Coding Challenge. 4

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Coding Challenge 3

Q.No.3 (a)

Readme file link

link to my Readme file

Clickable Link to the Manuscript

Manuscript Link

Q.No.6 (b)

File Tree of Github

```
fs::dir_tree()
```

```
## .
## +-- Coding challenge.4.Rmd
## +-- Coding Challenge.4.Rproj
## +-- Coding-challenge.4.docx
## +-- Coding-challenge.4.html
## +-- Coding-challenge.4.md
## +-- Coding-challenge.4.pdf
## +-- Coding-challenge.4.Rmd
## +-- Coding-challenge.4_files
## |   \-- figure-gfm
## |       +-- unnamed-chunk-10-1.png
## |       +-- unnamed-chunk-11-1.png
## |       +-- unnamed-chunk-13-1.png
## |       +-- unnamed-chunk-4-1.png
## |       +-- unnamed-chunk-6-1.png
## |       +-- unnamed-chunk-7-1.png
## |       +-- unnamed-chunk-8-1.png
## |       \-- unnamed-chunk-9-1.png
## \-- MycotoxinData.csv
```

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")
```
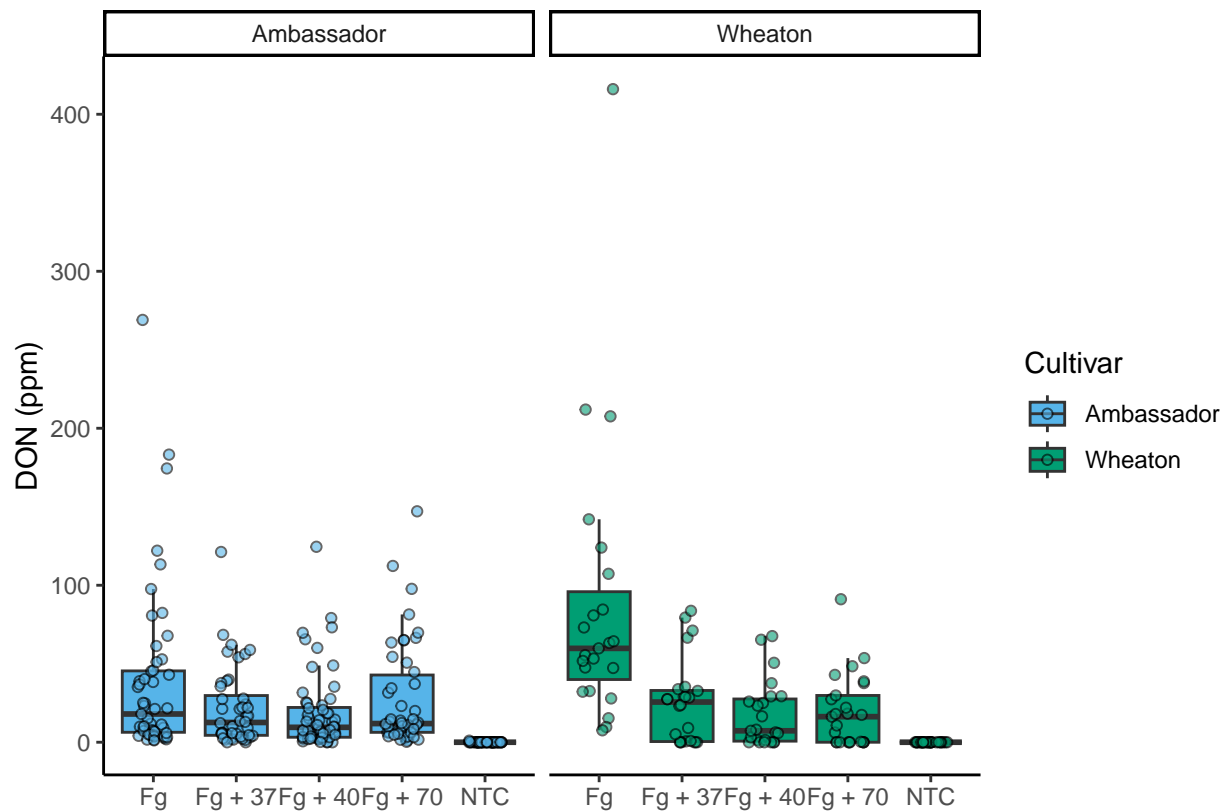
Q.No.3 (c)

Creating a ggplot box plot

```
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)
```

```
## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

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

Changing the factor levels

```
Mycotoxin_Data$Treatment <- factor(Mycotoxin_Data$Treatment, levels = c("NTC", "Fg", "Fg + 37", "Fg + 4
```

a. Using DON as Y variable

```
DON.Plot <- 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)
DON.Plot
```

```
## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

```
## Warning: Removed 8 rows containing missing values or values outside the scale range
## ('geom_point()').
```
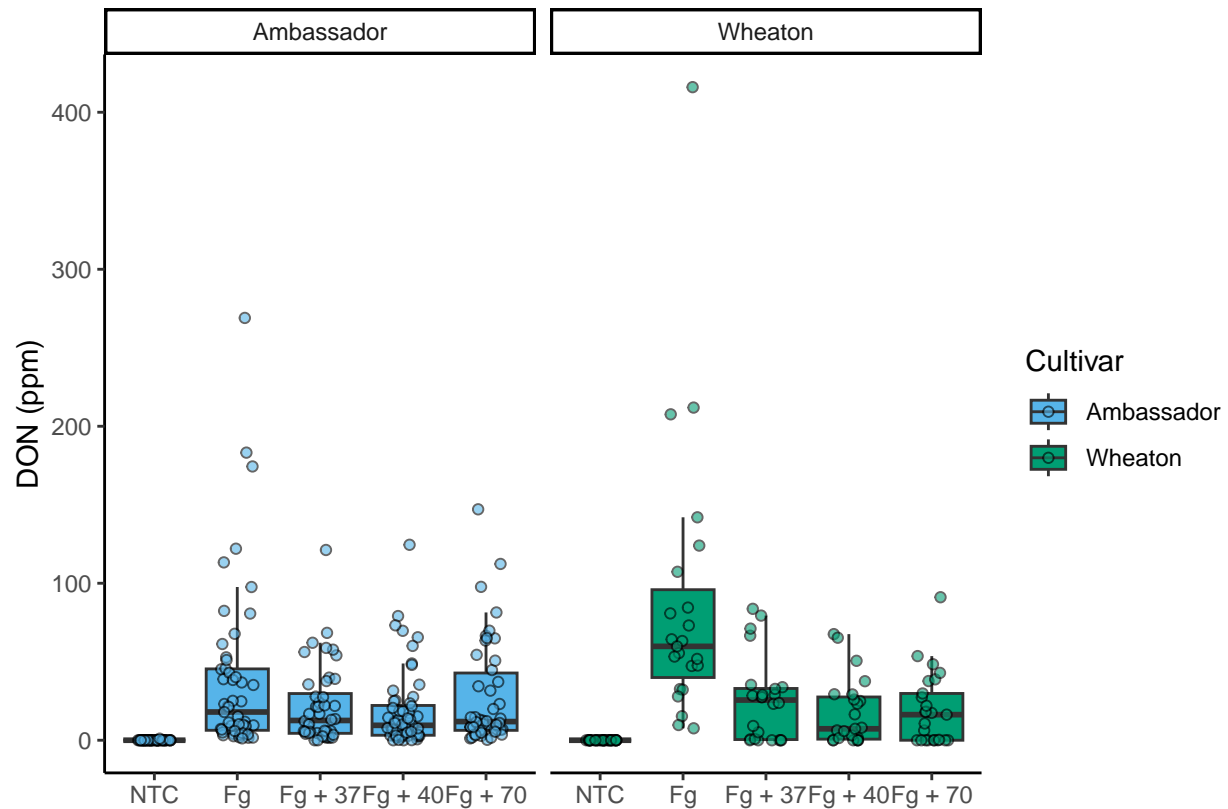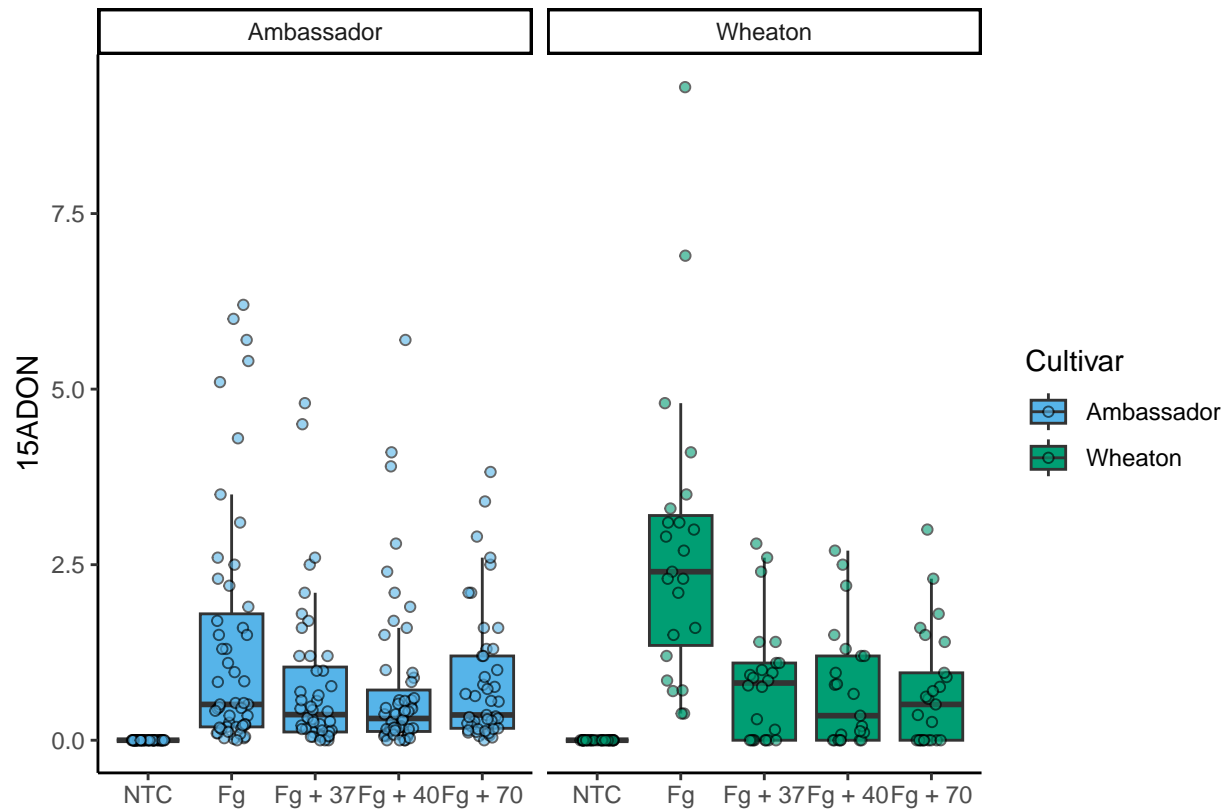
a. Using X15DON as Y variable

```
X15ADON.Plot <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = X15ADON, fill = Cultivar)) +
  geom_boxplot(outliers = F) +
  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)

X15ADON.Plot
```

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

```
## Warning: Removed 10 rows containing missing values or values outside the scale range
## ('geom_point()').
```

a. Using MassperSpeed as Y variable

```
Seed.mass.plot <- 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)

Seed.mass.plot
```

```
## Warning: Removed 2 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

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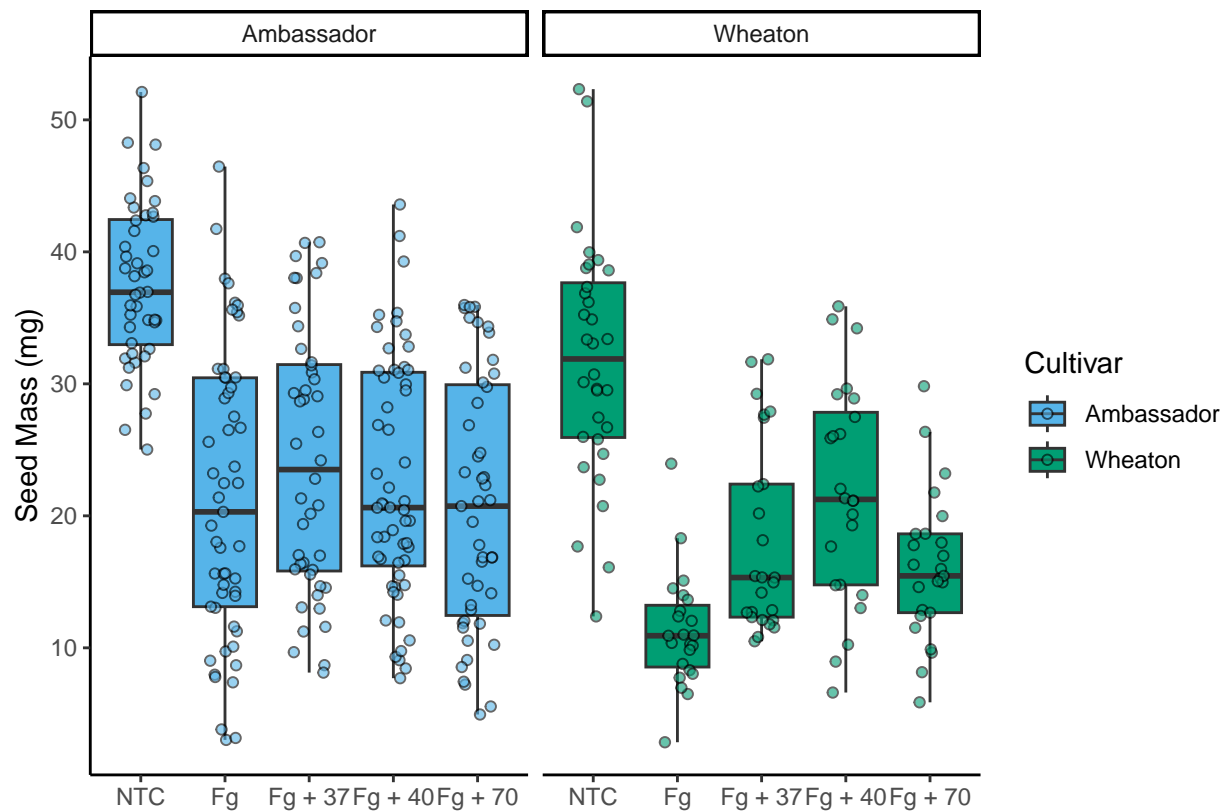
using ggarrange

```
Combine.plot <- ggarrange(
  DON.Plot,
  X15ADON.Plot,
  Seed.mass.plot,
  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 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 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 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 missing values or values outside the scale range
## ('geom_point()').
```
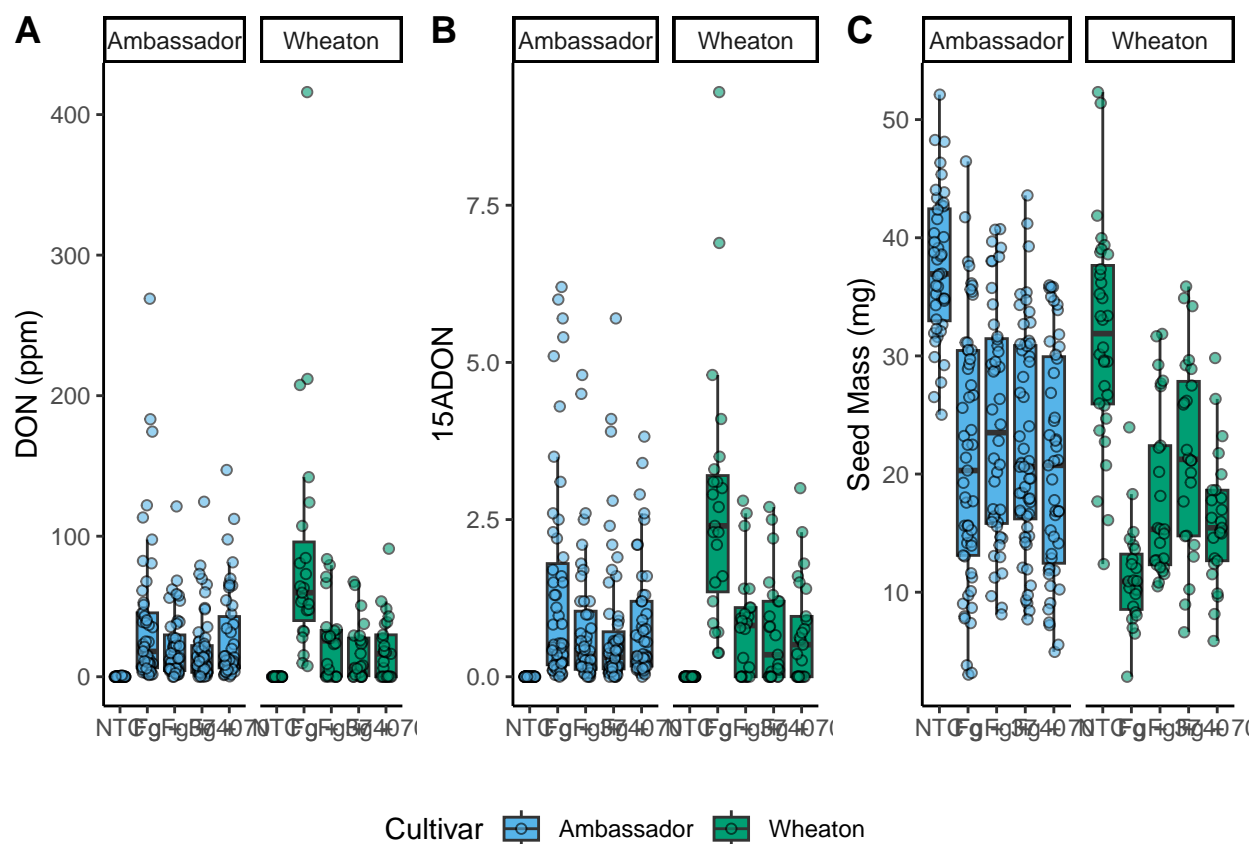
Combine.plot

Appling 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()`).
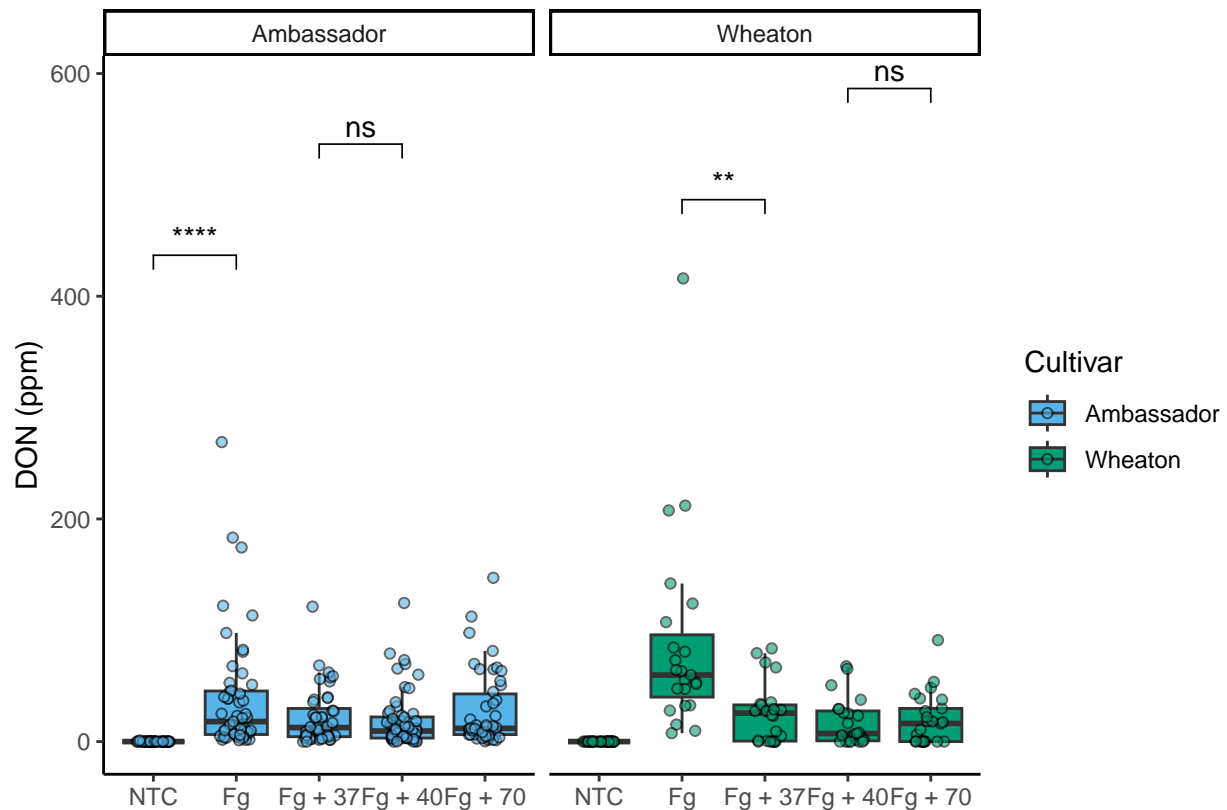
Warning: Removed 8 rows containing non-finite outside the scale range
(`stat_signif()`).

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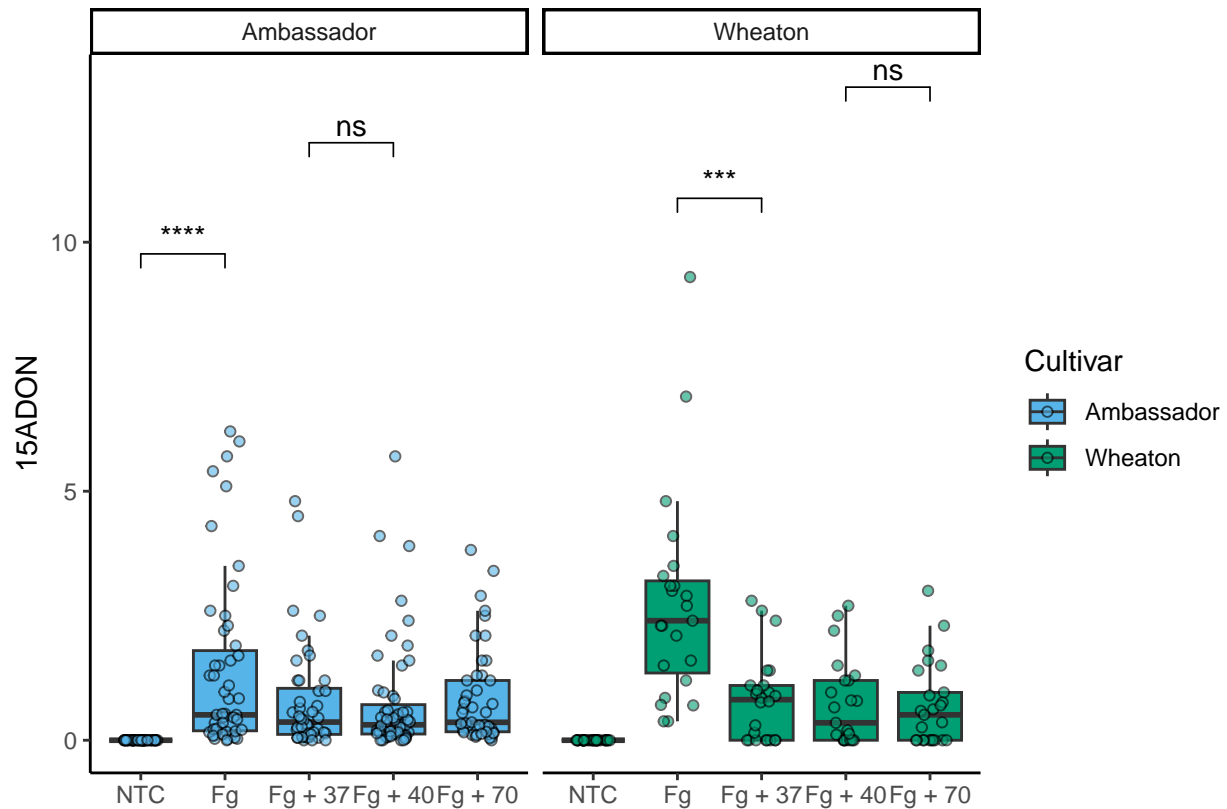## (`geom_point()`).

b.

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

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
```