

R SOFTWARE - OUR CODE

#charge the table modified by us

```
R <- read.csv("~/Downloads/RICA_isafe_students_vf.csv", sep=";", skip = 2, header = TRUE)
library(stats)
```

A) MAKE A BARPLOT

#create a sous ensemble of data for the region 76

```
R76 <- subset(R, NREG == 76)
```

#create a sous ensemble of data for the region 84

```
R84 <- subset(R, NREG == 84)
```

#count the number of observation for each production type of each region

```
observations_76 <- table(R76$OTEXE)
```

```
observations_84 <- table(R84$OTEXE)
```

#create a vector of regions name

```
regions <- c("Region 76", "Region 84")
```

#créer une matrice avec les données pour les deux régions

```
matrice_donnees <- rbind(observations_76, observations_84)
```

#barplot

```
barplot(matrice_donnees, beside = TRUE,
        main = "Répartition des types de productions pour les régions 76 et 84",
        xlab = "types de production", ylab = "Nombre d'observations",
        col = c("blue", "red"), legend = regions)
```

B) SHAPIRO WILK TEST (for a computer where the table is called R76)

shapiro test for each production type for only the region 76 (we can do it also for the region 84 if we want)

```
shapiro.test(R76$PRODV)
```

```
shapiro.test(R76$PRODA)
```

```
shapiro.test(R76$PRODT)
```

```
shapiro.test(R76$PRODH)
```

#representation plot for each

```
qqnorm(R76$PRODV)
```

to compare with normal distribution

```
qqline(rnorm(1000))
```

```
qqnorm(R76$PRODA)
```

to compare with normal distribution

```
qqline(rnorm(1000))
```

```
qqnorm(R76$PRODT)
```

to compare with normal distribution

```
qqline(rnorm(1000))
```

```
qqnorm(R76$PRODH)
```

to compare with normal distribution

```
qqline(rnorm(1000))
```

then to try to make with filtrating the values of PRODV, PRODA, PRODT, and PRODH different than zero

```
PRODV_non_zero <- R76$PRODV[R76$PRODV != 0]
```

```
PRODA_non_zero <- R76$PRODA[R76$PRODA != 0]
```

```
PRODT_non_zero <- R76$PRODT[R76$PRODT != 0]
```

```
PRODH_non_zero <- R76$PRODH[R76$PRODH != 0]
```

#to create a boxplot of the values of PRODV, PRODA, PRODT, and PRODH not equal to 0

```
boxplot(PRODV_non_zero,
```

```
+   main = "Boxplot of the PRODV variable (non zero values)",
```

```
+   ylab = "Value of PRODV")
```

```
boxplot(PRODA_non_zero,
```

```
+   main = "Boxplot of the PRODA variable (non zero values)",
```

```
+   ylab = "Value of PRODA")
```

```
boxplot(PRODT_non_zero,
```

```
+   main = "Boxplot of the PRODT variable (non zero values)",
```

```
+   ylab = "Value of PRODT")
```

```
boxplot(PRODH_non_zero,
```

```
+   main = "Boxplot of the PRODH variable (non zero values)",
```

```
+   ylab = "Value of PRODH")
```

Optional : example for PRODH :

to add precise value on the box plot

```

text(x = 1, y = min(PRODH_non_zero) - 2, labels = paste("Min =", min(PRODH_non_zero)), pos
= 1)
text(x = 1, y = quantile(PRODH_non_zero, 0.25), labels = paste("Q1 =",
quantile(PRODH_non_zero, 0.25)), pos = 1)
text(x = 1, y = median(PRODH_non_zero), labels = paste("Med =",
median(PRODH_non_zero)), pos = 1)
text(x = 1, y = quantile(PRODH_non_zero, 0.75), labels = paste("Q3 =",
quantile(PRODH_non_zero, 0.75)), pos = 1)
text(x = 1, y = max(PRODH_non_zero) + 2, labels = paste("Max =", max(PRODH_non_zero)),
pos = 1)

```

to have a pie plot of the production types distribution in the region 76

to select the columns corresponding to the type of production :

```
types_production <- R76[, c("PRODV", "PRODH", "PRODA", "PRODT")]
```

to count the number of values that are higher than zero, for each production type

```
type_counts <- colSums(types_production > 0)
```

to calculate the percentages

```
type_percentages <- type_counts / sum(type_counts) * 100
```

to create the pie plot

```

pie(type_percentages,
+   main = "Percentage of production types with values greater than zero",
+   labels = names(type_counts),
+   col = rainbow(length(type_percentages)),
+   cex = 0.8)

```

C) CHI SQUARE

a) Chisquare of surface and operating income

```

R$SUTOT_cat <- cut(R$SUTOT, breaks = c(0, 100, 500, 1000, Inf),
+                 labels = c("Petite", "Moyenne", "Grande", "Très grande"))

```

#create contingency table

```
tableau_contigence <- table(R$RESEX, R$SUTOT_cat)
```

#execute Chi-Square test of independence

```
resultat_test <- chisq.test(tableau_contigence)
```

#print the test results

```
print(resultat_chitest)
```

```
plot(R$SUTOT, R$RESEX,
```

```
+   xlab = "Surface", ylab = "Résultats d'exploitation",
```

```
+   main = "Nuage de points entre Surface et Résultat d'exploitation")
```

b) Charges correlation with surface

```
R <- apply(R, 2, as.numeric)
R_numeric <- R[, c("SUTOT", "CHRAM", "CHRSE", "CHRP", "CHRA", "CHRA", "CHRP",
"CHRA", "ELECTQUA", "ENTBT", "ENTMT", "LFRM", "LMATE", "ASSRE", "ASSAU",
"TXPRO", "TAXES", "AIMTX", "FPERS", "CHSOC", "CFINL", "CAGR4")]
# verify if conversion success :
str(R_numeric)

correlation_matrixRnum <- cor(R_numeric)
print(correlation_matrixRnum)

library(corrplot)
corrplot(correlation_matrixRnum, method = "color", type = "upper", order = "hclust", addrect = 2,
rect.col = "red")
```

D) VARIANCE (possible to do it for both regions to compare them but we only did it for the region 76 by adding "R84\$RESEX", after "R76\$RESEX" for example)

To make sure we have numerical values for OTEXE and RESEX :

```
class(R76$OTEXE)
class(R76$RESEX)
```

to convert R76\$OTEXE and R76\$RESEX into numerical values

```
R76$OTEXE <- as.numeric(R76$OTEXE)
R76$RESEX <- as.numeric(R76$RESEX)
```

to perform the variance test

```
var_test_result <- var.test(R76$OTEXE, R76$RESEX)
var_test_result
```

to calculate the mean of RESEX for each unique value of OTEXE

```
result <- aggregate(RESEX ~ OTEXE, data = R76, FUN = mean)
```

to calculate the mean of RESEX for each unique value of OTEXE

```
result <- tapply(R76$RESEX, R76$OTEXE, mean)
result
```

#to plot a barplot

```
barplot(result, xlab = "OTEXE", ylab = "Mean of RESEX",
+ main = "Mean of RESEX for each unique value of OTEXE")
```

E) T-test

```
resultat-test<- t.test(R76$RSESEX, R84$RSESEX)
print(resultat_test)
```

#We will make several test depending to the surface but also if the region is situated into a protected region or not :

```
resultat_test1 <- t.test(filtered_data_small_zenvi, filtered_data_small_nozenvi)
print(resultat_test1)
```

```
resultat_test2 <- t.test(filtered_data_medium_zenvi, filtered_data_medium_nozenvi)
print(resultat_test2)
```

```
resultat_test3 <- t.test(filtered_data_big_zenvi, filtered_data_big_nozenvi)
print(resultat_test3)
```

=> **Correlation** : for each PROD (for the region 76, but can also do it for the region 84 to compare), we know that the better would be with the OTEXE but it was longer to do it (because we have 17 different OTEXE)

```
R76_numericA <- R76[, c("PRODA","CHRAM", "CHRSE", "CHRPB", "CHRAE", "CHRAH",  
"CHRPV", "CHRCR", "ELECTQUA", "ENTBT", "ENTMT", "LFRM", "LMATE", "ASSRE",  
"ASSAU", "TXPRO", "TAXES", "AIMTX", "FPERS","CHSOC","CFINL","CAGR4")]  
R76_numericA <- sapply(R76_numericA, as.numeric, na.rm = TRUE)
```

```
R76_numericT <- R76[, c("PRODT","CHRAM", "CHRSE", "CHRPV", "CHRA", "CHRA", "CHRA",  
"CHRA", "CHRA", "ELECTQUA", "ENTBT", "ENTMT", "LFERM", "LMATE", "ASSRE",  
"ASSAU", "TXPRO", "TAXES", "AIMTX", "FPERS","CHSOC","CFINL","CAGR4")]  
R76_numericT <- sapply(R76_numericT, as.numeric, na.rm = TRUE)
```

```
R76_numericH <- R76[, c("PRODH","CHRAM", "CHRSE", "CHRPV", "CHRA", "CHRA", "CHRA",  
"CHRA", "CHRA", "ELECTQUA", "ENTBT", "ENTMT", "LFERM", "LMATE", "ASSRE",  
"ASSAU", "TXPRO", "TAXES", "AIMTX", "FPERS","CHSOC","CFINL","CAGR4")]  
R76_numericH <- sapply(R76_numericH, as.numeric, na.rm = TRUE)
```

to verify if the conversion succeed

```
str(R76_numericV)  
str(R76_numericA)  
str(R76_numericT)  
str(R76_numericH)
```

to calculate the 4 correlation

```
correlation_matrixV <- cor(R76_numericV)  
correlation_matrixA <- cor(R76_numericA)  
correlation_matrixT <- cor(R76_numericT)  
correlation_matrixH <- cor(R76_numericH)
```

to see the result if we want :

```
print(correlation_matrixV)  
print(correlation_matrixA)  
print(correlation_matrixT)  
print(correlation_matrixH)
```

#to plot a correlation plot

```
corrplot(correlation_matrixV, method = "color", type = "upper", order = "hclust", addrect = 2,  
rect.col = "red")  
corrplot(correlation_matrixA, method = "color", type = "upper", order = "hclust", addrect = 2,  
rect.col = "red")  
corrplot(correlation_matrixT, method = "color", type = "upper", order = "hclust", addrect = 2,  
rect.col = "red")  
corrplot(correlation_matrixH, method = "color", type = "upper", order = "hclust", addrect = 2,  
rect.col = "red")
```