

# Challenge 4

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## 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

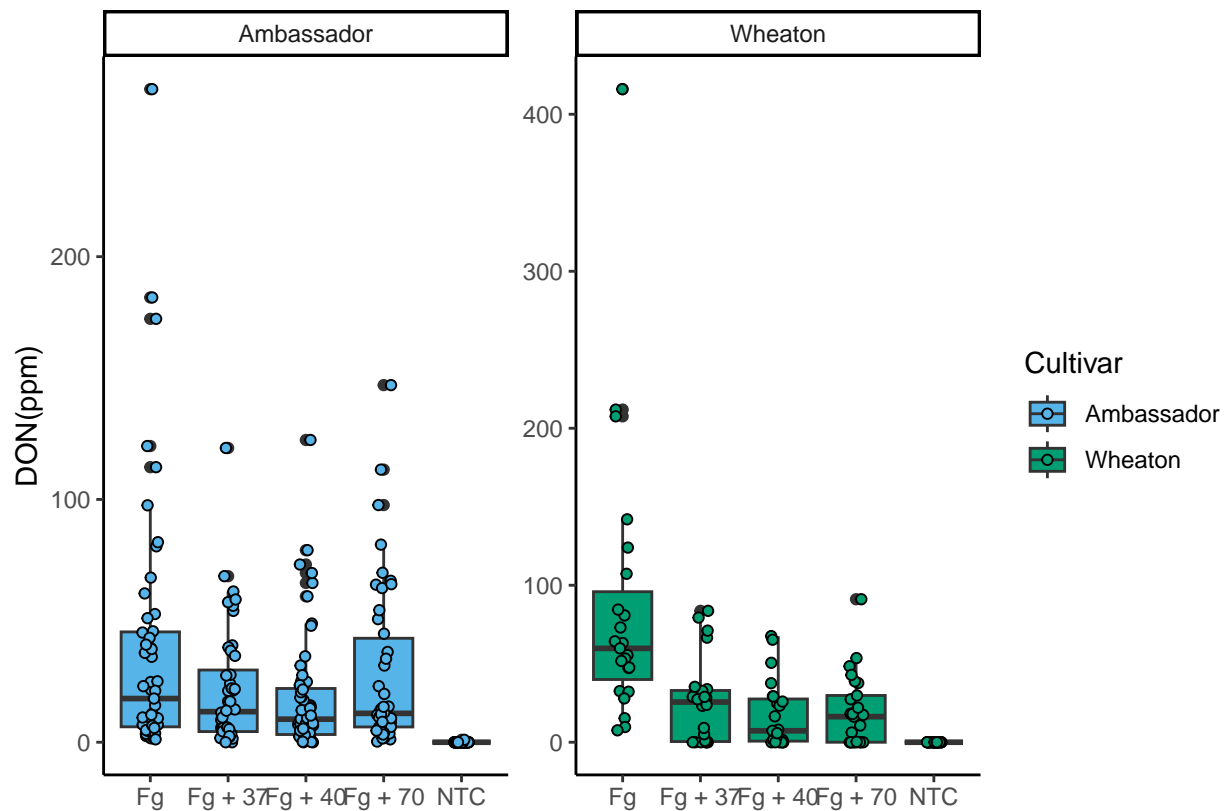
```
mycotoxin.data$Cultivar <- as.factor(mycotoxin.data$Cultivar)
mycotoxin.data$Treatment <- as.factor(mycotoxin.data$Treatment)
```

## 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

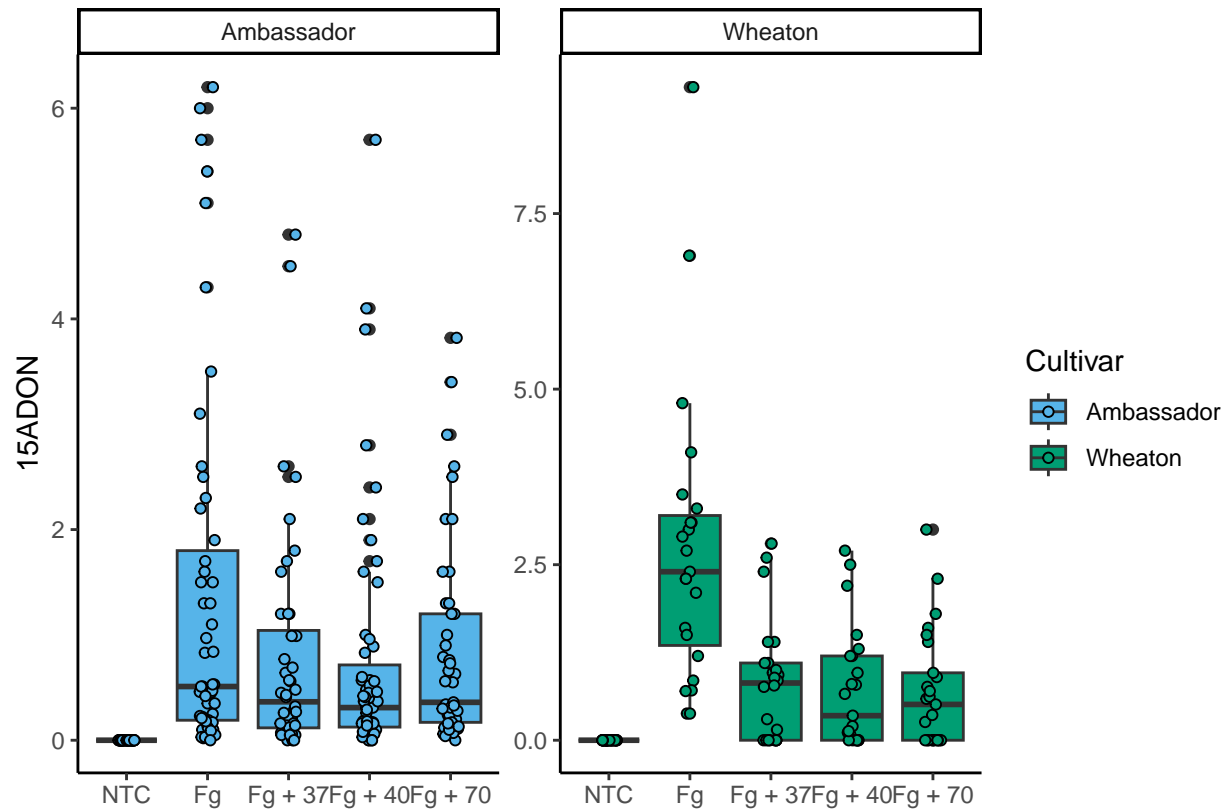
```
mycotoxin.data$Treatment <- factor(mycotoxin.data$Treatment, levels = c("NTC", "Fg", "Fg + 37", "Fg + 40", "Fg + 70"))
```

Plot X15ADON against treatment

```
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()').
```

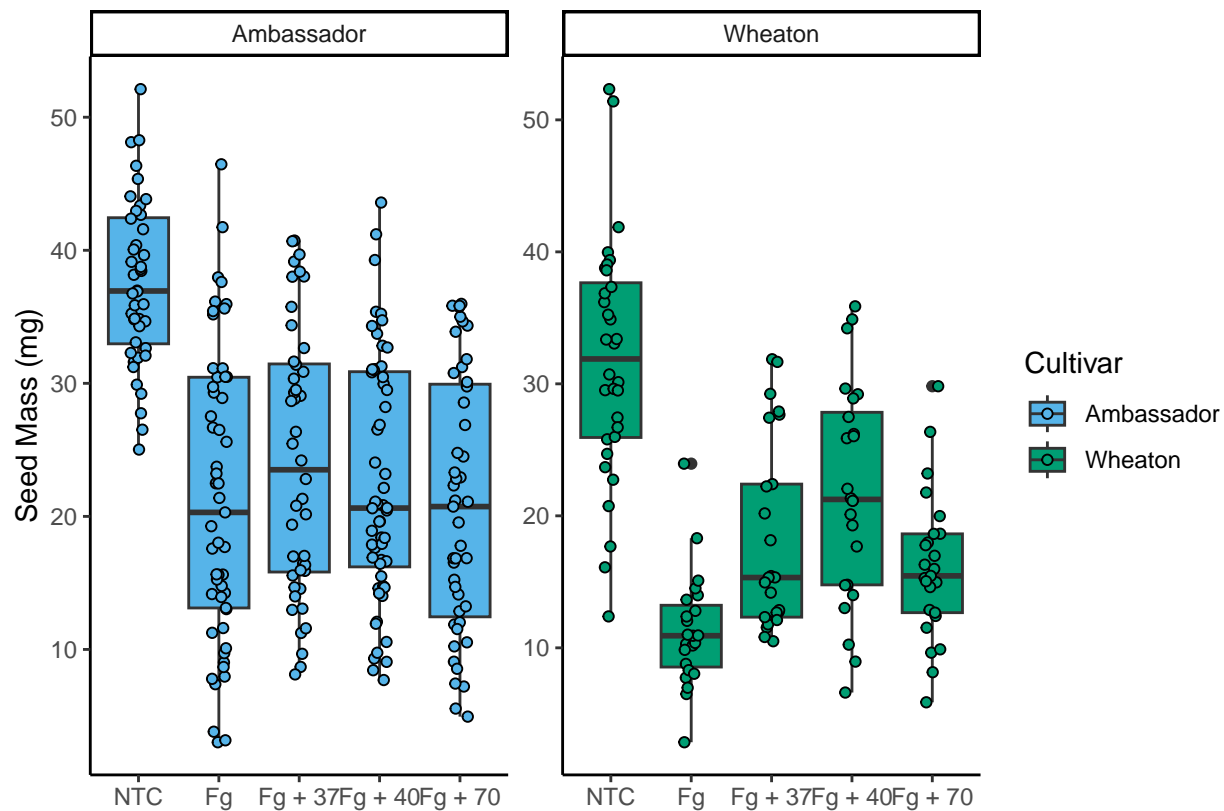


## Plot Massperseed against treatment

```
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

