Coding challenge 4

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2025-02-27

The data for this document is accessible here: [Manuscript with data](https://doi.org/10.1094/PDIS-06-21-1253-RE) Here is the full citation for this data: Noel, Z.A., Roze, L.V., Breunig, M., Trail, F. 2022. Endophytic fungi as promising biocontrol agent to protect wheat from Fusarium graminearum head blight. Plant Disease.https://doi.org/10.1094/PDIS-06-21-1253-RE

## Question 1

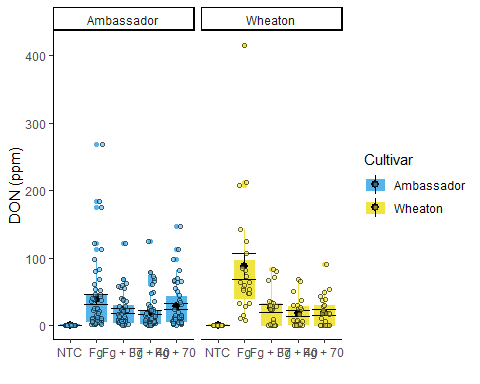
A YAML header is present at the top of a Markdown file that gives the title, author, and date of when the file was created. It also indicates what the format of the output should be, with common choices including pdf, word doc, and HTML files.

Literate programming is a mixture of input and output code that allow for fully reproducible documents.

## Question 2

This is the code chunk for the DON data.

data <- read.csv("MycotoxinData.csv", na.strings = "na") # reading in the data, specifying to not include the na values  
library(ggplot2) # loading ggplot  
library(tinytex)  
  
cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7") # created vector for colorblind colors  
  
q1 <- ggplot(data = data, aes(x = Treatment, y = DON, fill = Cultivar)) + # setting plot type and axes  
 geom\_boxplot(position = position\_dodge(width = 0.9), aes(color = Cultivar)) + # boxplot with cultivar colors  
 stat\_summary(fun = mean, position = "dodge") + # adding means   
 stat\_summary(fun.data = mean\_se, geom = "errorbar", position = "dodge")+ # adding error bars and setting dodge  
 geom\_point(position = position\_jitterdodge(dodge.width = 0.9), shape = 21, color = "black", alpha = 0.6) + # jittered data points, added transparency  
 xlab("") + # x axis label  
 ylab("DON (ppm)") + # y axis label  
 scale\_color\_manual(values = c("Ambassador" = "#56B4E9", "Wheaton" = "#F0E442")) + # setting color outline  
 scale\_fill\_manual(values = c("Ambassador" = "#56B4E9", "Wheaton" = "#F0E442")) + # setting color fill  
 theme\_classic() + # classic theme for plot  
 facet\_wrap(~Cultivar) # separate plots by subtype of cultivar  
  
# Question 2  
data$Treatment <- factor(data$Treatment, levels = c("NTC", "Fg", "Fg + 37", "Fg + 40", "Fg + 70")) # changing from default levels to ones specified  
  
ggplot(data = data, aes(x = Treatment, y = DON, fill = Cultivar)) +  
 geom\_boxplot(position = position\_dodge(width = 0.9), aes(color = Cultivar)) + # boxplot with cultivar colors  
 stat\_summary(fun = mean, position = "dodge") +  
 stat\_summary(fun.data = mean\_se, geom = "errorbar", position = "dodge")+  
 geom\_point(position = position\_jitterdodge(dodge.width = 0.9), shape = 21, color = "black", alpha = 0.6) + # jittered data points, added transparency  
 xlab("") +  
 ylab("DON (ppm)") +  
 scale\_color\_manual(values = c("Ambassador" = "#56B4E9", "Wheaton" = "#F0E442")) +   
 scale\_fill\_manual(values = c("Ambassador" = "#56B4E9", "Wheaton" = "#F0E442")) +  
 theme\_classic() + # classic theme for plot  
 facet\_wrap(~Cultivar)

 This is the code chunk for 15ADON data.

q3a <- ggplot(data = data, aes(x = Treatment, y = X15ADON, fill = Cultivar)) + # changed y variable  
 geom\_boxplot(position = position\_dodge(width = 0.9), aes(color = Cultivar)) + # boxplot with cultivar colors  
 stat\_summary(fun = mean, position = "dodge") +  
 stat\_summary(fun.data = mean\_se, geom = "errorbar", position = "dodge")+  
 geom\_point(position = position\_jitterdodge(dodge.width = 0.9), shape = 21, color = "black", alpha = 0.6) + # jittered data points, added transparency  
 xlab("") +  
 ylab("15ADON") + # changed label  
 scale\_color\_manual(values = c("Ambassador" = "#56B4E9", "Wheaton" = "#F0E442")) +   
 scale\_fill\_manual(values = c("Ambassador" = "#56B4E9", "Wheaton" = "#F0E442")) +  
 theme\_classic() + # classic theme for plot  
 facet\_wrap(~Cultivar)

This is the code chunk for Seedmass.

# plotting massperseed  
q3b <- ggplot(data = data, aes(x = Treatment, y = MassperSeed\_mg, fill = Cultivar)) + # changed y variable  
 geom\_boxplot(position = position\_dodge(width = 0.9), aes(color = Cultivar)) + # boxplot with cultivar colors  
 stat\_summary(fun = mean, position = "dodge") +  
 stat\_summary(fun.data = mean\_se, geom = "errorbar", position = "dodge")+  
 geom\_point(position = position\_jitterdodge(dodge.width = 0.9), shape = 21, color = "black", alpha = 0.6) + # jittered data points, added transparency  
 xlab("") +  
 ylab("Seed Mass (mg)") + # changed y label to be accurate  
 scale\_color\_manual(values = c("Ambassador" = "#56B4E9", "Wheaton" = "#F0E442")) +   
 scale\_fill\_manual(values = c("Ambassador" = "#56B4E9", "Wheaton" = "#F0E442")) +  
 theme\_classic() + # classic theme for plot  
 facet\_wrap(~Cultivar)

This is the code chunk for arranging the three figures using ggarrange.

library(tidyverse)

## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──  
## ✔ dplyr 1.1.4 ✔ readr 2.1.5  
## ✔ forcats 1.0.0 ✔ stringr 1.5.1  
## ✔ lubridate 1.9.4 ✔ tibble 3.2.1  
## ✔ purrr 1.0.4 ✔ tidyr 1.3.1  
## ── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
## ✖ dplyr::filter() masks stats::filter()  
## ✖ dplyr::lag() masks stats::lag()  
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

library(ggpubr)  
library(ggrepel)  
  
  
# common legend makes it to where there is one legend for all of the plots in the figure, whereas without it, the legend is displayed inside each subplot.   
  
# Question 5  
q5a <- q1 +   
 geom\_pwc(aes(group = Treatment), method = "t\_test", label = "p.adj.signif") # adding \* for significance  
  
q5b <- q3a +  
 geom\_pwc(aes(group = Treatment), method = "t\_test", label = "p.adj.signif") # adding \* for significance  
  
q5c <- q3b +  
 geom\_pwc(aes(group = Treatment), method = "t\_test", label = "p.adj.signif") # adding \* for significance  
  
# arranging plots again  
q5figure <- ggarrange(  
 q5a, # first plot  
 q5b, # second plot  
 q5c, # third plot  
 labels = c("A", "B", "C"), # manually specify capital labels  
 nrow = 1, # arrange plots in one row  
 ncol = 3, # three columns  
 common.legend = T  
)  
q5figure

