

Reproducibility_5820

title: "Coding Challenge. 4" author: "Maryam Saeed Noor Fatima" date: "2025-02-25" output:
md_document: variant: gfm html_document: toc: true toc_float: true word_document: default
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Coding Challenge 3

Q.No.3 (a)

Readme file link

```
{r} library(knitr)
```

link to my Markdown file

Clickable Link to the Manuscript

Manuscript Link

Q.No.6 (b)

File Tree of Github

```
{r} fs::dir_tree()
```

Libraries

```
{r} library(readr) library(ggplot2) library(tidyverse) library(ggpubr) library(ggrepel)  
cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73", "#F0E442",  
"#0072B2", "#D55E00", "#CC79A7")
```

Q.No.3 (b)

Importing the excel file

```
{r} Mycotoxin_Data <- read.csv("MycotoxinData.csv",na = "na")
```

Q.No.3 (c)

Changing the factor levels

```
{r} Mycotoxin_Data$Treatment <- factor(Mycotoxin_Data$Treatment, levels = c("NTC", "Fg",  
"Fg + 37", "Fg + 40", "Fg + 70"))
```

Applying Statistics using t test

a.

```
“{r} DONplot.pwc <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = DON, fill = Cultivar)) +
geom_boxplot(outliers = F) + xlab(“”) + ylab(“DON (ppm)”) + geom_point(alpha = 0.6, pch =
21, color = “black”, position = position_jitterdodge()) + scale_color_manual(values = c(cbbPalette[3],
cbbPalette[4])) + scale_fill_manual(values = c(cbbPalette[3], cbbPalette[4])) + theme_classic() +
facet_wrap(~Cultivar) + stat_compare_means(method = “t.test”, label = “p.signif”, comparisons =
list(c(“NTC”, “Fg”), c(“Fg”, “Fg + 37”), c(“Fg + 37”, “Fg + 40”), c(“Fg + 40”, “Fg + 70”)))
```

DONplot.pwc

b.

```
“{r}
X15ADONplot.pwc <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = X15ADON, fill = Cultivar)) +
  geom_boxplot(outliers = F) +
  xlab(“”) +
  ylab(“X15ADON”) +
  geom_point(alpha = 0.6, pch = 21, color = “black”, position = position_jitterdodge()) +
  scale_color_manual(values = c(cbbPalette[3], cbbPalette[4])) +
  scale_fill_manual(values = c(cbbPalette[3], cbbPalette[4])) +
  theme_classic() +
  facet_wrap(~Cultivar) +
  stat_compare_means(method = “t.test”, label = “p.signif”,
                    comparisons = list(c(“NTC”, “Fg”),
                                       c(“Fg”, “Fg + 37”),
                                       c(“Fg + 37”, “Fg + 40”),
                                       c(“Fg + 40”, “Fg + 70”)))
```

X15ADONplot.pwc

c.

```
{r} Seed.massplot.pwc <- ggplot(Mycotoxin_Data, aes(x = Treatment, y = MassperSeed_mg,
fill = Cultivar)) + geom_boxplot(outliers = F) + xlab(“”) + ylab(“Seed Mass
(mg)”) + geom_point(alpha = 0.6, pch = 21, color = “black”, position = position_jitterdodge())
+ scale_color_manual(values = c(cbbPalette[3], cbbPalette[4])) + scale_fill_manual(values
= c(cbbPalette[3], cbbPalette[4])) + theme_classic() + facet_wrap(~Cultivar) +
stat_compare_means(method = “t.test”, label = “p.signif”, comparisons
= list(c(“NTC”, “Fg”), c(“Fg”, “Fg + 37”), c(“Fg + 37”, “Fg + 40”), c(“Fg + 40”, “Fg +
70”)))
```

Combining all plots with statistics

```
“{r} Combineplot.pwc <- ggarrange( DONplot.pwc, X15ADONplot.pwc, Seed.massplot.pwc, labels = c(“A”,
“B”, “C”), nrow = 1, ncol = 3, common.legend = TRUE, legend = “bottom”)
```

Combineplot.pwc

“