

Coding Challenge. 4

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Coding Challenge 3

Q.No.3 (a)

Readme file link

```
library(knitr)
```

link to my Markdown fil

Clickable Link to the Manuscript

Manuscript Link

Q.No.6 (b)

File Tree of Github

```
fs::dir_tree()

## .
## +-- coding_challenge_4 Reproducibility.Rmd
## +-- coding-challenge_4-Reproducibility.html
## +-- coding-challenge_4-Reproducibility.Rmd
## +-- MycotoxinData.csv
## +-- README.html
## +-- README.md
## +-- README.pdf
## \-- Reproducibility_5820.Rproj
```

Libraries

```
library(readr)
library(ggplot2)
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.4      v stringr    1.5.1
## v forcats    1.0.0      v tibble     3.2.1
## v lubridate  1.9.4      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(ggrepel)
cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73",
               "#F0E442", "#0072B2", "#D55E00", "#CC79A7")
```

Q.No.3 (b)

Importing the excel file

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

Q.No.3 (c)

Changing the factor levels

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

Applying Statistics using t test

a.

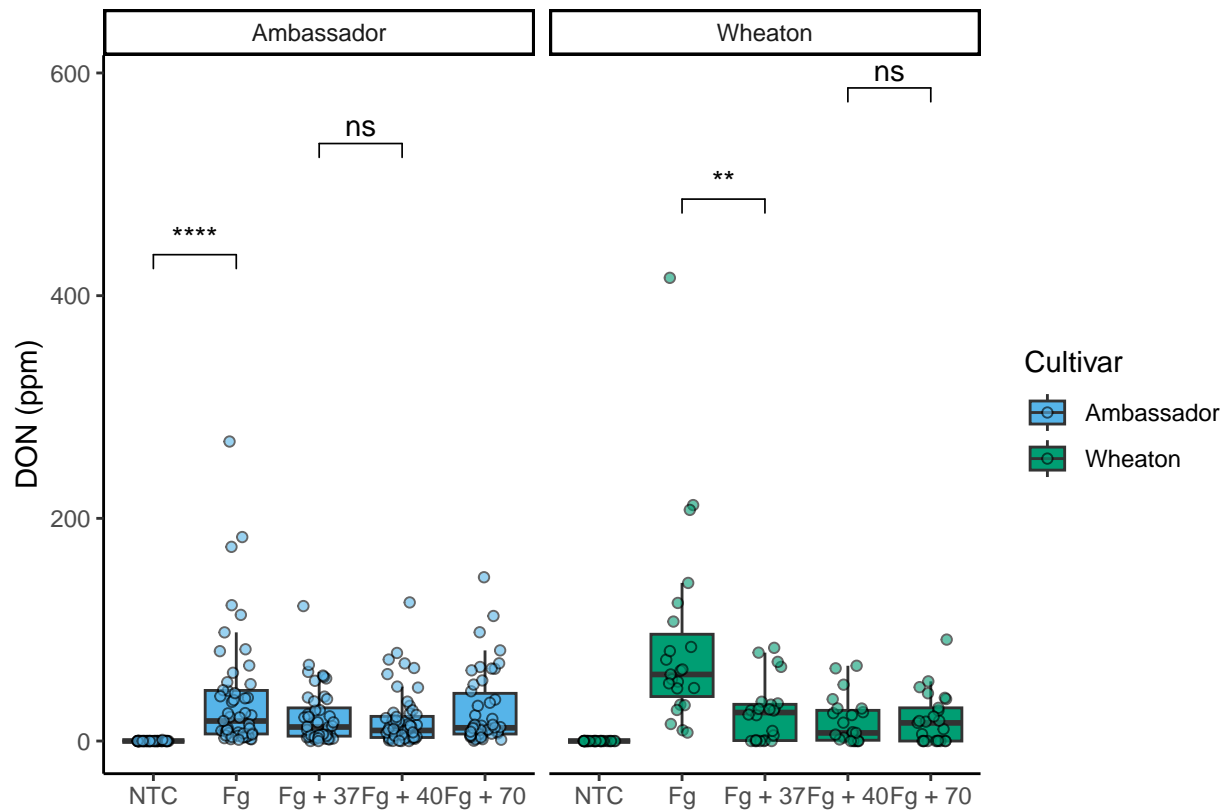
```
DONplot.pwc <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = DON, fill = Cultivar)) +
  geom_boxplot(outliers = F) +
  xlab("") +
  ylab("DON (ppm)") +
  geom_point(alpha = 0.6, pch = 21, color = "black", position = position_jitterdodge()) +
  scale_color_manual(values = c(cbbPalette[3], cbbPalette[4]))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



b.

```
X15ADONplot.pwc <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = X15ADON, fill = Cultivar)) +
  geom_boxplot(outliers = F) +
  xlab("") +
  ylab("X15ADON") +
  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"),
```

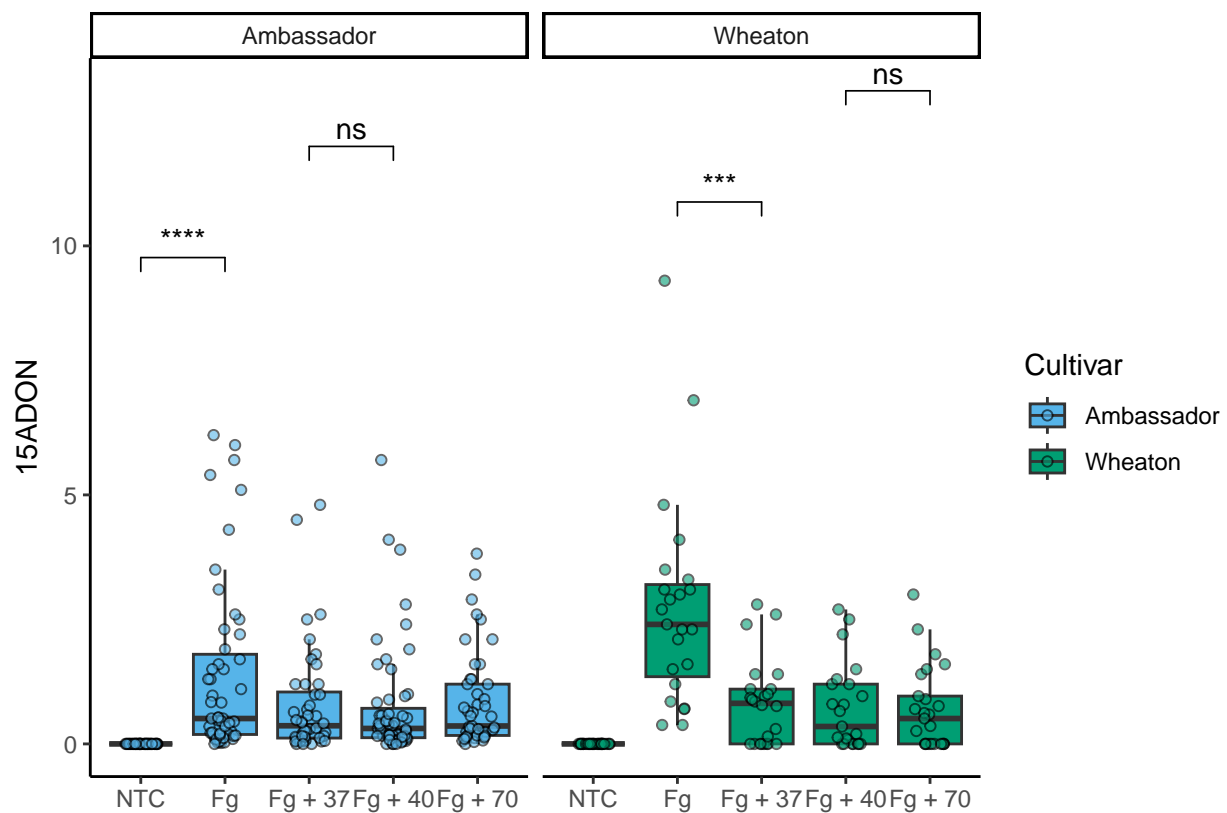
X15ADONplot.pwc

```
c("Fg + 37", "Fg + 40"),
c("Fg + 40", "Fg + 70"))
```

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



c.

```
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")))

```

Combining all plots with statistics

```

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

