

R_markdown_class_assignment

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Link to the manuscript

Plant Disease

Question 1.

Explain the following a.YAML header The YAML header is the R markdown's initial portion containing YAML arguments such as title, author, and output format demarcated by three dashes on either side. This is the example of YAML header. — title: “R markdown coding” author: “Bibechana Paudel” date: “2025-02-26” output: html_document: toc: true #table of content

-
- b. Literate programming Literate programming is the practice of mixing code and descriptive writing in order to execute and explain a data analysis simultaneously in the same document.

Question 2

Take the code you wrote for coding challenge 3, question 5, and incorporate it into your R markdown file. Some of you have already been doing this, which is great! Your final R markdown file should have the following elements.

a. At the top of the document, make a clickable link to the manuscript where these data are published. The link is here:

- 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>

b. Read the data using a relative file path with `na.strings` option set to "na". This means you need to put the `Mycotoxin.csv` file we have used for the past two weeks into your directory, which git tracks.

```
####Load the data
mycotoxin<-read.csv("Data_Visualization/MycotoxinData.csv", na.string="na")
####Load library
library(ggplot2)
library(ggpubr)
####Load cbbPalette
cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7")
```

c. Make a separate code chunk for the figures plotting the DON data, 15ADON, and Seedmass, and one for the three combined using `ggarrange`.

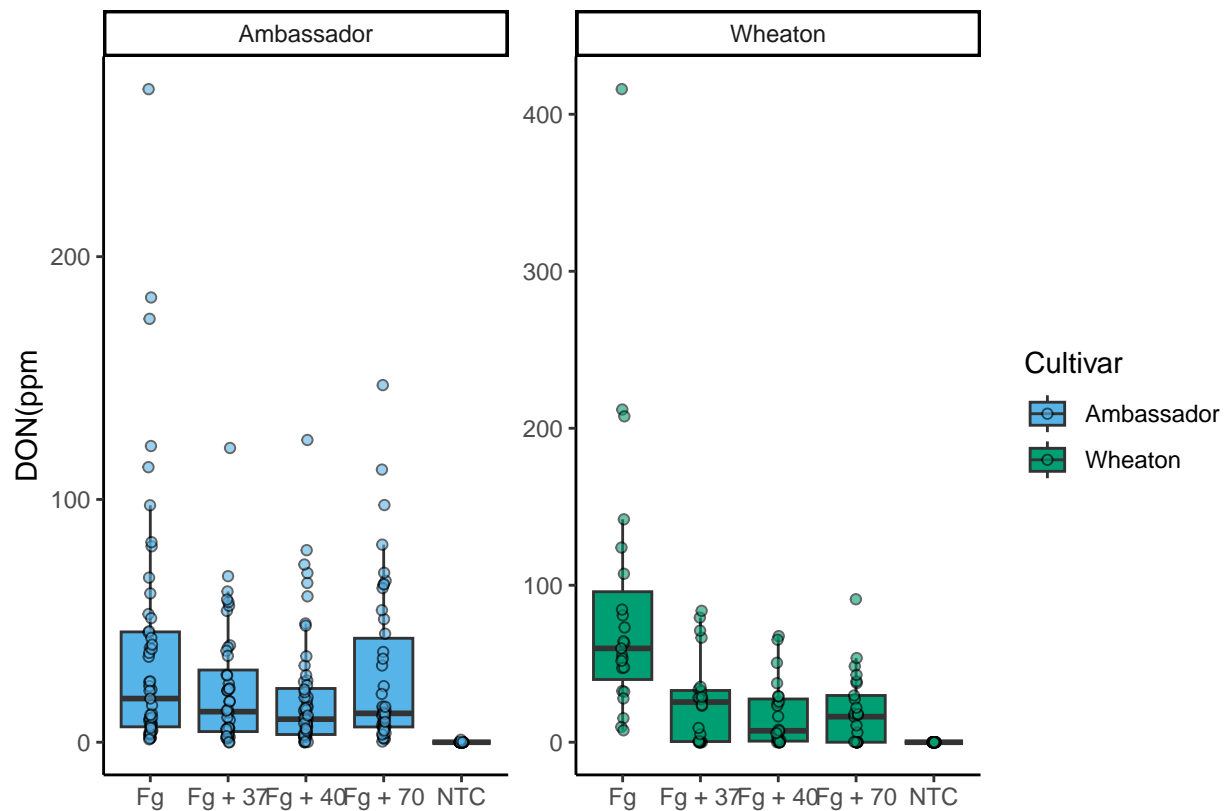
DON

```
####Using ggplot, create a boxplot of DON by Treatment so that the plot looks like the image below.
#a. Jitter points over the boxplot and fill the points and boxplots Cultivar with two colors from the c
#b. Change the transparency of the jittered points to 0.6.
#c. The y-axis should be labeled "DON (ppm)", and the x-axis should be left blank.
#d. The plot should use a classic theme
#e. The plot should also be faceted by Cultivar
```

```
mycotoxin.DON<-ggplot(mycotoxin,aes(Treatment,DON, fill=Cultivar))+
  geom_boxplot(outlier.shape=NA)+ # Add boxplots and remove the outlier shape that are missing.
  geom_point(position=position_jitterdodge(0.05), shape=21, alpha=0.6)+ ## Add jittered points to sh
  xlab("")+ #label the x-axis
  ylab("DON(ppm)")+ #label the y-axis
  scale_fill_manual(values=cbbPalette[c(3,4)])+ #fill the plot with colourblind friendly palette
  theme_classic()+
  facet_wrap(~Cultivar, scales="free") #facet wrap by cultivar
mycotoxin.DON
```

```
## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 8 rows containing missing values or values outside the scale range
## ('geom_point()').
```

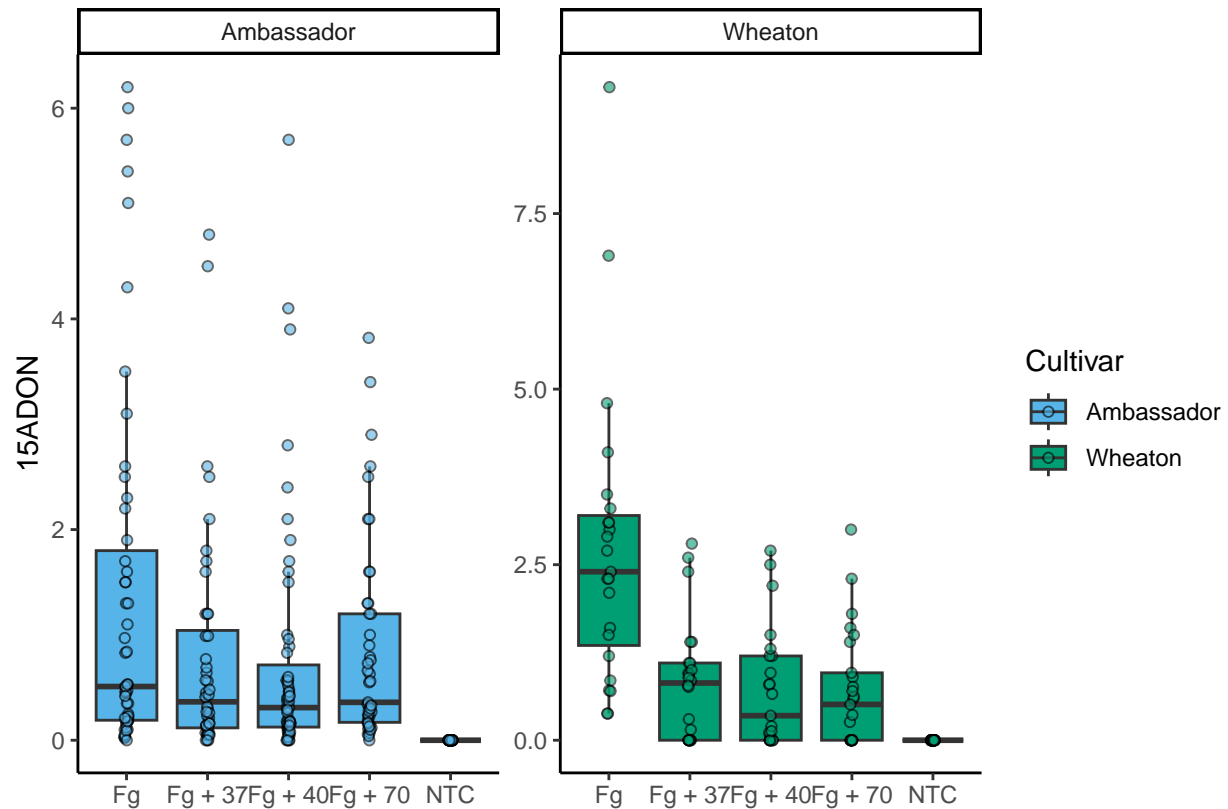


X15DON

```
####Change the y-variable to plot X15ADON and MassperSeed_mg. The y-axis label should now be "15ADON" a
mycotoxin.X15ADON<-ggplot(mycotoxin,aes(Treatment,X15ADON, fill=Cultivar))+ #define aesthetics x-axis
  geom_boxplot(outlier.shape=NA)+
  geom_point(position=position_jitterdodge(0.05), shape=21, alpha=0.6)+
  xlab("")+
  ylab("15ADON")+ #label y-axis as 15ADON
  scale_fill_manual(values=cbbPalette[c(3,4)])+
  theme_classic()+
  facet_wrap(~Cultivar, scales="free")
mycotoxin.X15ADON
```

```
## Warning: Removed 10 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 10 rows containing missing values or values outside the scale range
## ('geom_point()').
```

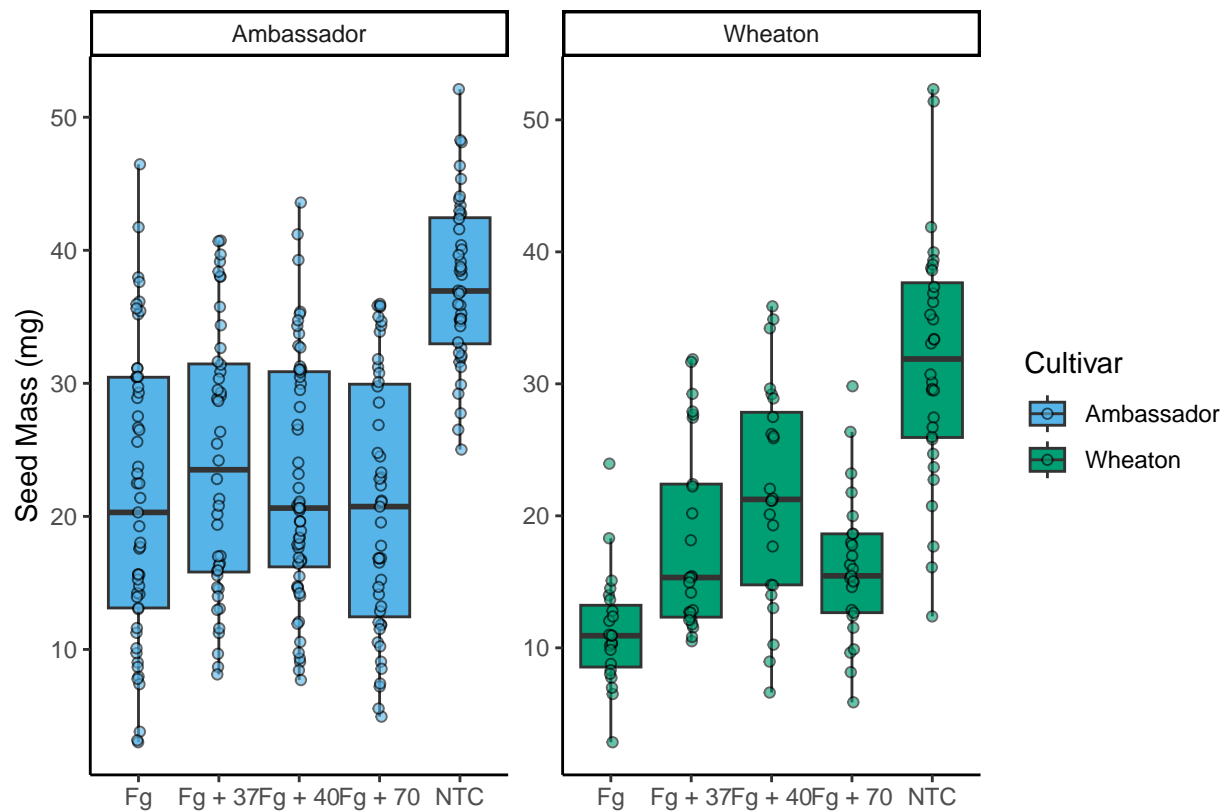


MassperSeed

```
mycotoxin.seed<-ggplot(mycotoxin,aes(Treatment,MassperSeed_mg, fill=Cultivar))+ #define aesthetics x-
  geom_boxplot(outlier.shape=NA)+
  geom_point(position=position_jitterdodge(0.05), shape=21, alpha=0.6)+
  xlab("")+
  ylab("Seed Mass (mg)")+ #label y axis as Seed Mass (mg)
  scale_fill_manual(values=cbbPalette[c(3,4)])+
  theme_classic()+
  facet_wrap(~Cultivar, scales="free")
mycotoxin.seed
```

```
## Warning: Removed 2 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 2 rows containing missing values or values outside the scale range
## ('geom_point()').
```



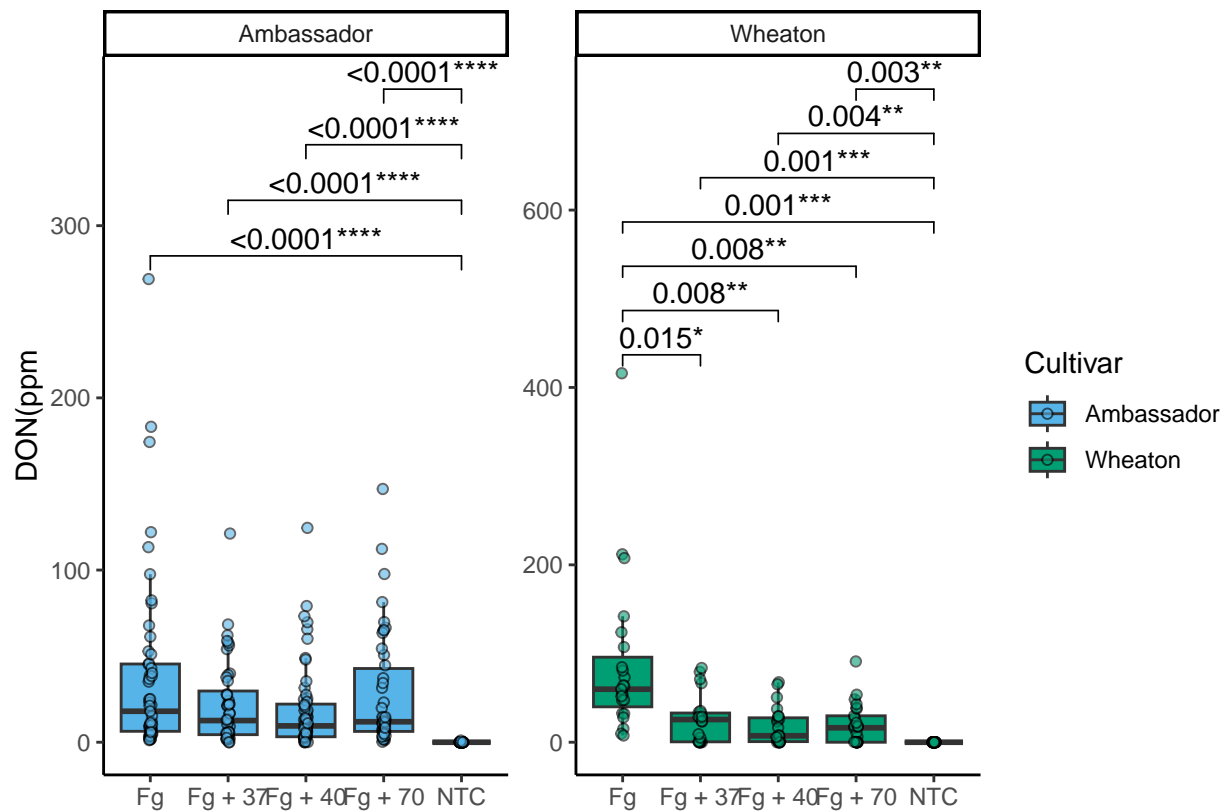
Combine fig

```
####Use geom_pwc() to add t.test pairwise comparisons to the three plots made above. Save each plot as a
mycotoxin.DON.significance<-mycotoxin.DON+
geom_pwc(aes(group=Treatment), method="t.test", label = "{p.adj.format}{p.adj.signif}", hide.ns=T) #
mycotoxin.DON.significance
```

```
## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_pwc()').
```

```
## Warning: Removed 8 rows containing missing values or values outside the scale range
## ('geom_point()').
```

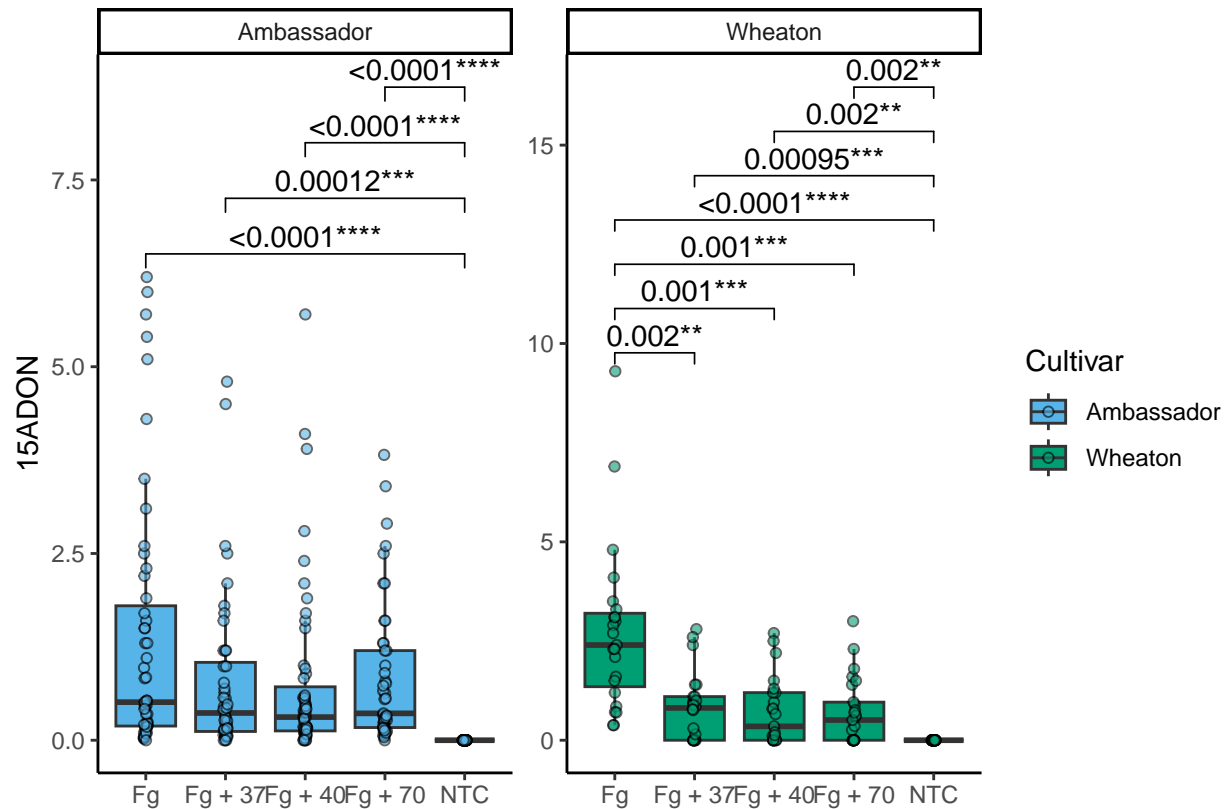


```
mycotoxin.X15ADON.significance<-mycotoxin.X15ADON+
geom_pwc(aes(group=Treatment), method="t.test", label = "{p.adj.format}{p.adj.signif}", hide.ns=T)
mycotoxin.X15ADON.significance
```

```
## Warning: Removed 10 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 10 rows containing non-finite outside the scale range
## ('stat_pwc()').
```

```
## Warning: Removed 10 rows containing missing values or values outside the scale range
## ('geom_point()').
```

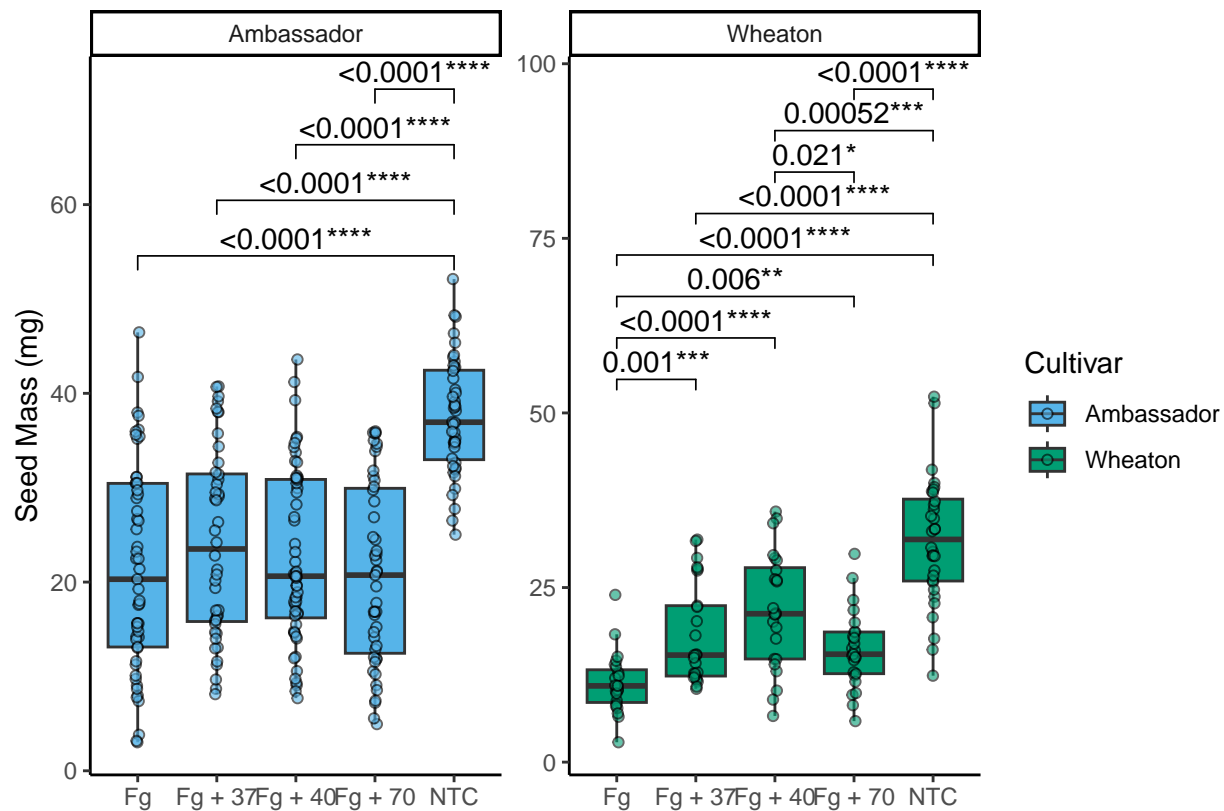


```
mycotoxin.seed.significance<-mycotoxin.seed+
geom_pwc(aes(group=Treatment), method="t.test", label = "{p.adj.format}{p.adj.signif}", hide.ns=T)
mycotoxin.seed.significance
```

```
## Warning: Removed 2 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 2 rows containing non-finite outside the scale range
## ('stat_pwc()').
```

```
## Warning: Removed 2 rows containing missing values or values outside the scale range
## ('geom_point()').
```



```
#Combining all the figures into one.
fig2 <- ggarrange(
  mycotoxin.DON.significance, # First plot
  mycotoxin.X15ADON.significance, # Second plot
  mycotoxin.seed.significance, # Third plot
  labels = c("A","B","C"), # label the plots A, B and C
  nrow = 1, # Arrange the plots in 3 rows
  ncol = 3, # Arrange the plots in 1 column
  common.legend = T #include a legend in the combined figure
)
```

```
## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_boxplot()').

## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_pwc()').

## Warning: Removed 8 rows containing missing values or values outside the scale range
## ('geom_point()').

## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_boxplot()').

## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_pwc()').
```



```
## Warning: Removed 8 rows containing missing values or values outside the scale range
## ('geom_point()').

## Warning: Removed 10 rows containing non-finite outside the scale range
## ('stat_boxplot()').

## Warning: Removed 10 rows containing non-finite outside the scale range
## ('stat_pwc()').

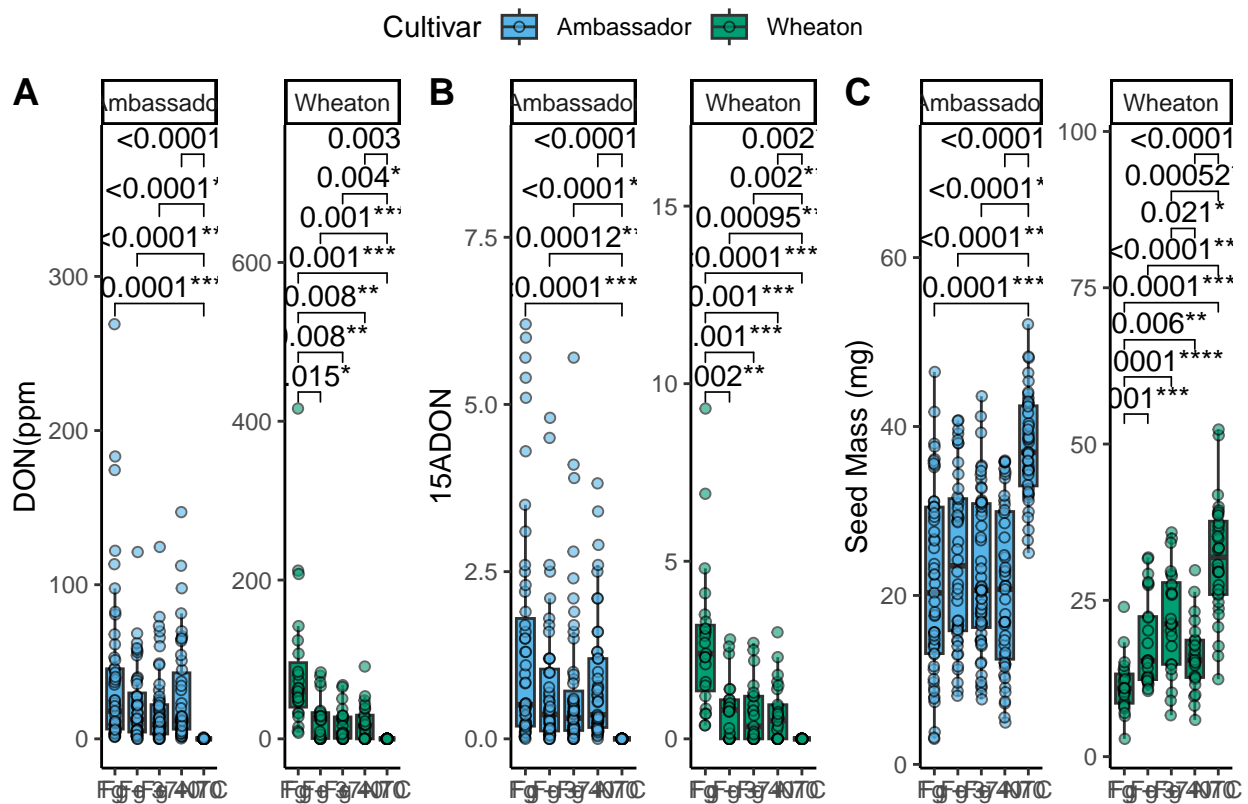
## Warning: Removed 10 rows containing missing values or values outside the scale range
## ('geom_point()').

## Warning: Removed 2 rows containing non-finite outside the scale range
## ('stat_boxplot()').

## Warning: Removed 2 rows containing non-finite outside the scale range
## ('stat_pwc()').

## Warning: Removed 2 rows containing missing values or values outside the scale range
## ('geom_point()').
```

fig2



Question 3.

Knit your document together in the following formats: a. .docx (word document) OR .pdf with a table of contents Link to pdf b. GitHub flavored markdown (.md file). Link to md

Question 4.

Push the .docx or .pdf and .md files to GitHub inside a directory called Coding Challenge 4. Done

Question 5.

Now edit, commit, and push the README file for your repository and include the following elements. a. A clickable link in your README to your GitHub flavored .md file b. A file tree of your GitHub repository. Done

Question 6.

Please provide me a clickable link to your GitHub

Reproducibility_class