Challenge 4

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Contents

Link to Manuscript

Load required packages

```
library (tidyverse)
```

```
## -- 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   3.5.1      v tibble    3.2.1
## v lubridate 1.9.4      v tidyr     1.3.1
## v purrr     1.0.4
## -- 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)
library(ggplot2)
```

Setting color palet

```
cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7")
```

Load the data in

```
mycotoxin.data <- read.csv("MycotoxinData.csv", na.strings = "na")
str (mycotoxin.data)
```

```
## 'data.frame':    375 obs. of  6 variables:
##  $ Treatment    : chr  "Fg" "Fg" "Fg" "Fg" ...
##  $ Cultivar     : chr  "Wheaton" "Wheaton" "Wheaton" "Wheaton" ...
##  $ BioRep       : int  2 2 2 2 2 2 2 2 2 3 ...
##  $ MassperSeed_mg: num  10.29 12.8 2.85 6.5 10.18 ...
##  $ DON          : num  107.3 32.6 416 211.9 124 ...
##  $ X15ADON      : num  3 0.85 3.5 3.1 4.8 3.3 6.9 2.9 2.1 0.71 ...
```
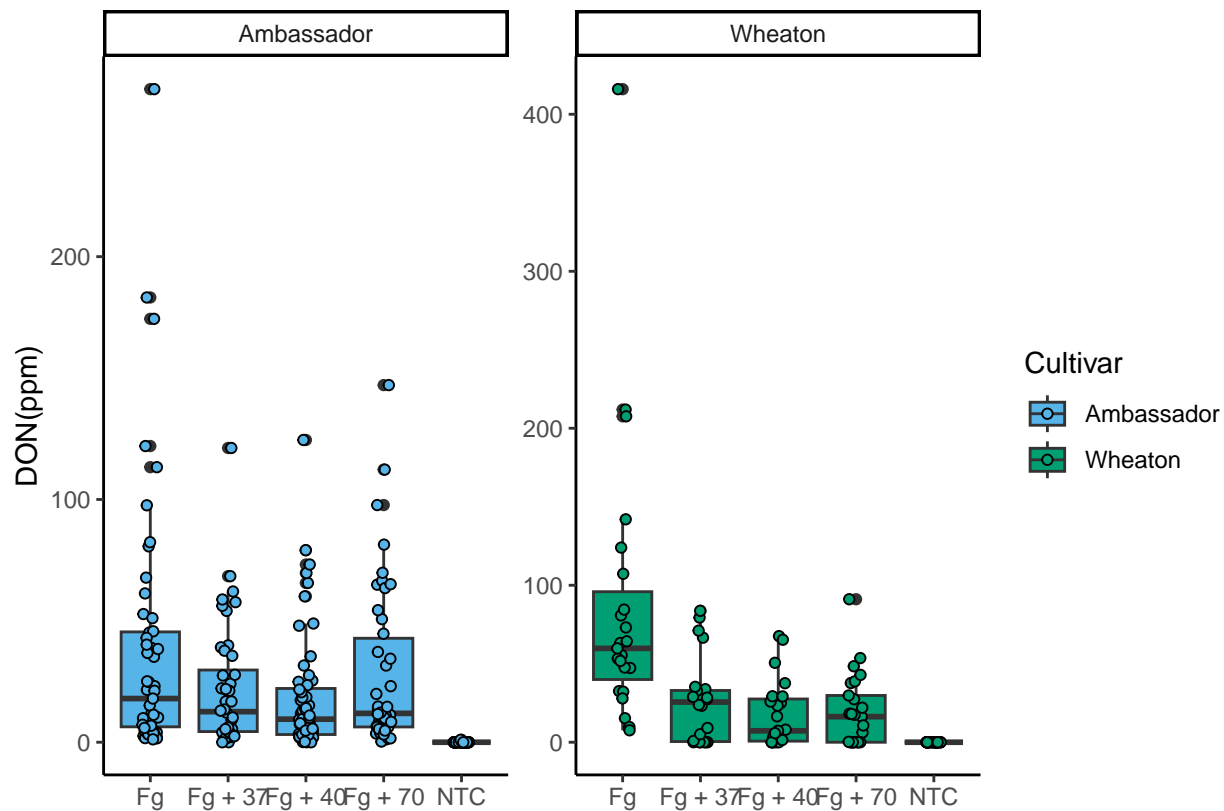
Make cultivar and treatment a factor

```
mycotoxin.data$Cultivar <- as.factor(mycotoxin.data$Cultivar)
mycotoxin.data$Treatment <- as.factor(mycotoxin.data$Treatment)
```

Plot DON against treatment

```
don.treatment.1 <- ggplot (mycotoxin.data, aes(x = Treatment, y = DON, fill = Cultivar)) +
  geom_boxplot(position = "dodge") +
  #geom_point(position = position_jitterdodge(0.6)) +
  geom_jitter(pch = 21, position = position_jitterdodge(), color = "black") +
  xlab("") +
  ylab("DON(ppm)") +
  scale_fill_manual(values = c(cbbPalette[[3]], cbbPalette[[4]])) +
  theme_classic() +
  facet_wrap(~Cultivar, scales = "free")
don.treatment.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()').
```

**Change the factor order level so that the treatment**

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

Plot X15ADON against treatment

```r
don.treatment.2 <- ggplot (mycotoxin.data, aes(x = Treatment, y = X15ADON, fill = Cultivar)) +
  geom_boxplot(position = "dodge") +
  #geom_point(position = position_jitterdodge(0.6)) +
  geom_jitter(pch = 21, position = position_jitterdodge(), color = "black") +
  xlab("") +
  ylab("15ADON") +
  scale_fill_manual(values = c(cbbPalette[[3]], cbbPalette[[4]])) +
  theme_classic() +
  facet_wrap(~Cultivar, scales = "free")
don.treatment.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()').
```
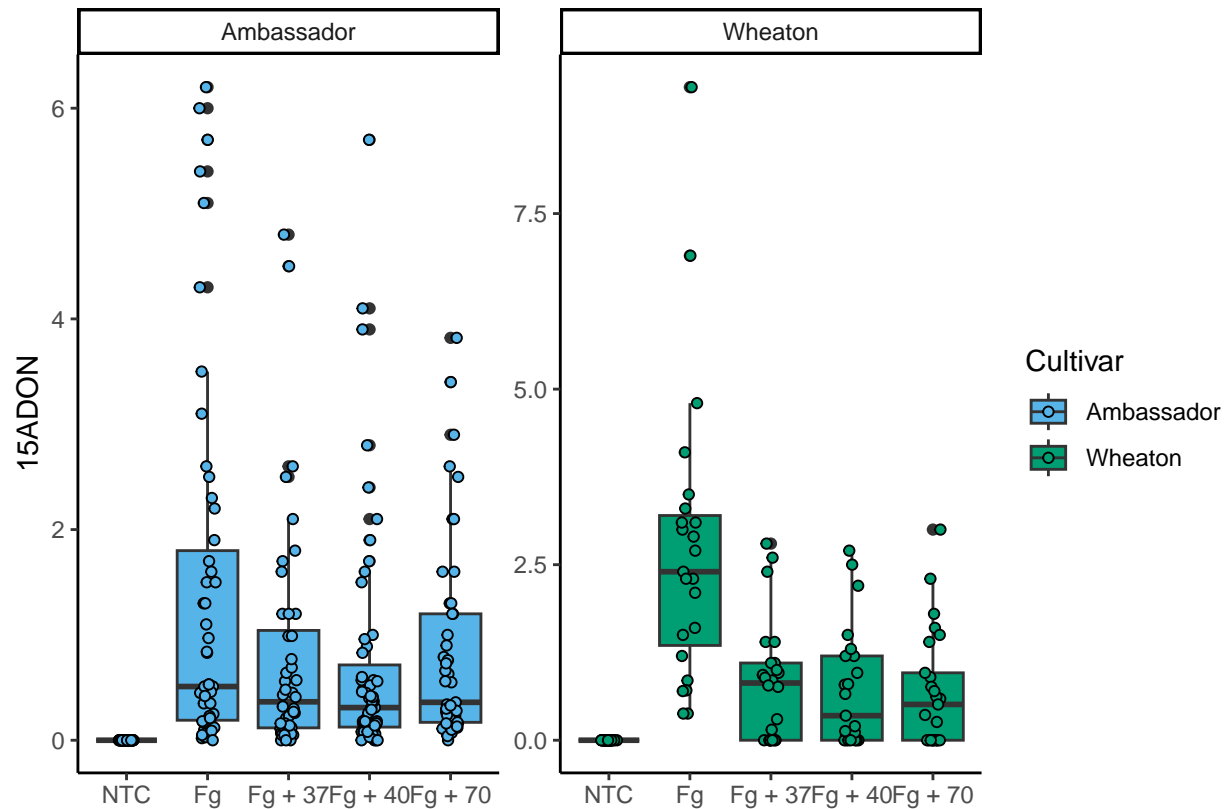
Plot Massperseed against treatment

```
don.treatment.3 <- ggplot (mycotoxin.data, aes(x = Treatment, y = MassperSeed_mg, fill = Cultivar)) +
  geom_boxplot(position = "dodge") +
  #geom_point(position = position_jitterdodge(0.6)) +
  geom_jitter(pch = 21, position = position_jitterdodge(), color = "black") +
  xlab("") +
  ylab("Seed Mass (mg)") +
  scale_fill_manual(values = c(cbbPalette[[3]], cbbPalette[[4]])) +
  theme_classic() +
  facet_wrap(~Cultivar, scales = "free")
don.treatment.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()').
```
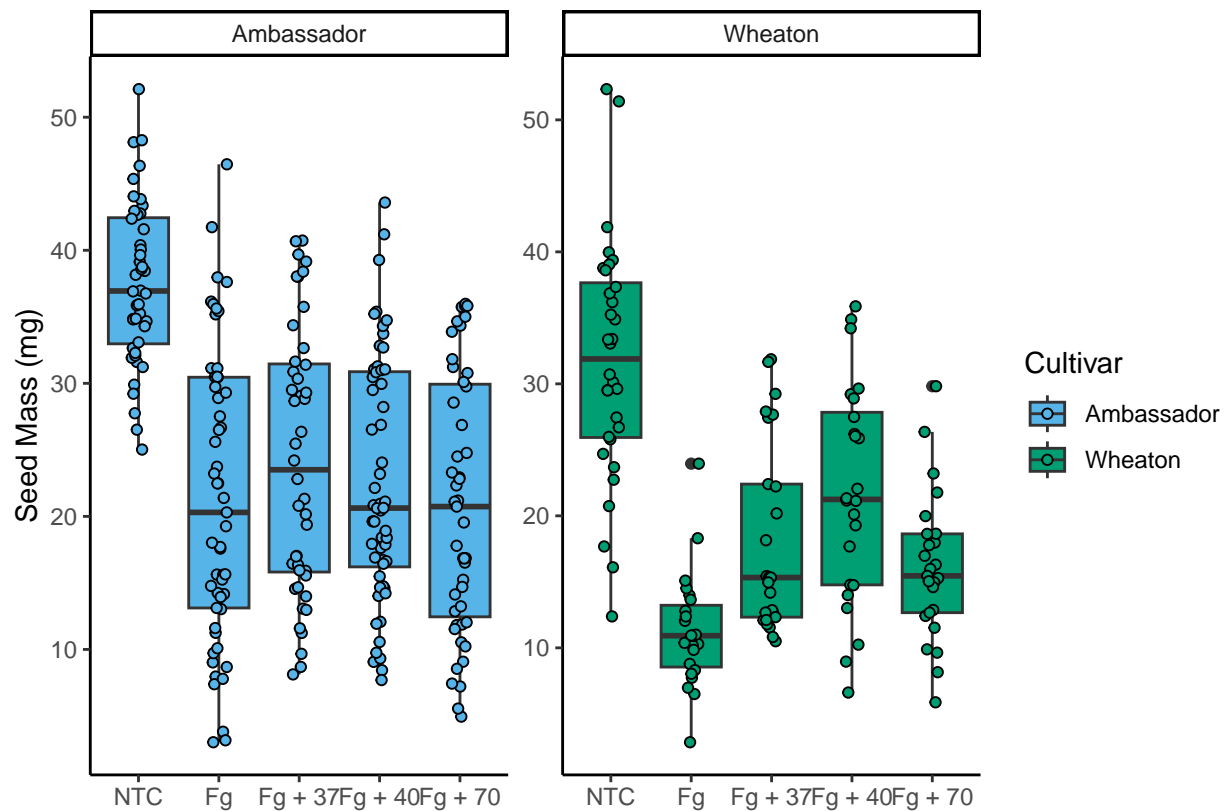
Perfrom a t-test comparison of treatments

```
Plot1 <- don.treatment.1 +
  geom_pwc(aes(group = Treatment), method = "t_test", label = "p.adj.format")

Plot2 <- don.treatment.2 +
  geom_pwc(aes(group = Treatment), method = "t_test", label = "p.adj.format")

Plot3 <- don.treatment.3 +
  geom_pwc(aes(group = Treatment), method = "t_test", label = "p.adj.format")
```

Stick many the three figures together for a publication ready figure

```
Figure_2 <- ggarrange(
  Plot1,
  Plot2,
  Plot3,
  nrow = 1,
  ncol = 3,
  labels = "auto",
  common.legend = TRUE
)
```

```
## 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_pwc()').

## 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_pwc()').

## 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_pwc()').

## 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_pwc()').

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

Figure_2

a

DON(ppm)

<0.000
<0.000
0.52
<0.0001
0.7
0.7
<0.0001
0.7
0.11
0.23

Ambassado | Wheaton

0.003
0.004
0.822
0.001
0.822
0.822
0.001
0.008
0.008
.015

b

15ADON

Ambassado

1
1
1
0.274
0.188
0.252
<0.0001
<0.0001
.00012
.0001

Wheaton

1
1
0.001
0.001
0.002
0.002
0.002
.00095
.0001

c

Seed Mass (mg)

Ambassado

1
0.7
1
1
1
1
<0.0001
<0.0001
0.0001
0.0001

Wheaton

0.02
0.26
0.21
0.006
<0.0001
0.001
<0.0001
0.00052
0.0001
0.0001