#### **Projet sensométrie**

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#### 1 Déclaration de répertoire de travail et Importation du ficher tableau

```
setwd("D:/Projet4/Partie R")
getwd()
library(readxl)
tableau=read xlsx("reponses JPO-rempli-centre revisé.xlsx", sheet=5)
inid=read xlsx("reponses JPO-rempli-centre revisé.xlsx", sheet=4)
attach(tableau)
attach(inid)
# Petite parenthése
decoupe_age = cut(tableau$age,breaks=c(0,30,56),labels = c("moins âgé","plus âgés"))
tableau_modif = cbind(tableau,decoupe_age)
table(decoupe age)
# Recodage de la variable CSP
tableau$CSP[tableau$CSP == "agriculteur"] <- "non etudiant"
tableau$CSP[tableau$CSP == "autre"] <- "non etudiant"</pre>
tableau$CSP[tableau$CSP == "cadre"] <- "non etudiant"</pre>
tableau$CSP[tableau$CSP == "employe"] <- "non etudiant"
table(tableau$CSP)
#write.table(tableau modif,file = "D:/Projet4/Partie R/ficher.csv")
```

#### 2 Test de normalité sur toutes les variables

```
# Creation de fonction de test de normalité
## Hypothéses
# H0: il y'a normalité
## Régle de normalité
## Régle de décision

# Rejet de H0 <-> p.value < 5% ou 1%
#Acceptation de H0 <-> p.value > 5% ou 1%
montest_norm<-function(A){

test_1 = shapiro.test(A)$p.value
test_2 = ks.test(A,"pnorm")$p.value</pre>
```

```
resum = cbind(test_1,test_2,test_1,test_2)
return(resum)
}
```

#### Excécution de la fonction

```
## La variable âge
var_age = montest_norm(tableau$age)
rownames(var_age)[nrow(var_age)]="âge"
## La variable Vintensite
Vint = montest norm(Vintensite)
rownames(Vint)[nrow(Vint)]="Vintensite"
## La variable Vcompact
Vcomp = montest_norm(Vcompact)
rownames(Vcomp)[nrow(Vcomp)]="Vcompact"
## La variable Vtexture
Vtext = montest norm(Vtexture)
rownames(Vtext)[nrow(Vtext)]="Vtexture"
## La variable Vtons
Vtons = montest_norm(tableau$Vtons)
rownames(Vtons)[nrow(Vtons)]="Vtons"
## La variable Vbrillance
Vbril = montest_norm(Vbrillance)
rownames(Vbril)[nrow(Vbril)]="Vbrillance"
## La variable Vattirance
Vatt = montest_norm(Vattirance)
rownames(Vatt)[nrow(Vatt)]="Vattirance"
## La variable Ofruit
Ofruit = montest_norm(tableau$Ofruit)
rownames(Ofruit)[nrow(Ofruit)]="Ofruit"
## La variable Oamer
```

```
Oamer = montest_norm(tableau$0amer)
rownames(Oamer)[nrow(Oamer)]="Oamer"
## La variable Oepice
Oepice = montest_norm(tableau$Oepice)
rownames(Oepice)[nrow(Oepice)]="Oepice"
## La variable Ovegetale
Oveg = montest norm(Ovegetale)
rownames(Oveg)[nrow(Oveg)]="Ovegetale"
## La variable Gdurete
Gdurete = montest norm(tableau$Gdurete)
rownames(Gdurete)[nrow(Gdurete)]="Gdurete"
## La variable Gintense
Gintense = montest_norm(tableau$Gintense)
rownames(Gintense)[nrow(Gintense)]="Gintense"
## La variable Gvegetal
Gveg = montest norm(Gvegetal)
rownames(Gveg)[nrow(Gveg)]="Gvegetal"
## La variable Giode
Giode = montest_norm(tableau$Giode)
rownames(Giode)[nrow(Giode)]="Giode"
## La variable Gsale
Gsale = montest_norm(tableau$Gsale)
rownames(Gsale)[nrow(Gsale)]="Gsale"
## La variable Gfruite
Gfruite = montest_norm(tableau$Gfruite)
rownames(Gfruite)[nrow(Gfruite)]="Gfruite"
## La variable Gepice
Gepice = montest_norm(tableau$Gepice)
```

```
rownames(Gepice)[nrow(Gepice)]="Gepice"
## La variable Gsucre
Gsucre = montest_norm(tableau$Gsucre)
rownames(Gsucre)[nrow(Gsucre)]="Gsucre"
## La variable Gacide
Gacide = montest_norm(tableau$Gacide)
rownames(Gacide)[nrow(Gacide)]="Gacide"
## La variable Gamer
Gamer = montest_norm(tableau$Gamer)
rownames(Gamer)[nrow(Gamer)]="Gamer"
## La variable Fagreable
Fagre = montest_norm(Fagreable)
rownames(Fagre)[nrow(Fagre)]="Fagreable"
## La variable Fagreable
Fintens = montest_norm(Fintensite)
rownames(Fintens)[nrow(Fintens)]="Fintensite"
## La variable Fpersistance
Fpersist = montest_norm(Fpersistance)
rownames(Fpersist)[nrow(Fpersist)]="Fpersistance"
## La variable Fnote
Fnote = montest_norm(tableau$Fnote)
rownames(Fnote)[nrow(Fnote)]="Fnote"
## La variable Fharmonie
Fharmo = montest_norm(Fharmonie)
rownames(Fharmo)[nrow(Fharmo)]="Fharmonie"
## La variable Farome
Farome = montest_norm(tableau$Farome)
rownames(Farome)[nrow(Farome)]="Farome"
## Création d'un récapitulatif des tests
```

```
tableau_recap = rbind(var_age, Vint, Vcomp, Vtext, Vtons, Vbril, Vatt, Ofruit, Oamer, O
epice, Oveg, Gdurete, Gintense, Gveg, Giode, Gsale, Gfruite, Gepice, Gsucre, Gacide, Ga
mer, Fagre, Fintens, Fpersist, Fnote, Fharmo, Farome)
colnames(tableau_recap)=c("test1_seuil1","test2_seuil1","test1_seuil2","test2_seuil2")
library(knitr)
kable(tableau_recap)
```

	test1_seuil1	test2_seuil1	test1_seuil2	test2_seuil2
âge	0.0000000	0.0000000	0.0000000	0.0000000
Vintensite	0.5529998	0.8056936	0.5529998	0.8056936
Vcompact	0.0167806	0.0182919	0.0167806	0.0182919
Vtexture	0.0213313	0.1573011	0.0213313	0.1573011
Vtons	0.1792710	0.1573011	0.1792710	0.1573011
Vbrillance	0.5982709	0.3635340	0.5982709	0.3635340
Vattirance	0.0465867	0.0366311	0.0465867	0.0366311
Ofruit	0.2129608	0.3364049	0.2129608	0.3364049
Oamer	0.0691517	0.3364049	0.0691517	0.3364049
Oepice	0.0915322	0.6199772	0.0915322	0.6199772
Ovegetale	0.1239082	0.1813051	0.1239082	0.1813051
Gdurete	0.0048602	0.0296859	0.0048602	0.0296859
Gintense	0.0048180	0.1666005	0.0048180	0.1666005
Gvegetal	0.0166196	0.1048569	0.0166196	0.1048569
Giode	0.0193038	0.0895842	0.0193038	0.0895842
Gsale	0.0004162	0.0023009	0.0004162	0.0023009
Gfruite	0.0135613	0.0159959	0.0135613	0.0159959
Gepice	0.0043877	0.0243141	0.0043877	0.0243141
Gsucre	0.0000021	0.0000096	0.0000021	0.0000096
Gacide	0.0808084	0.1519599	0.0808084	0.1519599
Gamer	0.2154469	0.2105516	0.2154469	0.2105516
Fagreable	0.0280508	0.1974827	0.0280508	0.1974827
Fintensite	0.0288554	0.0326751	0.0288554	0.0326751
Fpersistance	0.1081512	0.0569433	0.1081512	0.0569433
Fnote	0.0135102	0.0366311	0.0135102	0.0366311
Fharmonie	0.2798659	0.6993742	0.2798659	0.6993742
Farome	0.0624806	0.3364049	0.0624806	0.3364049
	/	C 1 115	15	

#write.table(tableau\_recap,file = "D:/Projet4/Partie\_R/Tab\_normalité.txt")

#### 2.1 Partie graphique de la normalité

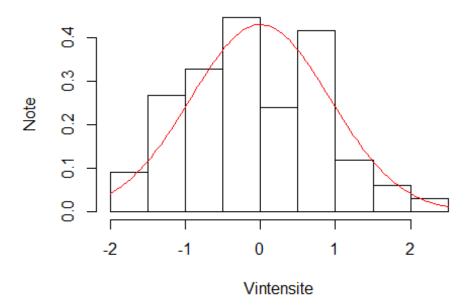
require(qqplotr)

# Histogramme

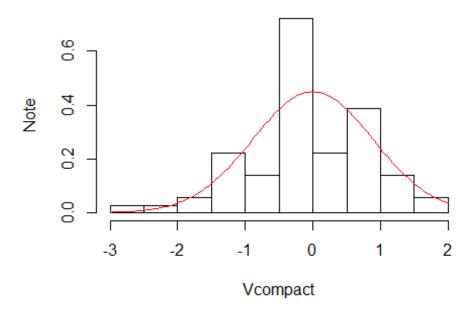
```
for(i in 12:37){
    #X11()
    hist(tableau[[i]], freq = FALSE,main =paste("Histogramme de la variable",colnames(tableau[,i])),xlab=colnames(tableau[,i]),ylab="Note")

    curve(dnorm(x, mean=mean(tableau[[i]],na.rm = TRUE), sd=sd(tableau[[i]],na.rm = TRUE)
), add=TRUE,col="red")
}
```

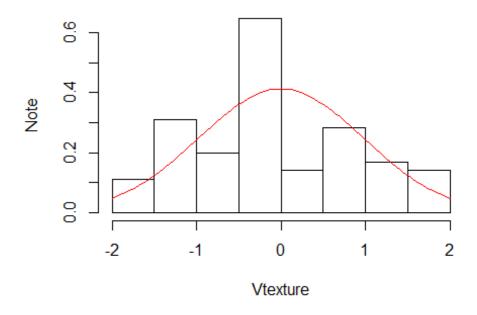
#### Histogramme de la variable Vintensite



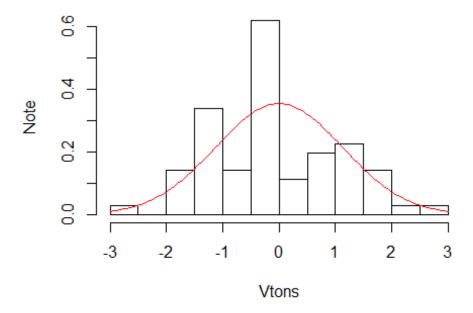
#### Histogramme de la variable Vcompact



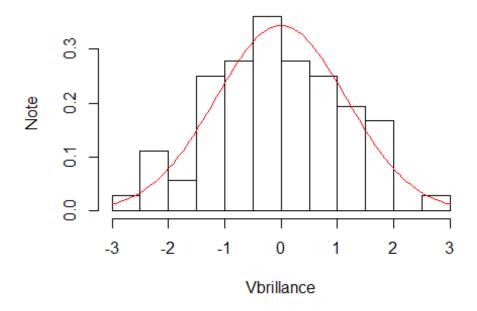
# Histogramme de la variable Vtexture



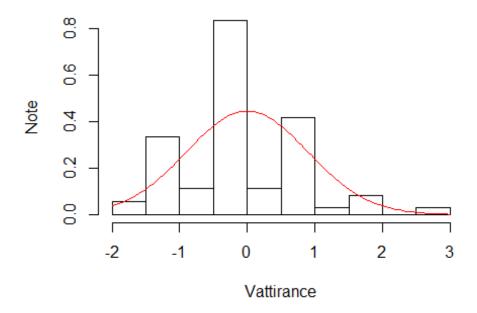
# Histogramme de la variable Vtons



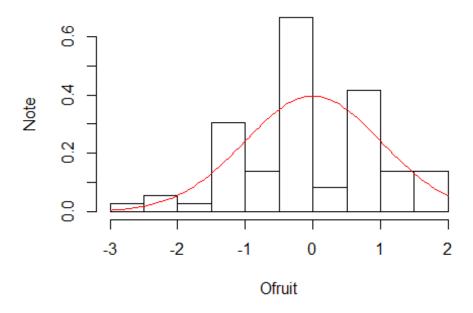
# Histogramme de la variable Vbrillance



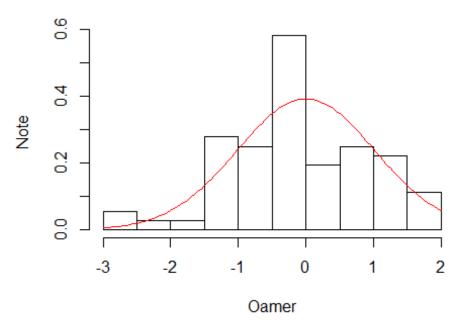
# Histogramme de la variable Vattirance



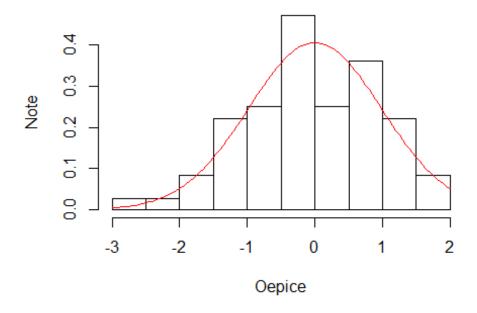
# Histogramme de la variable Ofruit



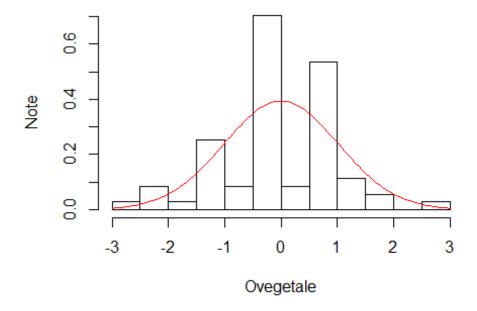
# Histogramme de la variable Oamer



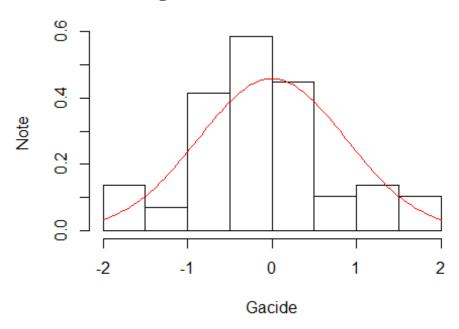
# Histogramme de la variable Oepice



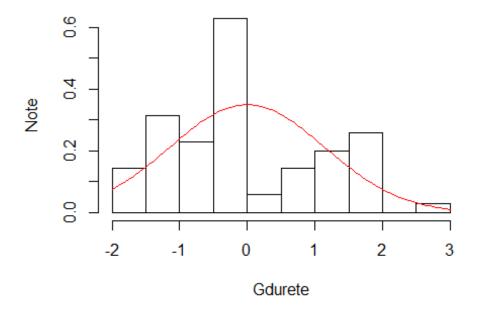
# Histogramme de la variable Ovegetale



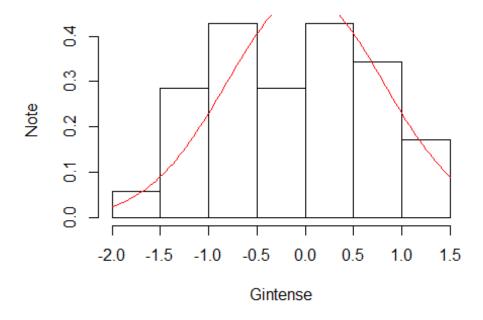
# Histogramme de la variable Gacide



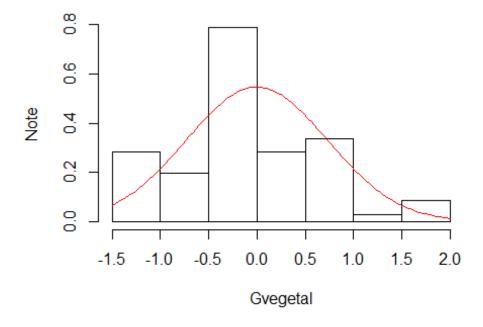
# Histogramme de la variable Gdurete



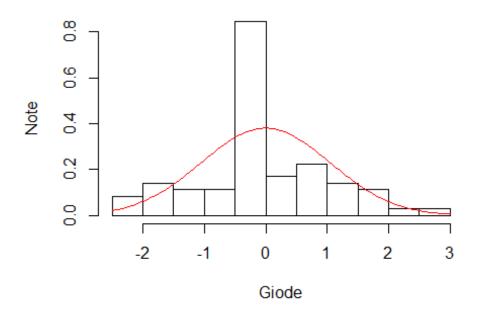
# Histogramme de la variable Gintense



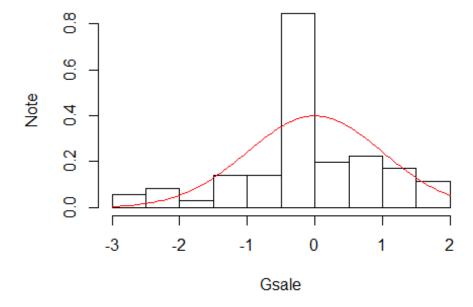
#### Histogramme de la variable Gvegetal



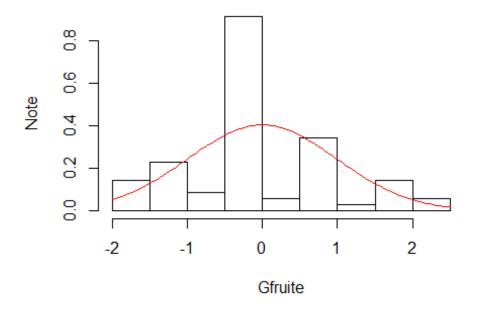
# Histogramme de la variable Giode



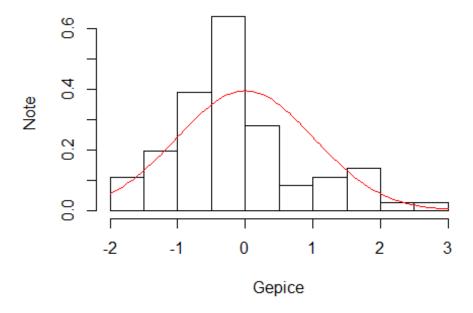
# Histogramme de la variable Gsale



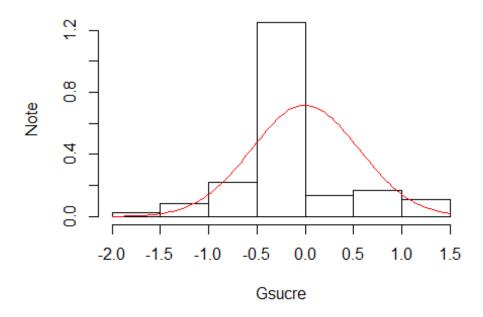
# Histogramme de la variable Gfruite



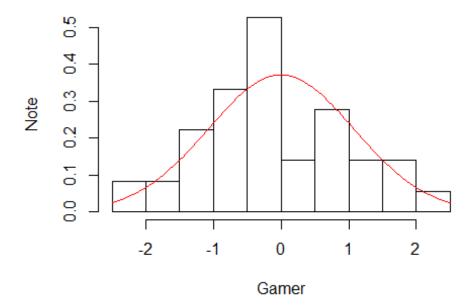
# Histogramme de la variable Gepice



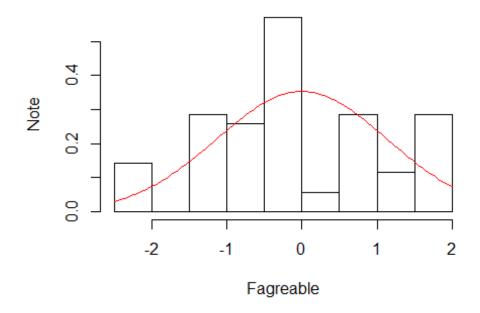
# Histogramme de la variable Gsucre



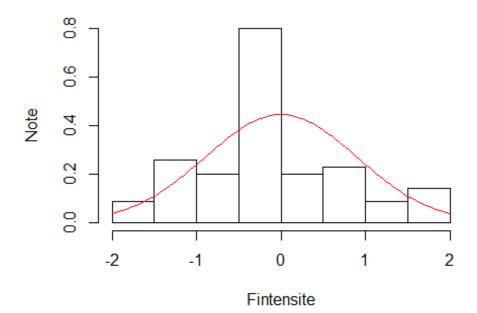
# Histogramme de la variable Gamer



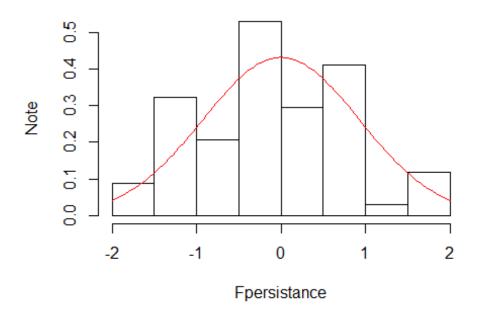
# Histogramme de la variable Fagreable



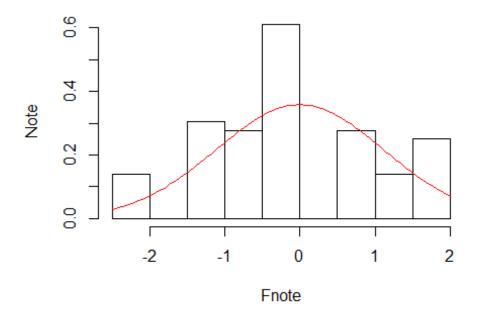
# Histogramme de la variable Fintensite



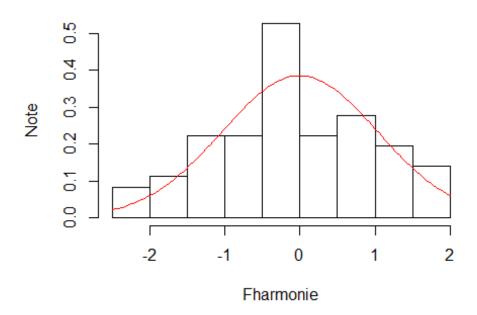
# Histogramme de la variable Fpersistance



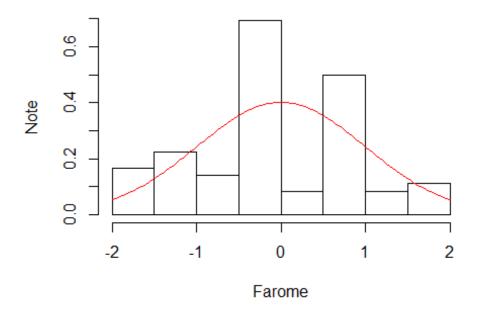
# Histogramme de la variable Fnote



#### Histogramme de la variable Fharmonie



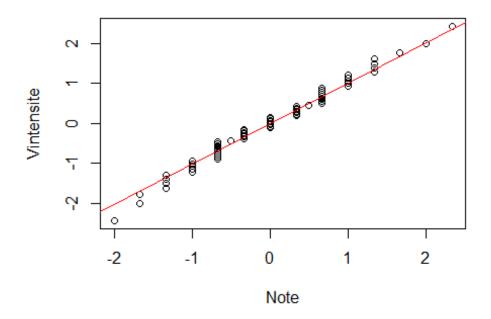
#### Histogramme de la variable Farome



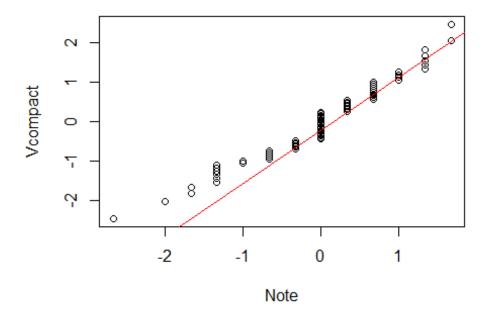
```
# QQplot

for(i in 12:37){
    qqnorm(tableau[[i]], datax=TRUE, main =paste("qqplot de la variable", colnames(tableau
[,i])),xlab=colnames(tableau[,i]),ylab="Note")
    qqline(tableau[[i]],datax=TRUE,col="red")
}
```

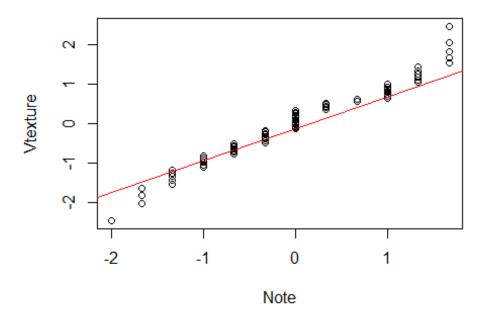
# qqplot de la variable Vintensite



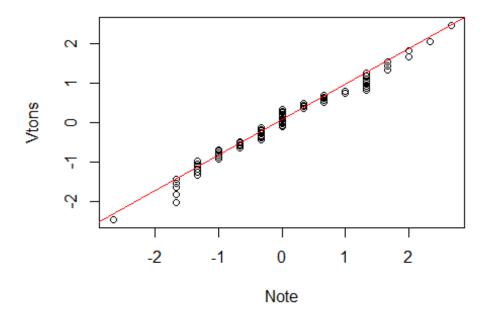
# qqplot de la variable Vcompact



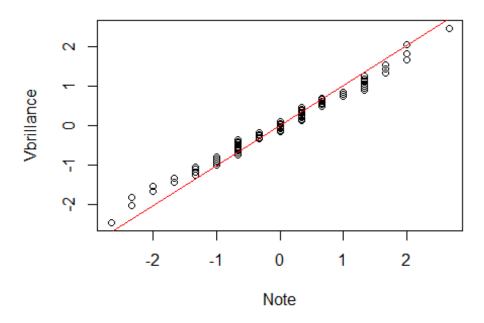
# qqplot de la variable Vtexture



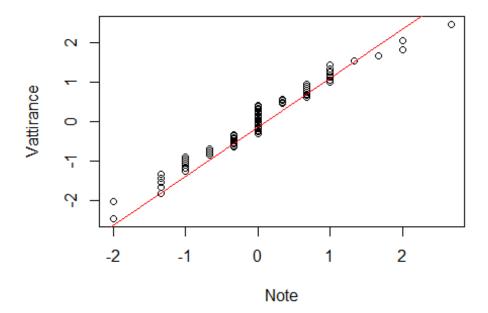
# qqplot de la variable Vtons



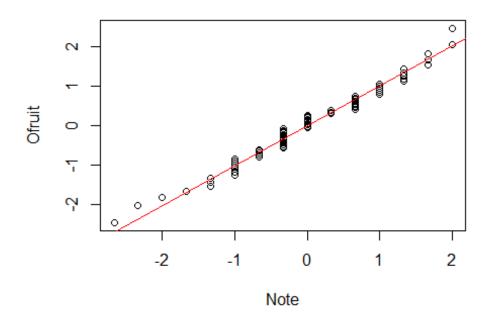
# qqplot de la variable Vbrillance



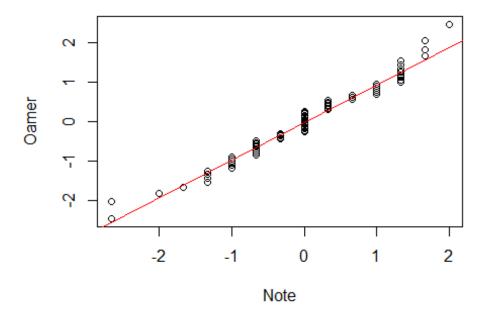
# qqplot de la variable Vattirance



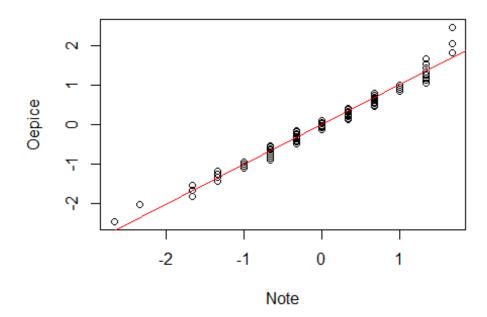
# qqplot de la variable Ofruit



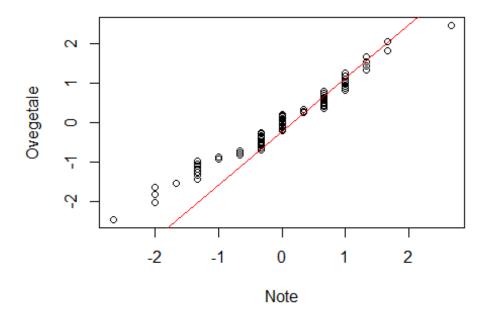
# qqplot de la variable Oamer



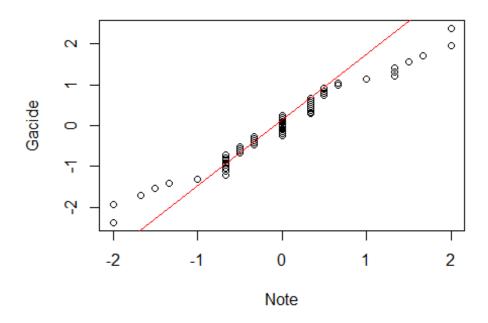
# qqplot de la variable Oepice



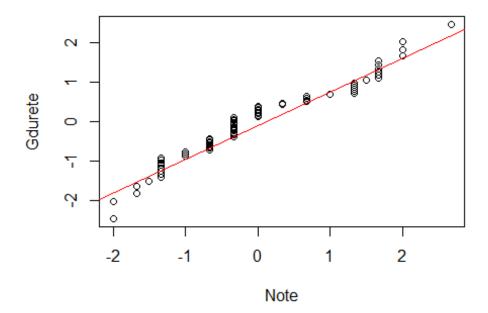
# qqplot de la variable Ovegetale



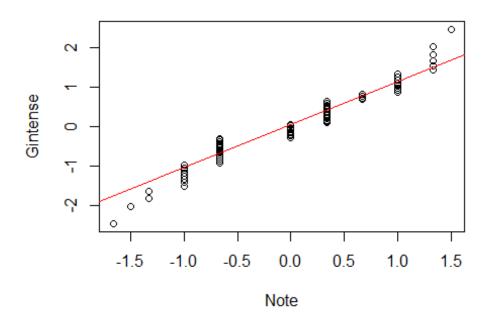
# qqplot de la variable Gacide



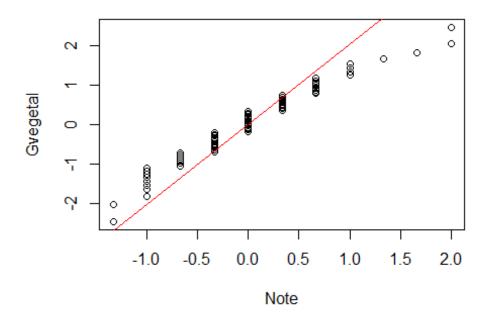
# qqplot de la variable Gdurete



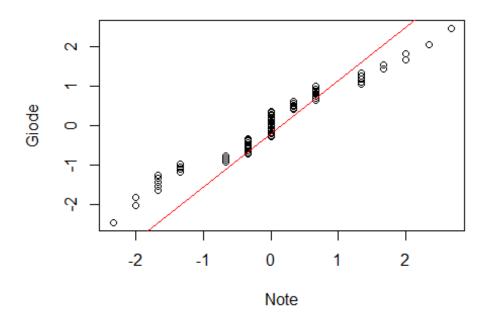
#### qqplot de la variable Gintense



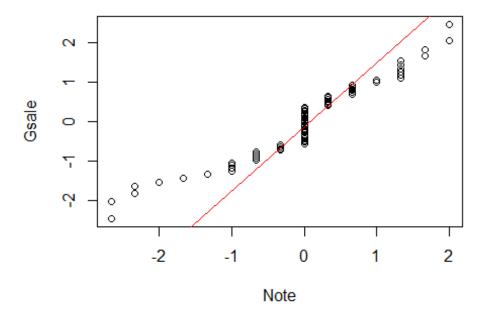
# qqplot de la variable Gvegetal



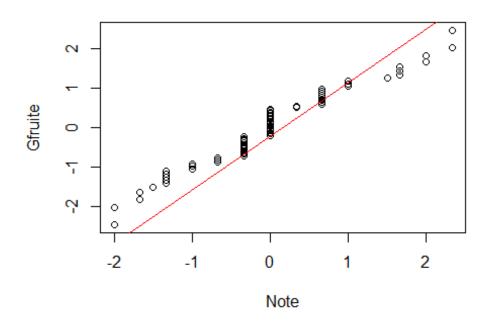
# qqplot de la variable Giode



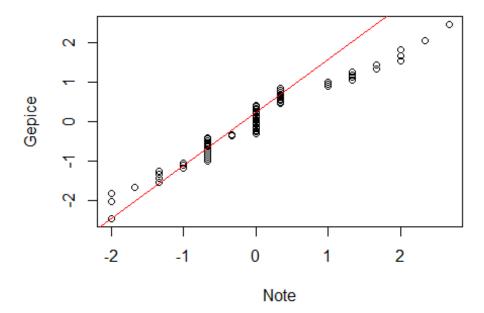
# qqplot de la variable Gsale



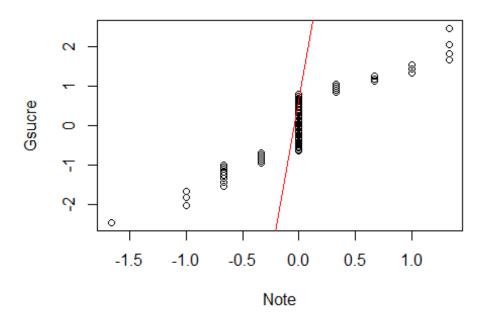
# qqplot de la variable Gfruite



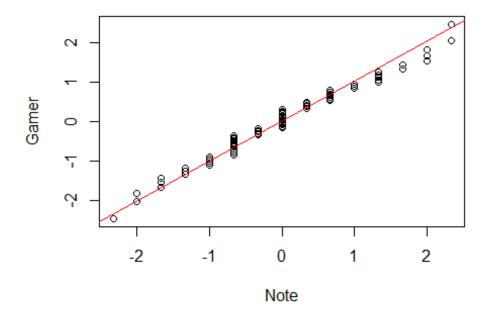
# qqplot de la variable Gepice



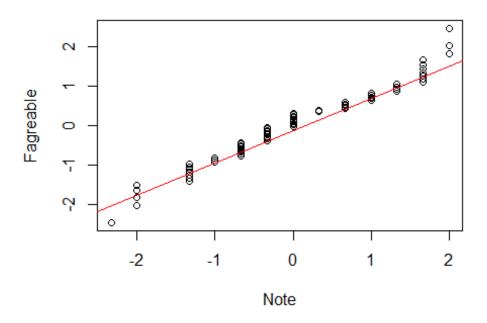
# qqplot de la variable Gsucre



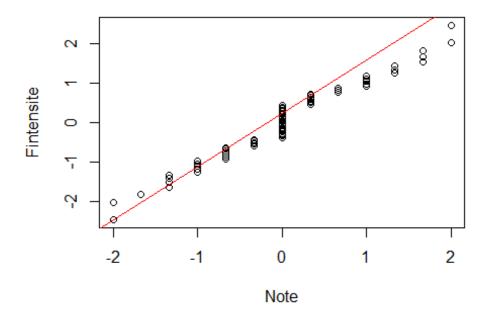
# qqplot de la variable Gamer



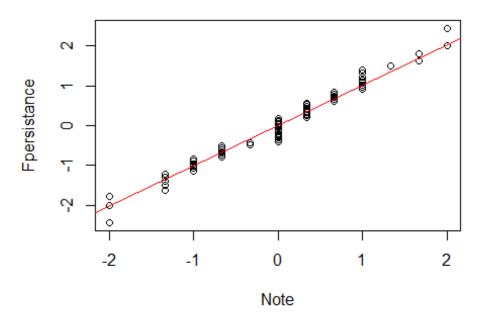
# qqplot de la variable Fagreable



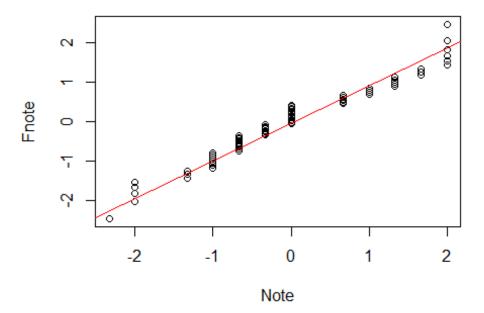
# qqplot de la variable Fintensite



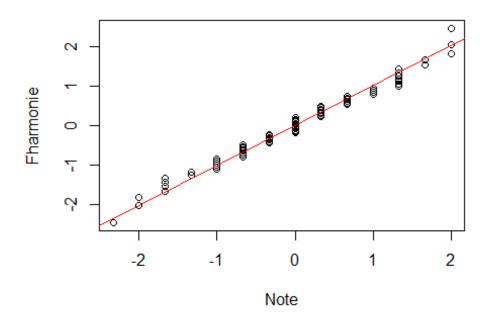
# qqplot de la variable Fpersistance



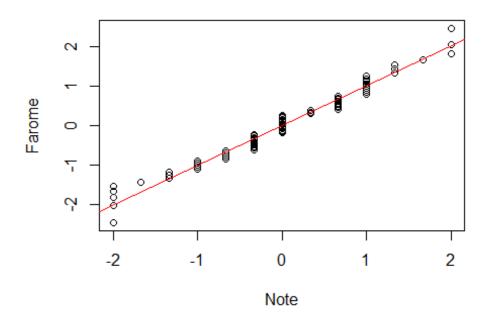
# qqplot de la variable Fnote



#### qqplot de la variable Fharmonie



#### qqplot de la variable Farome



#### 3 Test egalité des variances

```
# Creation de fonction de test de variance

## Hypothéses

# H0: il y'a égalité de variance

# H1: pas d'égalité de variance

## Régle de décision
```

```
# Rejet de H0 <-> p.value < 5% ou 1%
#Acceptation de H0 <-> p.value > 5% ou 1%
montest_var = function(A,B){
test var = var.test(A,B)$p.value
return(test_var)
}
      Caractéristique visuel
3.1
 # Intencité de la couleur
T1 vs T2 = montest var(T1.VintensiteC,T2.VintensiteC)
T1_vs_T3 = montest_var(T1.VintensiteC, T3.VintensiteC)
T2 vs T3 = montest var(T2.VintensiteC,T3.VintensiteC)
var int = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_int)[nrow(var_int)]="VintensiteC"
# copacité de la couleur
T1 vs T2 = montest var(T1.VcompactC, T2.VcompactC)
T1_vs_T3 = montest_var(T1.VcompactC,T3.VcompactC)
T2_vs_T3 = montest_var(T2.VcompactC,T3.VcompactC)
var_comp = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_comp)[nrow(var_comp)]="VcompactC"
# Granulosité texture
T1_vs_T2 = montest_var(T1.VtextureC,T2.VtextureC)
T1 vs T3 = montest var(T1.VtextureC, T3.VtextureC)
T2 vs T3 = montest var(T2.VtextureC,T3.VtextureC)
var_text = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_text)[nrow(var_text)]="VtextureC"
# Variété de tons
T1_vs_T2 = montest_var(T1.VtonsC,T2.VtonsC)
T1 vs T3 = montest var(T1.VtonsC,T3.VtonsC)
T2_vs_T3 = montest_var(T2.VtonsC,T3.VtonsC)
var_tons = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_tons)[nrow(var_tons)]="VtonsC"
# Brillance
T1 vs T2 = montest var(T1.VbrillanceC, T2.VbrillanceC)
T1 vs T3 = montest var(T1.VbrillanceC, T3.VbrillanceC)
T2_vs_T3 = montest_var(T2.VbrillanceC,T3.VbrillanceC)
var brill = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_brill)[nrow(var_brill)]="VbrillanceC"
```

```
# Attirance
T1_vs_T2 = montest_var(T1.VattiranceC, T2.VattiranceC)
T1 vs T3 = montest var(T1.VattiranceC,T3.VattiranceC)
T2_vs_T3 = montest_var(T2.VattiranceC,T3.VattiranceC)
var_att = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var att)[nrow(var att)]="VattiranceC"
# Tableau récapitulatif
tab visuel = rbind(var int,var comp,var text,var tons,var brill,var att)
colnames(tab_visuel)=c("T1 vs T2","T1 vs T3","T2 vs T3")
kable(tab visuel)
              T1 vs T2
                         T1 vs T3
                                    T2 vs T3
 VintensiteC 0.7591940 0.0631713 0.1225945
 VcompactC 0.8151354 0.3949479 0.2791895
 VtextureC
            0.9290364 0.8546618 0.7830335
 VtonsC
            0.3560290 0.6465475 0.6484002
 VbrillanceC 0.5444487 0.6330958 0.2801116
 VattiranceC 0.6860958 0.5022689 0.7890384
#write.table(tab_visuel,file = "D:/Projet4/Partie_R/VIsuel_égalité_Var.txt")
3.2
      Caractéristiques olfactives
# Odeur fruité
T1 vs T2 = montest var(T1.0fruitC,T2.0fruitC)
T1_vs_T3 = montest_var(T1.0fruitC,T3.0fruitC)
T2_vs_T3 = montest_var(T2.0fruitC,T3.0fruitC)
var_fruit = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var fruit)[nrow(var fruit)]="OfruitC"
# Odeur amer
T1 vs T2 = montest var(T1.OamerC, T2.OamerC)
T1_vs_T3 = montest_var(T1.OamerC,T3.OamerC)
T2 vs T3 = montest var(T2.OamerC, T3.OamerC)
var_amer = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_amer)[nrow(var_amer)]="0amerC"
# Odeur épicée
T1 vs T2 = montest var(T1.OepiceC, T2.OepiceC)
T1_vs_T3 = montest_var(T1.0epiceC,T3.0epiceC)
T2_vs_T3 = montest_var(T2.0epiceC,T3.0epiceC)
var epice = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var epice)[nrow(var epice)]="OepiceC"
# Odeur végétale
T1 vs T2 = montest var(T1.0vegetaleC,T2.0vegetaleC)
T1 vs T3 = montest var(T1.0vegetaleC,T3.0vegetaleC)
T2 vs T3 = montest var(T2.0vegetaleC,T3.0vegetaleC)
```

```
var veg = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_veg)[nrow(var_veg)]="OvegetaleC"
# Tableau récapitulatif
tab_olfactif = rbind(var_fruit,var_amer,var_epice,var veg)
colnames(tab_olfactif)=c("T1 vs T2","T1 vs T3","T2 vs T3")
kable(tab olfactif)
              T1 vs T2
                         T1 vs T3
                                     T2 vs T3
            0.8645847 \quad 0.7578460 \quad 0.6322406
 OfruitC
 OamerC
            0.7920666 0.7615939 0.5710406
 OepiceC
            0.8883277  0.3078481  0.2467145
 OvegetaleC 0.3277795 0.2233570 0.8070778
#write.table(tab_olfactif,file = "D:/Projet4/Partie_R/Olfactif_égalité_Var.txt")
3.3
      Caractéristique gustative
# Dureté texture
T1_vs_T2 = montest_var(T1.GdureteC, T2.GdureteC)
T1_vs_T3 = montest_var(T1.GdureteC, T3.GdureteC)
T2 vs T3 = montest var(T2.GdureteC, T3.GdureteC)
var_dur = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_dur)[nrow(var_dur)]="GdureteC"
# Intensité du gout
T1 vs T2 = montest var(T1.GintenseC, T2.GintenseC)
T1_vs_T3 = montest_var(T1.GintenseC,T3.GintenseC)
T2_vs_T3 = montest_var(T2.GintenseC,T3.GintenseC)
var int = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_int)[nrow(var_int)]="GintenseC"
#Gout Végétal
T1_vs_T2 = montest_var(T1.GvegetalC,T2.GvegetalC)
T1 vs T3 = montest var(T1.GvegetalC, T3.GvegetalC)
T2_vs_T3 = montest_var(T2.GvegetalC,T3.GvegetalC)
var_veg = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_veg)[nrow(var_veg)]="GvegetalC"
# Gout iodé
T1_vs_T2 = montest_var(T1.GiodeC, T2.GiodeC)
T1_vs_T3 = montest_var(T1.GiodeC, T3.GiodeC)
T2_vs_T3 = montest_var(T2.GiodeC,T3.GiodeC)
var iod = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_iod)[nrow(var_iod)]="GiodeC"
# Gout salé
T1_vs_T2 = montest_var(T1.GsaleC,T2.GsaleC)
T1_vs_T3 = montest_var(T1.GsaleC,T3.GsaleC)
T2_vs_T3 = montest_var(T2.GsaleC,T3.GsaleC)
```

```
var_sale = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_sale)[nrow(var_sale)]="GsaleC"
# Gout fruité
T1 vs T2 = montest var(T1.GfruiteC,T2.GfruiteC)
T1_vs_T3 = montest_var(T1.GfruiteC, T3.GfruiteC)
T2 vs T3 = montest var(T2.GfruiteC,T3.GfruiteC)
var fruit = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_fruit)[nrow(var_fruit)]="GfruiteC"
# Gout épicé
T1 vs T2 = montest var(T1.GepiceC, T2.GepiceC)
T1 vs T3 = montest var(T1.GepiceC, T3.GepiceC)
T2_vs_T3 = montest_var(T2.GepiceC,T3.GepiceC)
var_epice = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_epice)[nrow(var_epice)]="GepiceC"
# Gout sucré
T1 vs T2 = montest var(T1.GsucreC, T2.GsucreC)
T1_vs_T3 = montest_var(T1.GsucreC,T3.GsucreC)
T2 vs T3 = montest var(T2.GsucreC,T3.GsucreC)
var_sucre = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_sucre)[nrow(var_sucre)]="GsucreC"
# Gout acide
T1 vs T2 = montest var(T1.GacideC,T2.GacideC)
T1_vs_T3 = montest_var(T1.GacideC,T3.GacideC)
T2_vs_T3 = montest_var(T2.GacideC,T3.GacideC)
var acide = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_acide)[nrow(var_acide)]="GacideC"
# Gout amer
T1_vs_T2 = montest_var(T1.GamerC, T2.GamerC)
T1_vs_T3 = montest_var(T1.GamerC, T3.GamerC)
T2 vs T3 = montest var(T2.GamerC, T3.GamerC)
var amer = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_amer)[nrow(var_amer)]="GamerC"
# Tableau récapitulatif
tab_gustatif = rbind(var_dur,var_int,var_veg,var_iod,var_sale,var_fruit,var_epice,var_s
ucre,var acide,var amer)
colnames(tab_gustatif)=c("T1 vs T2","T1 vs T3","T2 vs T3")
kable(tab gustatif)
             T1 vs T2
                        T1 vs T3
                                   T2 vs T3
```

0.2170326

0.5608280

GdureteC

0.7204846 0.3694238

GintenseC 0.3984965 0.1541809

```
GvegetalC
           0.9672023  0.9637321  0.9969431
 GiodeC
           0.5652768 0.5115979 0.2222130
 GsaleC
           0.6891310 0.3437869 0.1825405
 GfruiteC
           0.8524015  0.8100544  0.9544701
 GepiceC
           0.0587135  0.0085203  0.4348459
 GsucreC
           0.0984493 0.7226878 0.0460607
 GacideC
           0.9295879 0.0800968 0.0951201
 GamerC
           0.4899163 0.5760957 0.8950615
#write.table(tab_gustatif,file = "D:/Projet4/Partie_R/Gustatif_égalité_Var.txt")
3.4
      Finalité en bouche
# Agréable
T1 vs T2 = montest var(T1.FagreableC,T2.FagreableC)
T1 vs T3 = montest var(T1.FagreableC,T3.FagreableC)
T2 vs T3 = montest var(T2.FagreableC,T3.FagreableC)
var_agre = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_agre)[nrow(var_agre)]="FagreableC"
# Intensité du gout
T1 vs T2 = montest var(T1FintensiteC,T2.FintensiteC)
T1_vs_T3 = montest_var(T1FintensiteC, T3.FintensiteC)
T2 vs T3 = montest var(T2.FintensiteC,T3.FintensiteC)
var intens = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_intens)[nrow(var_intens)]="FintensiteC"
# Persistence
T1 vs T2 = montest var(T1.FpersistanceC,T2.FpersistanceC)
T1 vs T3 = montest var(T1.FpersistanceC,T3.FpersistanceC)
T2_vs_T3 = montest_var(T2.FpersistanceC,T3.FpersistanceC)
var_pers = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var pers)[nrow(var pers)]="FpersistanceC"
# Note globale
T1_vs_T2 = montest_var(T1.FnoteC, T2.FnoteC)
T1 vs T3 = montest var(T1.FnoteC,T3.FnoteC)
T2 vs T3 = montest var(T2.FnoteC,T3.FnoteC)
var_note = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var note)[nrow(var note)]="FnoteC"
# Harmonie en bouche
T1 vs T2 = montest var(T1.FharmonieC,T2.FharmonieC)
T1 vs T3 = montest var(T1.FharmonieC, T3.FharmonieC)
T2_vs_T3 = montest_var(T2.FharmonieC,T3.FharmonieC)
var harm = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var harm)[nrow(var harm)]="FharmonieC"
# Riche en arome
```

```
T1_vs_T2 = montest_var(T1.FaromeC,T2.FaromeC)
T1_vs_T3 = montest_var(T1.FaromeC,T3.FaromeC)
T2_vs_T3 = montest_var(T2.FaromeC,T3.FaromeC)
var_arom = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_arom)[nrow(var_arom)]="FaromeC"

# Tableau récapitulatif

tab_fin_bouche = rbind(var_agre,var_intens,var_pers,var_note,var_harm,var_arom)
colnames(tab_fin_bouche)=c("T1 vs T2","T1 vs T3","T2 vs T3")
kable(tab_fin_bouche)
```

	T1 vs T2	T1 vs T3	T2 vs T3			
FagreableC	0.8625934	0.6704832	0.8019253			
FintensiteC	0.0925959	0.7577068	0.1605000			
FpersistanceC	0.2775852	0.9314236	0.3101299			
FnoteC	0.0573556	0.2840128	0.3965889			
FharmonieC	0.3031299	0.9353624	0.2670692			
FaromeC	0.1786381	0.8188646	0.2628465			
<pre>#write.table(tab_fin_bouche,file = "D:/Projet4/Partie_R/Fin_bouche_égalité_Var.txt")</pre>						

#### 4 Test de student d egalité des moyennes

```
# Fonction pour Le test des égalité des moyennes
## Hypothèses
# H0: il y'a égalité de moyenne
# H1: pas d'égalité de moyenne
## Régle de décision
# Rejet de H0 <-> p.value < 5% ou 1%
#Acceptation de H0 <-> p.value > 5% ou 1%
montest_var = function(A,B){

test_moy = t.test(A,B,conf.level=0.05)$p.value

return(test_moy)
}
# Hypothèse
## Hypothèse nulle H0: Les moyennes sont égales.(rouge)
## Hypothèse alternative : Les moyennes sont différentes.(vert)
```

# Règle de decision : rejet de H0 si et seulement si la p-value est inférieure au seuil alpha de 5%.

#### 4.1 Caractéristique visuel

```
# Intencité de la couleur
T1 vs T2 = montest var(T1.VintensiteC, T2.VintensiteC)
T1 vs T3 = montest var(T1.VintensiteC, T3.VintensiteC)
T2 vs T3 = montest var(T2.VintensiteC,T3.VintensiteC)
var int = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_int)[nrow(var_int)]="VintensiteC"
# copacité de la couleur
T1 vs T2 = montest var(T1.VcompactC, T2.VcompactC)
T1 vs T3 = montest var(T1.VcompactC, T3.VcompactC)
T2_vs_T3 = montest_var(T2.VcompactC,T3.VcompactC)
var_comp = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_comp)[nrow(var_comp)]="VcompactC"
# Granulosité texture
T1 vs T2 = montest var(T1.VtextureC,T2.VtextureC)
T1 vs T3 = montest var(T1.VtextureC, T3.VtextureC)
T2 vs T3 = montest var(T2.VtextureC,T3.VtextureC)
var text = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_text)[nrow(var_text)]="VtextureC"
# Variété de tons
T1_vs_T2 = montest_var(T1.VtonsC,T2.VtonsC)
T1_vs_T3 = montest_var(T1.VtonsC,T3.VtonsC)
T2_vs_T3 = montest_var(T2.VtonsC,T3.VtonsC)
var tons = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_tons)[nrow(var_tons)]="VtonsC"
# Brillance
T1 vs T2 = montest var(T1.VbrillanceC,T2.VbrillanceC)
T1 vs T3 = montest var(T1.VbrillanceC, T3.VbrillanceC)
T2 vs T3 = montest var(T2.VbrillanceC,T3.VbrillanceC)
var_brill = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_brill)[nrow(var_brill)]="VbrillanceC"
# Attirance
T1_vs_T2 = montest_var(T1.VattiranceC, T2.VattiranceC)
T1_vs_T3 = montest_var(T1.VattiranceC, T3.VattiranceC)
T2_vs_T3 = montest_var(T2.VattiranceC,T3.VattiranceC)
var_att = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_att)[nrow(var_att)]="VattiranceC"
# Tableau récapitulatif
tab_visuel = rbind(var_int,var_comp,var_text,var_tons,var_brill,var_att)
```

```
colnames(tab_visuel)=c("T1 vs T2","T1 vs T3","T2 vs T3")
kable(tab_visuel)
```

```
T1 vs T2 T1 vs T3 T2 vs T3

VintensiteC 0.3956438 0.0028927 0.0318967

VcompactC 0.5561335 0.0002187 0.0008851

VtextureC 0.5240857 0.7790506 0.7292601

VtonsC 0.0093354 0.7403064 0.0059877

VbrillanceC 0.0117133 0.0050061 1.0000000

VattiranceC 0.0404819 0.6202301 0.0076793

#write.table(tab visuel, file = "D:/Projet4/Partie R/VIsuel égalité Moy.txt")
```

#### 4.2 Caractéristiques olfactives

```
# Odeur fruité
T1_vs_T2 = montest_var(T1.0fruitC,T2.0fruitC)
T1 vs T3 = montest var(T1.0fruitC,T3.0fruitC)
T2 vs T3 = montest var(T2.0fruitC,T3.0fruitC)
var_fruit = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var fruit)[nrow(var fruit)]="OfruitC"
# Odeur amer
T1 vs T2 = montest var(T1.OamerC, T2.OamerC)
T1 vs T3 = montest var(T1.OamerC, T3.OamerC)
T2_vs_T3 = montest_var(T2.OamerC,T3.OamerC)
var_amer = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var amer)[nrow(var amer)]="OamerC"
# Odeur épicée
T1 vs T2 = montest var(T1.0epiceC,T2.0epiceC)
T1 vs T3 = montest var(T1.OepiceC, T3.OepiceC)
T2_vs_T3 = montest_var(T2.0epiceC,T3.0epiceC)
var epice = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_epice)[nrow(var_epice)]="OepiceC"
# Odeur végétale
T1 vs T2 = montest var(T1.0vegetaleC,T2.0vegetaleC)
T1_vs_T3 = montest_var(T1.0vegetaleC,T3.0vegetaleC)
T2 vs T3 = montest var(T2.0vegetaleC,T3.0vegetaleC)
var_veg = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var veg)[nrow(var veg)]="OvegetaleC"
# Tableau récapitulatif
tab olfactif = rbind(var fruit, var amer, var epice, var veg)
colnames(tab_olfactif)=c("T1 vs T2","T1 vs T3","T2 vs T3")
kable(tab olfactif)
```

T1 vs T2 T1 vs T3 T2 vs T3

```
OfruitC 0.0000160 0.0024312 0.0749891

OamerC 0.0291162 0.0755637 0.0002039

OepiceC 0.2076318 0.4884650 0.6736576

OvegetaleC 0.1347023 0.1276445 1.0000000

#write.table(tab olfactif, file = "D:/Projet4/Partie R/Olfactif égalité Moy.txt")
```

#### 4.3 Caractéristique qustative

```
# Dureté texture
T1_vs_T2 = montest_var(T1.GdureteC, T2.GdureteC)
T1_vs_T3 = montest_var(T1.GdureteC,T3.GdureteC)
T2 vs T3 = montest var(T2.GdureteC, T3.GdureteC)
var_dur = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_dur)[nrow(var_dur)]="GdureteC"
# Intensité du gout
T1 vs T2 = montest var(T1.GintenseC, T2.GintenseC)
T1 vs T3 = montest var(T1.GintenseC,T3.GintenseC)
T2_vs_T3 = montest_var(T2.GintenseC,T3.GintenseC)
var_int = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var int)[nrow(var int)]="GintenseC"
#Gout Végétal
T1_vs_T2 = montest_var(T1.GvegetalC,T2.GvegetalC)
T1 vs T3 = montest var(T1.GvegetalC,T3.GvegetalC)
T2_vs_T3 = montest_var(T2.GvegetalC,T3.GvegetalC)
var_veg = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_veg)[nrow(var_veg)]="GvegetalC"
# Gout iodé
T1 vs T2 = montest var(T1.GiodeC,T2.GiodeC)
T1_vs_T3 = montest_var(T1.GiodeC, T3.GiodeC)
T2_vs_T3 = montest_var(T2.GiodeC,T3.GiodeC)
var iod = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var iod)[nrow(var iod)]="GiodeC"
# Gout salé
T1 vs T2 = montest var(T1.GsaleC,T2.GsaleC)
T1_vs_T3 = montest_var(T1.GsaleC,T3.GsaleC)
T2_vs_T3 = montest_var(T2.GsaleC,T3.GsaleC)
var_sale = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_sale)[nrow(var_sale)]="GsaleC"
# Gout fruité
T1_vs_T2 = montest_var(T1.GfruiteC,T2.GfruiteC)
T1_vs_T3 = montest_var(T1.GfruiteC,T3.GfruiteC)
T2 vs T3 = montest var(T2.GfruiteC,T3.GfruiteC)
var_fruit = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_fruit)[nrow(var_fruit)]="GfruiteC"
```

```
# Gout épicé
T1_vs_T2 = montest_var(T1.GepiceC, T2.GepiceC)
T1_vs_T3 = montest_var(T1.GepiceC,T3.GepiceC)
T2 vs T3 = montest var(T2.GepiceC,T3.GepiceC)
var epice = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var epice)[nrow(var epice)]="GepiceC"
# Gout sucré
T1_vs_T2 = montest_var(T1.GsucreC, T2.GsucreC)
T1 vs T3 = montest var(T1.GsucreC, T3.GsucreC)
T2 vs T3 = montest var(T2.GsucreC,T3.GsucreC)
var sucre = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_sucre)[nrow(var_sucre)]="GsucreC"
# Gout acide
T1 vs T2 = montest var(T1.GacideC,T2.GacideC)
T1_vs_T3 = montest_var(T1.GacideC,T3.GacideC)
T2_vs_T3 = montest_var(T2.GacideC,T3.GacideC)
var_acide = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_acide)[nrow(var_acide)]="GacideC"
# Gout amer
T1_vs_T2 = montest_var(T1.GamerC, T2.GamerC)
T1_vs_T3 = montest_var(T1.GamerC, T3.GamerC)
T2 vs T3 = montest var(T2.GamerC, T3.GamerC)
var amer = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_amer)[nrow(var_amer)]="GamerC"
# Tableau récapitulatif
tab_gustatif = rbind(var_dur,var_int,var_veg,var_iod,var_sale,var_fruit,var_epice,var_s
ucre,var acide,var amer)
colnames(tab_gustatif)=c("T1 vs T2","T1 vs T3","T2 vs T3")
kable(tab_gustatif)
```

	T1 vs T2	T1 vs T3	T2 vs T3
GdureteC	0.0104851	0.0248859	0.0000108
GintenseC	0.0156131	0.5026443	0.1241435
GvegetalC	0.0177910	0.1106848	0.3969710
GiodeC	0.2454332	0.0417492	0.5012248
GsaleC	0.0635786	0.1984909	0.0021107
GfruiteC	0.6161846	0.8266686	0.7721369
GepiceC	0.5175034	0.3905428	0.2108153
GsucreC	0.4006308	0.4836117	0.1145540
GacideC	0.8698191	0.2255954	0.1577063

#### 4.4 Finalité en bouche

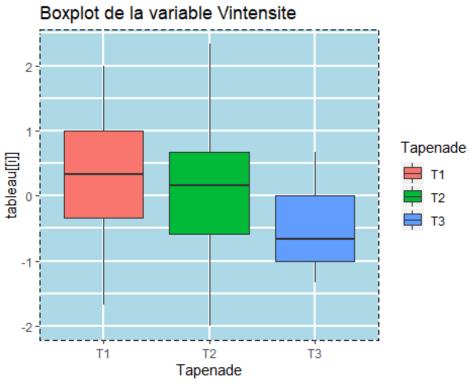
```
# Agréable
T1 vs T2 = montest var(T1.FagreableC,T2.FagreableC)
T1 vs T3 = montest var(T1.FagreableC, T3.FagreableC)
T2_vs_T3 = montest_var(T2.FagreableC,T3.FagreableC)
var_agre = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_agre)[nrow(var_agre)]="FagreableC"
# Intensité du gout
T1 vs T2 = montest var(T1FintensiteC,T2.FintensiteC)
T1_vs_T3 = montest_var(T1FintensiteC,T3.FintensiteC)
T2_vs_T3 = montest_var(T2.FintensiteC,T3.FintensiteC)
var intens = cbind(T1 vs T2,T1 vs T3,T2 vs T3)
rownames(var_intens)[nrow(var_intens)]="FintensiteC"
# Persistence
T1 vs T2 = montest var(T1.FpersistanceC,T2.FpersistanceC)
T1_vs_T3 = montest_var(T1.FpersistanceC,T3.FpersistanceC)
T2_vs_T3 = montest_var(T2.FpersistanceC,T3.FpersistanceC)
var_pers = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_pers)[nrow(var_pers)]="FpersistanceC"
# Note globale
T1_vs_T2 = montest_var(T1.FnoteC,T2.FnoteC)
T1_vs_T3 = montest_var(T1.FnoteC,T3.FnoteC)
T2 vs T3 = montest var(T2.FnoteC, T3.FnoteC)
var_note = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var_note)[nrow(var_note)]="FnoteC"
# Harmonie en bouche
T1_vs_T2 = montest_var(T1.FharmonieC,T2.FharmonieC)
T1_vs_T3 = montest_var(T1.FharmonieC,T3.FharmonieC)
T2_vs_T3 = montest_var(T2.FharmonieC,T3.FharmonieC)
var_harm = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var harm)[nrow(var harm)]="FharmonieC"
# Riche en arome
T1_vs_T2 = montest_var(T1.FaromeC, T2.FaromeC)
T1 vs T3 = montest var(T1.FaromeC, T3.FaromeC)
T2_vs_T3 = montest_var(T2.FaromeC,T3.FaromeC)
var_arom = cbind(T1_vs_T2,T1_vs_T3,T2_vs_T3)
rownames(var arom)[nrow(var arom)]="FaromeC"
# Tableau récapitulatif
tab fin_bouche = rbind(var_agre,var_intens,var_pers,var_note,var_harm,var_arom)
```

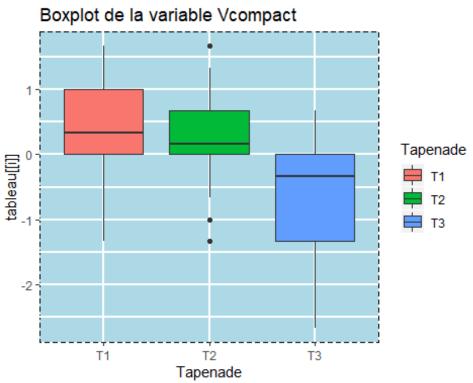
```
colnames(tab_fin_bouche)=c("T1 vs T2","T1 vs T3","T2 vs T3")
kable(tab_fin_bouche)
```

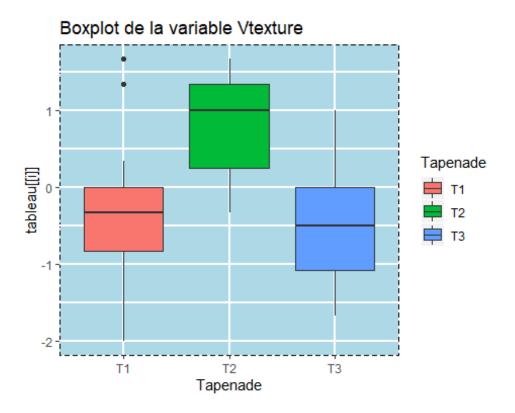
```
T1 vs T3
                                      T2 vs T3
                T1 vs T2
FagreableC
              0.1135408  0.5943863  0.3075122
FintensiteC.
              0.1217509  0.5606522  0.2856797
FpersistanceC
             0.0909009 0.7032300 0.1710171
FnoteC
              0.1223897 \quad 0.0225078 \quad 0.6300485
FharmonieC
              0.0602521 0.0157293 0.7828199
FaromeC
              0.0177446 0.0515889 0.4799714
#write.table(tab fin bouche, file = "D:/Projet4/Partie R/Fin bouche égalité Moy.txt")
```

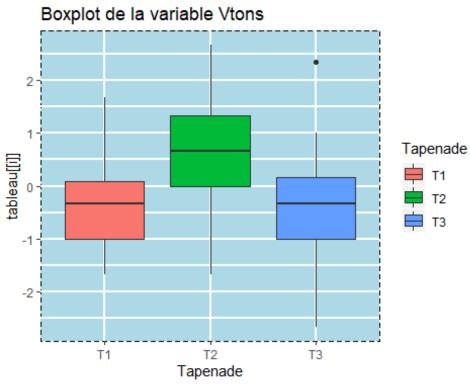
#### 5 ANOVA 1 facteur+tuckey

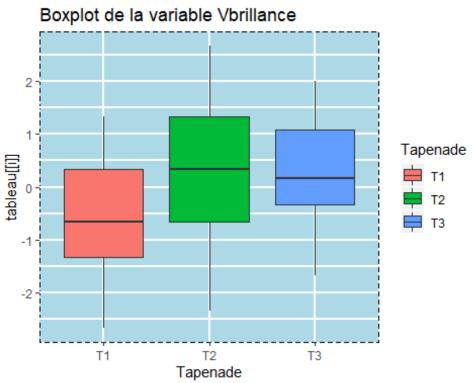
```
library(tidyr)
library(ggplot2)
library(multcomp)
library(car)
# Boite a moustache des différente tapenades
## Permet de voir la tapenade la mieux noté au niveau de chaque variable
for(i in 12:37){
 b = ggplot(data =tableau , aes(x=tableau$Tapenade, y=tableau[[i]], fill=Tapenade)) +
    geom boxplot() +
    xlab("") +
    theme(legend.position="right") +
    xlab("") +
ggtitle(paste("Boxplot de la variable",colnames(tableau[i]))) +
    xlab("Tapenade") +
  theme(panel.background = element rect(fill = "lightblue", colour = "lightblue", size
  linetype = 2), panel.grid.major = element_line(size = 0.9, linetype = 1,colour = "whi
  panel.grid.minor = element line(size = 0.9, linetype = 'solid',colour = "white"))
 print(b)
## Warning: Removed 5 rows containing non-finite values (stat boxplot).
```

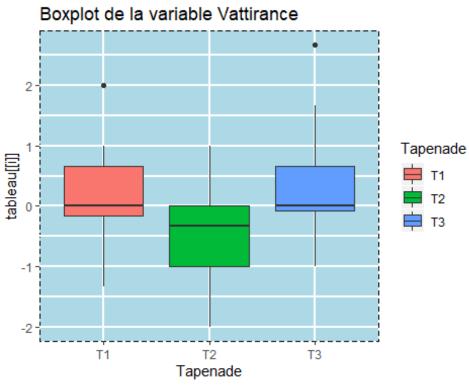


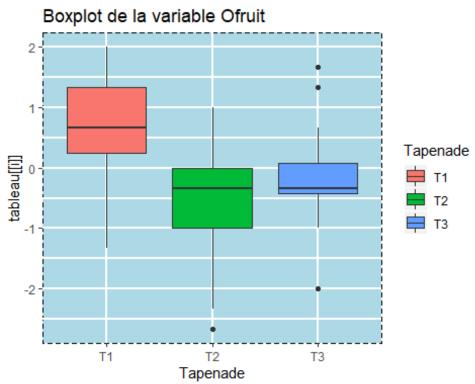


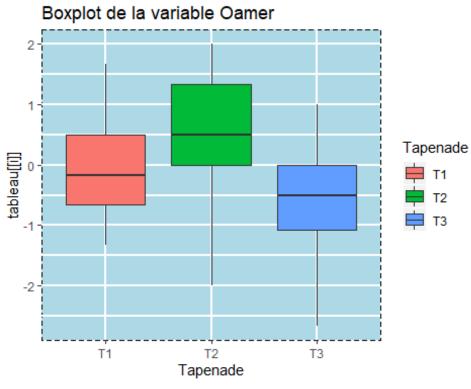


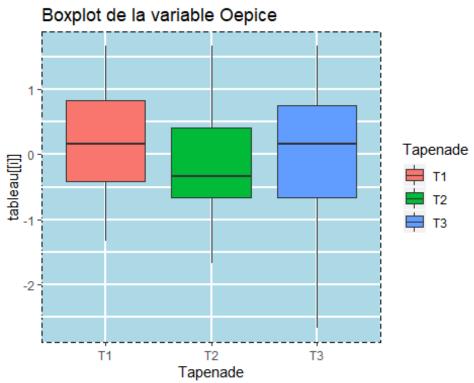


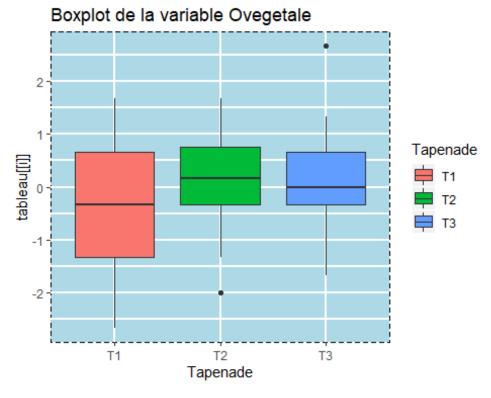


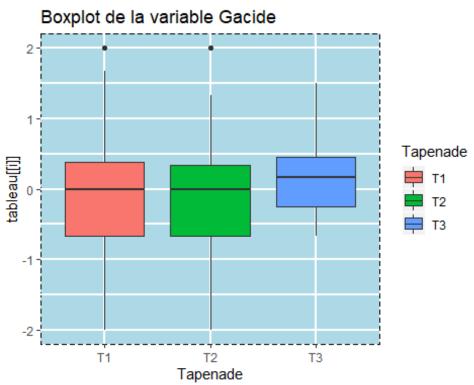


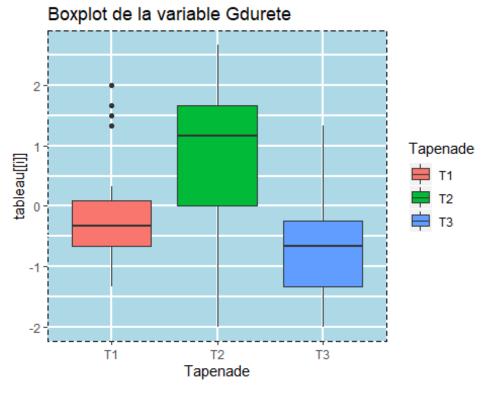


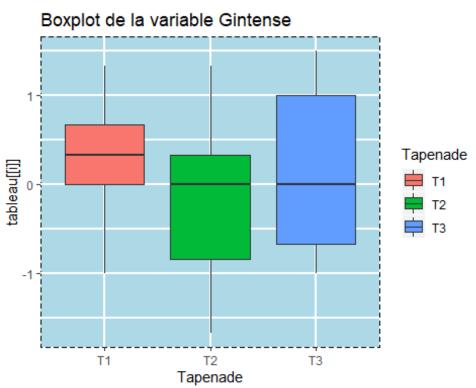


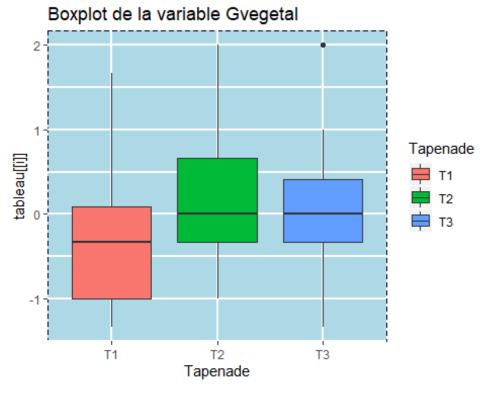


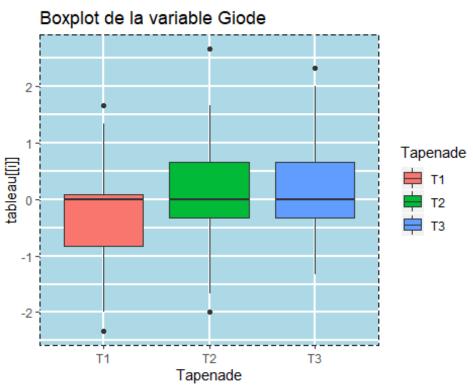


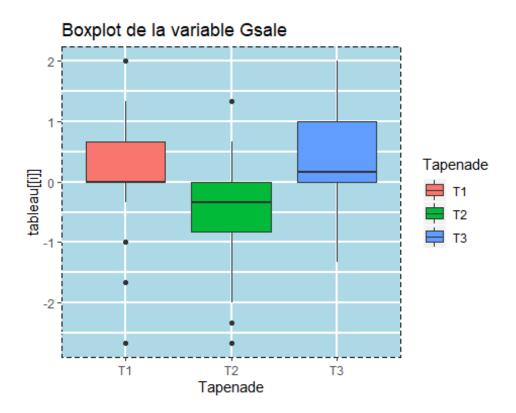


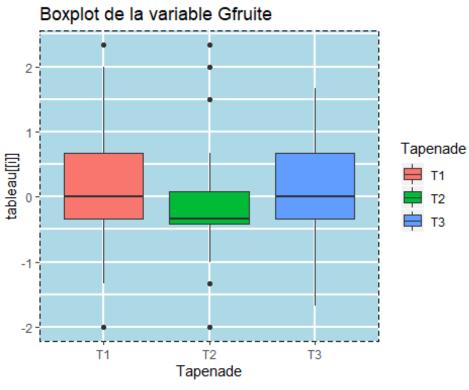


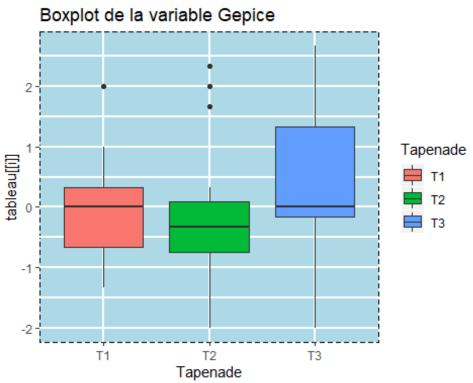


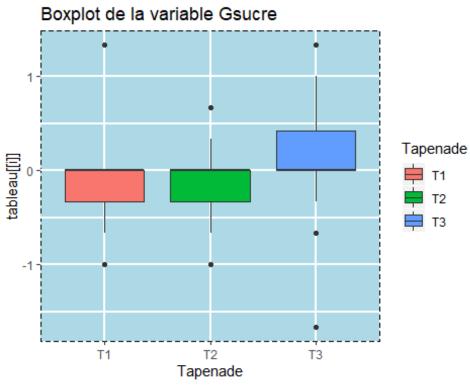


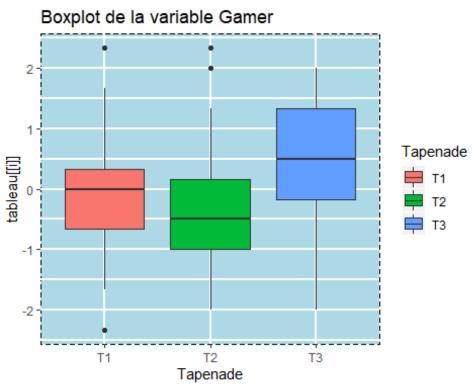


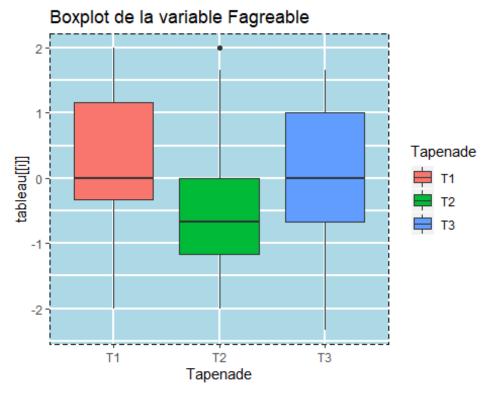


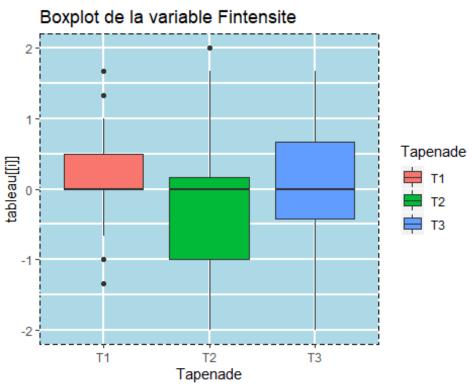


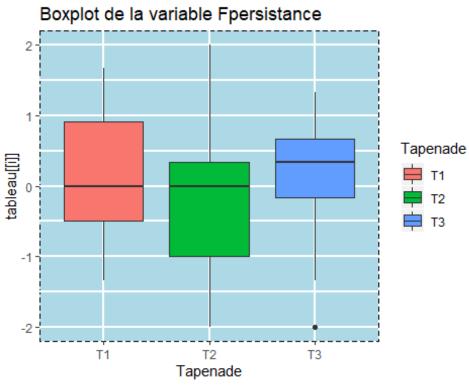


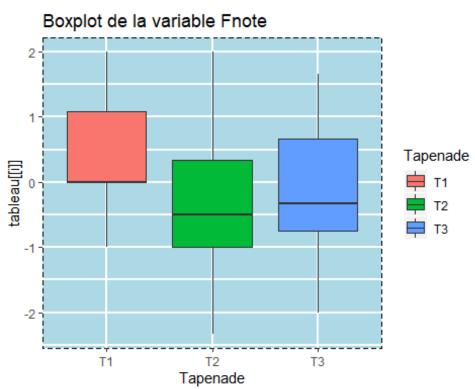


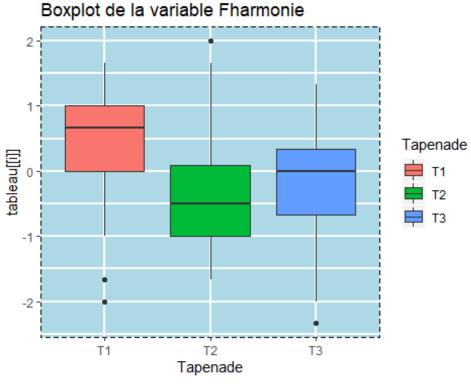


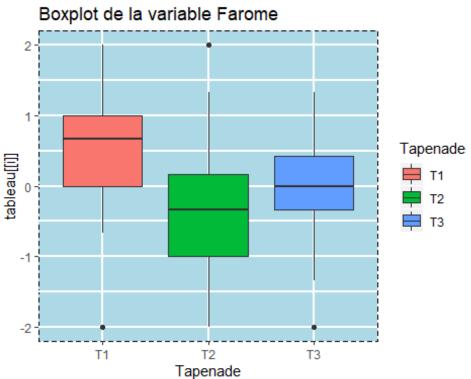










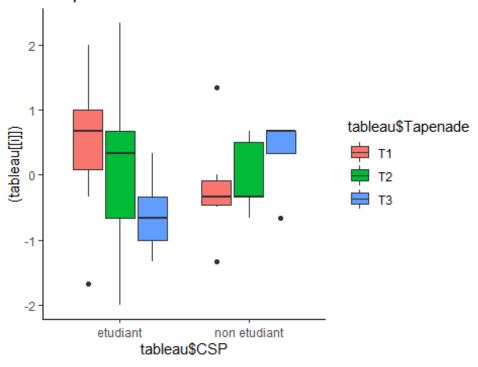


```
# Analyse par goupe

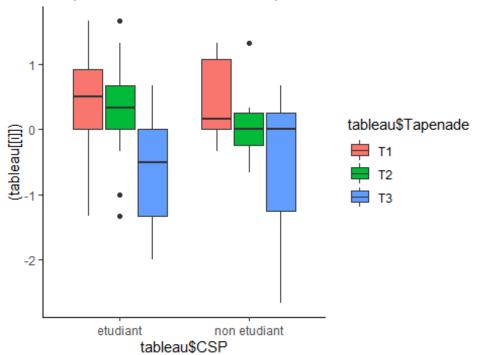
for(i in 12:37){

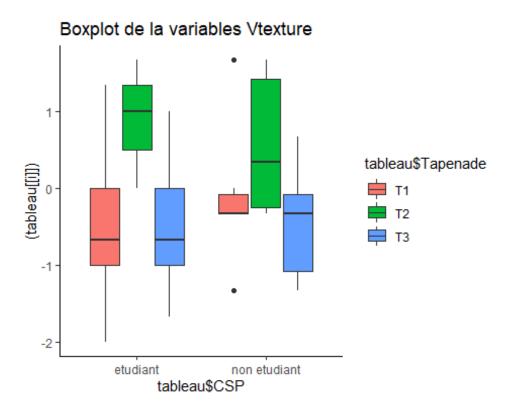
    p = ggplot(tableau, aes(tableau$CSP, (tableau[[i]]))) +
        geom_boxplot(aes(fill = tableau$Tapenade)) +
        ggtitle(paste("Boxplot de la variables",colnames(tableau[i]))) +
        theme_classic()
    print(p)
}
```

# Boxplot de la variables Vintensite

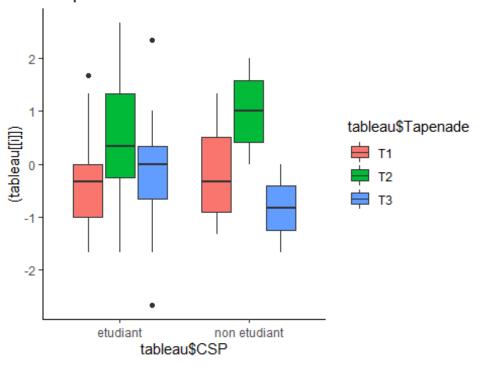


#### Boxplot de la variables Vcompact

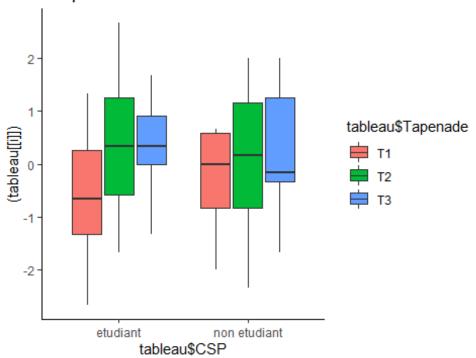




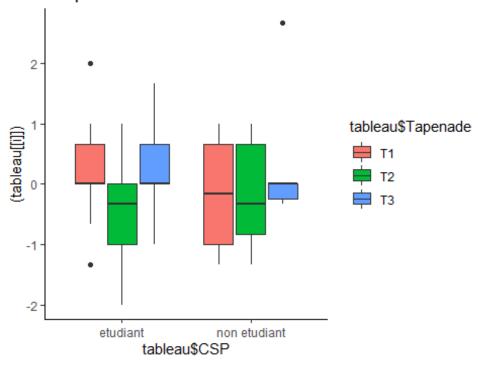
# Boxplot de la variables Vtons



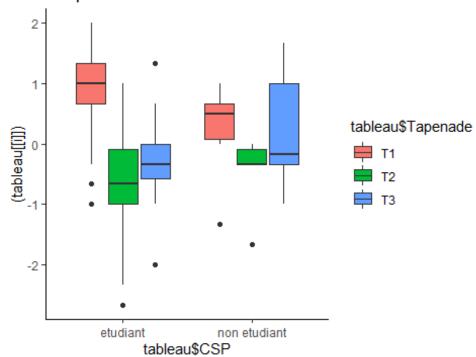
# Boxplot de la variables Vbrillance

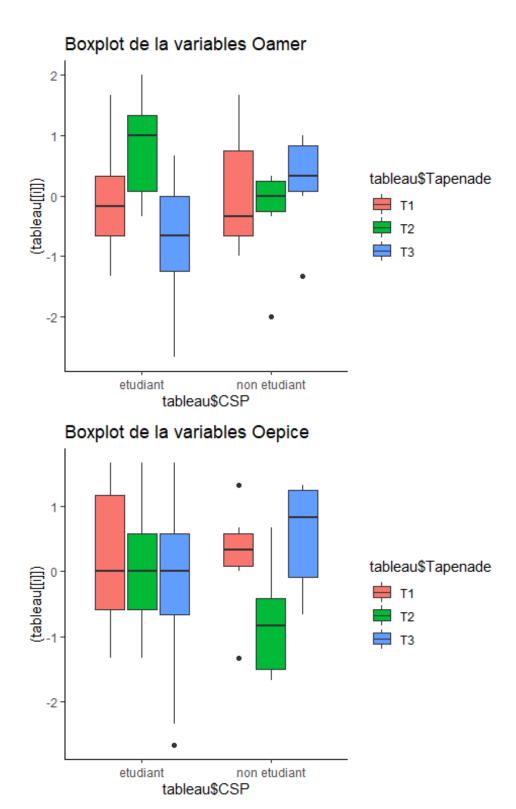


# Boxplot de la variables Vattirance

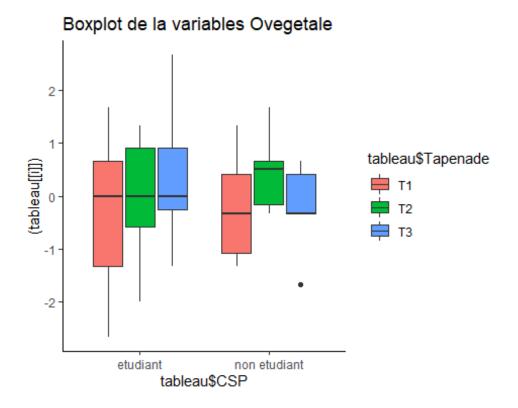


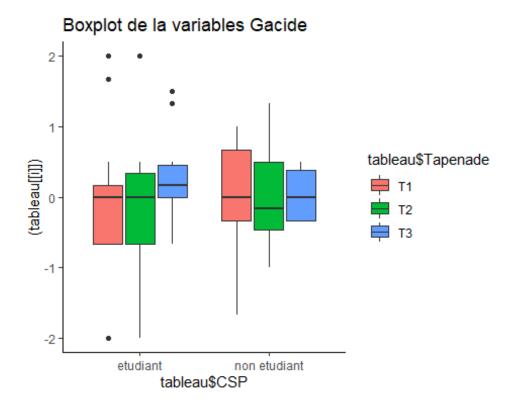
# Boxplot de la variables Ofruit



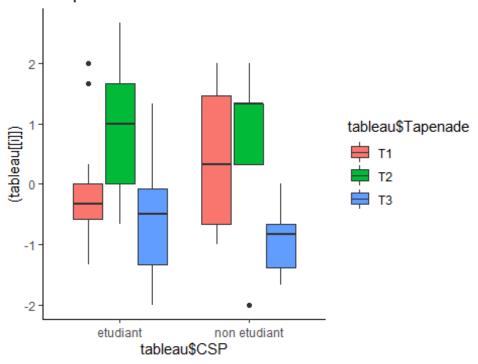


## Warning: Removed 1 rows containing non-finite values (stat\_boxplot).

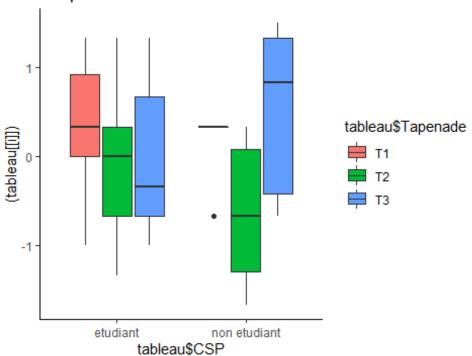




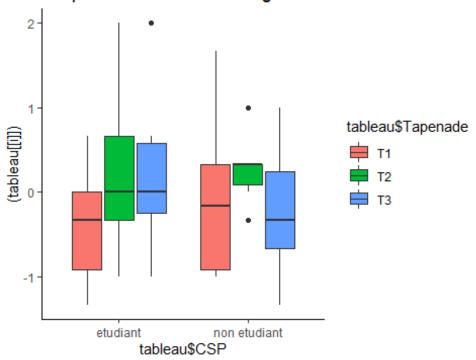
# Boxplot de la variables Gdurete



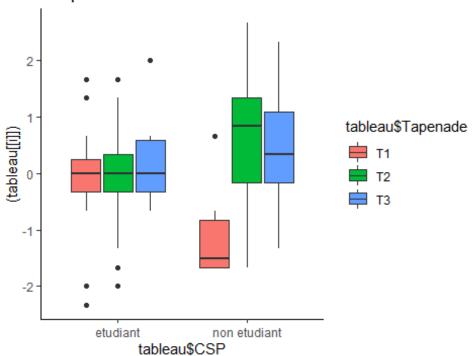
# Boxplot de la variables Gintense

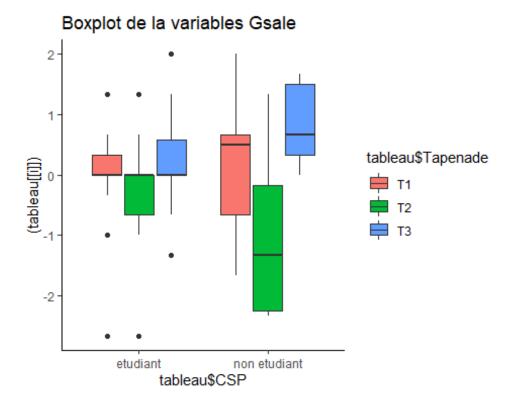


# Boxplot de la variables Gvegetal

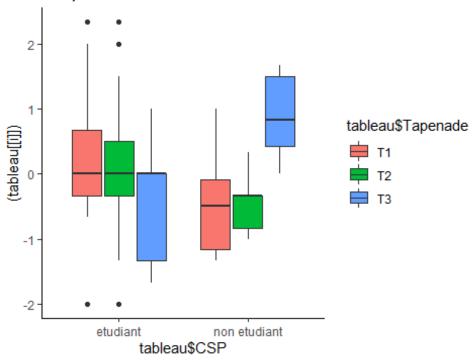


# Boxplot de la variables Giode

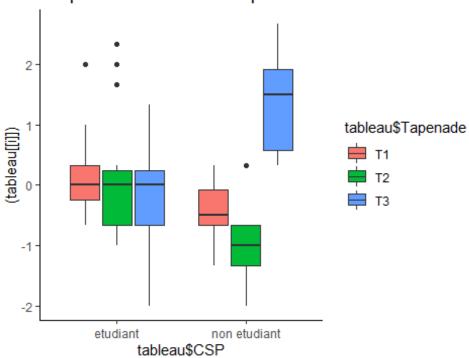


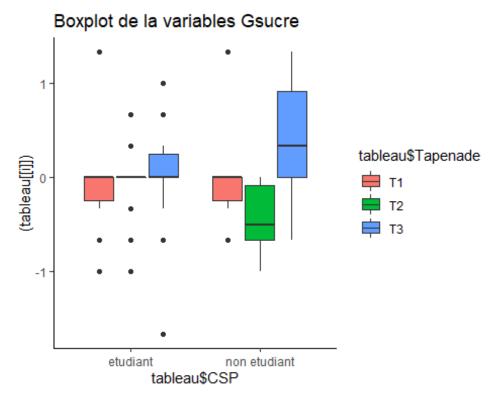


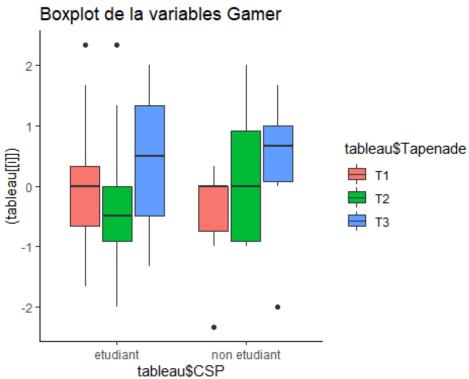
# Boxplot de la variables Gfruite



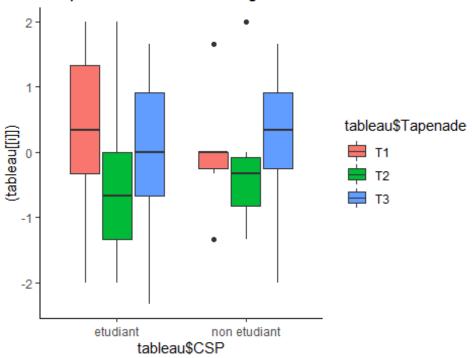
# Boxplot de la variables Gepice



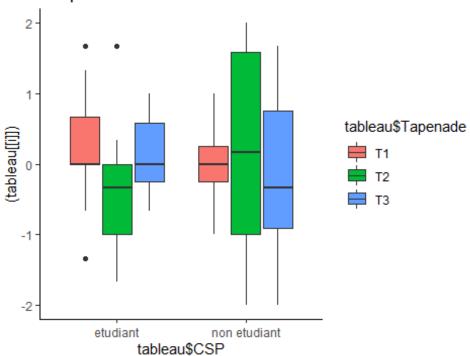




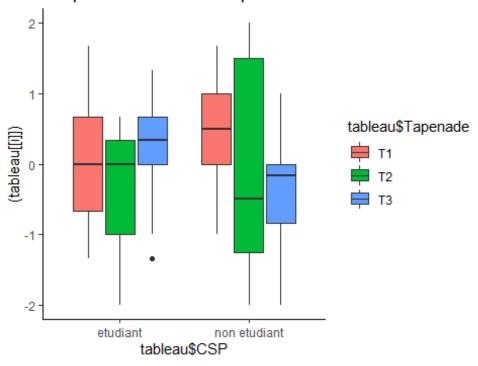
# Boxplot de la variables Fagreable



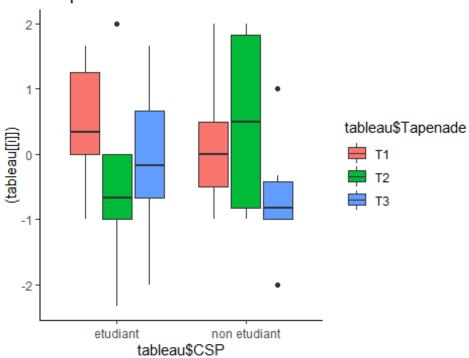
# Boxplot de la variables Fintensite



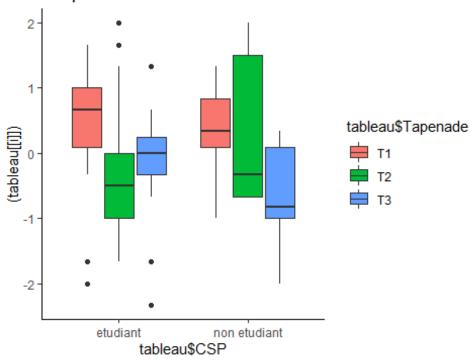
# Boxplot de la variables Fpersistance



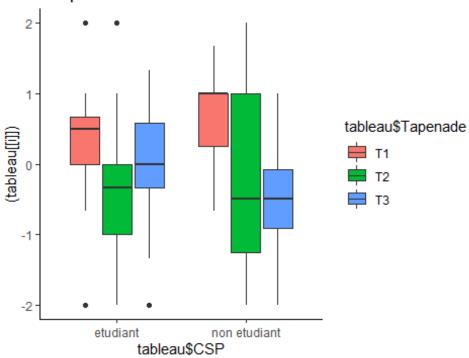
# Boxplot de la variables Fnote



#### Boxplot de la variables Fharmonie



#### Boxplot de la variables Farome



```
# Voir si les moyennes sont statistiquement differentes

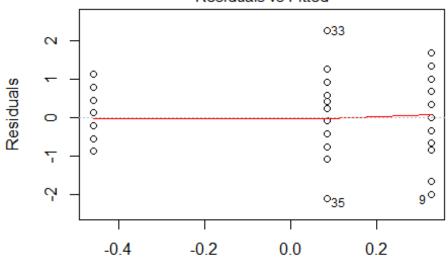
for(i in 12:37){
    anov = aov(tableau[[i]]~tableau$Tapenade, data =tableau) # Test ANOVA
## Vérification de la valité des résultats

    verif_indep1 = durbinWatsonTest(anov) # permet de vérifier l'indépendance
    verif_norm1 = shapiro.test(residuals(anov)) # permet de vérifier la normalité
```

```
#verif_homo1 = leveneTest(residuals(anov)~tableau$Tapenade)# permet de vérifier l'h
omogéneité
print(paste("ANOVA I pour la variable",colnames(tableau)[i]))
   print(summary(anov))
print(paste("Test d'indépendance des residus de la variable", colnames(tableau)[i]))
   print(verif indep1)
    #x11()
    print(plot(anov,1,main = paste("Indépendance : ",colnames(tableau)[i])))# Visualisa
tion de l'indépendance
print(paste("Test de normalité des residus de la variable",colnames(tableau)[i]))
   print(verif norm1)
   #x11()
    plot(anov,2,main = paste("Normalité : ",colnames(tableau)[i])) # Visualisation de l
a normalité
print(paste("Test de d'homogéneité des residus de la variable",colnames(tableau)[i]))
   #x11()
    plot(anov,3, main = paste("homogéneité : ",colnames(tableau)[i])) # Visualisation d
e l'homogéneité
   print(plot(TukeyHSD(anov))) # Test de Tukey et le plot
}
## "ANOVA I pour la variable Vintensite"
Interprétation : le test est signification à 5% car la pvalue(0.0131) est inférieur à 5%. Donc le f
acteur tapenade a un effet significatif sur l'intensité de couleur.
## "Test d'indépendance des residus de la variable Vintensite"
Ici la pvalue(0.916) est supérieur à 5% ,H0 n'est donc pas rejetée donc absence d'autoc
orrélation
```

#### Indépendance : Vintensite

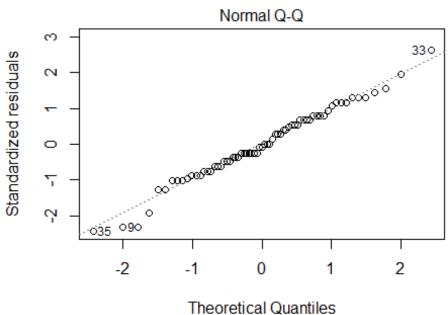
Residuals vs Fitted



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

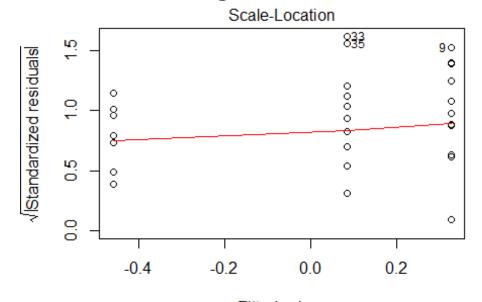
## "Test de normalité des residus de la variable Vintensite"
Ici la pvalue(0.5274) est supérieur à 5% ,H0 n'est donc pas rejetée donc normalité des résidus

## Normalité : Vintensite

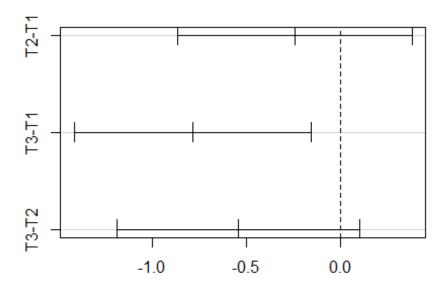


# "Test de d'homogéneité des residus de la variable Vintensite"

## homogéneité : Vintensite



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

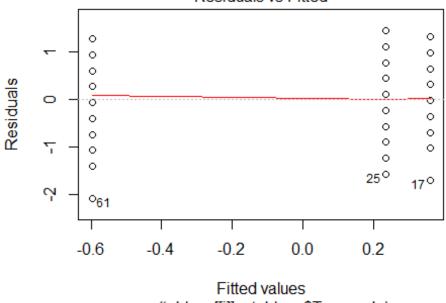


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Vcompact"
                   Df Sum Sq Mean Sq F value
                                               Pr(>F)
## tableau$Tapenade 2 13.03
                                       10.46 0.000108 ***
                               6.514
## Residuals
                      42.97
                   69
                               0.623
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Vcompact"
  lag Autocorrelation D-W Statistic p-value
##
##
               0.25347
                            1.482587
##
   Alternative hypothesis: rho != 0
```

## Indépendance : Vcompact

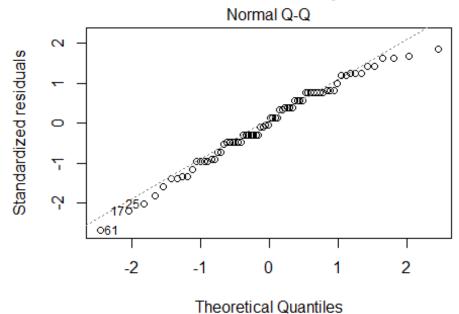
Residuals vs Fitted



aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Vcompact"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.98009, p-value = 0.3112
```

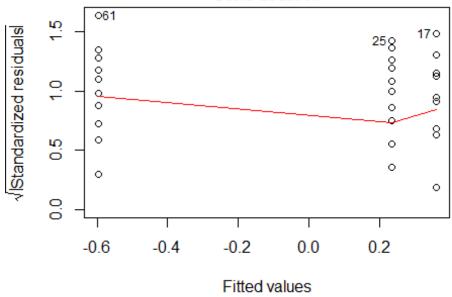
## Normalité : Vcompact



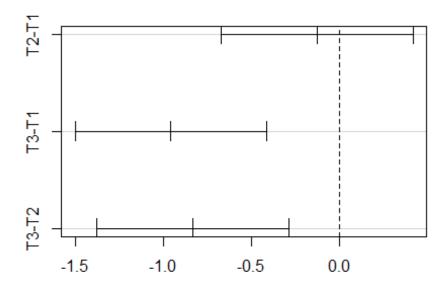
## [1] "Test de d'homogéneité des residus de la variable Vcompact"

## homogéneité: Vcompact

Scale-Location



aov(tableau[[i]] ~ tableau\$Tapenade)

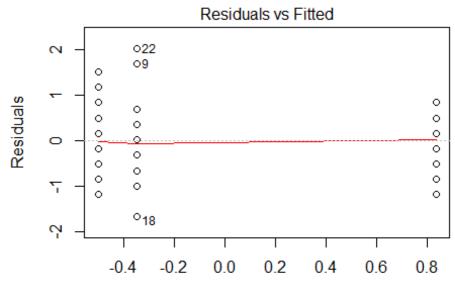


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Vtexture"
                   Df Sum Sq Mean Sq F value
                                               Pr(>F)
## tableau$Tapenade 2 25.45
                                        21.7 5.16e-08 ***
                              12.725
## Residuals
                      39.88
                               0.587
                   68
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## 1 observation deleted due to missingness
## [1] "Test d'indépendance des residus de la variable Vtexture"
## lag Autocorrelation D-W Statistic p-value
```

## 1 0.09383558 1.806055 0.296 ## Alternative hypothesis: rho != 0

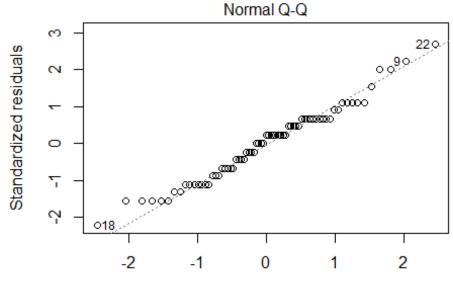
## Indépendance : Vtexture



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

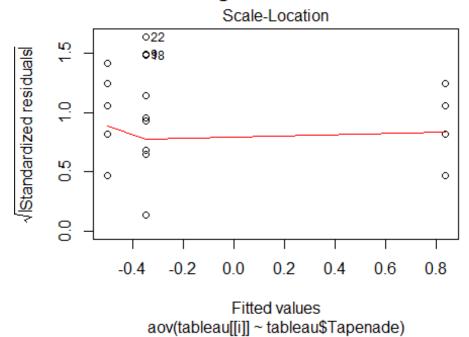
```
## NULL
## [1] "Test de normalité des residus de la variable Vtexture"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.97672, p-value = 0.2094
```

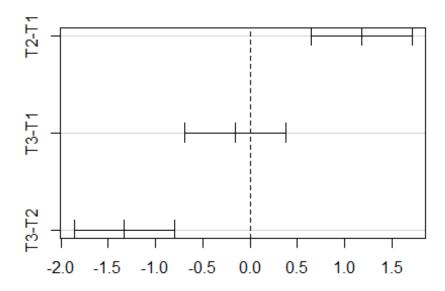
## Normalité: Vtexture



Theoretical Quantiles aov(tableau[[i]] ~ tableau\$Tapenade)

#### homogéneité : Vtexture



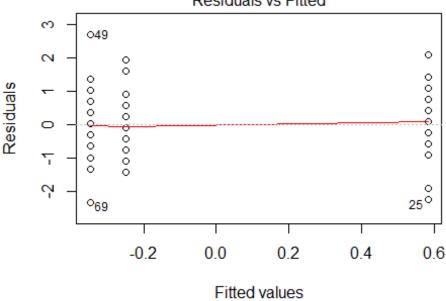


Differences in mean levels of tableau\$Tapenade

```
## lag Autocorrelation D-W Statistic p-value
## 1 0.1174269 1.761281 0.226
## Alternative hypothesis: rho != 0
```

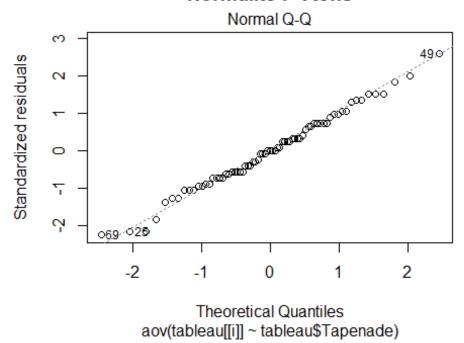
## Indépendance : Vtons

Residuals vs Fitted



```
## NULL
## [1] "Test de normalité des residus de la variable Vtons"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.98997, p-value = 0.847
```

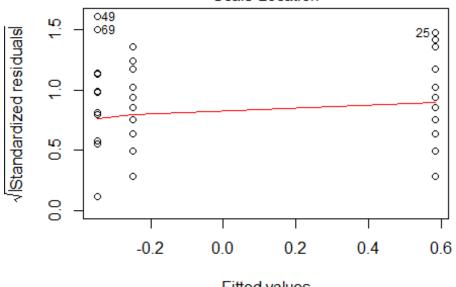
## Normalité : Vtons



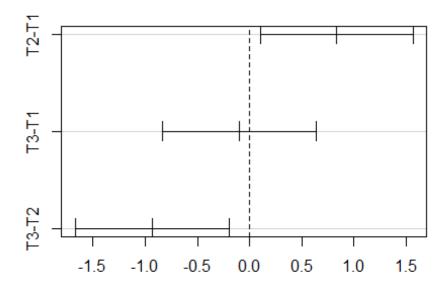
## [1] "Test de d'homogéneité des residus de la variable Vtons"

#### homogéneité: Vtons

Scale-Location



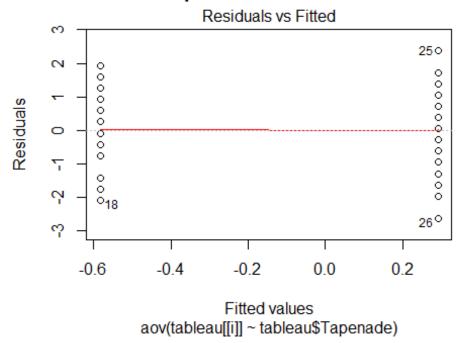
Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)



Differences in mean levels of tableau\$Tapenade

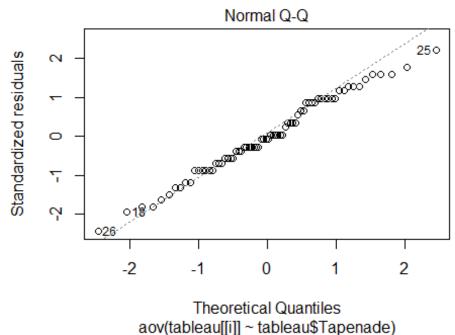
```
## NULL
## [1] "ANOVA I pour la variable Vbrillance"
                   Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2 12.25
                                       5.087 0.0087 **
                               6.125
## Residuals
                       83.08
                    69
                               1.204
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Vbrillance"
   lag Autocorrelation D-W Statistic p-value
##
##
             -0.1693205
                            2.330847
  Alternative hypothesis: rho != 0
##
```

#### Indépendance : Vbrillance



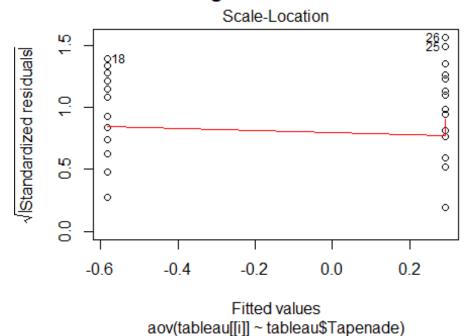
```
## NULL
## [1] "Test de normalité des residus de la variable Vbrillance"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.98606, p-value = 0.6116
```

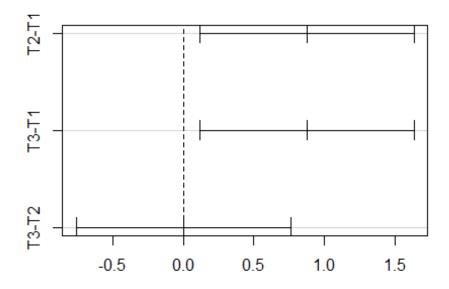
## Normalité : Vbrillance



## [1] "Test de d'homogéneité des residus de la variable Vbrillance"

## homogéneité : Vbrillance



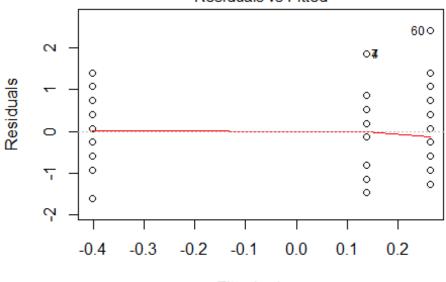


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Vattirance"
                   Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                        6.03 3.0139
                                       4.053 0.0217 *
## Residuals
                       51.31 0.7436
                   69
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Vattirance"
   lag Autocorrelation D-W Statistic p-value
##
##
             0.02839815
                            1.899601
##
   Alternative hypothesis: rho != 0
```

#### Indépendance : Vattirance

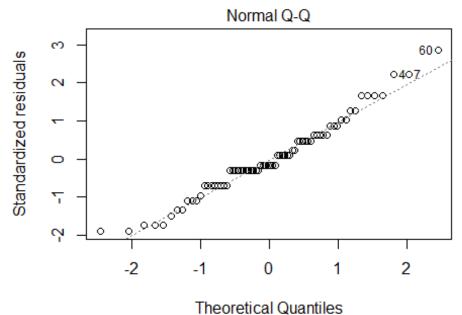
Residuals vs Fitted



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Vattirance"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.97383, p-value = 0.1382
```

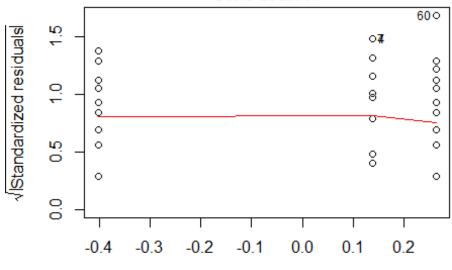
## Normalité : Vattirance



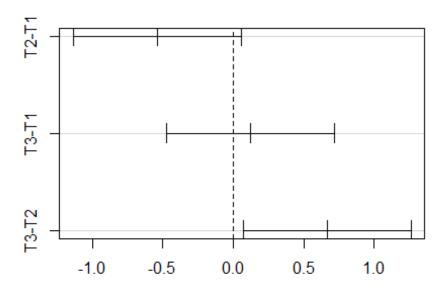
## [1] "Test de d'homogéneité des residus de la variable Vattirance"

#### homogéneité : Vattirance

Scale-Location



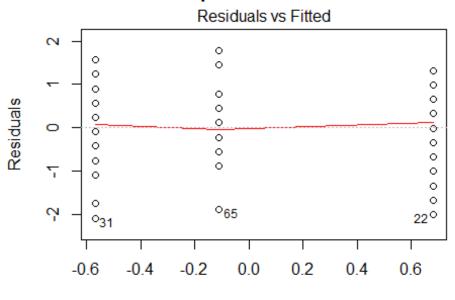
Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)



Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Ofruit"
                   Df Sum Sq Mean Sq F value
                                               Pr(>F)
## tableau$Tapenade 2
                                       12.54 2.26e-05 ***
                      19.19
                               9.597
## Residuals
                       52.81
                   69
                               0.765
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Ofruit"
   lag Autocorrelation D-W Statistic p-value
##
##
            -0.09633453
                            2.148244
   Alternative hypothesis: rho != 0
##
```

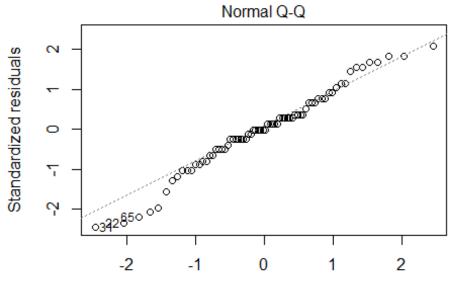
#### Indépendance : Ofruit



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Ofruit"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.97707, p-value = 0.2117
```

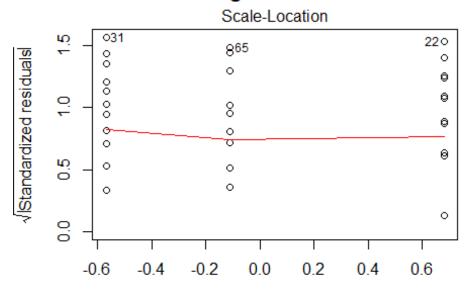
## Normalité : Ofruit



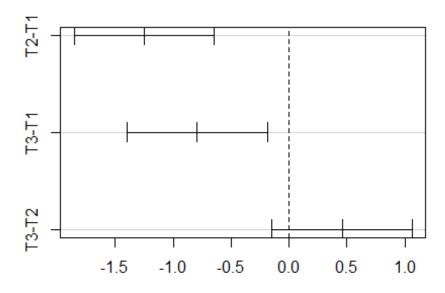
Theoretical Quantiles aov(tableau[[i]] ~ tableau\$Tapenade)

## [1] "Test de d'homogéneité des residus de la variable Ofruit"

#### homogéneité : Ofruit



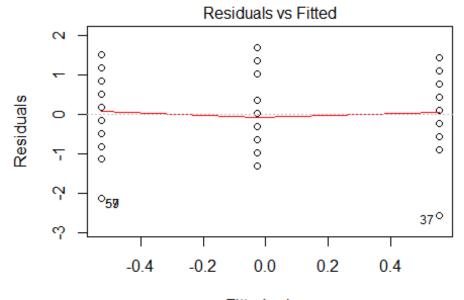
Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)



Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Oamer"
                   Df Sum Sq Mean Sq F value
                                               Pr(>F)
## tableau$Tapenade 2
                                        8.22 0.000628 ***
                      14.11
                               7.056
## Residuals
                       59.22
                    69
                               0.858
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Oamer"
   lag Autocorrelation D-W Statistic p-value
##
##
             0.07929435
                            1.830441
   Alternative hypothesis: rho != 0
##
```

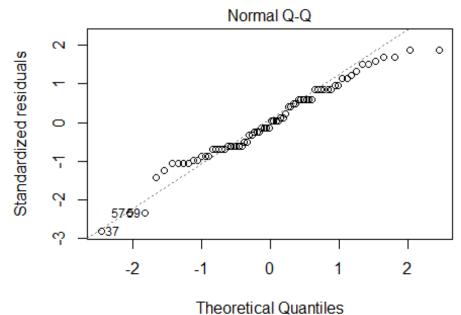
#### Indépendance : Oamer



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Oamer"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.97304, p-value = 0.1245
```

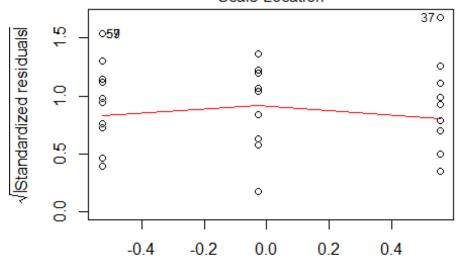
#### Normalité : Oamer



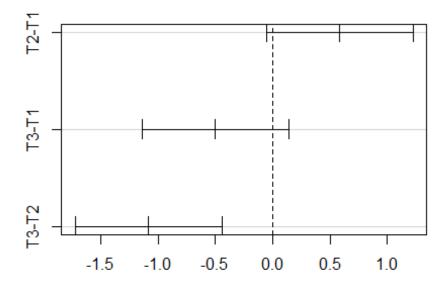
## [1] "Test de d'homogéneité des residus de la variable Oamer"

#### homogéneité : Oamer

Scale-Location



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

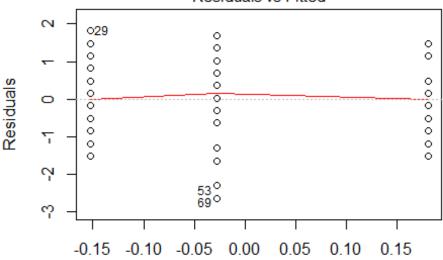


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Oepice"
##
                    Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                         1.36 0.6806
                                        0.698 0.501
                    69
                       67.31 0.9754
## [1] "Test d'indépendance des residus de la variable Oepice"
##
   lag Autocorrelation D-W Statistic p-value
##
             -0.2208207
                             2.433992
##
   Alternative hypothesis: rho != 0
```

## Indépendance : Oepice

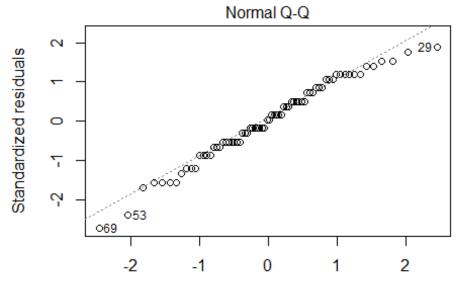
Residuals vs Fitted



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Oepice"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.97926, p-value = 0.2805
```

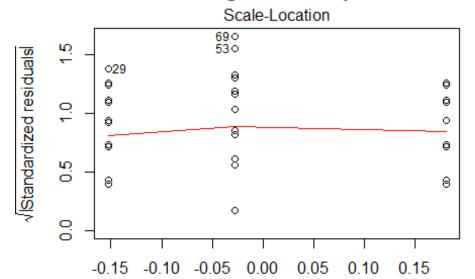
## Normalité : Oepice



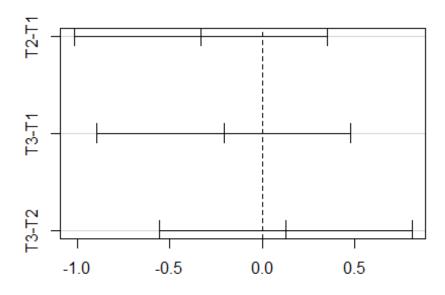
Theoretical Quantiles aov(tableau[[i]] ~ tableau\$Tapenade)

## [1] "Test de d'homogéneité des residus de la variable Oepice"

## homogéneité : Oepice



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)



Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Ovegetale"
##
                    Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                         3.46
                                1.729
                                        1.716 0.188
## Residuals
                    68
                       68.54
                                1.008
## 1 observation deleted due to missingness
## [1] "Test d'indépendance des residus de la variable Ovegetale"
   lag Autocorrelation D-W Statistic p-value
##
      1
            0.007095151
                             1.905046
   Alternative hypothesis: rho != 0
```

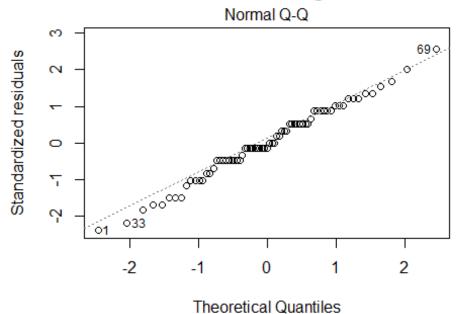
## Indépendance : Ovegetale

Residuals vs Fitted 690 N 0000000 000000000000 Residuals O 000 ۲ o 33° 01 -0.3-0.2-0.1 0.0 0.1

Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Ovegetale"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.98868, p-value = 0.7765
```

## Normalité : Ovegetale

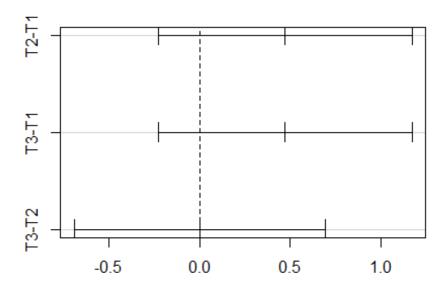


## [1] "Test de d'homogéneité des residus de la variable Ovegetale"

## homogéneité : Ovegetale

Scale-Location 690 LO, 01 330 √|Standardized residuals| 0 0 ٥ ٥ 0 0 0 0 0 0 Θ LQ. Ö 8 0 0.0 -0.2 -0.3-0.1 0.0 0.1

Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

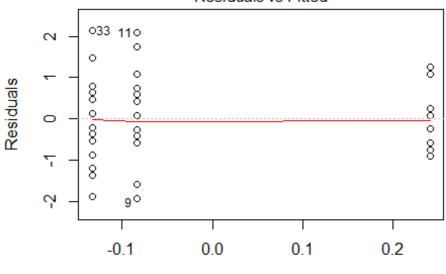


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Gacide"
##
                    Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                         1.54
                              0.7688
                                        1.016 0.369
## Residuals
                    55
                       41.63
                              0.7569
## 14 observations deleted due to missingness
## [1] "Test d'indépendance des residus de la variable Gacide"
##
   lag Autocorrelation D-W Statistic p-value
##
      1
             -0.2721562
                             2.528222
##
   Alternative hypothesis: rho != 0
```

## Indépendance : Gacide

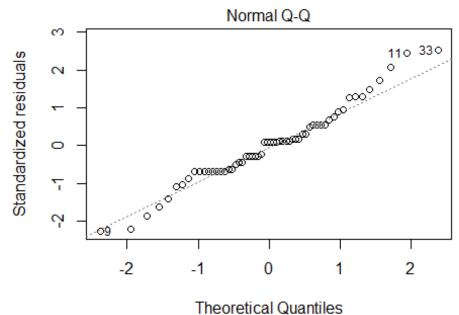
Residuals vs Fitted



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Gacide"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.97143, p-value = 0.1871
```

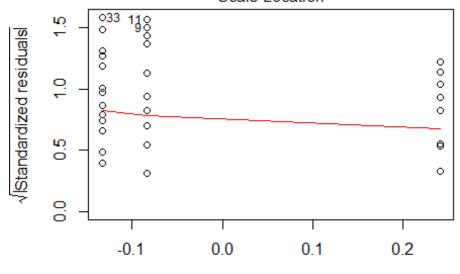
## Normalité : Gacide



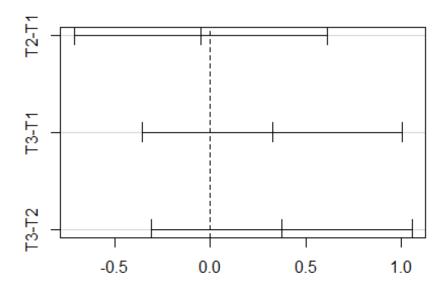
## [1] "Test de d'homogéneité des residus de la variable Gacide"

#### homogéneité : Gacide

Scale-Location



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

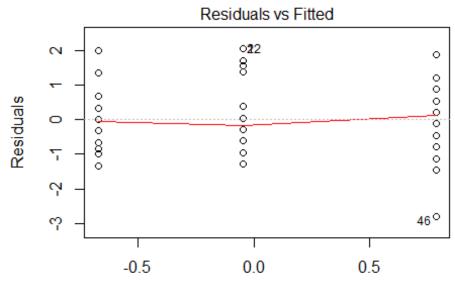


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Gdurete"
                   Df Sum Sq Mean Sq F value
                                               Pr(>F)
## tableau$Tapenade 2 24.60
                                       12.63 2.21e-05 ***
                              12.302
## Residuals
                      65.23
                               0.974
                   67
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## 2 observations deleted due to missingness
## [1] "Test d'indépendance des residus de la variable Gdurete"
## lag Autocorrelation D-W Statistic p-value
```

## 1 -0.07623979 2.081469 0.872 ## Alternative hypothesis: rho != 0

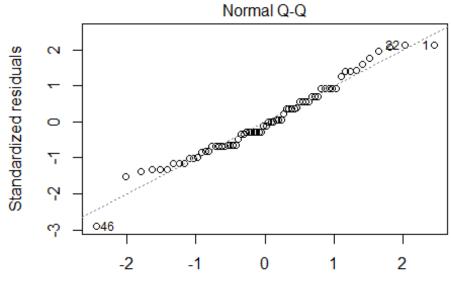
## Indépendance : Gdurete



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

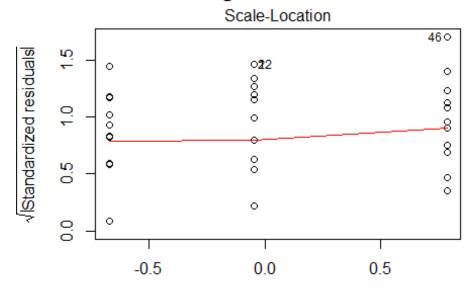
```
## NULL
## [1] "Test de normalité des residus de la variable Gdurete"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.97422, p-value = 0.1577
```

## Normalité : Gdurete

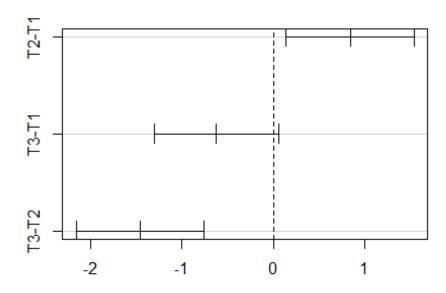


Theoretical Quantiles aov(tableau[[i]] ~ tableau\$Tapenade)

#### homogéneité : Gdurete



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

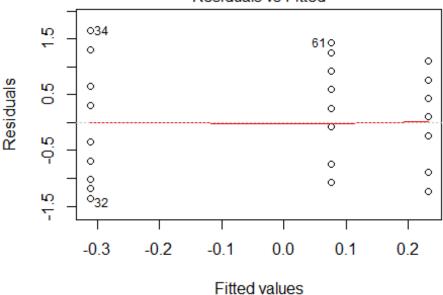


Differences in mean levels of tableau\$Tapenade

```
## lag Autocorrelation D-W Statistic p-value
## 1 0.3791581 1.227572 0.002
## Alternative hypothesis: rho != 0
```

## Indépendance : Gintense

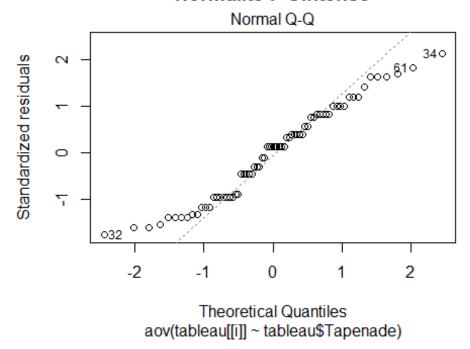




aov(tableau[[i]] ~ tableau\$Tapenade)

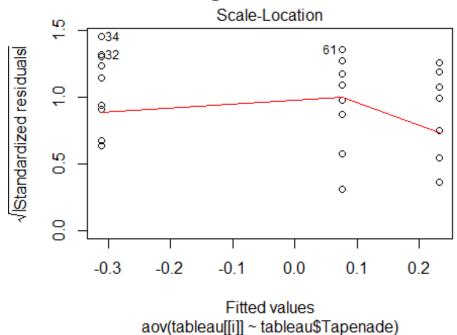
```
## NULL
## [1] "Test de normalité des residus de la variable Gintense"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.96183, p-value = 0.03161
```

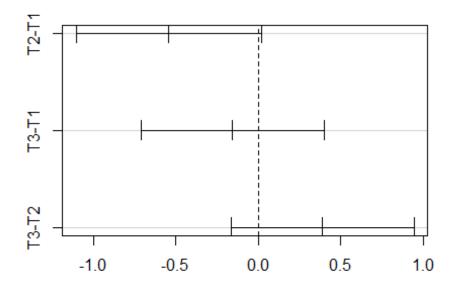
## Normalité : Gintense



## [1] "Test de d'homogéneité des residus de la variable Gintense"

## homogéneité : Gintense

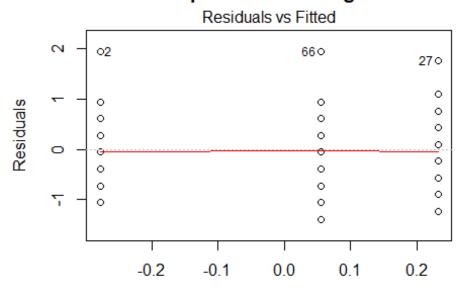




Differences in mean levels of tableau\$Tapenade

## 1 0.03361335 1.930425 0.57 ## Alternative hypothesis: rho != 0

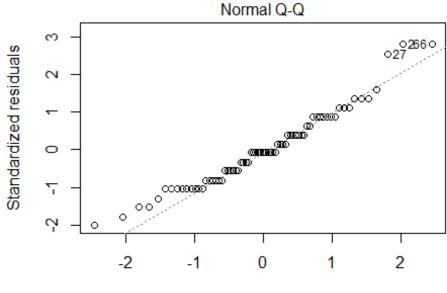
## Indépendance : Gvegetal



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

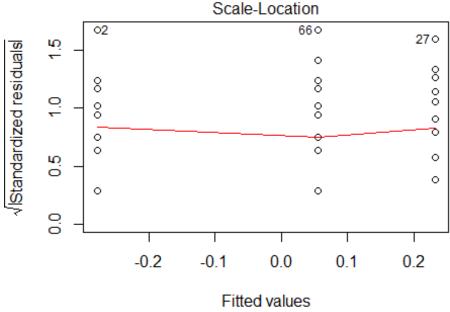
```
## NULL
## [1] "Test de normalité des residus de la variable Gvegetal"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.96074, p-value = 0.02588
```

## Normalité : Gvegetal

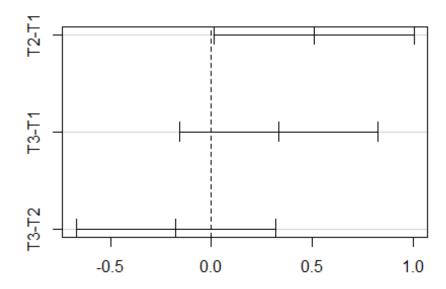


Theoretical Quantiles aov(tableau[[i]] ~ tableau\$Tapenade)

# homogéneité : Gvegetal



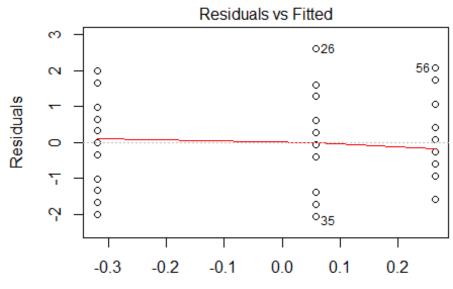
# aov(tableau[[i]] ~ tableau\$Tapenade)



Differences in mean levels of tableau\$Tapenade

## 1 -0.08329291 2.164217 0.644 ## Alternative hypothesis: rho != 0

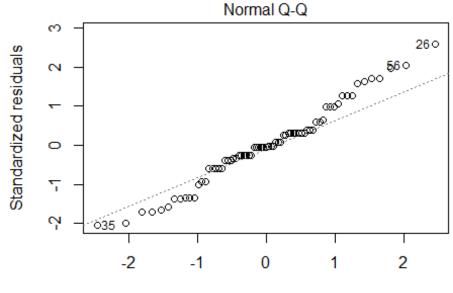
## Indépendance : Giode



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

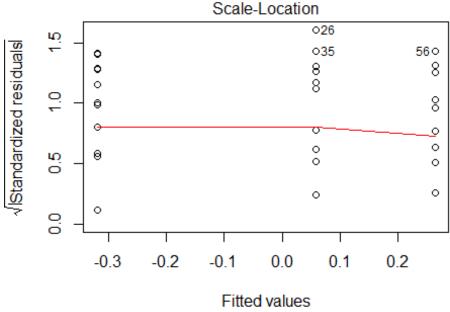
```
## NULL
## [1] "Test de normalité des residus de la variable Giode"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.97791, p-value = 0.2439
```

## Normalité : Giode

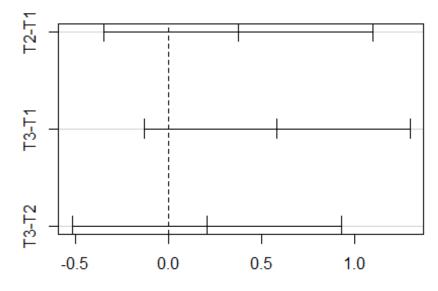


Theoretical Quantiles aov(tableau[[i]] ~ tableau\$Tapenade)

#### homogéneité : Giode



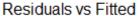
aov(tableau[[i]] ~ tableau\$Tapenade)

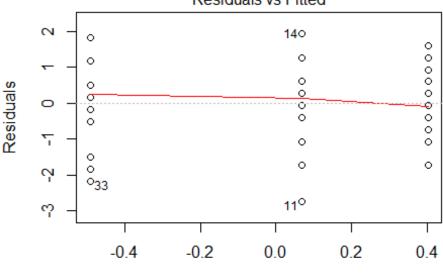


Differences in mean levels of tableau\$Tapenade

```
## lag Autocorrelation D-W Statistic p-value
## 1 0.1347287 1.727777 0.17
## Alternative hypothesis: rho != 0
```

## Indépendance : Gsale

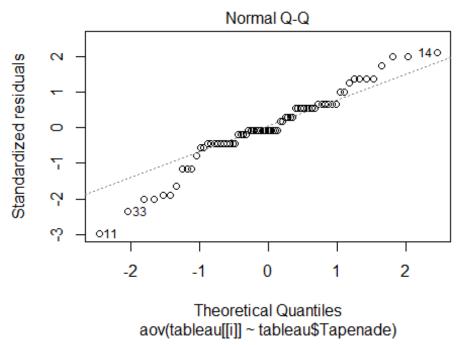




Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

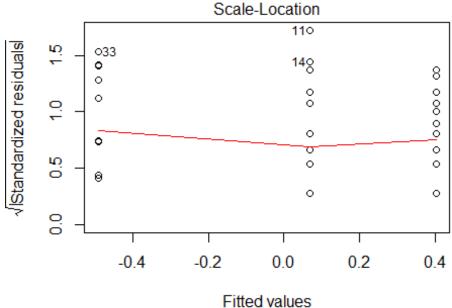
```
## NULL
## [1] "Test de normalité des residus de la variable Gsale"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.9571, p-value = 0.01625
```

## Normalité : Gsale

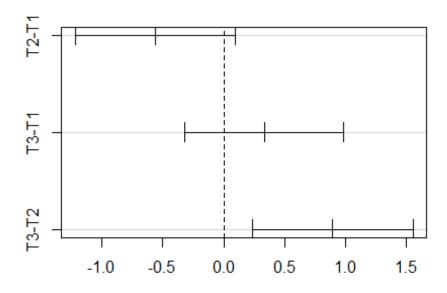


## [1] "Test de d'homogéneité des residus de la variable Gsale"

#### homogéneité : Gsale



aov(tableau[[i]] ~ tableau\$Tapenade)

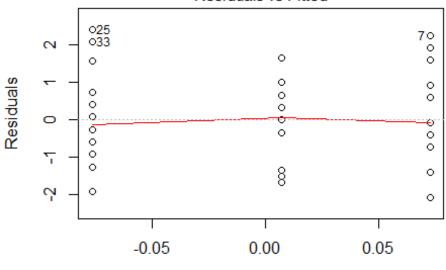


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Gfruite"
##
                    Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                         0.26
                              0.1310
                                        0.131 0.877
## Residuals
                    67
                        66.90
                              0.9986
## 2 observations deleted due to missingness
## [1] "Test d'indépendance des residus de la variable Gfruite"
   lag Autocorrelation D-W Statistic p-value
##
      1
            -0.03126923
                             2.054372
   Alternative hypothesis: rho != 0
```

## Indépendance : Gfruite

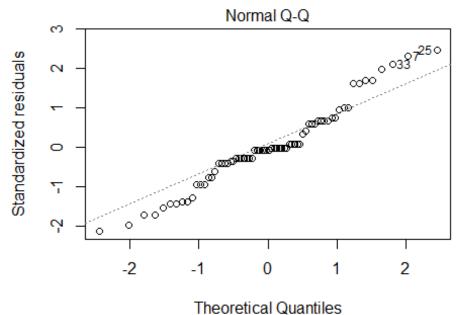
Residuals vs Fitted



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Gfruite"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.96502, p-value = 0.04767
```

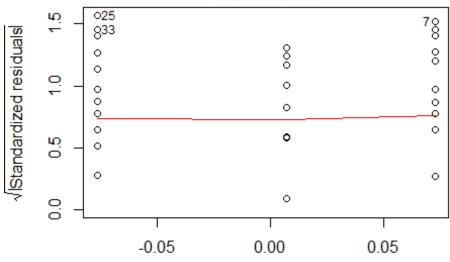
## Normalité : Gfruite



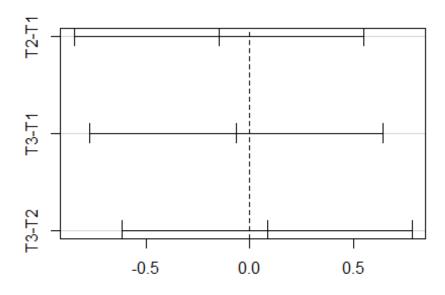
## [1] "Test de d'homogéneité des residus de la variable Gfruite"

### homogéneité : Gfruite

Scale-Location



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)



Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Gepice"
##
                    Df Sum Sq Mean Sq F value Pr(>F)
                         2.11
## tableau$Tapenade 2
                                        1.032 0.362
                                1.056
                    69
                        70.56
                                1.022
## [1] "Test d'indépendance des residus de la variable Gepice"
##
   lag Autocorrelation D-W Statistic p-value
##
            -0.03170385
                             2.062697
##
   Alternative hypothesis: rho != 0
```

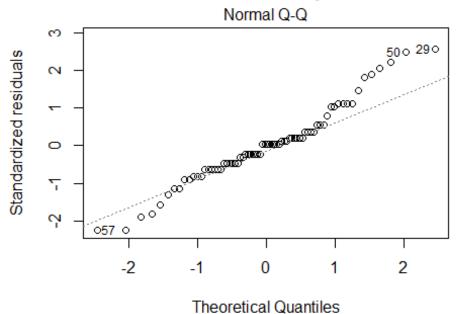
### Indépendance : Gepice

Residuals vs Fitted 029 50 o 0 0 N 0 0 0 Residuals 0 0 0 0 0 0 0 ۲ 0 0 Ņ 0 57° -0.2-0.10.0 0.1 0.2

Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

## NULL
## [1] "Test de normalité des residus de la variable Gepice"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.96486, p-value = 0.04179

### Normalité : Gepice



## [1] "Test de d'homogéneité des residus de la variable Gepice"

### homogéneité : Gepice

Scale-Location 029 <del>59</del>8 LO, 0 √|Standardized residuals| Ö 8 8 Θ 0 0 0 0 0 0 0 8 0.5 0 0 0 0 0.0

-0.2

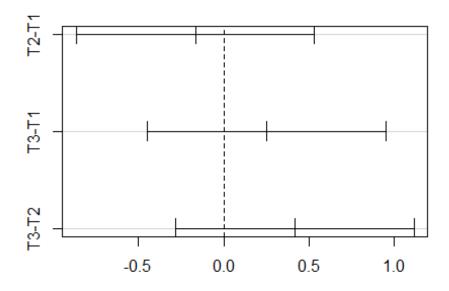
-0.1

Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

0.0

0.1

0.2

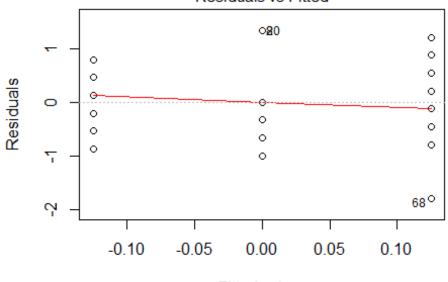


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Gsucre"
##
                    Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                         0.75
                                         1.218 0.302
                                0.375
                    69
                        21.25
                                0.308
## [1] "Test d'indépendance des residus de la variable Gsucre"
##
   lag Autocorrelation D-W Statistic p-value
##
             -0.2139706
                             2.343546
##
   Alternative hypothesis: rho != 0
```

### Indépendance : Gsucre

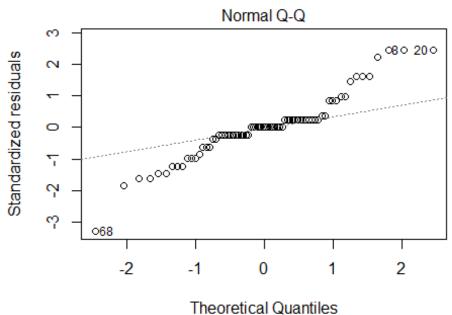
Residuals vs Fitted



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Gsucre"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.92937, p-value = 0.0005756
```

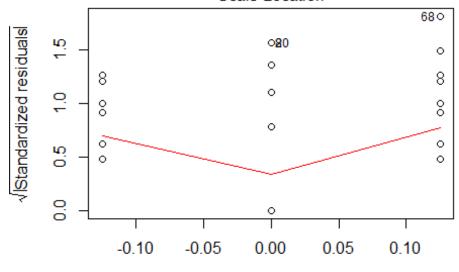
### Normalité : Gsucre



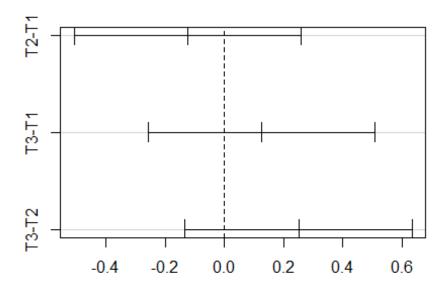
## [1] "Test de d'homogéneité des residus de la variable Gsucre"

### homogéneité: Gsucre

Scale-Location



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

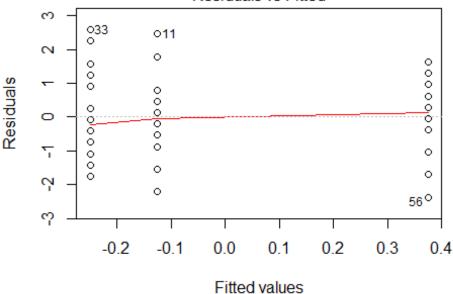


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Gamer"
##
                    Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                         5.25
                                 2.625
                                         2.36 0.102
                    69
                        76.75
                                1.112
## [1] "Test d'indépendance des residus de la variable Gamer"
##
   lag Autocorrelation D-W Statistic p-value
##
              0.1190282
                             1.759908
##
   Alternative hypothesis: rho != 0
```

### Indépendance : Gamer

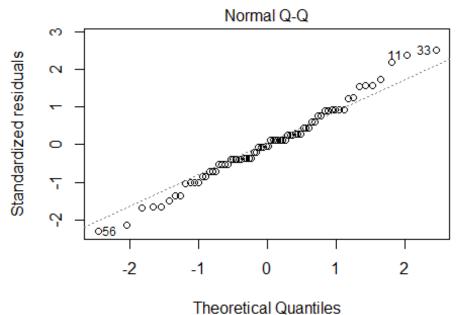
Residuals vs Fitted



aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Gamer"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.98674, p-value = 0.6527
```

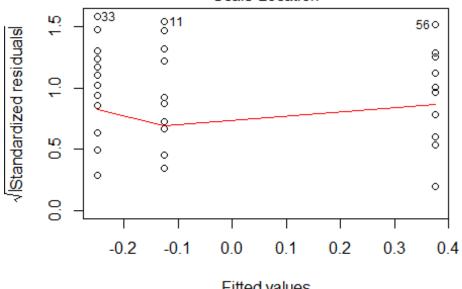
### Normalité : Gamer



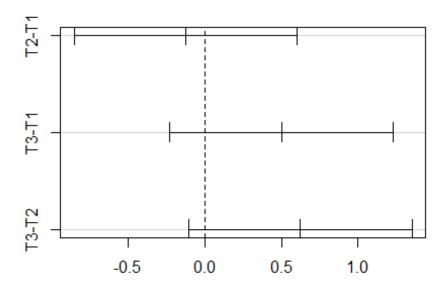
## [1] "Test de d'homogéneité des residus de la variable Gamer"

### homogéneité : Gamer

Scale-Location



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

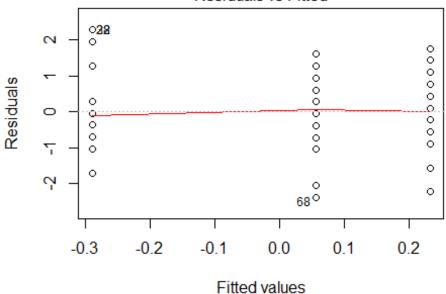


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Fagreable"
##
                    Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                         3.24
                                1.622
                                        1.282 0.284
## Residuals
                    67
                        84.76
                                1.265
## 2 observations deleted due to missingness
## [1] "Test d'indépendance des residus de la variable Fagreable"
   lag Autocorrelation D-W Statistic p-value
      1
##
              -0.177589
                             2.320366
   Alternative hypothesis: rho != 0
```

### Indépendance : Fagreable

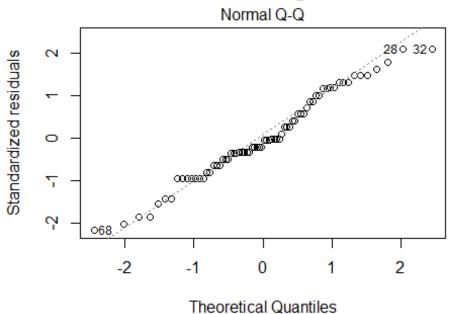
Residuals vs Fitted



aov(tableau[[i]] ~ tableau\$Tapenade)

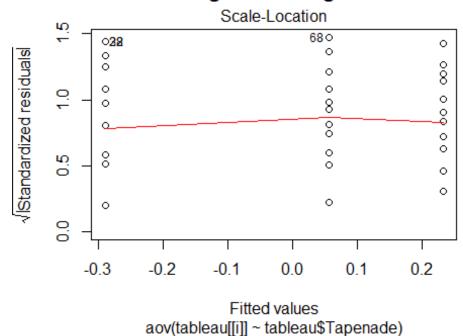
```
## NULL
## [1] "Test de normalité des residus de la variable Fagreable"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.97738, p-value = 0.2358
```

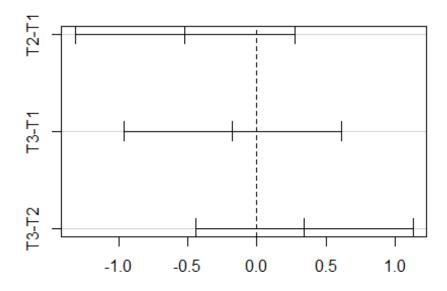
### Normalité : Fagreable



## [1] "Test de d'homogéneité des residus de la variable Fagreable"

### homogéneité : Fagreable



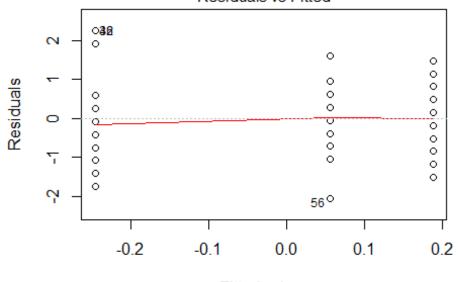


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Fintensite"
##
                    Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                         2.29
                               1.1433
                                        1.444 0.243
## Residuals
                    67
                        53.05
                              0.7917
## 2 observations deleted due to missingness
## [1] "Test d'indépendance des residus de la variable Fintensite"
##
   lag Autocorrelation D-W Statistic p-value
##
      1
              0.1597055
                             1.680135
##
   Alternative hypothesis: rho != 0
```

### Indépendance : Fintensite

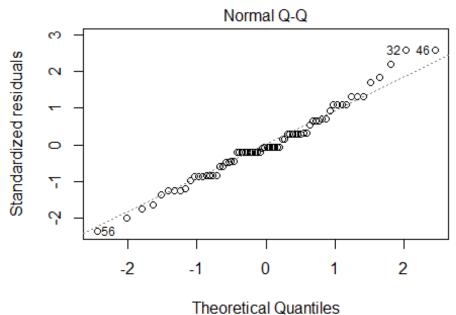
Residuals vs Fitted



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Fintensite"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.97938, p-value = 0.3021
```

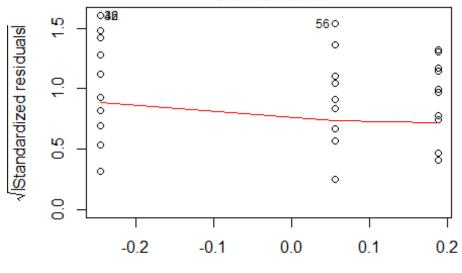
### Normalité : Fintensite



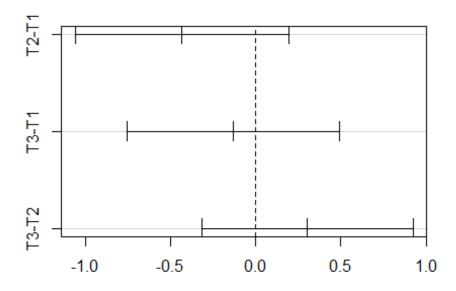
## [1] "Test de d'homogéneité des residus de la variable Fintensite"

### homogéneité: Fintensite

Scale-Location



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

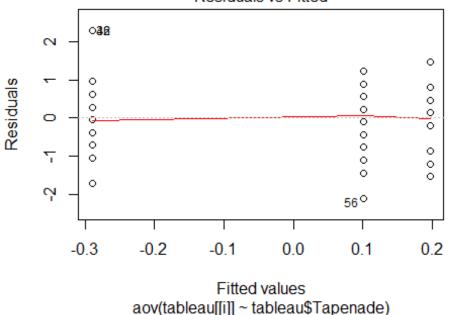


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Fpersistance"
##
                    Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                         3.02 1.5113
                                        1.809 0.172
## Residuals
                    65
                        54.31 0.8355
## 4 observations deleted due to missingness
## [1] "Test d'indépendance des residus de la variable Fpersistance"
   lag Autocorrelation D-W Statistic p-value
##
      1
              0.2168063
                             1.554324
   Alternative hypothesis: rho != 0
```

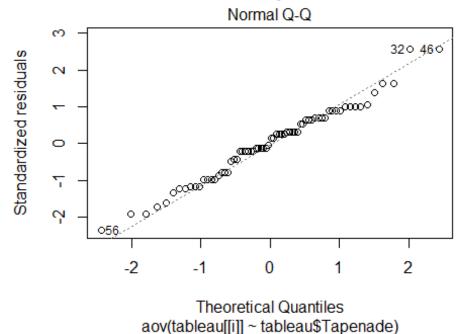
### Indépendance : Fpersistance

Residuals vs Fitted



```
## NULL
## [1] "Test de normalité des residus de la variable Fpersistance"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.98275, p-value = 0.4685
```

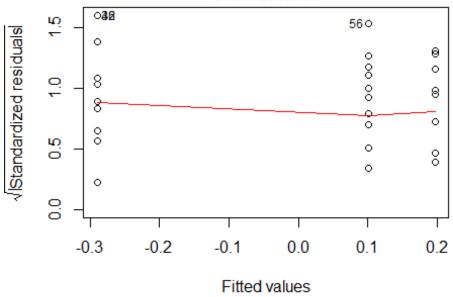
### Normalité : Fpersistance



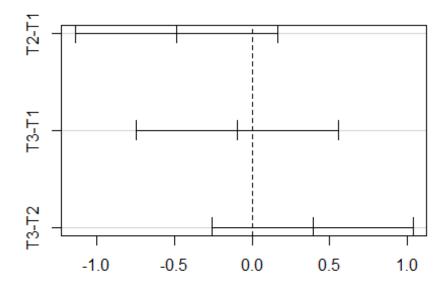
## [1] "Test de d'homogéneité des residus de la variable Fpersistance"

### homogéneité : Fpersistance

Scale-Location



## aov(tableau[[i]] ~ tableau\$Tapenade)

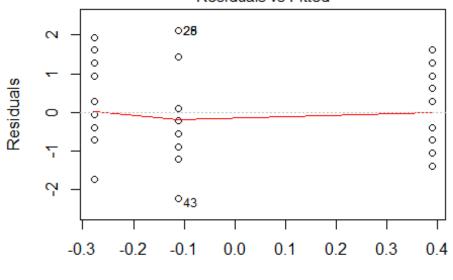


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Fnote"
                   Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                        5.78
                                2.889
                                       2.424 0.096 .
## Residuals
                       82.22
                    69
                                1.192
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Fnote"
   lag Autocorrelation D-W Statistic p-value
##
##
             -0.1098348
                            2.216892
##
   Alternative hypothesis: rho != 0
```

### Indépendance : Fnote

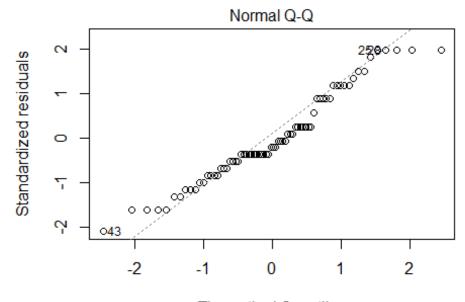
Residuals vs Fitted



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Fnote"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.9589, p-value = 0.01915
```

### Normalité: Fnote

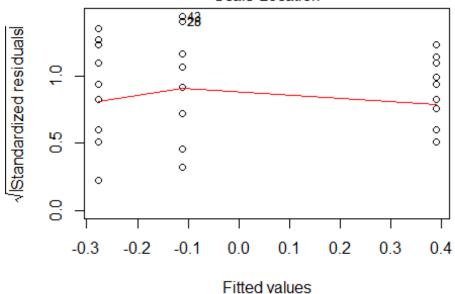


Theoretical Quantiles aov(tableau[[i]] ~ tableau\$Tapenade)

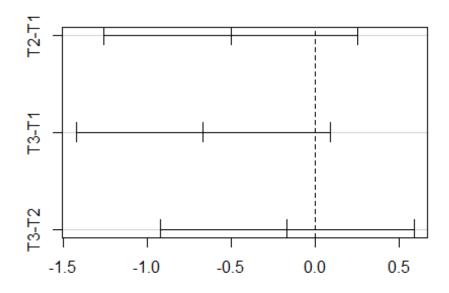
## [1] "Test de d'homogéneité des residus de la variable Fnote"

### homogéneité: Fnote

Scale-Location



# aov(tableau[[i]] ~ tableau\$Tapenade)

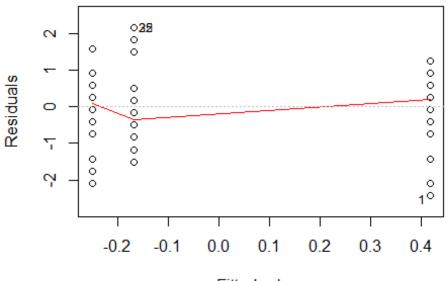


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Fharmonie"
                   Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                        6.33
                                3.167
                                       3.136 0.0497 *
## Residuals
                       69.67
                               1.010
                    69
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Fharmonie"
   lag Autocorrelation D-W Statistic p-value
##
##
             -0.1860048
                            2.287281
##
   Alternative hypothesis: rho != 0
```

### Indépendance : Fharmonie

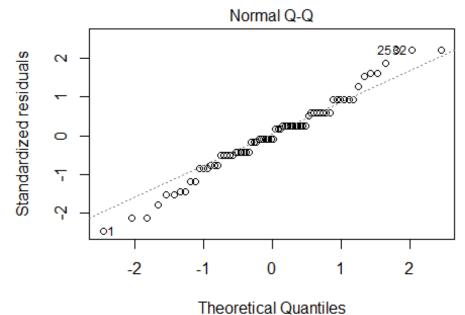
Residuals vs Fitted



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

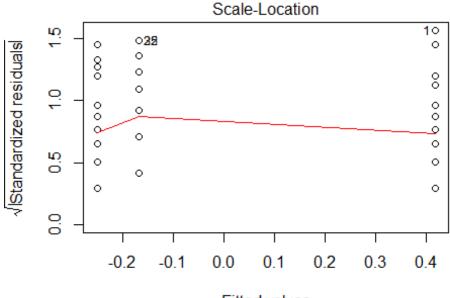
```
## NULL
## [1] "Test de normalité des residus de la variable Fharmonie"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.98032, p-value = 0.32
```

### Normalité : Fharmonie

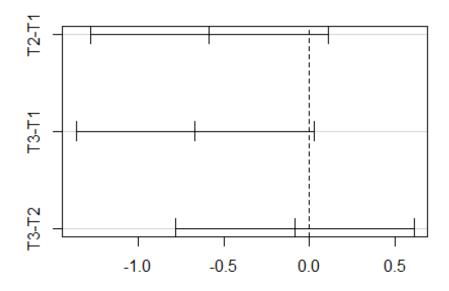


## [1] "Test de d'homogéneité des residus de la variable Fharmonie"

### homogéneité: Fharmonie



# Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

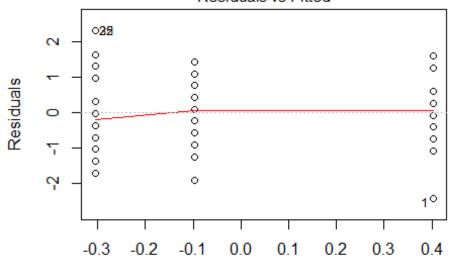


Differences in mean levels of tableau\$Tapenade

```
## NULL
## [1] "ANOVA I pour la variable Farome"
                   Df Sum Sq Mean Sq F value Pr(>F)
## tableau$Tapenade 2
                                       3.448 0.0374 *
                        6.36
                                3.181
## Residuals
                      63.64
                               0.922
                    69
##
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Farome"
  lag Autocorrelation D-W Statistic p-value
##
##
             -0.1300318
                            2.169195
  Alternative hypothesis: rho != 0
##
```

### Indépendance : Farome

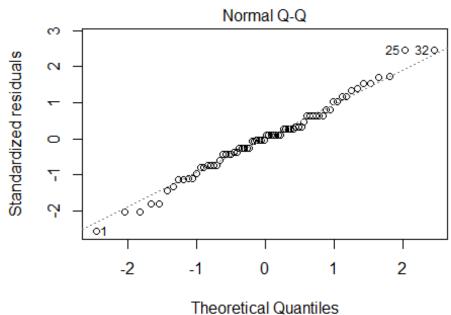
Residuals vs Fitted



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

```
## NULL
## [1] "Test de normalité des residus de la variable Farome"
##
## Shapiro-Wilk normality test
##
## data: residuals(anov)
## W = 0.98831, p-value = 0.7478
```

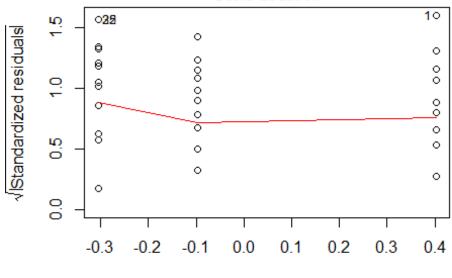
### Normalité: Farome



## [1] "Test de d'homogéneité des residus de la variable Farome"

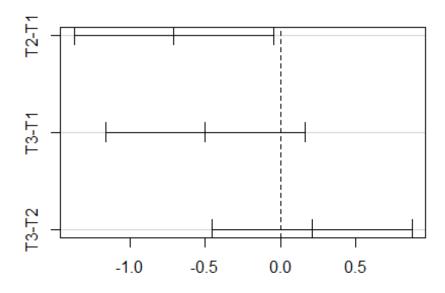
### homogéneité: Farome

Scale-Location



Fitted values aov(tableau[[i]] ~ tableau\$Tapenade)

### 95% family-wise confidence level



Differences in mean levels of tableau\$Tapenade

## NULL

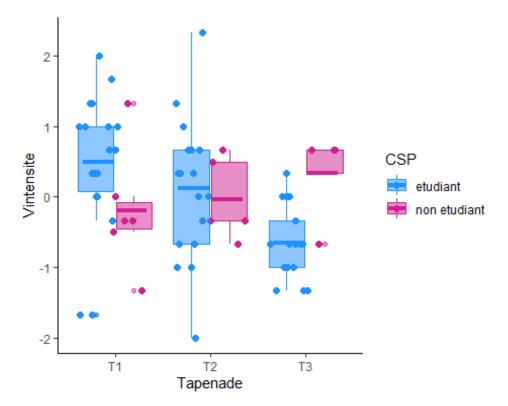
#### 6 ANOVA 2 facteur+tuckey

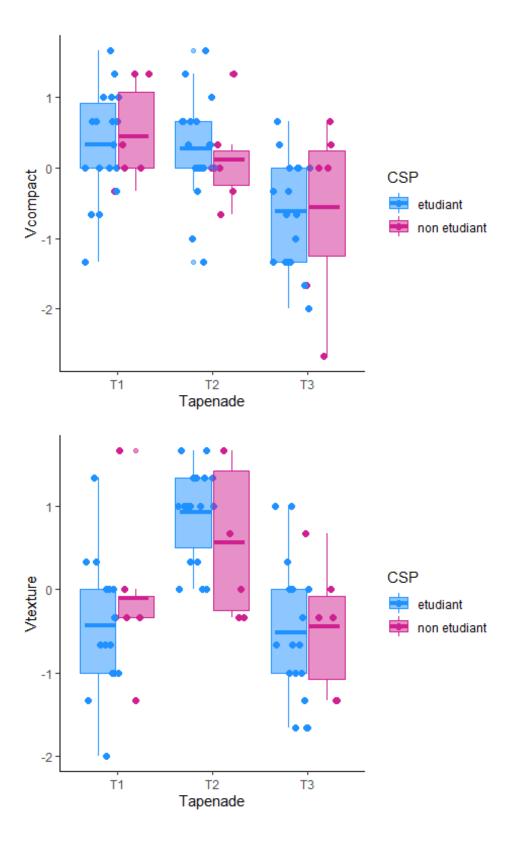
#Verifier qu'on peut appliquer une ANOVA 2

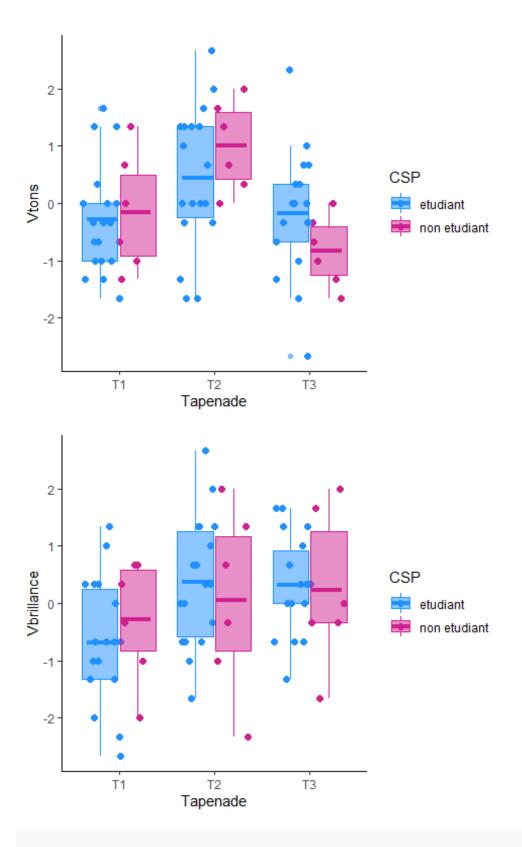
## Normalite: vérifier tout a fait en haut et nous avons constater que la majorité des données etait normalisése

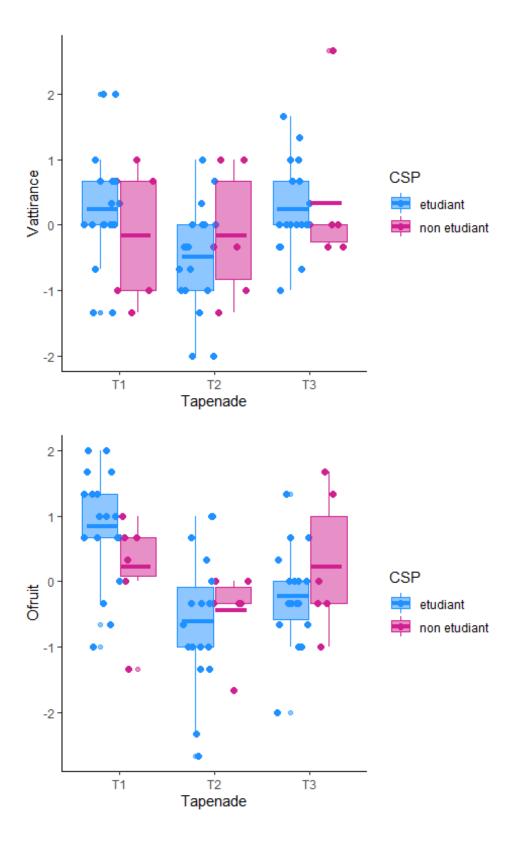
## L'homoscédasticité : c'est le cas pour l'égalité des variables car déja verifiée pré cédemment

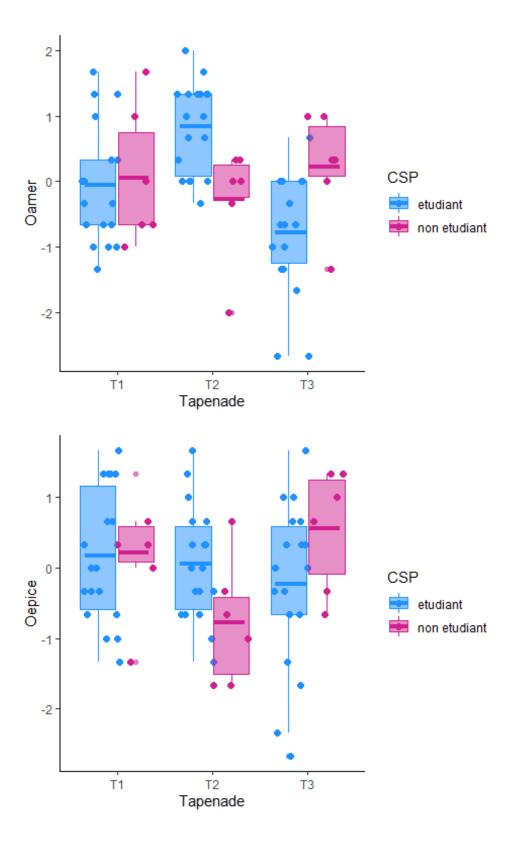
```
# Modele s'écrit classiquement
## Yijk = \mu + ai + bi + gij + Eijk
## Hypothéses
### HO_A:la tapenade a un effet sur les notes
### HO_B:le CSP a un effet sur les notes
### HO_AB: il y'ainteraction entre la tapenade et le CSP
### H1: hypothése alternative(à tester)
# Représentation des données
for(i in 12:37){
  print(ggplot(tableau, aes(x=Tapenade, y=tableau[[i]], colour=CSP, fill=CSP))+
        geom_point(position=position_jitterdodge(dodge.width=0.7), size=2) +
        geom_boxplot(alpha=0.5, position = position_dodge(width=0.8), fatten=NULL)+
        scale_colour_manual(values=c(c("#1E90FF", "#D02090", "#6FEB5D", "#FFFFFF")))+
        scale_fill_manual(values=c("#1E90FF", "#D02090", "#6FEB5D", "#FFFFFF"))+
        stat_summary(fun.y = mean, geom = "errorbar", aes(ymax = ..y.., ymin = ..y..),
       width=0.65, size = 1.5, linetype = "solid", position = position_dodge(width=0.7))+
       ylab(colnames(tableau[i]))+
       heme_classic())
}
```

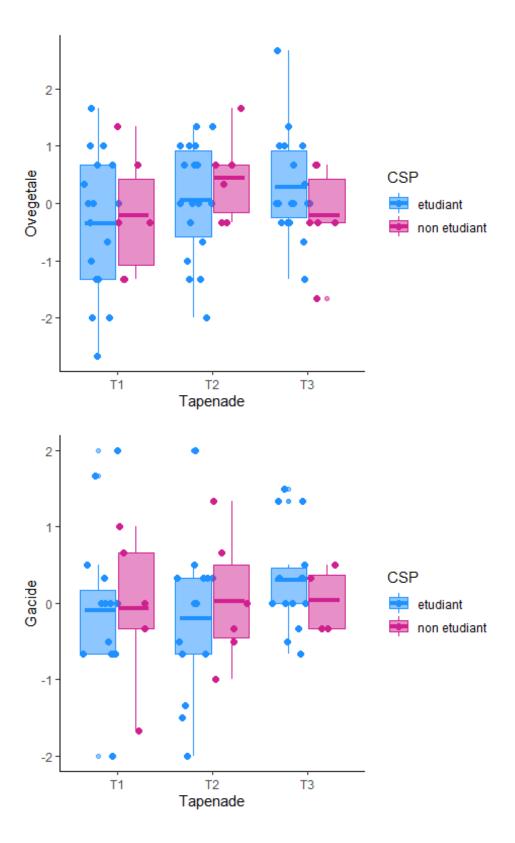


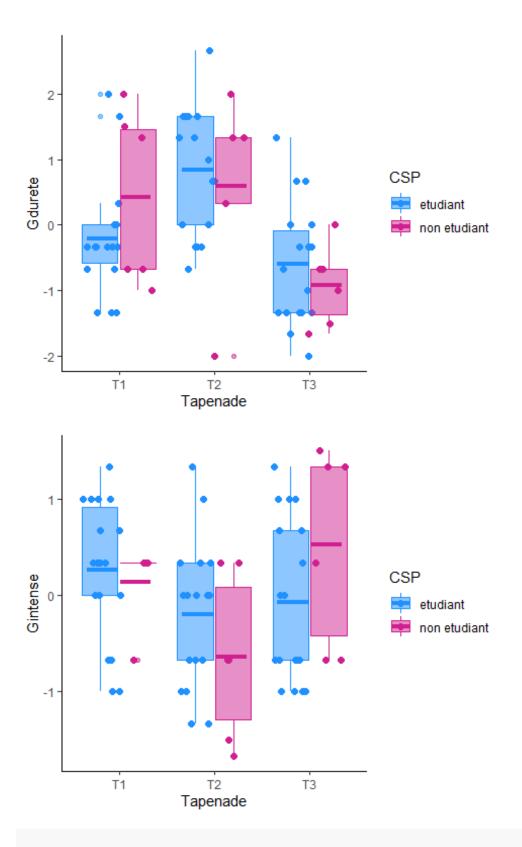


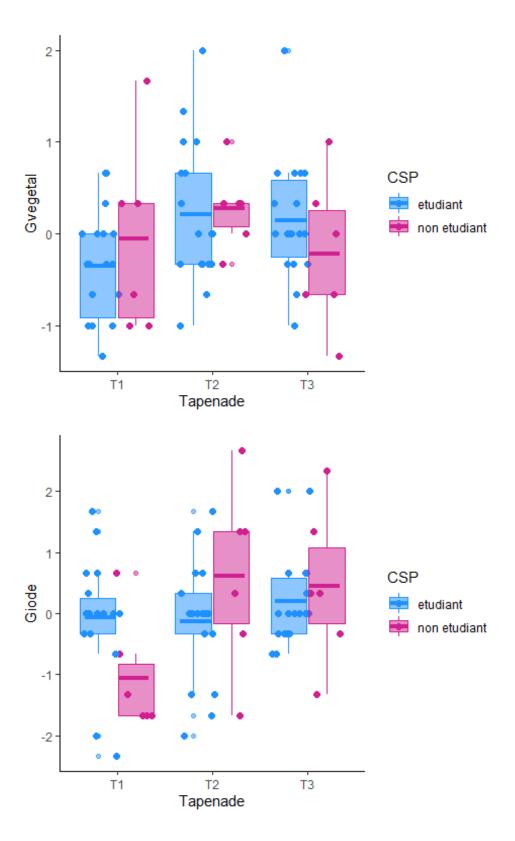


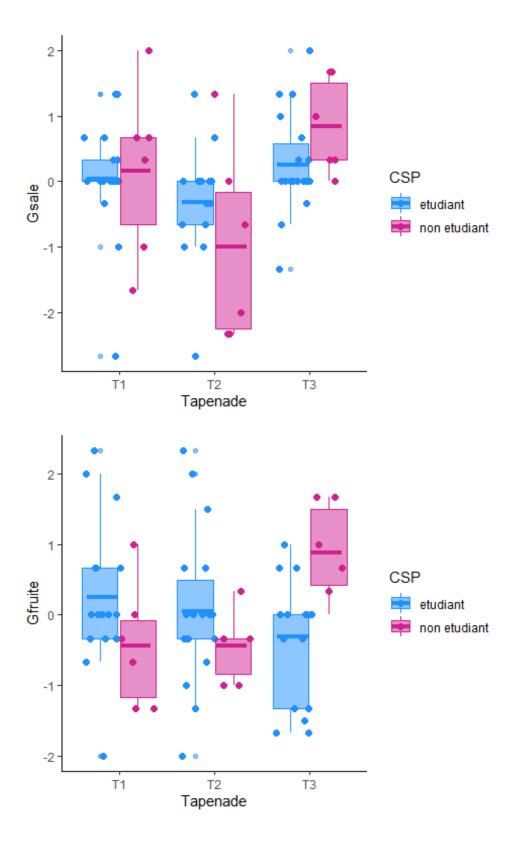


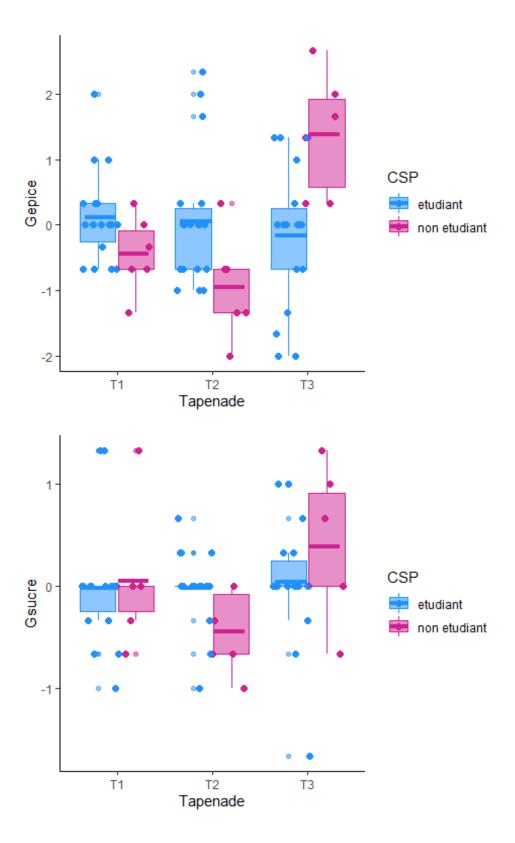


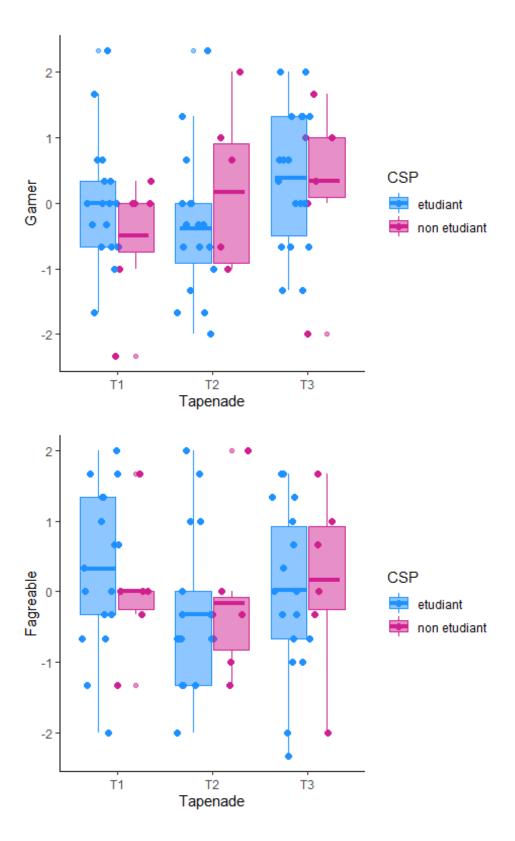


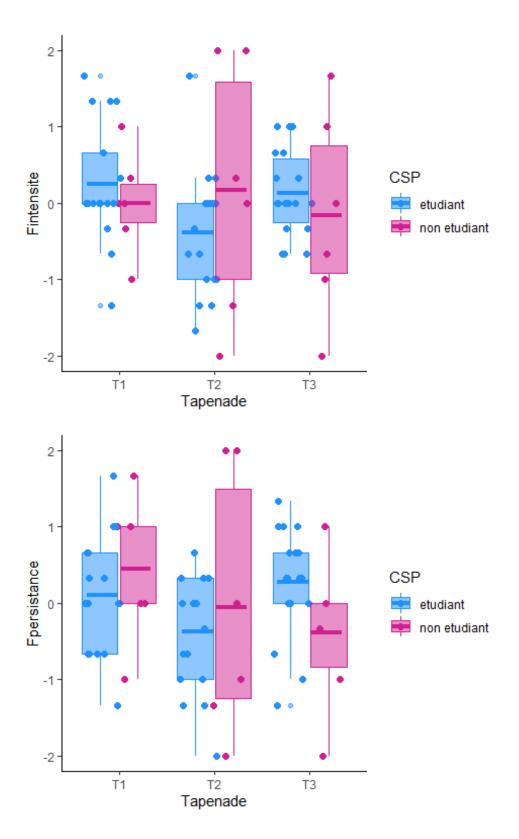


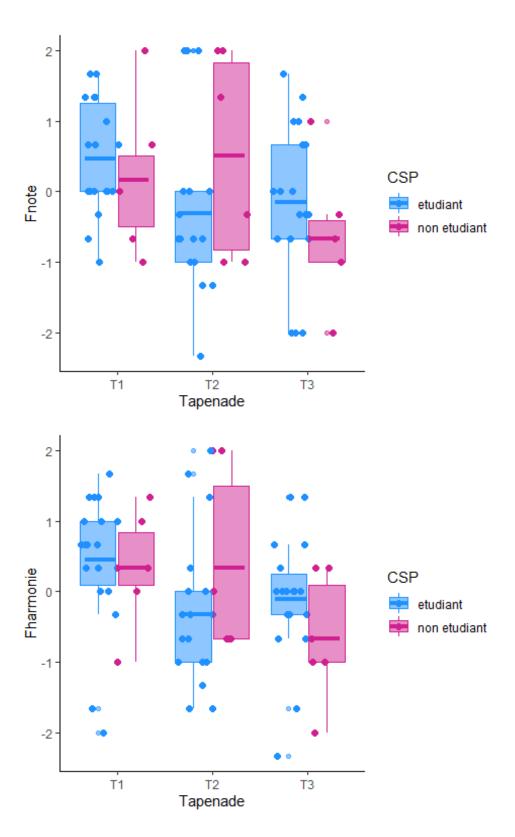


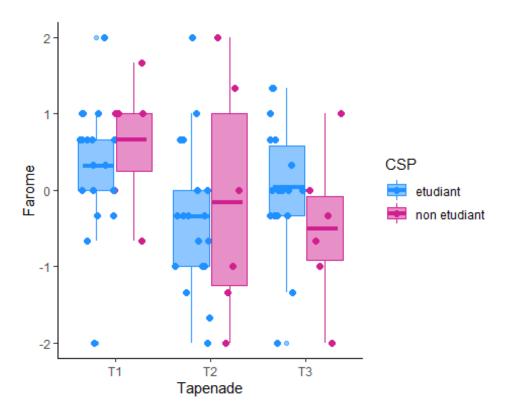










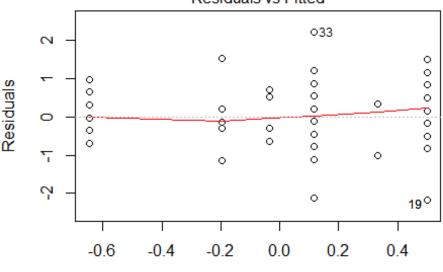


```
# Réalisation de l'ANOVA à 2 facteurs et Visualisation des résultats
## créé une variable "grp" correspondant au croisement des modalités des deux facteurs,
grâce à la fonction "interaction".
group = tableau$grp = interaction(tableau$Tapenade, tableau$CSP, sep=" ")
 for (i in 12:37) {
   mod1 = lm(tableau[[i]]~ Tapenade * CSP, contrasts = list(Tapenade=contr.sum, CSP=con
tr.sum), data=tableau)
res = Anova(mod1, type = 3)
verif indep = durbinWatsonTest(mod1) # permet de vérifier l'indépendance
verif_norm = shapiro.test(residuals(mod1)) # permet de vérifier la normalité
print(paste("ANOVA pour la variable",colnames(tableau)[i]))
   print(res)
print(paste("Test d'indépendance des residus de la variable",colnames(tableau)[i]))
   print(verif indep)
    #x11()
    print(plot(mod1,1,main = paste("Indépendance : ",colnames(tableau)[i])))# Visualisa
tion de l'indépendance
print(paste("Test de normalité des residus de la variable",colnames(tableau)[i]))
   print(verif norm)
   #x11()
    plot(mod1,2,main = paste("Normalité : ",colnames(tableau)[i])) # Visualisation de L
a normalité
print(paste("Test de d'homogéneité des residus de la variable",colnames(tableau)[i]))
    #x11()
    plot(mod1,3, main = paste("homogéneité : ",colnames(tableau)[i])) # Visualisation d
e l'homogéneité
 }
```

```
## [1] "ANOVA pour la variable Vintensite"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
##
                Sum Sq Df F value Pr(>F)
## (Intercept)
                 0.007
                       1 0.0102 0.91995
                 0.726 2
                          0.5035 0.60690
## Tapenade
## CSP
                 0.023 1
                          0.0320 0.85863
## Tapenade:CSP 5.346 2
                           3.7083 0.03021 *
## Residuals
                43.970 61
## ---
## Signif. codes:
                   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Vintensite"
    lag Autocorrelation D-W Statistic p-value
##
             -0.0192213
                             2.029924
##
  Alternative hypothesis: rho != 0
```

### Indépendance : Vintensite

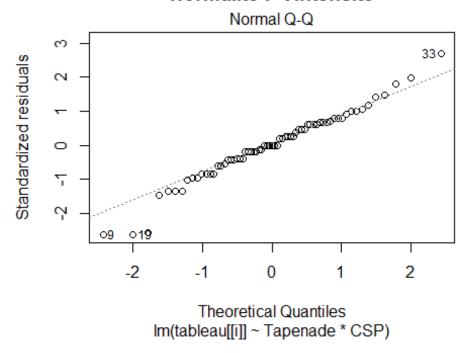




Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

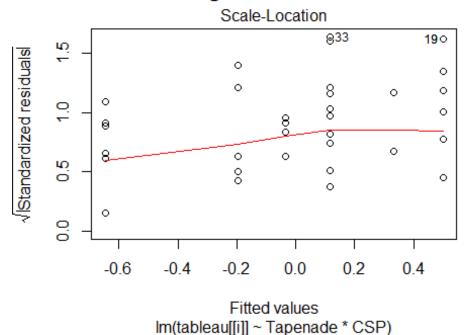
```
## NULL
## [1] "Test de normalité des residus de la variable Vintensite"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.97068, p-value = 0.1144
```

#### Normalité : Vintensite



## [1] "Test de d'homogéneité des residus de la variable Vintensite"

### homogéneité : Vintensite



```
## [1] "ANOVA pour la variable Vcompact"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value
##
                                     Pr(>F)
## (Intercept)
                 0.000
                              0.00 1.000000
                        1
## Tapenade
                        2
                 9.528
                              7.35 0.001313 **
## CSP
                       1
                 0.000
                              0.00 1.000000
```

```
## Tapenade:CSP 0.194 2 0.15 0.861001

## Residuals 42.778 66

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1

## [1] "Test d'indépendance des residus de la variable Vcompact"

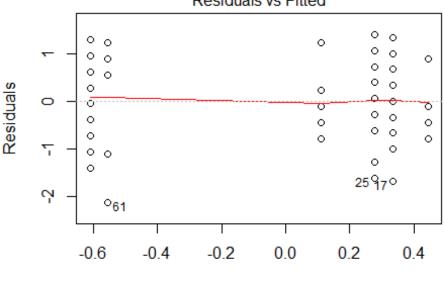
## lag Autocorrelation D-W Statistic p-value

## 1 0.2507215 1.487229 0.012

## Alternative hypothesis: rho != 0
```

### Indépendance : Vcompact

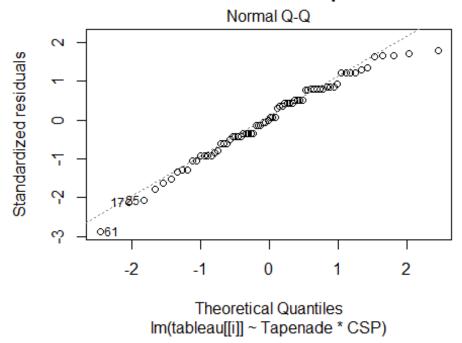
#### Residuals vs Fitted



Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

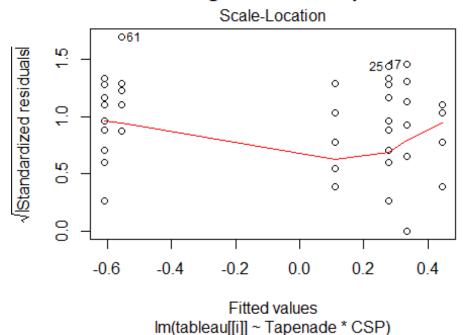
```
## NULL
## [1] "Test de normalité des residus de la variable Vcompact"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.98006, p-value = 0.31
```

### Normalité: Vcompact



## [1] "Test de d'homogéneité des residus de la variable Vcompact"

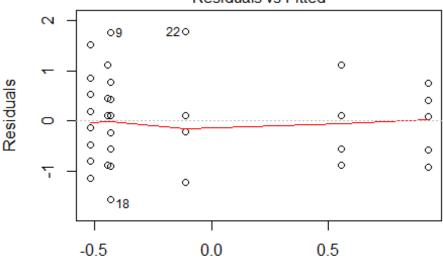
### homogéneité : Vcompact



```
## [1] "ANOVA pour la variable Vtexture"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value
##
                                      Pr(>F)
## (Intercept)
                 0.001
                       1 0.0014
                                      0.9699
## Tapenade
                       2 12.8653 1.962e-05 ***
                15.354
## CSP
                 0.001
                       1 0.0014
                                      0.9699
```

```
## Tapenade:CSP 1.096 2 0.9186 0.4042
## Residuals 38.787 65
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Vtexture"
## lag Autocorrelation D-W Statistic p-value
## 1 0.1201159 1.751563 0.16
## Alternative hypothesis: rho != 0
```

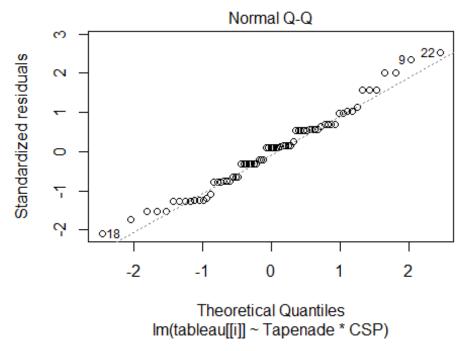
### Indépendance : Vtexture



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

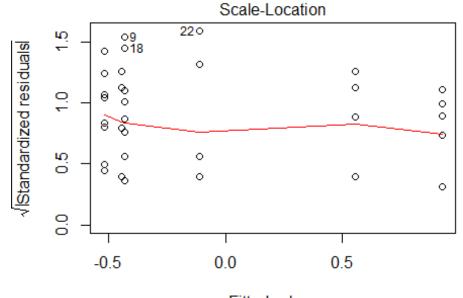
```
## NULL
## [1] "Test de normalité des residus de la variable Vtexture"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.97709, p-value = 0.2198
```

#### Normalité: Vtexture



## [1] "Test de d'homogéneité des residus de la variable Vtexture"

### homogéneité: Vtexture

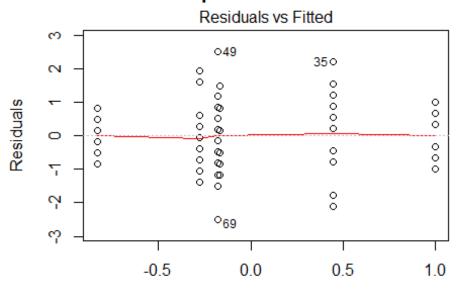


Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Vtons"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value
##
                                    Pr(>F)
## (Intercept)
                       1 0.0001 0.991008
                 0.000
## Tapenade
                       2
                          6.6017 0.002454 **
                14.800
## CSP
                 0.000 1 0.0001 0.991008
```

```
## Tapenade:CSP 3.357 2 1.4976 0.231283
## Residuals 72.859 65
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Vtons"
## lag Autocorrelation D-W Statistic p-value
## 1 0.1227015 1.752094 0.162
## Alternative hypothesis: rho != 0
```

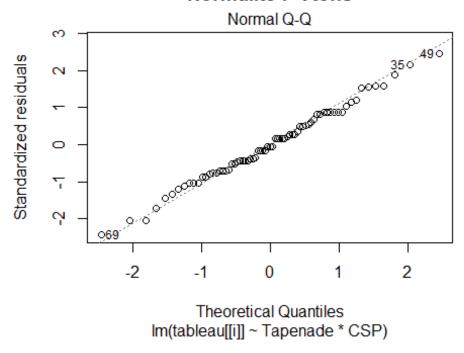
### Indépendance : Vtons



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

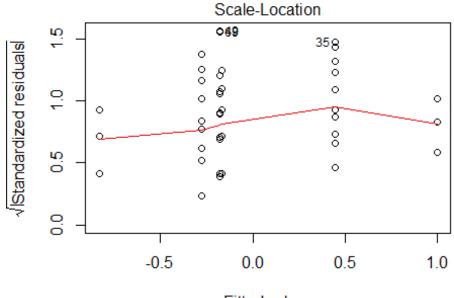
```
## NULL
## [1] "Test de normalité des residus de la variable Vtons"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.99211, p-value = 0.9389
```

#### Normalité: Vtons



## [1] "Test de d'homogéneité des residus de la variable Vtons"

### homogéneité: Vtons



Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Vbrillance"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                       1 0.0000 1.00000
                 0.000
## Tapenade
                        2
                 6.287
                           2.5347 0.08698
## CSP
                       1
                 0.000
                          0.0000 1.00000
```

```
## Tapenade:CSP 1.231 2 0.4965 0.61092
## Residuals 81.852 66
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Vbrillance"
## lag Autocorrelation D-W Statistic p-value
## 1 -0.1473521 2.288361 0.356
## Alternative hypothesis: rho != 0
```

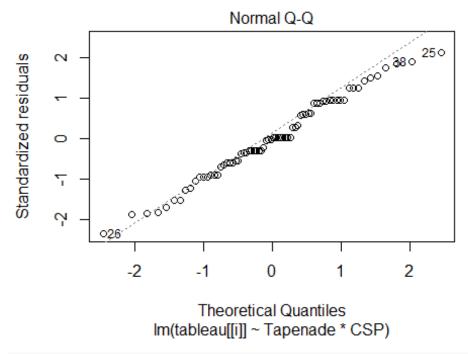
### Indépendance : Vbrillance

#### Residuals vs Fitted 250 0 0 0 0 ŏ 0 0 0 0 0 0 0 0 0 0 0 0 Ō 0 Ö 0 0 0 0 0 ō 0 0 47° 026 0.4 -0.6-0.4-0.20.0 0.2

Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

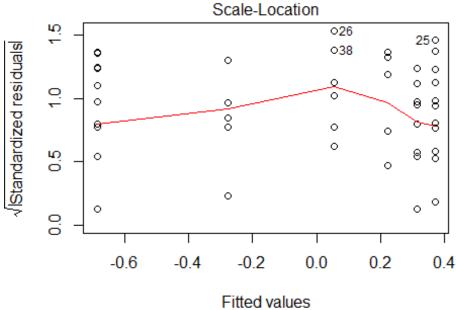
```
## NULL
## [1] "Test de normalité des residus de la variable Vbrillance"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.98458, p-value = 0.5253
```

#### Normalité : Vbrillance



## [1] "Test de d'homogéneité des residus de la variable Vbrillance"

### homogéneité : Vbrillance

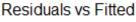


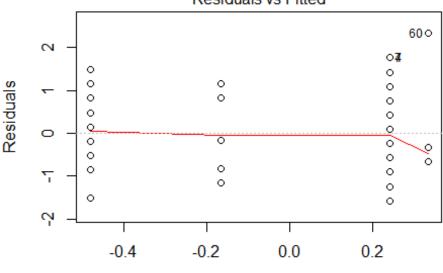
Fitted values
Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Vattirance"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                       1 0.0000 1.0000
                 0.000
## Tapenade
                        2
                 3.398
                           2.2395 0.1145
## CSP
                 0.000
                       1
                           0.0000 1.0000
```

```
## Tapenade:CSP 1.231 2 0.8116 0.4485
## Residuals 50.074 66
## [1] "Test d'indépendance des residus de la variable Vattirance"
## lag Autocorrelation D-W Statistic p-value
## 1 0.01082073 1.92772 0.602
## Alternative hypothesis: rho != 0
```

### Indépendance : Vattirance

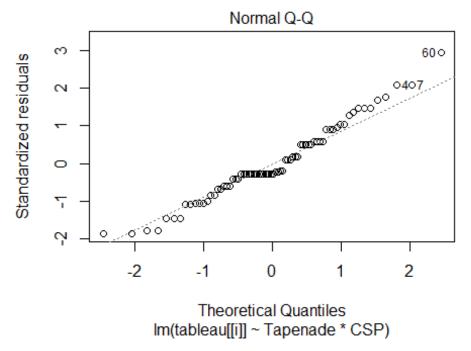




Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

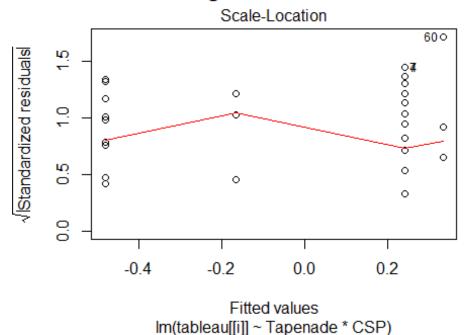
```
## NULL
## [1] "Test de normalité des residus de la variable Vattirance"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.97252, p-value = 0.1161
```

#### Normalité: Vattirance



## [1] "Test de d'homogéneité des residus de la variable Vattirance"

### homogéneité : Vattirance



```
## [1] "ANOVA pour la variable Ofruit"

## Anova Table (Type III tests)

##

## Response: tableau[[i]]

## Sum Sq Df F value Pr(>F)

## (Intercept) 0.000 1 0.0000 1.00000

## Tapenade 10.028 2 6.6037 0.00243 **

## CSP 0.000 1 0.00000 1.00000
```

```
## Tapenade:CSP 2.694 2 1.7744 0.17758

## Residuals 50.111 66

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1

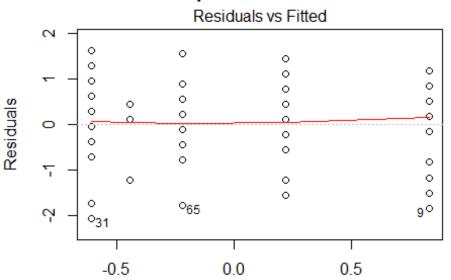
## [1] "Test d'indépendance des residus de la variable Ofruit"

## lag Autocorrelation D-W Statistic p-value

## 1 -0.0908475 2.138766 0.74

## Alternative hypothesis: rho != 0
```

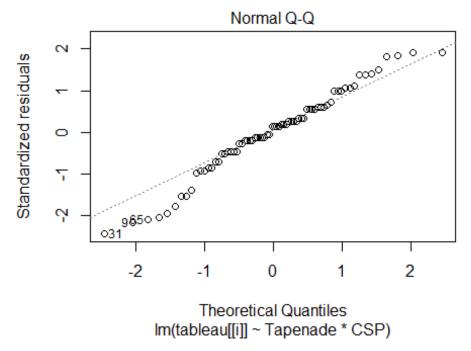
### Indépendance : Ofruit



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

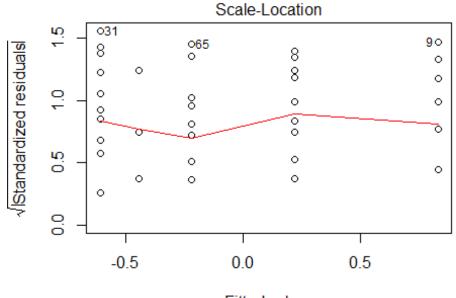
```
## NULL
## [1] "Test de normalité des residus de la variable Ofruit"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.97535, p-value = 0.1691
```

### Normalité: Ofruit



## [1] "Test de d'homogéneité des residus de la variable Ofruit"

### homogéneité : Ofruit

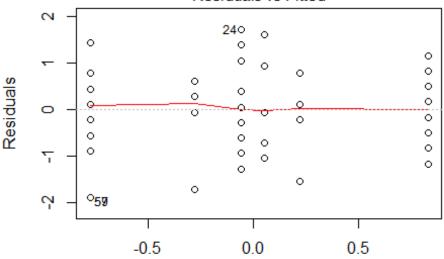


Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Oamer"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value
##
                                    Pr(>F)
## (Intercept)
                       1 0.0000 1.000000
                 0.000
## Tapenade
                        2
                 2.778
                           1.8665 0.162734
## CSP
                       1
                 0.000
                          0.0000 1.000000
```

```
## Tapenade:CSP 10.111 2 6.7941 0.002075 **
## Residuals
               49.111 66
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Oamer"
   lag Autocorrelation D-W Statistic p-value
##
            -0.0513449
                            2.096342
##
  Alternative hypothesis: rho != 0
```

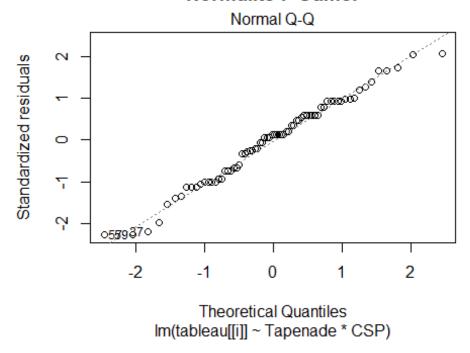
### Indépendance : Oamer



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

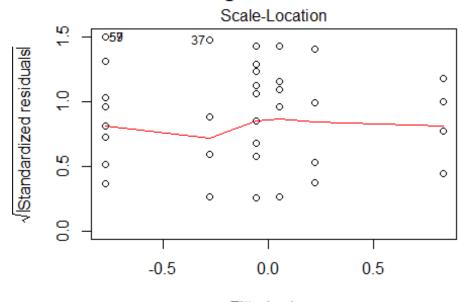
```
## [1] "Test de normalité des residus de la variable Oamer"
##
##
    Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.98347, p-value = 0.465
```

### Normalité : Oamer



## [1] "Test de d'homogéneité des residus de la variable Oamer"

### homogéneité : Oamer



Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Oepice"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                       1 0.0000 1.00000
                 0.000
## Tapenade
                        2
                 3.528
                           1.8947 0.15846
## CSP
                 0.000
                       1
                           0.0000 1.00000
```

```
## Tapenade:CSP 5.861 2 3.1478 0.04946 *

## Residuals 61.444 66

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1

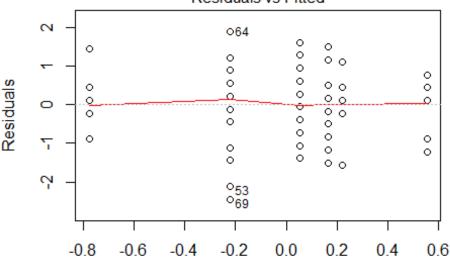
## [1] "Test d'indépendance des residus de la variable Oepice"

## lag Autocorrelation D-W Statistic p-value

## 1 -0.1883163 2.363321 0.228

## Alternative hypothesis: rho != 0
```

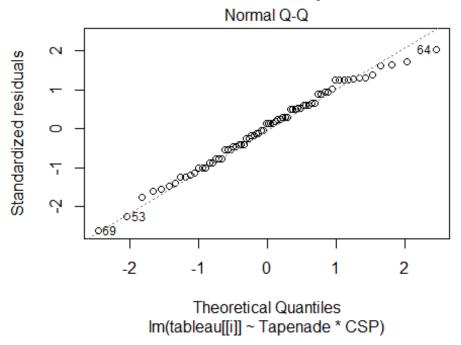
### Indépendance : Oepice



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

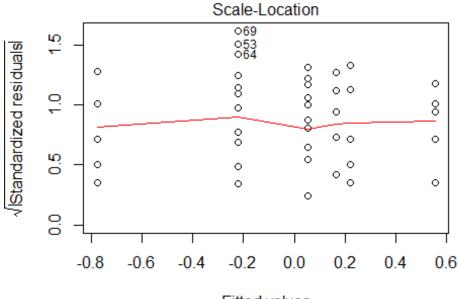
```
## NULL
## [1] "Test de normalité des residus de la variable Oepice"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.98714, p-value = 0.6769
```

### Normalité : Oepice



## [1] "Test de d'homogéneité des residus de la variable Oepice"

### homogéneité : Oepice

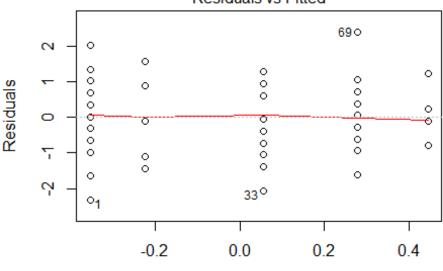


Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Ovegetale"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                 0.001
                       1 0.0006 0.9812
                       2
## Tapenade
                 2.606
                           1.2704 0.2876
## CSP
                 0.001
                       1
                          0.0006 0.9812
```

```
## Tapenade:CSP 1.881 2 0.9170 0.4048
## Residuals 66.660 65
## [1] "Test d'indépendance des residus de la variable Ovegetale"
## lag Autocorrelation D-W Statistic p-value
## 1 0.0342365 1.850062 0.318
## Alternative hypothesis: rho != 0
```

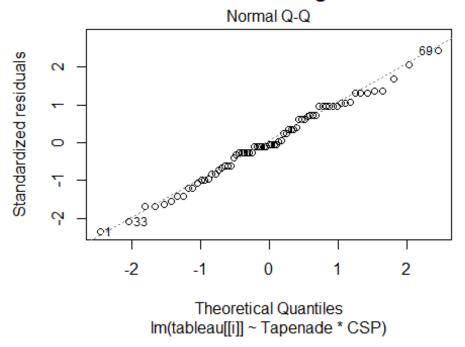
### Indépendance : Ovegetale



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

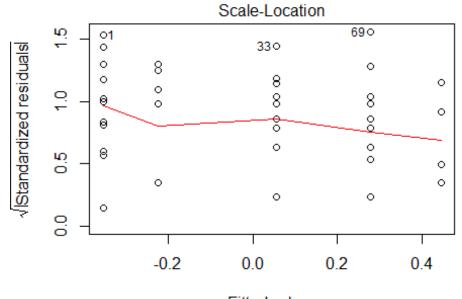
```
## NULL
## [1] "Test de normalité des residus de la variable Ovegetale"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.98978, p-value = 0.8374
```

### Normalité : Ovegetale



## [1] "Test de d'homogéneité des residus de la variable Ovegetale"

### homogéneité : Ovegetale

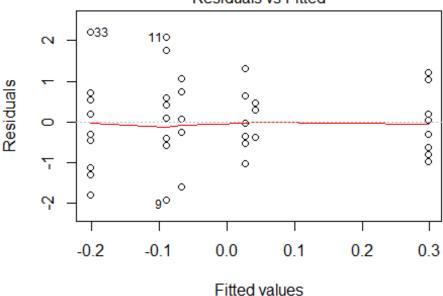


Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Gacide"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
## Sum Sq Df F value Pr(>F)
## (Intercept) 0.000 1 0.0001 0.9910
## Tapenade 0.571 2 0.3602 0.6993
## CSP 0.000 1 0.0000 0.9965
```

```
## Tapenade:CSP 0.422 2 0.2665 0.7671
## Residuals 41.201 52
## [1] "Test d'indépendance des residus de la variable Gacide"
## lag Autocorrelation D-W Statistic p-value
## 1 -0.2425706 2.467376 0.132
## Alternative hypothesis: rho != 0
```

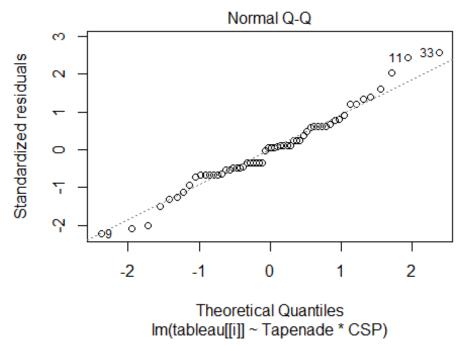
### Indépendance : Gacide



Im(tableau[[i]] ~ Tapenade \* CSP)

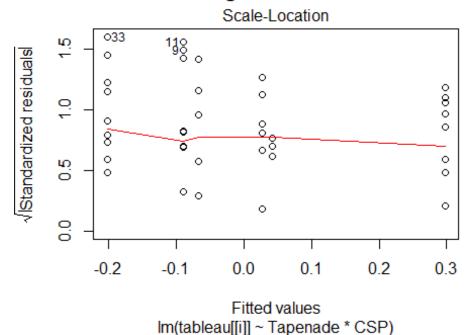
```
## NULL
## [1] "Test de normalité des residus de la variable Gacide"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.9774, p-value = 0.3504
```

#### Normalité : Gacide



## [1] "Test de d'homogéneité des residus de la variable Gacide"

### homogéneité : Gacide



```
## [1] "ANOVA pour la variable Gdurete"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value
##
                                     Pr(>F)
## (Intercept)
                       1 0.0312 0.8602478
                 0.031
                        2
## Tapenade
                18.496
                           9.4251 0.0002584 ***
## CSP
                 0.004 1 0.0041 0.9491748
```

```
## Tapenade:CSP 2.421 2 1.2336 0.2980756

## Residuals 62.797 64

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1

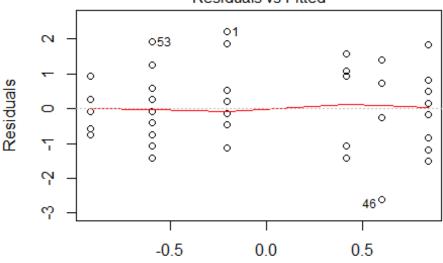
## [1] "Test d'indépendance des residus de la variable Gdurete"

## lag Autocorrelation D-W Statistic p-value

## 1 -0.1448941 2.203717 0.57

## Alternative hypothesis: rho != 0
```

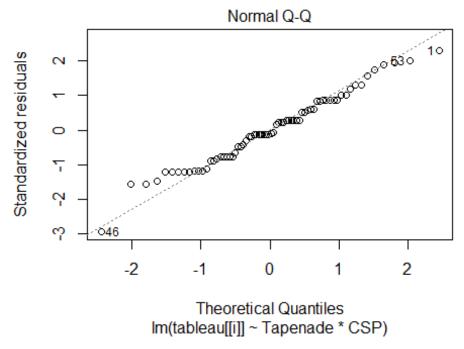
### Indépendance : Gdurete



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

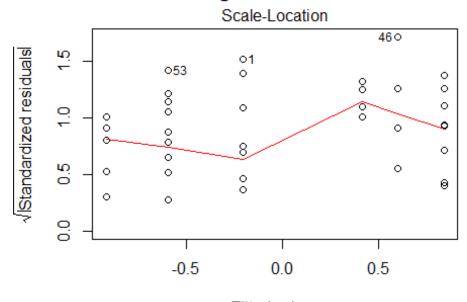
```
## NULL
## [1] "Test de normalité des residus de la variable Gdurete"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.98387, p-value = 0.5062
```

#### Normalité : Gdurete



## [1] "Test de d'homogéneité des residus de la variable Gdurete"

### homogéneité : Gdurete



Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Gintense"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
## Sum Sq Df F value Pr(>F)
## (Intercept) 0.000 1 0.0003 0.98636
## Tapenade 4.620 2 3.7275 0.02942 *
## CSP 0.002 1 0.0025 0.96015
```

```
## Tapenade:CSP 2.557 2 2.0628 0.13546

## Residuals 39.662 64

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1

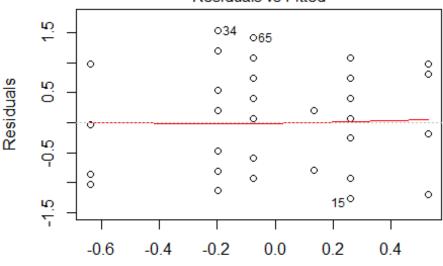
## [1] "Test d'indépendance des residus de la variable Gintense"

## lag Autocorrelation D-W Statistic p-value

## 1 0.416258 1.153511 0

## Alternative hypothesis: rho != 0
```

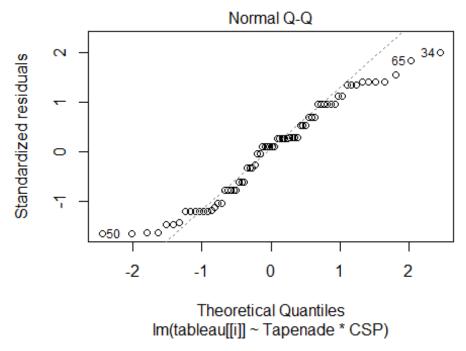
### Indépendance : Gintense



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

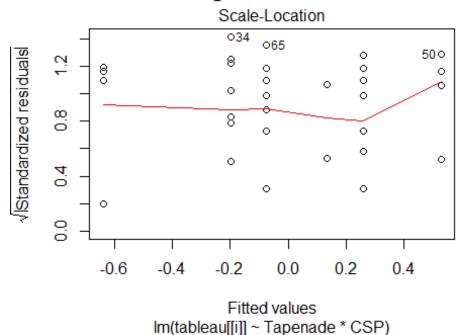
```
## NULL
## [1] "Test de normalité des residus de la variable Gintense"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.95671, p-value = 0.01653
```

#### Normalité : Gintense



## [1] "Test de d'homogéneité des residus de la variable Gintense"

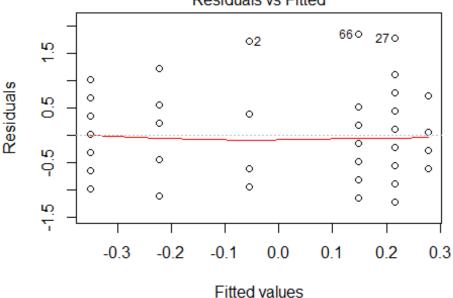
### homogéneité : Gintense



```
## [1] "ANOVA pour la variable Gvegetal"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                       1 0.0004 0.9837
                 0.000
## Tapenade
                 1.851
                        2
                           1.8156 0.1709
## CSP
                 0.000
                       1
                          0.0004 0.9837
```

```
## Tapenade:CSP 1.029 2 1.0093 0.3701
## Residuals 33.141 65
## [1] "Test d'indépendance des residus de la variable Gvegetal"
## lag Autocorrelation D-W Statistic p-value
## 1 0.07646187 1.842678 0.328
## Alternative hypothesis: rho != 0
```

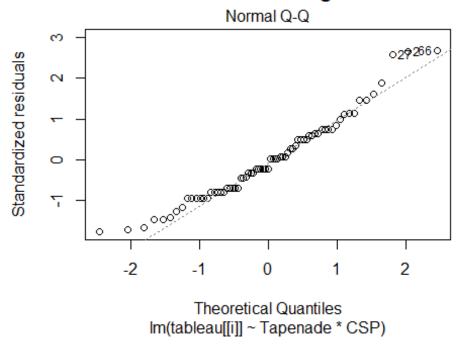
### Indépendance : Gvegetal



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

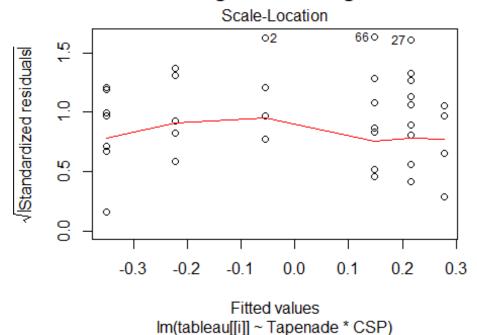
```
## NULL
## [1] "Test de normalité des residus de la variable Gvegetal"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.96512, p-value = 0.04569
```

### Normalité : Gvegetal



## [1] "Test de d'homogéneité des residus de la variable Gvegetal"

### homogéneité : Gvegetal



```
## [1] "ANOVA pour la variable Giode"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
## Sum Sq Df F value Pr(>F)
## (Intercept) 0.000 1 0.0001 0.99262
## Tapenade 8.628 2 4.2884 0.01781 *
## CSP 0.000 1 0.0001 0.99262
```

```
## Tapenade:CSP 7.079 2 3.5186 0.03541 *

## Residuals 65.390 65

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1

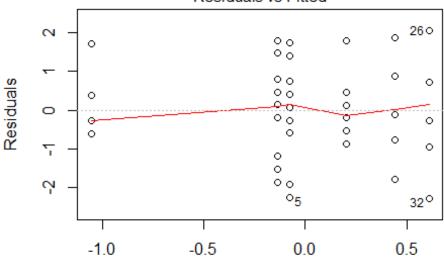
## [1] "Test d'indépendance des residus de la variable Giode"

## lag Autocorrelation D-W Statistic p-value

## 1 -0.1352088 2.269699 0.404

## Alternative hypothesis: rho != 0
```

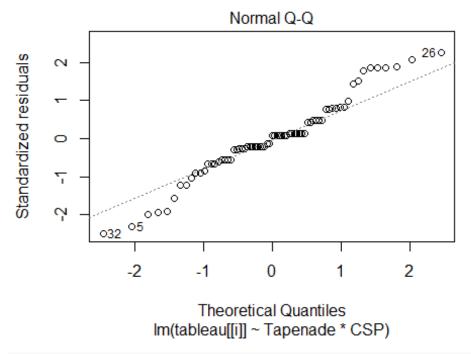
### Indépendance : Giode



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

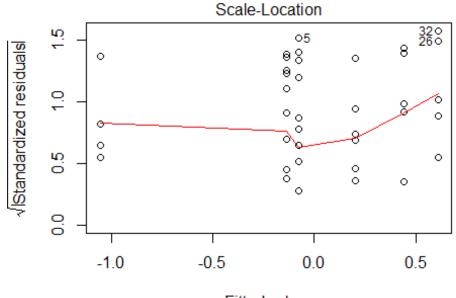
```
## NULL
## [1] "Test de normalité des residus de la variable Giode"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.9614, p-value = 0.02817
```

#### Normalité : Giode



## [1] "Test de d'homogéneité des residus de la variable Giode"

### homogéneité : Giode



Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Gsale"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value
##
                                    Pr(>F)
## (Intercept)
                       1 0.0005 0.981889
                 0.000
## Tapenade
                        2
                13.213
                           7.5655 0.001112 **
## CSP
                       1 0.0005 0.981889
                 0.000
```

```
## Tapenade:CSP 3.646 2 2.0878 0.132196

## Residuals 56.759 65

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1

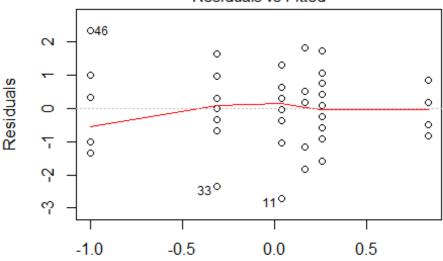
## [1] "Test d'indépendance des residus de la variable Gsale"

## lag Autocorrelation D-W Statistic p-value

## 1 0.07814604 1.8425 0.314

## Alternative hypothesis: rho != 0
```

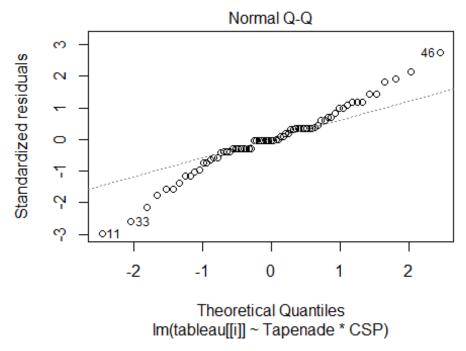
### Indépendance : Gsale



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

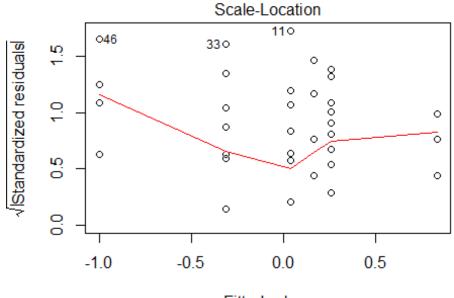
```
## NULL
## [1] "Test de normalité des residus de la variable Gsale"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.97134, p-value = 0.1038
```

#### Normalité : Gsale



## [1] "Test de d'homogéneité des residus de la variable Gsale"

### homogéneité : Gsale



Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Gfruite"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value
##
                                    Pr(>F)
## (Intercept)
                       1 0.0000 0.997213
                 0.000
## Tapenade
                        2
                 2.390
                           1.3338 0.270698
## CSP
                 0.000 1
                          0.0000 0.997213
```

```
## Tapenade:CSP 9.562 2 5.3364 0.007187 **

## Residuals 57.342 64

## ---

## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1

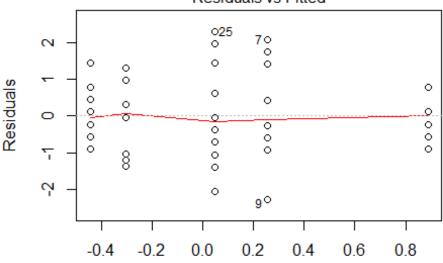
## [1] "Test d'indépendance des residus de la variable Gfruite"

## lag Autocorrelation D-W Statistic p-value

## 1 0.007492928 1.968592 0.688

## Alternative hypothesis: rho != 0
```

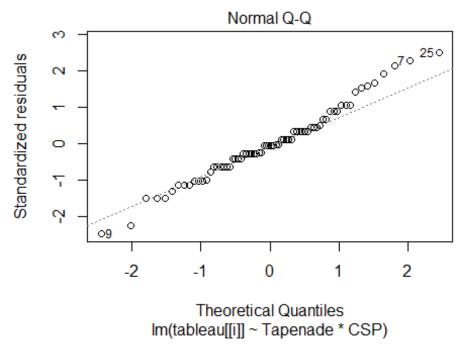
### Indépendance : Gfruite



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

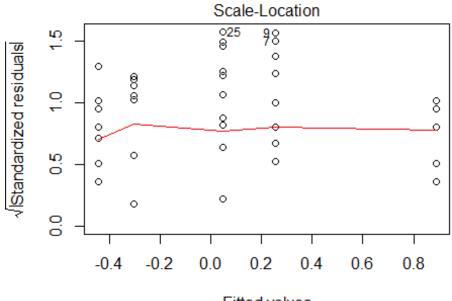
```
## NULL
## [1] "Test de normalité des residus de la variable Gfruite"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.98271, p-value = 0.446
```

#### Normalité : Gfruite



## [1] "Test de d'homogéneité des residus de la variable Gfruite"

### homogéneité : Gfruite

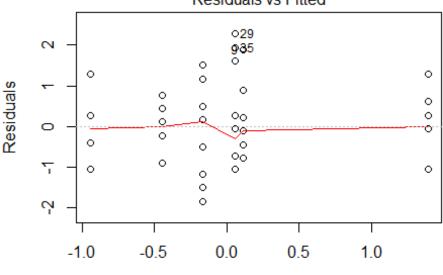


Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Gepice"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value
##
                                     Pr(>F)
## (Intercept)
                       1 0.0000 1.0000000
                 0.000
## Tapenade
                        2
                10.778
                           6.6136 0.0024104 **
## CSP
                 0.000
                       1
                          0.0000 1.0000000
```

```
## Tapenade:CSP 16.778 2 10.2955 0.0001283 ***
## Residuals 53.778 66
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Gepice"
## lag Autocorrelation D-W Statistic p-value
## 1 0.03380395 1.931646 0.52
## Alternative hypothesis: rho != 0
```

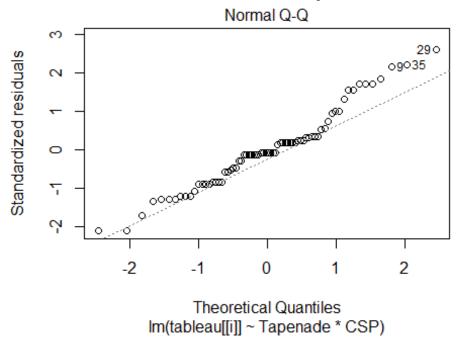
### Indépendance : Gepice



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

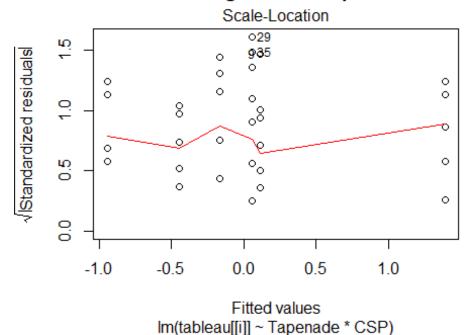
```
## NULL
## [1] "Test de normalité des residus de la variable Gepice"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.96457, p-value = 0.04023
```

### Normalité : Gepice



## [1] "Test de d'homogéneité des residus de la variable Gepice"

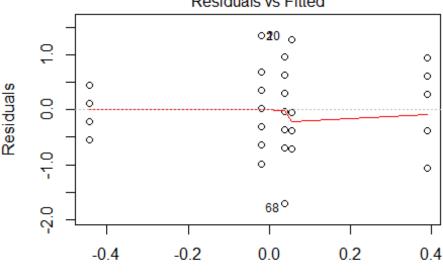
### homogéneité : Gepice



```
## [1] "ANOVA pour la variable Gsucre"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                 Sum Sq Df F value Pr(>F)
##
## (Intercept)
                 0.0000
                        1 0.0000 1.00000
## Tapenade
                 1.7870
                         2
                            2.9706 0.05817
## CSP
                 0.0000 1
                           0.0000 1.00000
```

```
## Tapenade:CSP 1.3981 2 2.3242 0.10583
## Residuals
               19.8519 66
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Gsucre"
  lag Autocorrelation D-W Statistic p-value
##
            -0.2729236
                            2.453721
##
  Alternative hypothesis: rho != 0
```

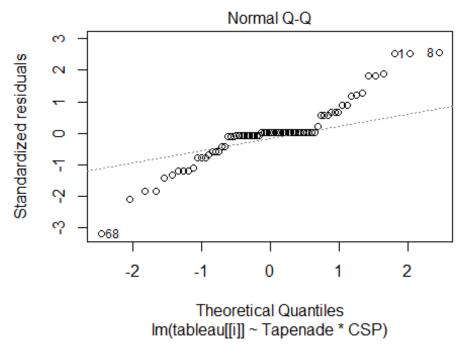
### Indépendance : Gsucre



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

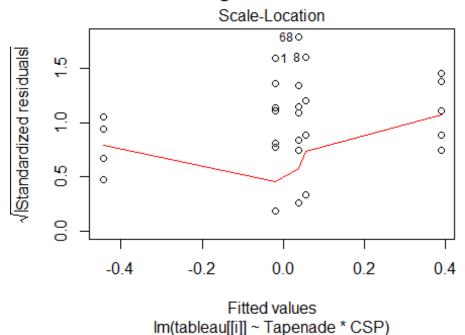
```
## [1] "Test de normalité des residus de la variable Gsucre"
##
##
   Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.91465, p-value = 0.0001245
```

#### Normalité : Gsucre



## [1] "Test de d'homogéneité des residus de la variable Gsucre"

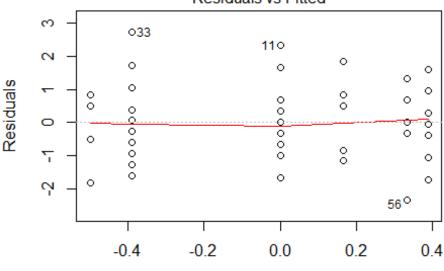
### homogéneité : Gsucre



```
## [1] "ANOVA pour la variable Gamer"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                       1 0.0000 1.0000
                 0.000
## Tapenade
                 3.694
                        2
                           1.6426 0.2013
## CSP
                           0.0000 1.0000
                 0.000
                       1
```

```
## Tapenade:CSP 2.528 2 1.1239 0.3312
## Residuals 74.222 66
## [1] "Test d'indépendance des residus de la variable Gamer"
## lag Autocorrelation D-W Statistic p-value
## 1 0.1402611 1.71744 0.152
## Alternative hypothesis: rho != 0
```

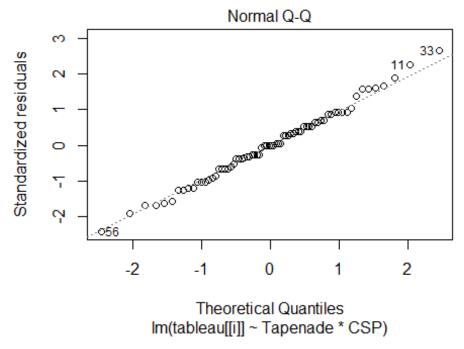
### Indépendance : Gamer



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

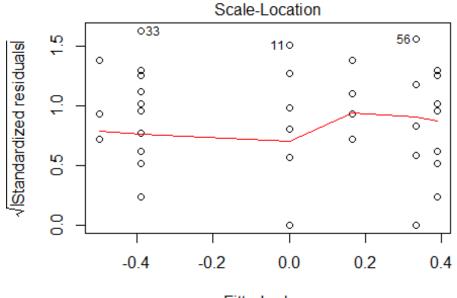
```
## NULL
## [1] "Test de normalité des residus de la variable Gamer"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.99092, p-value = 0.8881
```

#### Normalité : Gamer



## [1] "Test de d'homogéneité des residus de la variable Gamer"

# homogéneité : Gamer

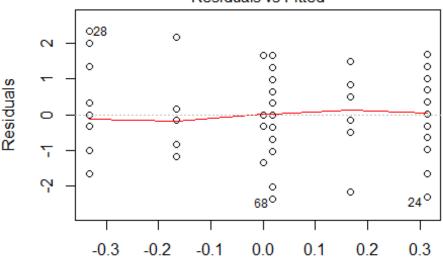


Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Fagreable"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                       1 0.0000 0.9991
                 0.000
## Tapenade
                        2
                 1.700
                           0.6467 0.5272
## CSP
                 0.000
                       1 0.0000 0.9991
```

```
## Tapenade:CSP 0.658 2 0.2505 0.7791
## Residuals 84.098 64
## [1] "Test d'indépendance des residus de la variable Fagreable"
## lag Autocorrelation D-W Statistic p-value
## 1 -0.1574951 2.270506 0.386
## Alternative hypothesis: rho != 0
```

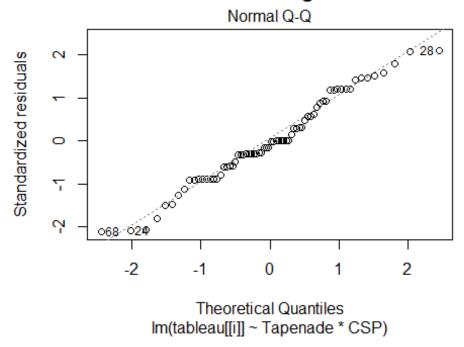
#### Indépendance : Fagreable



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

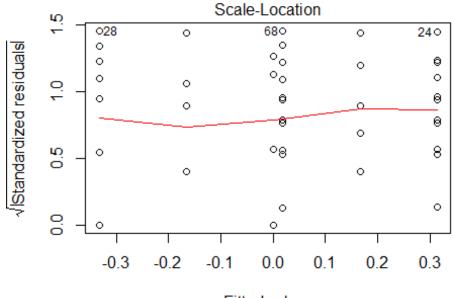
```
## NULL
## [1] "Test de normalité des residus de la variable Fagreable"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.97766, p-value = 0.2444
```

#### Normalité : Fagreable



## [1] "Test de d'homogéneité des residus de la variable Fagreable"

#### homogéneité : Fagreable

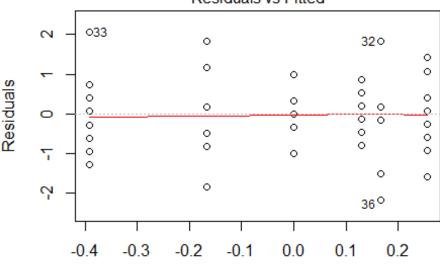


Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Fintensite"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                       1 0.0001 0.9917
                 0.000
## Tapenade
                        2
                           0.3262 0.7228
                 0.520
## CSP
                 0.000 1
                          0.0001 0.9917
```

```
## Tapenade:CSP 2.068 2 1.2982 0.2801
## Residuals
                50.979 64
## [1] "Test d'indépendance des residus de la variable Fintensite"
   lag Autocorrelation D-W Statistic p-value
##
              0.2280831
                             1.541325
   Alternative hypothesis: rho != 0
##
```

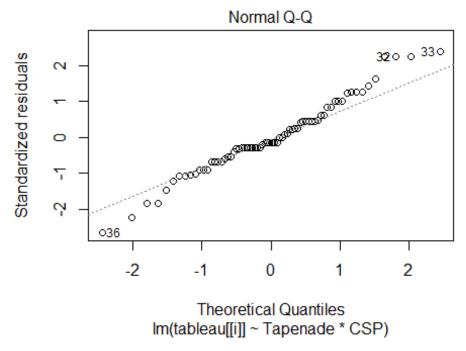
# Indépendance : Fintensite



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

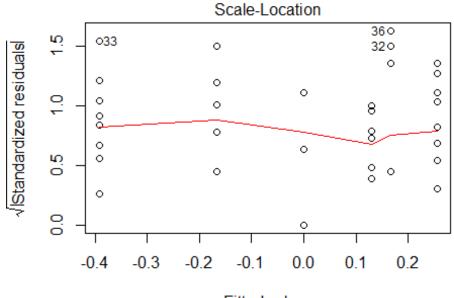
```
## NULL
## [1] "Test de normalité des residus de la variable Fintensite"
##
##
    Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.9815, p-value = 0.3886
```

#### Normalité : Fintensite



## [1] "Test de d'homogéneité des residus de la variable Fintensite"

# homogéneité : Fintensite

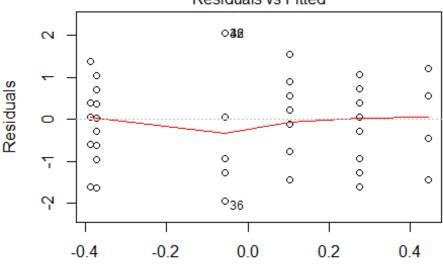


Fitted values Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Fpersistance"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
## Sum Sq Df F value Pr(>F)
## (Intercept) 0.000 1 0.0001 0.9935
## Tapenade 2.184 2 1.3171 0.2753
## CSP 0.000 1 0.0001 0.9935
```

```
## Tapenade:CSP 2.902 2 1.7502 0.1822
## Residuals 51.408 62
## [1] "Test d'indépendance des residus de la variable Fpersistance"
## lag Autocorrelation D-W Statistic p-value
## 1 0.2398943 1.512742 0.028
## Alternative hypothesis: rho != 0
```

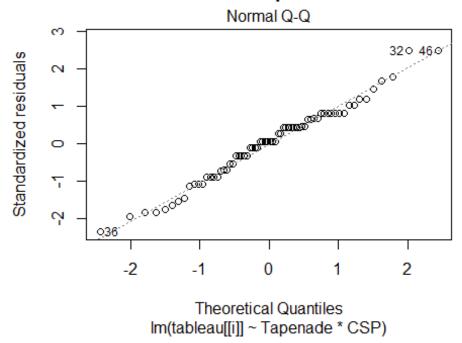
# Indépendance : Fpersistance



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

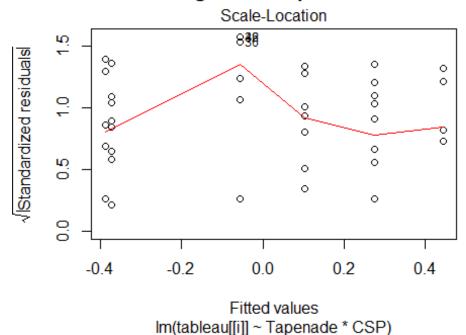
```
## NULL
## [1] "Test de normalité des residus de la variable Fpersistance"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.98251, p-value = 0.4565
```

#### Normalité : Fpersistance



## [1] "Test de d'homogéneité des residus de la variable Fpersistance"

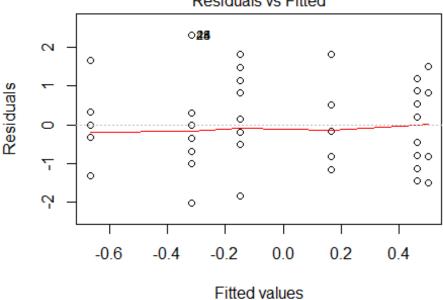
# homogéneité: Fpersistance



```
## [1] "ANOVA pour la variable Fnote"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                       1 0.0000 1.0000
                 0.000
## Tapenade
                        2
                 4.926
                           2.0940 0.1313
## CSP
                 0.000
                       1
                          0.0000 1.0000
```

```
## Tapenade:CSP 4.593 2 1.9523 0.1501
## Residuals 77.630 66
## [1] "Test d'indépendance des residus de la variable Fnote"
## lag Autocorrelation D-W Statistic p-value
## 1 -0.1144817 2.22592 0.504
## Alternative hypothesis: rho != 0
```

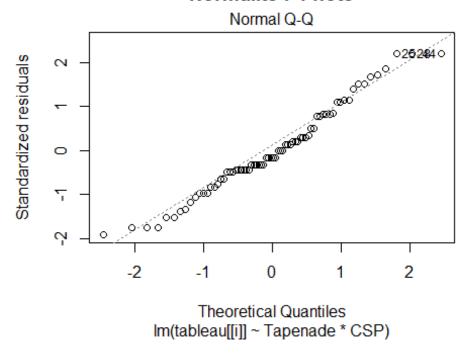
# Indépendance : Fnote



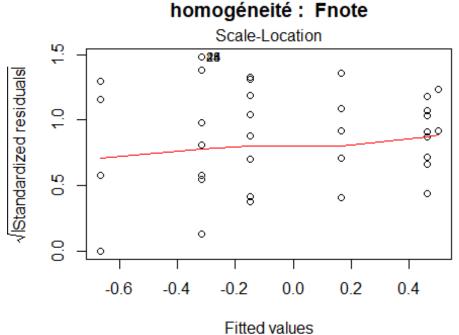
Im(tableau[[i]] ~ Tapenade \* CSP)

```
## NULL
## [1] "Test de normalité des residus de la variable Fnote"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.97518, p-value = 0.1652
```

#### Normalité: Fnote



## [1] "Test de d'homogéneité des residus de la variable Fnote"



Im(tableau[[i]] ~ Tapenade \* CSP)

```
## [1] "ANOVA pour la variable Fharmonie"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                       1 0.0000 1.00000
                 0.000
## Tapenade
                        2
                 5.444
                           2.7131 0.07373
## CSP
                       1
                 0.000
                          0.0000 1.00000
```

```
## Tapenade:CSP 3.444 2 1.7164 0.18763
## Residuals 66.222 66
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Fharmonie"
## lag Autocorrelation D-W Statistic p-value
## 1 -0.1181954 2.145973 0.74
## Alternative hypothesis: rho != 0
```

#### Indépendance : Fharmonie

#### Residuals vs Fitted 025 0 0 o 0000 0 0 0 0 Ö Ō Q. 0 Ö 0 0 0 0 0 0 0 0 O<sub>68</sub> 10

Residuals

0

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-0.6

-0.4

Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

-0.2

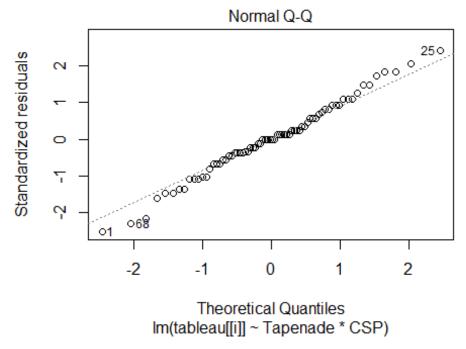
0.0

```
## NULL
## [1] "Test de normalité des residus de la variable Fharmonie"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.98847, p-value = 0.7573
```

0.2

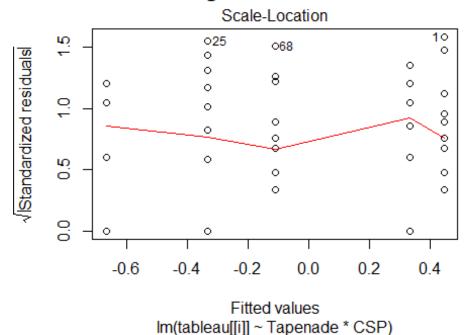
0.4

#### Normalité: Fharmonie



## [1] "Test de d'homogéneité des residus de la variable Fharmonie"

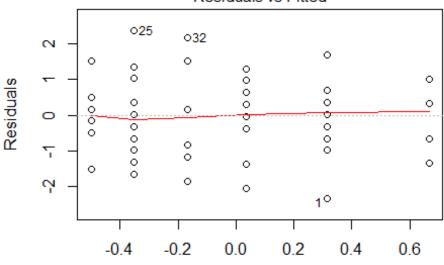
# homogéneité : Fharmonie



```
## [1] "ANOVA pour la variable Farome"
## Anova Table (Type III tests)
##
## Response: tableau[[i]]
                Sum Sq Df F value Pr(>F)
##
## (Intercept)
                       1 0.0000 1.00000
                 0.000
## Tapenade
                        2
                           3.4854 0.03639 *
                 6.509
## CSP
                       1
                          0.0000 1.00000
                 0.000
```

```
## Tapenade:CSP 2.009 2 1.0759 0.34690
## Residuals 61.630 66
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "Test d'indépendance des residus de la variable Farome"
## lag Autocorrelation D-W Statistic p-value
## 1 -0.08931513 2.091663 0.91
## Alternative hypothesis: rho != 0
```

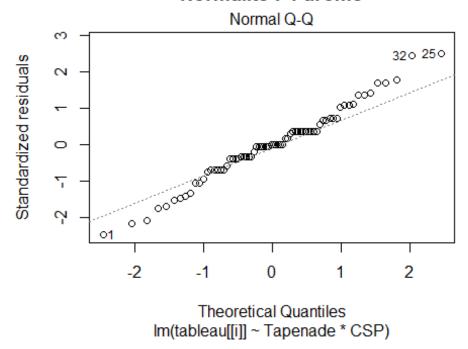
#### Indépendance : Farome



Fitted values lm(tableau[[i]] ~ Tapenade \* CSP)

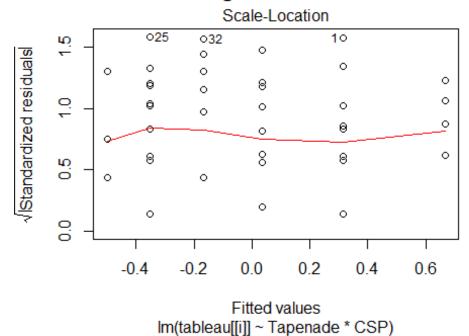
```
## NULL
## [1] "Test de normalité des residus de la variable Farome"
##
## Shapiro-Wilk normality test
##
## data: residuals(mod1)
## W = 0.98637, p-value = 0.6304
```

#### Normalité: Farome



## "Test de d'homogéneité des residus de la variable Farome"

# homogéneité: Farome



# verif\_homo <- leveneTest(residuals(mod1)~tableau\$grp)# permet de vérifier l'homogén
eité</pre>

# <u>Conclusion générale sur l'ANOVA2</u> : le facteur CSP n'a pas d'effet sur les notes des t apenades.