

# Biol432 Tutorial - 1 Markdown

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## Load Required Libraries and Data

```
# Load necessary libraries
library(dplyr)

##
## 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(ggplot2)
library(tidyr)
library(tinytex)

# Load the revised measurements.csv
data <- read.csv("measurements.csv")

# Display the first few rows of the dataset
head(data)

##      Species Limb_width Limb_length Observer  Volume
## 1 Species_C    4.439524    8.579187   Charlie 132.8033
## 2 Species_B    4.769823   10.513767   Charlie 187.8679
## 3 Species_E    6.558708    9.506616   Charlie 321.1829
## 4 Species_B    5.070508    9.304915     Alice 187.8907
## 5 Species_C    5.129288    8.096763     Alice 167.3075
## 6 Species_C    6.715065    9.909945   Charlie 350.9632
```

## Sorting of the data

```
# Sort data by Species, Observer, and Volume
sorted_data <- data %>%
  arrange(Species, Observer, Volume)

# Display the sorted dataset
head(sorted_data)
```

```
##      Species Limb_width Limb_length Observer  Volume
```

```
## 1 Species_A 3.973579 7.629040 Alice 94.60705
## 2 Species_A 4.527209 7.951742 Alice 128.00095
## 3 Species_A 4.554338 11.837993 Alice 192.84949
## 4 Species_A 4.674068 11.508108 Alice 197.46218
## 5 Species_A 4.399740 13.994427 Alice 212.76447
## 6 Species_A 4.779513 9.527441 Bob 170.93599
```

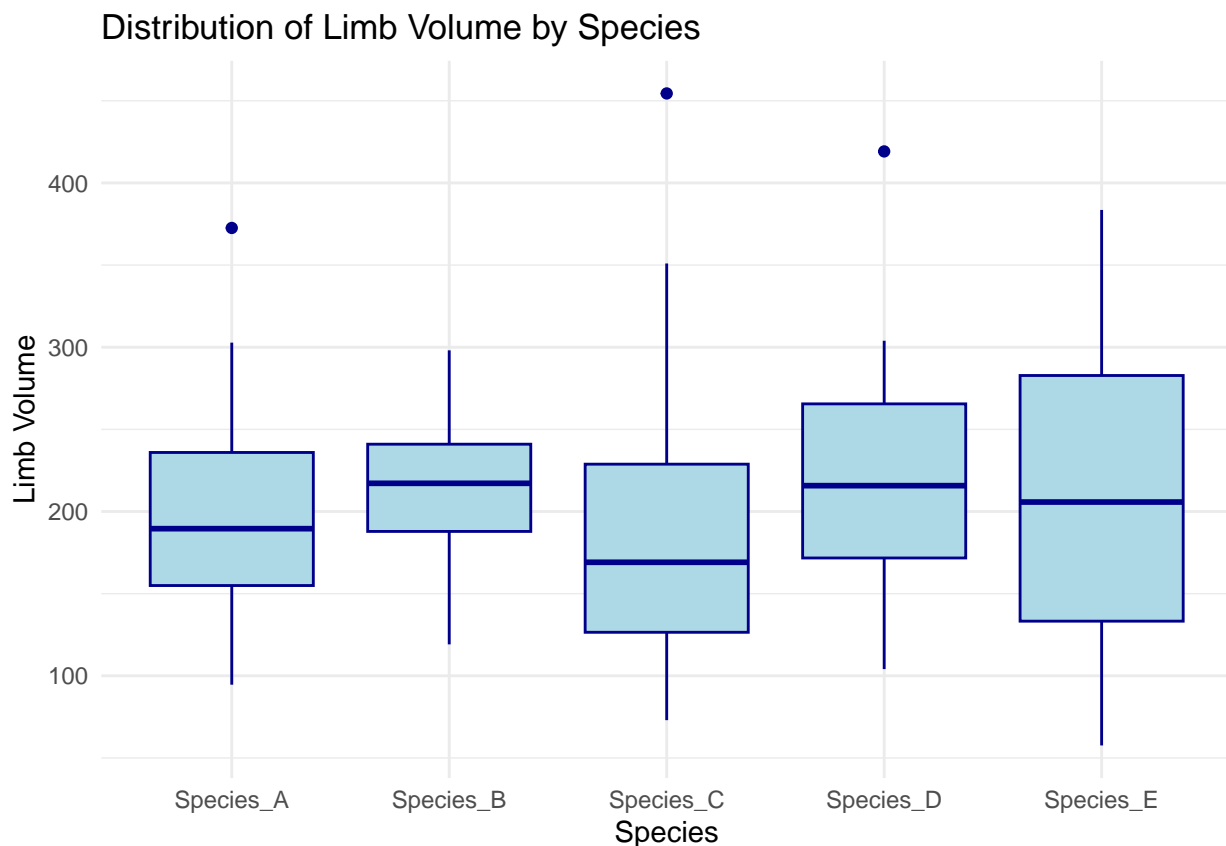
## Calculating the average limb volume of species

```
# Create a table showing the average volume for each species
```

```
average_volume <- data %>%
  group_by(Species) %>%
  summarize(Average_Volume = mean(Volume, na.rm = TRUE))
```

```
## Create a box plot comparing limb volumes by species
```

```
ggplot(data, aes(x = Species, y = Volume)) +
  geom_boxplot(fill = "lightblue", color = "darkblue") +
  theme_minimal() +
  labs(
    title = "Distribution of Limb Volume by Species",
    x = "Species",
    y = "Limb Volume")
```



```
# Create frequency histograms for limb volume by species
```

```
ggplot(data, aes(x = Volume)) +
```

```
geom_histogram(binwidth = 1, fill = "lightgreen", color = "darkgreen") +
facet_wrap(~ Species, scales = "free_y") +
theme_minimal() +
labs(
  title = "Frequency Histograms of Limb Volume by Species",
  x = "Limb Volume",
  y = "Frequency"
)
```

