Codingchallenge4

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Contents

1 Question

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.

2 Question2a

-PaperLink

3 Question2b

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.4.3
```

```
## Warning: package 'ggplot2' was built under R version 4.4.3
```

```
## -- Attaching core tidyverse packages ----------------------- tidyverse 2.0.0 --
## v dplyr      1.1.4     v readr      2.1.5
## v forcats    1.0.0     v stringr    1.5.1
## v ggplot2    4.0.2     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(ggplot2)
library(ggpubr)
```

```
## Warning: package 'ggpubr' was built under R version 4.4.3
```

```
mycotoxin<- read.csv(file.choose())
mycotoxin$Treatment <- as.factor(mycotoxin$Treatment)
mycotoxin$Cultivar <- as.factor(mycotoxin$Cultivar)
str(mycotoxin)
```

```
## 'data.frame':    375 obs. of  6 variables:
##  $ Treatment     : Factor w/ 5 levels "Fg","Fg + 37",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ Cultivar      : Factor w/ 2 levels "Ambassador","Wheaton": 2 2 2 2 2 2 2 2 2 2 ...
##  $ BioRep        : int  2 2 2 2 2 2 2 2 2 3 ...
##  $ MassperSeed_mg: chr  "10.29130435" "12.80322581" "2.846666667" "6.5" ...
##  $ DON           : chr  "107.3" "32.6" "416" "211.9" ...
##  $ X15ADON       : chr  "3" "0.85" "3.5" "3.1" ...
```
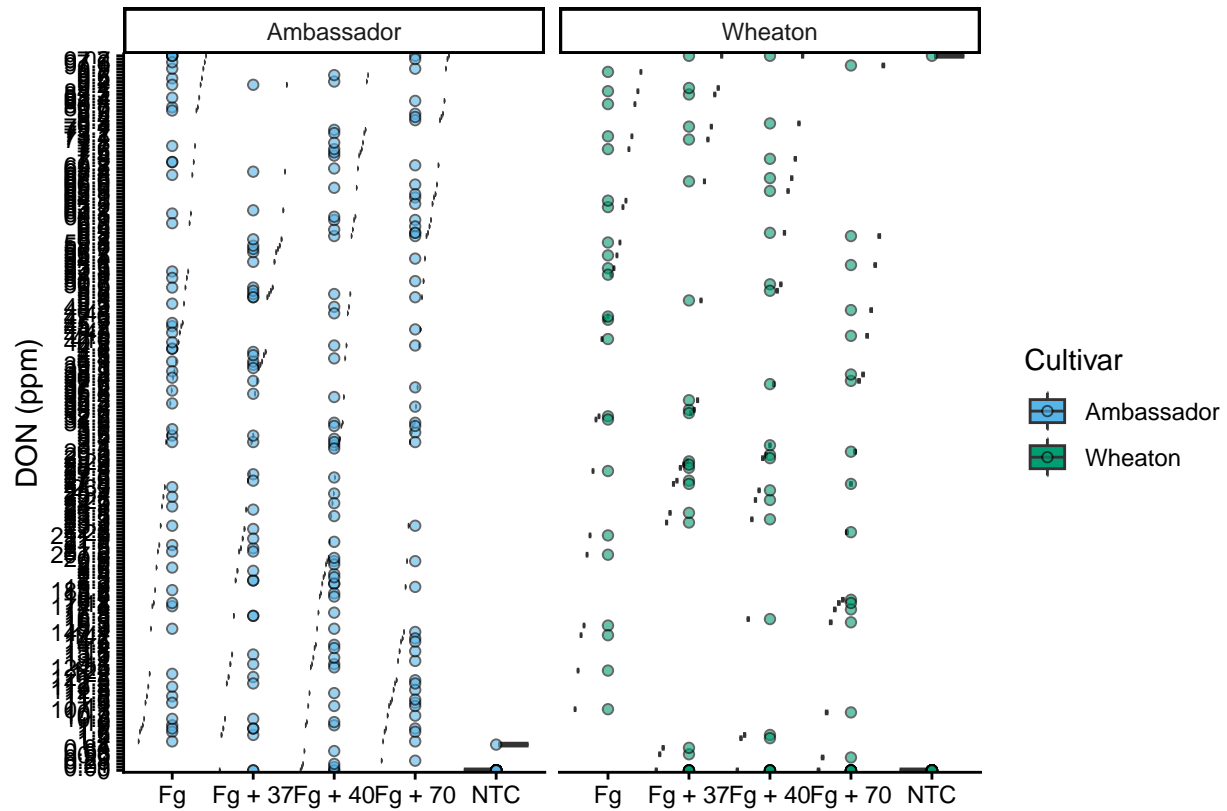
4 Question2c

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

5 DON_PLOT1

```
Plot1 <- ggplot(mycotoxin, aes(x = Treatment, y = DON, fill = Cultivar)) +
  geom_boxplot(position = position_dodge(0.85)) +
  xlab("") +
  ylab("DON (ppm)") +
```

```
geom_point(alpha = 0.6,pch = 21, color = "black") +
scale_fill_manual(values = cbbPalette)+
facet_wrap(~Cultivar)+
theme_classic()
Plot1
```
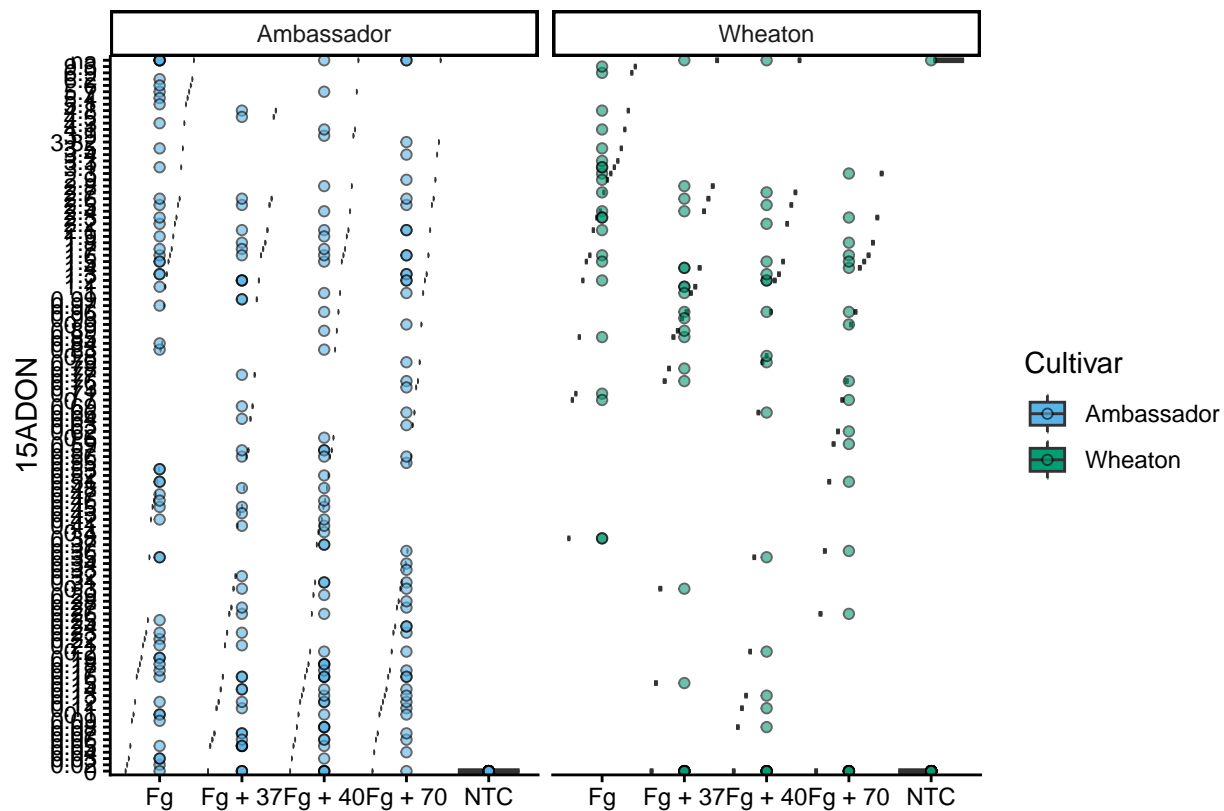

6 Plot X15ADON

```
Plot2 <- ggplot(mycotoxin, aes(x = Treatment, y = X15ADON, fill = Cultivar)) +
  geom_boxplot(position = position_dodge(0.85)) +
  xlab("") +
  ylab("15ADON") +
  geom_point(alpha = 0.6,pch = 21, color = "black") +
  scale_fill_manual(values = cbbPalette)+
  facet_wrap(~Cultivar)+
  theme_classic()
Plot2
```
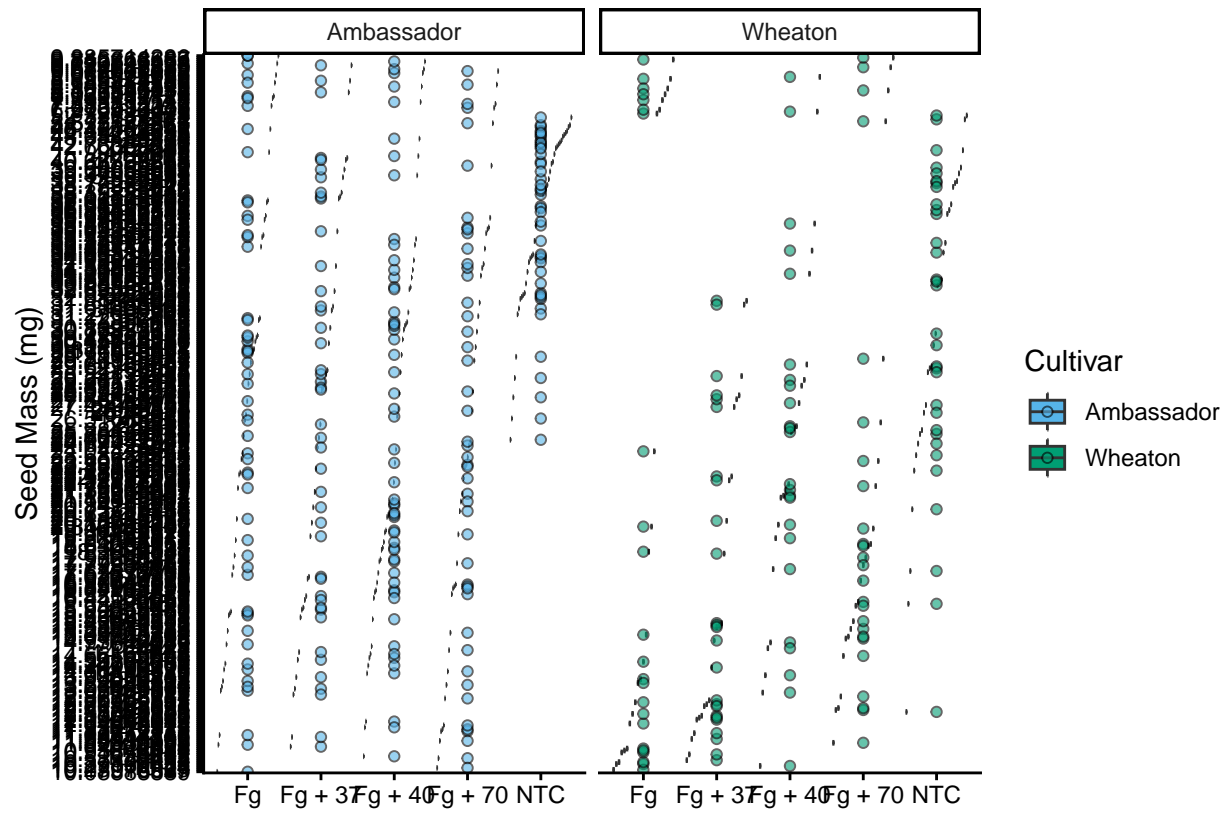
7 SeedMass

```
#Plot 3

Plot3<- ggplot(mycotoxin, aes(x = Treatment, y = MassperSeed_mg, fill = Cultivar)) +
geom_boxplot(position = position_dodge(0.85)) +
  xlab("") +
  ylab("Seed Mass (mg)") +
  geom_point(alpha = 0.6,pch = 21, color = "black") +
  scale_fill_manual(values = cbbPalette)+
  facet_wrap(~Cultivar)+
  theme_classic()
Plot3
```

8 Question5

README

9 Question6

Github