Project Title: Effects of hydrogen peroxide (H_2O_2) on the growth of different bloom-forming cyanobacteria

1. Creating the "FACETED LINE PLOT"

#Load Necessary Packages

```
library(readxl)
library(dplyr)
library(writexl)
library(ggplot2)
library(scales)
```

 # Set the file path

```
file_path <- "C:/Users/ASUS/Desktop/Exp_1.9.xlsx"
```

 # Read the data from the first sheet

```
data <- read_excel(file_path, sheet = 1)
```

 # Calculate the average and standard deviation

```
data_summary <- data %>%
 mutate(
  Average = rowMeans(select(., R1, R2), na.rm = TRUE),
  SD = apply(select(., R1, R2), 1, sd, na.rm = TRUE)
 )
```

 # View the result

```
print(data_summary)
```

 # CREATING PLOT
 # Make sure variables are formatted correctly

```
exp <- data_summary %>%
 mutate(
  Treatment = as.factor(Treatment),
  Pigment = as.factor(Pigment),
  Phytoplankton = as.factor(Phytoplankton)
 )
```

 # Create the plot

```
ggplot(exp, aes(x = Day, y = Average, color = Treatment, fill = Treatment)) +
 geom_point(size = 2) +
 geom_errorbar(aes(ymin = Average - SD, ymax = Average + SD), width = 0.3) +
 geom_smooth(method = "loess", se = FALSE) +
 facet_grid(Pigment ~ Phytoplankton, scales = "free") +
 theme(text = element_text(size = 14)) +
 labs(
  title = "Effects of Hydrogen Peroxide on Cyanobacteria",
  subtitle = "Exp_1.9",
  x = "Days",
```

```
  y = "Pigment (RFU)",
   color = "Treatment",
   shape = "Treatment"
  ) +
  scale_y_continuous(labels = comma) +
  theme_minimal()
```

2. ANOVA
 # Load required packages
```
library(readxl)
library(dplyr)
library(tidyr)
library(writexl)
library(ggplot2)
library(openxlsx)
```

 # Load data
```
raw_data <- read_excel("C:/Users/ASUS/Desktop/Exp_1.9.xlsx", sheet = 1)
```

 # Convert wide to long format
```
data <- raw_data %>%
  pivot_longer(cols = starts_with("R"), names_to = "REP", values_to = "READ") %>%
  mutate(
   REP = ifelse(REP == "R1", 1, 2),
   log10READ = log10(READ)
  )
```
 # Step 3: Load the existing workbook
```
wb <- loadWorkbook("C:/Users/ASUS/Desktop/Exp_1.9.xlsx")

addWorksheet(wb, "Sheet2")
writeData(wb, sheet = "Sheet2", data)
```

 # Step 5: Save the updated workbook
```
saveWorkbook(wb, "C:/Users/ASUS/Desktop/Exp_1.9.xlsx", overwrite = TRUE)
```

#factor Treatment
```
data$Treatment <- as.factor(data$Treatment)
```

 # Filter only Chl-a pigment
```
chl_data <- data %>%
  filter(Pigment == "Chl-a")
```

 # Calculate growth rate: slope of ln(Chl-a) vs Day for each Phytoplankton and Treatment
```
growth_rates <- chl_data %>%
  group_by(Phytoplankton, Treatment,REP) %>%
```

```r
  arrange(Day) %>%
  summarise(Growth_Rate = coef(lm(log10READ ~ Day))[2], .groups = "drop")
```

View results
```r
print(growth_rates)
```

Save the growth rate data to an Excel file
```r
write_xlsx(growth_rates, "Cyanobacteria_Growth_Rates.xlsx")
```

2.1 Filter by phytoplankton - MC first
```r
MC_growth<- growth_rates %>%
  filter(Phytoplankton == "Microcystis LE21")
```

ANOVA (indicates that a single factor has a significant effect on your population)
```r
MC_aov <- aov(Growth_Rate~Treatment, data=MC_growth)
summary(MC_aov)
```

Create a formatted table
```r
anova_table <- as.data.frame(anova(MC_aov))
```

Save the table as CSV
```r
write.csv(format(anova_table, scientific = FALSE), "MC_anova_results_clean.csv")
```

2.2 Filter by phytoplankton - PLK
```r
PLK_growth<- growth_rates %>%
  filter(Phytoplankton == "Planktothrix 1808")
```

ANOVA
```r
PLK_aov <- aov(Growth_Rate~Treatment, data=PLK_growth)
summary(PLK_aov)
```

Create a formatted table
```r
anova_table <- as.data.frame(anova(PLK_aov))
```

Save the table as CSV
```r
write.csv(format(anova_table, scientific = FALSE), "PLK_anova_results_clean.csv")
```

2.3 Filter by phytoplankton - FIS
```r
FIS_growth<- growth_rates %>%
  filter(Phytoplankton == "Fischerella 1.5")
```

ANOVA
```r
FIS_aov <- aov(Growth_Rate~Treatment, data=FIS_growth)
summary(FIS_aov)
```

Create a formatted table
```r
anova_table <- as.data.frame(anova(FIS_aov))
```

Save the table as CSV
```r
write.csv(format(anova_table, scientific = FALSE), "FIS_anova_results_clean.csv")
```