Inclass_assignment_R_markdown

Arpan

2025-02-27

Contents

DOM

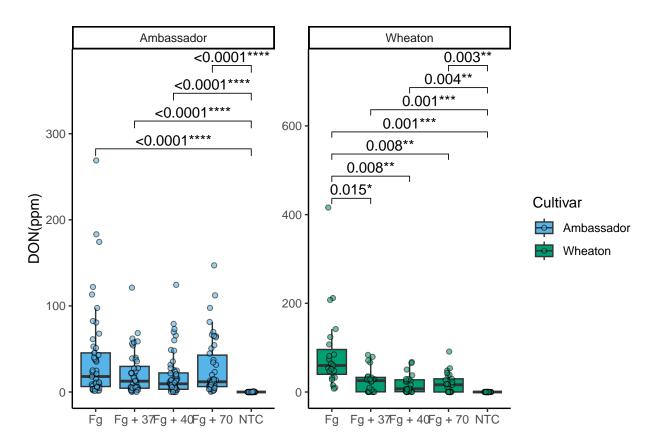
DON	
15ADON	
Seed mass	
Manuscript link: https://doi.org/10.1094/PDIS-06-21-1253-RE	
<pre>library(ggplot2) library(ggpubr) #Reading the data and converting "na" strings to NA values datum=read.csv("Data_Visualization_class1/MycotoxinData.csv",na.strings="na")</pre>	
# Convert categorical variables to factors datum\$Treatment=as.factor(datum\$Treatment) # Convert treatment column to a categorical variable datum\$Cultivar=as.factor(datum\$Cultivar)# Convert cultivar column to a categorical variable datum\$BioRep=as.factor(datum\$BioRep) # Convert biological replicate column to a categorical	
#Using colour blind palette cbbPalette <- c("#E69F00", "#56B4E9", "#009E73", "#F0E442", "#0072B2", "#D55E00", "#CC79A7"	',"#000000")

DON

```
plot1<-ggplot(datum, aes(Treatment,DON,fill=Cultivar))+
   geom_boxplot(outlier.shape = NA)+ #adding boxplot in figure but removing outliers(the black dots that
   geom_point(position=position_jitterdodge(dodge.width=0.9),shape=21,alpha=0.6)+#Adding jitter points o
   scale_fill_manual(values = cbbPalette[c(2, 3)])+#filling the points and boxplots Cultivar with two co
   xlab("")+#Changing x label
   ylab("DON(ppm)")+#Changing y label
   facet_wrap(~Cultivar,scales="free")+#faceting by cultivar
   theme_classic() + #Using classic theme
   geom_pwc(aes(group=Treatment),method="t.test",label="{p.adj.format}-{p.adj.signif}-",hide.ns=T)#Using g
plot1</pre>
```

```
## 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()').



15ADON

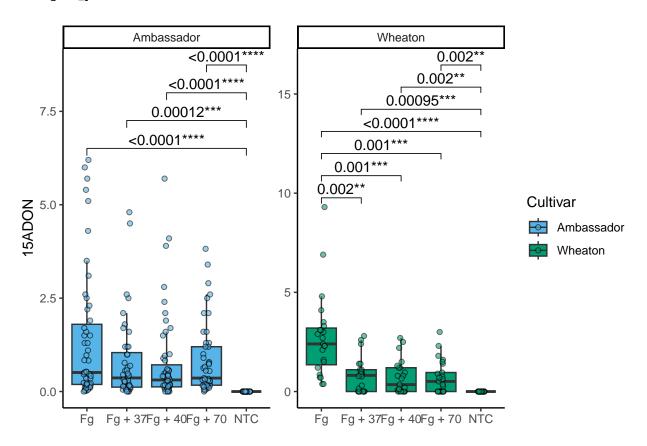
('stat_boxplot()').

```
# Change the y-variable to plot X15ADON and MassperSeed_mg. The y-axis label should now be
plot2<-ggplot(datum, aes(Treatment,X15ADON,fill=Cultivar))+#Changing y variable to X15DON
geom_boxplot(outlier.shape = NA)+
geom_point(position=position_jitterdodge(dodge.width=0.9),shape=21,alpha=0.6)+
scale_fill_manual(values = cbbPalette[c(2, 3)])+
xlab("")+
ylab("15ADON")+#Changing the label as per y variable used
facet_wrap(~Cultivar,scales="free")+
theme_classic()+
geom_pwc(aes(group=Treatment),method="t.test",label="{p.adj.format}{p.adj.signif}",hide.ns=T)
plot2

## Warning: Removed 10 rows containing non-finite outside the scale range</pre>
```

```
## 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()').



Seed mass

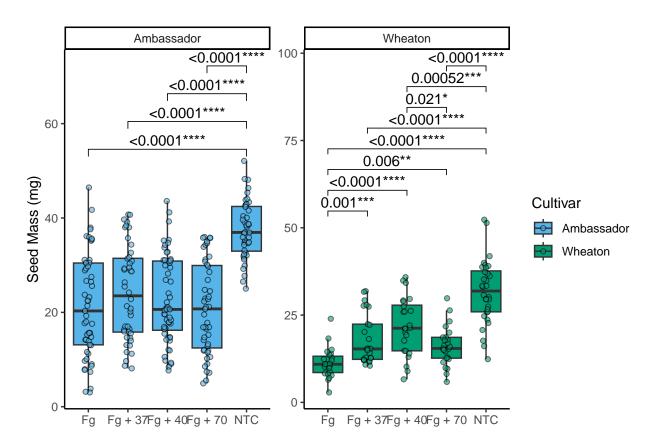
```
plot3<-ggplot(datum, aes(Treatment,MassperSeed_mg,fill=Cultivar))+#Changing y variable to MassperSpeed_
    geom_boxplot(outlier.shape = NA)+
    geom_point(position=position_jitterdodge(dodge.width=0.9),shape=21,alpha=0.6)+
    scale_fill_manual(values = cbbPalette[c(2, 3)])+
    xlab("")+
    ylab("Seed Mass (mg)")+#Changing y label as per y variable used
    facet_wrap(-Cultivar,scales="free")+
    theme_classic()+
    geom_pwc(aes(group=Treatment),method="t.test",label="{p.adj.format}{p.adj.signif}",hide.ns=T)

plot3

## 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()').</pre>
```

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



Combined

```
# combining all three figures into one with three columns and one row.
figure <- ggarrange(plot1,plot2,plot3,labels = c("A","B","C"),nrow = 1,ncol = 3, 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()').</pre>
```

```
## 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

