CodingChallenge4

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Contents

Coding Challenge 4

Manuscript

Noel, Z.A., Roze, L.V., Breunig, M., Trail, F. 2022. Endophytic fungi as promising biocontrol agent to protect wheat from Fusarium graminearum head blight. Plant Disease.https://doi.org/10.1094/PDIS-06-21-1253-RE

Call in the required packages and dataset ("Housekeeping")

```r
#Calling in packages
library(ggplot2)
library(ggpubr)
library(ggrepel)
library(tinytex)
library(knitr)
library(rmarkdown)
library(pandoc)
```

```
##
## Attaching package: 'pandoc'

## The following objects are masked from 'package:rmarkdown':
##
##     pandoc_available, pandoc_convert, pandoc_version
```

```r
#Calling in Dataset
MycotoxinData <- read.csv("MycotoxinData.csv",na.strings="na")

#Call in Color Blind Palette for ggplot
cbbPalette <- c("#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7","#000000")
```
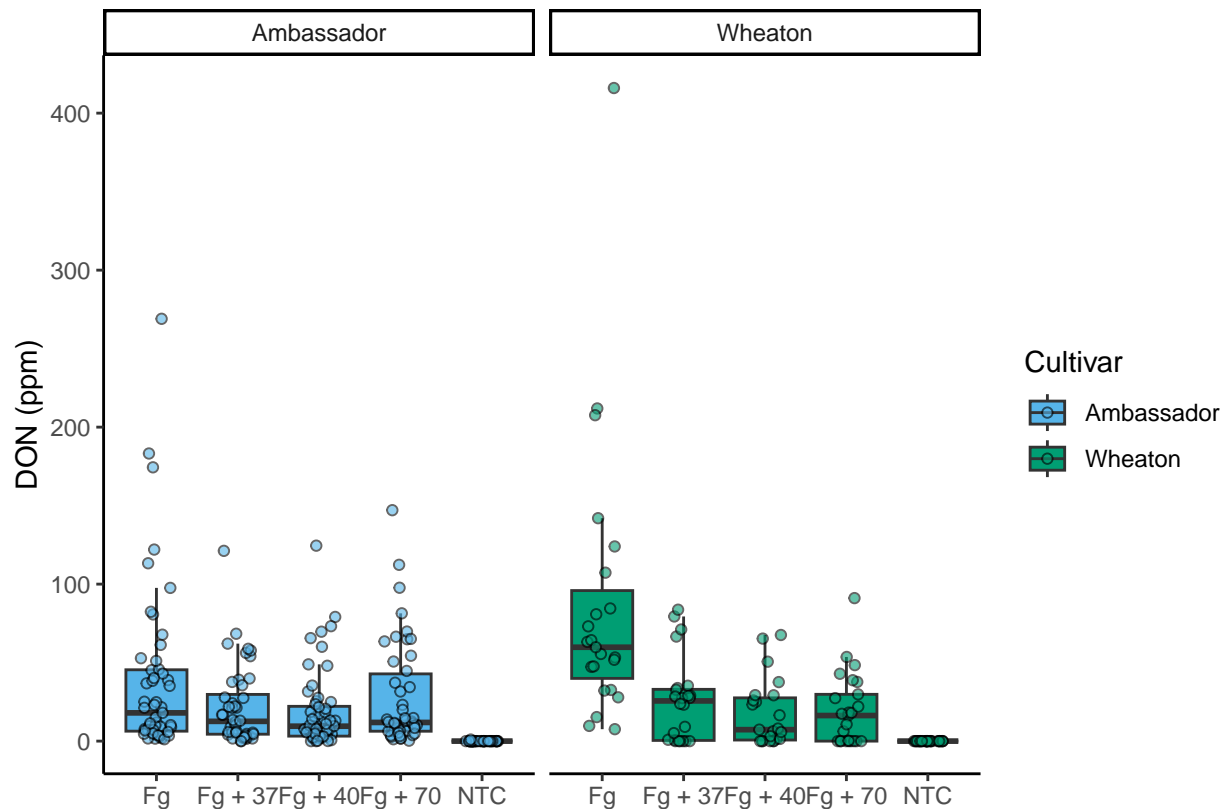
Question 2

Plotting DON x Treatment

```
DON <- ggplot(MycotoxinData, aes(x=Treatment, y=DON, fill=Cultivar)) +
  geom_boxplot(outlier.shape=NA) +
  geom_point(position = position_jitterdodge(dodge.width=0.9), shape=21,alpha=0.6)+ #jitter dodge point
  scale_fill_manual(values = c(cbbPalette[[2]],cbbPalette[[3]]))+ #manually insert two colors from CbbP
  xlab("")+ #label x-axis
  ylab("DON (ppm)")+ #label y-axis
  theme_classic() + #classic theme
  facet_wrap(~Cultivar) #facet by Cultivar
DON
```

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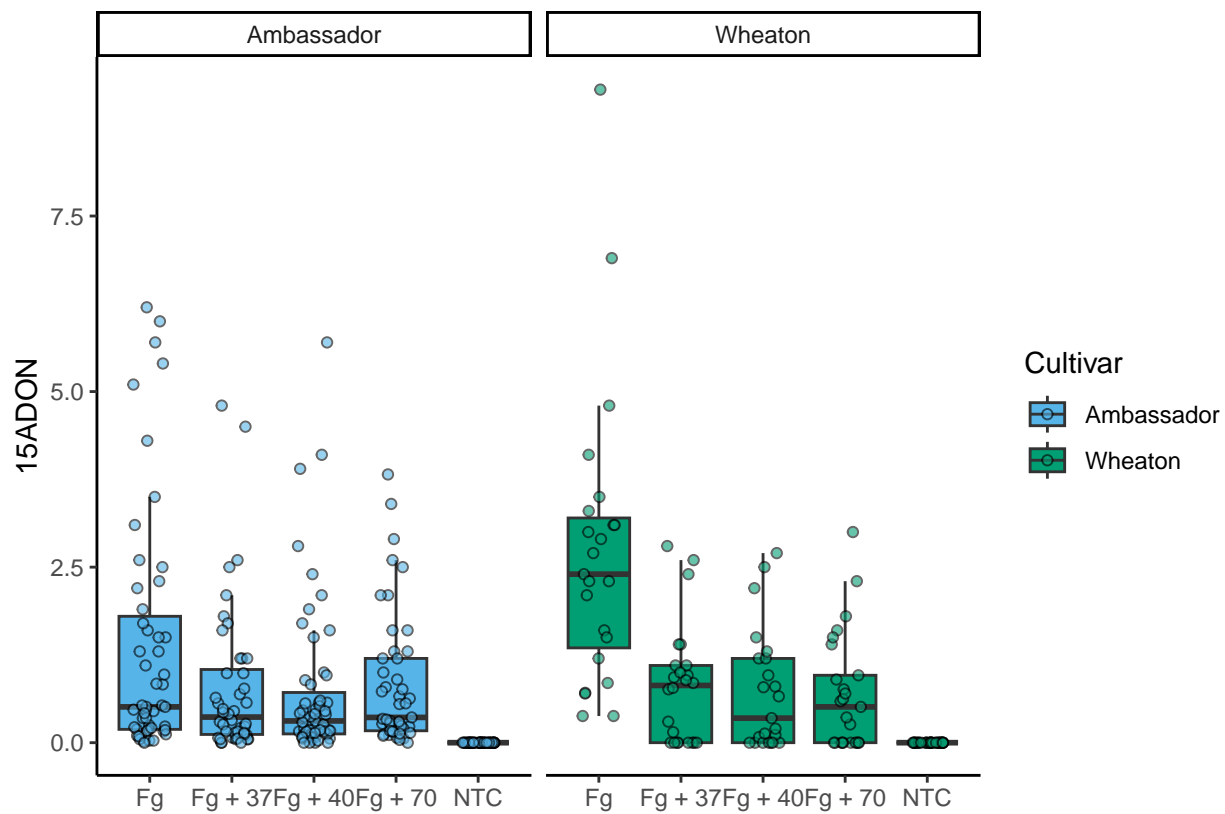

Plotting X15ADON x Treatment

```
X15ADON <- ggplot(MycotoxinData, aes(x=Treatment, y=X15ADON, fill=Cultivar)) +
  geom_boxplot(outlier.shape=NA) +
  geom_point(position = position_jitterdodge(dodge.width=0.9), shape=21,alpha=0.6)+ #jitter dodge point.
  scale_fill_manual(values = c(cbbPalette[[2]],cbbPalette[[3]]))+ #manually insert two colors from CbbP
  xlab("")+ #label x-axis
  ylab("15ADON")+ #label y-axis
  theme_classic() + #classic theme
  facet_wrap(~Cultivar) #facet by Cultivar
X15ADON
```

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


Plotting MassperSeed_mg x Treatment

```
MassperSeed <- ggplot(MycotoxinData, aes(x=Treatment, y=MassperSeed_mg, fill=Cultivar)) +
  geom_boxplot(outlier.shape=NA) +
  geom_point(position = position_jitterdodge(dodge.width=0.9), shape=21,alpha=0.6)+ #jitter dodge point.
  scale_fill_manual(values = c(cbbPalette[[2]],cbbPalette[[3]]))+ #manually insert two colors from CbbP
```

```
  xlab("")+ #label x-axis
  ylab("Seed Mass (mg)")+ #label y-axis
  theme_classic() + #classic theme
  facet_wrap(~Cultivar) #facet by Cultivar
MassperSeed
```
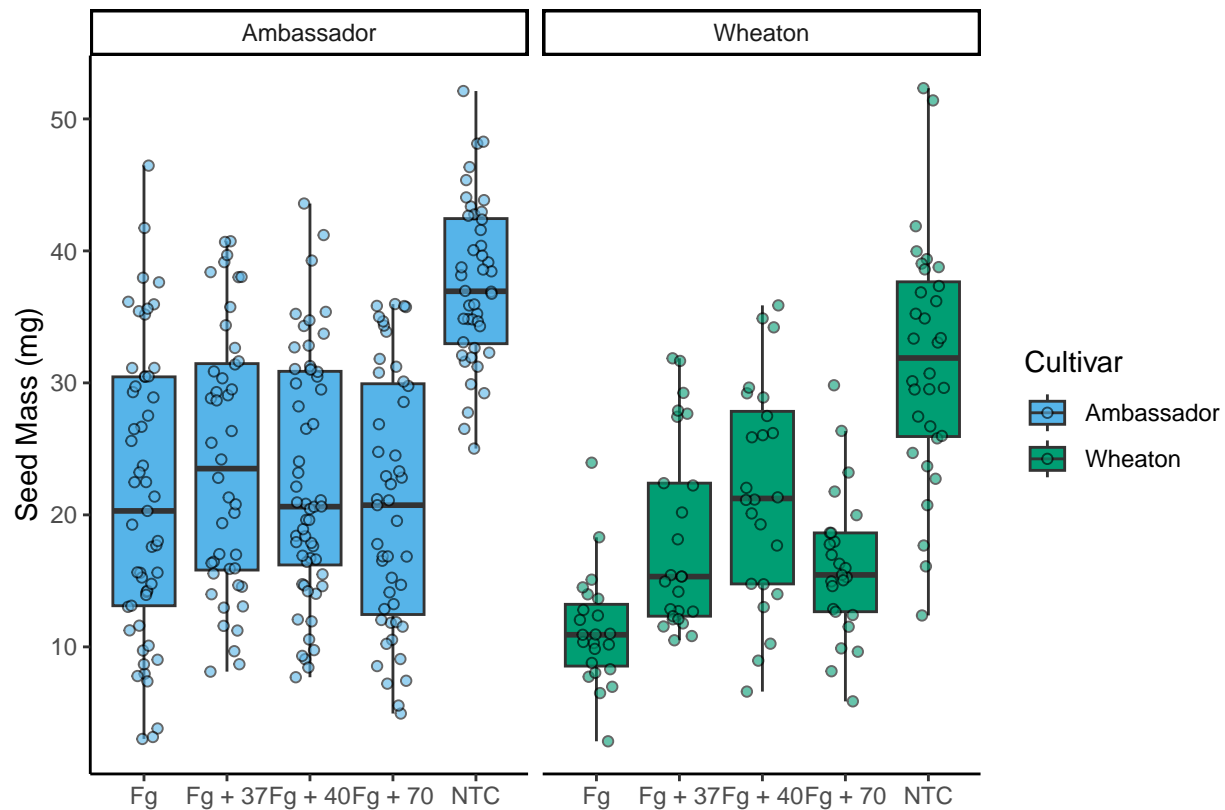
```
## Warning: Removed 2 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

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


Use geom_pwc() to add t.test pairwise comparisons to the three plots made above. Combine three figures into group via ggarrange

```
#Calculating t-tests for the three figures
Stat1 <-  DON +
  geom_pwc(aes(group=Treatment), method = "t_test",label = "p.adj.format") #Adding t-test to Question 1

Stat2 <- X15ADON +
  geom_pwc(aes(group=Treatment),method = "t_test",label = "p.adj.format")  #Adding t-test to Question 2
```

```
Stat3 <- MassperSeed +
  geom_pwc(aes(group=Treatment),method = "t_test",label = "p.adj.format")  #Adding t-test to Question 3

#Plotting three figures with t-test calculations
figure1 <- ggarrange(
  Stat1,  # First plot: water.imbibed
  Stat2,  # Second plot: bac.even
  Stat3,  # Third plot: water.imbibed.cor
  labels = "auto",  # Automatically label the plots (A, B, C, etc.)
  nrow = 1,  # Arrange the plots in 3 rows
  ncol = 3,  # Arrange the plots in 1 column
  common.legend = TRUE  # Do not include a legend in the combined figure
)
```

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

```
figure1
```