

Coding_Challenge4_Markdown_mer0127_kat0084

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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

```
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 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

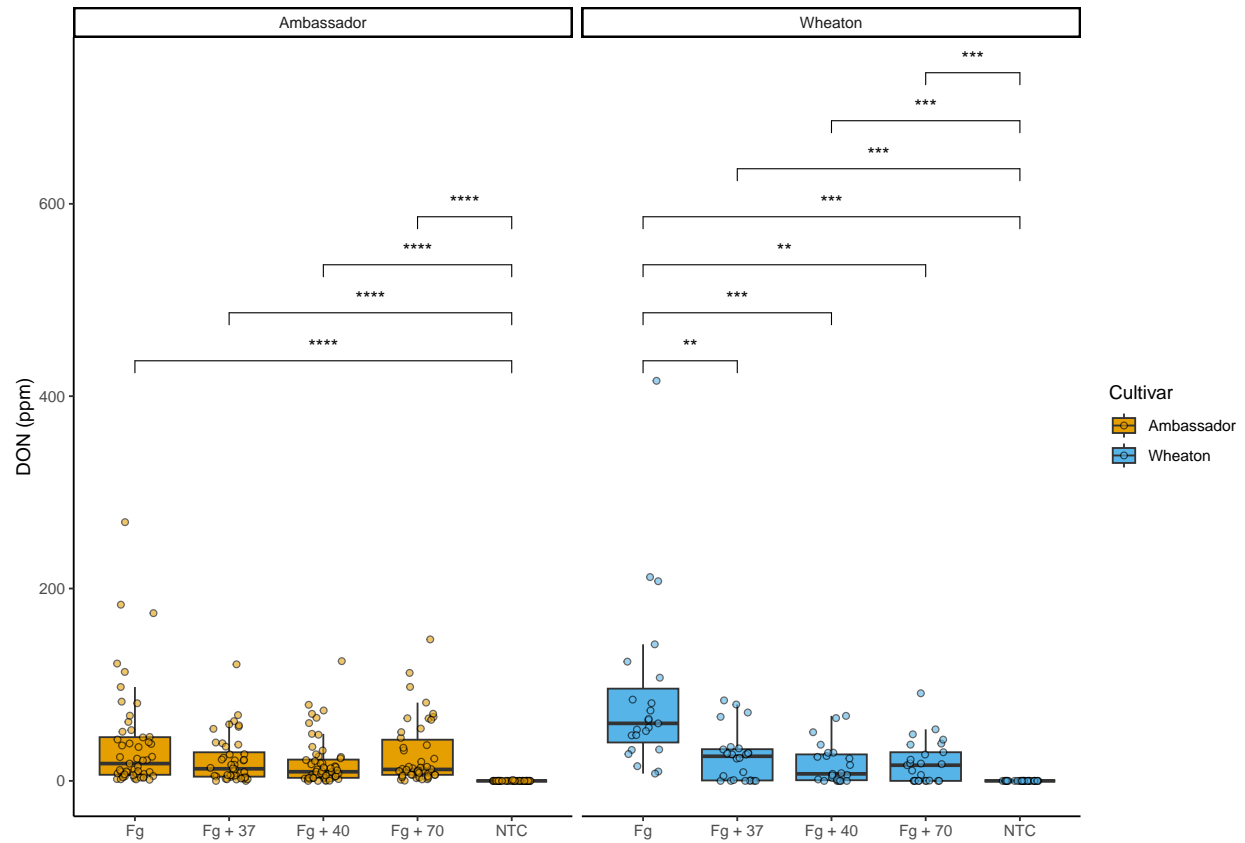
```
plot1 <- ggplot(Mycotoxin, aes(x=Treatment, y=DON, fill=Cultivar)) +

  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
```



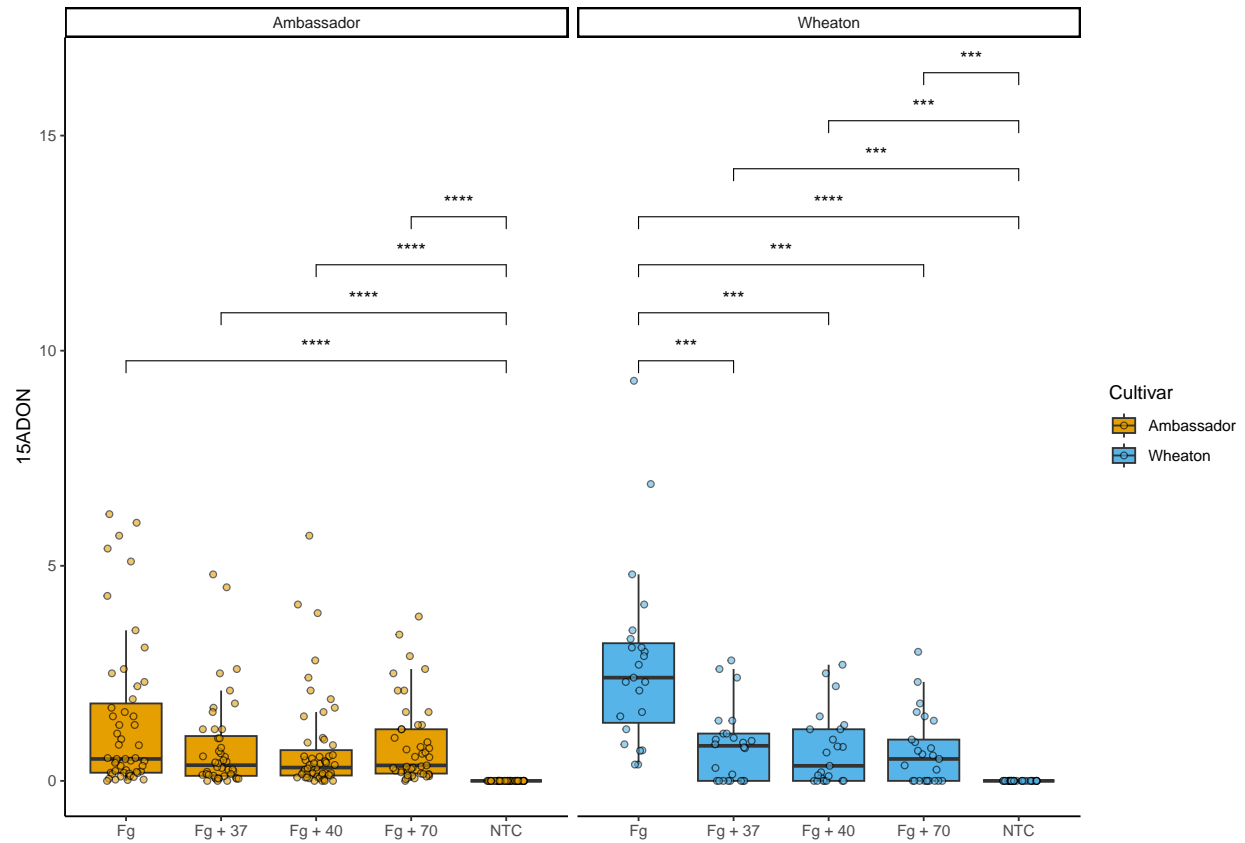
X15ADON with pairwise comparisons

```
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("X15ADON") +

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

plot2



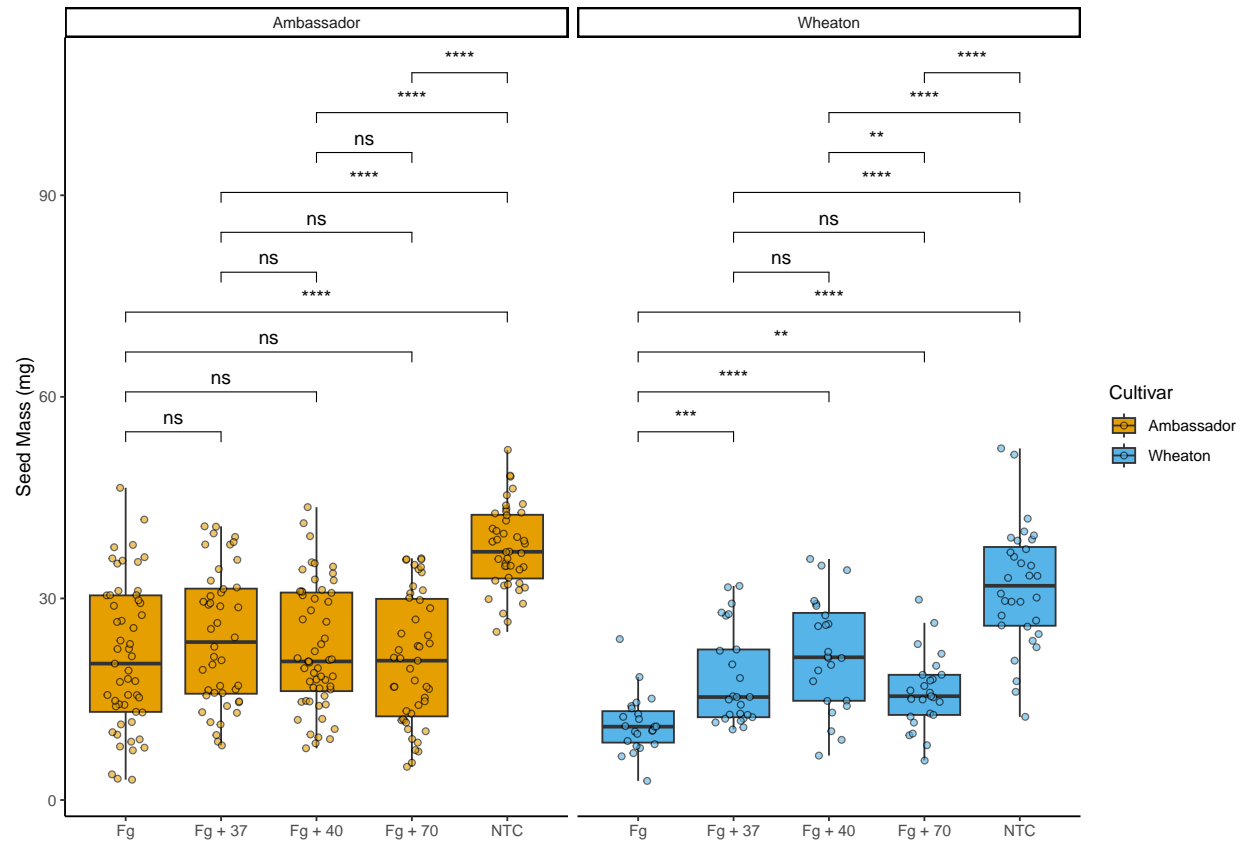
MassperSeed_mg with pairwise comparisons

```
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)
```

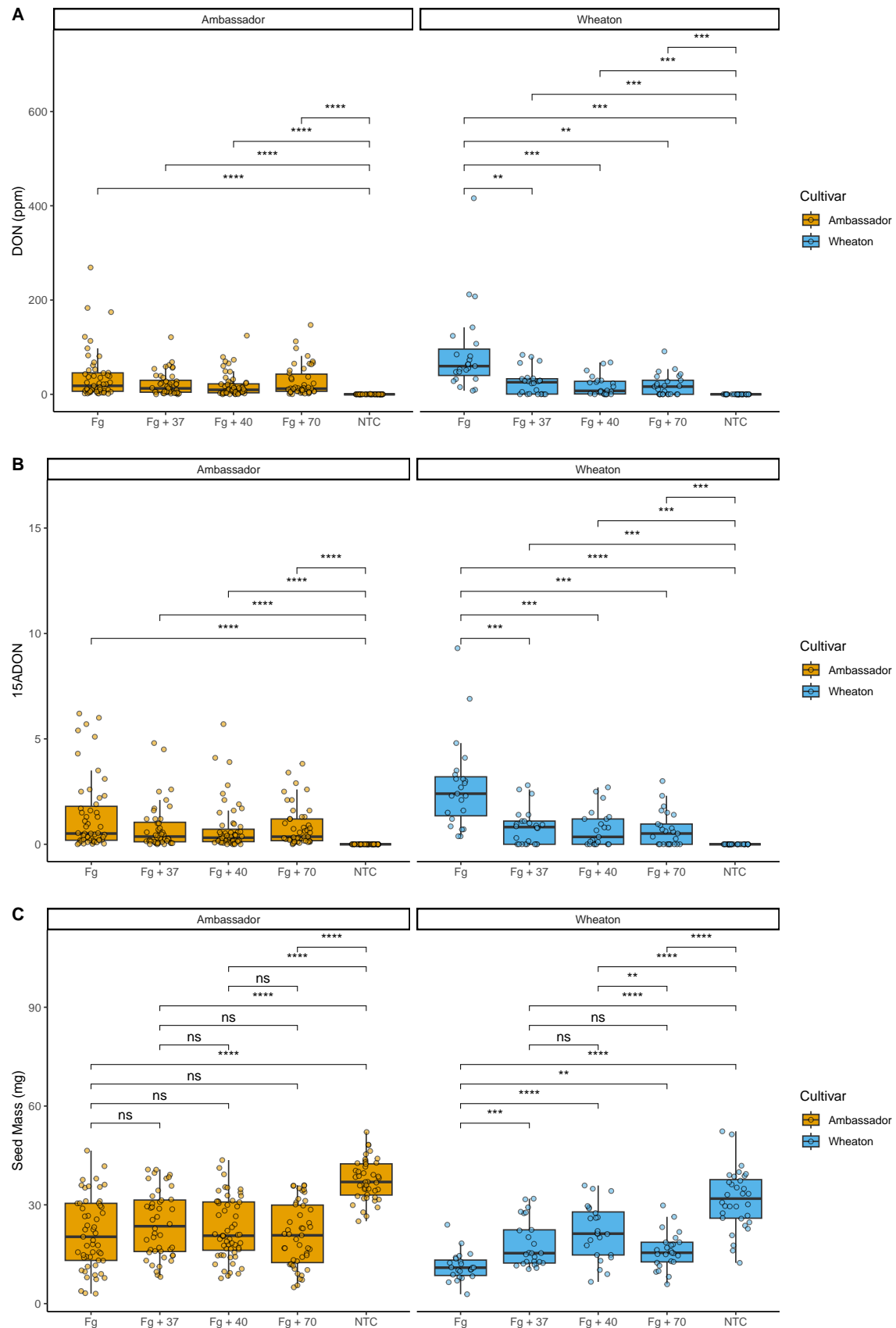
plot3



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