**Barplot horizontal**

Importer depuis excel

> data <- data.frame(PP) « PP nom du fichier importé »

> barplot(height=data$Abondance, names=data$Espece, col="#69b3a2", horiz=T , las=1)

Version 2 :

ggplot(data1, aes(x=Taille, y=Fréquence, fill=Mature))+

geom\_bar(stat="identity", color="black")+

scale\_fill\_manual(values=c("#999999", "#56B4E9"))+

theme\_minimal()+ scale\_x\_discrete(limits=c("[08-12[", "[12-14[", "[14-18[", "[18-20[", "[20-22["))

Kruskall wallis

kruskal.test(weight ~ group, data = my\_data)

Marge

Avant la formule

par(mai = c(1.5, 1.5, 1.5, 1.5))

**Diagramme**

Importer depuis excel

> data <- data.frame(PP) « PP nom du fichier importé »

ggplot(data, aes(x="", y=Pourcentage, fill=Stade)) + geom\_bar(stat="identity", width=1) + coord\_polar("y", start=0)

+ Palette couleurs

+ scale\_fill\_brewer(palette="Blues")+ theme\_minimal()

Ordre apparition des variables

+ scale\_x\_discrete(limits=c("Printemps", "Eté", "Automne", "Hiver"))

**Basic Diagramme**

# Basic piechart

ggplot(data, aes(x="", y=value, fill=group)) +

geom\_bar(stat="identity", width=1, color="white") +

coord\_polar("y", start=0) +

theme\_void() # remove background, grid, numeric labels

**ACP**

> pacman::p\_load(readxl, FactoMineR, factoextra, tidyverse, Factoshiny)

> library(readxl)

> Lithium <- read\_excel("data/Lithium.xlsx")

> View(Lithium)

> data <- data.frame(Lithium)

> res <- PCA(Lithium, quali.sup = 1)

> fviz\_pca\_biplot(res, habillage = "Dose", geom = "point", pointsize = 2, addEllipses = TRUE, ellipse.type = "confidence", label = "var", ind.shape = 21, pointshape = 20)

Exporter

> ggsave(filename = "Lithium.png",fviz\_pca\_biplot(res, habillage = "Dose", geom = "point", pointsize = 2, addEllipses = TRUE, ellipse.type = "confidence", label = "var", ind.shape = 21, pointshape = 20) , width = 8.3, height = 5.5, dpi = 300, units = "in", device='png')

**Boxplot**

ggplot(data5) +

geom\_bar( aes(x=Saison, y=Abondance), stat="identity", fill="skyblue", alpha=0.7)

+

geom\_signif(comparisons = list(c("versicolor", "virginica")),

map\_signif\_level=TRUE)

Ajout des diff signnificatives

library(ggsignif)

rajouter moyenne

+ stat\_summary(fun.y=mean, geom="point", shape=23, size=4)

ggplot(data, aes(x=Techniques, y=CPUE, color=Techniques)) +

geom\_boxplot(outlier.shape = NA) + coord\_cartesian(ylim = c(0, 2000)) + stat\_summary(fun.y=mean, geom="point", shape=20, size=4)

Plot 1

> ggplot(data1, aes(x=Dose, y=Value)) + geom\_boxplot(alpha=0.7) + stat\_summary(fun.y=mean, geom="point", shape=20, size=3, color="black", fill="red") + theme(legend.position="none") + scale\_fill\_brewer(palette="Set2") + xlab("Dose") + ylab("MDA nmoles/mg of protein")

Plot 2

ggplot(data2, aes(x=Dose, y=Value)) + geom\_boxplot(alpha=0.7) + stat\_summary(fun.y=mean, geom="point", shape=20, size=3, color="black", fill="red") + theme(legend.position="none") + scale\_fill\_brewer(palette="Set2") + xlab("Dose") + ylab("H202 nmoles/mg of protein")

Plot3

ggplot(data3, aes(x=Dose, y=Value)) + geom\_boxplot(alpha=0.7) + stat\_summary(fun.y=mean, geom="point", shape=20, size=3, color="black", fill="red") + theme(legend.position="none") + scale\_fill\_brewer(palette="Set2") + xlab("Dose") + ylab("AOPP µmoles/mg of protein")

**Plot 4**

ggplot(data4, aes(x=Dose, y=Value)) + geom\_boxplot(alpha=0.7) + stat\_summary(fun.y=mean, geom="point", shape=20, size=3, color="black", fill="red") + theme(legend.position="none") + scale\_fill\_brewer(palette="Set2") + xlab("Dose") + ylab("PCO µmoles/mg of protein")

Sans nomm legende abcsisse

Plot 1

> ggplot(data1, aes(x=Dose, y=Value)) + geom\_boxplot(alpha=0.7) + stat\_summary(fun.y=mean, geom="point", shape=20, size=3, color="black", fill="red") + theme(legend.position="none") + scale\_fill\_brewer(palette="Set2") + xlab("") + ylab("MDA nmoles/mg of protein")

Plot 2

ggplot(data2, aes(x=Dose, y=Value)) + geom\_boxplot(alpha=0.7) + stat\_summary(fun.y=mean, geom="point", shape=20, size=3, color="black", fill="red") + theme(legend.position="none") + scale\_fill\_brewer(palette="Set2") + xlab("") + ylab("H202 nmoles/mg of protein")

Plot3

ggplot(data3, aes(x=Dose, y=Value)) + geom\_boxplot(alpha=0.7) + stat\_summary(fun.y=mean, geom="point", shape=20, size=3, color="black", fill="red") + theme(legend.position="none") + scale\_fill\_brewer(palette="Set2") + xlab("") + ylab("AOPP µmoles/mg of protein")

**Plot 4**

ggplot(data4, aes(x=Dose, y=Value)) + geom\_boxplot(alpha=0.7) + stat\_summary(fun.y=mean, geom="point", shape=20, size=3, color="black", fill="red") + theme(legend.position="none") + scale\_fill\_brewer(palette="Set2") + xlab("") + ylab("PCO µmoles/mg of protein")

**Grouper les graphs**

library(ggplot2)

p1 <- ggplot(mtcars, aes(wt, mpg)) +

geom\_point()

p2 <- ggplot(mtcars, aes(factor(cyl))) +

geom\_bar()

p3 <- ggplot(mtcars, aes(factor(cyl), mpg)) +

geom\_violin()

p4 <- ggplot(mtcars, aes(factor(cyl), mpg)) +

geom\_boxplot()

library(cowplot)

plot\_grid(p1, p2, p3, p4)

**Matrice correlation**

library(ggplot2)

library(Hmisc)

library(corrplot)

cor(Lit2)

rcorr(as.matrix(Lit2), type=c("spearman"))

> corrplot(cor(Lit2), method="ellipse")

corrplot(cor(Lit2), method="circle")

corrplot(cor(Lit2), method="color")

corrplot(cor(Lit2), method="number")

> corrplot(cor(Lit2), method="circle", type = "upper")

corrplot(cor(Lit2), method="circle", type = "lower")

Heatmpap

[Comment Créer une Superbe Heatmap Interactive dans R - Datanovia](https://www.datanovia.com/en/fr/blog/comment-creer-une-superbe-heatmap-interactive-dans-r/)

**library**("heatmaply")

df <- normalize(mtcars)

heatmaply(df)

pheatmap(data)

tiff(filename="test.tiff", width=2300, height=2000, res=300)

$ plot\_bar(physeq\_ASV\_r, "description", fill="Phylum") + geom\_bar(stat="identity", position="fill") + facet\_grid(~environment, scales="free\_x") + scale\_y\_continuous(labels=percent) + labs(x="Sample", y="Relative abundance") + scale\_fill\_manual(values = PhylaPalette) + theme(text=element\_text(family="Arial", size=12))

$dev.off()

tiff(filename="test.tiff", width=2300, height=2000, res=300)

ggplot(df, aes(x=Mois, y=Pourcentage))+

geom\_bar(stat="identity", color="black")+

scale\_fill\_manual(values=c("#999999", "#56B4E9"))+

theme\_minimal()+ scale\_x\_discrete(limits=c("Juin", "Juillet", "Août", "Septembre", "Octobre"))+ geom\_col(aes(fill = Mois)) + scale\_fill\_manual(values = c("#ff5145", "#ff9b94", "#fff6f6", "#800800", "#f61000")) dev.off()

**Lollipop Chart**

ggplot(data, aes(x= Espèce, y=Pourcentage)) +

geom\_segment(aes(x= reorder(Espèce, Pourcentage), xend= reorder(Espèce, Pourcentage), y=0, yend=Pourcentage), color="skyblue") +

geom\_point( color="blue", size=4, alpha=0.6) +

theme\_light() +

coord\_flip() +

theme(

panel.grid.major.y = element\_blank(),

panel.border = element\_blank(),

axis.ticks.y = element\_blank()

)

V2

ggplot(data2, aes(x=Saison, y=Shannon, color=Saison)) +

geom\_segment( aes(x=Saison, xend=Saison, y=0, yend=Shannon) , size=1, color="black", linetype="F1" ) +

geom\_point(size=5)+ scale\_x\_discrete(limits=c("Printemps", "Eté", "Automne", "Hiver", "Année"))