

```
# Installation du package du cours depuis GitHub
remotes::install_github(
  "vguillemot/intro2r",
  build_vignettes = TRUE
)
```

```
library(intro2r)
?"intro2r-package"
```

```
# Guillemets
```

```
chaine1 <- "Je souhaite dire 'Bonjour'"
chaine2 <- "J'aime le chocolat !"
chaine3 <- 'Je souhaite dire "Bonjour"'
chaine4 <- 'Voilà'
chaine5 <- "Je souhaite dire 'J'aime le chocolat'"
```

```
chaine1
chaine2
chaine3
chaine4
chaine5
```

Exercice

Que se passe-t-il quand on oublie les parenthèses dans la commande `fruits[-(1:3),]` ? Commentez !

Faites de même avec le jeu de données `mtcars`.

```
data("fruits", package = "intro2r")
fruits[-(1:3), ]
```

Erreur dans `xj[i]` : les indices négatifs ne peuvent être mélangés qu'à des 0

Error in xj[i] : only 0's may be mixed with negative subscripts

```
fruits$Eau
```

```
fruits$Eau >= 60
```

```
fruits[fruits$Eau >= 60, ]
```

```
fruits[fruits$groupe == "secs" & fruits$Sucres < 40, ]
```

```
Data1<-read.table("nutrimenu/nutrimenu.txt", header = TRUE, sep = "\t")
```

MERCREDI APRES-MIDI

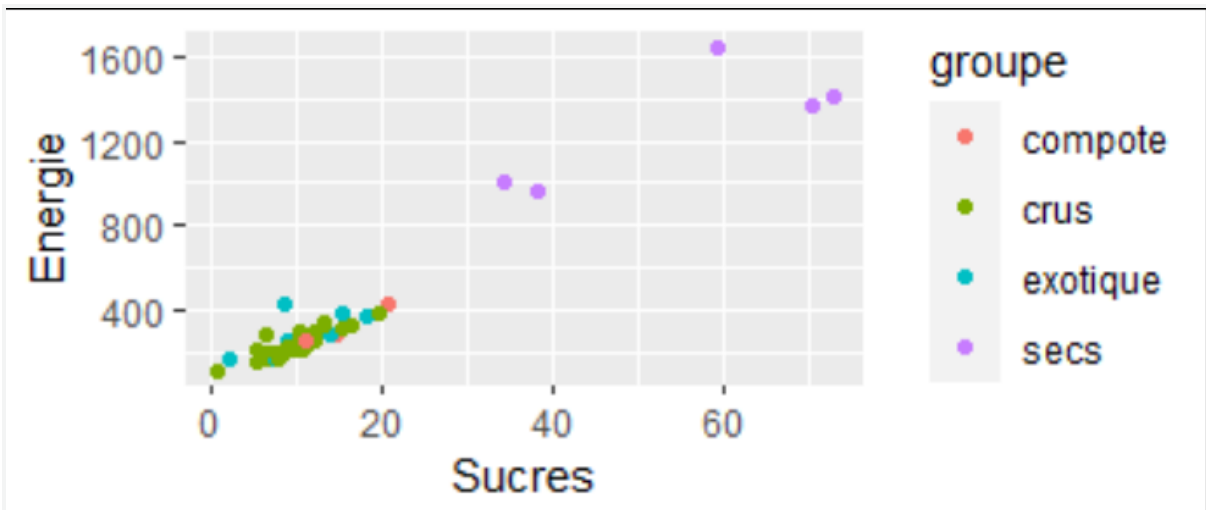
```
# Package des représentations graphiques
```

```
library(ggplot2)
```

```
data("fruits", package = "intro2r")
```

Erreur : le chargement du package ou de l'espace de noms a échoué pour
'ggplot2' in loadNamespace(i, c(lib.loc, .libPaths()), versionCheck = vI[[i]]) :
aucun package nommé 'colorspace' n'est trouvé

```
ggplot(data = fruits,  
       aes(x = Sucres,  
          y = Energie,  
          color = groupe)) +  
geom_point()
```



```
fruits$SucreSup10 <- fruits$Sucre > 10
```

```
ggplot(fruits,
  aes(SucreSup10,
    fill = SucreSup10))
```

Erreur dans FUN(X[[i]], ...) : objet 'sucreSup10' introuvable

>

```
fruits$sucreSup10 <- fruits$Sucre > 10
```

```
ggplot(data=fruits,
  aes(x = sucreSup10))+
  geom_bar()
```

```
fruits$Eau2groupes <- cut(fruits$Eau, c(0, 84.2, 100))
```

```
ggplot(fruits, aes(Eau2groupes)) +
  geom_bar(fill = "steelblue")
```

```
fruits$Eau3gpe <- cut(fruits$Eau, c(0, 50, 70, 100))
```

```
ggplot(fruits, aes(x=Eau3gpe)) +
  geom_bar(fill = "steelblue")
```

```
dat.col <- as.data.frame(
  table(cut(fruits$Eau, c(0, 50, 70, 100))))
```

```

ggplot(dat.col, aes(Var1, Freq)) +
  geom_col()

# Comment modifier les deux commandes précédentes
# pour faire un diagramme en bâtons montrant le nombre ayant
# une teneur en Eau supérieure à 80 g / 100 g par groupe ?
#### Etape 1 : création de la variable Eau > 80
fruits$EauSup80 <- fruits$Eau > 80
fruits$EauSup80
#### Etape 2 : comptage des fruits Eau > 80 / groupe
tab.esup80.grp <- table(fruits$EauSup80, fruits$groupe)
tab.esup80.grp
#### Etape 3 : Transformer en data.frame
df.esup80.grp <- as.data.frame(tab.esup80.grp)
df.esup80.grp
#### Etape 4 : sélectionner les fruits Eau > 80
df.esup80.grp.filt <- df.esup80.grp[df.esup80.grp$Var1 == "TRUE",]
df.esup80.grp.filt
#### Etape 5 : le graphe !
ggplot(data = df.esup80.grp.filt, aes(x=Var2, y=Freq)) +
  geom_col()
#### Graphe alternatif : représenter tous les fruits
ggplot(df.esup80.grp, aes(x = Var2, y = Freq, fill = Var1)) +
  geom_col()
##histogramme des sucres
ggplot(data=fruits,aes(x=Sucres))+geom_histogram(breaks=seq(from=0,to=75,
by=5))

# Diagramme en violons
ggplot(fruits,
  aes(x = Fibres > 1.5,
    y = Proteines,
    fill = Fibres > 1.5)) +

```

```
geom_violin()
```

Erreur : Cannot use `+.gg()` with a single argument. Did you accidentally put + on a new line?

Run `rlang::last_error()` to see where the error occurred.

```
## Exercice : theme_bw
```

```
ggplot(fruits, aes(y = Fibres)) +  
  geom_boxplot() +  
  theme_classic()
```

```
##### JEUDI MATIN #####
```

```
library(ggplot2)
```

```
data("fruits", package = "intro2r")
```

```
ggplot(fruits, aes(Magnesium)) +  
  geom_histogram() +  
  theme(  
    panel.grid.major = element_line(color = "black",  
                                     linetype = "dotted"))
```

```
#### Paramètres esthétiques
```

```
ggplot(fruits,  
  aes(x = Phosphore,  
      y = Calcium,  
      color = ifelse(Phosphore >= 20, "P >= 20", "P < 20"),  
      size = Zinc,  
      shape = groupe)) +  
  geom_point() +  
  geom_vline(
```

```

    xintercept = 20,
    color = "black",
    linetype = "dotted") +
geom_text(x = 17,
  y = 55,
  size = 2,
  angle = 90,
  label = "Seuil de teneur\en Phosphore",
  inherit.aes = FALSE,
  hjust = 0,
  vjust = 0) +
labs(color = "Phosphore") +
theme_bw() +
theme(legend.position = "right")

#-----
#Graphique très moche !!
#-----
ggplot(fruits, aes(Magnesium))+
  geom_histogram()+
  geom_vline(xintercept = 20, color= "yellow", size=9 )+
  geom_text(x=23, y=7, label="seuil",
    color="purple", angle =45, size=12)+
  theme(panel.grid.major = element_line(linetype = "dotted",
    color = "black"),
    panel.grid.minor = element_blank())

```

##↑ Exercice : personnalisation d'un nuage de points

```
ggplot(fruits,
  aes(x = Sucres,
      y = Proteines,
      *** = Magnesium,
      *** = ***) +
  geom_***() +
  ***(title = "Fruits",
      x = "Sucres (g/100 g)",
      y = "Protéines, N x 6.25 (g/100 g)",
      size = "Magnésium\n(mg/100 g)",
      ***= "Groupe") +
  theme_***())
```

```
ggplot(fruits,
  aes(x = Sucres,
      y = Proteines,
      size = Magnesium,
      color = groupe)) +
  geom_point() +
  labs(title = "Fruits",
      x = "Sucres (g/100 g)",
      y = "Protéines, N x 6.25 (g/100 g)",
      size = "Magnésium\n(mg/100 g)",
      color= "Groupe") +
  theme_bw())
```

```
## Personnalisation des échelles
```

```
ggplot(fruits,  
      aes(Phosphore,  
          Calcium)) +  
geom_point(*** = "white") +  
scale_***() +  
scale_***() +  
labs(x = "log10(Phosphore)",  
     y = "log10(Calcium)") +  
theme_dark()
```

```
ggplot(fruits,  
      aes(Phosphore,  
          Calcium)) +  
geom_point(color = "white") +  
scale_x_log10() +  
scale_y_log10() +  
labs(x = "log10(Phosphore)",  
     y = "log10(Calcium)") +  
theme_dark()
```

```
## On enlève tout ce qui déborde
```

```
ggplot(fruits,  
      aes(x = Phosphore,  
          y = Calcium,  
          color = groupe)) +  
geom_point(size = 2) +  
theme_bw() +  
xlim(c(0, 20)) +  
ylim(c(0, 20)) +  
theme(legend.position =
```



```

    "left")
## On fait un Zoom
ggplot(fruits,
      aes(x = Phosphore,
          y = Calcium,
          color = groupe)) +
  geom_point(size = 2) +
  theme_bw() +
  coord_cartesian(xlim = c(0, 20), ylim = c(0, 20)) +
  theme(legend.position =
        "left")

##### Couleurs #####

library(RColorBrewer)

# Exercice : Couleurs alternées
barplot(c(1:5, 1:5),
      col = rep(c("steelblue", "indianred2"),5),
      axes = FALSE)

barplot(rep(1:5, 2), col = rep(c("steelblue", "indianred2"),5), axes = FALSE)
barplot(rep(1:5, 2), col = rep(c(4, 2),5), axes = FALSE)

barplot(rep(1:5, 2), col = c(4, 2), axes = FALSE)

##### JEUDI APRES-MIDI #####

library(ggplot2)
library(RColorBrewer)

data("fruits", package = "intro2r")

display.brewer.all()
brewer.pal(n = 12, name = "Set3")

```

```
barplot(rep(1, 3), col = brewer.pal(n = 3, name = "Set3"))
```

```
## Exercice : choisir sa palette
```

```
pal <- brewer.pal(n=7, name ="Set1")
```

```
barplot(rep(1, 7),  
        col = pal,  
        axes = FALSE,  
        border = FALSE)
```

Erreur dans barplot.default(rep(1, 7), col = pal, axes = FALSE, border = FALSE) :

objet 'pal' introuvable

```
colfun <- colorRampPalette(  
  c(4,3,2))
```

```
barplot(rep(1, 100),  
        col = colfun(100),  
        axes = F, border = NA)
```

```
## Personnaliser les couleurs avec la palette Set1
```

```
ggplot(fruits, aes(x = groupe,  
                  fill = groupe)) +  
  geom_bar() +  
  scale_fill_brewer(palette = "Set1") +  
  theme_bw()
```

```
## Personnaliser les couleurs avec la palette divergente PuOr
```

```
ggplot(fruits, aes(x = Phosphore,  
                  y = Calcium,  
                  color = Magnesium)) +  
  geom_point() +  
  scale_color_distiller(palette = "PuOr") +  
  theme_bw()
```

```
ggplot(fruits, aes(x = groupe,  
  fill = groupe)) +  
  geom_bar() +  
  scale_fill_manual(  
    values = c(crus = "violet",  
      secs = "brown3",  
      exotique = "limegreen",  
      compote = "skyblue")) +  
  theme_bw()
```

```
ggplot(data = fruits, aes(groupe, VitamineC)) +  
  geom_boxplot(aes(color = groupe)) +  
  geom_signif(  
    comparisons = list(2:3),  
    textsize = 2.5) +  
  theme_bw()
```

```
ggplot(data = fruits, aes(groupe, VitamineC)) +  
  geom_boxplot(aes(color = groupe)) +  
  geom_signif(  
    comparisons = list(2:3, 1:2, 3:4, c(1, 4)),  
    textsize = 2.5, step_increase = 0.1) +  
  theme_bw()
```

```
ggplot(data = fruits, aes(groupe, VitamineC)) +  
  geom_boxplot(aes(color = groupe)) +  
  geom_signif(  
    comparisons = list(2:3, 1:2, 3:4, c(1, 4)),  
    textsize = 2.5, step_increase = c(0, 0, 0, 0.1)) +  
  theme_bw()
```

```

## GGARRANGE
g1 <- ggplot(fruits, aes(Eau)) + geom_histogram()
g2 <- ggplot(fruits, aes(Energie)) + geom_histogram()
ggarrange(g1, g2, labels = "AUTO")

## Avec des facettes
ggplot(fruits, aes(Eau)) +
  geom_histogram() +
  facet_wrap(vars(groupe))

moyenne <- mean(fruits$Eau)
ecarttype <- sd(fruits$Eau)

ggplot(fruits, aes(Eau)) +
  geom_histogram(aes(y = ..density..), color = "white") +
  geom_density(color = "steelblue", bw = 5) +
  stat_function(
    fun = dnorm,
    n = 101, args = list(mean = moyenne, sd = ecarttype)) +
  theme_bw()

#### Tests
energiequal <- cut(fruits$Energie, c(0, 250, 2000))
eauqual <- cut(fruits$Eau, c(0, 85, 100))
(tab <- table(energiequal, eauqual))
prop.table(tab)

```