R Markdown Coding Challenge

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```r
library(knitr)
```

- Link of manuscript

File Tree

```r
library("fs")
fs::dir_tree(path = "Assignments/CodingChallenge4")
```

```
## Assignments/CodingChallenge4
## +-- 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 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("MycotoxinData.csv", na.strings = "na")
```

```r
# 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)
```

```r
library(ggplot2)
```

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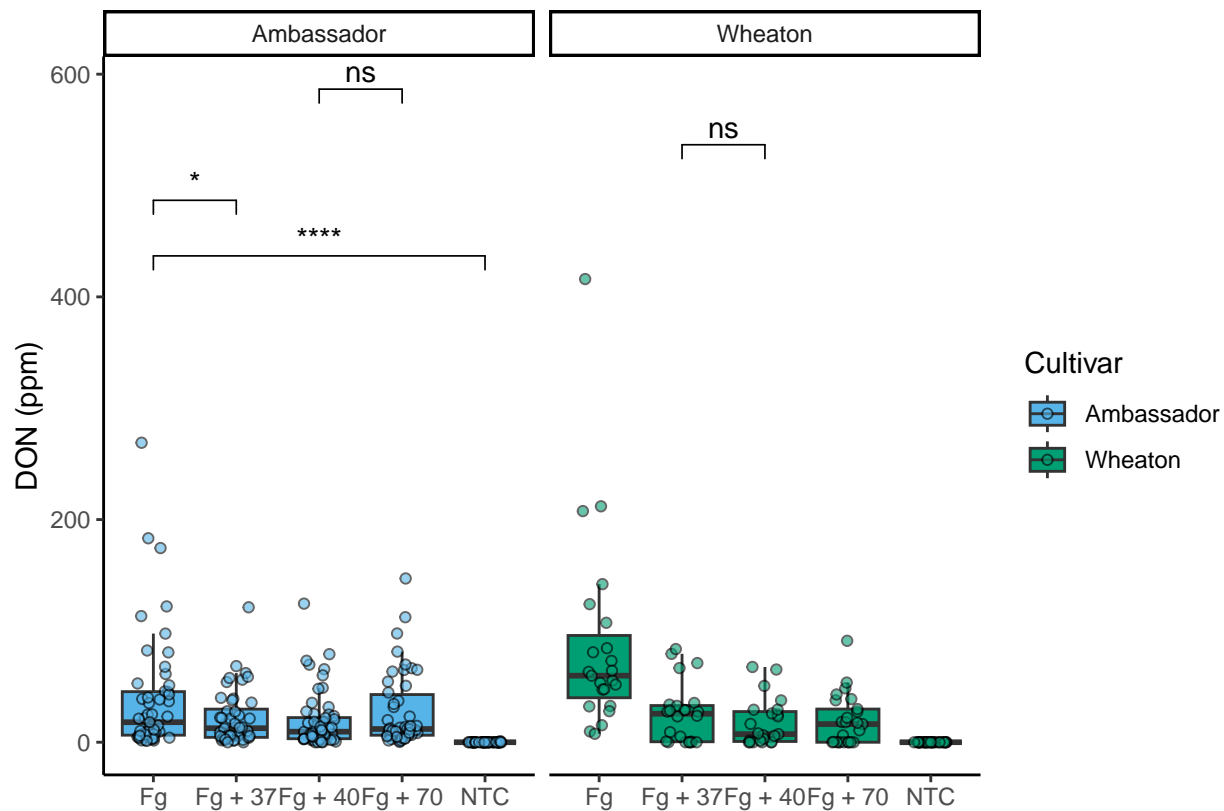
```r
library(ggplot2)
library(ggpubr)
```

```r
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()').
```

2

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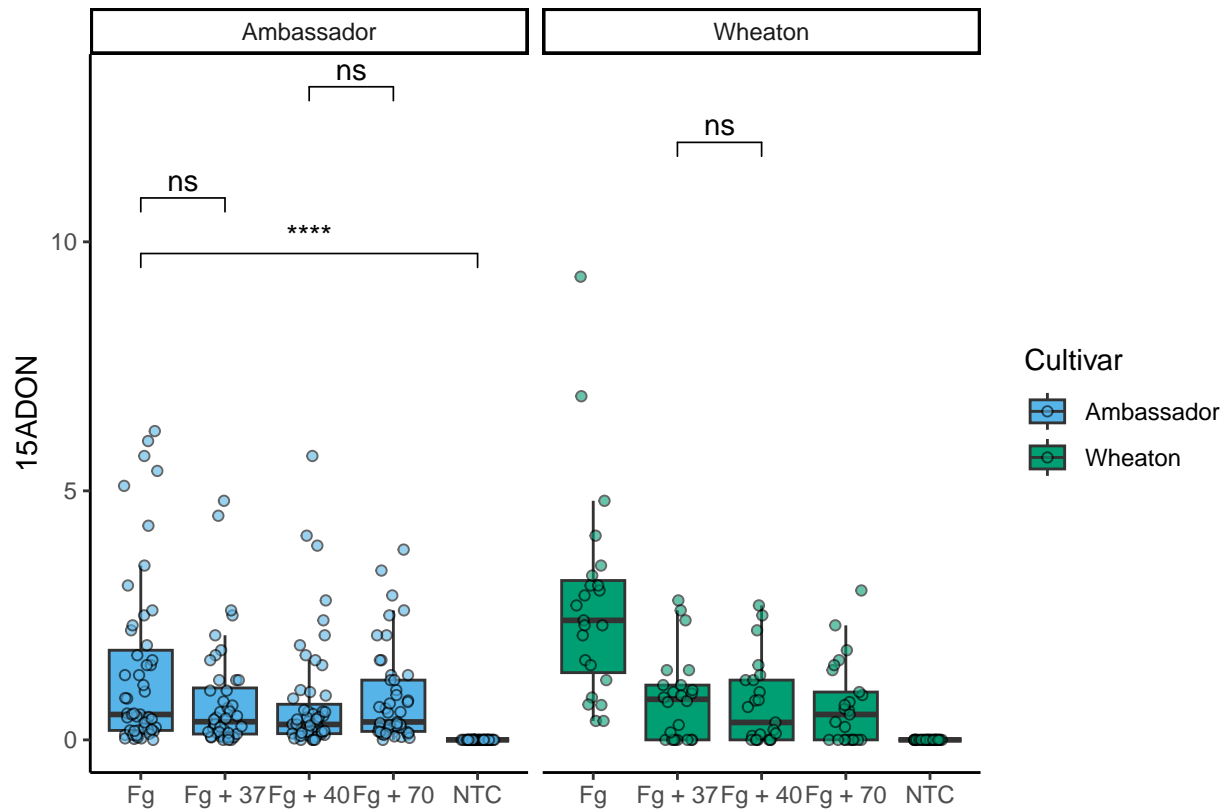
```
## Warning: Removed 10 rows containing non-finite outside the scale range
## ('stat_boxplot()').

## 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()`).


```r
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()`).
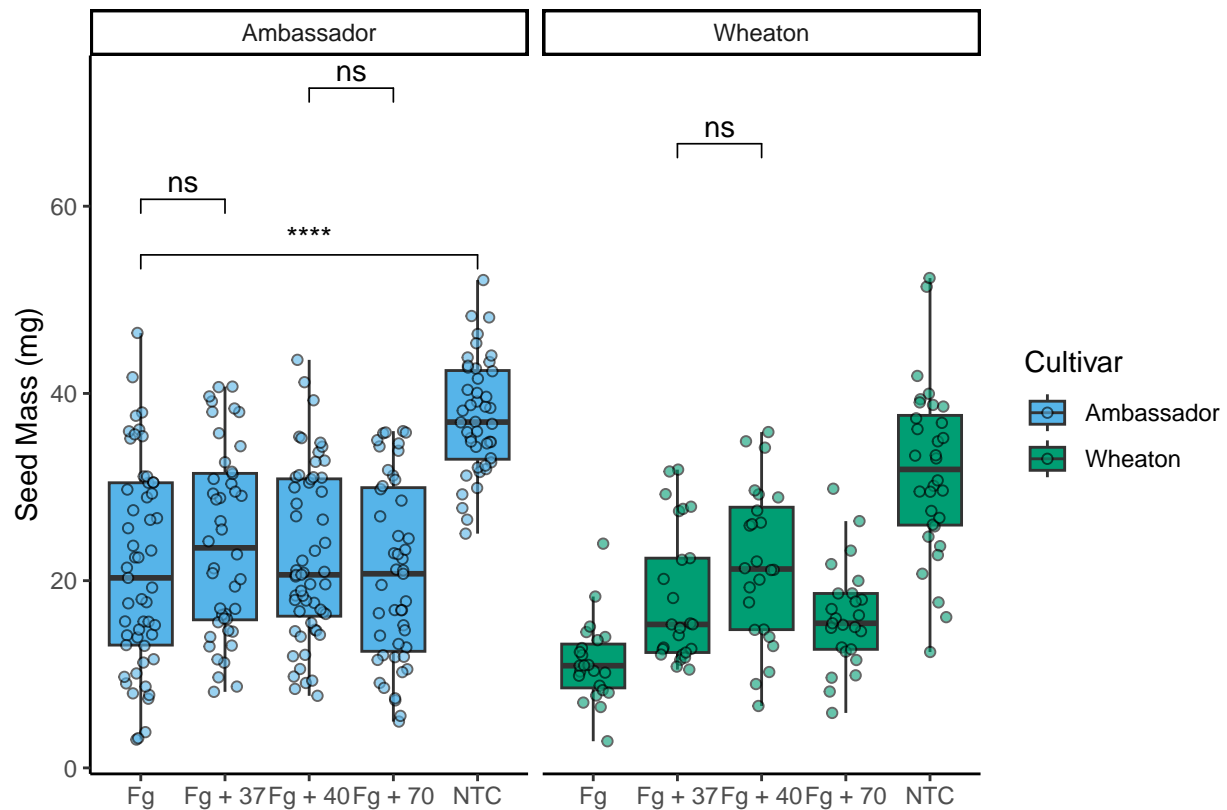

```
Combineplot.pwc <- ggarrange(
  DONplot.pwc,
  X15ADONplot.pwc,
  Seed.massplot.pwc,
  labels = c("A", "B", "C"),
  nrow = 1,
  ncol = 3,
  common.legend = TRUE,
  legend = "bottom"
)
```

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