

Coding Challenge. 4

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Coding Challenge 3

Q.No.3 (a)

Q.No.6 (b)

###Readme file link

link to my Readme file

Clickable Link to the ManuscDript

Manuscript Link

Q.No.6 (b)

##File Tree of Github

pdf file

word file

md file

Mycotoxin csv file

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

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

Q.No.3 (c)

Creating a ggplot box plot

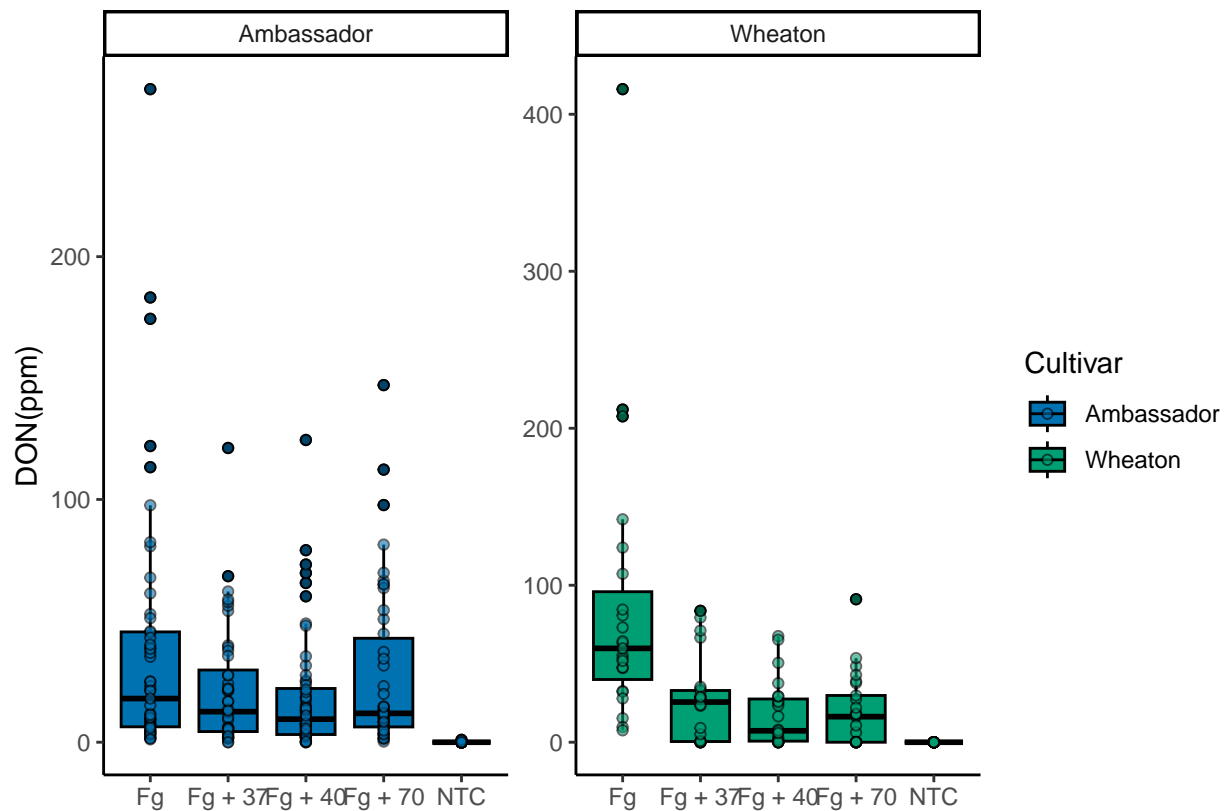
```
plot.1 <- ggplot(data = MycotoxinData, aes(x = Treatment, y = DON, fill = Cultivar)) +
  geom_boxplot(color = "black") +
  geom_point(aes(fill = Cultivar), shape = 21, color = "black", alpha = 0.6,
            width = 0.9) +
  scale_fill_manual(values = c(cbbPalette[6], cbbPalette[4])) +
  xlab("") +
  ylab("DON(ppm)") +
  theme_classic() +
  facet_wrap(~Cultivar, scale = "free")
```

```
## Warning in geom_point(aes(fill = Cultivar), shape = 21, color = "black", :
## Ignoring unknown parameters: 'width'
```

```
plot.1
```

```
## 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

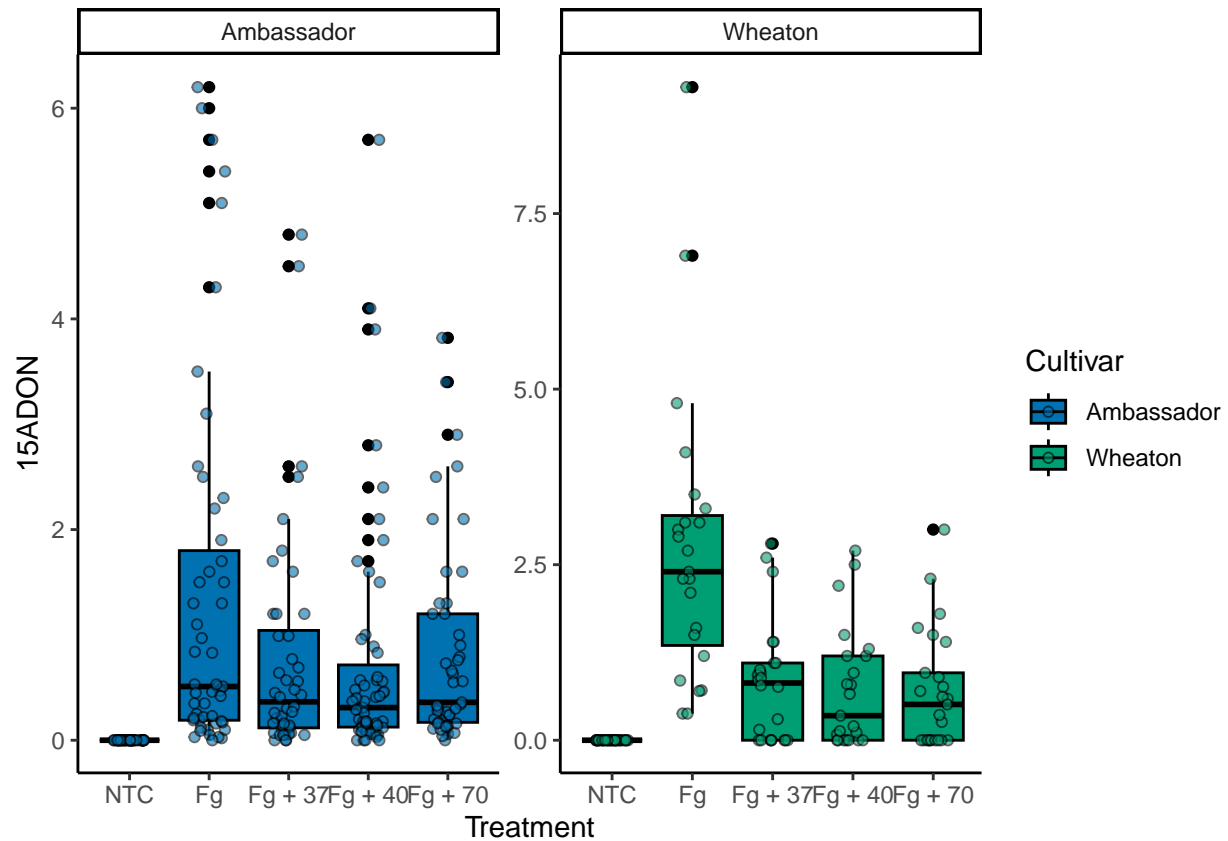
```
MycotoxinData$Treatment <- factor(MycotoxinData$Treatment,
                                   levels = c("NTC", "Fg", "Fg + 37", "Fg + 40", "Fg + 70"))
```

a. Using 15ADON as Y variable

```
plot.2 <- ggplot(data = MycotoxinData, aes(x = Treatment, y = X15ADON, fill = Cultivar)) +
  geom_boxplot(color = "black") +
  geom_point(aes(fill = Cultivar), shape = 21, color = "black", alpha = 0.6,
             position = position_jitterdodge(dodge.width = 0.9)) +
  scale_fill_manual(values = c(cbbPalette[6], cbbPalette[4])) +
  ylab("15ADON") +
  theme_classic() +
  facet_wrap(~Cultivar, scale = "free")
plot.2
```

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



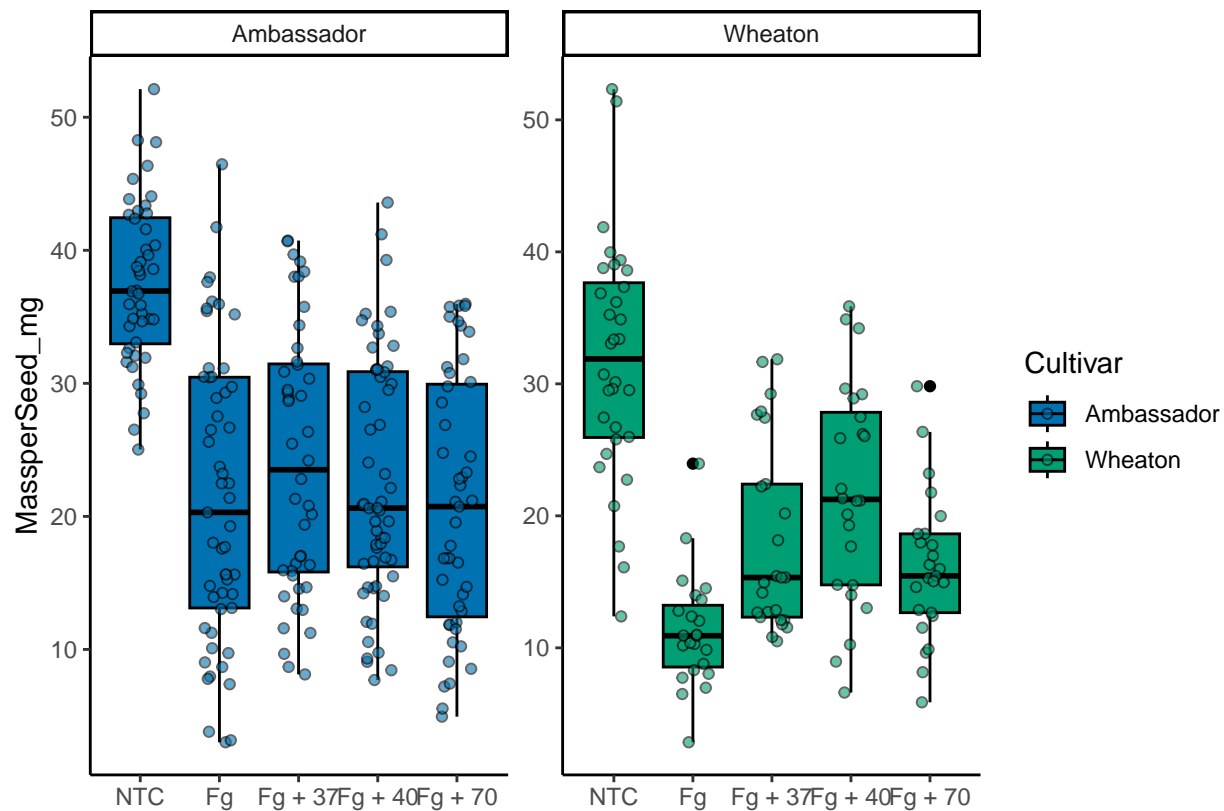
b. using MassperSeed_mg as Y variable

```
plot.3 <- ggplot(data = MycotoxinData, aes(x = Treatment, y = MassperSeed_mg, fill = Cultivar)) +
  geom_boxplot(color = "black") +
  geom_point(aes(fill = Cultivar), shape = 21, color = "black", alpha = 0.5,
             position = position_jitterdodge(dodge.width = 0.9)) +
  scale_fill_manual(values = c(cbbPalette[6], cbbPalette[4])) +
  xlab("") +
  ylab("MassperSeed_mg") +
  theme_classic() +
  facet_wrap(~Cultivar, scale = "free")

plot.3
```

```
## 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

```
plot.4<- ggarrange(plot.1, plot.2, plot.3,
```

```
  nrow =3,
  ncol= 1,
  labels = "auto",
  common.legend = T)
```

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

plot.4

