Coding_Challenge4_Markdown_mer0127_kat0084

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Contents

Data Information

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. DOI

Coding Challenge 3

Question One

Explain the following: **YAML header**

A YAML header contains arguments "title", "author", "output", "toc", and "theme" within three dashes (- - -) above and below the arguments.

Literate programming

A mix of code and descriptive writing to explain and execute data analysis.

Quesiton Two

- Use geom_pwc() to add t.test pairwise comparisons to the three plots made above.
- Save each plot as a new R object, and combine them again with ggarange as you did in question

```r
library(ggplot2) #version 3.5.1
library(ggpubr) #version 0.6.0
library(ggrepel)  #version 0.9.6
```

Data Set

```
Mycotoxin<- read.csv("MycotoxinData.csv", na.strings = "na")
head(Mycotoxin)
```

```
##   Treatment Cultivar BioRep MassperSeed_mg   DON X15ADON
## 1        Fg  Wheaton      2      10.291304 107.3    3.00
## 2        Fg  Wheaton      2      12.803226  32.6    0.85
## 3        Fg  Wheaton      2       2.846667 416.0    3.50
## 4        Fg  Wheaton      2       6.500000 211.9    3.10
## 5        Fg  Wheaton      2      10.179167 124.0    4.80
## 6        Fg  Wheaton      2      12.044444  73.1    3.30
```

```
str(Mycotoxin)
```

```
## '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 ...
```

New Color Palette

```
cbbPalette <- c( "#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2",
                 "#D55E00", "#CC79A7","#000000")
```

DON with pairwise comparisons

```
plot1 <- ggplot(Mycotoxin, aes(x=Treatment, y=DON, fill=Cultivar)) +

  geom_boxplot(outlier.color=NA) +
  geom_point(pch=21, alpha=0.6, color="black",
             position=position_jitterdodge(dodge.width=0.9)) +
  geom_pwc(aes(group = Treatment),
           method = "t_test", label = "p.signif", hide.ns = TRUE)+

  xlab("") +
  ylab("DON (ppm)") +

  theme_classic() +
  scale_fill_manual(values= cbbPalette) +
  facet_wrap(~Cultivar)

plot1
```
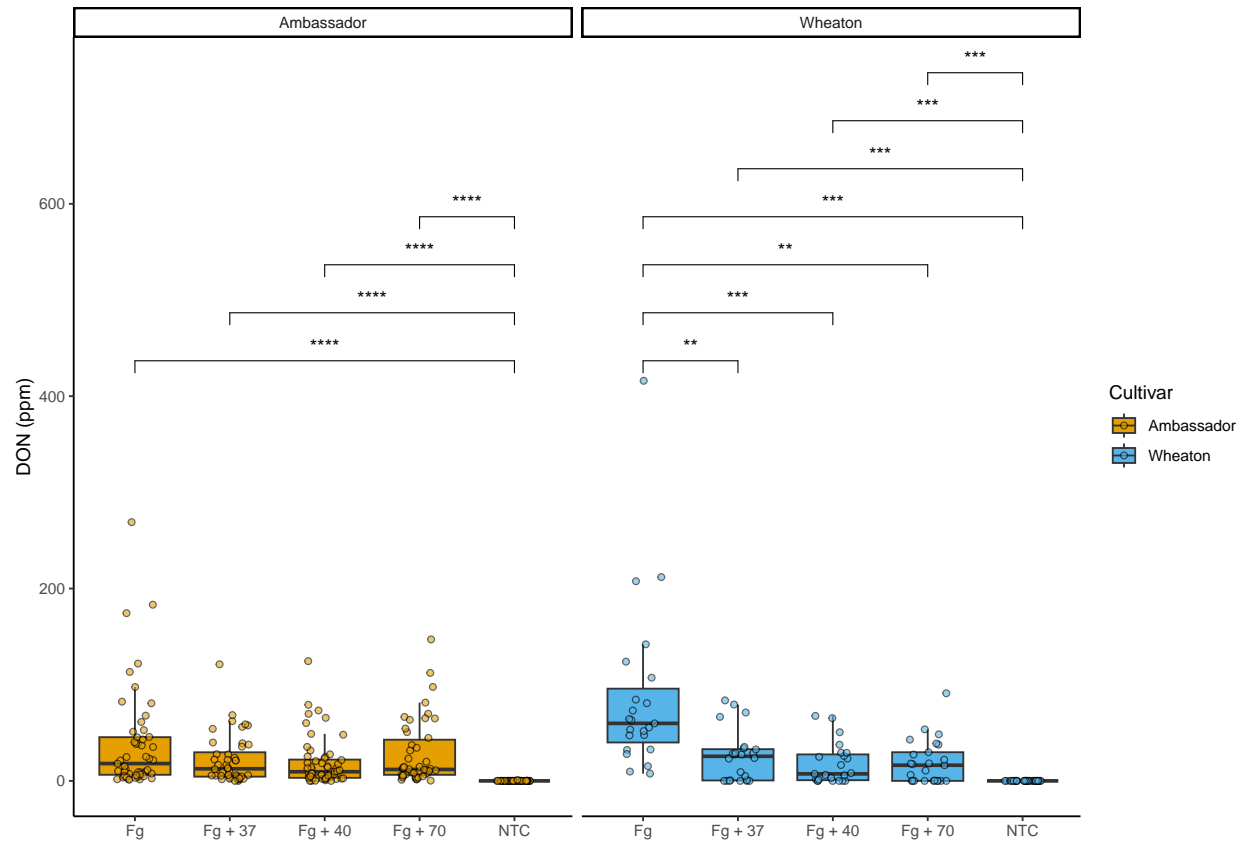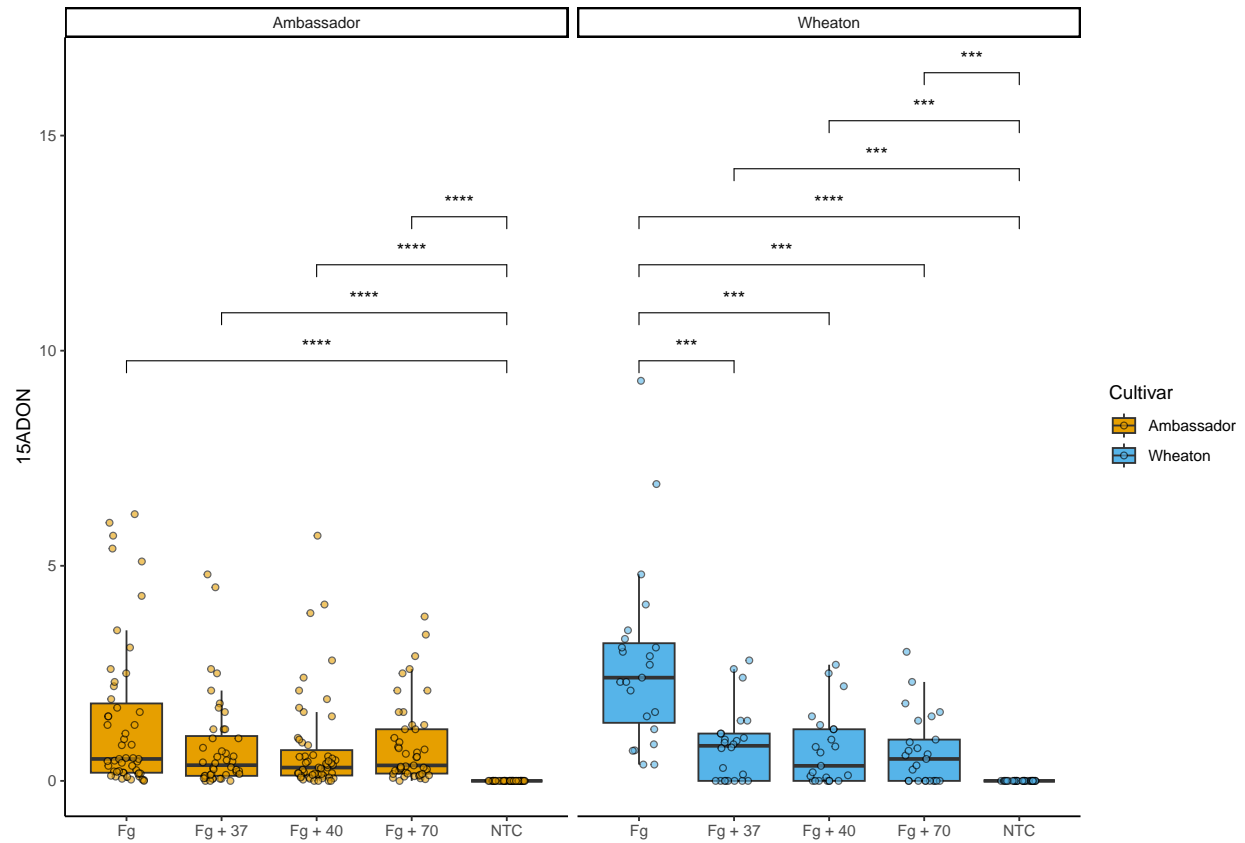
X15ADON with pairwise comparisons

```
plot2 <- ggplot(Mycotoxin, aes(x=Treatment, y=X15ADON, fill=Cultivar)) +
  geom_boxplot(outlier.color=NA) +
  geom_point(pch=21, alpha=0.6, color="black",
             position=position_jitterdodge(dodge.width=0.9)) +
  geom_pwc(aes(group = Treatment),method = "t_test", label = "p.signif",
           hide.ns = TRUE)+

  xlab("") +
  ylab("15ADON") +

  theme_classic() +
  scale_fill_manual(values=cbbPalette) +
  facet_wrap(~Cultivar)


plot2
```

MassperSeed_mg with pairwise comparisons

```
plot3 <- ggplot(Mycotoxin, aes(x=Treatment, y=MassperSeed_mg, fill=Cultivar)) +
  geom_boxplot(outlier.color=NA) +
  geom_point(pch=21, alpha=0.6, color="black",
             position=position_jitterdodge(dodge.width=0.9)) +
  geom_pwc(aes(group = Treatment), method = "t_test", label = "p.signif")+

  xlab("") +
  ylab("Seed Mass (mg)") +

  theme_classic() +
  scale_fill_manual(values=cbbPalette) +
  facet_wrap(~Cultivar)


plot3
```
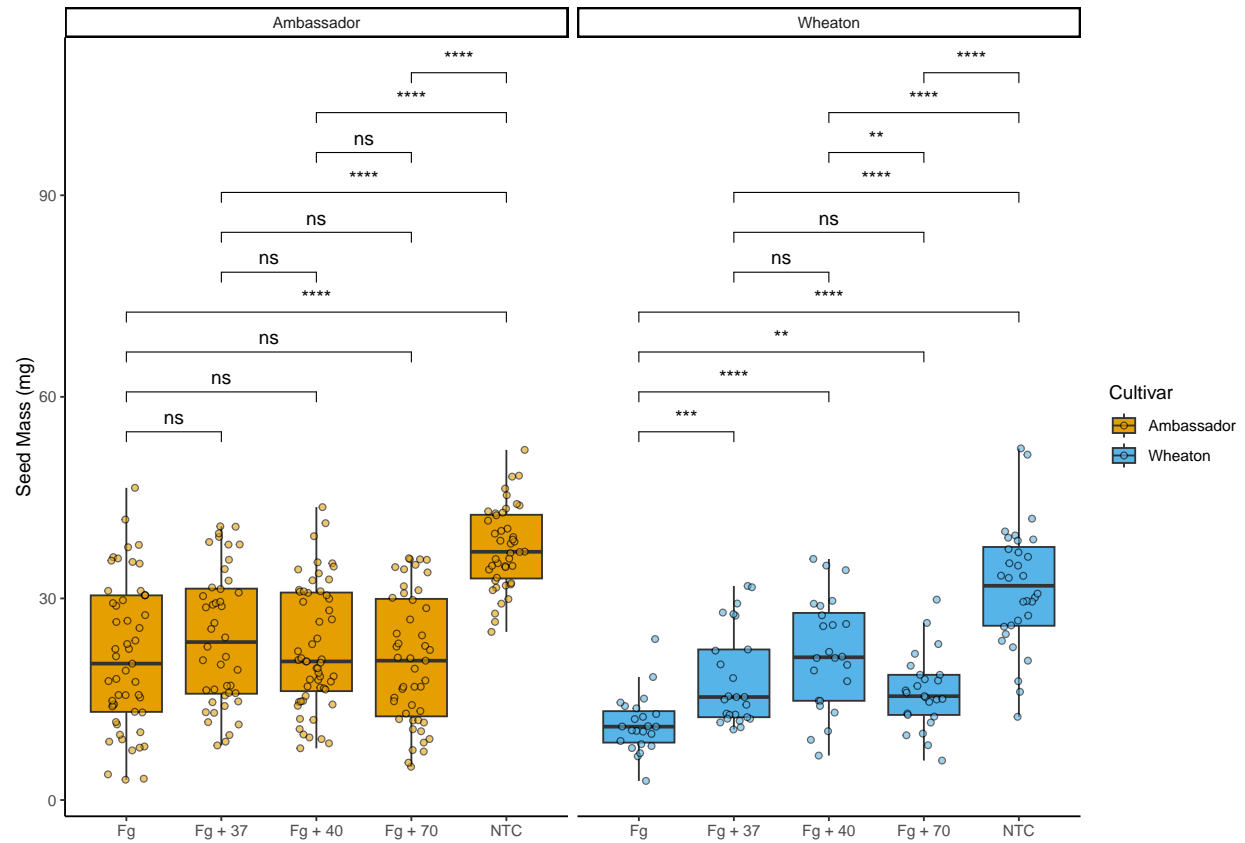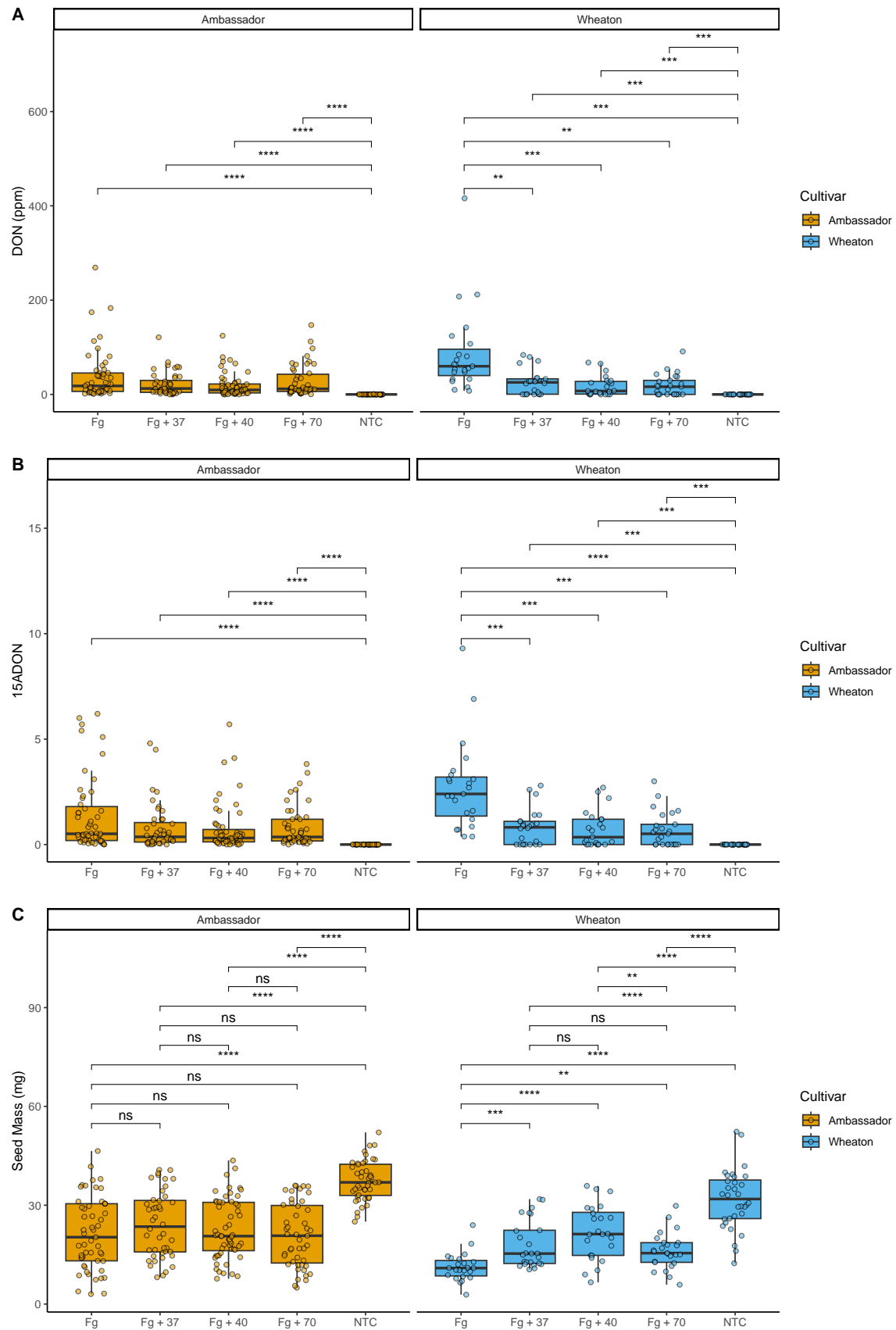
Combining the three plots into one file

```
combined_plots <- ggarrange(plot1, plot2, plot3,
                            ncol = 1, nrow = 3,
                            labels = c("A", "B", "C"))

combined_plots
```

```
ggsave("combined_plot.jpeg", plot = combined_plots, width =15 , height = 10)
#Saving Plot to Rproject Folder
```

Question 6

link to GitHub