A1_McLEOD_20294254

AHM

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Assignment 1 Aidan McLeod 20294254

Repository link: https://github.com/AidanMcLeod/BIOL432A1

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())
```

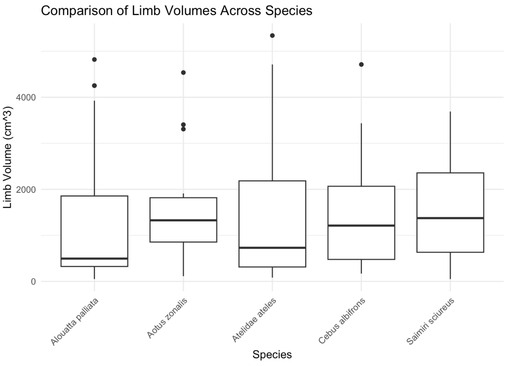
```
## `summarise()` has grouped output by 'species_name'. You can override using the
## `.groups` argument.
```

```
#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 (cm³)",
       y = "Frequency")
```