

A1_McLEOD_20294254

AHM

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Assignment 1 Aidan McLeod 20294254

1. Loading the revised measurements csv generated in “dataGenerato.R” and “volumeEstimato.R:

```
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)  
  
#load file  
limb_measurements <- read.csv("measurements.csv")  
head(limb_measurements)
```

```
##           species_name limb_width limb_length observer_name      Volume  
## 1      Aotus zonalis         8.5         60          Mari 3404.70104  
## 2 Alouatta palliata         8.5         14          Kyle  794.43024  
## 3   Atelidae ateles         2.0         26          Kyle   81.68141  
## 4 Alouatta palliata         5.0         20           Cam  392.69908  
## 5   Atelidae ateles         2.5         66           Cam  323.97674  
## 6   Cebus albifrons        10.0         24           Cam 1884.95559
```

2. Sorting the variables in the file into order:

```
#sort data by species, then by observer, then by limb volume  
measurements_sorted <- limb_measurements %>%  
  arrange(species_name, observer_name, Volume)
```

3. Table of the calculated average volumes for each species:

```
#calculate average volume for each species  
avg_volume <- measurements_sorted %>%  
  group_by(species_name) %>%  
  summarize(Average_Volume = mean(Volume, na.rm = TRUE))  
  
#display the average volume table  
avg_volume
```

```
## # A tibble: 5 × 2  
##   species_name      Average_Volume  
##   <chr>              <dbl>  
## 1 Alouatta palliata      1308.  
## 2 Aotus zonalis         1602.  
## 3 Atelidae ateles       1518.  
## 4 Cebus albifrons       1519.  
## 5 Saimiri sciureus      1510.
```

4. Table of the number of observations by observers per species:

```
#Count the number of observations for each combination of species and observer  
observation_count <- measurements_sorted %>%  
  group_by(species_name, observer_name) %>%  
  summarize(Num_Observations = n())
```

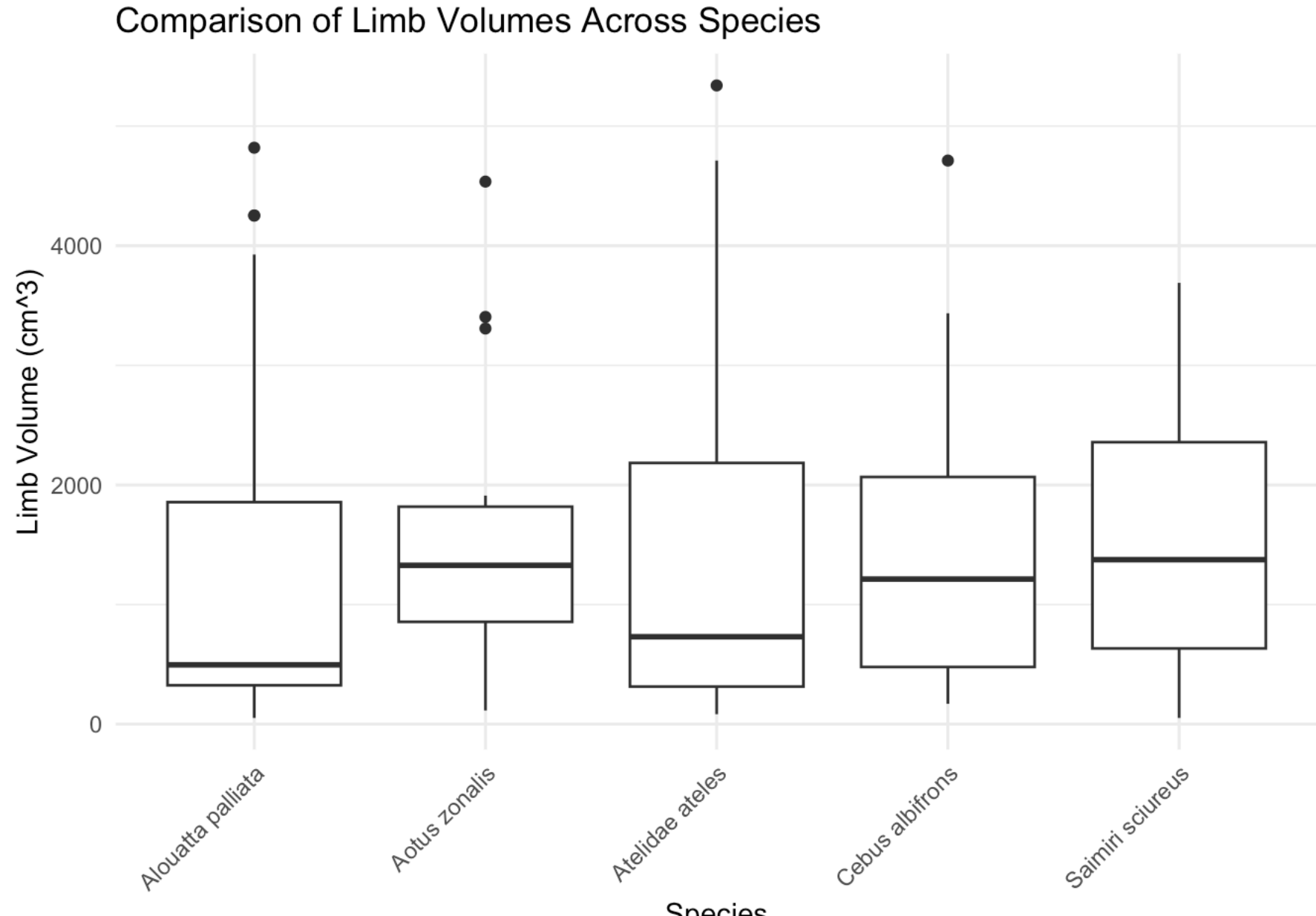
```
## `summarise()` has grouped output by 'species_name'. You can override using the  
## ``.groups` argument.
```

```
#Display the observation count table  
observation_count
```

```
## # A tibble: 15 × 3  
## # Groups:   species_name [5]  
##   species_name      observer_name Num_Observations  
##   <chr>          <chr>              <int>  
## 1 Alouatta palliata Cam                 7  
## 2 Alouatta palliata Kyle                10  
## 3 Alouatta palliata Mari                12  
## 4 Aotus zonalis    Cam                 6  
## 5 Aotus zonalis    Kyle                 7  
## 6 Aotus zonalis    Mari                 2  
## 7 Atelidae ateles  Cam                 5  
## 8 Atelidae ateles  Kyle                 6  
## 9 Atelidae ateles  Mari                 8  
## 10 Cebus albifrons Cam                13  
## 11 Cebus albifrons Kyle                 3  
## 12 Cebus albifrons Mari                 2  
## 13 Saimiri sciureus Cam                 8  
## 14 Saimiri sciureus Kyle                 5  
## 15 Saimiri sciureus Mari                 6
```

5. Boxplot of the distribution of limb volumes (cm^3) in each species:

```
#Create boxplot comparison of limb volumes between species  
ggplot(measurements_sorted, aes(x = species_name, y = Volume)) +  
  geom_boxplot() +  
  theme_minimal() +  
  labs(title = "Comparison of Limb Volumes Across Species",  
        x = "Species",  
        y = "Limb Volume (cm^3)") +  
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



6. Histogram panels showing the frequency distribution of limb volumes in each species:

```
#Convert data to long format for easier plotting  
measurements_long <- measurements_sorted %>%  
  gather(key = "Measurement_Type", value = "Value", Volume)  
  
#Create multi-panel plot histograms of limb volume by species  
ggplot(measurements_long, aes(x = Value)) +  
  geom_histogram(bins = 15, fill = "skyblue", color = "black", alpha = 0.7) +  
  facet_wrap(~ species_name, scales = "free_x") +  
  theme_minimal() +  
  labs(title = "Distribution of Limb Volume by Species",  
        x = "Limb Volume (cm^3)",  
        y = "Frequency")
```

