Treball aliments

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# Pràctica 1:

## Grafics Pràctica 1:

# modificat de paractica 4 a practica 1  
  
# p <- ggplot(  
# practica\_1,  
# aes("Tipus de mostra", "Mitjana")  
# )  
# p  
#   
# p <- p +   
# geom\_bar(stat='identity') +   
# geom\_errorbar(  
# aes(x="Tipus de mostra", ymin="Mitjana" - "Error", ymax= "Mitjana" + "Error"),  
# width=0.1, colour="black",  
# alpha=1,  
# size=0.3) +   
# labs (x = "Tipus de mostra", y = "% Humitat", title = "Percentatge d'humitat en funció de cada Tipus de # formatge" )  
#   
# p <- p + scale\_fill\_brewer(palette = "Dark2")  
# p

El shapiro test ens permet contrastar la normalitat d’un conjunt de dades. Així, la hipòtesi nul·la que es planteja és que les mostres segueixen una distribució normal (ho he cercat wiki però es pot contrastar)

data <- practica\_1  
colnames(data) <- c("Mostra", "Contingut", "Mitjana", "Error")  
  
shapiro.test(data$Contingut)

##   
## Shapiro-Wilk normality test  
##   
## data: data$Contingut  
## W = 0.71897, p-value = 0.0001338

# suposam normalitat (si no hi ha normalitat tot i aixi ho feim)  
one.way <- aov(data$Contingut ~ data$Mostra)  
summary(one.way)

## Df Sum Sq Mean Sq F value Pr(>F)   
## data$Mostra 4 5563 1391 470.8 6.41e-14 \*\*\*  
## Residuals 13 38 3   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

pwc <- pairwise.t.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "bonferroni")  
pwc

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Mermelada Pinya Semicurat  
## Mermelada 2.3e-07 - - -   
## Pinya 7.4e-14 1.9e-11 - -   
## Semicurat 0.12685 4.6e-06 1.9e-13 -   
## Tendre 0.00048 0.00024 5.3e-13 0.09081   
##   
## P value adjustment method: bonferroni

# suposam NO normalitat  
kt <- kruskal.test(data$Contingut ~ data$Mostra)  
kt

##   
## Kruskal-Wallis rank sum test  
##   
## data: data$Contingut by data$Mostra  
## Kruskal-Wallis chi-squared = 16.07, df = 4, p-value = 0.002926

pwc2 <- pairwise.wilcox.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "holm")  
pwc2

##   
## Pairwise comparisons using Wilcoxon rank sum exact test   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Mermelada Pinya Semicurat  
## Mermelada 0.46 - - -   
## Pinya 0.46 0.46 - -   
## Semicurat 0.46 0.46 0.46 -   
## Tendre 0.29 0.46 0.46 0.29   
##   
## P value adjustment method: holm

# Practica 2

## Pràctica 2.1.

## Including Plots

# titol <-   
#p\_21 <- ggplot(  
# practica\_21,  
# aes("Formatge", "Mitjana", fill="Formatge")  
#)  
#  
#p\_31 <- p\_21 +  
# geom\_bar(stat='identity') +  
# geom\_errorbar( aes(x="Formatge", ymin="Mitjana" - "Error", ymax= "Mitjana" + "Error"),  
# width=0.1, colour="black", alpha=1, size=0.3) +  
# labs (x = "Tipus de formatge", y = "% Humitat", title = "Percentatge d'humitat en funció de cada Tipus de formatge" )  
#  
#p\_31 <- p\_31 + scale\_fill\_brewer(palette = "Dark2")  
#p\_31  
# save png

El shapiro test ens permet contrastar la normalitat d’un conjunt de dades. Així, la hipòtesi nul·la que es planteja és que les mostres segueixen una distribució normal (ho he cercat wiki però es pot contrastar)

data <- practica\_22  
colnames(data) <- c("Mostra", "Contingut", "Mitjana", "Error")  
  
shapiro.test(data$Contingut)

##   
## Shapiro-Wilk normality test  
##   
## data: data$Contingut  
## W = 0.93706, p-value = 0.5513

one.way <- aov(data$Contingut ~ data$Mostra)  
summary(one.way)

## Df Sum Sq Mean Sq F value Pr(>F)  
## data$Mostra 2 26.07 13.04 0.672 0.545  
## Residuals 6 116.38 19.40

pwc <- pairwise.t.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "bonferroni")  
pwc

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Semicurat  
## Semicurat 0.87 -   
## Tendre 1.00 1.00   
##   
## P value adjustment method: bonferroni

kt <- kruskal.test(data$Contingut ~ data$Mostra)  
kt

##   
## Kruskal-Wallis rank sum test  
##   
## data: data$Contingut by data$Mostra  
## Kruskal-Wallis chi-squared = 1.6, df = 2, p-value = 0.4493

pwc2 <- pairwise.wilcox.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "holm")  
pwc2

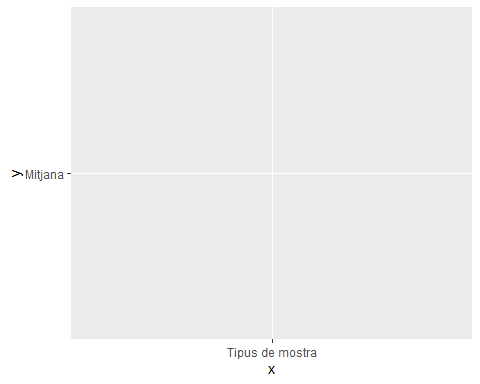
##   
## Pairwise comparisons using Wilcoxon rank sum exact test   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Semicurat  
## Semicurat 1 -   
## Tendre 1 1   
##   
## P value adjustment method: holm

# Pràctica 2.2

practica\_32 <- read\_excel(paste0(directori, "/Ignorar/Practica 32.xlsx"))  
## !!!

## Including Plots

p2 <- ggplot(practica\_32, aes("Tipus de mostra", "Mitjana", fill="Tipus de mostra"))  
  
#p2 <- p2 + geom\_bar(stat='identity') + geom\_errorbar( aes(x="Tipus de mostra", ymin="Mitjana" - "Error", ymax= "Mitjana" + "Error"), width=0.1, colour="black", alpha=1, size=0.3) + labs (x = "Tipus de Mostra", y = "% Humitat", title = "Percentatge d'humitat en funció de cada Tipus de formatge" )  
  
p2 <- p2 + scale\_fill\_brewer(palette = "Dark2")  
p2



El shapiro test ens permet contrastar la normalitat d’un conjunt de dades. Així, la hipòtesi nul·la que es planteja és que les mostres segueixen una distribució normal (ho he cercat wiki però es pot contrastar)

data <- practica\_22  
colnames(data) <- c("Mostra", "Contingut", "Mitjana", "Error")  
  
shapiro.test(data$Contingut)

##   
## Shapiro-Wilk normality test  
##   
## data: data$Contingut  
## W = 0.93706, p-value = 0.5513

one.way <- aov(data$Contingut ~ data$Mostra)  
summary(one.way)

## Df Sum Sq Mean Sq F value Pr(>F)  
## data$Mostra 2 26.07 13.04 0.672 0.545  
## Residuals 6 116.38 19.40

pwc <- pairwise.t.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "bonferroni")  
pwc

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Semicurat  
## Semicurat 0.87 -   
## Tendre 1.00 1.00   
##   
## P value adjustment method: bonferroni

kt <- kruskal.test(data$Contingut ~ data$Mostra)  
kt

##   
## Kruskal-Wallis rank sum test  
##   
## data: data$Contingut by data$Mostra  
## Kruskal-Wallis chi-squared = 1.6, df = 2, p-value = 0.4493

pwc2 <- pairwise.wilcox.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "holm")  
pwc2

##   
## Pairwise comparisons using Wilcoxon rank sum exact test   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Semicurat  
## Semicurat 1 -   
## Tendre 1 1   
##   
## P value adjustment method: holm

# Practica 3

## Pràctica 3.1.

# p\_31 <- ggplot(practica\_31, aes("Formatge", "Mitjana", fill="Formatge"))  
#   
# p\_31 <- p\_31 +  
# geom\_bar(stat='identity') +   
# geom\_errorbar( aes(x="Formatge", ymin="Mitjana" - "Error", ymax= "Mitjana" + "Error"),   
# width=0.1, colour="black", alpha=1, size=0.3) +   
# labs (x = "Tipus de formatge", y = "% Humitat", title = "Percentatge d'humitat en funció de cada Tipus de formatge" )  
#   
# p\_31 <- p\_31 + scale\_fill\_brewer(palette = "Dark2")  
# p\_31

data <- practica\_31  
colnames(data) <- c("Mostra", "Contingut", "Mitjana", "Error")  
  
shapiro.test(data$Contingut)

##   
## Shapiro-Wilk normality test  
##   
## data: data$Contingut  
## W = 0.96201, p-value = 0.8191

one.way <- aov(data$Contingut ~ data$Mostra)  
summary(one.way)

## Df Sum Sq Mean Sq F value Pr(>F)   
## data$Mostra 2 0.011615 0.005808 4.996 0.0528 .  
## Residuals 6 0.006974 0.001162   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

pwc <- pairwise.t.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "bonferroni")  
pwc

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Semicurat  
## Semicurat 0.144 -   
## Tendre 0.078 1.000   
##   
## P value adjustment method: bonferroni

kt <- kruskal.test(data$Contingut ~ data$Mostra)  
kt

##   
## Kruskal-Wallis rank sum test  
##   
## data: data$Contingut by data$Mostra  
## Kruskal-Wallis chi-squared = 5.4222, df = 2, p-value = 0.06646

pwc2 <- pairwise.wilcox.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "holm")  
pwc2

##   
## Pairwise comparisons using Wilcoxon rank sum exact test   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Semicurat  
## Semicurat 0.3 -   
## Tendre 0.3 1.0   
##   
## P value adjustment method: holm

# Pràctica 3.2

## Including Plots

#practica\_2\_proc<-practica\_2\_proc %>% select(Muestra,M,SEM)  
#plot <- practica\_2\_proc[!duplicated(practica\_2\_proc$Muestra),]  
  
# p2 <- ggplot(practica\_32, aes("Tipus de mostra", "Mitjana", fill="Tipus de mostra"))  
#   
# p2 <- p2 +   
# geom\_bar(stat='identity') +   
# geom\_errorbar( aes(x="Tipus de mostra", ymin="Mitjana" - "Error", ymax= "Mitjana" + "Error")  
# , width=0.1, colour="black", alpha=1, size=0.3) +   
# labs (x = "Tipus de Mostra", y = "% Humitat", title = "Percentatge d'humitat en funció de cada Tipus de formatge" )  
#   
# p2 <- p2 + scale\_fill\_brewer(palette = "Dark2")  
# p2

data <- practica\_32  
colnames(data) <- c("Mostra", "Contingut", "Mitjana", "Error")  
  
shapiro.test(data$Contingut)

##   
## Shapiro-Wilk normality test  
##   
## data: data$Contingut  
## W = 0.85684, p-value = 0.02754

one.way <- aov(data$Contingut ~ data$Mostra)  
summary(one.way)

## Df Sum Sq Mean Sq F value Pr(>F)   
## data$Mostra 4 1.9823 0.4956 65.94 1.15e-06 \*\*\*  
## Residuals 9 0.0676 0.0075   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
## 1 observation deleted due to missingness

pwc <- pairwise.t.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "bonferroni")  
pwc

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Oli d'oliva Oli girasol Semicurat  
## Oli d'oliva - - - -   
## Oli girasol - - - -   
## Semicurat - - - -   
## Tendre - - - -   
##   
## P value adjustment method: bonferroni

kt <- kruskal.test(data$Contingut ~ data$Mostra)  
kt

##   
## Kruskal-Wallis rank sum test  
##   
## data: data$Contingut by data$Mostra  
## Kruskal-Wallis chi-squared = 11, df = 4, p-value = 0.02656

pwc2 <- pairwise.wilcox.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "holm")  
pwc2

##   
## Pairwise comparisons using Wilcoxon rank sum exact test   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Oli d'oliva Oli girasol Semicurat  
## Oli d'oliva 0.57 - - -   
## Oli girasol 0.57 0.80 - -   
## Semicurat 1.00 1.00 1.00 -   
## Tendre 1.00 0.80 0.80 1.00   
##   
## P value adjustment method: holm

# Pràctica 3.3.

## Including Plots

#practica\_2\_proc<-practica\_2\_proc %>% select(Muestra,M,SEM)  
#plot <- practica\_2\_proc[!duplicated(practica\_2\_proc$Muestra),]  
  
#p3 <- ggplot(practica33, aes("Formatge", "Mitjana", fill="Formatge"))  
#  
#p3 <- p3 + geom\_bar(stat='identity') +  
# geom\_errorbar( aes(x="Formatge", ymin="Mitjana" - "Error", ymax= "Mitjana" + "Error"),  
# width=0.1, colour="black", alpha=1, size=0.3) +   
# labs (x = "Tipus de Mostra", y = "% Humitat", title = "Percentatge d'humitat en funció de cada Tipus de formatge" )  
#  
#p3 <- p3 + scale\_fill\_brewer(palette = "Dark2")  
#p3

data <- practica\_33  
colnames(data) <- c("Mostra", "Contingut", "Mitjana", "Error")  
  
shapiro.test(data$Contingut)

##   
## Shapiro-Wilk normality test  
##   
## data: data$Contingut  
## W = 0.79521, p-value = 0.03672

one.way <- aov(data$Contingut ~ data$Mostra)  
summary(one.way)

## Df Sum Sq Mean Sq F value Pr(>F)   
## data$Mostra 2 14980 7490 97.38 0.000405 \*\*\*  
## Residuals 4 308 77   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
## 2 observations deleted due to missingness

pwc <- pairwise.t.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "bonferroni")  
pwc

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Semicurat  
## Semicurat 0.00124 -   
## Tendre 0.00073 0.68285   
##   
## P value adjustment method: bonferroni

kt <- kruskal.test(data$Contingut ~ data$Mostra)  
kt

##   
## Kruskal-Wallis rank sum test  
##   
## data: data$Contingut by data$Mostra  
## Kruskal-Wallis chi-squared = 5.3571, df = 2, p-value = 0.06866

pwc2 <- pairwise.wilcox.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "holm")  
pwc2

##   
## Pairwise comparisons using Wilcoxon rank sum exact test   
##   
## data: data$Contingut and data$Mostra   
##   
## Curat Semicurat  
## Semicurat 0.6 -   
## Tendre 0.6 0.6   
##   
## P value adjustment method: holm

# Practica 4

## Including Plots

# p <- ggplot(practica\_4, aes("Embutit", "Mitjana", fill="Embutit"))  
#   
# p <- p +  
# geom\_bar(stat='identity') +  
# geom\_errorbar( aes(x="Embutit", ymin="Mitjana" - "Error", ymax= "Mitjana" + "Error"),  
# width=0.1, colour="black", alpha=1, size=0.3) +  
# labs (x = "Embutit", y = "% Humitat", title = "Percentatge d'humitat en funció de cada Tipus de formatge" )  
#   
# p <- p + scale\_fill\_brewer(palette = "Dark2")  
# p

data <- practica\_4  
colnames(data) <- c("Mostra", "Contingut", "Mitjana", "Error")  
  
shapiro.test(data$Contingut)

##   
## Shapiro-Wilk normality test  
##   
## data: data$Contingut  
## W = 0.92383, p-value = 0.4997

one.way <- aov(data$Contingut ~ data$Mostra)  
summary(one.way)

## Df Sum Sq Mean Sq F value Pr(>F)   
## data$Mostra 2 293.68 146.84 7.875 0.041 \*  
## Residuals 4 74.59 18.65   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
## 2 observations deleted due to missingness

pwc <- pairwise.t.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "bonferroni")  
pwc

##   
## Pairwise comparisons using t tests with pooled SD   
##   
## data: data$Contingut and data$Mostra   
##   
## Mortadel·la Salsitxó  
## Salsitxó 0.088 -   
## Xoriço 0.088 1.000   
##   
## P value adjustment method: bonferroni

kt <- kruskal.test(data$Contingut ~ data$Mostra)  
kt

##   
## Kruskal-Wallis rank sum test  
##   
## data: data$Contingut by data$Mostra  
## Kruskal-Wallis chi-squared = 4.5, df = 2, p-value = 0.1054

pwc2 <- pairwise.wilcox.test(data$Contingut, data$Mostra, paired = FALSE, p.adjust.method = "holm")  
pwc2

##   
## Pairwise comparisons using Wilcoxon rank sum exact test   
##   
## data: data$Contingut and data$Mostra   
##   
## Mortadel·la Salsitxó  
## Salsitxó 0.6 -   
## Xoriço 0.6 1.0   
##   
## P value adjustment method: holm