

05_InClass_Assignment_RMarkdown

Sachida Pokhrel

2025-02-27

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Clickable link to the manuscript

DOI

Read data

```
#read data
Mycotoxin <- read.csv("03_Visualization/MycotoxinData.csv",
                      na.strings = "na")

#load library
library(ggplot2)
```

Plot DON

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

#making box plot
DON <- ggplot(Mycotoxin, aes(x = Treatment,
                             y = DON,
                             fill = Cultivar))+

  geom_boxplot(outlier.shape = NA)+
  #removing NA outliers from the boxplot
  geom_point(shape = 21, color = "black",
             position = position_jitterdodge(dodge.width = 0.9),
```

```

        alpha = 0.6 )+
#giving shape to fill the color and dodge away from the bar plot, alpha value provides transparency t
scale_fill_manual(values = cbbPalette)+
theme_classic()+
xlab("")+
ylab("DON (ppm)")+
facet_wrap(~Cultivar)
#facet wrap according to the Cultivar, here I didnot use scale free since all all the plot space is use

```

Plot X15ADON

```

#making y-axis as 15ADON
X15ADON <- ggplot(Mycotoxin, aes(Treatment,
                                X15ADON,
                                fill = Cultivar))+
#change x axis only since the data is ordered for that column
geom_boxplot(outlier.shape = NA)+ #removing NA outliers from the boxplot
geom_point(shape = 21, color = "black",
           position = position_jitterdodge(dodge.width = 0.9),
           alpha=0.6 )+
scale_fill_manual(values = cbbPalette)+
theme_classic()+
xlab("")+
ylab("15ADON")+
facet_wrap(~Cultivar)

```

Plot Seed mass

```

#making y-axis as mass per seed
Seedmass <- ggplot(Mycotoxin, aes(Treatment,
                                MassperSeed_mg,
                                fill = Cultivar))+
geom_boxplot(outlier.shape = NA)+
geom_point(shape = 21, color = "black",
           position = position_jitterdodge(dodge.width = 0.9),
           alpha=0.6 )+
scale_fill_manual(values = cbbPalette)+
theme_classic()+
xlab("")+
ylab("Seed Mass (mg)")+
facet_wrap(~Cultivar)

```

Combine plots

```

#load library
library(ggpubr)

```

```

DON_stat <- DON+
  geom_pwc(aes(group = Treatment),
    method = "t.test",
    label = "{p.adj.format}.{p.adj.signif}",
    hide.ns = T)
# takes Treatment as a group to compare using t-test and provides label for p-adjusted value and signif

X15ADON_stat <- X15ADON+
  geom_pwc(aes(group = Treatment),
    method = "t.test",
    label = "{p.adj.format}.{p.adj.signif}",
    hide.ns = T)

Seedmass_stat <- Seedmass+
  geom_pwc(aes(group = Treatment),
    method = "t.test",
    label = "{p.adj.format}.{p.adj.signif}",
    hide.ns = T)

stat_plot <- ggarrange(
  DON_stat,
  X15ADON_stat,
  Seedmass_stat,
  ncol = 3,
  nrow = 1,
  labels = c("A", "B", "C"), #we can also provide label to the plot manually
  common.legend = T
)

```

```

## 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()').

```

