# R Markdown Coding Challenge

## Vaibhav Shelar

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- Link of manuscript

**Q1**

# YAML Header:

YAML header is a short blob of text, specially formatted with key: value pairs tags, that seats at the top of our Rmarkdown document. It contains YAML arguments such as "Title", "Author", and "Output", demarcated by three dashes (—) on either end.

# Literate Programming:

A methodology that combines a programming language with a documentation language, thereby making programs more robust, more portable, more easily maintained, and arguably more fun to write than programs that are written only in a high-level language.

**Q2**

```r
# Load dataset of MycotoxinData
Mycotoxin_Data <- read.csv("D:/Spring 2025/PLPA7820/Class-Reports/MycotoxinData.csv", na.strings = "na")

# structure of the dataframe
str(Mycotoxin_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 ...
```

```r
# plotting data using ggplota2 (Boxplot)

library(ggplot2)

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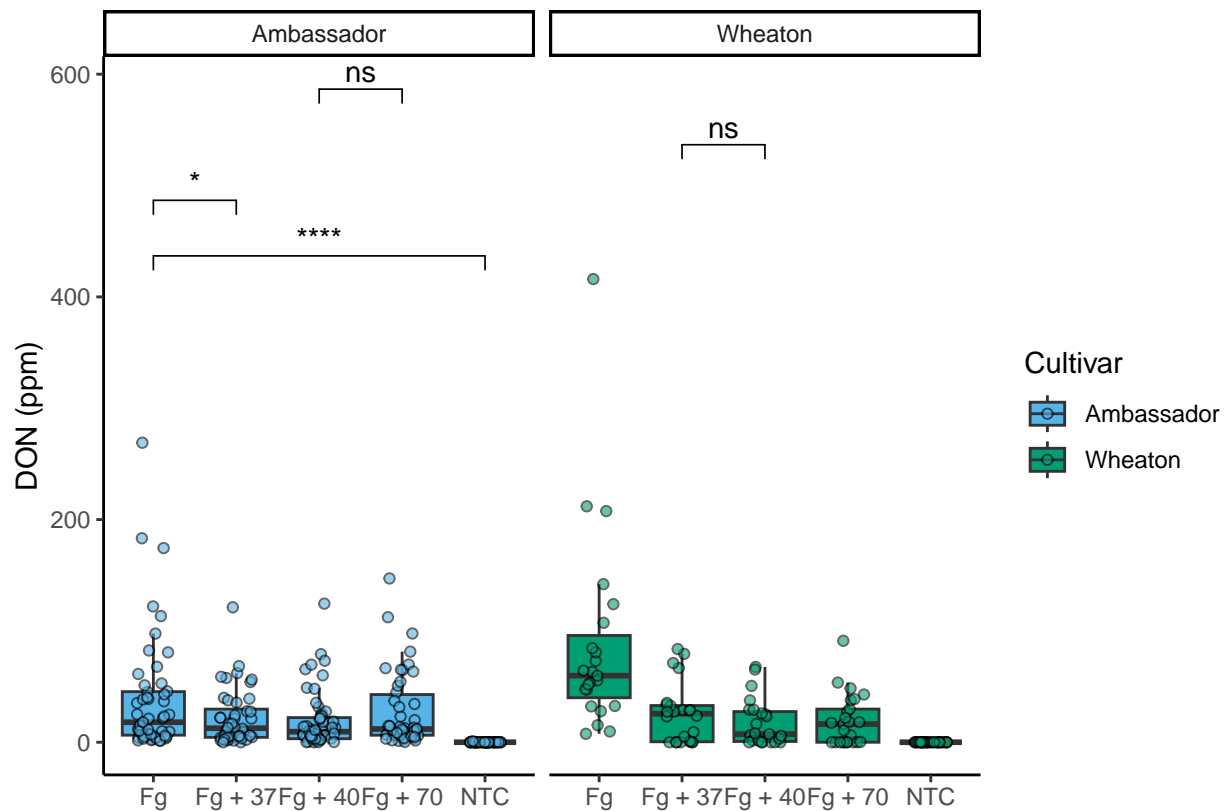
```r
library(ggplot2)
library(ggpubr)

DONplot.pwc <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = DON, fill = Cultivar)) +
  geom_boxplot(outliers = F) +
  xlab("") +
  ylab("DON (ppm)") +
  geom_point(alpha = 0.6, pch = 21, color = "black", position = position_jitterdodge()) +
  scale_color_manual(values = c(cbbPalette[3], cbbPalette[4])) +
  scale_fill_manual(values = c(cbbPalette[3], cbbPalette[4])) +
  theme_classic() +
  facet_wrap(~Cultivar) +
  stat_compare_means(method = "t.test", label = "p.signif",
                     comparisons = list(c("NTC", "Fg"),
                                        c("Fg", "Fg + 37"),
                                        c("Fg + 37", "Fg + 40"),
                                        c("Fg + 40", "Fg + 70")))

DONplot.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_signif()').
```

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

```r
X15ADONplot.pwc <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = X15ADON, fill = Cultivar)) +
  geom_boxplot(outlier.shape = NA) +
  xlab("") +
  ylab("15ADON") +
  geom_point(alpha = 0.6, pch = 21, color = "black", position = position_jitterdodge()) +
  scale_color_manual(values = c(cbbPalette[3], cbbPalette[4])) +
  scale_fill_manual(values = c(cbbPalette[3], cbbPalette[4])) +
  theme_classic() +
  facet_wrap(~Cultivar) +
  stat_compare_means(method = "t.test", label = "p.signif",
                     comparisons = list(
                       c("NTC", "Fg"),
                       c("Fg", "Fg + 37"),
                       c("Fg + 37", "Fg + 40"),
                       c("Fg + 40", "Fg + 70")
                     ))

X15ADONplot.pwc
```
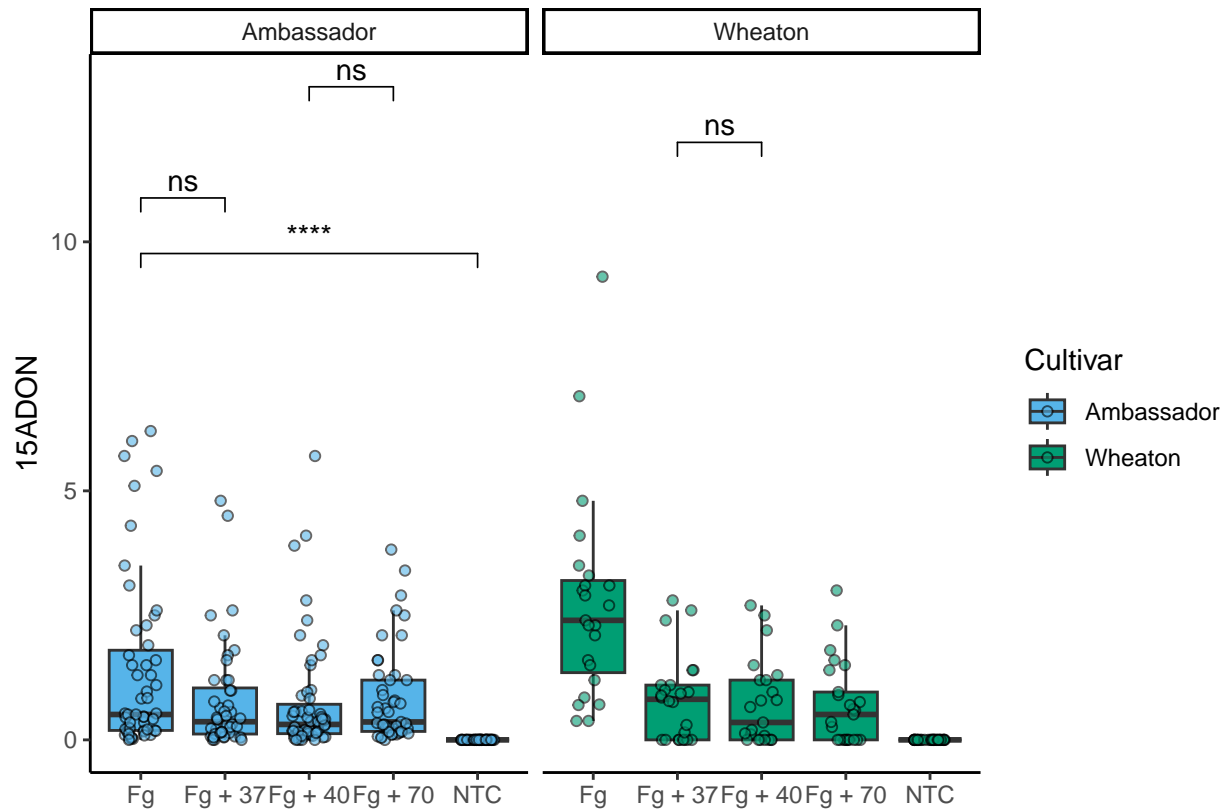
```
## Warning: Removed 10 rows containing non-finite outside the scale range
## ('stat_boxplot()').

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

## Warning: Removed 10 rows containing missing values or values outside the scale range
```

## (`geom_point()`).



```
Seed.massplot.pwc <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = MassperSeed_mg, fill = Cultivar)) +
  geom_boxplot(outliers = F) +
  xlab("") +
  ylab("Seed Mass (mg)") +
  geom_point(alpha = 0.6, pch = 21, color = "black", position = position_jitterdodge()) +
  scale_color_manual(values = c(cbbPalette[3], cbbPalette[4])) +
  scale_fill_manual(values = c(cbbPalette[3], cbbPalette[4])) +
  theme_classic() +
  facet_wrap(~Cultivar) +
  stat_compare_means(method = "t.test", label = "p.signif",
                     comparisons = list(c("NTC", "Fg"),
                                        c("Fg", "Fg + 37"),
                                        c("Fg + 37", "Fg + 40"),
                                        c("Fg + 40", "Fg + 70")))

Seed.massplot.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_signif()`).

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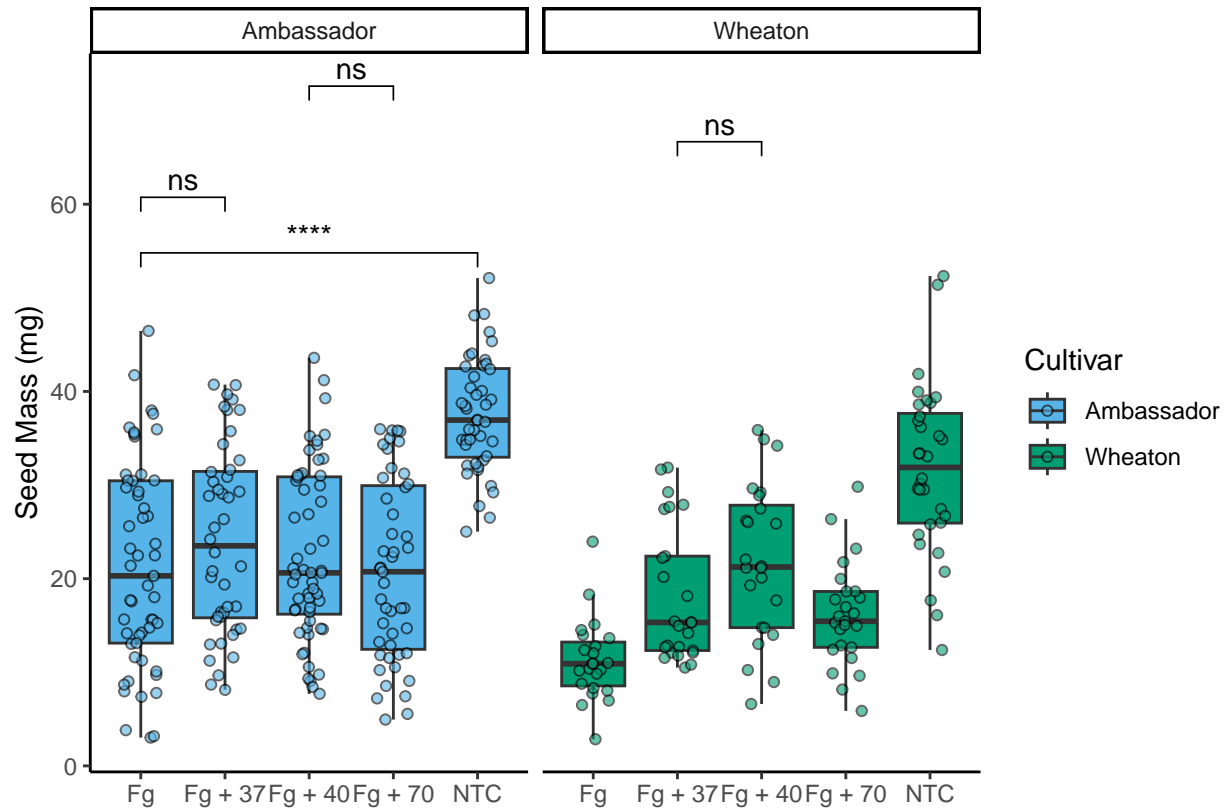


```
Combineplot.pwc <- ggarrange(
  DONplot.pwc,
  X15ADONplot.pwc,
  Seed.massplot.pwc,
  labels = c("A", "B", "C"),
  nrow = 1,
  ncol = 3,
  common.legend = TRUE,
  legend = "bottom"
)
```

## 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_signif()`).

## 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_signif()').

## 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_signif()').

## 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_signif()').

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

Combineplot.pwc