Data Visualization Analysis

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0.1 Introduction

This tutorial is designed to help you learn data visualization analysis by providing simple and useful information in a way that is easy to follow and understand.

0.2 Preparation

In order to draw a chart, we need to include the required packages for visualization and dataset. For example, ggplot2 package is for drawing charts, gcookbook is for using pg_mean dataset, and palmerpenguins provides the penguins dataset.

```
library(ggplot2)
library(gcookbook)
library(dplyr)  # Provides %>% operator

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':
    filter, lag

The following objects are masked from 'package:base':
    intersect, setdiff, setequal, union

library(palmerpenguins) # Provides penguins dataset

Warning: package 'palmerpenguins' was built under R version 4.4.2
```

0.3 Bar chart

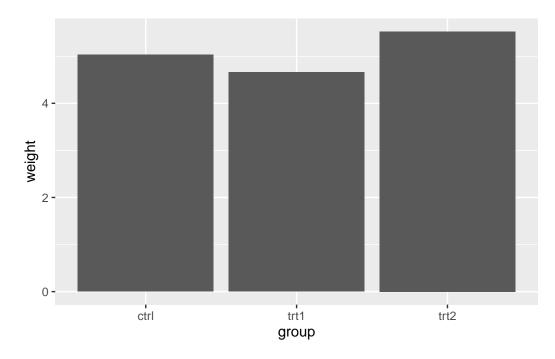
In this section, we will draw a bar chart using pg_mean dataset. The dataset has two columns: group, weight.

pg_mean

```
group weight
1 ctrl 5.032
2 trt1 4.661
3 trt2 5.526
```

This dataset compares the weight across three groups:

- ctrl: Control group (baseline, weight = 5.032).
- trt1: Treatment 1 group (weight = 4.661).
- trt2: Treatment 2 group (weight = 5.526).



It initializes a ggplot with the dataset pg_mean.

aes(x = group, y = weight) specifies the aesthetics:

- x = group: Assign the group variable to the x-axis (categorical data, such as ctrl, trt1, trt2).
- y = weight: Assign the weight variable to the y-axis (numerical data).

geom_col():

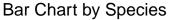
- Adds a column geometry to the plot.
- geom_col() creates bars where the height of each bar corresponds to the value of weight for each group.

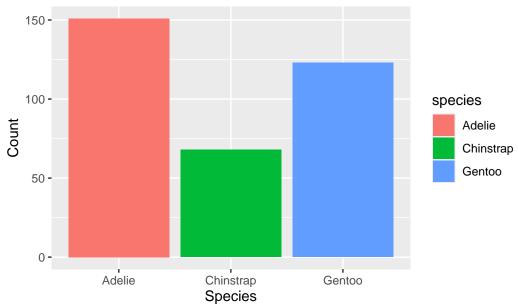
0.4 Bar Chart with Color

```
# Sample data
data <- penguins %>% filter(!is.na(body_mass_g))

# Bar chart by species
p <- ggplot(data, aes(x = species, fill = species)) +
    geom_bar() +
    labs(title = "Bar Chart by Species", x = "Species", y = "Count")

print(p)</pre>
```





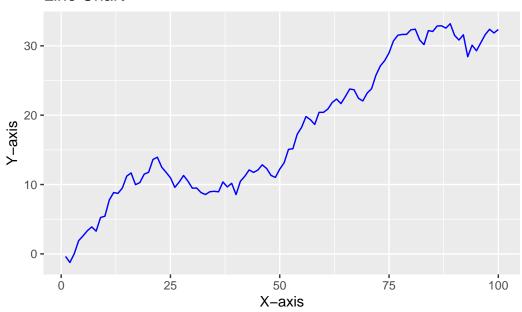
0.5 Line Chart

```
# Sample data
line_data <- tibble(
    x = 1:100,
    y = cumsum(rnorm(100))
)

# Line chart
p <- ggplot(line_data, aes(x = x, y = y)) +
    geom_line(color = "blue") +
    labs(title = "Line Chart", x = "X-axis", y = "Y-axis")

print(p)</pre>
```

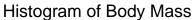
Line Chart

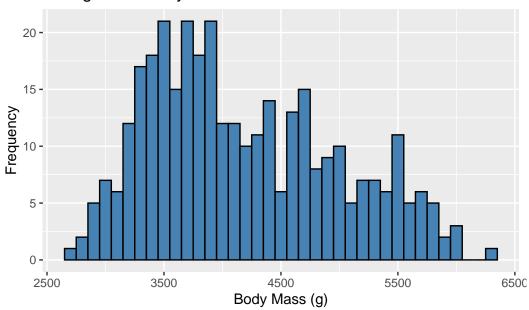


0.6 Histogram

```
# Histogram of penguin body mass
p <- ggplot(data, aes(x = body_mass_g)) +
geom_histogram(binwidth = 100, fill = "steelblue", color = "black") +</pre>
```

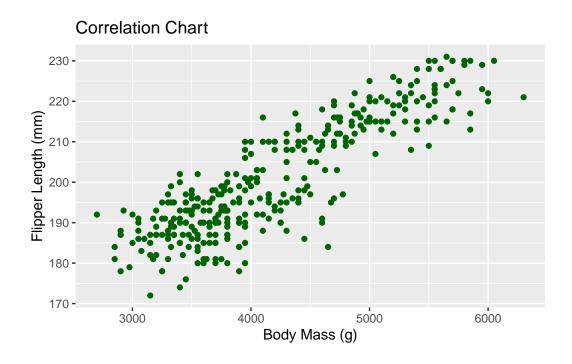
```
labs(title = "Histogram of Body Mass", x = "Body Mass (g)", y = "Frequency")
print(p)
```





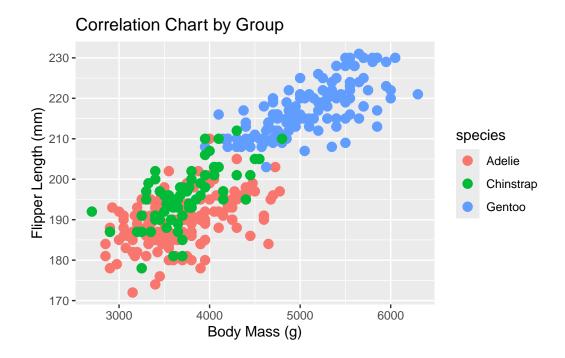
0.7 Correlation Chart

```
# Scatter plot of body mass vs. flipper length
p <- ggplot(data, aes(x = body_mass_g, y = flipper_length_mm)) +
    geom_point(color = "darkgreen") +
    labs(title = "Correlation Chart", x = "Body Mass (g)", y = "Flipper Length (mm)")
print(p)</pre>
```



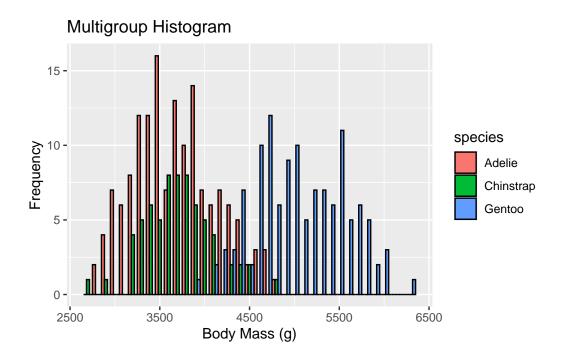
0.8 Correlation Chart: Color by Group

```
# Scatter plot with color by species
p <- ggplot(data, aes(x = body_mass_g, y = flipper_length_mm, color = species)) +
   geom_point(size = 3) +
   labs(title = "Correlation Chart by Group", x = "Body Mass (g)", y = "Flipper Length (mm)")
print(p)</pre>
```



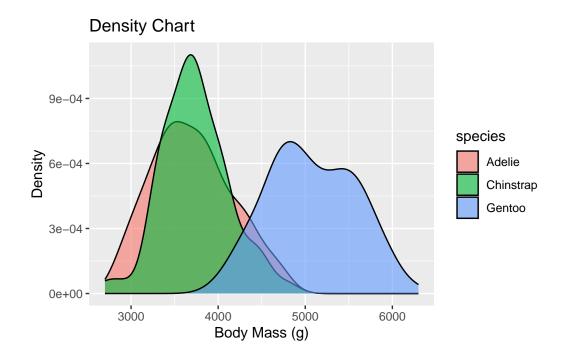
0.9 Multigroup Histogram

```
# Histogram of body mass by species
p <- ggplot(data, aes(x = body_mass_g, fill = species)) +
    geom_histogram(binwidth = 100, position = "dodge", color = "black") +
    labs(title = "Multigroup Histogram", x = "Body Mass (g)", y = "Frequency")
print(p)</pre>
```



0.10 Density Chart

```
# Density chart of body mass
p <- ggplot(data, aes(x = body_mass_g, fill = species)) +
  geom_density(alpha = 0.6) +
  labs(title = "Density Chart", x = "Body Mass (g)", y = "Density")
print(p)</pre>
```



0.11 Box Plot

```
# Box plot of body mass by species
p <- ggplot(data, aes(x = species, y = body_mass_g, fill = species)) +
    geom_boxplot() +
    labs(title = "Box Plot by Species", x = "Species", y = "Body Mass (g)")
print(p)</pre>
```

