

R Markdown Coding Challenge

Vaibhav Shelar

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- Link of manuscript
- GitHub flavored .md file

File Tree

```
library("fs")
fs::dir_tree(path = "D:/Spring 2025/PLPA7820/Class-Reports/Assignments/Coding Challenge 4")

## D:/Spring 2025/PLPA7820/Class-Reports/Assignments/Coding Challenge 4
## +-- R Markdown Coding Challenge.Rmd
## +-- R-Markdown-Coding-Challenge.docx
## +-- R-Markdown-Coding-Challenge.html
## +-- R-Markdown-Coding-Challenge.md
## +-- R-Markdown-Coding-Challenge.pdf
## \-- R-Markdown-Coding-Challenge_files
##     \-- figure-gfm
##         +-- unnamed-chunk-6-1.png
##         +-- unnamed-chunk-7-1.png
##         +-- unnamed-chunk-8-1.png
##         \-- unnamed-chunk-9-1.png
```

Q1

YAML Header:

YAML header is a short blob of text, specially formatted with key: value pairs tags, that sits 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

```
# 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 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 ...
```

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

```
library(ggplot2)
```

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

```
library(ggplot2)
```

```
library(ggpubr)
```

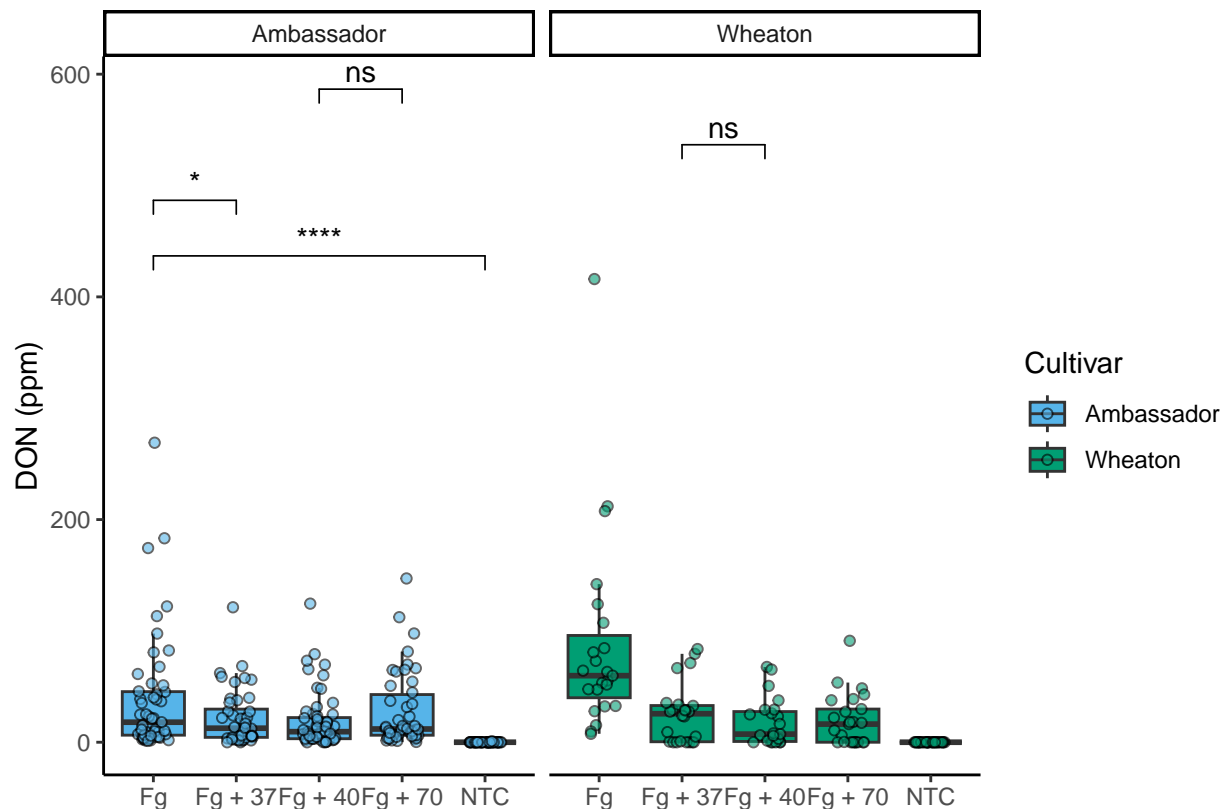
```
DONplot.pwc <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = DON, fill = Cultivar)) +
  geom_boxplot(outliers = F) +
  xlab("") +
  ylab("DON (ppm)") +
  geom_point(alpha = 0.6, pch = 21, color = "black", position = position_jitterdodge()) +
  scale_color_manual(values = c(cbbPalette[3], cbbPalette[4])) +
  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()').
```



```
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")
    )
  )
```

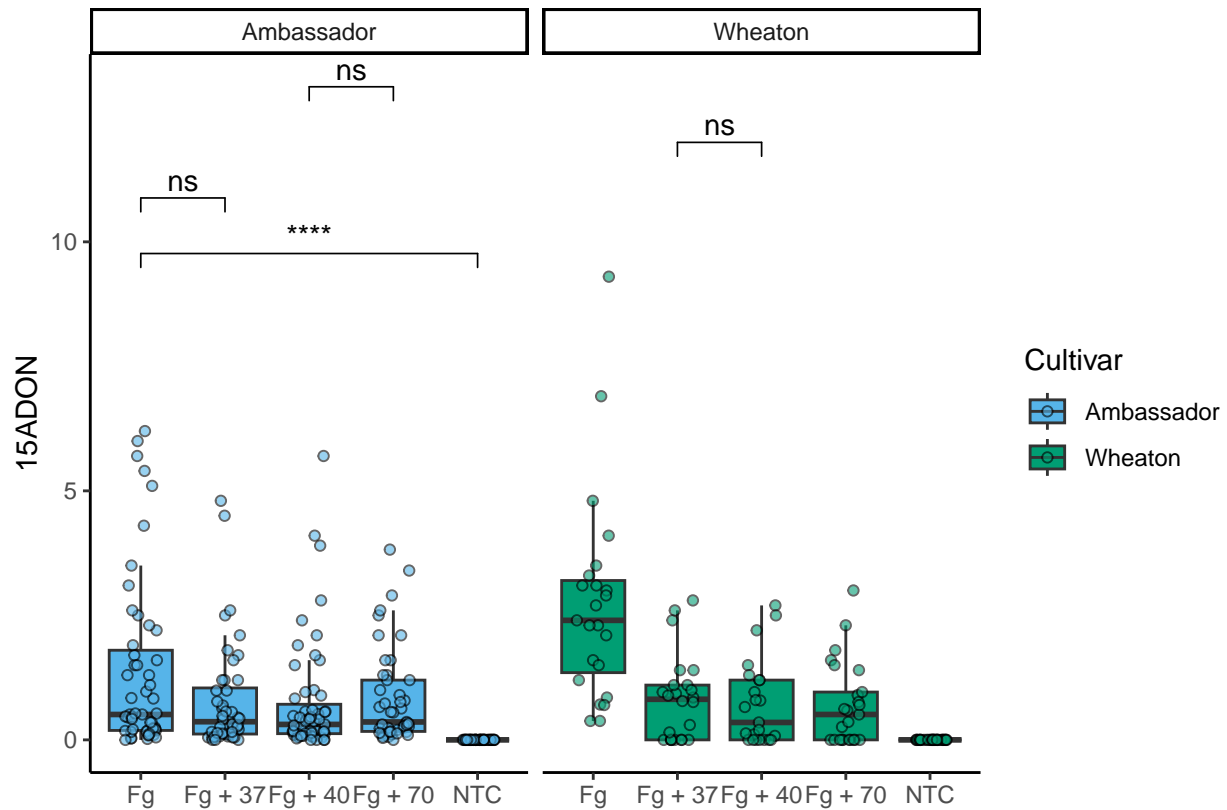
X15ADONplot.pwc

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



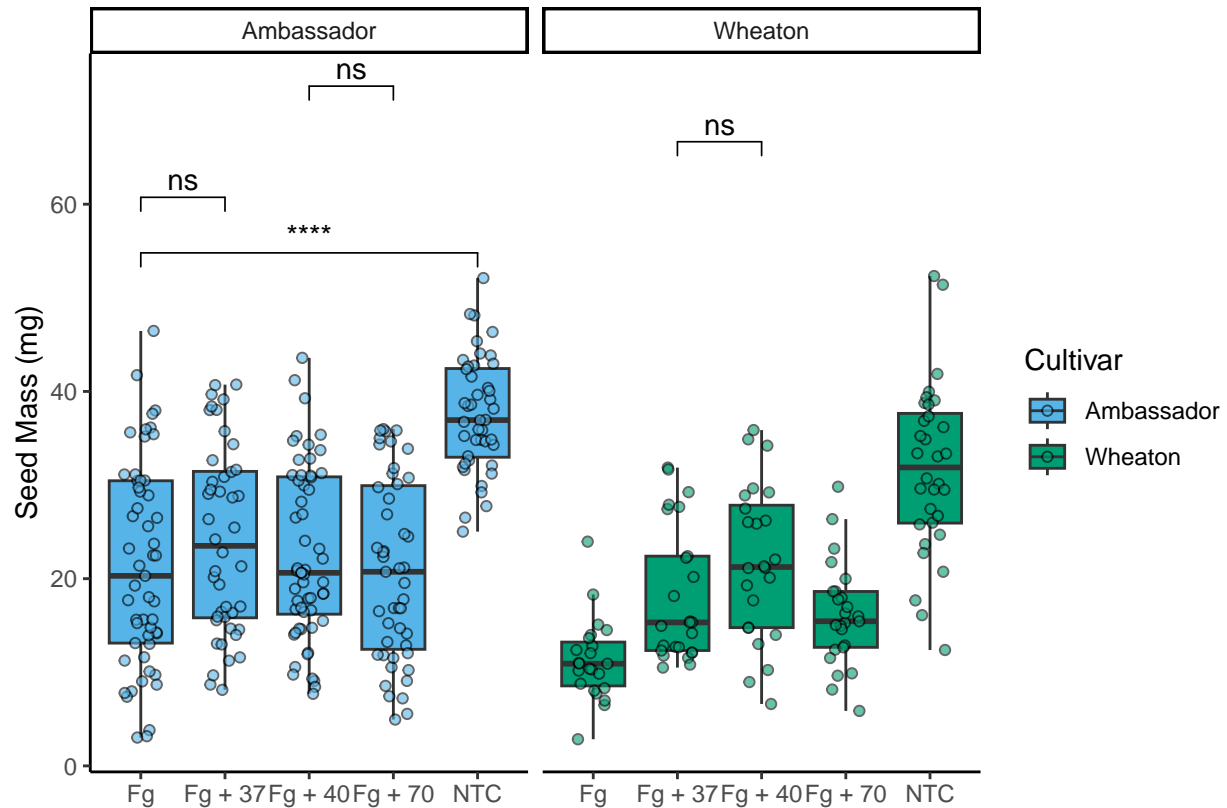
```
Seed.massplot.pwc <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = MassperSeed_mg, fill = Cultivar)) +
  geom_boxplot(outliers = F) +
  xlab("") +
  ylab("Seed Mass (mg)") +
  geom_point(alpha = 0.6, pch = 21, color = "black", position = position_jitterdodge()) +
  scale_color_manual(values = c(cbbPalette[3], 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

