

Coding Challenge 4

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Link for the Paper

- [Link for paper](#)

Q1

In the context of R Markdown , the YAML header appears at the top of the document, enclosed by — lines, and it contains metadata about the document. Literate Programming(For eg. R Markdown) is documentation and code live together in the same file, making it easy for others (and your future self!) to understand not just what the code does, but why it was written that way.

Q2

2 (B)

```
mycotoxin=read.csv("MycotoxinData.csv", na.strings = "na")
mycotoxin$Treatment <- as.factor(mycotoxin$Treatment)
mycotoxin$Cultivar <- as.factor(mycotoxin$Cultivar)
```

2(C)

CbbPalette

```
cbbPalette <- c("#56B4E9", "#009E73")
```

DON_PLOT1

```
Plot1 <- ggplot(mycotoxin, aes(x = Treatment, y = DON, fill = Cultivar)) +
  geom_boxplot() + # add boxplot layer
  xlab("Treatment") +
  ylab("DON (ppm)") + # y label
  geom_point(alpha = 0.6, pch = 21, color = "black", position = position_jitterdodge()) +
```

```

scale_fill_manual(values = cbbPalette)+ # transparency of the jittered points to 0.6. #Jitter points
facet_wrap(~Cultivar)+ #faceted by Cultivar
theme_classic() # for classic theme
Plot1

```

```

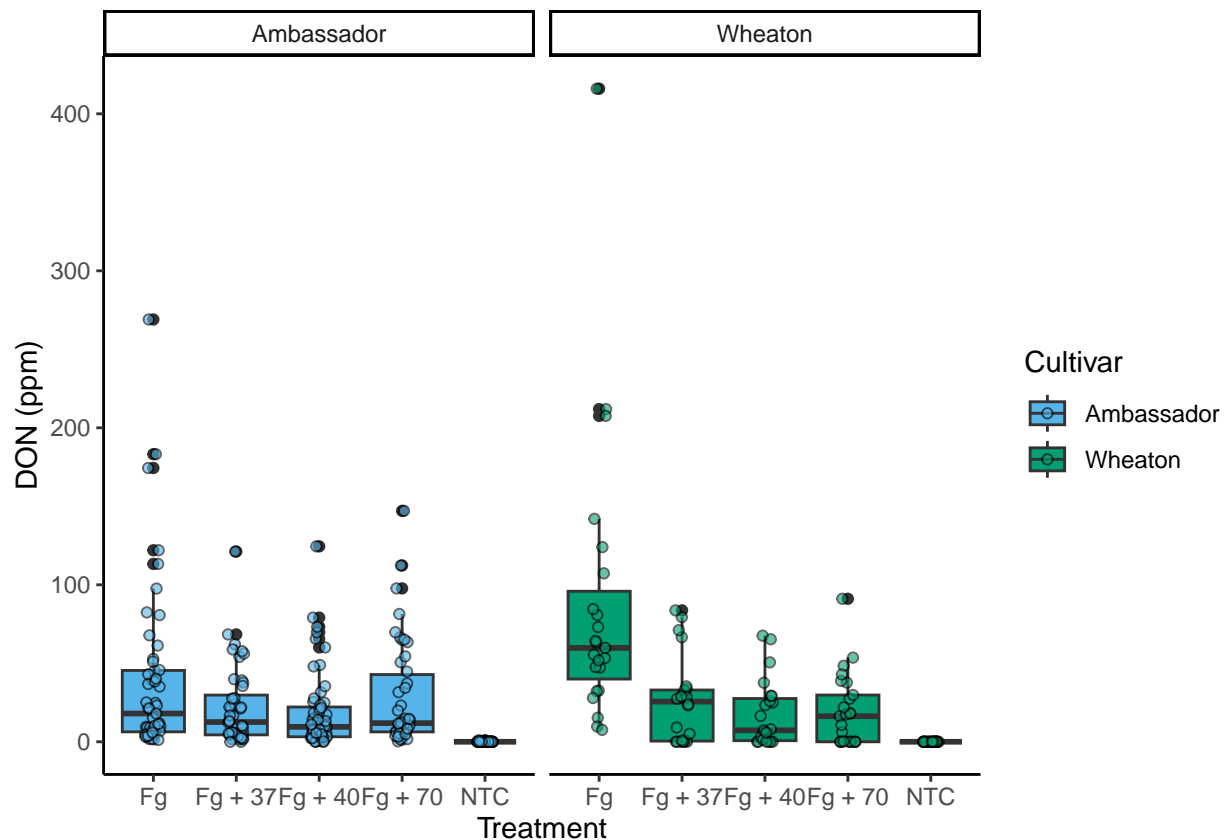
## Warning: Removed 8 rows containing non-finite outside the scale range
## ('stat_boxplot()').

```

```

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

```



15XADON_PLOT2

```

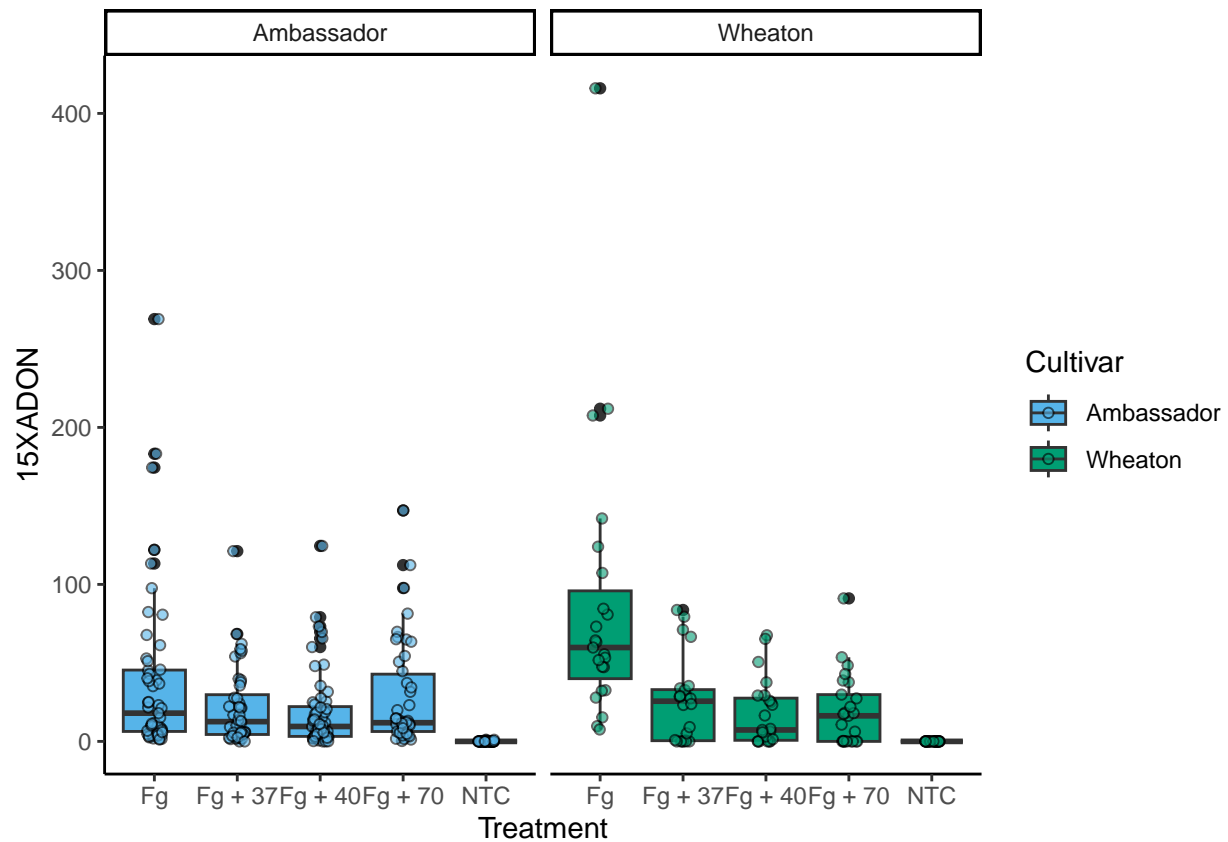
Plot2 <- ggplot(mycotoxin, aes(x = Treatment, y = DON, fill = Cultivar)) +
  geom_boxplot() + # add boxplot layer
  xlab("Treatment") +
  ylab("15XADON") + # y label
  geom_point(alpha = 0.6, pch = 21, color = "black", position = position_jitterdodge()) +
  scale_fill_manual(values = cbbPalette)+ # transparency of the jittered points to 0.6. #Jitter points
  facet_wrap(~Cultivar)+ #faceted by Cultivar
  theme_classic() # for classic theme

```

Plot2

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

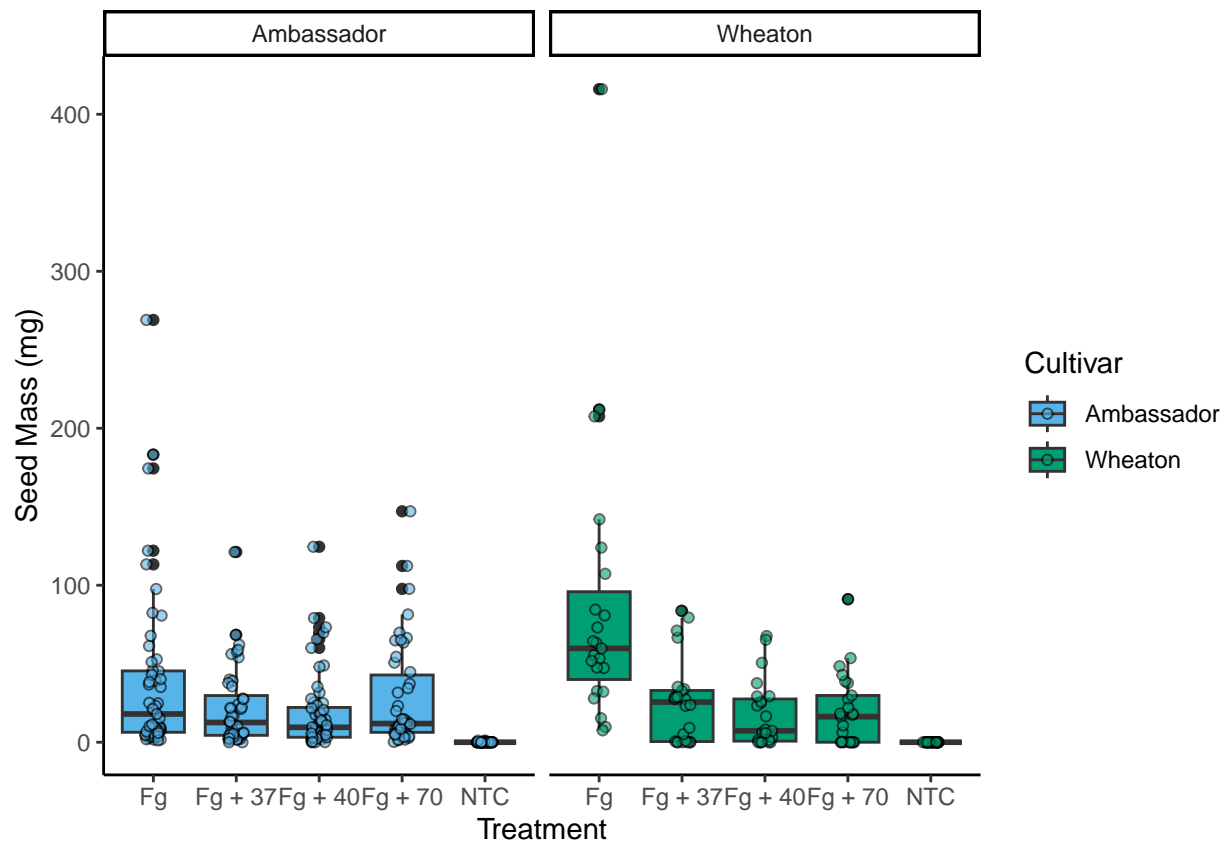


SeedMass_PLOT3

```
Plot3 <- ggplot(mycotoxin, aes(x = Treatment, y = DON, fill = Cultivar)) +
  geom_boxplot() + # add boxplot layer
  xlab("Treatment") +
  ylab("Seed Mass (mg)") + # y label
  geom_point(alpha = 0.6, pch = 21, color = "black", position = position_jitterdodge()) +
  scale_fill_manual(values = cbbPalette) + # transparency of the jittered points to 0.6. #Jitter points
  facet_wrap(~Cultivar) + # faceted by Cultivar
  theme_classic() # for classic theme
Plot3
```

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



3Combined_PLOT

```
figure=ggarrange(
  Plot1,
  Plot2,
  Plot3,
  labels = c("A", "B", "C"),
  nrow = 1,
  ncol = 3,
  common.legend=TRUE
)
```

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

figure

