Bio-Data Science Task 1 Report

Summary: In this week's task, I carried out two tasks to strengthen my skills inR-programming for data science.

First, I performed simple visualization on the data set "astrocyte_data". I created barplots, histograms, boxplots, added legends and labels. Next, I installed all the packages that would enable me perform ggplots on the data set "aflatoxin_data". I continued to melt data, stack barplots, create pie-chart, histogram and scatter plot while applying colors. I then created heatmaps which I manipulated severally to create what suits my taste.

In conclusion, this task has strengthened my skills in R-programmingfor statistical analysis/visualization.

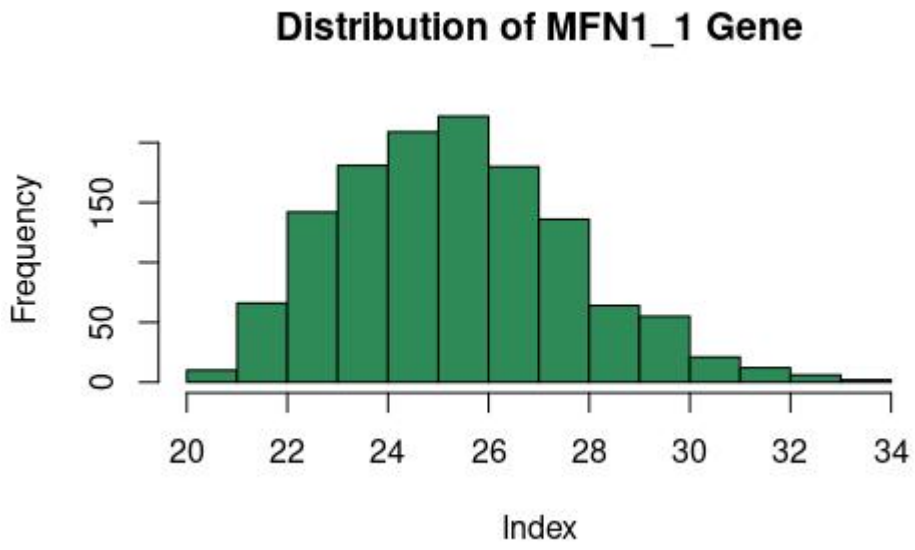
Explanations of codes and visualizations are provided below:

1. Mitochondria-endoplasmic reticulum contacts in reactive astrocytes promote vascular remodelling. Goebel et al. I want to perform the comparison of FACS-enriched astrocytes from uninjured and injured wild-type mice at different time points.I have already downloaded my data as .csv, next I will import my file in R

```
astrocyte_data <- read.csv(file.choose())
astrocyte_data
```

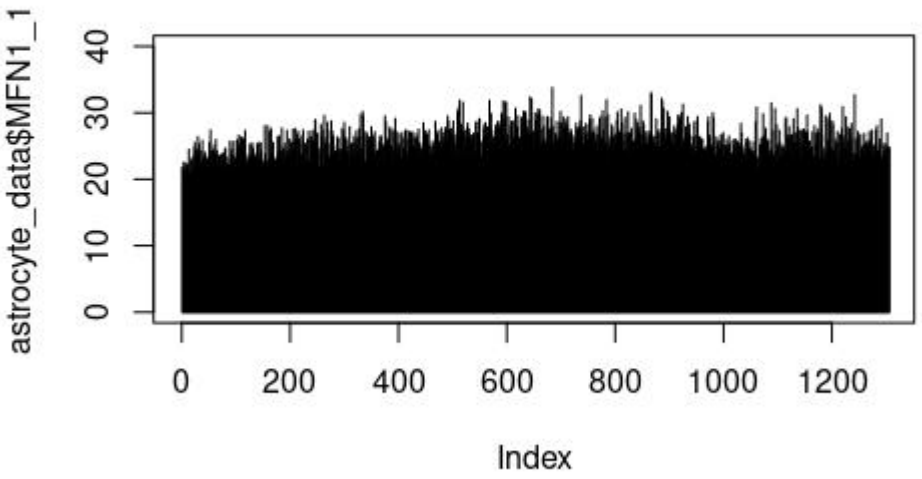
2. I want to perform Data Visualization in R. Let me construct a histogram for the distribution of MFN1_1 Gene

```
hist(astrocyte_data$MFN1_1, col = "Sea green", main = "Distribution of MFN1_1 Gene",
xlab = "Index")
```



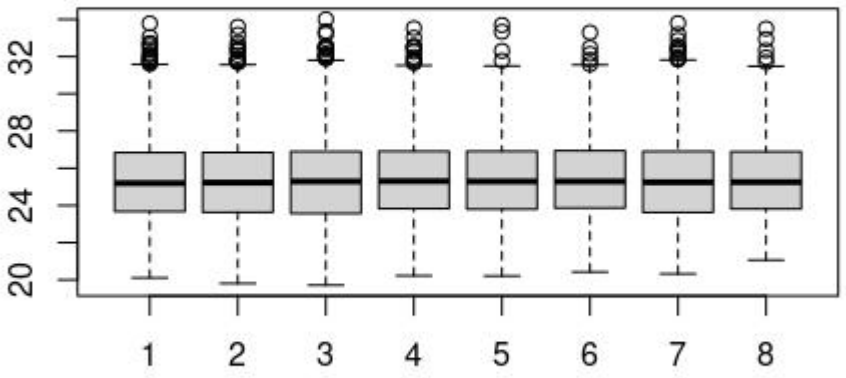
3. I want to plot lineplots for the distribution of MFN1_1 Gene

```
plot(astrocyte_data$MFN1_1, type = "h", xlim = c(0,1300), ylim = c(0, 40))
```



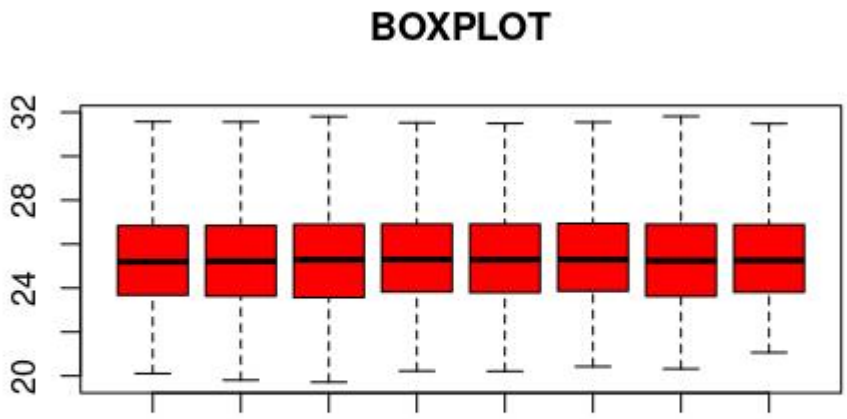
4. I want to create black and white boxplots for my genes

```
boxplot(astrocyte_data$MFN1_1, astrocyte_data$MFN1_2, astrocyte_data$MFN1_4,
astrocyte_data$WT_1, astrocyte_data$WT_3, astrocyte_data$WT_4, astrocyte_data$MFN1,
astrocyte_data$WT)
```



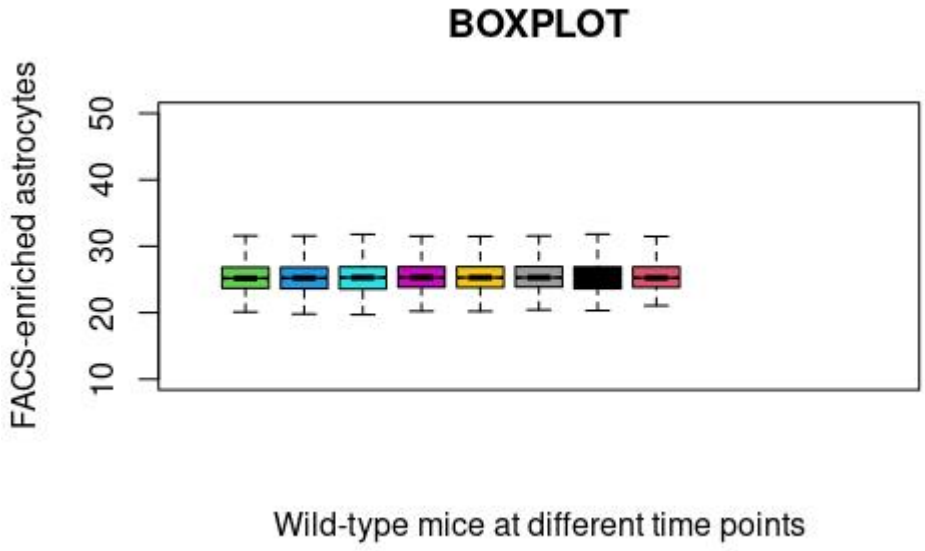
5. Let me add red color and title to my boxplot

```
boxplot(astrocyte_data$MFN1_1, astrocyte_data$MFN1_2, astrocyte_data$MFN1_4,
astrocyte_data$WT_1, astrocyte_data$WT_3, astrocyte_data$WT_4, astrocyte_data$MFN1,
astrocyte_data$WT, col = 'red', outline = F, main = 'BOXPLOT')
```



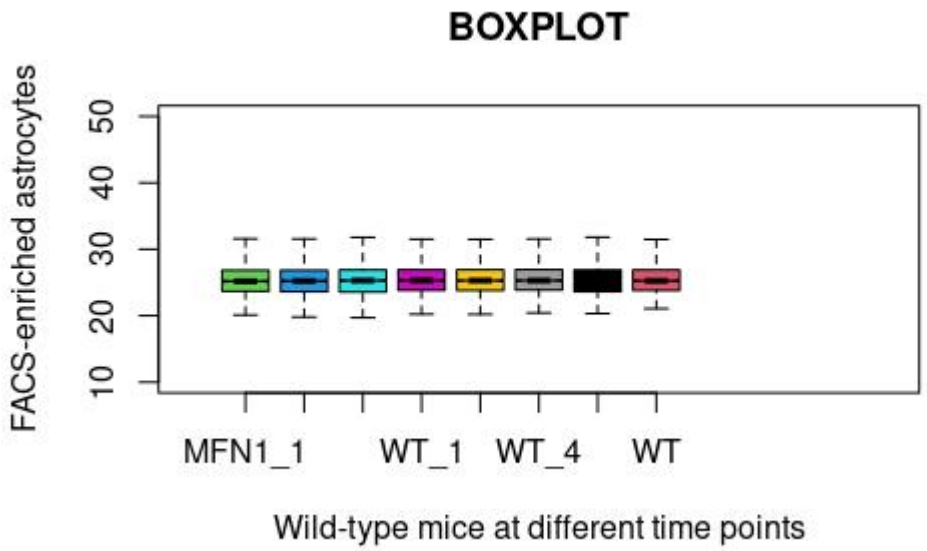
6. I want to color by gene types

```
boxplot(astrocyte_data$MFN1_1, astrocyte_data$MFN1_2, astrocyte_data$MFN1_4, astrocyte_data$WT_1, astrocyte_data$WT_3, astrocyte_data$WT_4, astrocyte_data$MFN1, astrocyte_data$WT, col = 3:10, notch = T, outline = F, main = 'BOXPLOT', xaxt = 'n', xlab = 'Wild-type mice at different time points', ylab = 'FACS-enriched astrocytes', ylim = c(10,50), xlim = c(0,12))
```



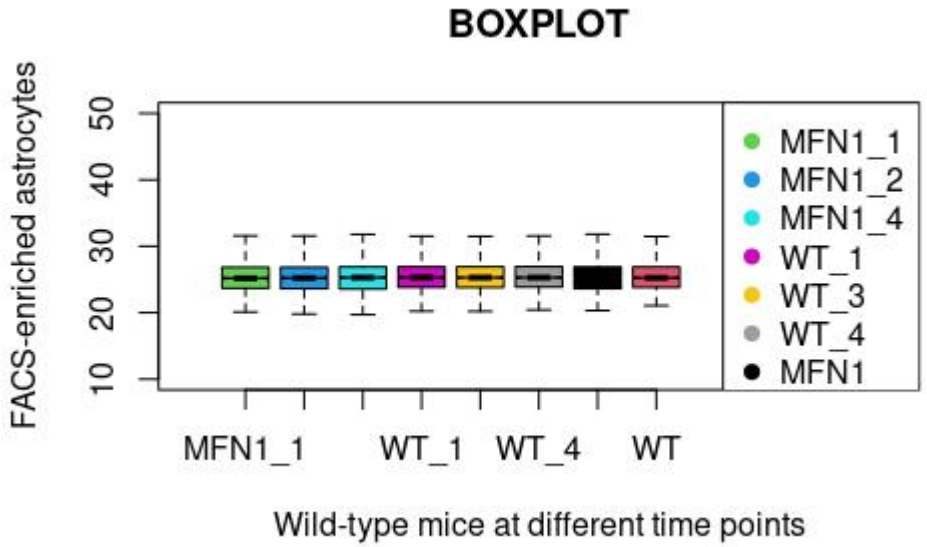
7. I want to add axis

```
axis(side = 1, at = c(1,2,3,4,5,6,7,8), labels = c('MFN1_1', 'MFN1_2', 'MFN1_4', 'WT_1', 'WT_3', 'WT_4', 'MFN1', 'WT'))
```



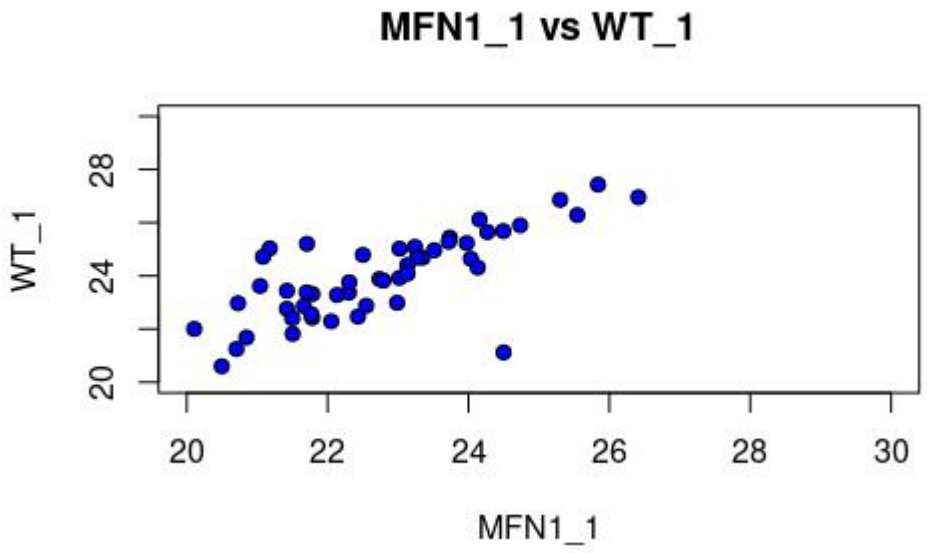
8. Finally I will add legend

```
legend('topright', legend = c('MFN1_1', 'MFN1_2', 'MFN1_4', 'WT_1', 'WT_3', 'WT_4', 'MFN1', 'WT'), col = 3:10, pch = 19)
```



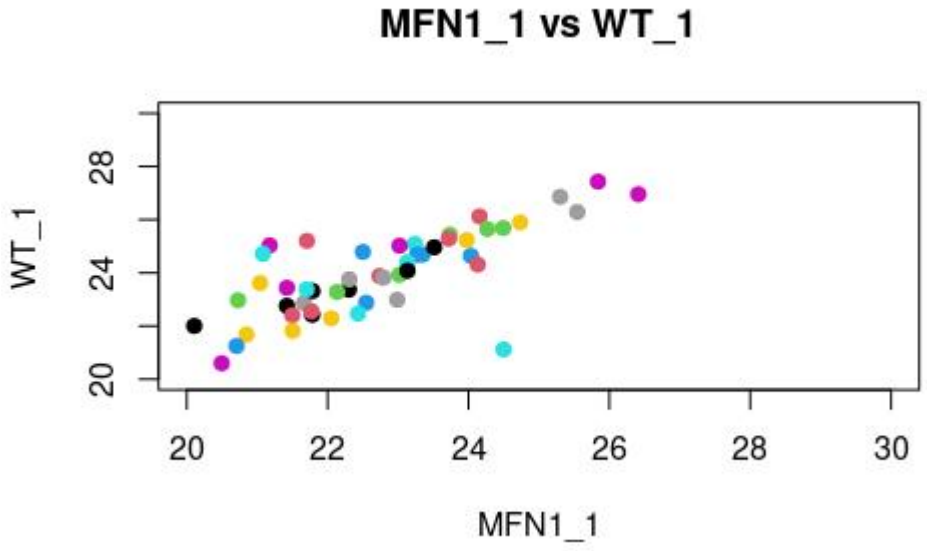
9. I want to create a scatterplot of MFN1_1 vs WT_1. I will color it black with a background of blue.

```
plot(x = astrocyte_data$MFN1_1[1:50], y = astrocyte_data$WT_1[1:50], col = 'black', pch = 21, bg = 'blue', main = 'MFN1_1 vs WT_1', xlab = 'MFN1_1', ylab = 'WT_1', xlim = c(20,30), ylim = c(20,30))
```



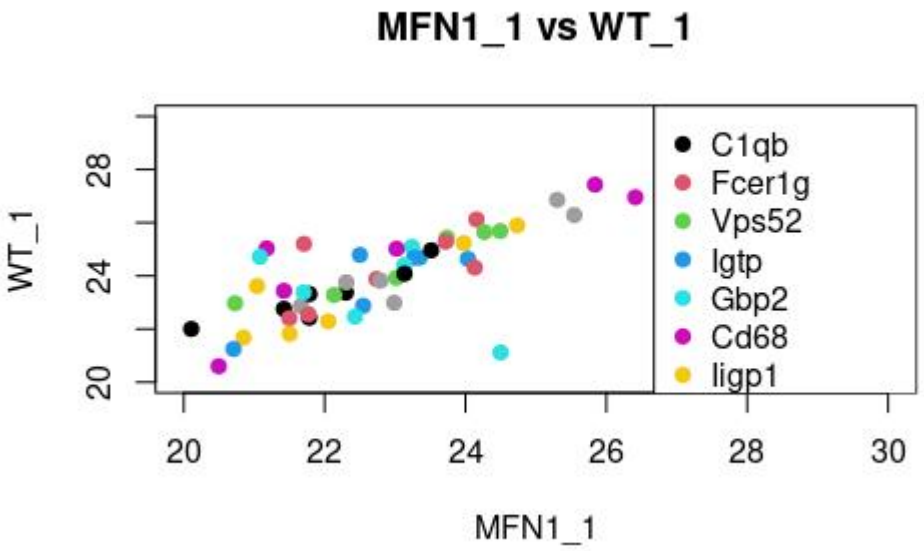
10. I want to color by gene type.

```
plot(astrocyte_data$MFN1_1[1:50], astrocyte_data$WT_1[1:50], col = 1:50, pch = 19, main = 'MFN1_1 vs WT_1', xlab = 'MFN1_1', ylab = 'WT_1', xlim = c(20,30), ylim = c(20,30))
```



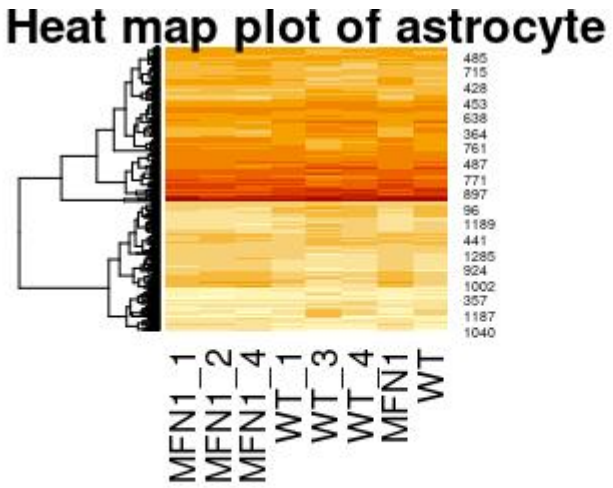
11. Let me add legend to my plot

```
legend('topright', legend = c(astrocyte_data$T..Gene.names[1:50]), pch = 19, col = 1:50)
```



12. I plot the heatmap next.

```
heatmap(as.matrix(astrocyte_data[2:9]), Colv = NA, scale = 'col', margins = c(10,10), main = 'Heat map plot of astrocyte')
```

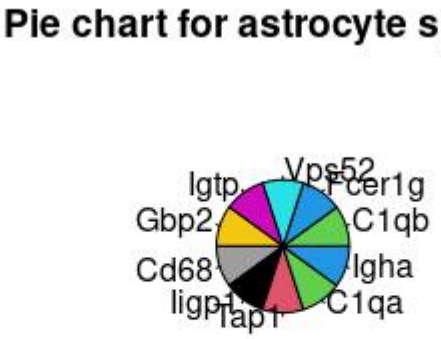


13. Let me now plot Pie Charts

```
table(astrocyte_data$T..Gene.names[1:10])
item <- unique(astrocyte_data$T..Gene.names[1:10])
itemCount <- as.vector(table(astrocyte_data$T..Gene.names[1:10]))
```

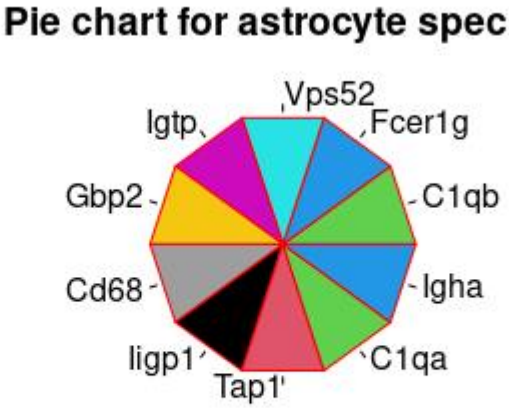
14. I will start by plotting a simple pie chart for astrocyte species

```
pie (x = itemCount, labels = item, radius = 0.5, col = 11:20, main = 'Pie chart for astrocyte species')
```



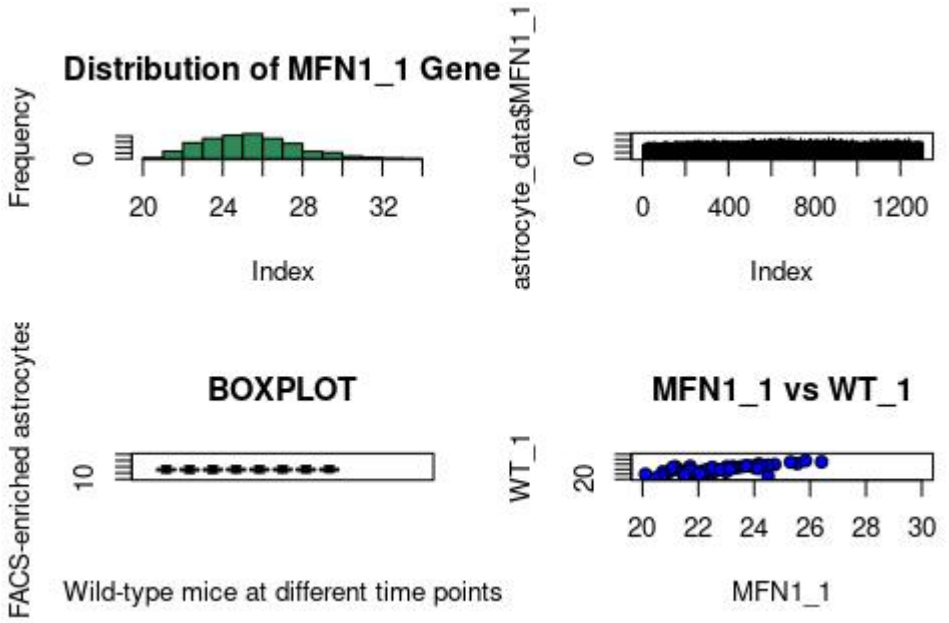
15. Next, let me add edges and color my borders

```
pie (x = itemCount, labels = item, radius = 1.0, edge = T, border = 'red', col = 11:20, main = 'Pie chart for astrocyte species')
```



16. Let's practice how to arrange some of these plots as we usually see in publications

```
par(mfrow = c(2,2))
```



LET US NOW GO FULLY INTO GGPLOTS

17. We are going to work with a new dataset

About data set: Growth and Toxigenicity of A. flavus on Resistant and Susceptible Peanut Genotypes. This study seeks to determine the reaction of peanut genotypes to Aflatoxigenic and non-aflatoxigenic A. flavus inoculation and also determine the mechanisms of their resistance. It was established that non-aflatoxigenic A. flavus grows faster than aflatoxigenic A. flavus. There was no significant difference in the incidence and severity of the A. flavus resistant genotypes (L027B and ICGV-03401) however, there were significant differences between resistant genotypes and the susceptible check Manipinta. This study also confirmed that non-aflatoxigenic A. flavus inoculation did not lead to aflatoxin production. Non-aflatoxigenic A. flavus identified could serve as a good biocontrol against aflatoxin contamination under field conditions. Additionally, peanut genotypes with resistance to post-harvest aflatoxin accumulation will resist the growth of A. flavus and subsequent aflatoxin accumulation.

18. Install ggplot2

```
install.packages("ggplot2")
library(ggplot2)
```

19. Import .csv file in R

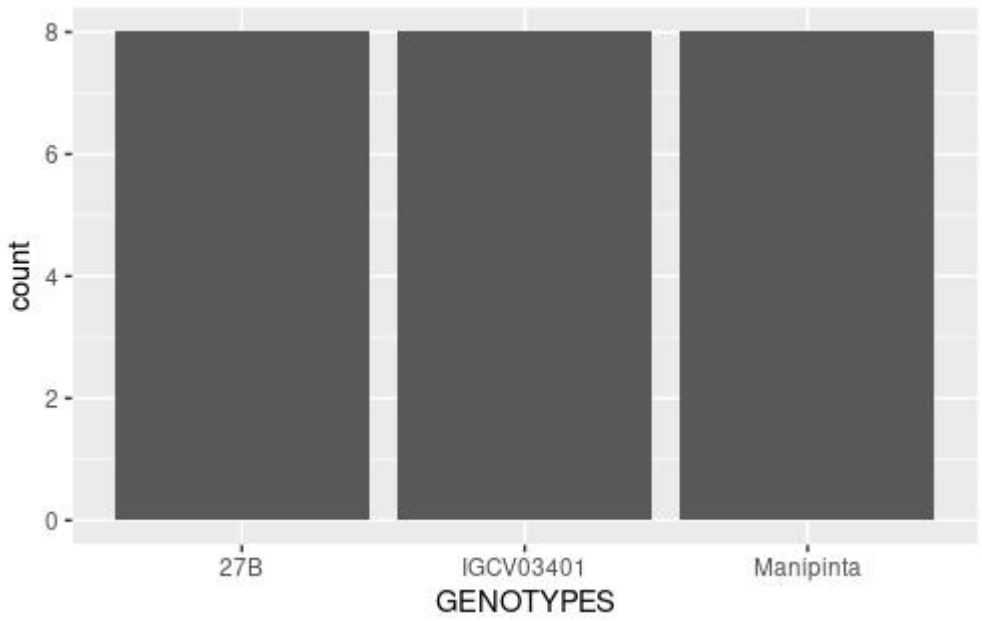
```
aflatoxin_data <- read.csv(file.choose())
aflatoxin_data
```

20. Start with defining the base data for ggplot

```
pl <- ggplot(data = aflatoxin_data)
```

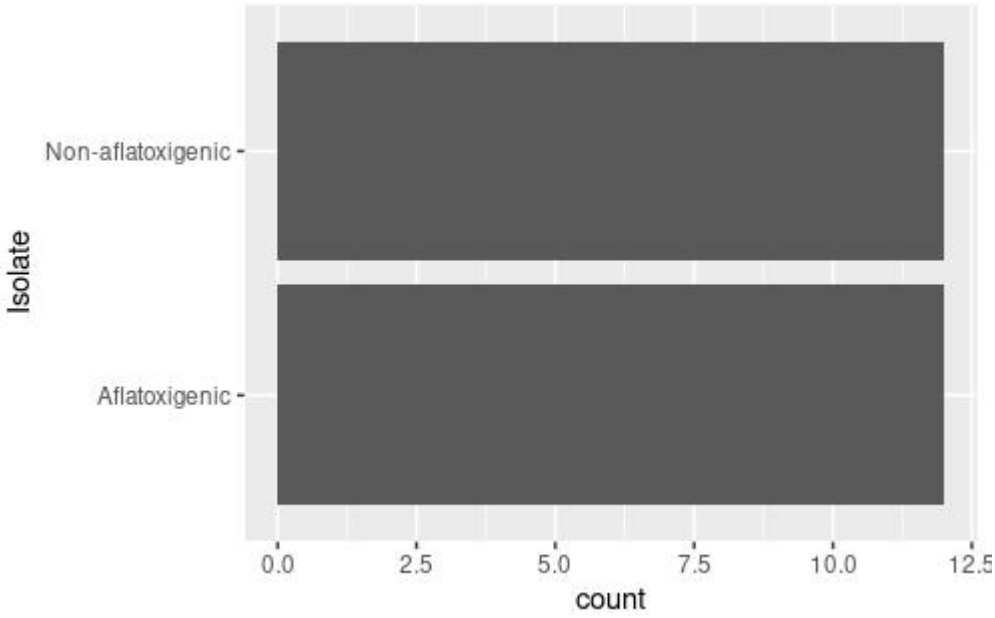
21. To the base, I will add what I want to plot and color

```
pl + geom_bar(aes(x=GENOTYPES))
```



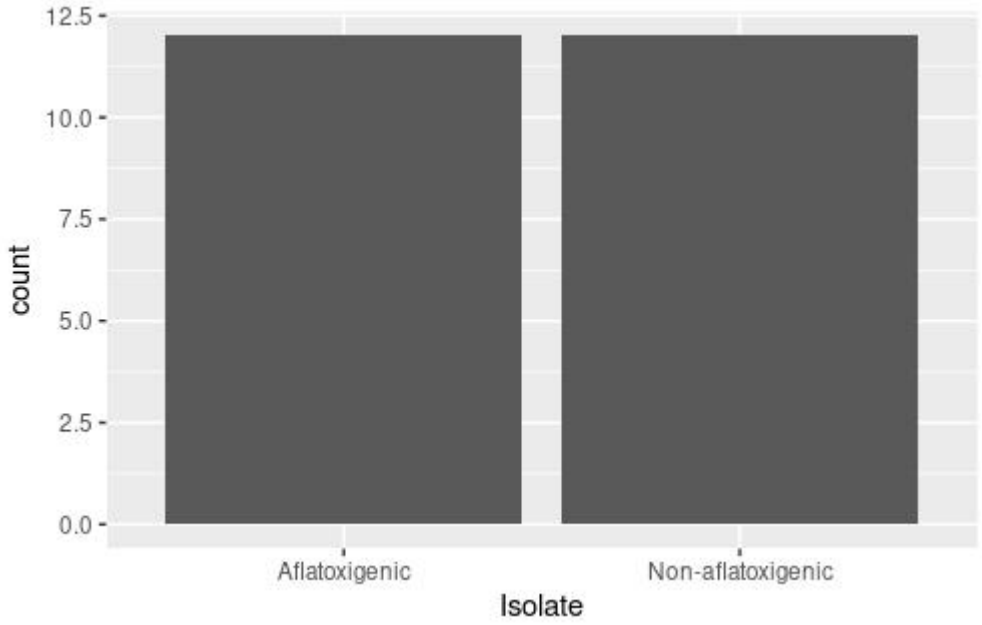
22. I will plot frequency of the data from a single column

```
pl + geom_bar(aes(y=Isolate))
```



23. Let me flip the coordinates

```
pl + geom_bar(aes(y=Isolate))+coord_flip()
```

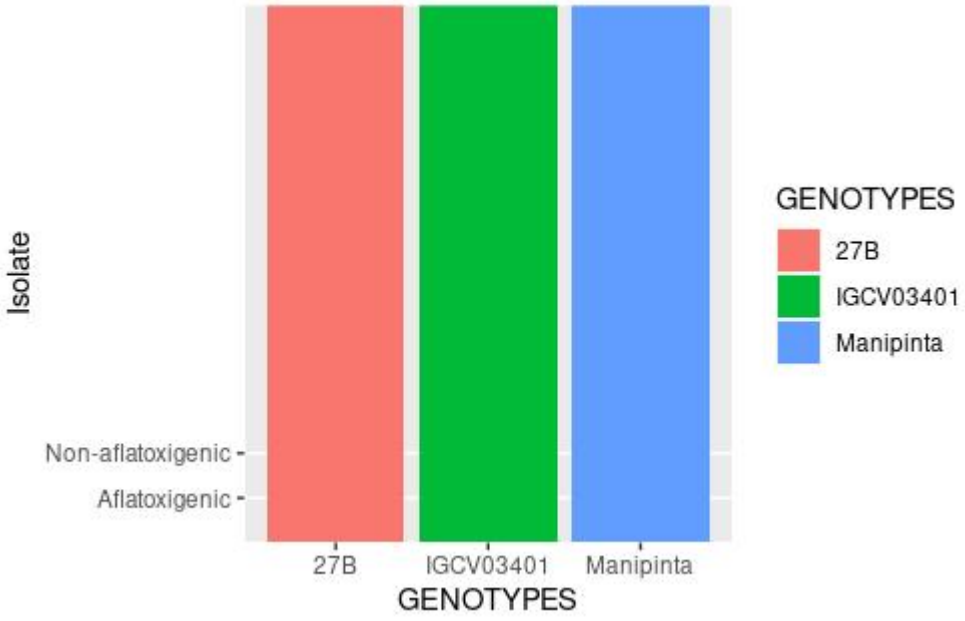


24. See the frequency of each variable within the species. Install.package(reshape2). Melt the data to have something understandable by ggplot better.

```
install.packages("reshape2")
install.packages("Rcpp")
library(reshape2)
melted_aflatoxin_data <- melt(aflatoxin_data)
```

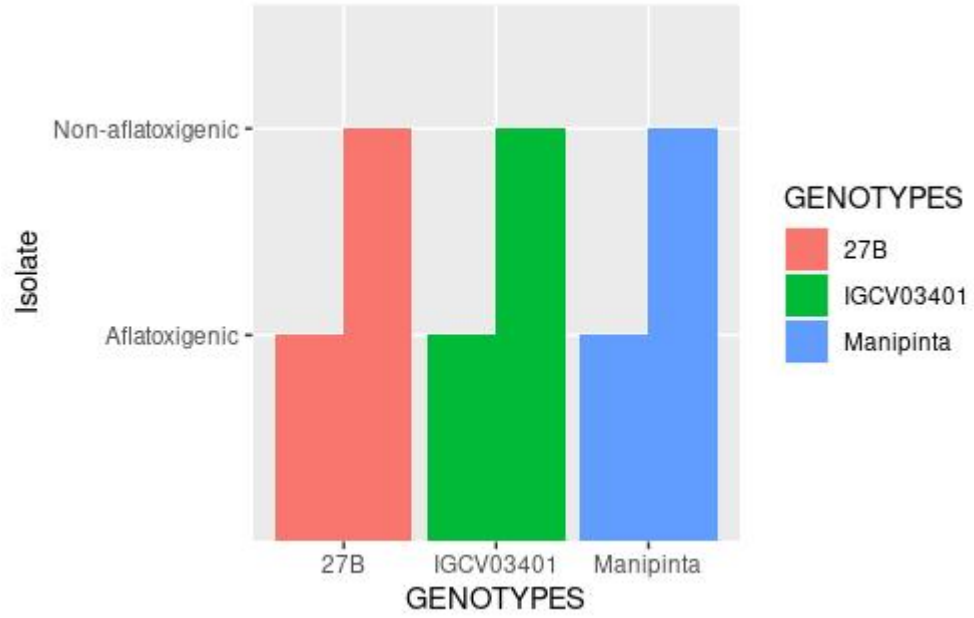
25. I want to produce a ttacked/continuous bar plot for genotypes.

```
ggplot(data = aflatoxin_data) + geom_bar(aes(x=GENOTYPES, y=Isolate, fill = GENOTYPES), stat = "identity")
```



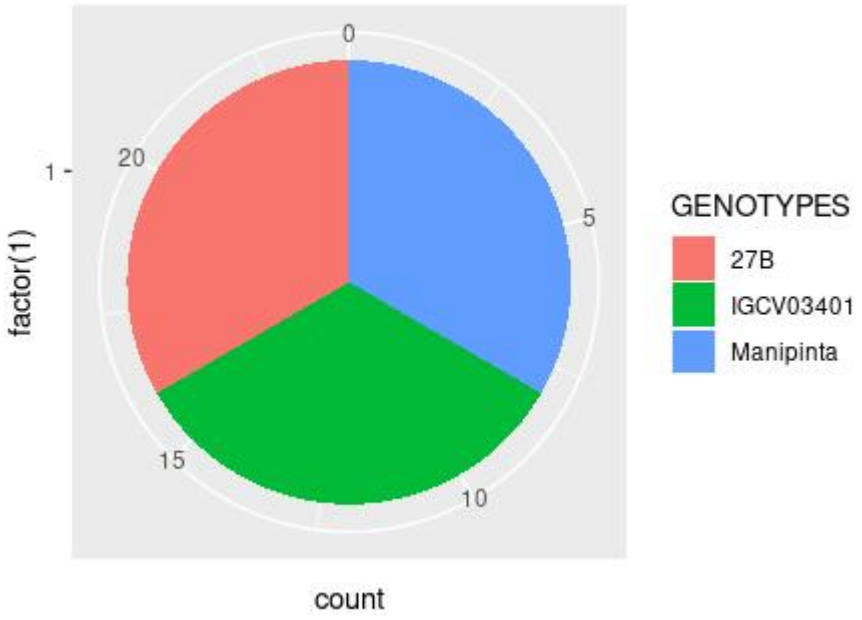
26. Let me produce a multiple bar plot

```
ggplot(data = aflatoxin_data) + geom_bar(aes(x=GENOTYPES, y=Isolate, fill = GENOTYPES), stat = "identity", position = 'dodge')
```



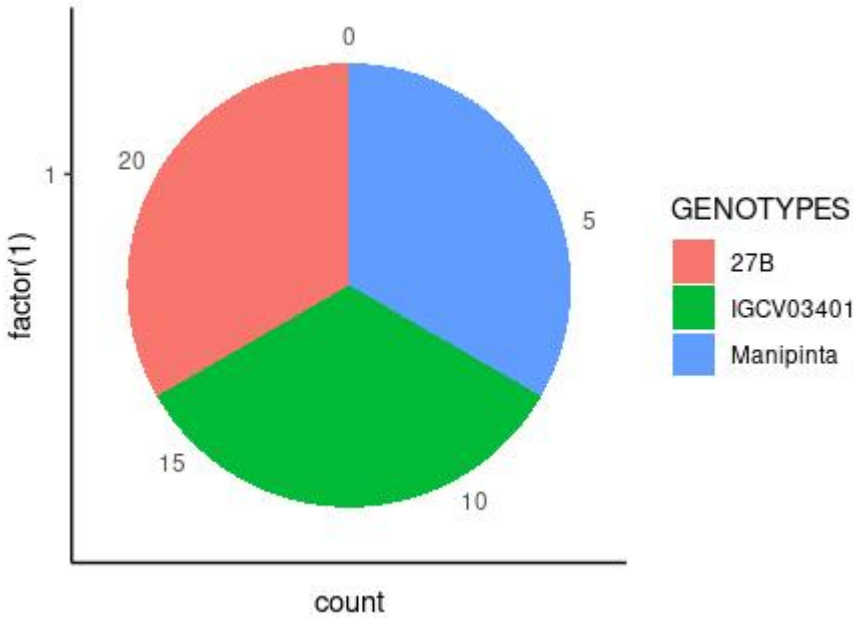
27. Let me plot a simple pie chart and label by genotypes

```
ggplot(data = aflatoxin_data) + geom_bar(aes(x=factor(1), fill = GENOTYPES), width = 1) + coord_polar(theta = 'y')
```



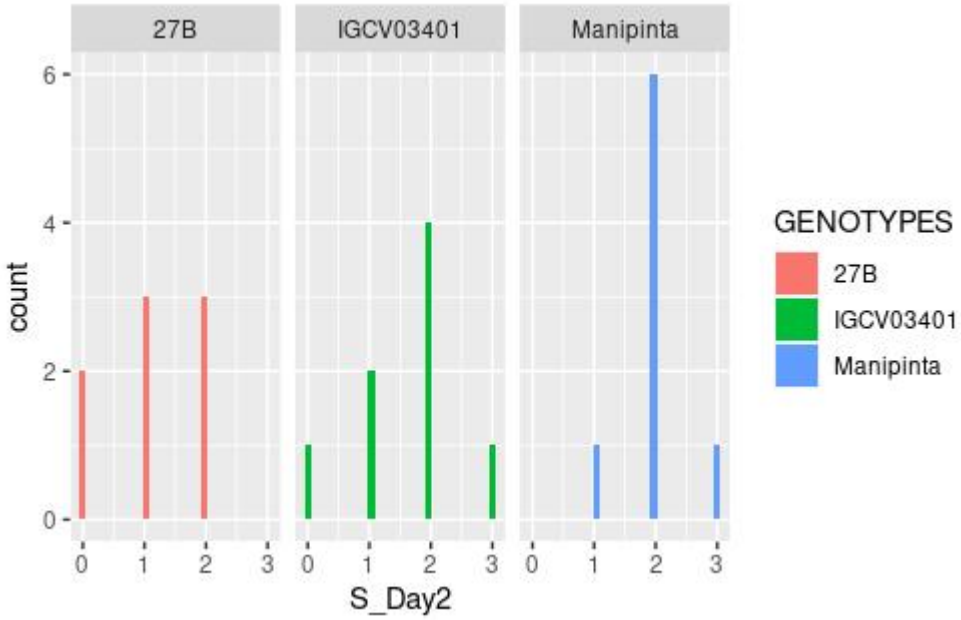
28. I will add a theme of my choice

```
ggplot(data = aflatoxin_data) + geom_bar(aes(x=factor(1), fill = GENOTYPES), width = 1) + coord_polar(theta = 'y') + theme_classic()
```



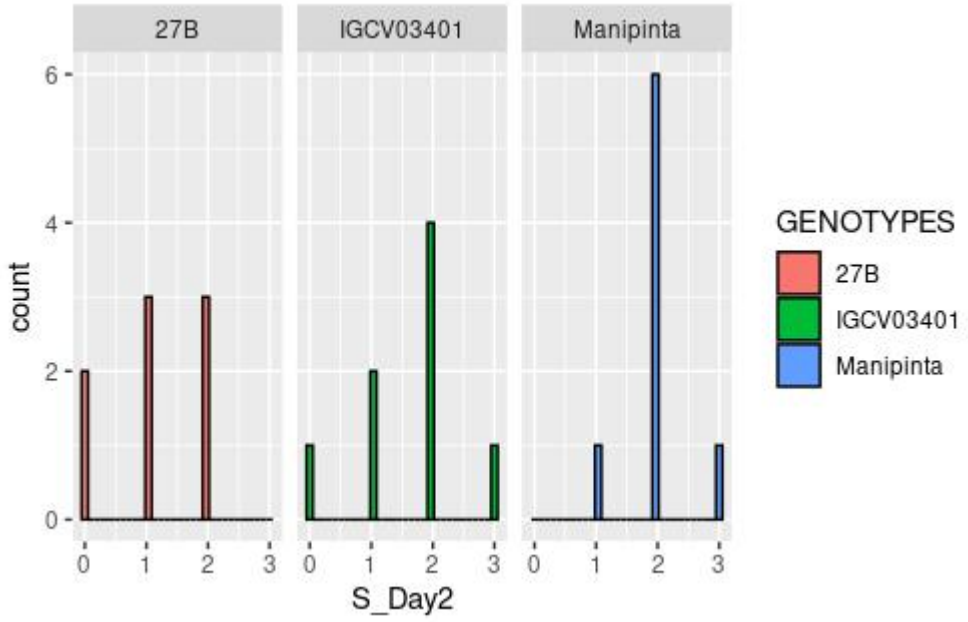
29. Let me plot a simple histogram for aflatoxin_data

```
pl <- ggplot(data = aflatoxin_data)
pl + geom_histogram(aes(x=S_Day2, fill = GENOTYPES)) + facet_grid(. ~GENOTYPES)
```



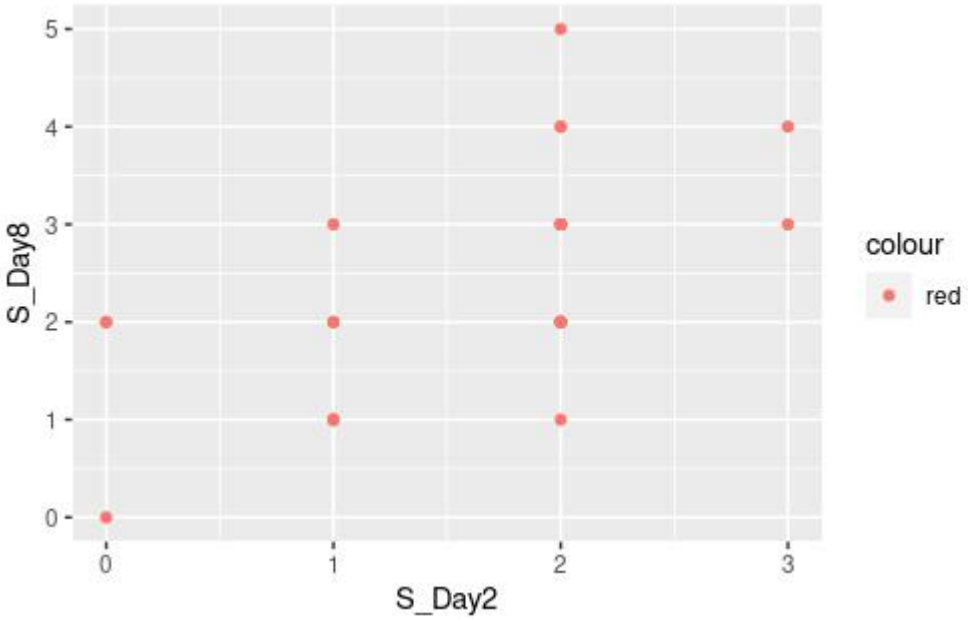
30. I will add a color parameter

```
pl + geom_histogram(aes(x=S_Day2, fill = GENOTYPES), color = "black") + facet_grid(. ~GENOTYPES)
```



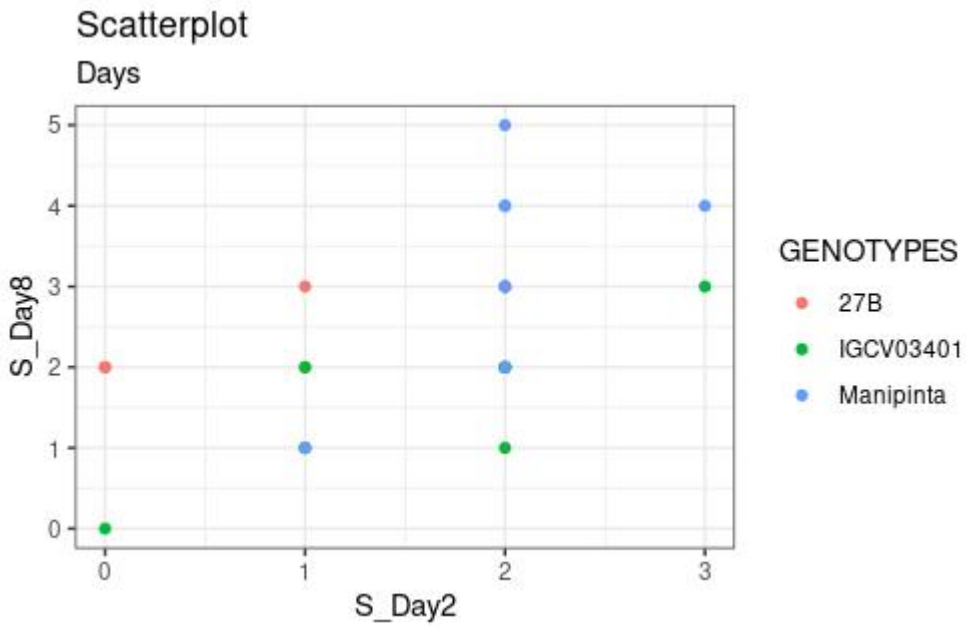
31. Let me construct a Scatter plot of S_Day8 against S_Day2 with red color

```
pl + geom_point(aes(x = S_Day2, y = S_Day8, color = 'red'))
```



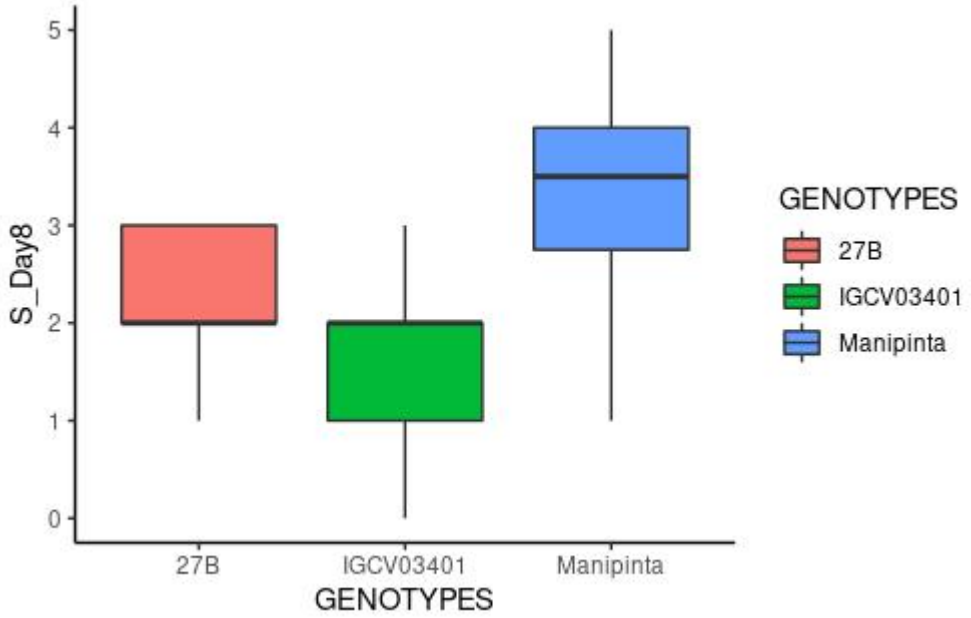
32. I will Color by Genotype (quite automated)

```
pl + geom_point(aes(x = S_Day2, y = S_Day8, color = GENOTYPES)) + theme_bw() +
ggtitle(label = 'Scatterplot', subtitle = 'Days')
```



33. I will construct a boxplot plus a theme

```
pl + geom_boxplot(notch = F, aes(x= GENOTYPES, y = S_Day8, fill = GENOTYPES)) +
theme_classic()
```

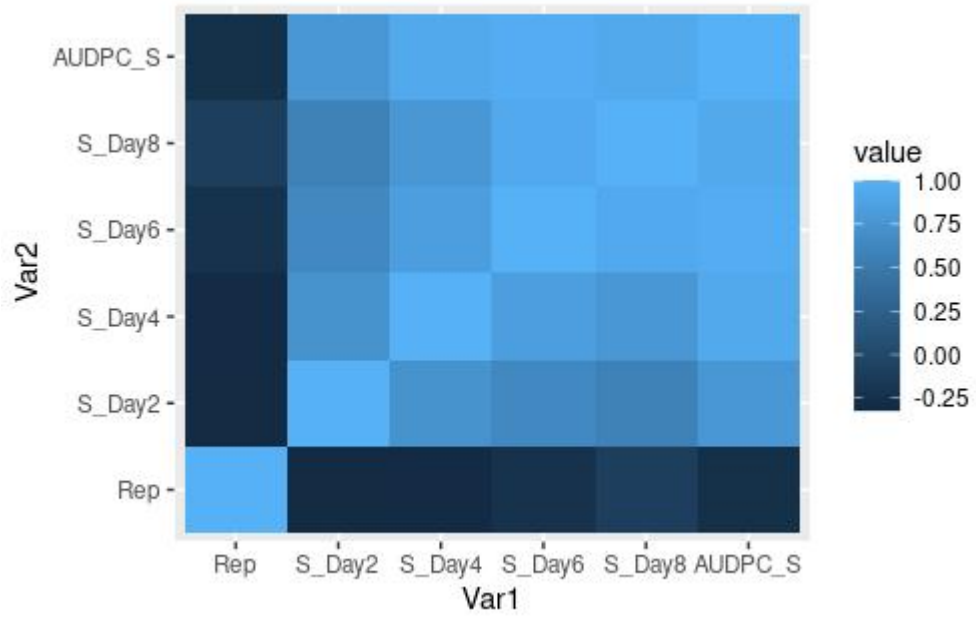


34. Heat map plotting. I will use melting methods to create heat map with ggtiles.

```
meltCorData <- melt(cor(aflatoxin_data[3:8]))
```

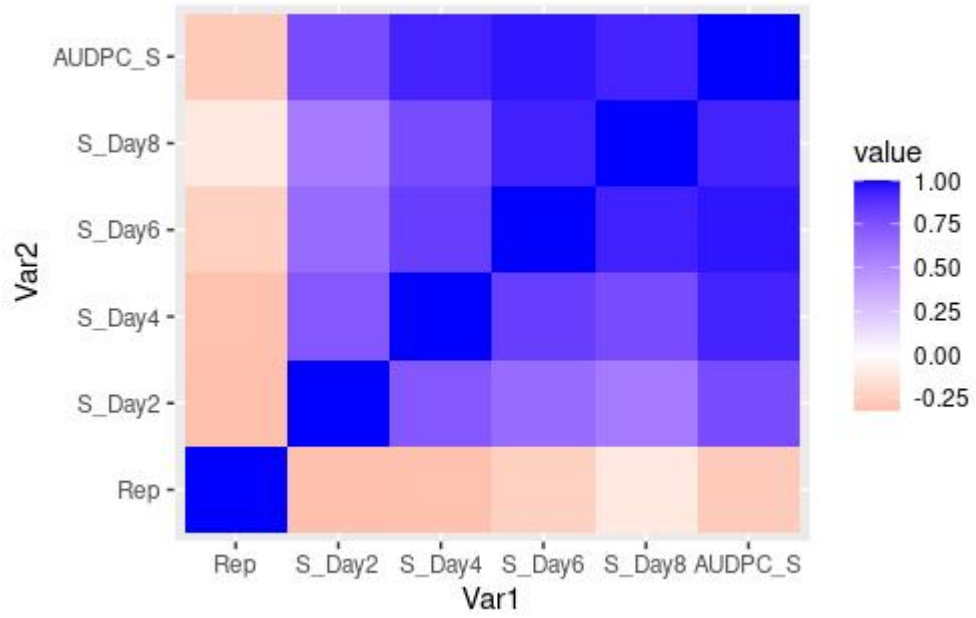
35. I start by setting my new ggplot

```
hm <- ggplot(data = meltCorData)
hm + geom_tile(aes(x = Var1, y = Var2, fill = value))
```



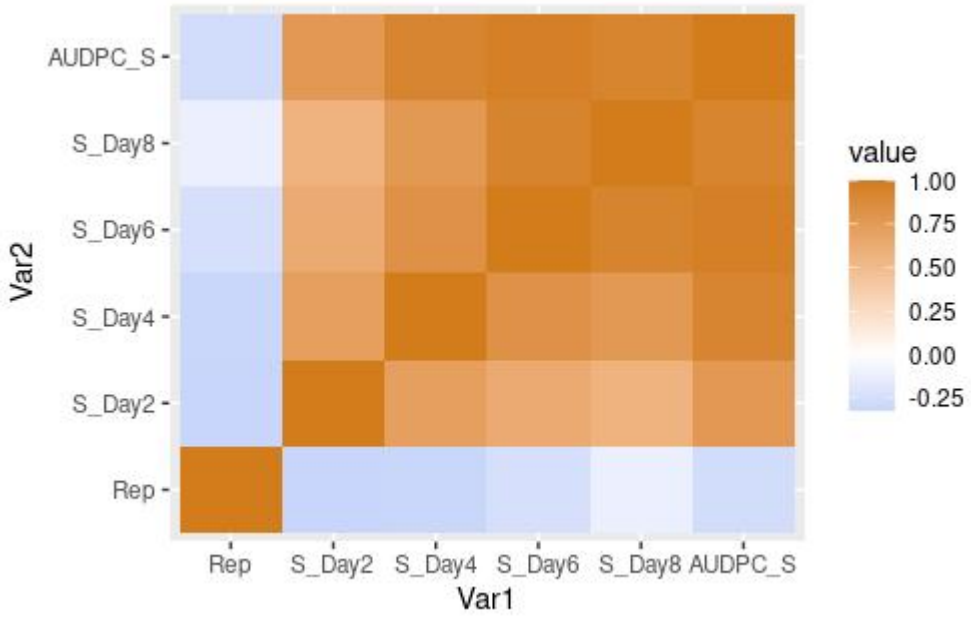
36. Let me start changing colors in heatmaps

```
hm + geom_tile(aes(x = Var1, y = Var2, fill = value)) + scale_fill_gradient2(low = 'red', high = 'blue')
```



37. I will also use hex code

```
hm + geom_tile(aes(x = Var1, y = Var2, fill = value)) + scale_fill_gradient2(low = '#1687ee', high = '#d27C1c')
```



38. Let me change my x and y labels

```
hm + geom_tile(aes(x = Var1, y = Var2, fill = value)) + scale_fill_gradient2() + xlab('First Variable') + ylab('Second Variable')
```