R Markdown Assignment

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Contents

Markdown – 25 pts

PLEASE READ THIS BEFORE CONTINUING

This assignment will help you practice integrating markdown into your R scripts for literate programming. It will also involve some more practice with GitHub. You may collaborate with a partner to enhance your learning experience. Please ensure the following:

• Collaboration: If you work with a partner, include both names on the final submission by editing the YAML header. • Submission: Only one person should submit the assignment to Canvas in a Word document or .pdf file generated through R markdown. Additionally, you should provide a link to your GitHub, where the assignment should be viewable by rendering it as a GitHub-flavored markdown file. • Setup: It is also assumed you already have a GitHub repository for this class.

1. 4 pts. Explain the following

   a. YAML header: YAML header is situated at the top of the R markdown script which includes information such as title of the document, author of the document, date and output format. Using different options in output, we can render our document as html, word document, pdf document etc. This documents are not recognized by github so, for github we can use option md document to obtain markdown formatted document which is an intermediate markdown format with extension .md and is recognized by github.

   b. Literate programming: Literate programming is an approach to make codes easily readable and understandable by humans thus it uses methods of writing codes along with detailed explanations of the codes. For example: R Markdown allows us to write chunks of codes with detailed explanations within a single document.

2. 6 pts. 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:

b. 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

c. 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.

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

MANUSCRIPT LINK

Data

```
datum <- read.csv ("MycotoxinData.csv" , na.strings = "na") #loading data in R
str(datum)  #viewing the structure of the data
```

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

```
library(ggplot2) #loading library ggplot2
library(ggpubr) #loading library ggpubr
cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7")
```

DON data boxplot

```
boxplot_DON <- ggplot(data = datum, aes(x = Treatment, y = DON, fill=Cultivar)) + #defining aesthetics
  geom_boxplot(position = position_dodge(), outlier.shape = NA) +  #creating box plot without overlap a
  geom_point(position = position_jitterdodge(dodge.width = 0.8), aes(fill=Cultivar),alpha = 0.6, shape=
  scale_fill_manual(values = c(cbbPalette[[4]], cbbPalette[[7]])) + #setting fills of boxplot and data
  xlab("") + #labelling x axis
  ylab("DON (ppm)") + #labelling y axis
  theme_classic() + #setting theme classic to make plain white background
  facet_wrap(~Cultivar) #separating the plots according to cultivars
boxplot_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()').
```
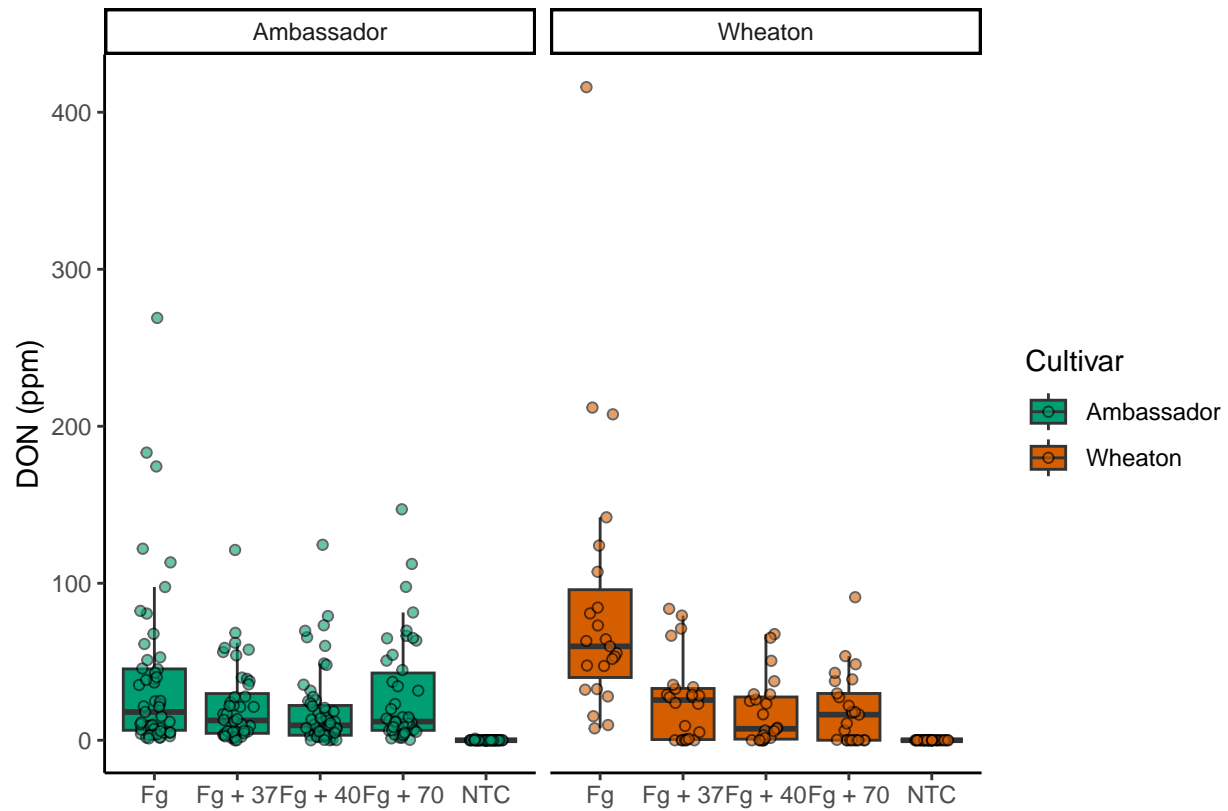
```
boxplot_DON_pwc <- boxplot_DON +
  geom_pwc(aes(group = Treatment), method = "t.test", label = "p.adj.format") #pair-wise comparisons be
boxplot_DON_pwc
```

```
## 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()').
```
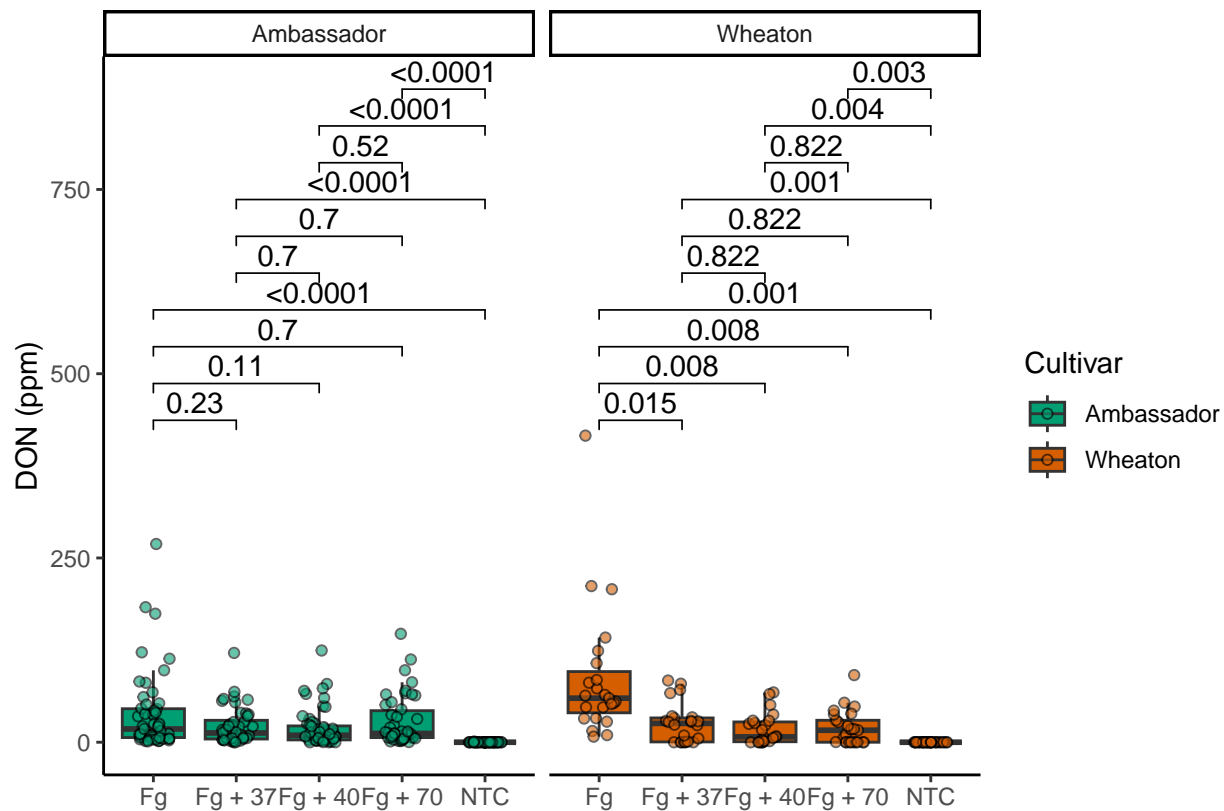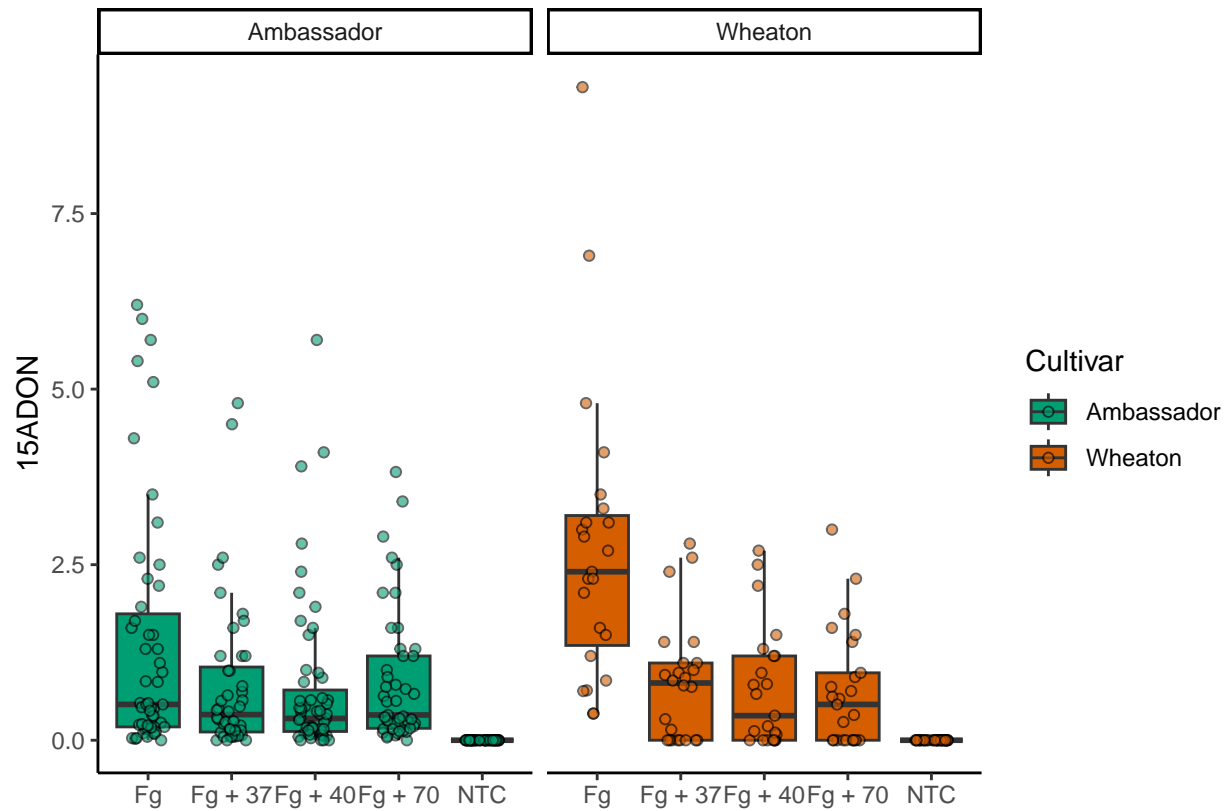
15ADON data boxplot

```
boxplot_15ADON <- ggplot(data = datum, aes(x = Treatment, y = X15ADON, fill = Cultivar)) + #defining ae
  geom_boxplot(position = position_dodge(), outlier.shape = NA) + #creating box plot without overlap an
  geom_point(position = position_jitterdodge(dodge.width = 0.8), aes(fill=Cultivar),alpha = 0.6, shape=
  scale_fill_manual(values = c(cbbPalette[[4]], cbbPalette[[7]])) + #setting fills of boxplot and data
  xlab("") + #labelling x axis
  ylab("15ADON") + #labelling y axis
  theme_classic() + #setting theme classic to make plain white background
  facet_wrap(~Cultivar) #separating the plots according to cultivars
boxplot_15ADON
```

```
## 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()').
```

```
boxplot_15ADON_pwc <- boxplot_15ADON +
  geom_pwc(aes(group = Treatment), method = "t.test", label = "p.adj.format")  #pair-wise comparisons b
 boxplot_15ADON_pwc
```

```
## 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()').
```
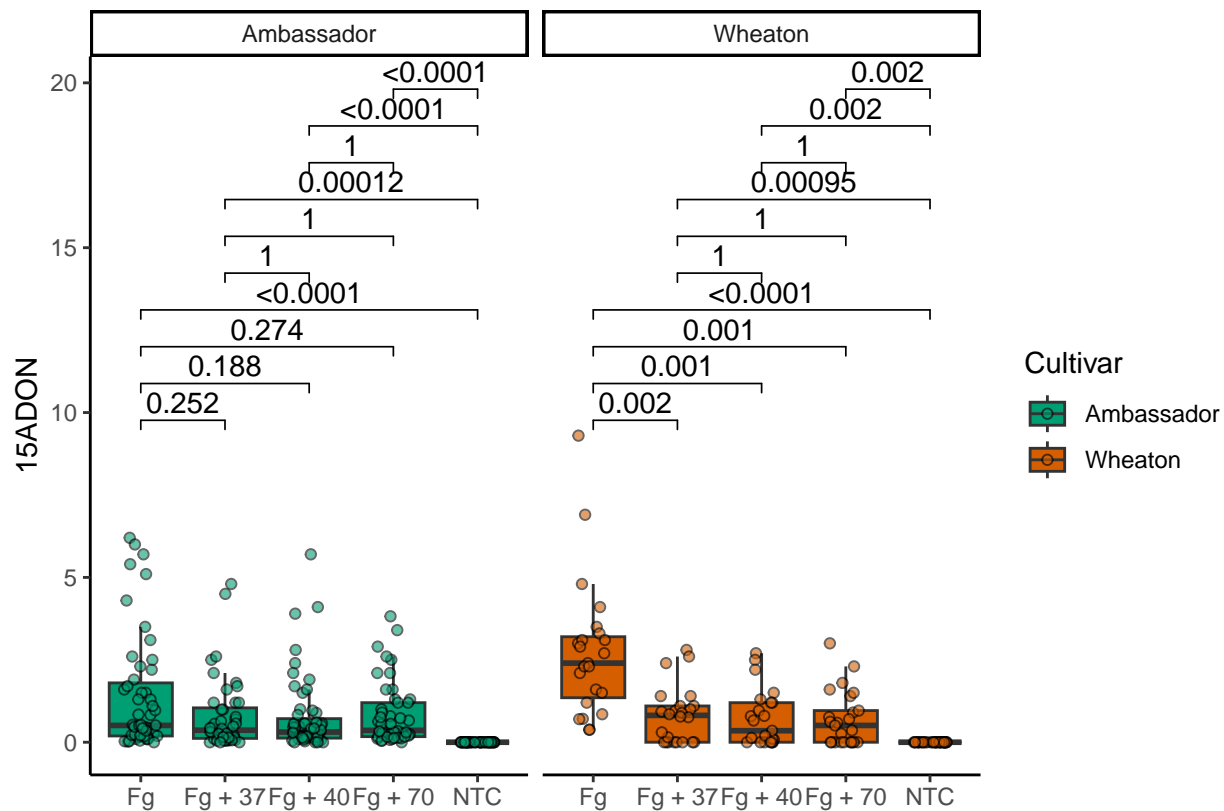
Seedmass boxplot

```
boxplot_massperseed <- ggplot(data = datum, aes(x = Treatment, y = MasperSeed_mg, fill = Cultivar)) +
  geom_boxplot(position = position_dodge(), outlier.shape = NA) + #creating box plot without overlap an
  geom_point(position = position_jitterdodge(dodge.width = 0.8), aes(fill=Cultivar),alpha = 0.6, shape=
  scale_fill_manual(values = c(cbbPalette[[4]], cbbPalette[[7]])) + #setting fills of boxplot and data
  xlab("") + #labelling x axis
  ylab("Seed Mass (mg)") + #labelling y axis
  theme_classic() + #setting theme classic to make plain white background
  facet_wrap(~Cultivar) #separating the plots according to cultivars
boxplot_massperseed
```

```
## 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()').
```
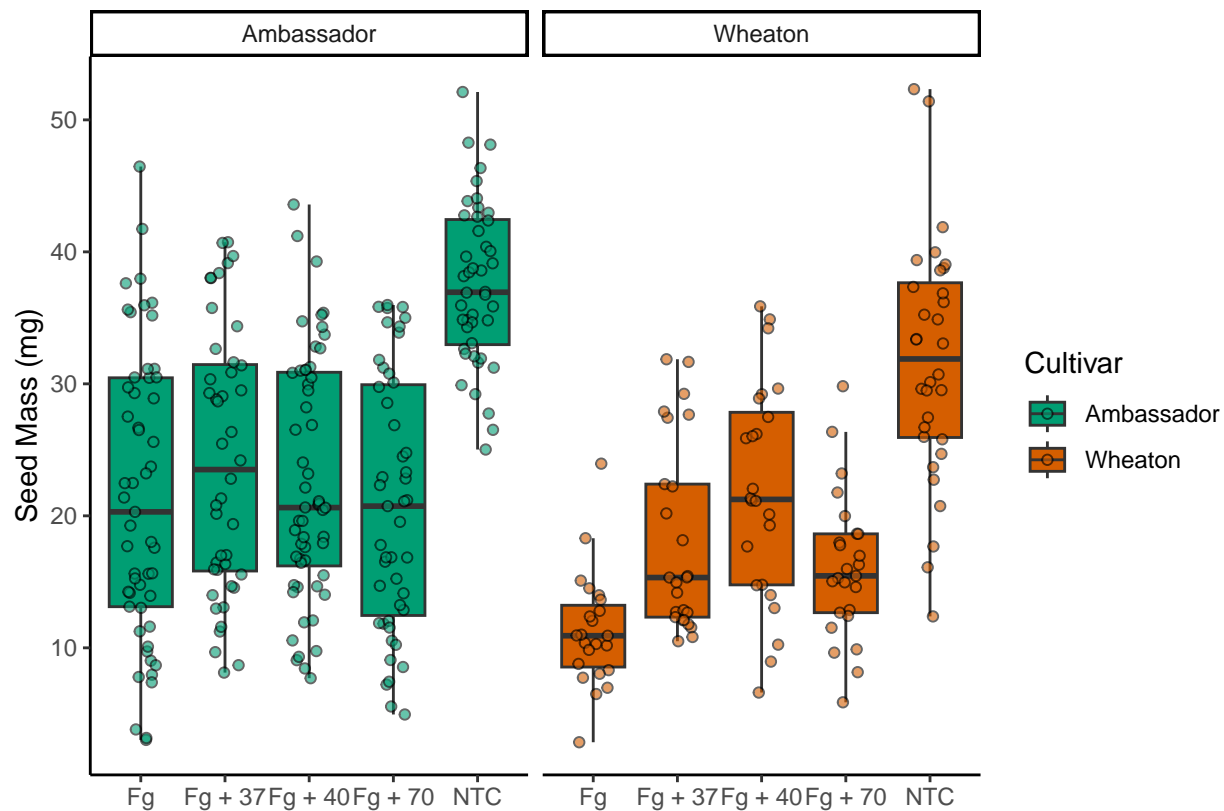
```
boxplot_massperseed_pwc <- boxplot_massperseed +
  geom_pwc(aes(group = Treatment), method = "t.test", label = "p.adj.format") #pair-wise comparisons be
boxplot_massperseed_pwc
```

```
## 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()').
```
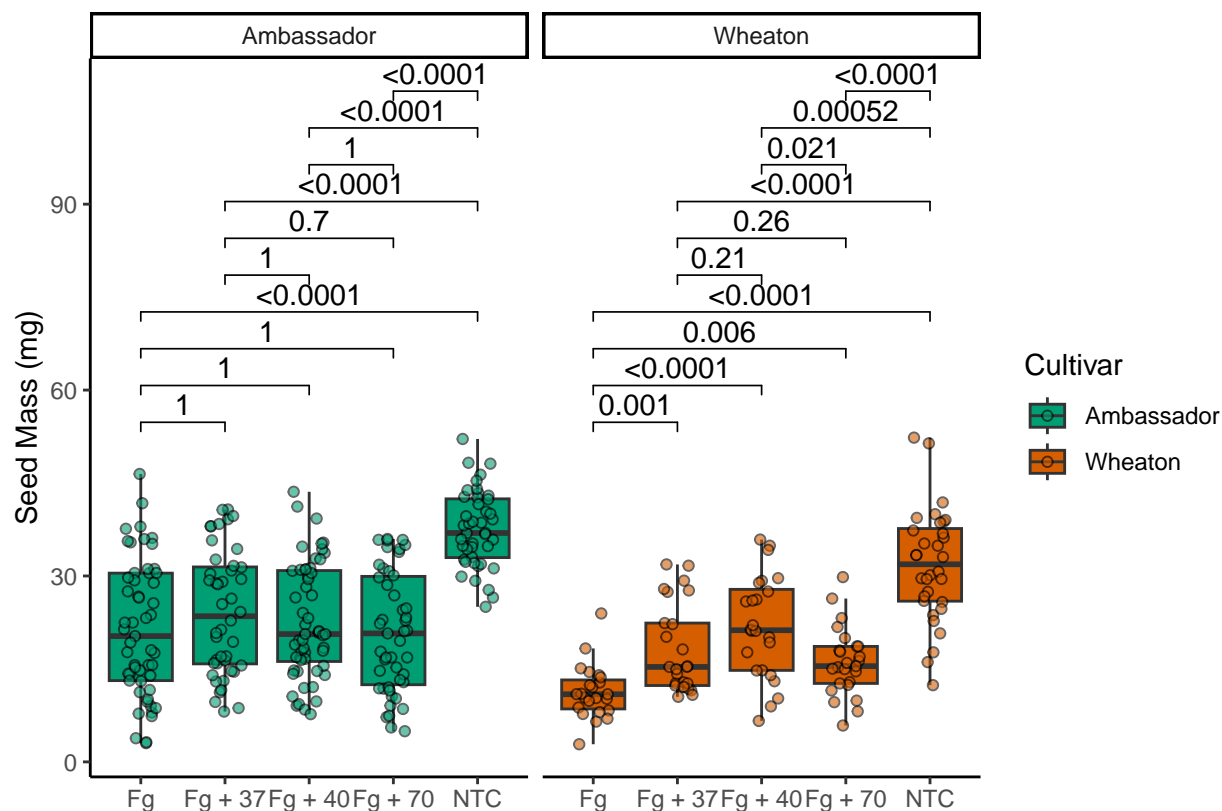
Combined figure

```r
figure_pwc <- ggarrange(
  boxplot_DON_pwc, #plotting boxplot1_pwc
  boxplot_15ADON_pwc, #plotting boxplot_15ADON_pwc
  boxplot_massperseed_pwc, #plotting boxplot_massperseed_pwc
  labels = "AUTO", #setting labels as A, B and C
  nrow = 1, #combining figures with single row
  ncol = 3, #combining figures with 3 columns
  common.legend = TRUE, #combining legends for all three figures as one
  legend = TRUE #displaying legend
)
```

```
## 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()`).
```
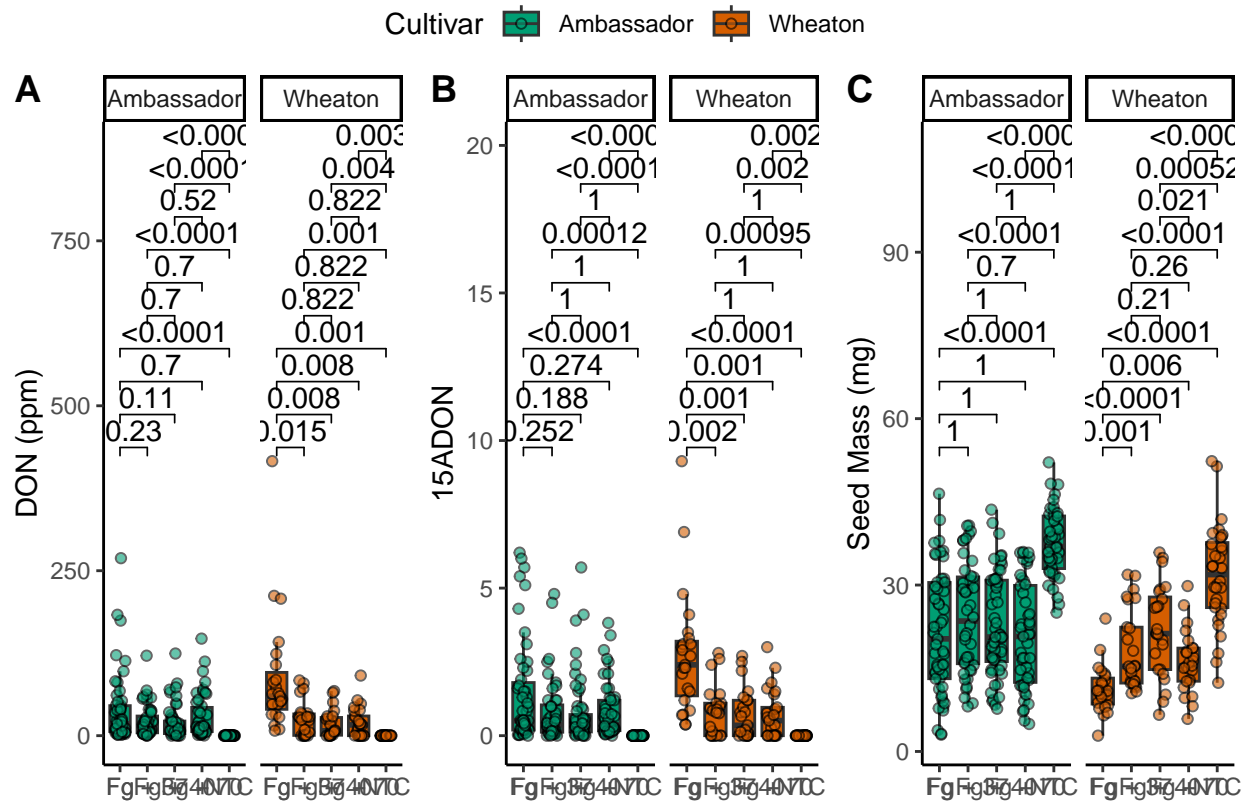
```
figure_pwc
```

3. 6 pts. 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).

4. 2 pts. Push the .docx or .pdf and .md files to GitHub inside a directory called Coding Challenge 4.

5. 6 pts. 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.

6. 1 pt. Please provide me a clickable link to your GitHub

GitHub Link