

# Coding\_Challenge4\_Markdown

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## Coding Challenge 4 Answers

Q1) Explain the following a. YAML header YAMLS helps in writing the configuration of the files and is on the top of the markdown files.

b. Literate programming In literate programming along with our code we will have its explanations and provide the chunks of codes. It explains the codes in better way.

Q2)

## Clickable link to manuscript where these data are published

Noel et al., 2022. Endophytic fungi as promising biocontrol agent to protect wheat from Fusarium graminearum head blight. Plant Disease

```
## Load libraries
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v readr      2.1.5
## v forcats    1.0.0      v stringr   1.5.1
## v ggplot2    3.5.1      v tibble    3.2.1
## v lubridate  1.9.3      v tidyr     1.3.1
## v purrr      1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(ggpubr)
library("knitr") # required for knitting
```

```
## Reading data by relative path
```

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

```
## 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
```

```
## Codes needed for complete analysis
```

```
#Plot1 Treatment on Y
```

```
P1 <- ggplot(csv, aes(x = Treatment, y = DON, fill = Cultivar))+
  theme_classic() + # removes the grids
  geom_boxplot() +
  xlab("") +
  ylab("DON (ppm)") +
  geom_point(alpha = 0.6, shape = 21, position = position_jitterdodge()) +
  scale_fill_manual (values = c("#56B4E9", "#009E73")) +
  facet_wrap(~ Cultivar)

str(csv)
```

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

```
csv$Treatment <- factor(csv$Treatment, levels = c("NTC", "Fg", "Fg + 37", "Fg + 40", "Fg + 70"))
```

```
#Plot2 X15ADON on Y
```

```
P2 <- ggplot(csv, aes(x = Treatment, y = X15ADON, fill = Cultivar))+
  theme_classic() + # removes the grids
  geom_boxplot() +
  xlab("") +
  ylab("X15ADON") +
  geom_point(alpha = 0.6, shape = 21, position = position_jitterdodge()) +
  scale_fill_manual (values = c("#56B4E9", "#009E73")) +
  facet_wrap(~ Cultivar)
```

```
#Plot3 MassperSeed_mg on Y
```

```
P3 <- ggplot(csv, aes(x = Treatment, y = MassperSeed_mg, fill = Cultivar))+
  theme_classic() + # removes the grids
  geom_boxplot() +
  xlab("") +
  ylab("Seed Mass (mg)") +
```

```
geom_point(alpha = 0.6, shape = 21, position = position_jitterdodge()) +
scale_fill_manual (values = c("#56B4E9", "#009E73")) +
facet_wrap(~ Cultivar)
```

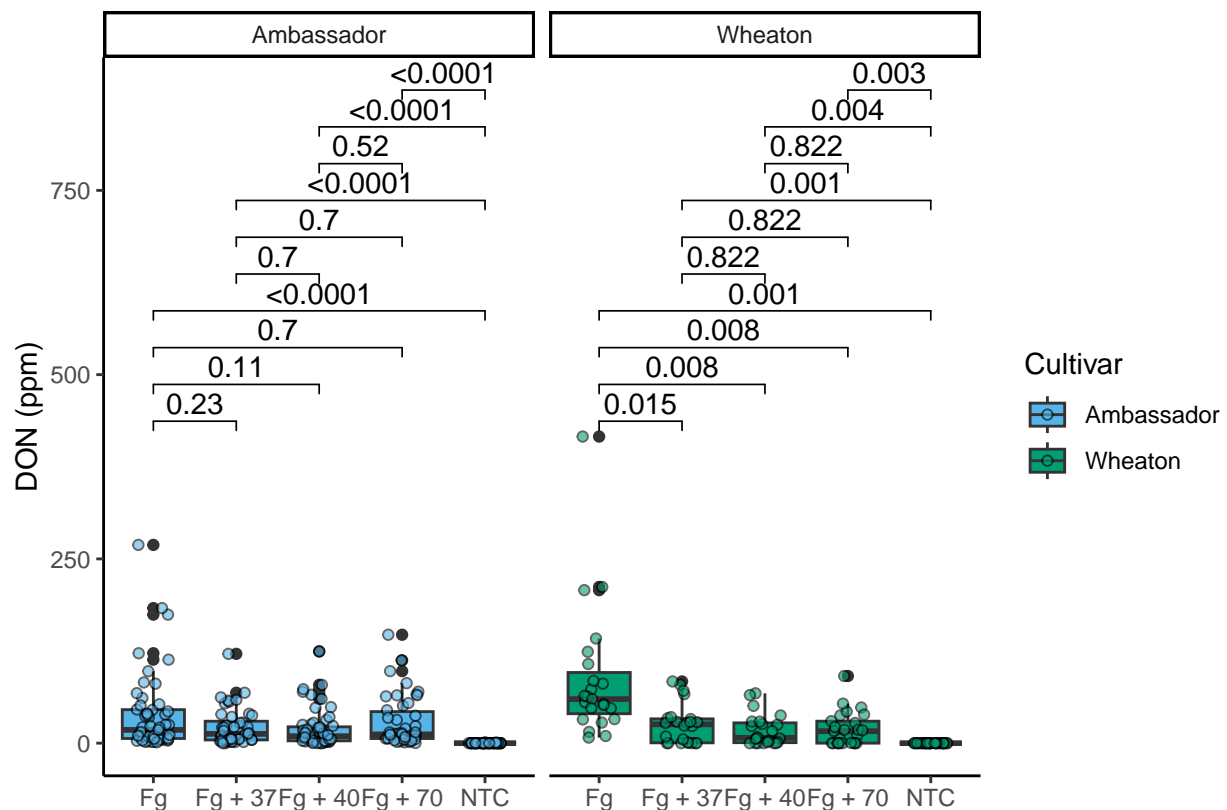
Code from coding challenge 3, question 5 & sepreated code chunks for each plot

```
P1_stat <- P1 +
  geom_pwc(aes(group = Treatment), method = "t_test", label = "p.adj.format")
P1_stat
```

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

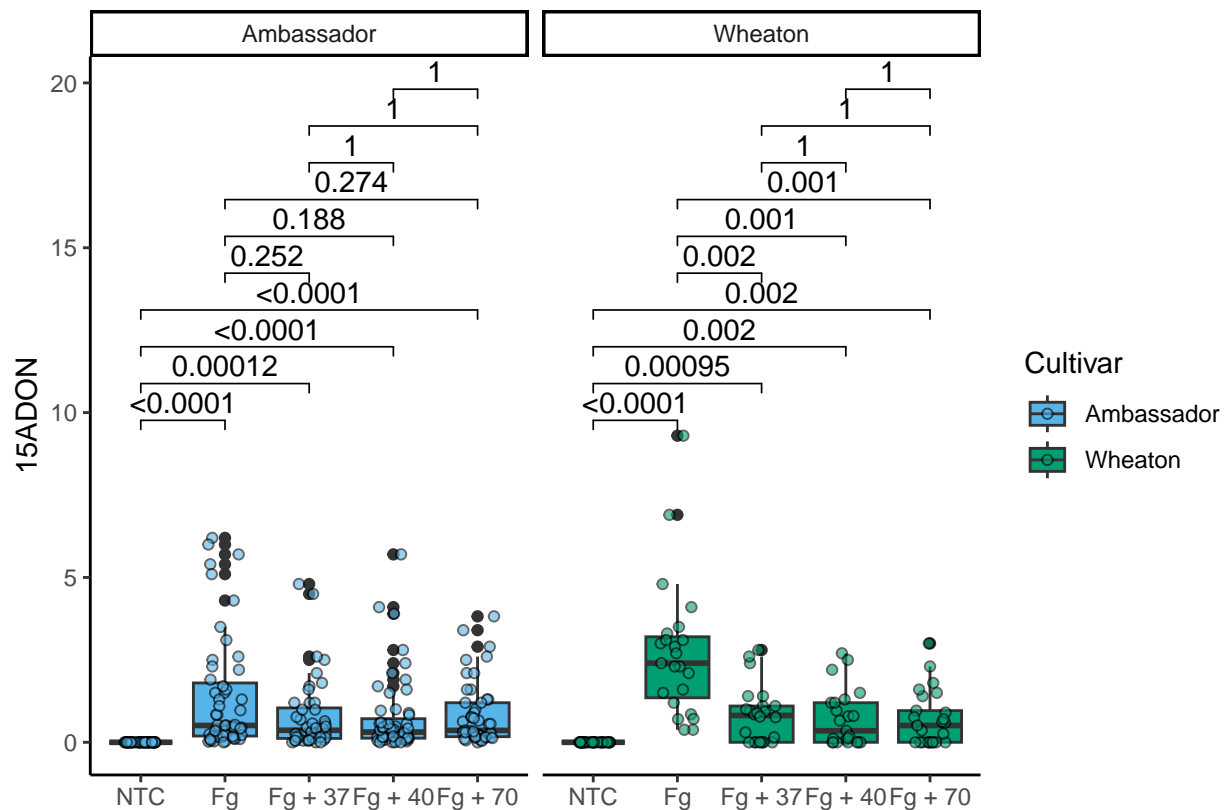


```
P2_stat <- P2 +
  geom_pwc(aes(group = Treatment), method = "t_test", label = "p.adj.format")
P2_stat
```

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

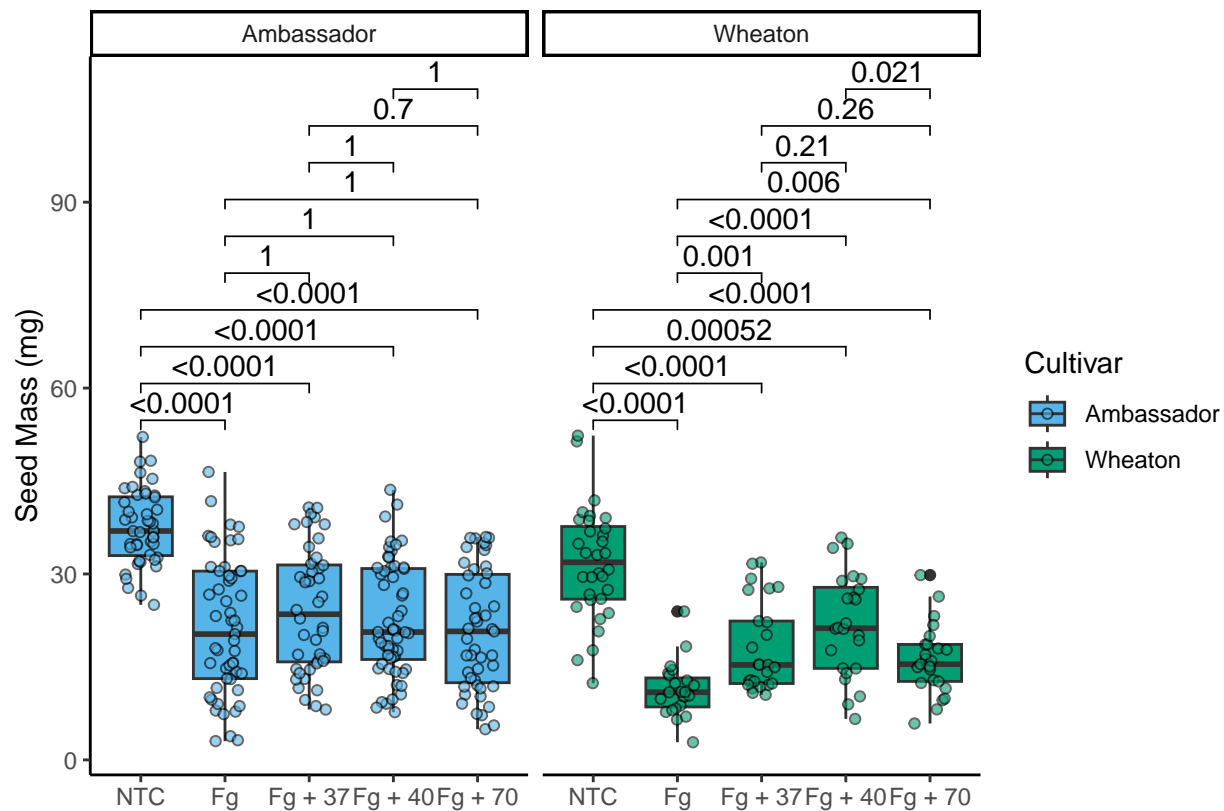


```
P3_stat <- P3 +
  geom_pwc(aes(group = Treatment), method = "t_test", label = "p.adj.format")
P3_stat
```

```
## 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
Combined_plot_stat <- ggarrange(
  P1_stat, ## add the plots onf interest subsequently
  P2_stat,
  P3_stat,
  labels = "auto", # Automatically label the plots (A, B, C, etc.)
  nrow = 1, # Arrange the plots in # rows
  ncol = 3, # Arrange the plots in # column
  common.legend = T
)

## 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()').
```