For **box plot**

# Load the libraries

library(readxl)

library(dplyr)

library(ggplot2)

library(janitor) # Optional

# Import data from Excel

data <- read\_excel("C:/Users/prathibha\_liyanawad1/Desktop/mi\_data.xlsx")

# Clean column names (to avoid spaces or weird symbols)

data <- clean\_names(data)

# Calculate the mean mitotic index and standard error (SE) by concentration

summary\_data <- data %>%

group\_by(concentration) %>%

summarize(

mean\_mitotic\_index = mean(mitotic\_index, na.rm = TRUE),

se\_mitotic\_index = sd(mitotic\_index, na.rm = TRUE) / sqrt(n()) # Standard error formula

)

# Relabel concentrations to show 0, 25, 75, 100 instead of 0, 0.25, 0.75, 1

summary\_data$concentration <- factor(summary\_data$concentration,

levels = c(0, 0.25, 0.75, 1),

labels = c("0", "25", "75", "100"))

# Check the summary data to confirm error bars are non-zero

print(summary\_data)

# Create the bar plot with error bars (standard error)

plot <- ggplot(summary\_data, aes(x = concentration, y = mean\_mitotic\_index, fill = concentration)) +

geom\_bar(stat = "identity", position = "dodge") +

geom\_errorbar(aes(

ymin = mean\_mitotic\_index - se\_mitotic\_index,

ymax = mean\_mitotic\_index + se\_mitotic\_index),

width = 0.2, color = "black") + # Error bars

labs(

title = "Mean Mitotic Index vs Concentration",

x = "Concentration (%)",

y = "Mean Mitotic Index",

caption = "Figure 1: Mitotic index (MI) data shown as mean ± standard error of the mean (SEM) for %, 25%, 75%, 100% concentrations"

) +

theme(

# Customizing the plot background

panel.background = element\_rect(fill = "white", color = "white"), # White background

plot.background = element\_rect(fill = "white", color = "white"), # White background for the entire plot

legend.background = element\_rect(fill = "white"), # White background for legend

legend.key = element\_rect(fill = "white"), # White background for legend key

text = element\_text(color = "black"), # Ensure text is black

axis.text = element\_text(color = "black"), # Axis text in black

axis.title = element\_text(color = "black"), # Axis titles in black

plot.margin = margin(10, 10, 40, 10), # Increased bottom margin for caption

plot.caption = element\_text(hjust = 0) # Left-justify the caption

) +

scale\_fill\_brewer(palette = "Set2") # Change palette

# Save the plot as a .png file on Desktop with bigger height to accommodate the caption

ggsave("C:/Users/prathibha\_liyanawad1/Desktop/mean\_mitotic\_index\_vs\_concentration.png",

plot = plot,

width = 8,

height = 6, # Increased height to ensure full caption space

dpi = 300,

units = "in") # Adjusting size for more space for caption

**For one-way ANOVA test**

# Load the libraries

library(readxl)

library(dplyr)

library(ggplot2)

library(janitor) # Optional

# Import data from Excel

data <- read\_excel("C:/Users/prathibha\_liyanawad1/Desktop/mi\_data.xlsx")

# Clean column names (to avoid spaces or weird symbols)

data <- clean\_names(data)

# Calculate the mean mitotic index and standard error (SE) by concentration

summary\_data <- data %>%

group\_by(concentration) %>%

summarize(

mean\_mitotic\_index = mean(mitotic\_index, na.rm = TRUE),

se\_mitotic\_index = sd(mitotic\_index, na.rm = TRUE) / sqrt(n()) # Standard error formula

)

# Relabel concentrations to show 0, 25, 75, 100 instead of 0, 0.25, 0.75, 1

summary\_data$concentration <- factor(summary\_data$concentration,

levels = c(0, 0.25, 0.75, 1),

labels = c("0", "25", "75", "100"))

# Check the summary data to confirm error bars are non-zero

print(summary\_data)

# Create the bar plot with error bars (standard error)

plot <- ggplot(summary\_data, aes(x = concentration, y = mean\_mitotic\_index, fill = concentration)) +

geom\_bar(stat = "identity", position = "dodge") +

geom\_errorbar(aes(

ymin = mean\_mitotic\_index - se\_mitotic\_index,

ymax = mean\_mitotic\_index + se\_mitotic\_index),

width = 0.2, color = "black") + # Error bars

labs(

title = "Mean Mitotic Index vs Concentration",

x = "Concentration (%)",

y = "Mean Mitotic Index",

caption = "Figure 1: Mitotic index (MI) data shown as mean ± standard error of the mean (SEM) for %, 25%, 75%, 100% concentrations"

) +

theme(

# Customizing the plot background

panel.background = element\_rect(fill = "white", color = "white"), # White background

plot.background = element\_rect(fill = "white", color = "white"), # White background for the entire plot

legend.background = element\_rect(fill = "white"), # White background for legend

legend.key = element\_rect(fill = "white"), # White background for legend key

text = element\_text(color = "black"), # Ensure text is black

axis.text = element\_text(color = "black"), # Axis text in black

axis.title = element\_text(color = "black"), # Axis titles in black

plot.margin = margin(10, 10, 40, 10), # Increased bottom margin for caption

plot.caption = element\_text(hjust = 0) # Left-justify the caption

) +

scale\_fill\_brewer(palette = "Set2") # Change palette

# Save the plot as a .png file on Desktop with bigger height to accommodate the caption

ggsave("C:/Users/prathibha\_liyanawad1/Desktop/mean\_mitotic\_index\_vs\_concentration.png",

plot = plot,

width = 8,

height = 6, # Increased height to ensure full caption space

dpi = 300,

units = "in") # Adjusting size for more space for caption