Coding Challenge 4: Markdown

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### Question 1

1. A YAML header is the section of the top of .rmd code that sets the title, output options, and other global settings. You can set the output as a html, word, pdf, or github flavored markdown document. You can also set a table of contents in the YAML header.
2. Literate programming is writing code in a way that is human-readable and easy to understand. It is a key part of a reproducible workflow.

### Question 2

Data are published here:

[Noel, Z.A., Roze, L.V., Breunig, M., Trail, F. 2022. Endophytic fungi aspromising biocontrol agent to protect wheat from Fusarium graminearum head blight. Plant Disease.](https://apsjournals.apsnet.org/doi/10.1094/PDIS-06-21-1253-RE)

Load in the MycotinData.csv dataframe.

# load in data, assigning na with <NA>  
mycotoxindf <- read.csv("MycotoxinData.csv", na.strings = "na")  
str(mycotoxindf) #check that it's right

## 'data.frame': 375 obs. of 6 variables:  
## $ Treatment : chr "Fg" "Fg" "Fg" "Fg" ...  
## $ Cultivar : chr "Wheaton" "Wheaton" "Wheaton" "Wheaton" ...  
## $ BioRep : int 2 2 2 2 2 2 2 2 2 3 ...  
## $ MassperSeed\_mg: num 10.29 12.8 2.85 6.5 10.18 ...  
## $ DON : num 107.3 32.6 416 211.9 124 ...  
## $ X15ADON : num 3 0.85 3.5 3.1 4.8 3.3 6.9 2.9 2.1 0.71 ...

Load in packages and colorblind palette.

library(ggplot2)  
library(ggpubr)  
#color blind palette vector   
cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7")

Create DON~Treatment boxplot.

# relevel the df so that NTC is the first group in the plot   
mycotoxindf$Treatment <- factor(mycotoxindf$Treatment, levels = c("NTC", "Fg", "Fg + 37", "Fg + 40", "Fg + 70"))  
  
#create a boxplot of DON~Treatment   
DON.bp <- ggplot(mycotoxindf, aes(x= Treatment, y = DON, fill = Cultivar)) +  
 geom\_boxplot(outliers = F) +   
 geom\_point(shape = 21, alpha = 0.6, position = position\_jitter(0.25)) +  
 xlab(" ") +  
 ylab("DON (ppm)") +  
 scale\_fill\_manual(values = c(cbbPalette[3], cbbPalette[4])) +  
 theme\_classic() +  
 facet\_wrap(~Cultivar)

Create Mass~Treatment boxplot.

mass.bp <- ggplot(mycotoxindf, aes(x= Treatment, y = MassperSeed\_mg , fill = Cultivar)) +  
 geom\_boxplot(outliers = F) +   
 geom\_point(shape = 21, alpha = 0.6, position = position\_jitter(0.25)) +  
 xlab(" ") +  
 ylab("Seed Mass (mg)") +  
 scale\_fill\_manual(values = c(cbbPalette[3], cbbPalette[4])) +  
 theme\_classic() +  
 facet\_wrap(~Cultivar)

Create X15adon~Treatment boxplot.

X15ADON.bp <- ggplot(mycotoxindf, aes(x= Treatment, y = X15ADON , fill = Cultivar)) +  
 geom\_boxplot(outliers = FALSE) +   
 geom\_point(shape = 21, alpha = 0.6, position = position\_jitter(0.25)) +  
 xlab(" ") +  
 ylab("15ADON") +  
 scale\_fill\_manual(values = c(cbbPalette[3], cbbPalette[4])) +  
 theme\_classic() +  
 facet\_wrap(~Cultivar)

Use ggarange to combine all figures and add p-values to figures

# adds t-test pairwise p-values to each of the figures  
X15ADON.bp.ttest <- X15ADON.bp +  
 geom\_pwc(aes(group = Treatment), method = "t.test", label = "p.adj.format")   
  
mass.bp.ttest <- mass.bp +  
 geom\_pwc(aes(group = Treatment), method = "t.test", label = "p.adj.format")   
  
DON.bp.ttest <- DON.bp +  
 geom\_pwc(aes(group = Treatment), method = "t.test", label = "p.adj.format")   
  
#combines those three plots with the ttest pvalues into a single plot with 3 panels  
figure.ttest <- ggarrange(  
 DON.bp.ttest,   
 mass.bp.ttest,   
 X15ADON.bp.ttest,  
 nrow = 3,   
 ncol = 1,   
 labels = c("A)", "B)", "C)"),   
 common.legend = TRUE,   
 legend = "bottom"  
)  
figure.ttest

