Analyse de la variance (anova)

quantitatif ~ f(qualitatif)

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Définition et objetif

Modèle général :

$$y_{ij...nr} = \mu + \alpha_i + \beta_j + \ldots + \gamma_n + \ldots + \alpha\beta_{ij} + \ldots + \beta\gamma_{jn} + \epsilon_{ij...nr}$$

$$\epsilon_{ij...nr} \to N(0, \sigma^2) \qquad cov(\epsilon_{ij...nr}, \epsilon_{i'j'...n'r'}) = 0$$

- μ : intercept
- α, β, γ : variables qualitatives
- α_i : valeur pour la modalité i de la variable associée au paramètre α
- $\alpha\beta$: interaction entre α et β
- ϵ : erreur résiduelle

Objectif principal :

Tester et étudier l'influence de variables qualitatives sur une variable numérique.

Hypothèses :

- Sur les résidus
- Sur les coefficients : $\alpha_{ref} = 0$ ou $\sum_i \alpha_i = 0$

Exemple

- Expérimentation en plein champ avec I = 3 variétés différentes de blé et J = 2 types de fongicides

- 54 parcelles : 9 répétitions pour chaque pair de variété et fongicide

- Question : existe t-il des différences de rendement entre les variétés de blé et selon le fongicide utilisé ?

- Model :

$$rendement_{ijr} = \mu + \alpha_{variete=i} + \beta_{fongicide=j} + \alpha\beta_{variete=i,fongicide=j} + \epsilon_{ijr}$$

Estimation par moindres carrés (modèle à 1 facteur !)

```
# Par défaut dans R
#
#
```

- $\hat{\mu} = \bar{y}_{i=ref}$
- $\hat{\alpha}_{i=ref} = 0$
  $\hat{\alpha}_{i \neq ref} = \bar{y}_{i \neq ref} - \mu$

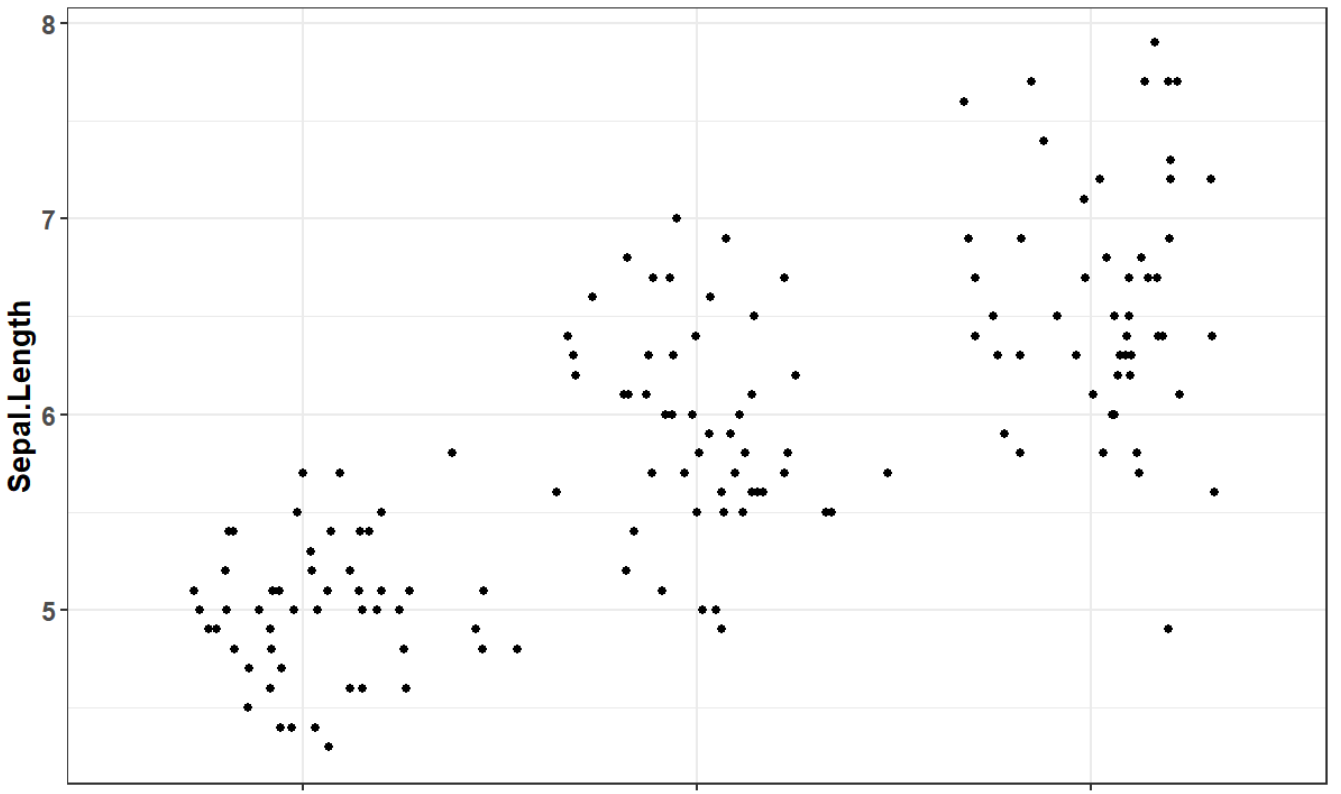
```
options(contrasts=c("contr.sum","contr.sum"))
# ou
FactoMineR::AovSum()
```

- $\hat{\mu} = \bar{y}$
- $\hat{\alpha}_i = \bar{y}_i - \mu$

- $\hat{y}_{ik} = \hat{\mu} + \hat{\alpha}_i$
- $e_{ik} = y_{ik} - \hat{y}_{ik}$
- $\hat{\sigma}^2 = \frac{\sum_{ik} \epsilon_{ik}^2}{n-I}$
- $\hat{\sigma}^2_{\hat{\alpha}_i} = \frac{I-1}{n} \hat{\sigma}^2$

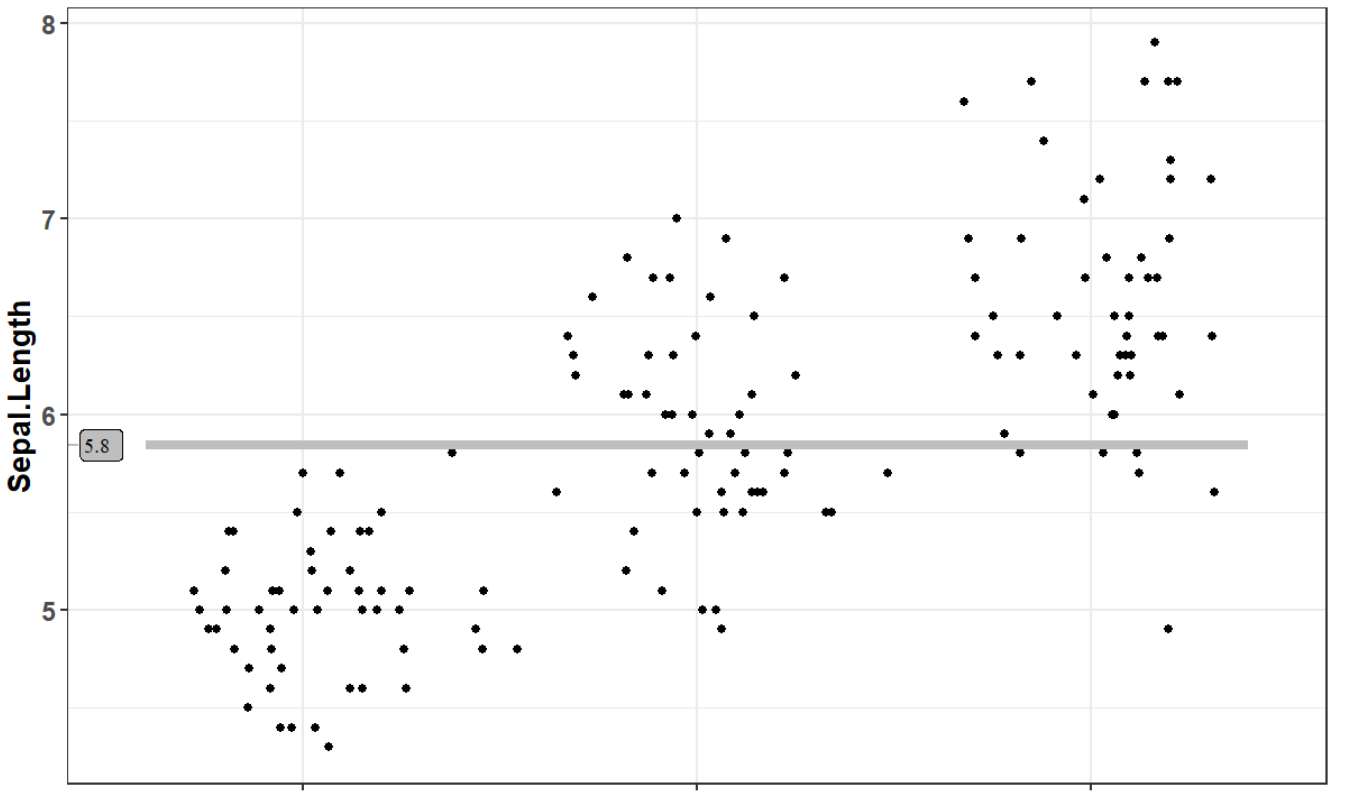
Illustration

Sepal.Length_{ik}



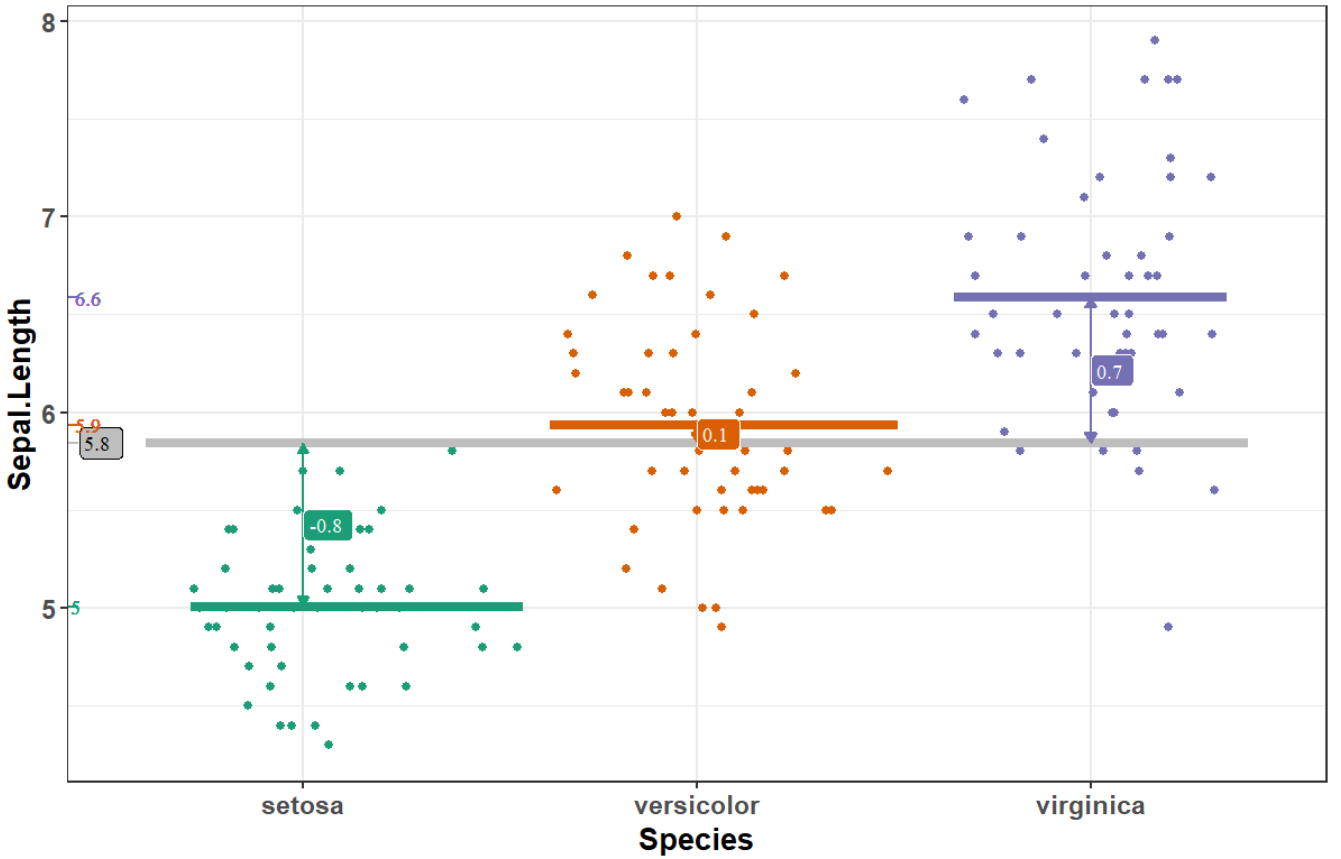
Illustration

$\text{Sepal.Length}_{ik} = \mu$



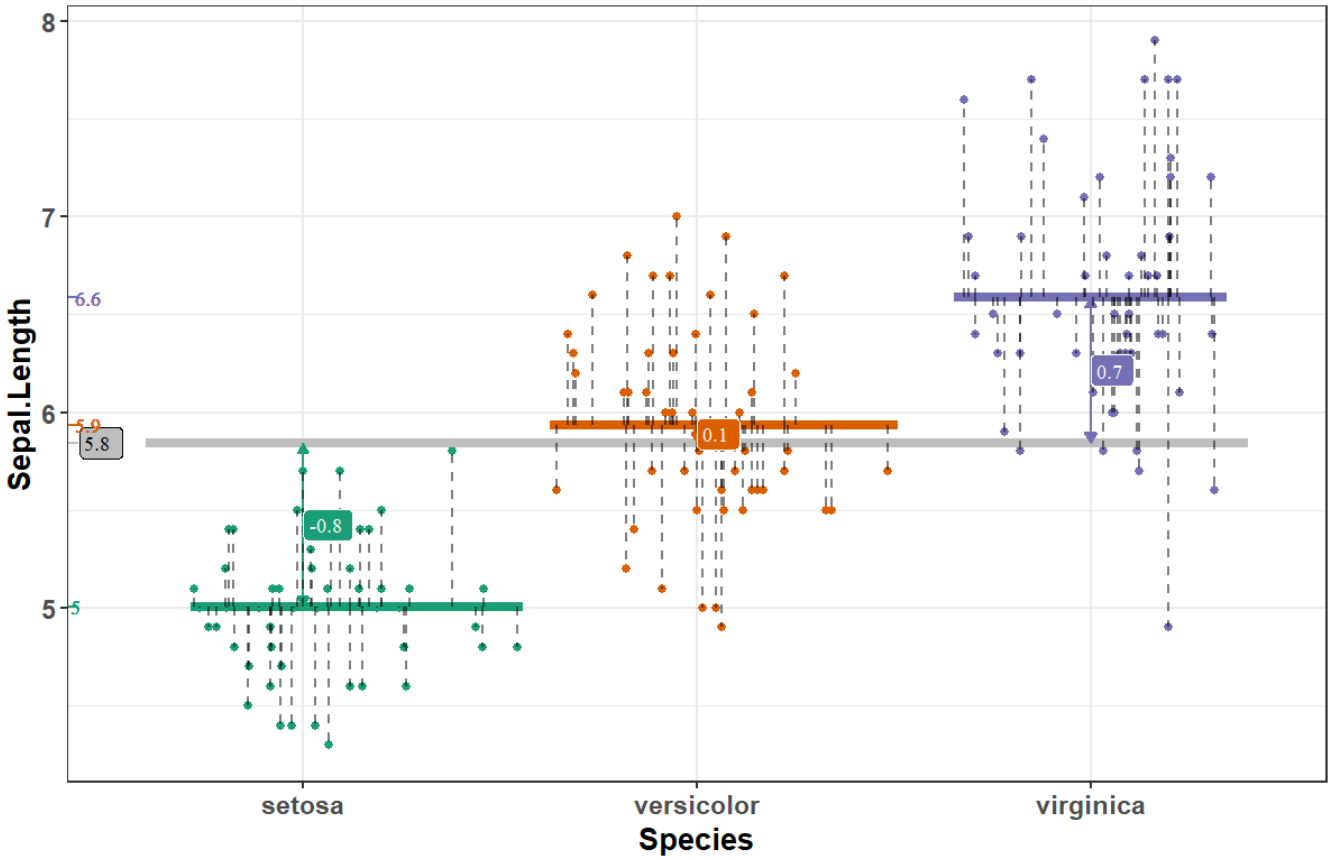
Illustration

$\text{Sepal.Length}_{ik} = \mu + \alpha_i$, i = {setosa | versicolor | virginica}



Illustration

$\text{Sepal.Length}_{ik} = \mu + \alpha_i + \varepsilon_{ik}$, i = {setosa | versicolor | virginica}



Test de l'effet d'une variable

➔ **La variabilité de y entre les modalités de la variable est elle *significativement* plus grande que la variabilté résiduelle ?**

⚠ **Dans le cas d'un plan équilibré** ⚠ **:**

$$\sum_{ij}\left(y_{ij}-\bar{y}\right)^2 = \frac{n}{I}\sum_{i}\left(\hat{\alpha}_i\right)^2 + \sum_{ij}\left(e_{ij}\right)^2$$

Variabilité totale	=	Variabilité interclasse (*between group*)	+	Variabilité interclasse (*whithin group*)
SS_T	=	SS_F	+	SS_R

Test : à quel point SS_F est plus grande que SS_R ? (Plus il y a de groupes/observations, plus les valeurs risques d'être élevées !)

➔ Il faut normaliser avec les ***degrés de libertés*** *(_df)*!

$$CM_F = \frac{SS_F}{I-1} \qquad CM_R = \frac{SS_R}{n-(I-1)-1}$$

Dans R

```
options(contrasts=c("contr.sum","contr.sum"))
mod = lm(Sepal.Length ~ Species, data = iris)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: Sepal.Length
##            Df Sum Sq Mean Sq F value    Pr(>F)
## Species     2 63.212  31.606  119.26 < 2.2e-16 ***
## Residuals 147 38.956   0.265
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Test de l'effet d'une variable

Hypothèse :

$H_0 : \alpha_i = 0, \ \forall \ i$, tous les coefficients sont égaux, donc nuls

$H_1 : \exists \ \alpha_i \neq 0$, un coefficient au moins n'est pas nul

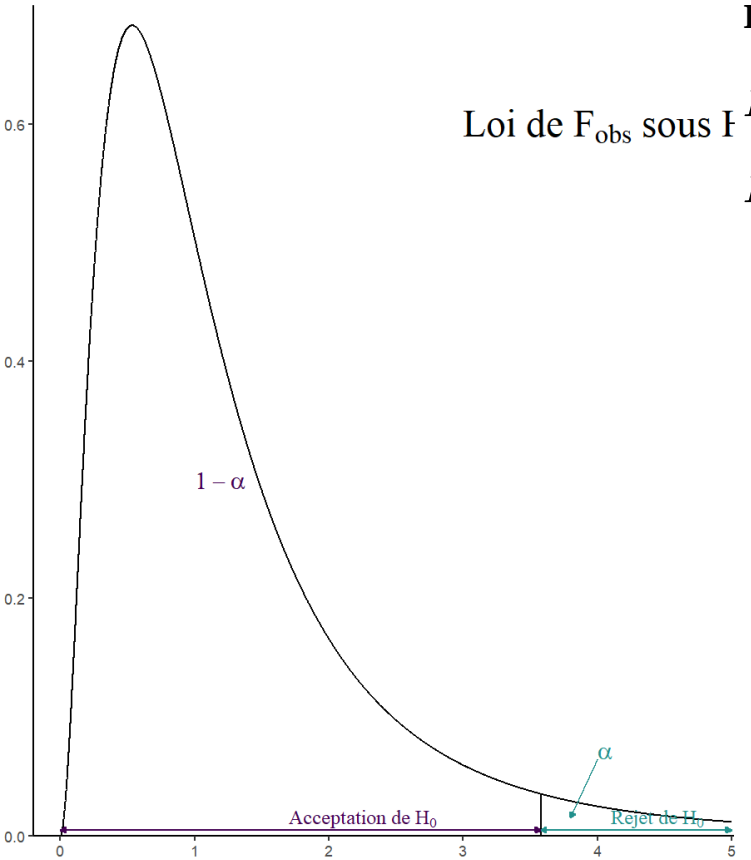
Statistique de test :

$$F_{obs} = \frac{CM_F}{CM_R}$$

Sous H_0 :

$$F_{obs} \rightarrow F_{n-I}^{I-1}$$

Test de l'effet d'une variable



Règle de décision

$F_{obs} < F_{n-I}^{I-1}(1-\alpha) \Rightarrow$ acceptation de H_0

$F_{obs} \geq F_{n-I}^{I-1}(1-\alpha) \Rightarrow$ rejet de H_0

Dans R

```
options(contrasts=c("contr.sum","contr.sum"))
mod = lm(Sepal.Length ~ Species, data = iris)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: Sepal.Length
##             Df Sum Sq Mean Sq F value    Pr(>F)
## Species      2 63.212  31.606  119.26 < 2.2e-16 ***
## Residuals  147 38.956   0.265
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
pf(119.26, 2, 147, lower.tail = FALSE)
```

Exemples avec plus de facteurs

```
library(agricolae)
data(greenhouse)
data <- greenhouse$greenhouse1
mod <- lm(weight ~ variety*method, data = data)
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: weight
##                  Df Sum Sq Mean Sq  F value Pr(>F)
## variety           2   2297    1148   0.7279 0.4835
## method            3 483322  161107 102.1204 <2e-16 ***
## variety:method    6 150619   25103  15.9120 <2e-16 ***
## Residuals       468 738326    1578
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Summary

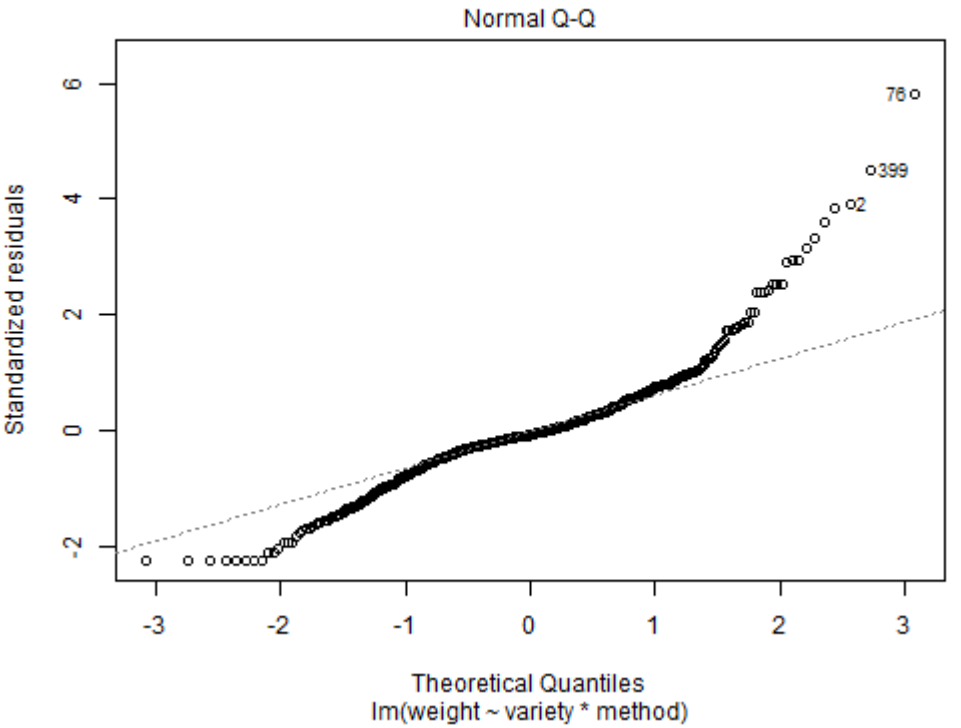
Énormément d'information donné par le `summary()` !!!

```
summary(mod)
```

```
##
## Call:
## lm(formula = weight ~ variety * method, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -88.547 -17.871  -3.492  15.626 227.944
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         72.664      1.813  40.081  < 2e-16 ***
## variety1             1.056      2.564   0.412  0.68067
## variety2             1.990      2.564   0.776  0.43799
## method1              2.022      3.140   0.644  0.51996
## method2             11.814      3.140   3.762  0.00019 ***
## method3            -50.440      3.140 -16.063  < 2e-16 ***
## variety1:method1   -35.589      4.441  -8.014 8.92e-15 ***
## variety2:method1    18.681      4.441   4.207 3.11e-05 ***
## variety1:method2     2.014      4.441   0.454  0.65035
## variety2:method2    10.335      4.441   2.327  0.02038 *
## variety1:method3     2.855      4.441   0.643  0.52054
## variety2:method3    -9.963      4.441  -2.243  0.02533 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 39.72 on 468 degrees of freedom
## Multiple R-squared:  0.4629,    Adjusted R-squared:  0.4502
## F-statistic: 36.66 on 11 and 468 DF,  p-value: < 2.2e-16
```

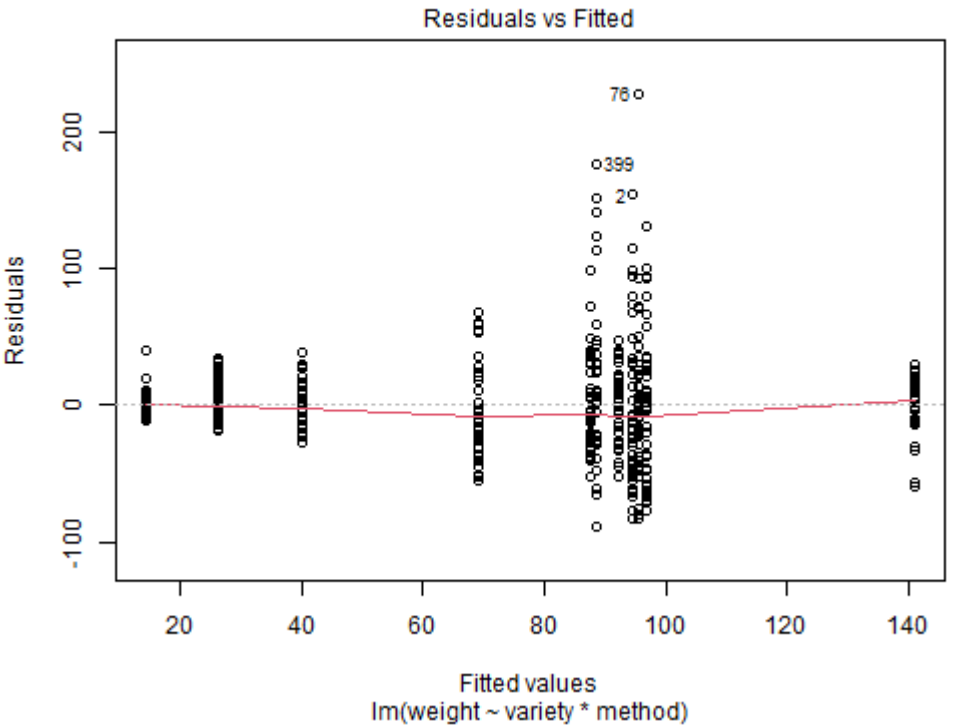
Vérification hypothèses

```
plot(mod, which = 2)
```



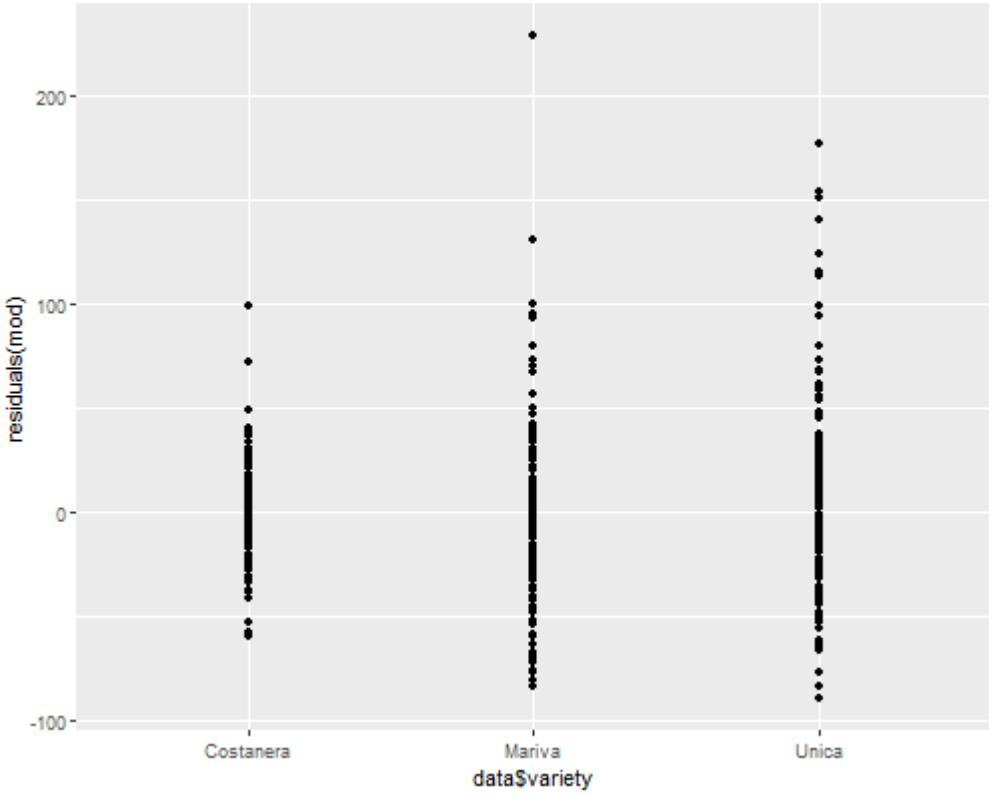
Vérification hypothèses

```
plot(mod, which = 1)
```



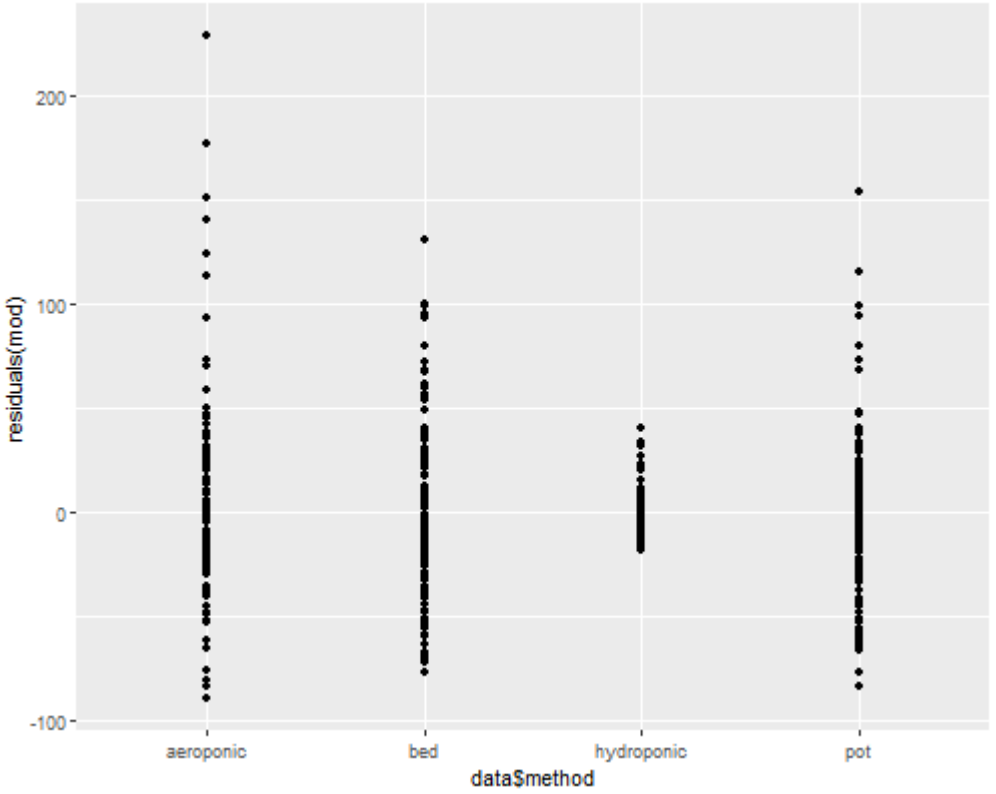
Vérification hypothèses

```
qplot(x = data$variety, y = residuals(mod), geom = "point")
```



Vérification hypothèses

```
qplot(x = data$method, y = residuals(mod), geom = "point")
```



Tests post-hoc (comparaisons multiples)

```
library(emmeans)
pairs(emmeans(mod, ~method))
```

```
## NOTE: Results may be misleading due to involvement in interactions

##  contrast               estimate   SE  df t.ratio p.value
##  aeroponic - bed           -9.79 5.13 468  -1.910 0.2253
##  aeroponic - hydroponic    52.46 5.13 468  10.231 <.0001
##  aeroponic - pot          -34.58 5.13 468  -6.744 <.0001
##  bed - hydroponic          62.25 5.13 468  12.141 <.0001
##  bed - pot                -24.79 5.13 468  -4.834 <.0001
##  hydroponic - pot         -87.04 5.13 468 -16.975 <.0001
##
## Results are averaged over the levels of: variety
## P value adjustment: tukey method for comparing a family of 4 estimates
```

Tests post-hoc (comparaisons multiples)

```
pairs(emmeans(mod, ~variety|method))
```

```
## method = aeroponic:
##  contrast           estimate   SE  df t.ratio p.value
##  Costanera - Mariva   -55.20 8.88 468 -6.216  <.0001
##  Costanera - Unica    -48.40 8.88 468 -5.449  <.0001
##  Mariva - Unica         6.81 8.88 468  0.767  0.7237
##
## method = bed:
##  contrast           estimate   SE  df t.ratio p.value
##  Costanera - Mariva    -9.26 8.88 468 -1.042  0.5507
##  Costanera - Unica     18.46 8.88 468  2.079  0.0953
##  Mariva - Unica        27.72 8.88 468  3.121  0.0054
##
## method = hydroponic:
##  contrast           estimate   SE  df t.ratio p.value
##  Costanera - Mariva    11.88 8.88 468  1.338  0.3748
##  Costanera - Unica     -0.15 8.88 468 -0.017  0.9998
##  Mariva - Unica       -12.03 8.88 468 -1.355  0.3656
##
## method = pot:
##  contrast           estimate   SE  df t.ratio p.value
##  Costanera - Mariva    48.84 8.88 468  5.499  <.0001
##  Costanera - Unica     46.49 8.88 468  5.234  <.0001
##  Mariva - Unica        -2.35 8.88 468 -0.265  0.9621
##
## P value adjustment: tukey method for comparing a family of 3 estimates
```

p-value !!!

Tableau d'Anova

	fongicide	variete	interaction
p-value	0.0500205	0.0006926	0.231347

Comparaisons fongicides

	Estimate	p-value
F1-F2	9.81	0.0500205

Comparaisons variétés

	Estimate	p-value
V1-V2	2.58	0.0284387
V1-V3	3.36	0.0173694
V2-V3	0.78	0.1120579

Quelles conclusions peut-on faire de ces résultats ?

p-value !!!

- **Les *p-value* dépendent de la qualité ET de la quantité des données !**
- **Le seuil de 0.05 est arbitraire !**
- **Les résultats des tests statistiques ne sont pas la fin de l'analyse. Il est important de prendre du recul et d'évaluer la qualité des résultats !**
- **Les résultats des tests ne consituent pas des conclusions/décisions ! Ce sont des outils qui aident les experts à conclure/décider !**

Exercice 2

Analyse du fichier *cow.csv* : mesure de rendement de production laitière par différentes vaches. Les vaches ont reçu soit la ration R1, soit la ration R2 de nourriture et sont à des âges différents (1ère, 2ème, 3ème ou 4ème lactation).

Existe t-il une influence de la ration et/ou de la lactation sur la production de lait ?

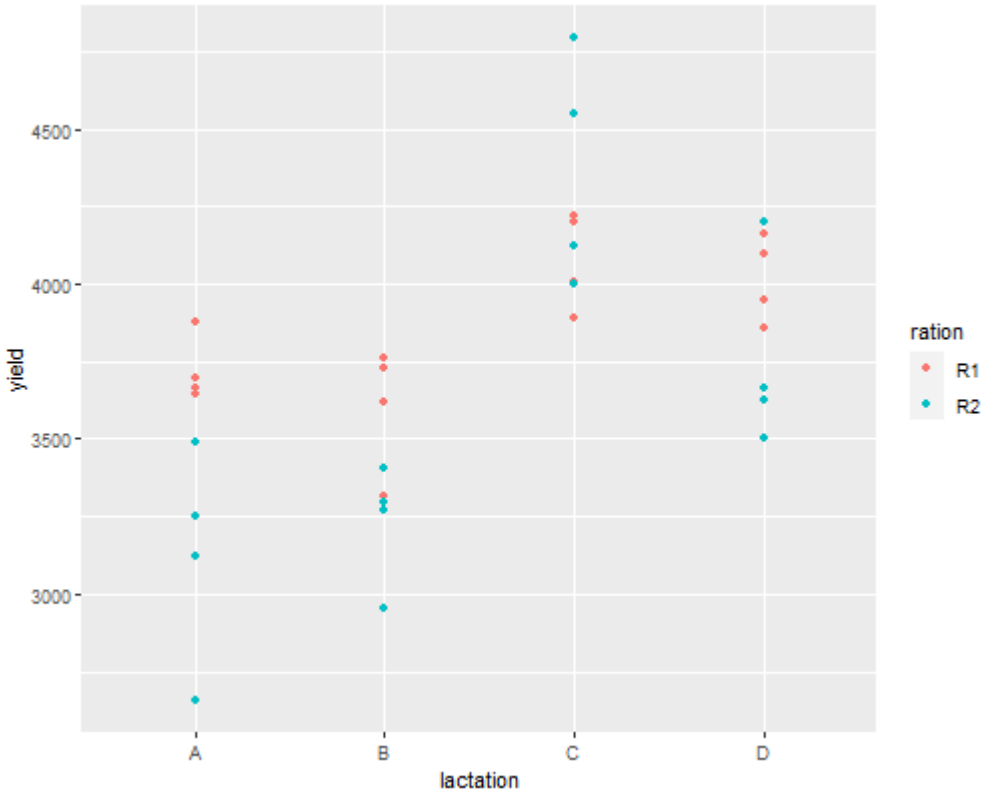
Correction exercice 2

```
library(readr)
library(ggplot2)
library(emmeans)
library(dplyr)
data <- read_delim(here::here("static/data/cows.csv"), delim = ";")
summary(data)
```

```
##     ration           lactation           yield
##  Length:32          Length:32          Min.   :2660
##  Class :character   Class :character   1st Qu.:3470
##  Mode  :character   Mode  :character   Median :3716
##                                        Mean   :3738
##                                        3rd Qu.:4030
##                                        Max.   :4792
```

Correction exercice 2

```
ggplot(data) +
  aes(x = lactation, y = yield, color = ration) +
geom_point()
```



Correction exercice 2

```
mod <- lm(yield ~ ration + lactation + ration:lactation, data = data)
anova(mod)
```

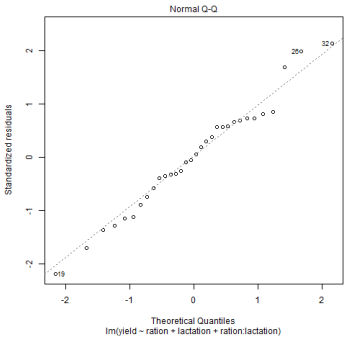
```
## Analysis of Variance Table
##
## Response: yield
##                  Df  Sum Sq Mean Sq F value    Pr(>F)
## ration            1  448404  448404  7.3174   0.01236 *
## lactation         3 3631550 1210517 19.7540 1.136e-06 ***
## ration:lactation  3  838933  279644  4.5634   0.01148 *
## Residuals        24 1470708   61280
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Correction exercice 2

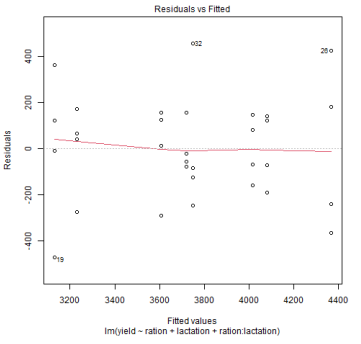
```
summary(mod)
```

```
##
## Call:
## lm(formula = yield ~ ration + lactation + ration:lactation, data = data)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -471.0 -133.0    0.5  142.8  456.0
##
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)         3737.63      43.76  85.411  < 2e-16 ***
## ration1              118.37      43.76   2.705 0.012362 *
## lactation1          -311.63      75.80  -4.111 0.000397 ***
## lactation2          -317.62      75.80  -4.191 0.000325 ***
## lactation3           484.87      75.80   6.397 1.29e-06 ***
## ration1:lactation1   176.62      75.80   2.330 0.028525 *
## ration1:lactation2    69.63      75.80   0.919 0.367450
## ration1:lactation3  -261.88      75.80  -3.455 0.002059 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 247.5 on 24 degrees of freedom
## Multiple R-squared:  0.7698,    Adjusted R-squared:  0.7027
## F-statistic: 11.47 on 7 and 24 DF,  p-value: 2.562e-06
```

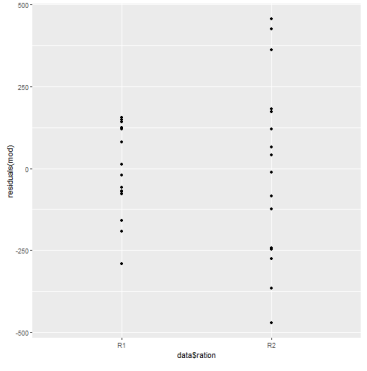
```
plot(mod, which = 2)
```



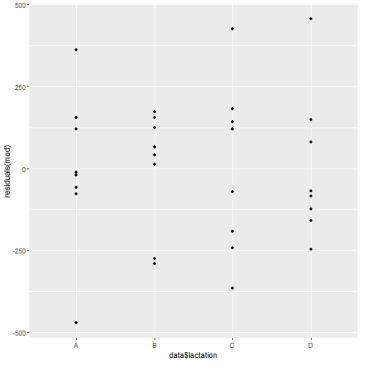

```
plot(mod, which = 1)
```




```
qplot(x = data$ration,
      y = residuals(mod),
      geom = "point")
```




```
qplot(x = data$lactation,
      y = residuals(mod),
      geom = "point")
```



Correction exercice 2

```
library(emmeans)
pairs(emmeans(mod,~ration))
```

```
## NOTE: Results may be misleading due to involvement in interactions

##  contrast estimate   SE df t.ratio p.value
##  R1 - R2       237 87.5 24 2.705   0.0124
##
## Results are averaged over the levels of: lactation
```

```
pairs(emmeans(mod,~lactation))
```

```
## NOTE: Results may be misleading due to involvement in interactions

##  contrast estimate  SE df t.ratio p.value
##  A - B           6 124 24  0.048  1.0000
##  A - C        -796 124 24 -6.435  <.0001
##  A - D        -456 124 24 -3.684  0.0060
##  B - C        -802 124 24 -6.484  <.0001
##  B - D        -462 124 24 -3.733  0.0053
##  C - D         340 124 24  2.751  0.0508
##
## Results are averaged over the levels of: ration
## P value adjustment: tukey method for comparing a family of 4 estimates
```

Correction exercice 2

```
pairs(emmeans(mod,~ration|lactation))
```

```
## lactation = A:
##  contrast estimate  SE df t.ratio p.value
##  R1 - R2       590 175 24  3.371  0.0025
##
## lactation = B:
##  contrast estimate  SE df t.ratio p.value
##  R1 - R2       376 175 24  2.148  0.0420
##
## lactation = C:
##  contrast estimate  SE df t.ratio p.value
##  R1 - R2      -287 175 24 -1.640  0.1141
##
## lactation = D:
##  contrast estimate  SE df t.ratio p.value
##  R1 - R2       268 175 24  1.531  0.1388
```

Correction exercice 2

```
pairs(emmeans(mod,~lactation|ration))
```

```
## ration = R1:
##  contrast estimate  SE df t.ratio p.value
##  A - B         113 175 24  0.646  0.9161
##  A - C        -358 175 24 -2.045  0.1999
##  A - D        -295 175 24 -1.685  0.3530
##  B - C        -471 175 24 -2.691  0.0577
##  B - D        -408 175 24 -2.331  0.1190
##  C - D          63 175 24  0.360  0.9836
##
## ration = R2:
##  contrast estimate  SE df t.ratio p.value
##  A - B        -101 175 24 -0.577  0.9380
##  A - C       -1235 175 24 -7.055  <.0001
##  A - D        -617 175 24 -3.525  0.0088
##  B - C       -1134 175 24 -6.478  <.0001
##  B - D        -516 175 24 -2.948  0.0331
##  C - D         618 175 24  3.531  0.0087
##
## P value adjustment: tukey method for comparing a family of 4 estimates
```