**Experiment 1 :-**

**1)dplyr – Data Manipulation**

library(dplyr)

# Sample data

data <- data.frame(name = c("A", "B", "C"), score = c(85, 90, 75))

# Filter and summarize

result <- data %>%

filter(score > 80) %>%

summarise(avg\_score = mean(score))

print(result)

**2) ggplot2 – Data Visualization**

library(ggplot2)

# Sample data

data <- data.frame(x = c(1, 2, 3), y = c(3, 7, 4))

# Line plot

ggplot(data, aes(x = x, y = y)) +

geom\_line(color = "blue") +

ggtitle("Simple Line Plot")

**3) readr – Reading CSV Data**

library(readr)

# Read sample CSV from URL

data <- read\_csv("https://raw.githubusercontent.com/mwaskom/seaborn-data/master/iris.csv")

# Show first few rows

head(data)

**Experiment 7 :-**

# Load required libraries

library(readr)

library(dplyr)

library(ggplot2)

# Import data (Iris dataset)

data <- read\_csv("https://raw.githubusercontent.com/mwaskom/seaborn-data/master/iris.csv")

# Check for missing values

sum(is.na(data))

# View column names and structure

str(data)

# Rename columns (if needed)

colnames(data) <- gsub("\\.", "\_", colnames(data))

summary(data)

# Mean petal length by species

data %>%

group\_by(species) %>%

summarise(mean\_petal\_length = mean(petal\_length))

# Histogram of Sepal Length

ggplot(data, aes(x = sepal\_length)) +

geom\_histogram(fill = "skyblue", bins = 20) +

labs(title = "Distribution of Sepal Length")

# Scatter Plot - Sepal Dimensions

ggplot(data, aes(x = sepal\_length, y = sepal\_width, color = species)) +

geom\_point(size = 2) +

labs(title = "Sepal Length vs Sepal Width")

# Boxplot - Petal Length by Species

ggplot(data, aes(x = species, y = petal\_length, fill = species)) +

geom\_boxplot() +

labs(title = "Petal Length by Species")

**Experiment 8 :-**

# Load required libraries

library(readr)

library(ggplot2)

library(corrplot)

# Load sample data (Iris dataset)

data <- read\_csv("https://raw.githubusercontent.com/mwaskom/seaborn-data/master/iris.csv")

# Scatter plot: Sepal Length vs Sepal Width

ggplot(data, aes(x = sepal\_length, y = sepal\_width, color = species)) +

geom\_point(size = 2) +

labs(title = "Sepal Length vs Sepal Width")

# Scatter plot: Petal Length vs Petal Width

ggplot(data, aes(x = petal\_length, y = petal\_width, color = species)) +

geom\_point(size = 2) +

labs(title = "Petal Length vs Petal Width")

# Correlation Analysis

numeric\_data <- data[, sapply(data, is.numeric)]

# Compute correlation matrix

cor\_matrix <- cor(numeric\_data)

# Plot correlation matrix

corrplot(cor\_matrix, method = "circle", type = "upper",

title = "Correlation Matrix", tl.col = "black", addCoef.col = "black")