Coding Challenge4

Samit Kafle

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Contents

Figures generated below are published here

Project Github repository: Click Here

Definition

    a. **YAML Header:** It is the structural block that defines metadata such as title, authors, date, output-format and other document settings.

    b. **Literate Programming:** It is the method that combines a programming language with a documentation language that makes it easy to understand what is being executed.

Knitr Options

```r
# turn off the warning display
knitr::opts_chunk$set(warning = FALSE, message = FALSE)
```

Read the data

```
library(tinytex)
library(ggplot2)
library(ggpubr)
datum=read.csv("MycotoxinData.csv",na.strings="na")
datum$Treatment=as.factor(datum$Treatment)
```

Define color palette

```
#colorblind palette
cbbPalette <- c("#000000", "#E69F00", "#56B4E9", "#009E73",
                "#F0E442", "#0072B2", "#D55E00", "#CC79A7")
```

Figures

Box plot of DON

```
plot_DON<-ggplot(datum, aes(x = Treatment, y = DON, fill = Cultivar)) +
  geom_boxplot(alpha=0.6) +
  geom_jitter(aes(color = Cultivar), width = 0.2, alpha = 0.6) + #b transparency of jitter point
  scale_fill_manual(values = c(cbbPalette[[6]], cbbPalette[[4]])) +
  scale_color_manual(values = c(cbbPalette[[6]], cbbPalette[[4]])) +
  labs(y = "DON (ppm)", x = "") +#c
  theme_classic() +#d
  facet_wrap(~Cultivar)#e

plot_DON
```
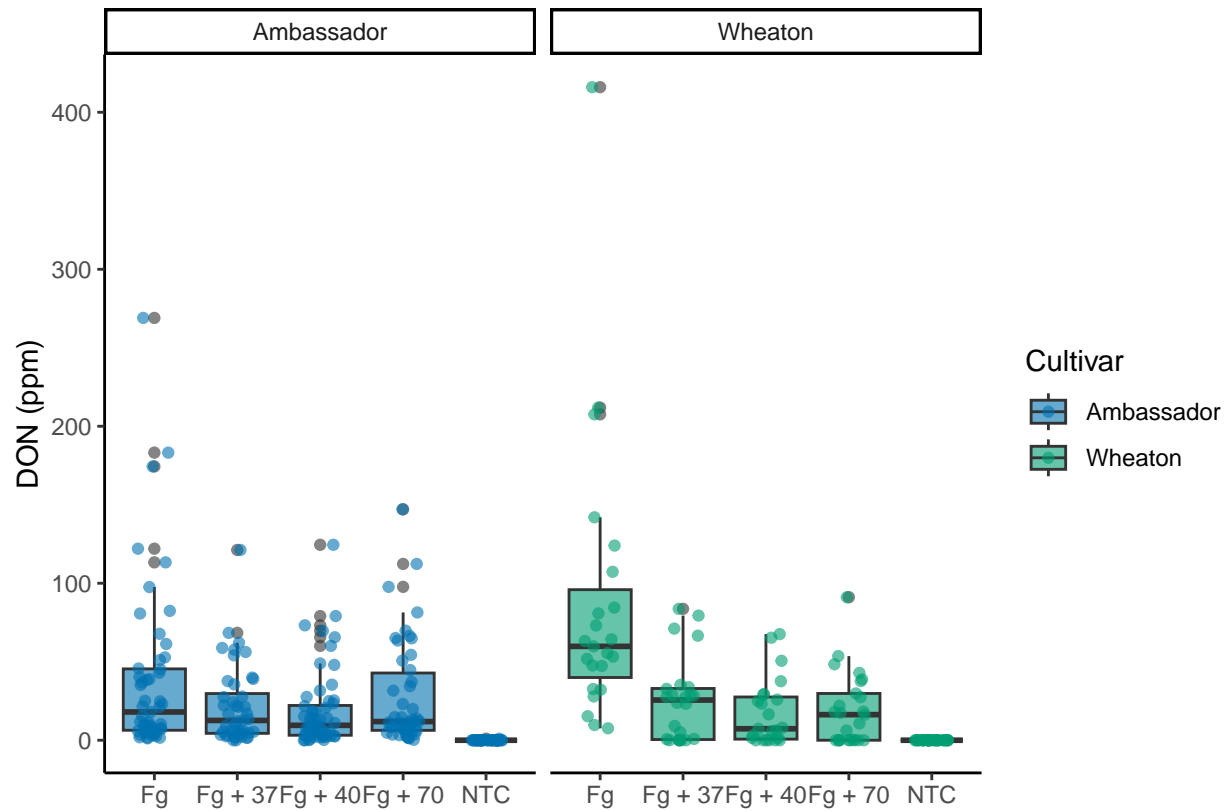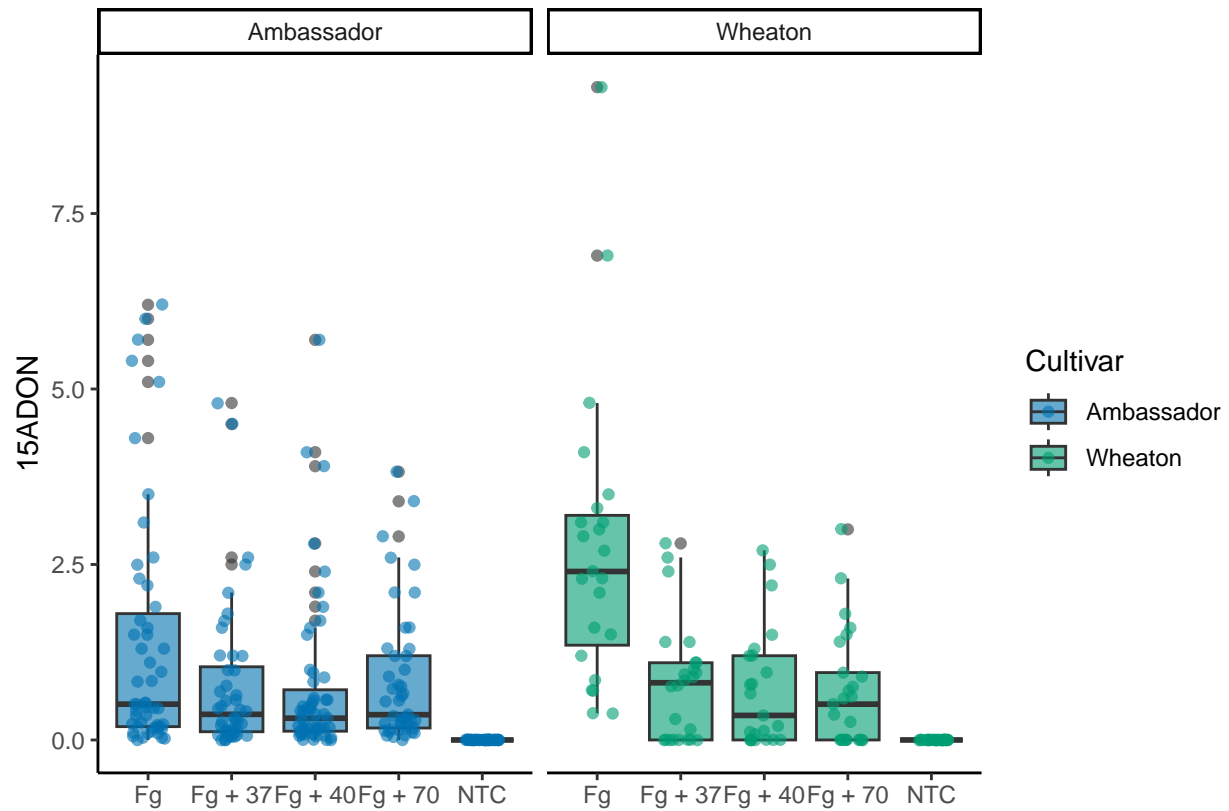
Box plot of 15 ADON

```
plot_15ADON <- ggplot(datum, aes(x = Treatment, y = X15ADON, fill = Cultivar)) +
  geom_boxplot(alpha = 0.6) +
  geom_jitter(aes(color = Cultivar), width = 0.2, alpha = 0.6) +
  scale_fill_manual(values = c(cbbPalette[[6]], cbbPalette[[4]])) +
  scale_color_manual(values = c(cbbPalette[[6]], cbbPalette[[4]])) +
  labs(y = "15ADON", x = "") +
  theme_classic() +
  facet_wrap(~Cultivar)

plot_15ADON
```
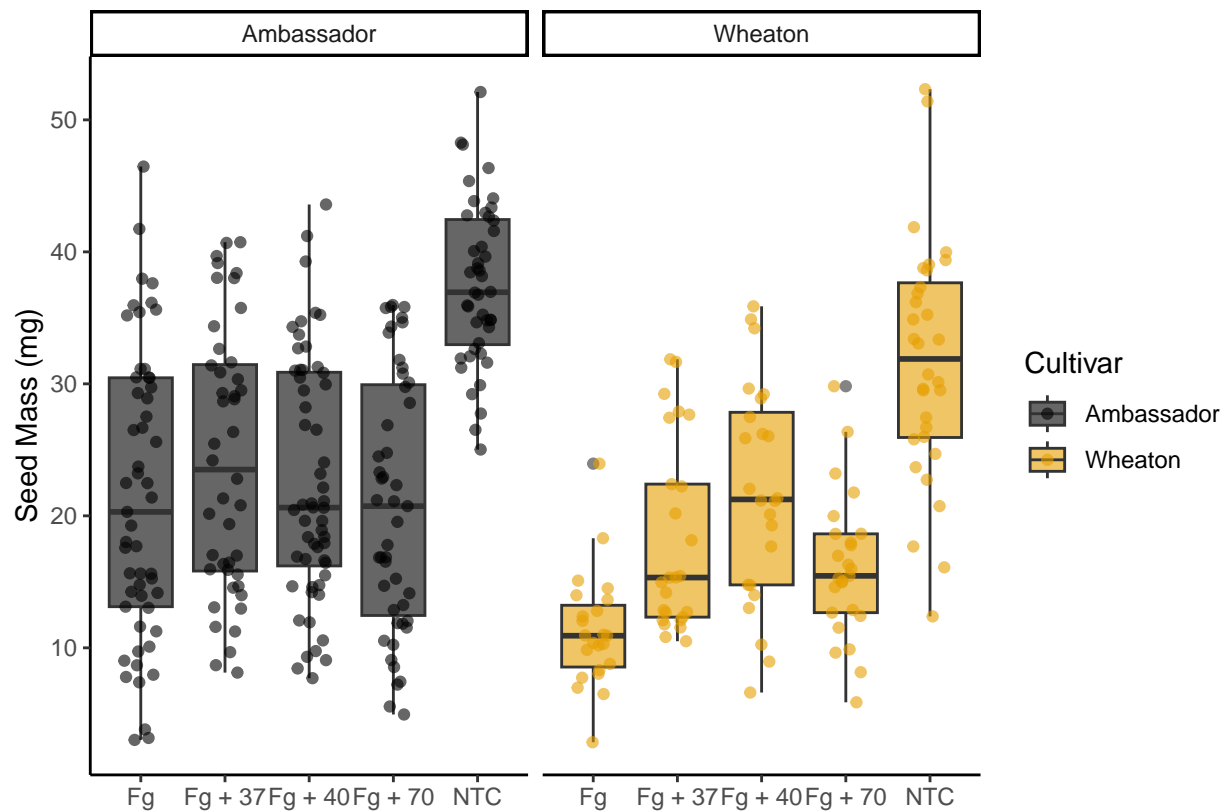
Box plot of SeedMass

```r
plot_SeedMass <- ggplot(datum, aes(x = Treatment, y = MassperSeed_mg, fill = Cultivar)) +
  geom_boxplot(alpha = 0.6) +
  geom_jitter(aes(color = Cultivar), width = 0.2, alpha = 0.6) +
  scale_fill_manual(values = cbbPalette) +
  scale_color_manual(values = cbbPalette) +
  labs(y = "Seed Mass (mg)", x = "") +
  theme_classic() +
  facet_wrap(~Cultivar)


plot_SeedMass
```

Combined Plot with t test metrics

```
plot_DON_ttest <- plot_DON + geom_pwc(aes(group=Treatment),method = "t.test")
plot_15ADON_ttest <- plot_15ADON + geom_pwc(aes(group=Treatment),method = "t.test")
plot_SeedMass_ttest <- plot_SeedMass + geom_pwc(aes(group=Treatment),method = "t.test")
combined_plot_ttest <- ggarrange(plot_DON_ttest, plot_15ADON_ttest, plot_SeedMass_ttest,
                                 labels = c("A", "B", "C"),
                                 ncol = 3, nrow = 1, common.legend = TRUE, legend = "right")


combined_plot_ttest
```