R_markdown_class_assignment

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Contents

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

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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.

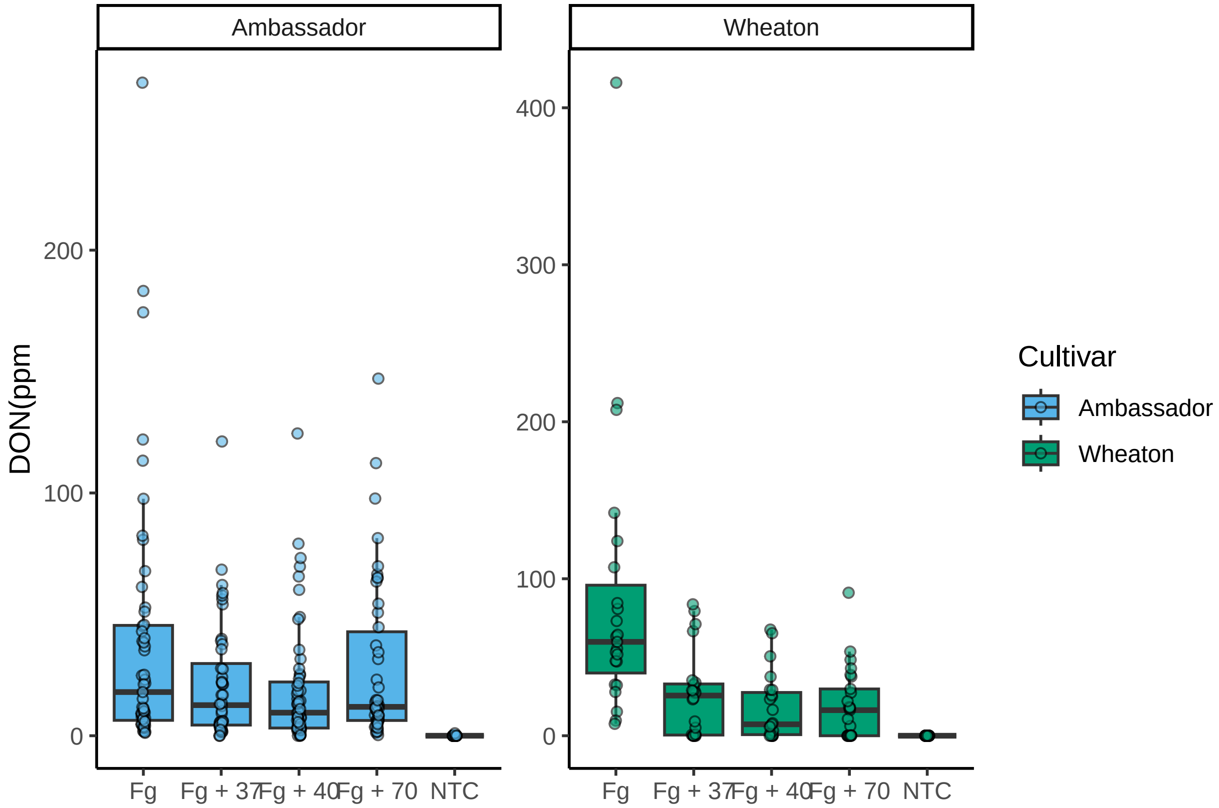
DON

```
####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 sho
  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()‘).
```

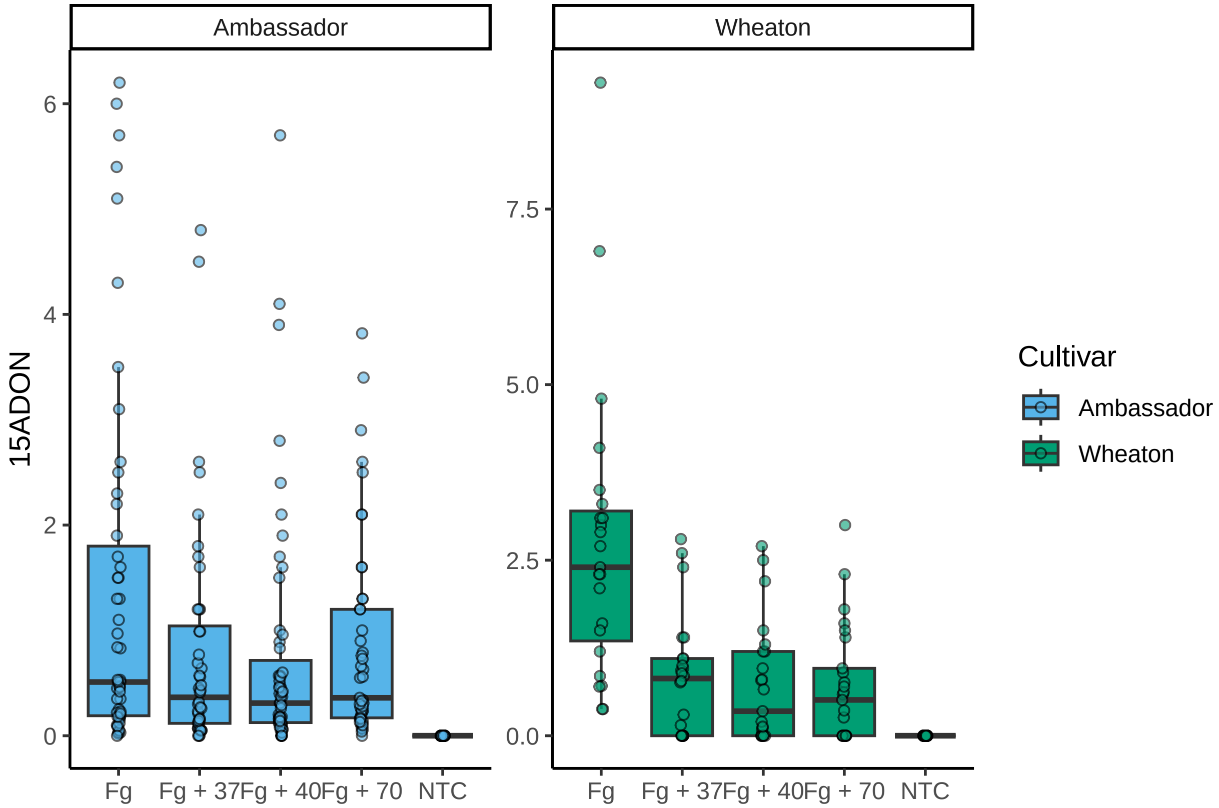


X15DON

```
####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 asthetics 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()‘).
```

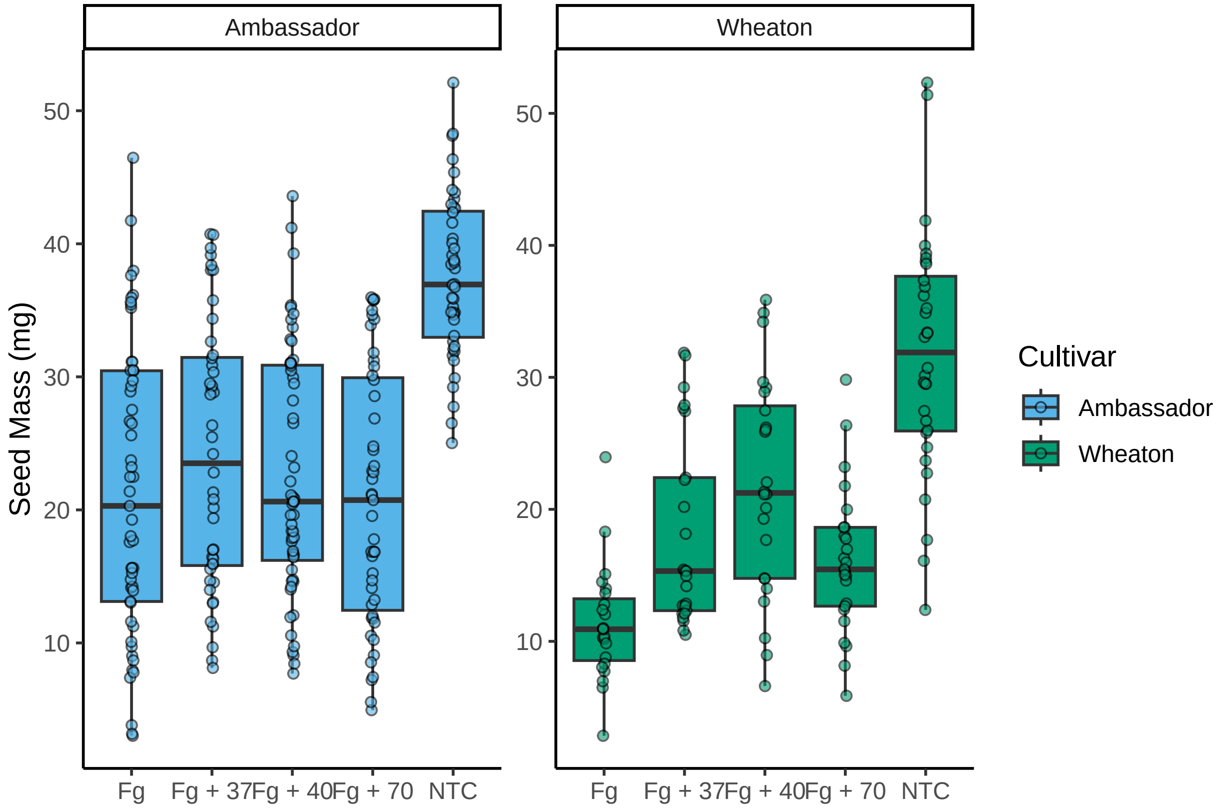


MassperSeed

```
mycotoxin.seed<-ggplot(mycotoxin,aes(Treatment,MassperSeed_mg, fill=Cultivar))+    #define asthetics 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()‘).
```



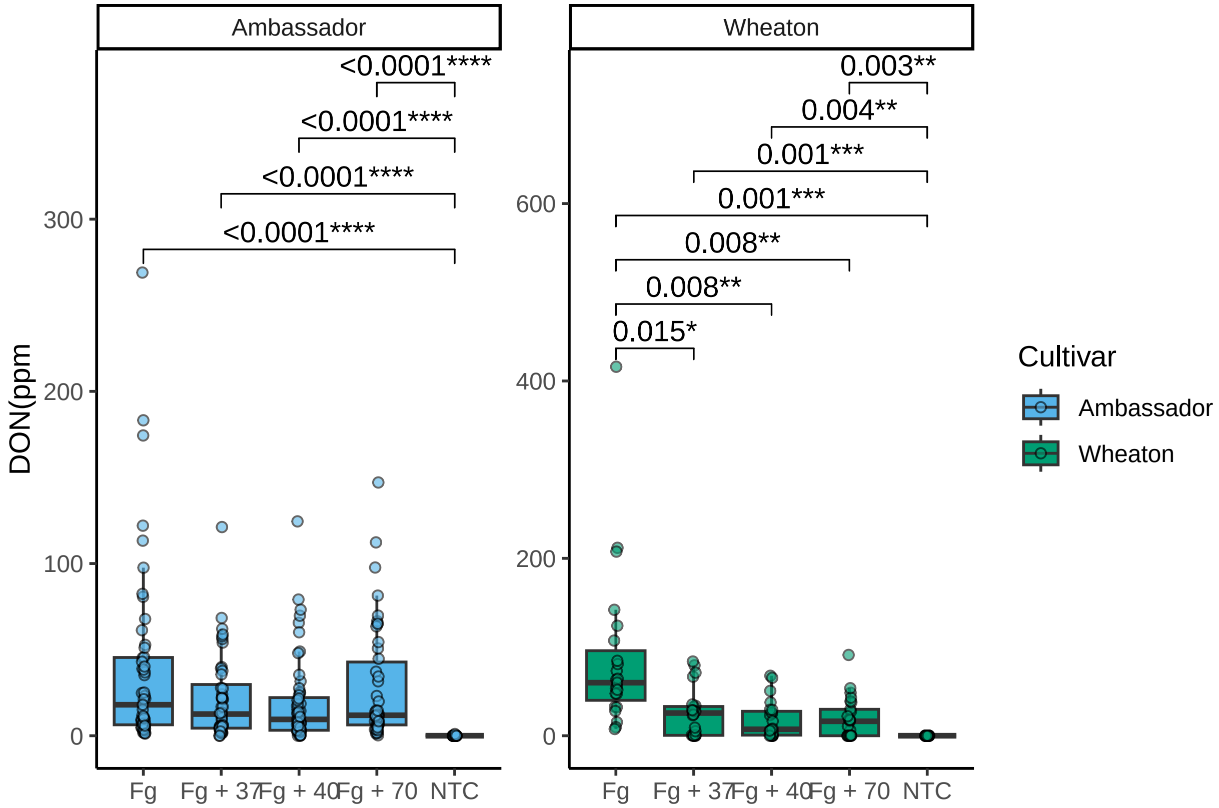
Combine fig

```
####Use geom_pwc() to add t.test pairwise comparisons to the three plots made above. Save each plot as
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()‘).
```

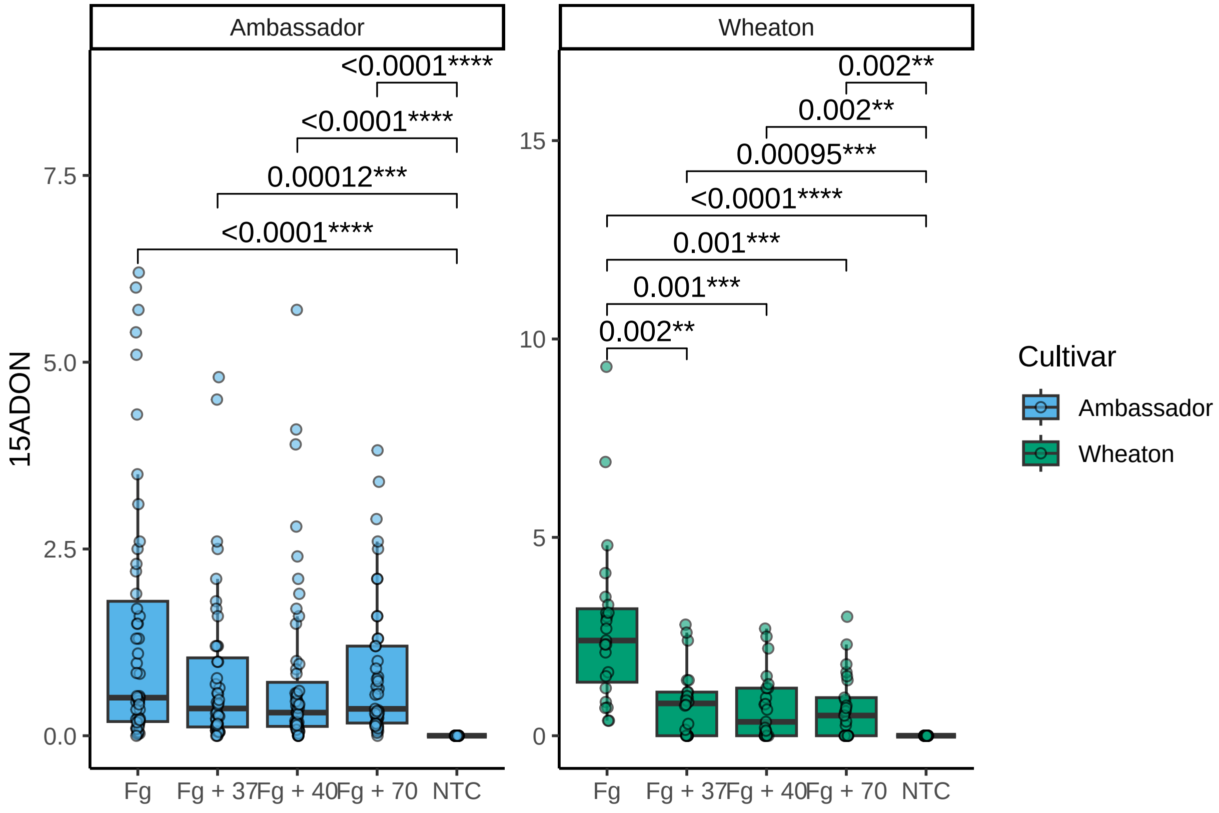


```
mycotoxin.X15ADON.significance<-mycotoxin.X15ADON+
geom_pwc(aes(group=Treatment), method="t.test", label = "{p.adj.format}{p.adj.signif}", hide.ns=T)
mycotoxin.X15ADON.significance
```

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

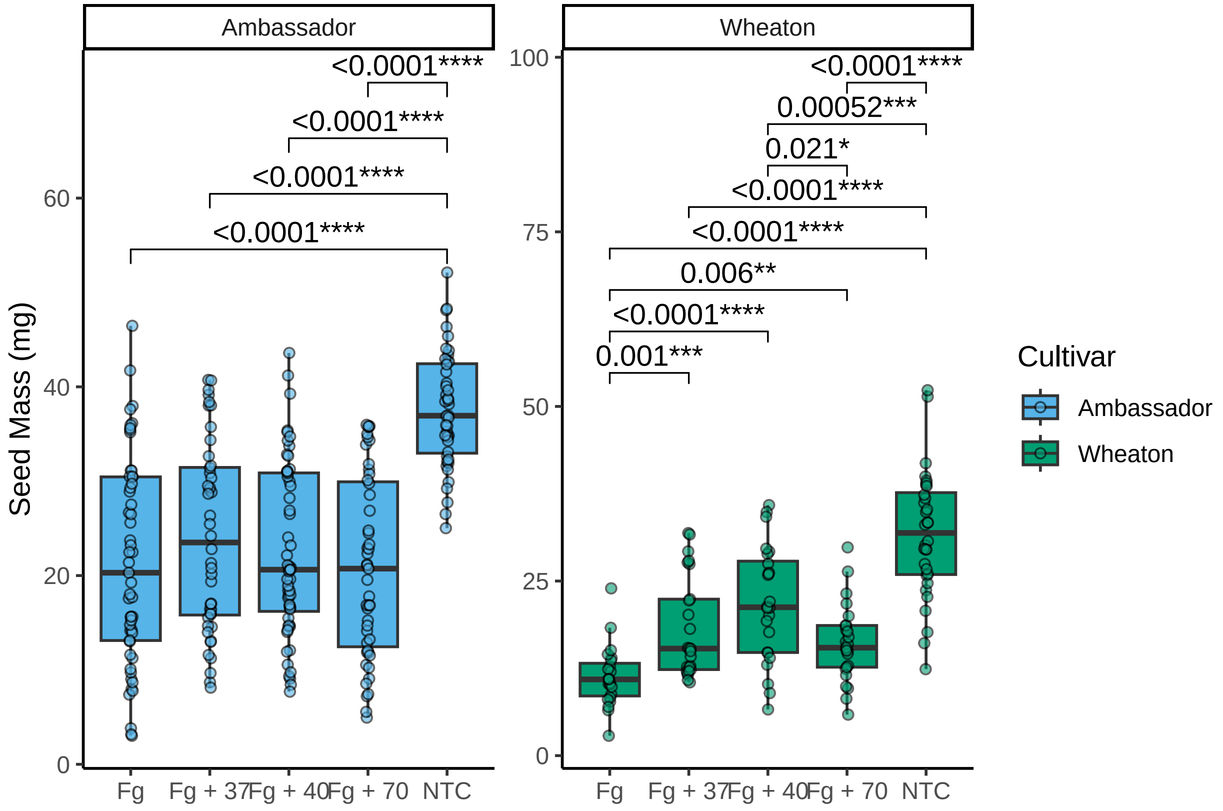

```
 #Combining all the figures into one.
fig2 <- ggarrange(
          mycotoxin.DON.significance,  # First plot
          mycotoxin.X15ADON.significance,  # Second plot
          mycotoxin.seed.significance,  # Third plot
          labels = c("A","B","C"),  # label the plots A, B and C
          nrow = 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()‘).

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

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## (‘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()‘).
```
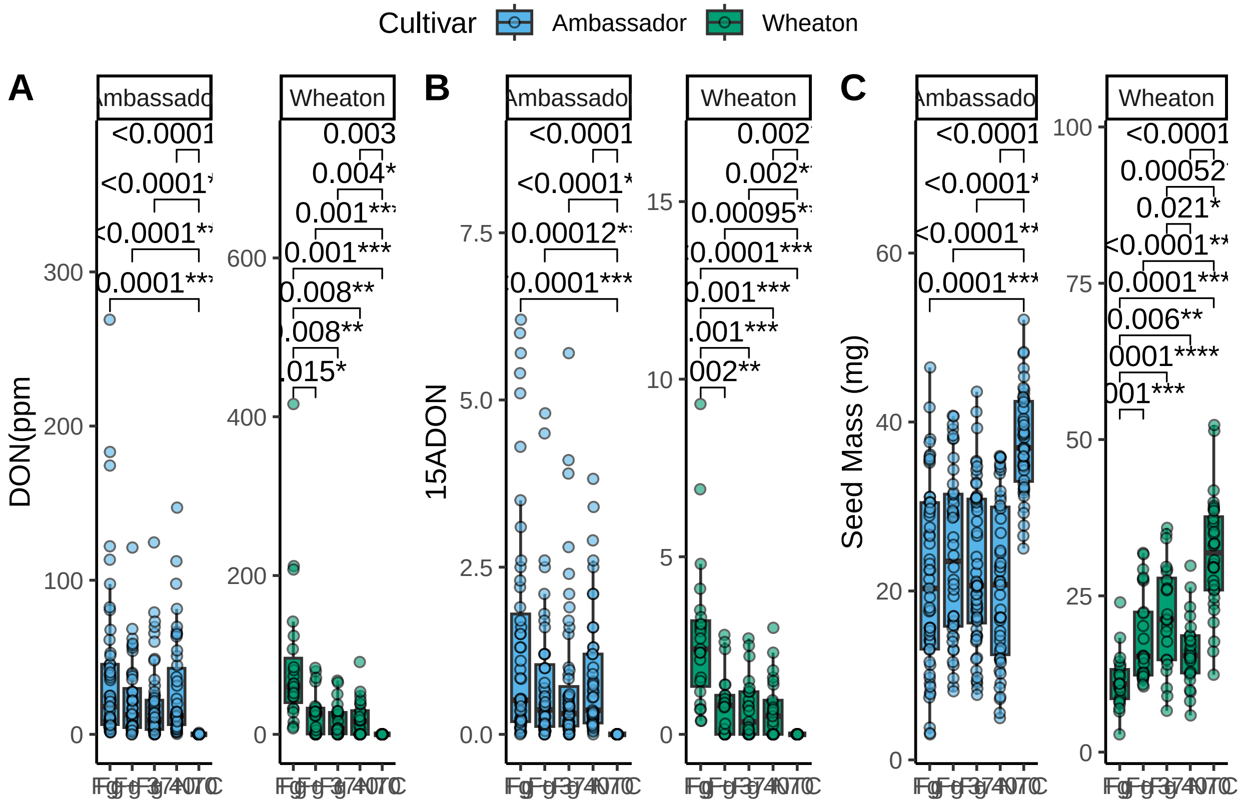

```
fig2
```



Question 3.

Knit your document together in the following formats: a. .docx (word document) OR .pdf with a table of contents

b. GitHub flavored markdown (.md file). Done

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