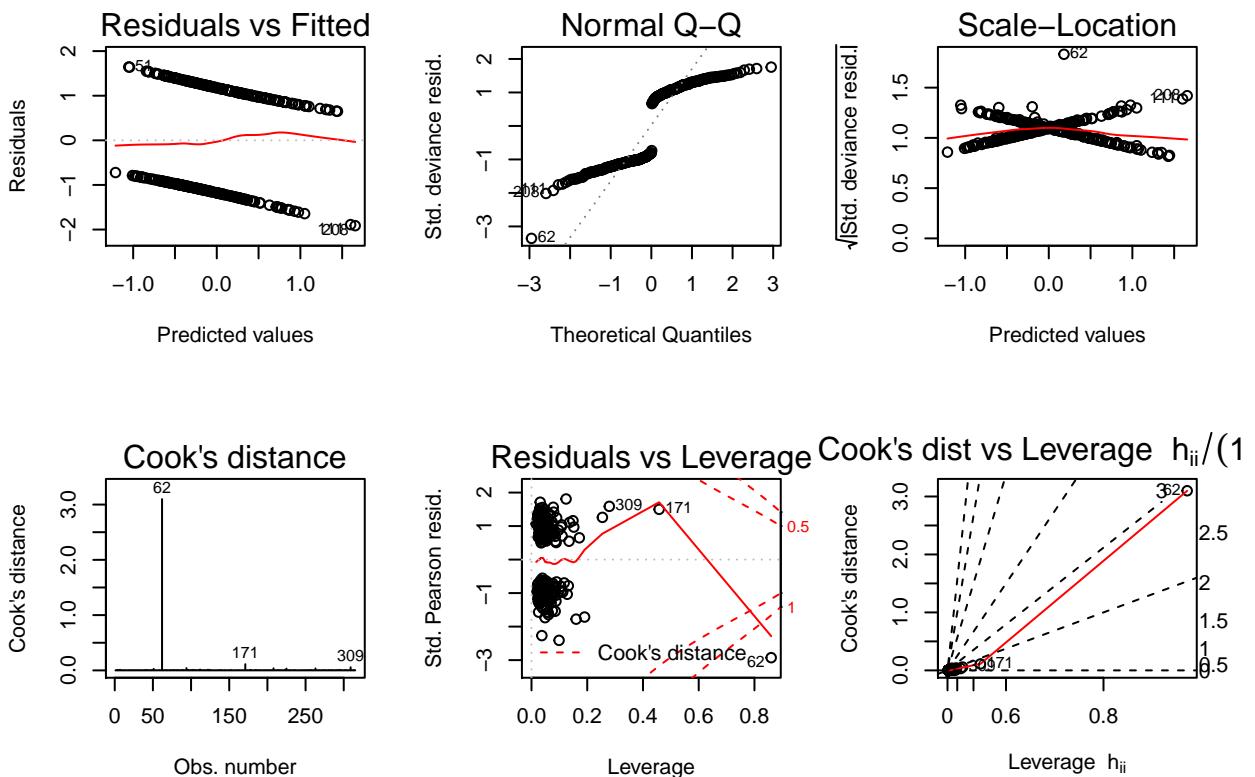
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre fibres et betadiet", col.names = c(
        "Variable", "OR", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + fibres*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 157: Régression linéaire multiple avec interaction entre fibres et retdiet

	OR	IC	p
(Intercept)	1.029	[1.01;1.049]	0.0024
age	0.697	[0.317;1.503]	0.3607
sexeFemmes	1.214	[0.727;2.035]	0.4585
tabacAutrefois	0.963	[0.45;2.037]	0.9224
tabacFumeur	1.018	[0.978;1.06]	0.3854
bmi	1.094	[0.617;1.94]	0.7591
vitamineSouvent	1.122	[0.607;2.077]	0.7142
vitaminePas-souvent	1	[0.999;1.002]	0.4982
calories	0.995	[0.976;1.015]	0.6259
graisses	0.993	[0.881;1.119]	0.9105
fibres	0.991	[0.961;1.022]	0.5325
alcool	1	[0.997;1.002]	0.8582
cholesterol	1	[1;1]	0.8484
betadiet	1.001	[0.999;1.002]	0.5002
retdiet	1.002	[1;1.003]	0.0515
betaplasma	NA	[NA;NA]	0.5078
fibres:retinol[, "retdiet"]	1	[1;1]	0.0578
0.108	[0.01;1.057]	0.0578	(Intercept)

```

## Waiting for profiling to be done...

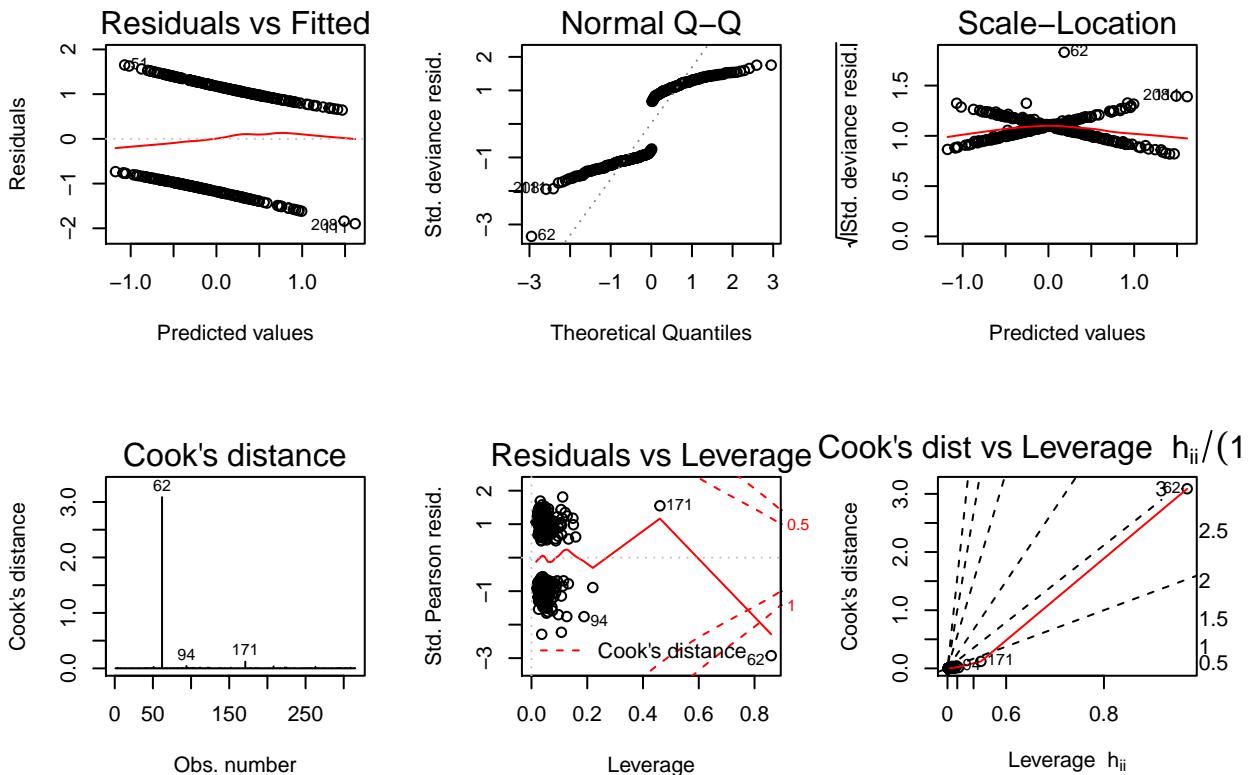
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre fibres et retdiet", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + fibres*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 158: Régression linéaire multiple avec interaction entre fibres et betaplasma

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0019
age	0.699	[0.318;1.505]	0.3636
sexeFemmes	1.218	[0.728;2.045]	0.4528
tabacAutrefois	0.978	[0.457;2.067]	0.9539
tabacFumeur	1.017	[0.977;1.059]	0.4113
bmi	1.105	[0.624;1.957]	0.7324
vitamineSouvent	1.121	[0.606;2.08]	0.7163
vitaminePas-souvent	1	[0.999;1.002]	0.4474
calories	0.994	[0.975;1.014]	0.5567
graisses	0.961	[0.883;1.045]	0.3594
fibres	0.99	[0.96;1.021]	0.5069
alcool	1	[0.997;1.002]	0.8738
cholesterol	1	[1;1]	0.8771
betadiet	1	[1;1]	0.8926
retdiet	1.002	[0.998;1.005]	0.3523
betaplasma	NA	[NA;NA]	0.9978
fibres:retinol[, "betaplasma"]	1	[1;1]	0.0857
0.157	[0.018;1.278]	0.0857	(Intercept)

```

## Waiting for profiling to be done...

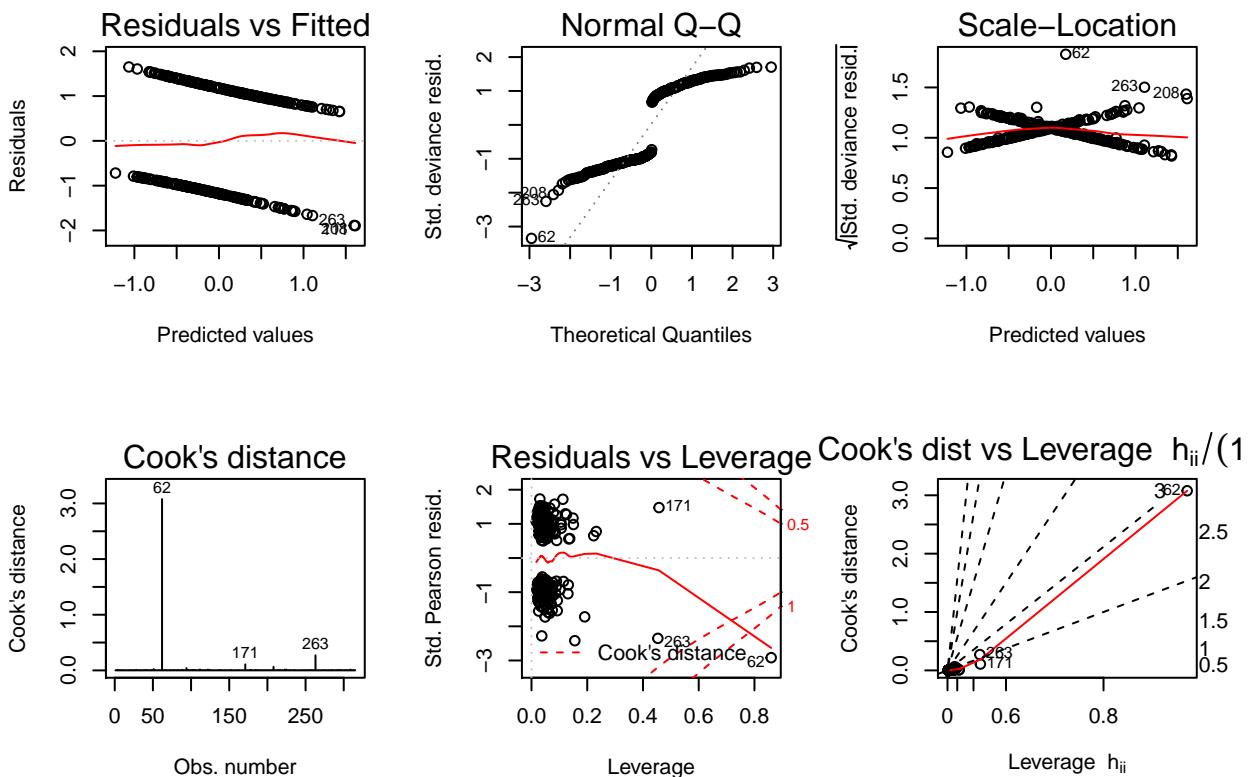
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre fibres et betaplasma", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.9 Interaction avec l'alcool

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + alcool*retinol[, "cholesterol"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4)

## Waiting for profiling to be done...
## Warning in cbind(exp(stats:::coef(x)), exp(stats:::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats:::coef(x)), exp(stats:::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 159: Régression linéaire multiple avec interaction entre alcool et cholesterol

	OR	IC	p
(Intercept)	1.032	[1.013;1.051]	0.0011
age	0.776	[0.35;1.693]	0.5267
sexeFemmes	1.117	[0.663;1.886]	0.6772
tabacAutrefois	1.003	[0.465;2.138]	0.994
tabacFumeur	1.024	[0.983;1.067]	0.2596
bmi	1.207	[0.676;2.161]	0.525
vitamineSouvent	1.147	[0.617;2.138]	0.6653
vitaminePas-souvent	1.001	[0.999;1.002]	0.3535
calories	0.993	[0.973;1.012]	0.4597
graisses	0.959	[0.893;1.029]	0.2466
fibres	1.101	[0.998;1.224]	0.0618
alcool	1	[0.997;1.003]	0.9286
cholesterol	1	[1;1]	0.8274
betadiet	1	[1;1.001]	0.8613
retdiet	1.001	[1;1.003]	0.0659
betaplasma	NA	[NA;NA]	0.0342
alcool:retinol[, "cholesterol"]	1	[1;1]	0.0212
0.084	[0.01;0.675]	0.0212	(Intercept)

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

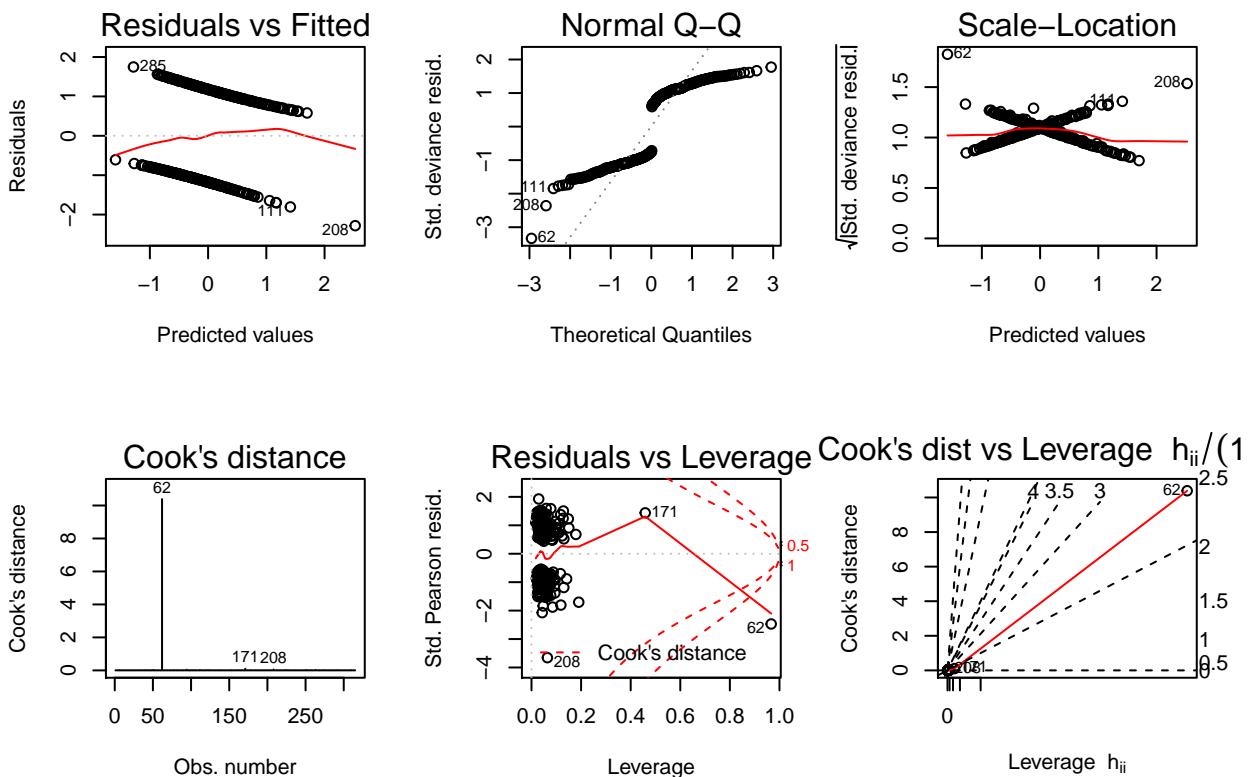
## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre alcool et cholesterol", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

## Warning in sqrt(crit * p * (1 - hh)/hh): production de NaN
## Warning in sqrt(crit * p * (1 - hh)/hh): production de NaN

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + alcool*retinol[, "betadiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 160: Régression linéaire multiple avec interaction entre alcool et betadiet

	OR	IC	p
(Intercept)	1.029	[1.01;1.048]	0.0027
age	0.67	[0.3;1.461]	0.3191
sexeFemmes	1.243	[0.742;2.09]	0.41
tabacAutrefois	0.989	[0.459;2.103]	0.9764
tabacFumeur	1.02	[0.979;1.062]	0.3406
bmi	1.135	[0.64;2.017]	0.6651
vitamineSouvent	1.158	[0.622;2.165]	0.644
vitaminePas-souvent	1.001	[0.999;1.002]	0.4134
calories	0.993	[0.974;1.013]	0.4859
graisses	0.96	[0.892;1.03]	0.2566
fibres	1.099	[0.999;1.227]	0.068
alcool	1	[0.997;1.002]	0.8843
cholesterol	1	[1;1]	0.3833
betadiet	1	[1;1.001]	0.8893
rettdiet	1.002	[1;1.003]	0.0526
betaplasma	NA	[NA;NA]	0.0348
alcool:retinol[, "betadiet"]	1	[1;1]	0.0423
0.119	[0.015;0.911]	0.0423	(Intercept)

```

## Waiting for profiling to be done...

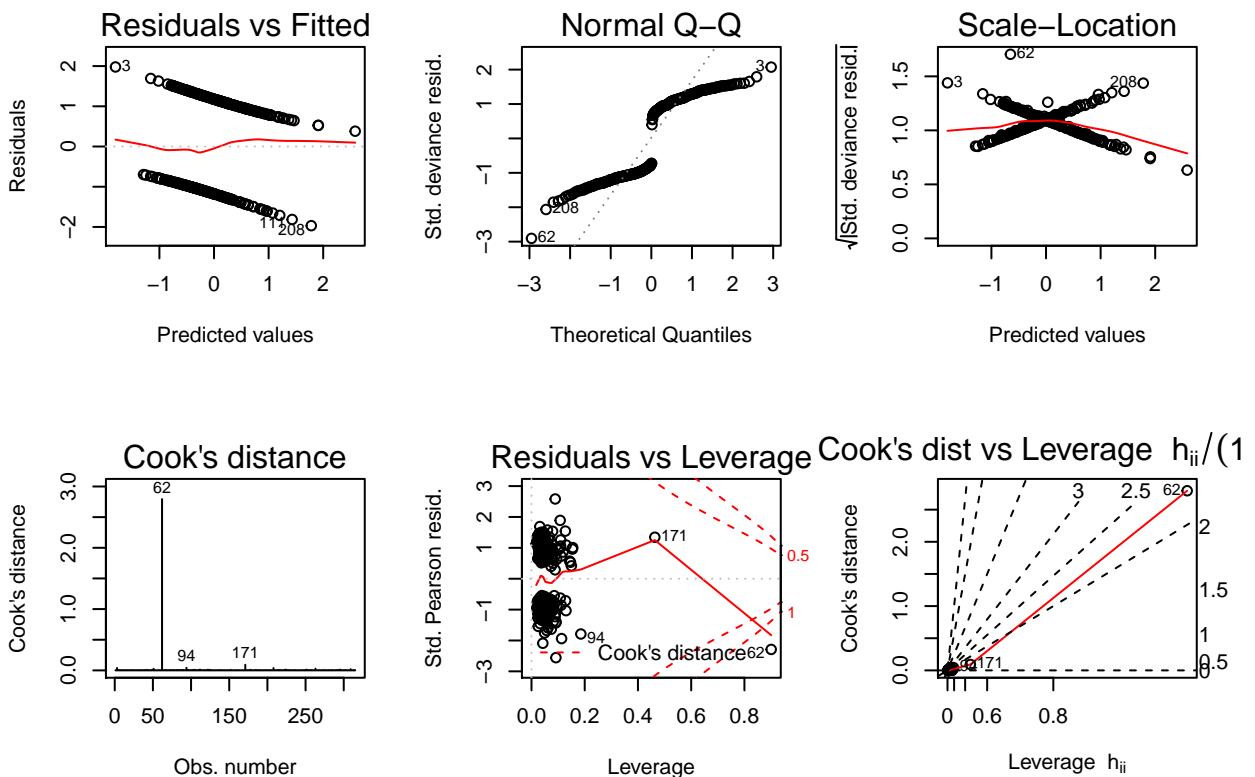
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre alcool et betadiet", col.names = c
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + alcool*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 161: Régression linéaire multiple avec interaction entre alcool et retdiet

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0019
age	0.757	[0.341;1.65]	0.4857
sexeFemmes	1.169	[0.697;1.966]	0.5545
tabacAutrefois	0.992	[0.462;2.105]	0.9839
tabacFumeur	1.02	[0.979;1.062]	0.349
bmi	1.1	[0.62;1.952]	0.745
vitamineSouvent	1.1	[0.594;2.043]	0.7612
vitaminePas-souvent	1	[0.999;1.002]	0.454
calories	0.994	[0.975;1.014]	0.5459
graisses	0.962	[0.896;1.032]	0.281
fibres	1.058	[0.957;1.175]	0.2807
alcool	1	[0.997;1.002]	0.7916
cholesterol	1	[1;1]	0.8552
betadiet	1	[1;1.001]	0.3961
retdiet	1.002	[1;1.003]	0.0545
betaplasma	NA	[NA;NA]	0.184
alcool:retinol[, "retdiet"]	1	[1;1]	0.0411
0.116	[0.014;0.899]	0.0411	(Intercept)

```

## Waiting for profiling to be done...

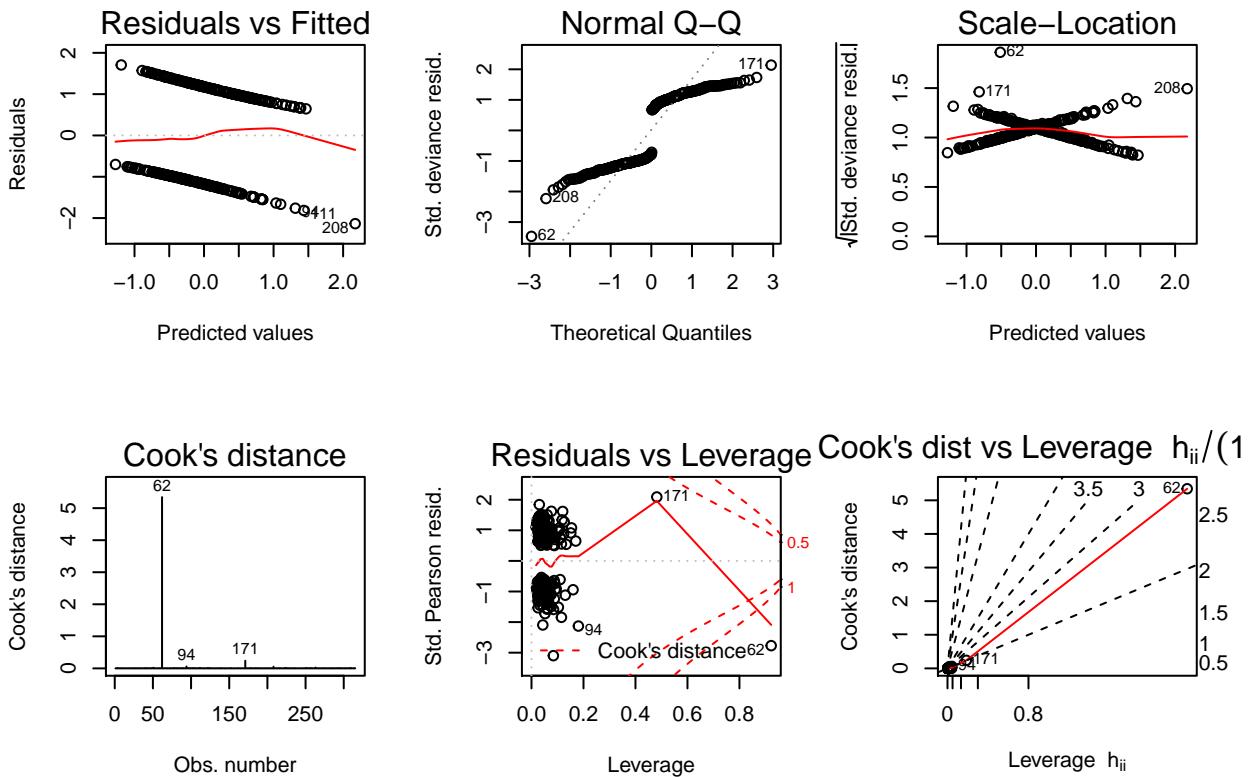
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre alcool et retdiet", col.names = c(
        kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + alcool*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 162: Régression linéaire multiple avec interaction entre alcool et betaplasma

	OR	IC	p
(Intercept)	1.029	[1.011;1.049]	0.0022
age	0.699	[0.318;1.504]	0.3629
sexeFemmes	1.236	[0.736;2.085]	0.4235
tabacAutrefois	0.98	[0.458;2.071]	0.9578
tabacFumeur	1.017	[0.977;1.059]	0.4107
bmi	1.101	[0.622;1.952]	0.7416
vitamineSouvent	1.124	[0.608;2.081]	0.7094
vitaminePas-souvent	1	[0.999;1.002]	0.4566
calories	0.994	[0.975;1.014]	0.56
graisses	0.961	[0.894;1.03]	0.2649
fibres	0.995	[0.952;1.038]	0.8219
alcool	1	[0.997;1.002]	0.8778
cholesterol	1	[1;1]	0.8866
betadiet	1	[1;1]	0.8863
retdiet	1.002	[1;1.004]	0.0699
betaplasma	NA	[NA;NA]	0.7127
alcool:retinol[, "betaplasma"]	1	[1;1]	0.0711
0.157	[0.02;1.155]	0.0711	(Intercept)

```

## Waiting for profiling to be done...

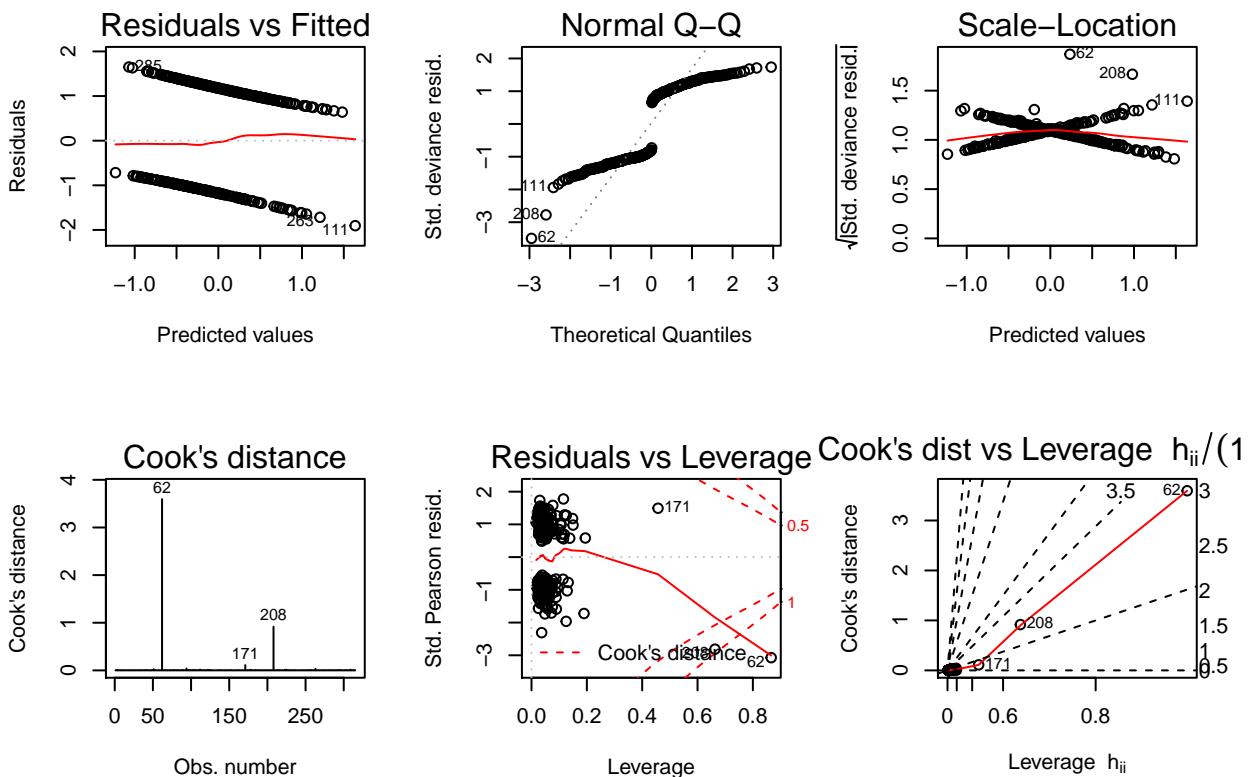
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre alcool et betaplasma", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.10 Interaction avec le cholestérol

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + cholesterol*retinol[, "betadiet"],
               data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 163: Régression linéaire multiple avec interaction entre cholesterol et betadiet

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.002
age	0.722	[0.327;1.564]	0.4126
sexeFemmes	1.288	[0.768;2.171]	0.339
tabacAutrefois	0.944	[0.438;2.005]	0.8812
tabacFumeur	1.018	[0.978;1.06]	0.3843
bmi	1.132	[0.637;2.014]	0.6733
vitamineSouvent	1.1	[0.594;2.042]	0.762
vitaminePas-souvent	1	[0.999;1.002]	0.4545
calories	0.995	[0.975;1.015]	0.6043
graisses	0.959	[0.893;1.029]	0.2473
fibres	0.992	[0.962;1.024]	0.6059
alcool	1.003	[0.999;1.007]	0.2015
cholesterol	1	[1;1.001]	0.1064
betadiet	1	[1;1]	0.9105
retdiet	1.001	[1;1.003]	0.066
betaplasma	NA	[NA;NA]	0.0633
cholesterol:retinol[, "betadiet"]	1	[1;1]	0.0195
0.075	[0.008;0.641]	0.0195	(Intercept)

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

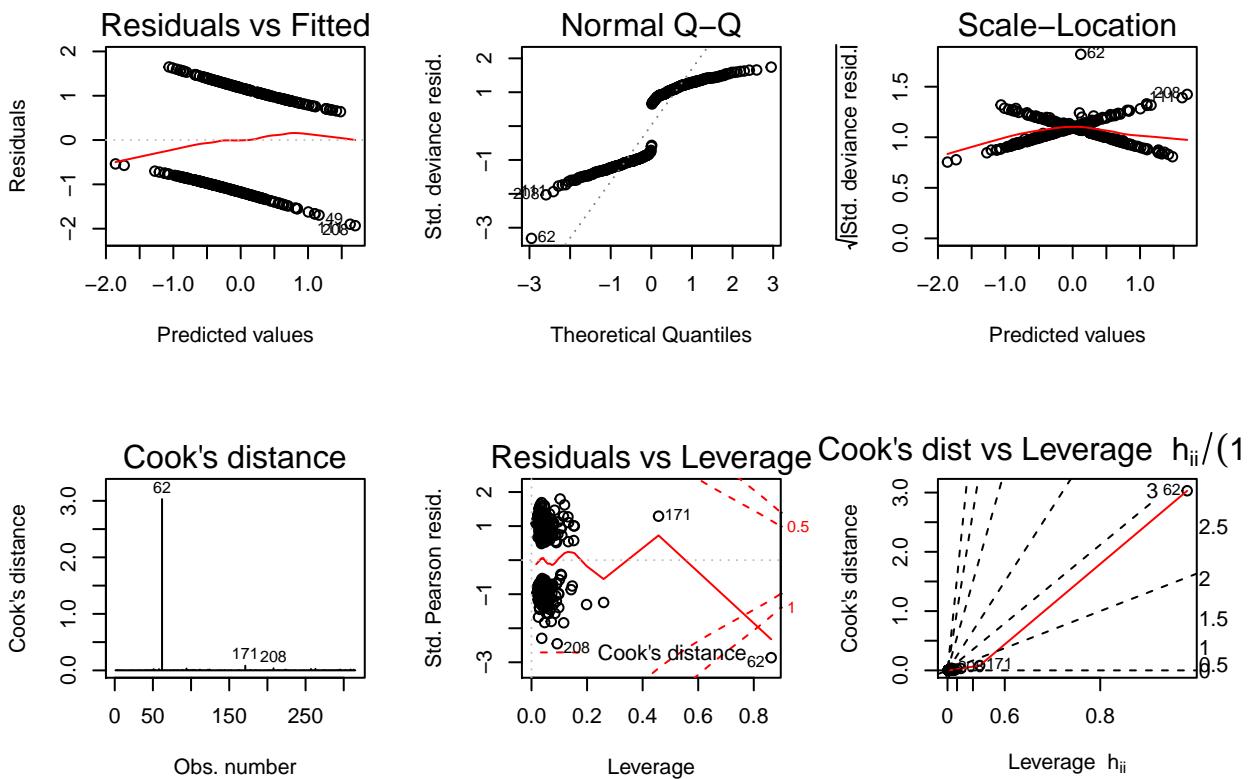
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre cholesterol et betadiet", col.names = c("Variable", "OR", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + cholesterol*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3),"]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 164: Régression linéaire multiple avec interaction entre cholesterol et retdiet

	OR	IC	p
(Intercept)	1.03	[1.011;1.049]	0.0021
age	0.695	[0.314;1.504]	0.3601
sexeFemmes	1.234	[0.737;2.074]	0.4248
tabacAutrefois	0.965	[0.448;2.05]	0.9266
tabacFumeur	1.018	[0.978;1.06]	0.3862
bmi	1.163	[0.654;2.073]	0.6072
vitamineSouvent	1.14	[0.616;2.117]	0.6769
vitaminePas-souvent	1	[0.999;1.001]	0.7514
calories	0.996	[0.976;1.015]	0.6633
graisses	0.967	[0.9;1.037]	0.3521
fibres	0.996	[0.965;1.028]	0.7747
alcool	1.002	[0.999;1.006]	0.238
cholesterol	1	[1;1]	0.8351
betadiet	1.001	[1;1.002]	0.0882
retdiet	1.001	[1;1.003]	0.054
betaplasma	NA	[NA;NA]	0.0703
cholesterol:retinol[, "retdiet"]	1	[1;1]	0.0267
0.092	[0.011;0.742]	0.0267	(Intercept)

```

## Waiting for profiling to be done...

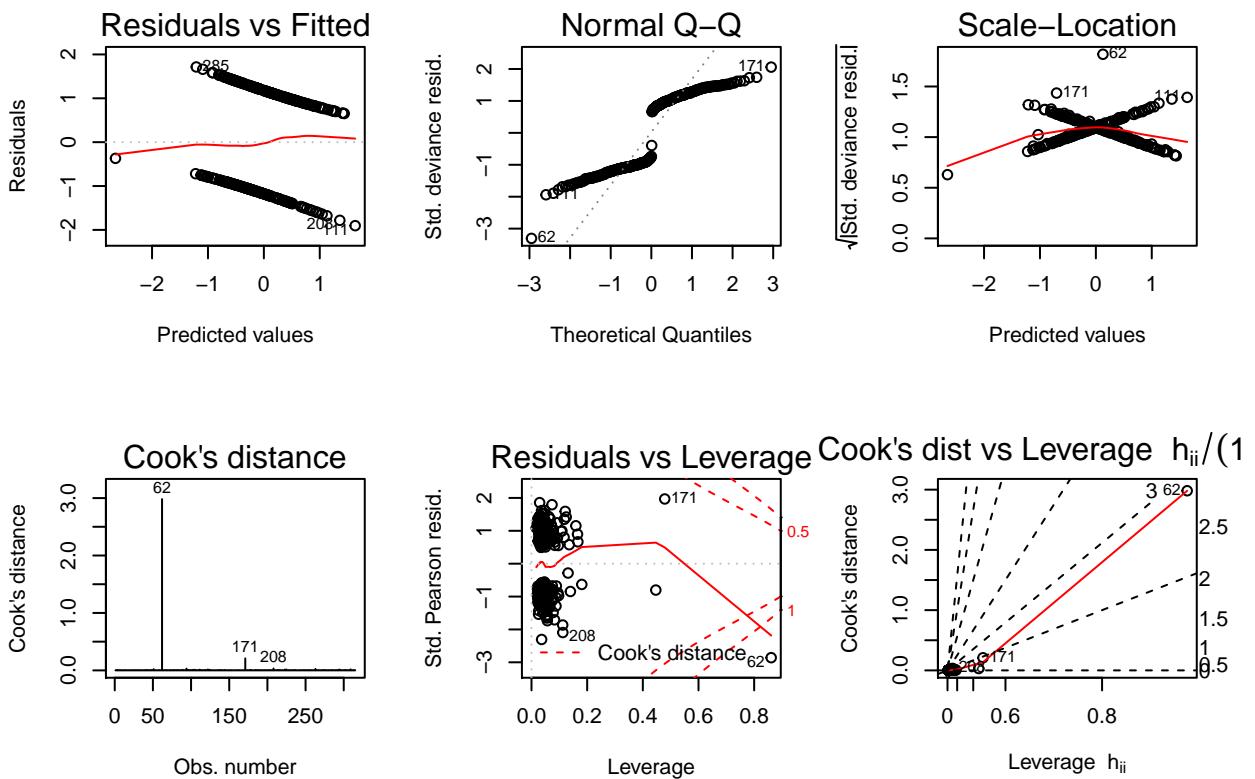
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre cholesterol et retdiet", col.names
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + cholesterol*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 165: Régression linéaire multiple avec interaction entre cholesterol et betaplasma

	OR	IC	p
(Intercept)	1.032	[1.013;1.052]	0.001
age	0.668	[0.296;1.471]	0.3218
sexeFemmes	1.281	[0.763;2.161]	0.3498
tabacAutrefois	1.008	[0.466;2.151]	0.9838
tabacFumeur	1.018	[0.977;1.06]	0.3939
bmi	1.103	[0.62;1.966]	0.7379
vitamineSouvent	1.087	[0.585;2.025]	0.7915
vitaminePas-souvent	1.001	[0.999;1.002]	0.324
calories	0.992	[0.972;1.012]	0.4127
graisses	0.955	[0.887;1.025]	0.2044
fibres	0.989	[0.958;1.021]	0.4587
alcool	0.997	[0.993;1.001]	0.1081
cholesterol	1	[1;1]	0.7193
betadiet	1	[1;1.001]	0.9501
retdiet	0.997	[0.993;1.001]	0.1489
betaplasma	NA	[NA;NA]	0.0227
cholesterol:retinol[, "betaplasma"]	1	[1;1]	0.2234
0.272	[0.033;2.197]	0.2234	(Intercept)

```

## Waiting for profiling to be done...

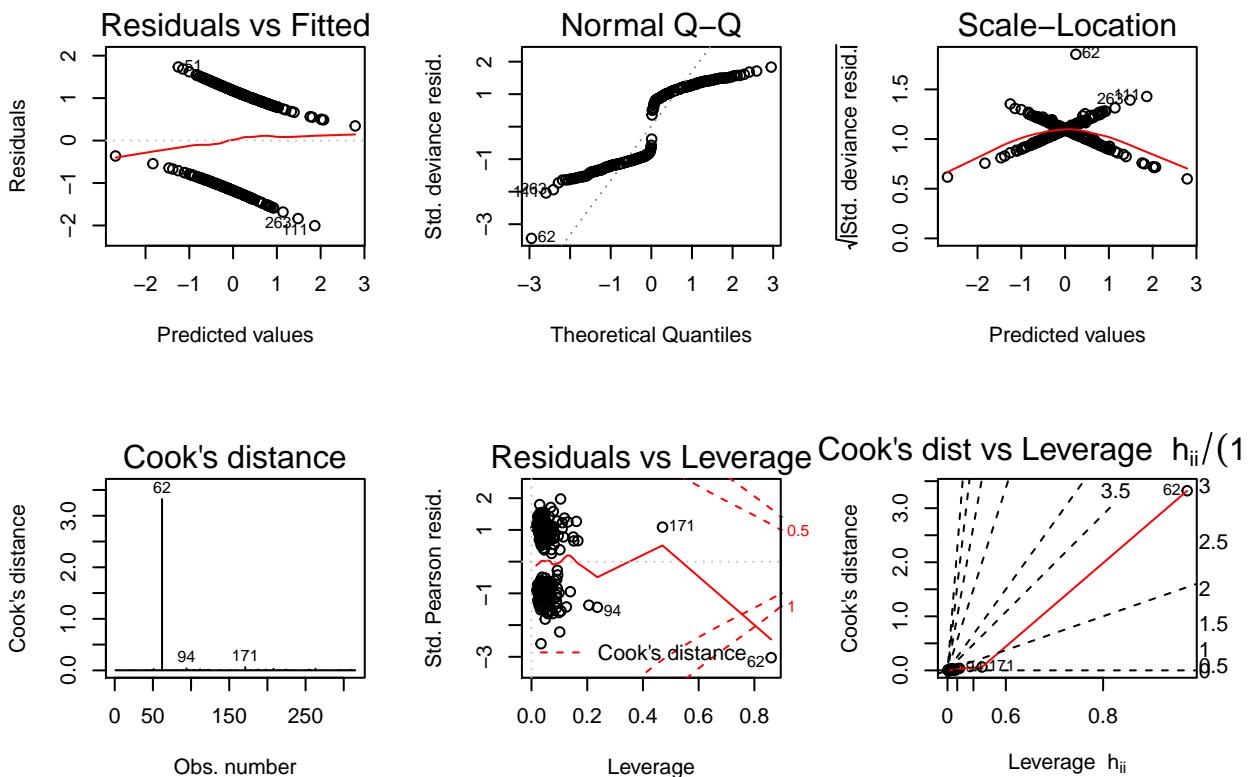
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre cholesterol et betaplasma", col.names = c("Variable", "OR", "IC", "p"),
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1"))

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.11 Interaction avec betadiet

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + betadiet*retinol[, "retdiet"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 166: Régression linéaire multiple avec interaction entre betadiet et retdiet

	OR	IC	p
(Intercept)	1.031	[1.012;1.05]	0.0015
age	0.693	[0.314;1.494]	0.3535
sexeFemmes	1.275	[0.76;2.148]	0.3583
tabacAutrefois	0.963	[0.449;2.038]	0.9215
tabacFumeur	1.019	[0.979;1.061]	0.3638
bmi	1.106	[0.624;1.965]	0.7296
vitamineSouvent	1.108	[0.598;2.057]	0.7451
vitaminePas-souvent	1.001	[0.999;1.002]	0.386
calories	0.994	[0.975;1.013]	0.5394
graisses	0.962	[0.895;1.031]	0.2762
fibres	0.989	[0.959;1.02]	0.4665
alcool	1	[0.997;1.003]	0.9038
cholesterol	1	[1;1.001]	0.2195
betadiet	1.001	[1;1.001]	0.1858
retdiet	1.001	[1;1.003]	0.0617
betaplasma	NA	[NA;NA]	0.1112
betadiet:retinol[, "retdiet"]	1	[1;1]	0.0277
0.092	[0.011;0.754]	0.0277	(Intercept)

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

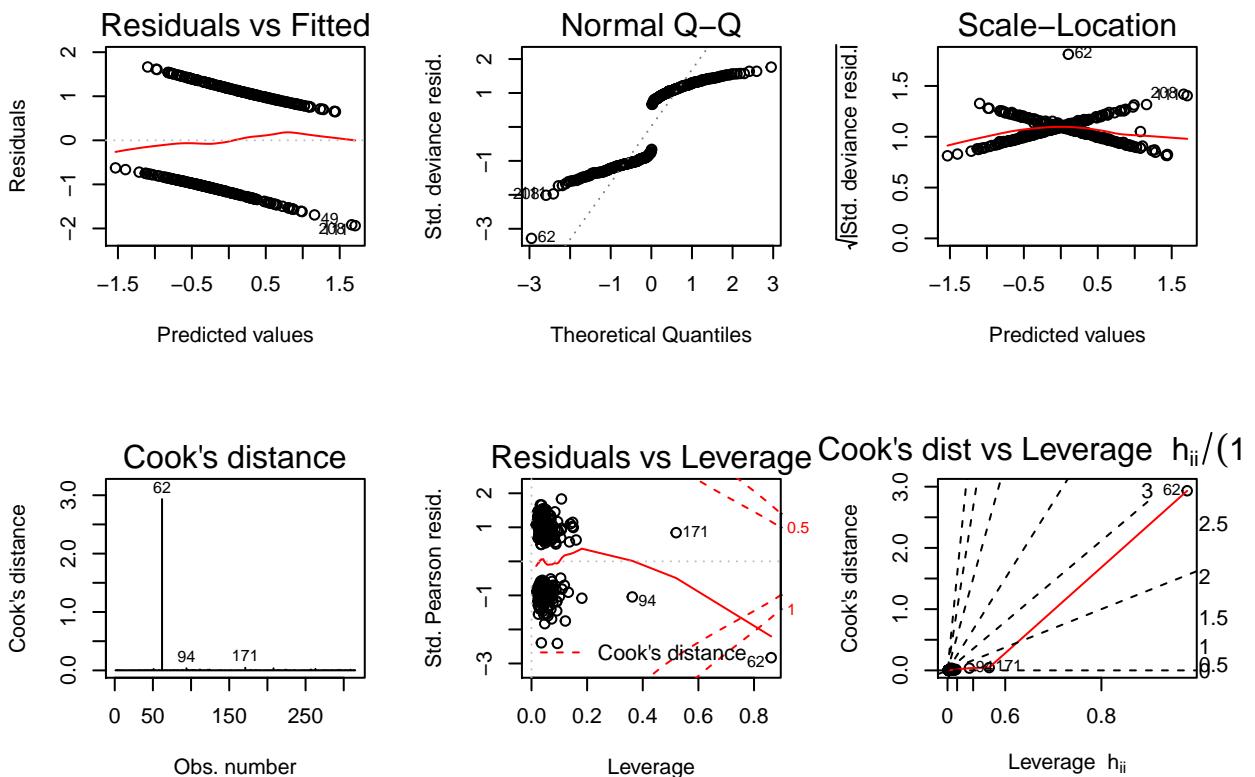
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre betadiet et retdiet", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```

rm(mod.tmp)
rm(res.tmp)

mod.tmp = glm(retplasmaBin ~ . -retplasma + betadiet*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4 )

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

```

Table 167: Régression linéaire multiple avec interaction entre betadiet et betaplasma

	OR	IC	p
(Intercept)	1.031	[1.012;1.05]	0.0016
age	0.696	[0.317;1.498]	0.3574
sexeFemmes	1.225	[0.734;2.052]	0.4387
tabacAutrefois	0.975	[0.455;2.06]	0.9468
tabacFumeur	1.017	[0.977;1.059]	0.4171
bmi	1.106	[0.624;1.961]	0.7303
vitamineSouvent	1.136	[0.614;2.106]	0.6851
vitaminePas-souvent	1	[0.999;1.002]	0.4601
calories	0.995	[0.975;1.014]	0.591
graisses	0.96	[0.894;1.03]	0.2611
fibres	0.99	[0.96;1.022]	0.5137
alcool	1	[0.997;1.002]	0.8299
cholesterol	1	[1;1]	0.566
betadiet	1	[1;1.001]	0.8508
retdiet	1.001	[0.998;1.004]	0.6789
betaplasma	NA	[NA;NA]	0.513
betadiet:retinol[, "betaplasma"]	1	[1;1]	0.0993
0.179	[0.022;1.367]	0.0993	(Intercept)

```

## Waiting for profiling to be done...

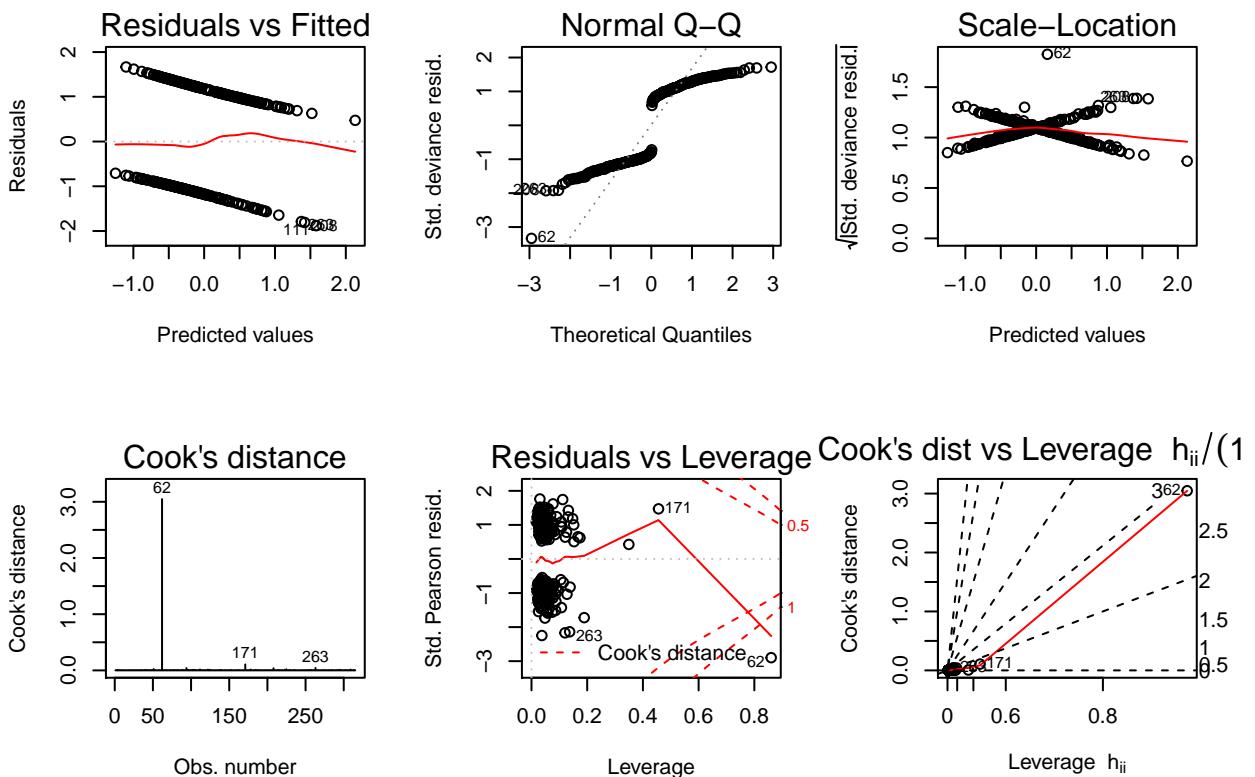
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : la longueur des données [71] n'est pas un diviseur ni un
## multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre betadiet et betaplasma", col.names
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

6.3.12 Interaction avec retdiet

```
mod.tmp = glm(retplasmaBin ~ . -retplasma + retdiet*retinol[, "betaplasma"],
              data = retinol,family = "binomial")
res.tmp = matrix(c(rownames(summary(mod.tmp)$coefficient),
                  round(odds.ratio(mod.tmp)[,1],3),
                  paste0("[",round(odds.ratio(mod.tmp)[,2],3),";",
                         round(odds.ratio(mod.tmp)[,3],3), "]"),
                  round(odds.ratio(mod.tmp)[,4],4)), ncol = 4)

## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)
## Waiting for profiling to be done...
```

Table 168: Régression linéaire multiple avec interaction entre retdiet et betaplasma

	OR	IC	p
(Intercept)	1.03	[1.011;1.05]	0.002
age	0.666	[0.3;1.445]	0.308
sexeFemmes	1.275	[0.76;2.148]	0.3582
tabacAutrefois	1.002	[0.467;2.123]	0.9954
tabacFumeur	1.019	[0.978;1.061]	0.3682
bmi	1.155	[0.649;2.058]	0.6244
vitamineSouvent	1.167	[0.629;2.171]	0.6249
vitaminePas-souvent	1.001	[0.999;1.002]	0.3599
calories	0.993	[0.973;1.013]	0.4886
graisses	0.956	[0.889;1.026]	0.2139
fibres	0.988	[0.958;1.02]	0.4497
alcool	1	[0.997;1.003]	0.9133
cholesterol	1	[1;1]	0.9194
betadiet	0.999	[0.998;1]	0.0727
retdiet	0.998	[0.995;1.002]	0.3392
betaplasma	NA	[NA;NA]	0.0383
retdiet:retinol[, "betaplasma"]	1	[1;1]	0.1716
0.236	[0.029;1.856]	0.1716	(Intercept)

```

## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Waiting for profiling to be done...

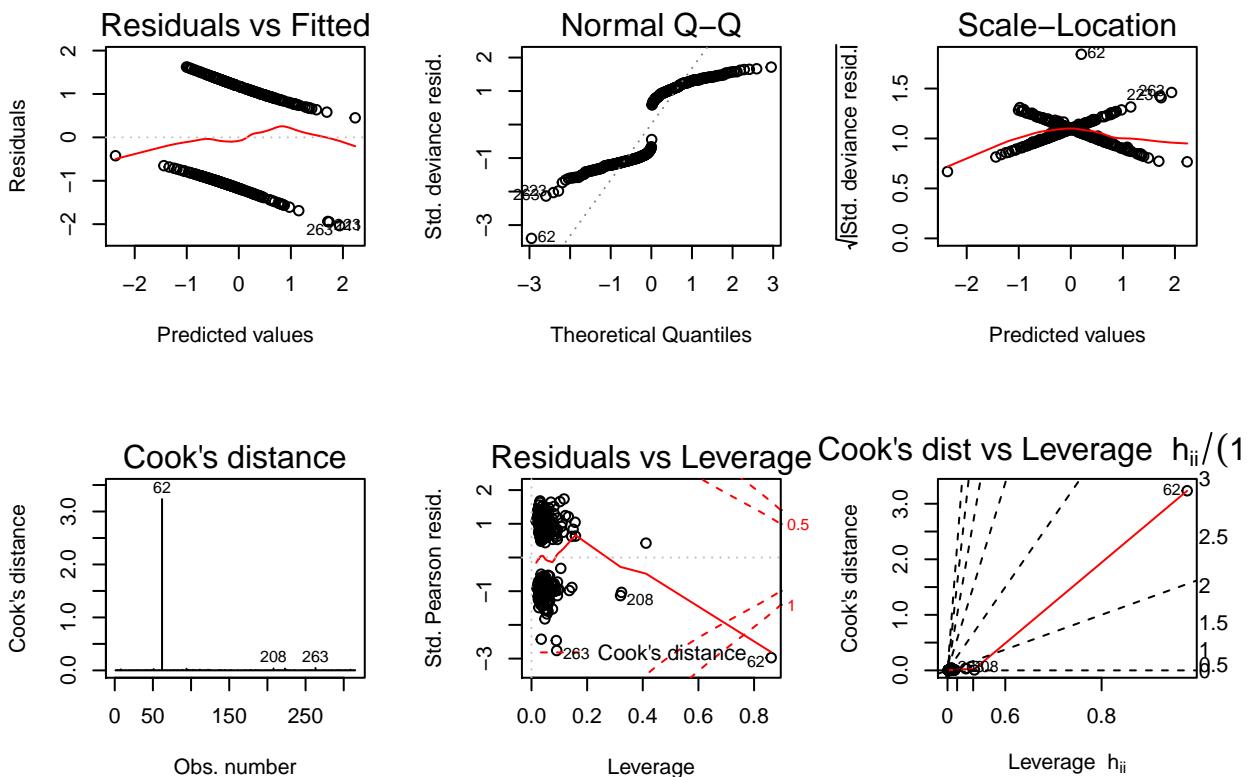
## Warning in cbind(exp(stats::coef(x)), exp(stats::confint(x, level =
## level)), : number of rows of result is not a multiple of vector length (arg
## 3)

## Warning in matrix(c(rownames(summary(mod.tmp)$coefficient),
## round(odds.ratio(mod.tmp)[, : la longueur des données [71] n'est pas un
## diviseur ni un multiple du nombre de lignes [18]

kable(res.tmp,
      caption = "Régression linéaire multiple avec interaction entre retdiet et betaplasma", col.names =
      kable_styling(latex_options = "striped", stripe_color = "#BBD2E1")

par(mfrow = c(2,3))
plot(mod.tmp, which = 1:6)

```



```
rm(mod.tmp)
rm(res.tmp)
```

7. Ouverture, améliorations.

Pour que l'analyse que nous venons d'effectuer aie plus de "sens", il faudrait commencer par repérer les valeurs aberrantes comme dans la variable `alcool`. D'ailleurs, une idée serait de catégoriser cette variable en 3 classes : non-buveurs, buveurs modérés et buveurs. Cela pourrait faciliter l'interprétation des résultats d'une régression (logistique ou linéaire). De plus, on pourrait être plus fins dans la recherche d'interactions entre variables explicatives en recherchant ce qui a du sens plutôt qu'en faisant une recherche systématique. Je ne l'ai pas fait car j'ai plusieurs fois lu que le but du devoir portait plus sur l'utilisation de R et des tests de régressions vues en cours que sur une réelle analyse du dataset.

Bon courage à vous pour la correction.

Cordialement,

Odélia Guedj