2023 RIKEN-KI Doctoral Course in Yokohama

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The Tasks in WEEK 1

Task 1

link: https://github.com/xufengshu/xufengshu.github.io/blob/main/task%201 (https://github.com/xufengshu/xufengshu.github.io/blob/main/task%201)

Task 2-3

Get ready for the Github repository and install necessary packages

```
##  install Bioconductor
## if (!require("BiocManager", quietly = TRUE))
## install.packages("BiocManager")
## BiocManager::install(version = "3.16")

## install Tidyverse
## install.packages("tidyverse")
library(tidyverse)
```

```
## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──
## ✔ dplyr     1.1.2     ✔ readr     2.1.4
## ✔ forcats   1.0.0     ✔ stringr   1.5.0
## ✔ ggplot2   3.4.2     ✔ tibble    3.2.1
## ✔ lubridate 1.9.3     ✔ tidyr     1.3.0
## ✔ purrr     1.0.1
## ── Conflicts ────────────────────────────────────────── tidyverse_conflicts() ──
## ✖ dplyr::filter() masks stats::filter()
## ✖ dplyr::lag()    masks stats::lag()
## ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

Task 4

```
## Q: What is the average and median CO2 uptake of the plants from Quebec
# and Mississippi?

data("CO2")
help("CO2")
# extract out CO2 uptake of the plants from Quebec
Quebec_CO2_uptake = CO2[which(CO2$Type == "Quebec"), c(2,5)]
Quebec_average = mean(Quebec_CO2_uptake$uptake)
Quebec_average
```

```
## [1] 33.54286
```

```
Quebec_median = median(Quebec_CO2_uptake$uptake)
Quebec_median
```

```
## [1] 37.15
```

```
# extract out CO2 uptake of the plants from Mississippi
Mississippi_CO2_uptake = CO2[which(CO2$Type == "Mississippi"), c(2,5)]
Mississippi_average = mean(Mississippi_CO2_uptake$uptake)
Mississippi_average
```

```
## [1] 20.88333
```

```
Mississippi_median = median(Mississippi_CO2_uptake$uptake)
Mississippi_median
```

```
## [1] 19.3
```

Task 5

```
## use CO2 uptake vector as an example to execute the functions.

## Q: Write a function that calculates the ratio of the mean and the
# median of a given vector.
# function
ratio_mean_median = function(data_vector){
  mean = mean(data_vector)
  median = median(data_vector)
  ratio = mean / median
  return(ratio)
}
#test
ratio = ratio_mean_median(CO2$uptake)
print(ratio)
```

```
## [1] 0.9615935
```

```r
## Q: Write a function that ignores the lowest and the highest value
# from a given vector and calculate the mean.
#function
calculate_mean_without_extremes <- function(data_vector) {
  # Check if the vector has at least 3 elements
  if (length(data_vector) < 3) {
    stop("Input vector must have at least 3 elements.")
  }
  # Sort the vector in ascending order
  sorted_data <- sort(data_vector)
  # Remove the lowest and highest values
  trimmed_data <- sorted_data[-c(1, length(sorted_data))]
  # Calculate the mean of the trimmed data
  mean_value <- mean(trimmed_data)
  return(mean_value)
}
#test
mean = calculate_mean_without_extremes(CO2$uptake)
print(mean)
```

```
## [1] 27.22805
```

```r
## piping
library(magrittr)
```

```
##
## Attaching package: 'magrittr'
```

```
## The following object is masked from 'package:purrr':
##
##     set_names
```

```
## The following object is masked from 'package:tidyr':
##
##     extract
```

```
## Q3: Familiarize yourself with piping
##  *Why use pipes in R:
# **Readability**: Pipes allow you to chain together operations in a left-to-right
fashion,
# making your code more readable and resembling a natural language flow.

# **Reduced Nesting**: Using pipes, you can avoid deeply nested function calls,
# which can be hard to read and debug. This leads to cleaner, more maintainable co
de.

# **Code Efficiency**: Pipes can make your code more efficient since intermediate
results
# are stored automatically, and you don't have to repeatedly assign variables.

# **Interactive Data Exploration**: For interactive data exploration, pipes can be
# especially helpful because they allow you to build up your analysis step by ste
p.

## *How to use pipes in R:
# the `%>%` operator passes the result of one operation as the first argument to t
he
# next operation, allowing you to chain together multiple data manipulation functi
ons.

## *When not to use pipes in R:
# **Overly Complex Chains**: Avoid creating overly complex chains of operations.
# If your pipe chain becomes too long and convoluted, it may reduce code readabili
ty
# and make debugging more challenging.

# **Conditional Execution**: If you need conditional execution of functions or com
plex
# branching in your code, it might be better to use traditional control flow struc
tures
# like `if`, `else`, or loops.

# **Performance Critical Code**: For highly performance-critical code, using pipes
might
# introduce some overhead. In such cases, you may need to optimize your code diffe
rently.

# **Non-Pipe-Friendly Functions**: Some functions may not work well with pipes,
# especially if they have unconventional argument orders or side effects.




## Q4: Familiarize yourself with the apply-family of functions (apply, lapply, sap
ply etc.)

## **Applying Functions to Data Frames or Matrices**:
# `apply()`: Useful for applying a function to the rows or columns of a matrix or
data frame.
# For example, calculating row-wise or column-wise means or sums.
```

```
# `lapply()`: Used to apply a function to each element of a list or data frame col
umn,
# returning a list as output. This is handy for transforming and summarizing data.

## **Simplifying Code**:
#`sapply()`: Similar to `lapply()`, but it tries to simplify the result into a vec
tor or
# matrix whenever possible, which can lead to cleaner code.

## **Multiple Input Lists**:
#`mapply()`: Useful when you have multiple input lists or vectors, and you want to
# apply a function element-wise to each combination of inputs.

## **Split-Apply-Combine Operations**:
#`tapply()`: Great for performing split-apply-combine operations, where you split
your data
# into groups based on one or more factors, apply a function to each group, and th
en
# combine the results.

## **Working with Complex Data Structures**:
# The apply family can handle complex nested data structures and can help you extr
act,
# transform, or summarize data buried within lists or data frames.

## **Custom Function Application**:
# You can use these functions to apply your custom functions to data, allowing for
# flexible and customized data processing.

## **Speed and Efficiency**:
#In many cases, the apply family functions can be more efficient than using loops,
# especially when working with large datasets. They are often implemented in C,
# which can be faster than writing equivalent R code.

## **Functional Programming Paradigm**:
#The apply family functions align with the functional programming paradigm,
# which can lead to more concise and expressive code, enhancing the maintainabilit
y of your scripts.

## **Parallel Processing**:
#Some of the apply functions can be used in parallel environments,
# which can significantly speed up computations on multi-core machines.
```

Task 6

```
## install.packages("remotes")
library(remotes)
## install_url("http://emotion.utu.fi/wp-content/uploads/2019/11/nummenmaa_1.0.ta
r.gz",dependencies=TRUE)

library(tidyverse)
library(gridExtra)
```

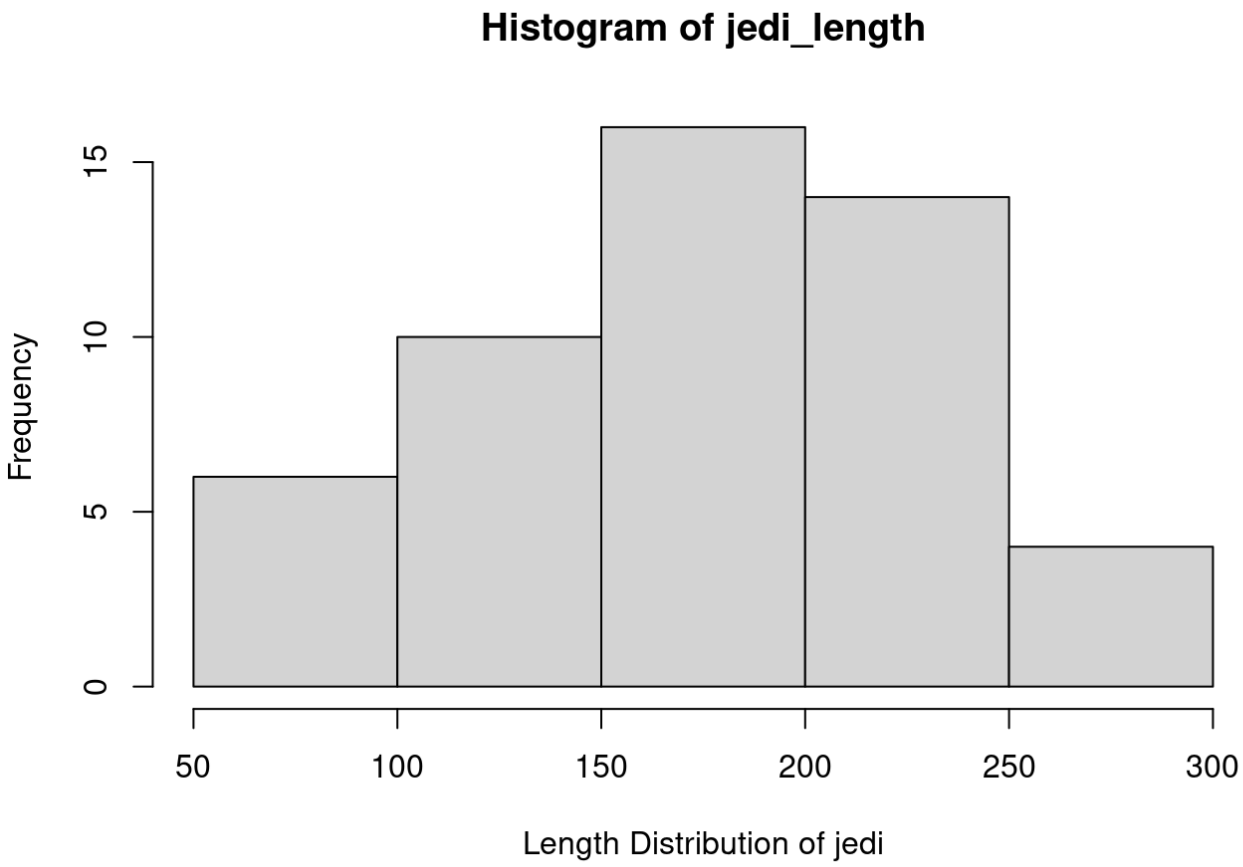
```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

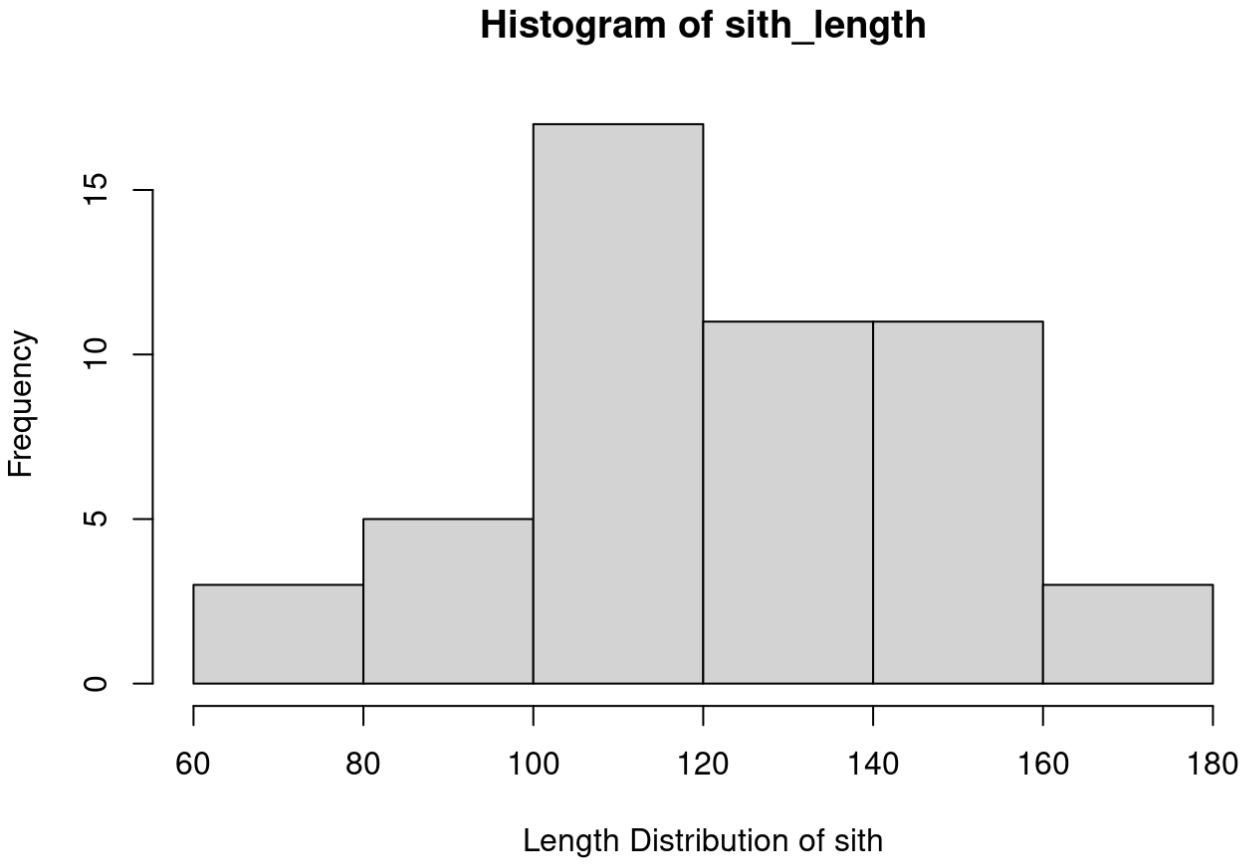
```
library(nummenmaa)


## Q1:
magic.guys <- read.csv("magic_guys.csv", header=TRUE, stringsAsFactors=FALSE)

head(magic.guys)
```

```
##   uniqId species length weight
## 1     p1    jedi  174.6   71.3
## 2     p2    jedi  252.2   70.8
## 3     p3    jedi  229.8   70.7
## 4     p4    jedi  176.2   80.4
## 5     p5    jedi  213.3   82.0
## 6     p6    jedi  112.5   64.2
```

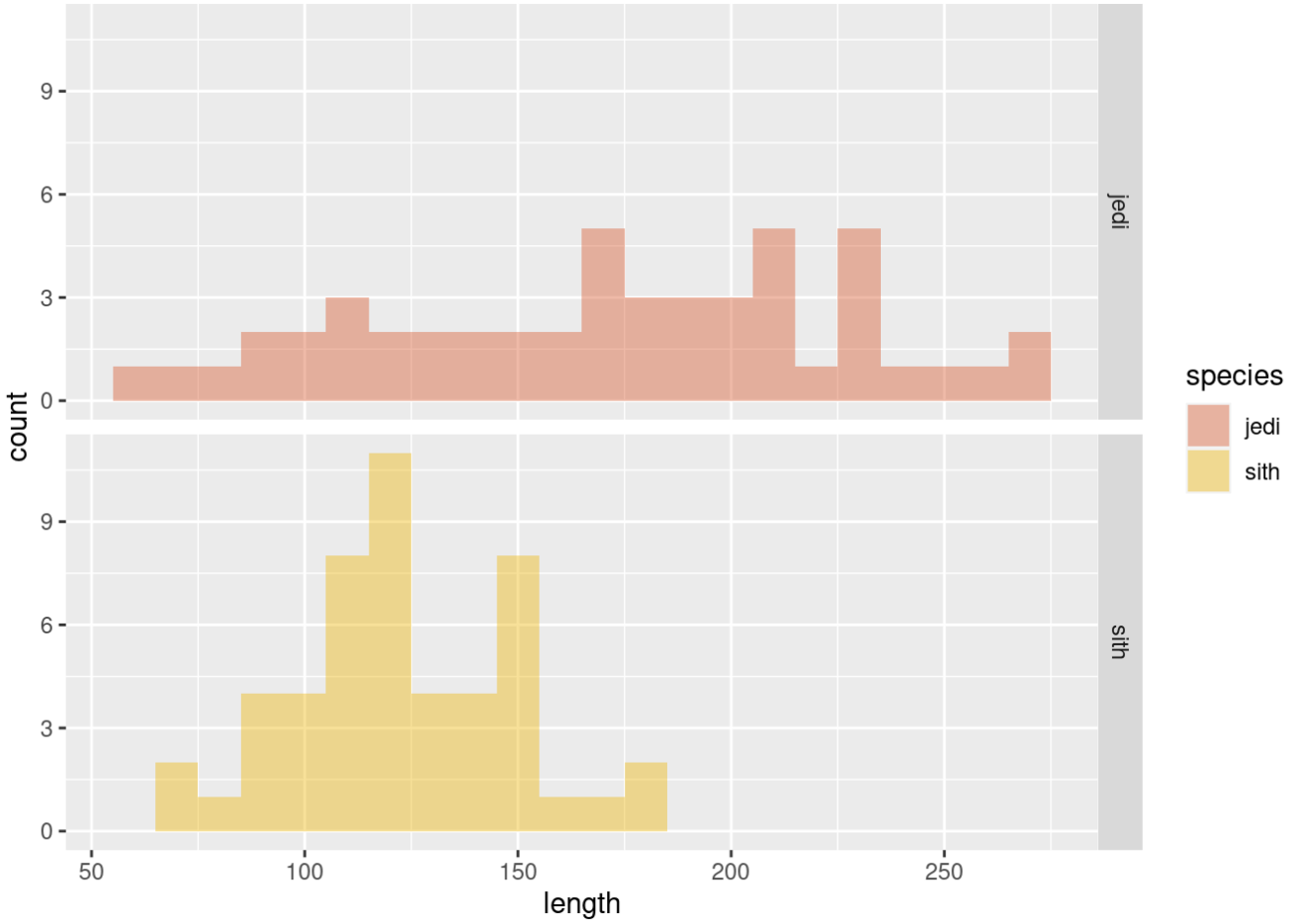
```
## histogram plot
jedi_length = magic.guys[which(magic.guys$species == "jedi"), 3]
sith_length = magic.guys[which(magic.guys$species == "sith"), 3]

hist(jedi_length, xlab = "Length Distribution of jedi")
```



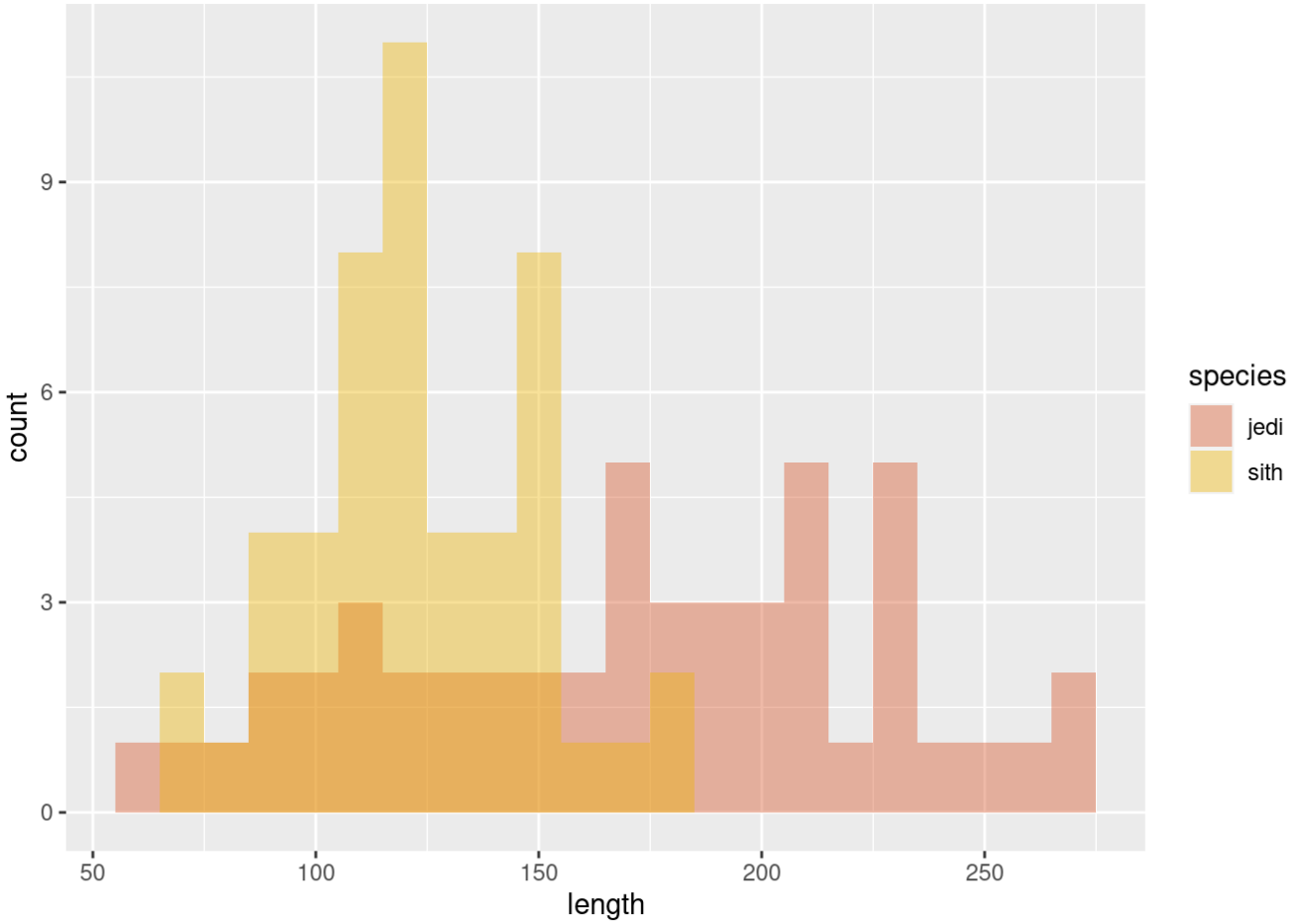

```
hist(sith_length, xlab = "Length Distribution of sith")
```



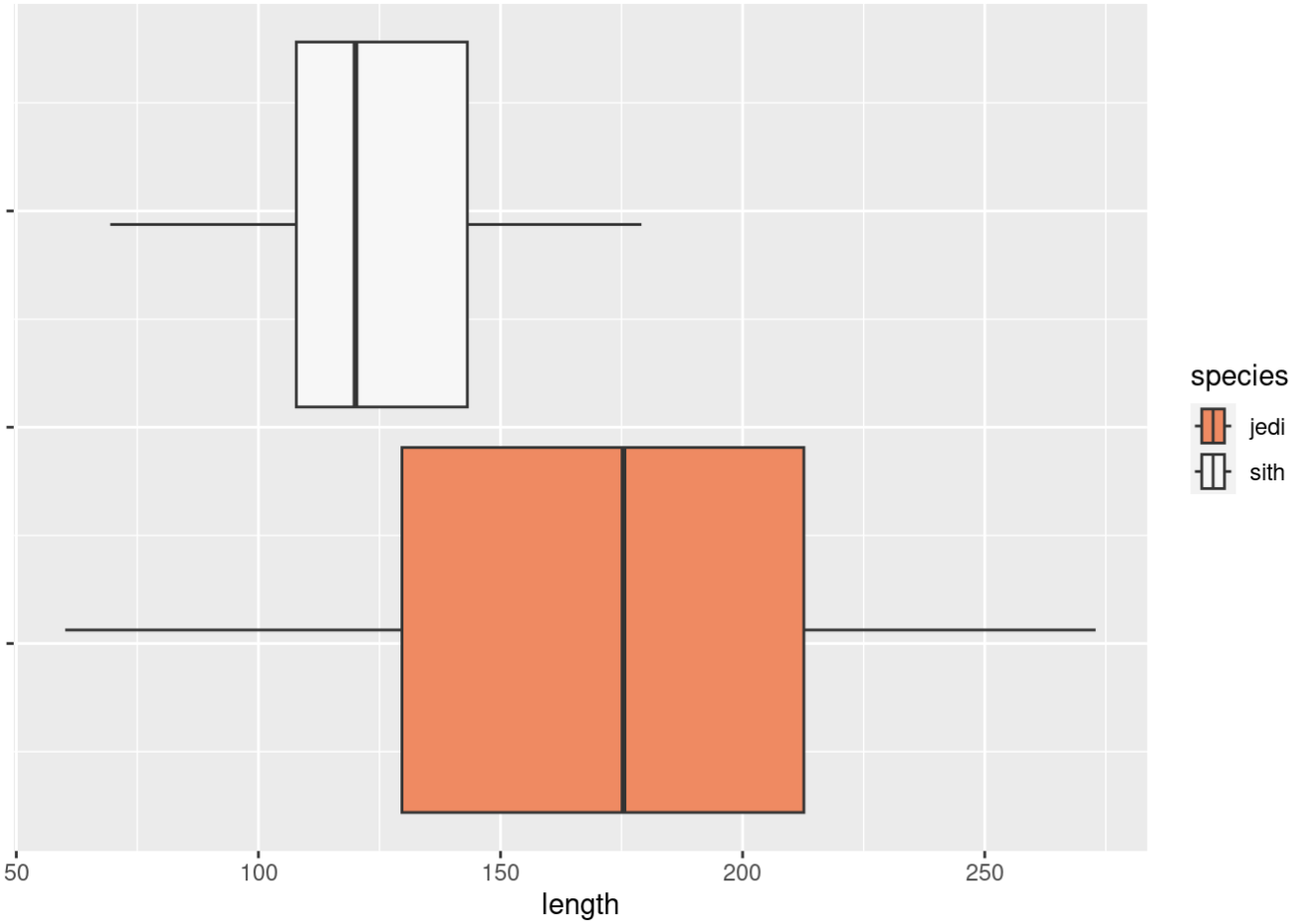
```
#seperate
compare.length = magic.guys %>%
  ggplot( aes(x=length, fill=species)) +
    geom_histogram(binwidth = 10, alpha=0.4, position = 'identity') +
    scale_fill_manual(values=c("#d75427","#eeb401")) +
    facet_grid(species ~ .)

compare.length
```




```
#merge
compare.length = magic.guys %>%
  ggplot( aes(x=length, fill=species)) +
    geom_histogram(binwidth = 10, alpha=0.4, position = 'identity') +
    scale_fill_manual(values=c("#d75427","#eeb401"))

compare.length
```




```
## box plot
compare.length = magic.guys %>%
  ggplot( aes(x=length, fill=species)) +
    geom_boxplot(outlier.colour="red", outlier.shape=8,outlier.size=4) +
    scale_fill_brewer(palette="RdBu") +
    theme(axis.text.y = element_blank())

compare.length
```




```
## save plots with pdf format
pdf("/home/xufeng/joint_KI_RIKEN/ompare.length.pdf")
plot(compare.length)
dev.off()
```

```
## png
##   2
```

```
## save plots with svg format
svg("/home/xufeng/joint_KI_RIKEN/ompare.length.svg")
plot(compare.length)
dev.off()
```

```
## png
##   2
```

```
## save plots with png format
png("/home/xufeng/joint_KI_RIKEN/ompare.length.png")
plot(compare.length)
dev.off()
```

```
## png
##   2
```

```
# The PDF format for saving images is the most used for creating scientific documents,
# as they are easy to add to LaTeX and maintain the resolution even if you zoom in.
# However, if you need to edit the image after saving in order to add some decoration
# or perform some modifications you should use SVG. And png image file format is
# known to weight less than JPEG with better quality, as it supports transparent backgrounds.


## Q2:
microarray <- read.table("/home/xufeng/joint_KI_RIKEN/microarray_data.tab", header = T, stringsAsFactors=FALSE, sep = "\t")

nrow(microarray)
```

```
## [1] 553
```

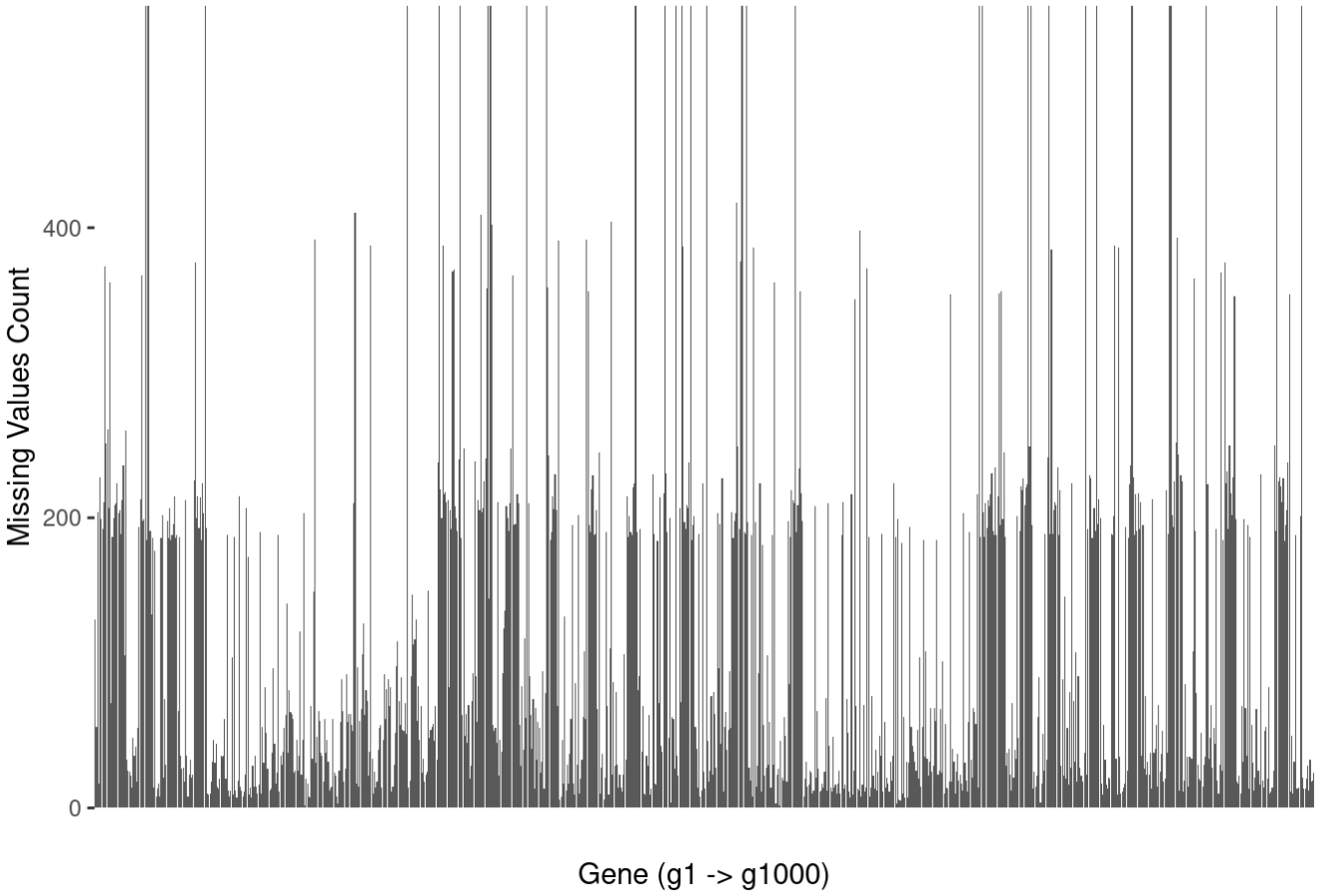
```
ncol(microarray)
```

```
## [1] 1000
```

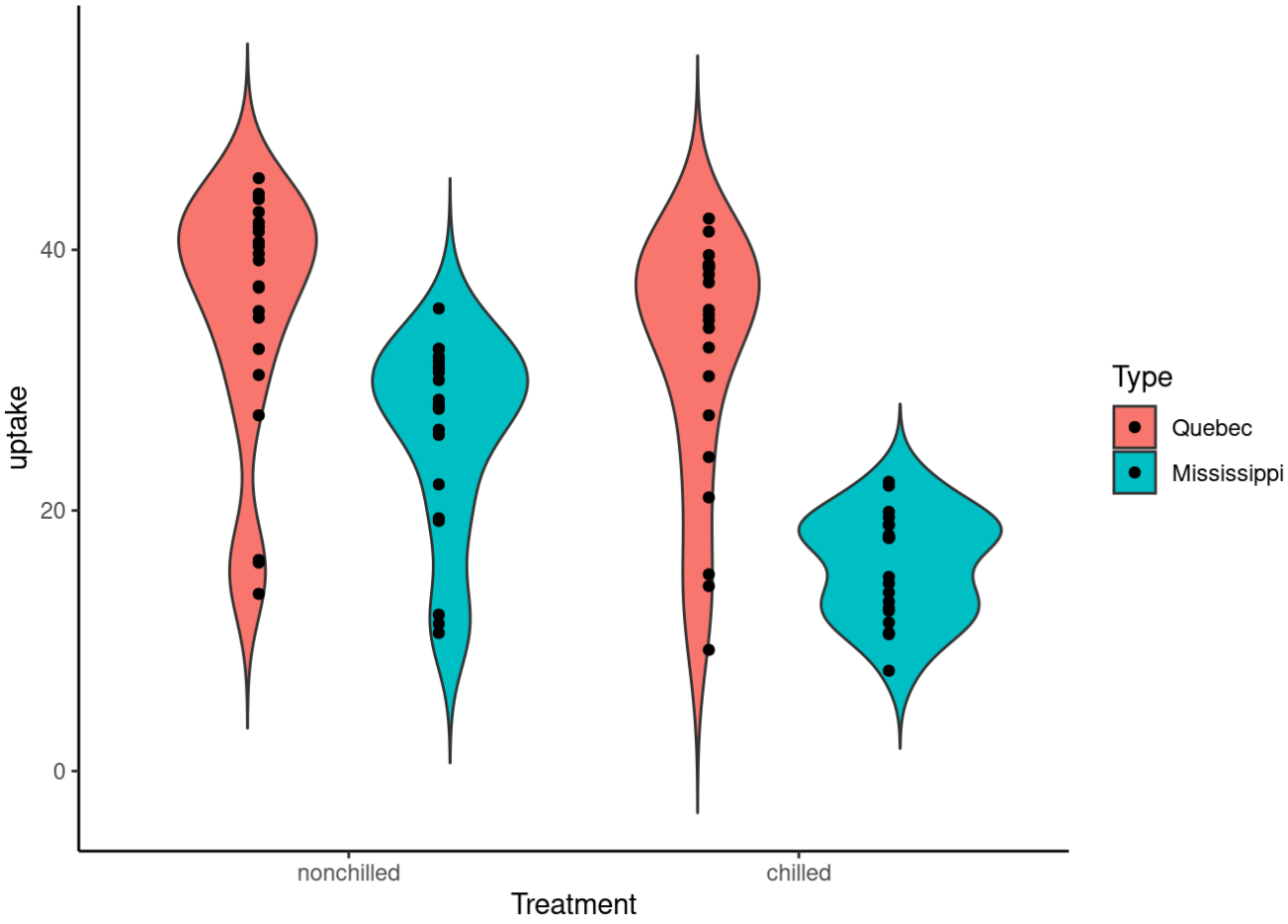
```
dim(microarray)
```

```
## [1]  553 1000
```

```
## Count the missing values per gene and visualize this result.
missing_values_per_gene = colSums(is.na(microarray))

gene_missing_counts <- data.frame(Gene = colnames(microarray), Missing_Values = missing_values_per_gene)

ggplot(gene_missing_counts, aes(x = Gene, y = Missing_Values)) +
  geom_bar(stat = "identity") +
  labs(x = "Gene (g1 -> g1000)", y = "Missing Values Count") +
  theme(axis.text.x=element_blank(),
        axis.ticks.x=element_blank())
```


Missing Values Count
400
200
0
Gene (g1 -> g1000)

```
## Find the genes for which there are more than X% (X=10%, 20%, 50%) missing value
s.

p_10 = gene_missing_counts[which(gene_missing_counts$Missing_Values > (nrow(microa
rray)*0.1)), 1]

p_20 = gene_missing_counts[which(gene_missing_counts$Missing_Values > (nrow(microa
rray)*0.2)), 1]

p_50 = gene_missing_counts[which(gene_missing_counts$Missing_Values > (nrow(microa
rray)*0.5)), 1]


## Replace the missing values by the average expression value for the particular g
ene.

# Calculate the row-wise means for each gene, ignoring NA values
gene_means <- apply(microarray, 2, function(x) mean(x, na.rm = TRUE))
# Replace NA values with corresponding gene means
for (gene_col in 1:ncol(microarray)) {
  microarray[is.na(microarray[, gene_col]), gene_col] <- gene_means[gene_col]
}


## Q3: Visualize the data in the CO2 dataset in a way that gives you a deeper unde
rstanding of the
# data. What do you see?

# Load the CO2 dataset
data("CO2")

ggplot(data = CO2, aes(x = Treatment, y = uptake, fill = Type))+
  theme_classic() +
  geom_violin(trim = FALSE) +
  geom_point(position = position_dodge(width = 0.8))
```



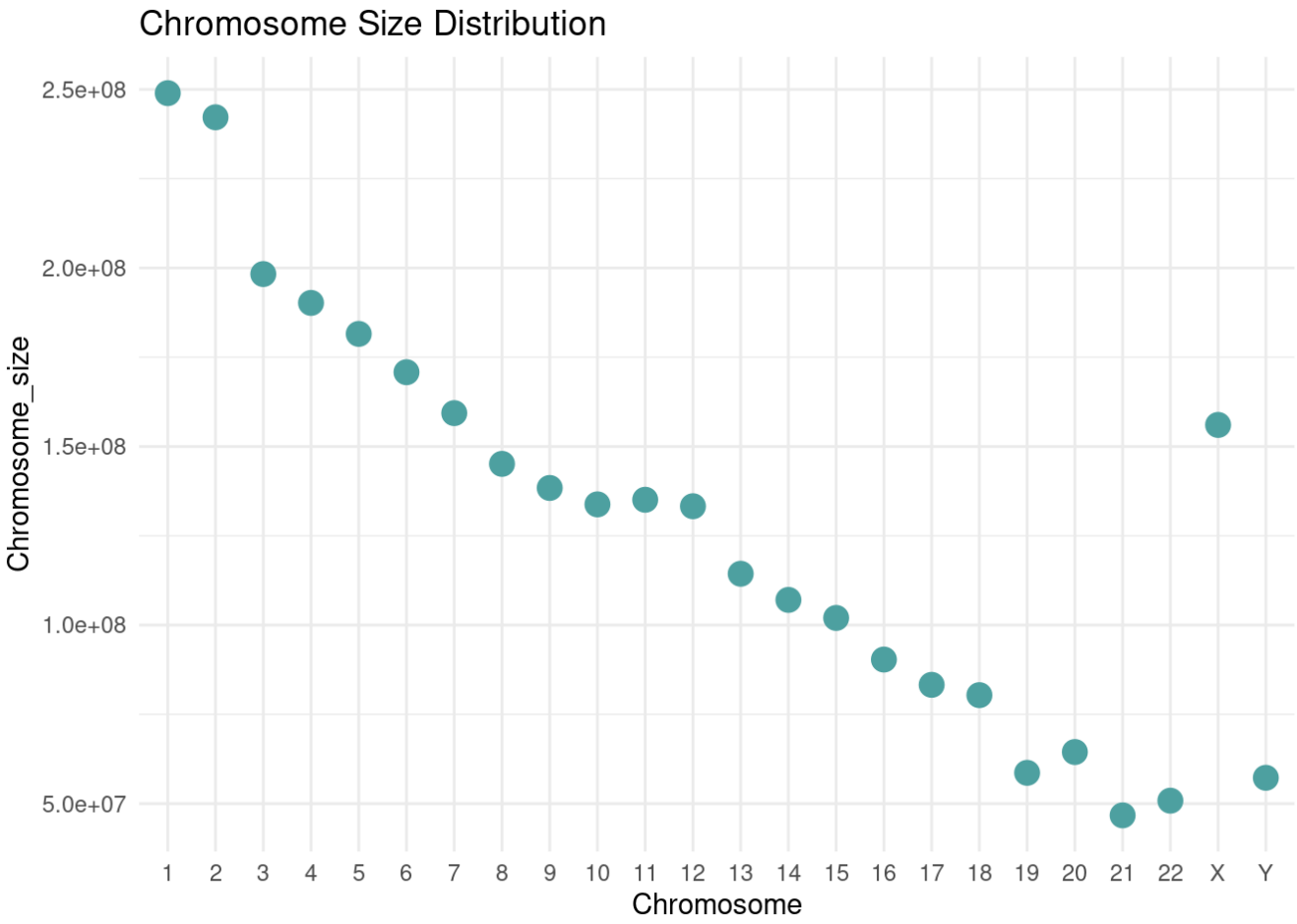

```
# I found : nonchilled is a better condition for uptaking CO2. And in the same con
dition,
# Quebec can uptake more CO2 versus to Mississippi.
```

Task 7

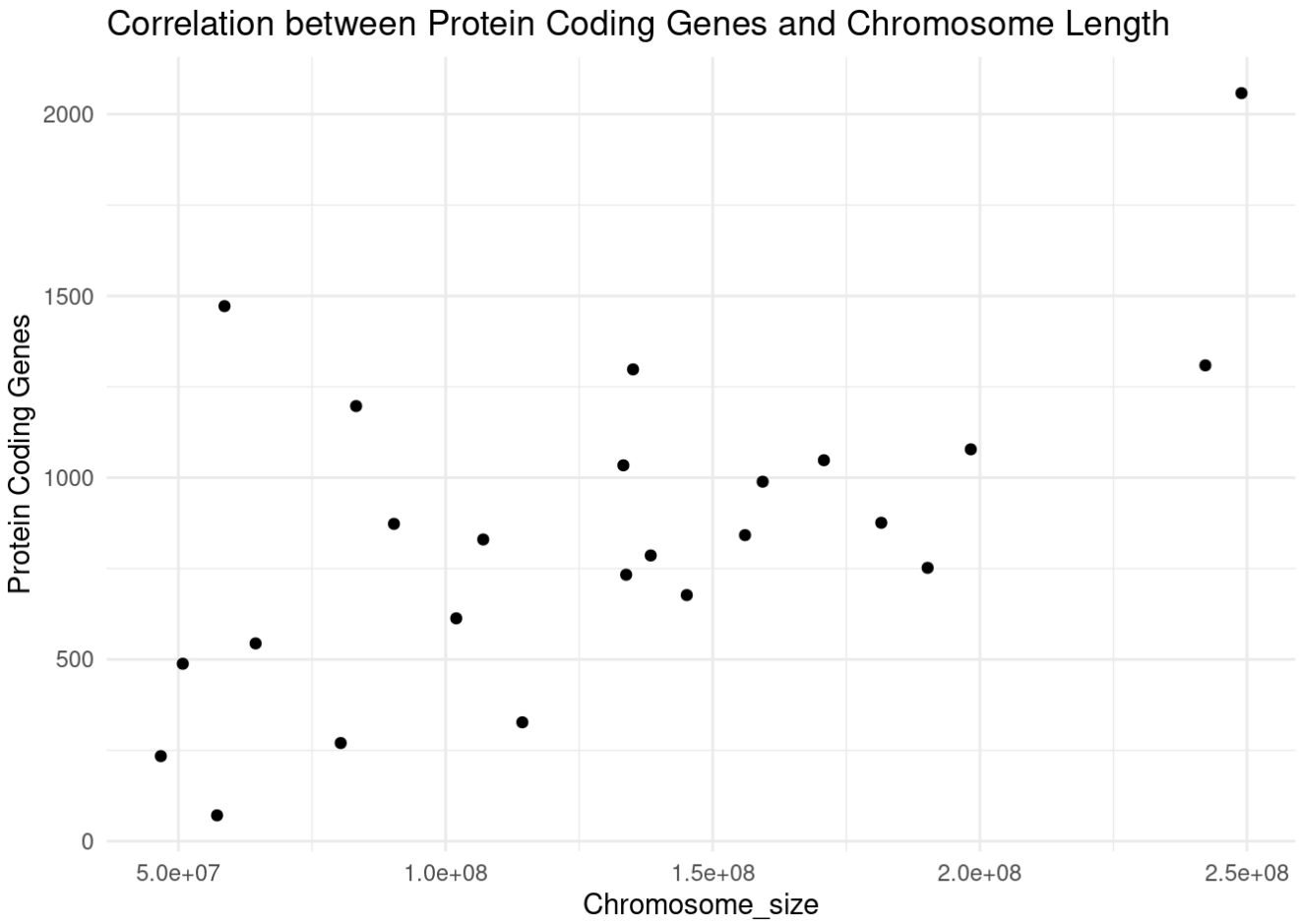
```
## devtools::install_github("hirscheylab/tidybiology")

## a. Extract summary statistics (mean, median and maximum) for the following vari
ables
# from the ‘chromosome’ data: variations, protein coding genes, and miRNAs.
# Utilize the tidyverse functions to make this as simply as possible.

library(tidybiology)
# Load the 'chromosome' data
data("chromosome")
# Use tidyverse functions to extract summary statistics
summary_stats <- chromosome %>%
  summarise(
    Mean_Variations = mean(variations, na.rm = TRUE),
    Median_Variations = median(variations, na.rm = TRUE),
    Max_Variations = max(variations, na.rm = TRUE),
    Mean_Protein_Coding_Genes = mean(protein_codinggenes, na.rm = TRUE),
    Median_Protein_Coding_Genes = median(protein_codinggenes, na.rm = TRUE),
    Max_Protein_Coding_Genes = max(protein_codinggenes, na.rm = TRUE),
    Mean_miRNAs = mean(mi_rna, na.rm = TRUE),
    Median_miRNAs = median(mi_rna, na.rm = TRUE),
    Max_miRNAs = max(mi_rna, na.rm = TRUE)
  )

summary_stats
```

```
## # A tibble: 1 × 9
##   Mean_Variations Median_Variations Max_Variations Mean_Protein_Coding_Genes
##             <dbl>             <dbl>          <dbl>                     <dbl>
## 1        6484572.           6172346       12945965                      850.
## # ℹ 5 more variables: Median_Protein_Coding_Genes <dbl>,
## #   Max_Protein_Coding_Genes <int>, Mean_miRNAs <dbl>, Median_miRNAs <dbl>,
## #   Max_miRNAs <int>
```

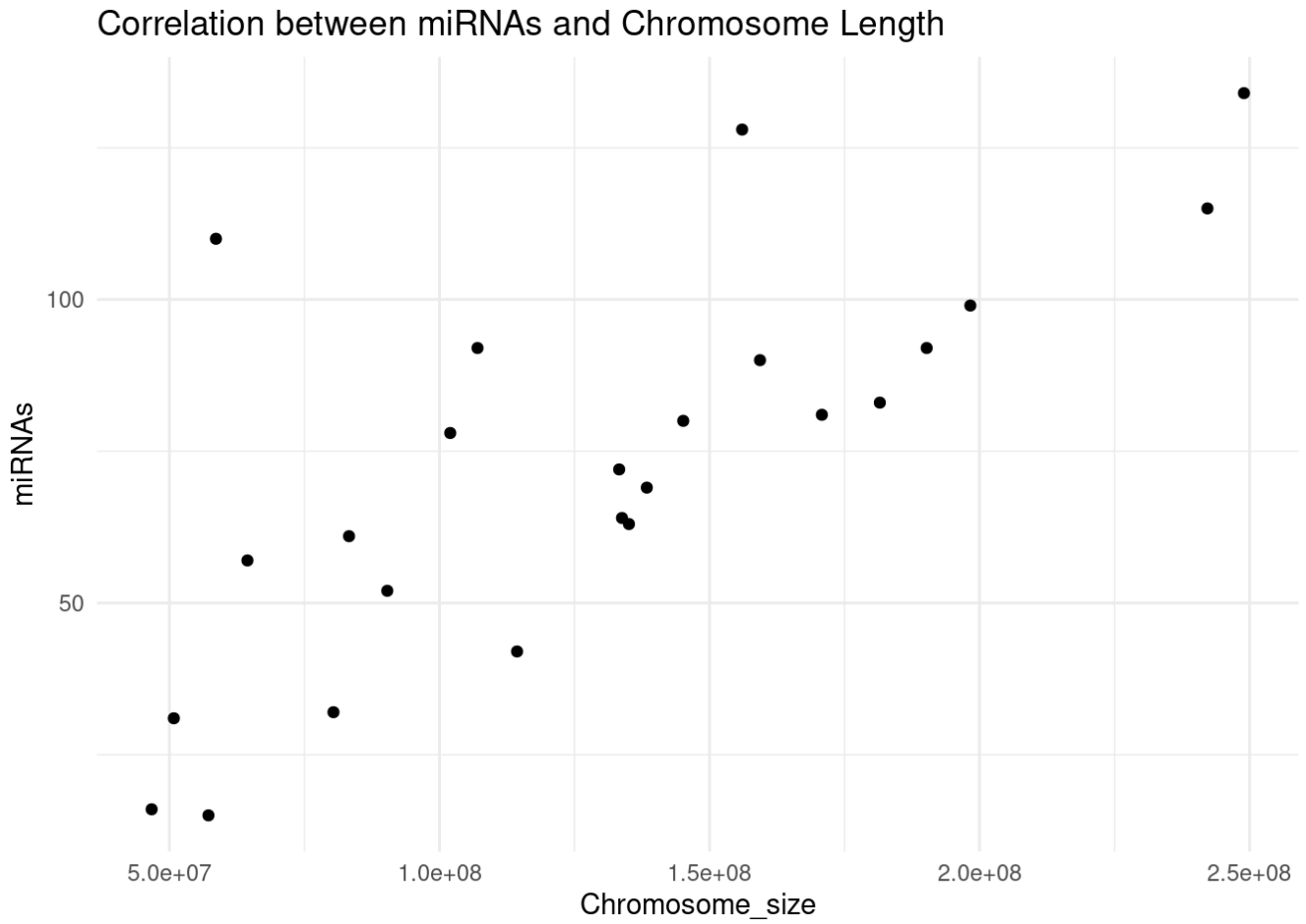
```
## b. How does the chromosome size distribute? Plot a graph that helps to visualiz
e
# this by using ggplot2 package functions.

# Create a scatter plot to visualize chromosome size distribution
ggplot(chromosome, aes(x = id, y = basepairs)) +
  geom_point(color = "#4da0a0", size = 4) +
  labs(title = "Chromosome Size Distribution",
       x = "Chromosome",
       y = "Chromosome_size") +
  theme_minimal()
```




```
## c. Does the number of protein coding genes or miRNAs correlate with the length
# of the chromosome? Make two separate plots to visualize these relationships.

# Scatter plot to visualize correlation between protein coding genes and chromosom
e length
ggplot(chromosome, aes(x = basepairs, y = protein_codinggenes)) +
  geom_point() +
  labs(title = "Correlation between Protein Coding Genes and Chromosome Length",
       x = "Chromosome_size",
       y = "Protein Coding Genes") +
  theme_minimal()
```



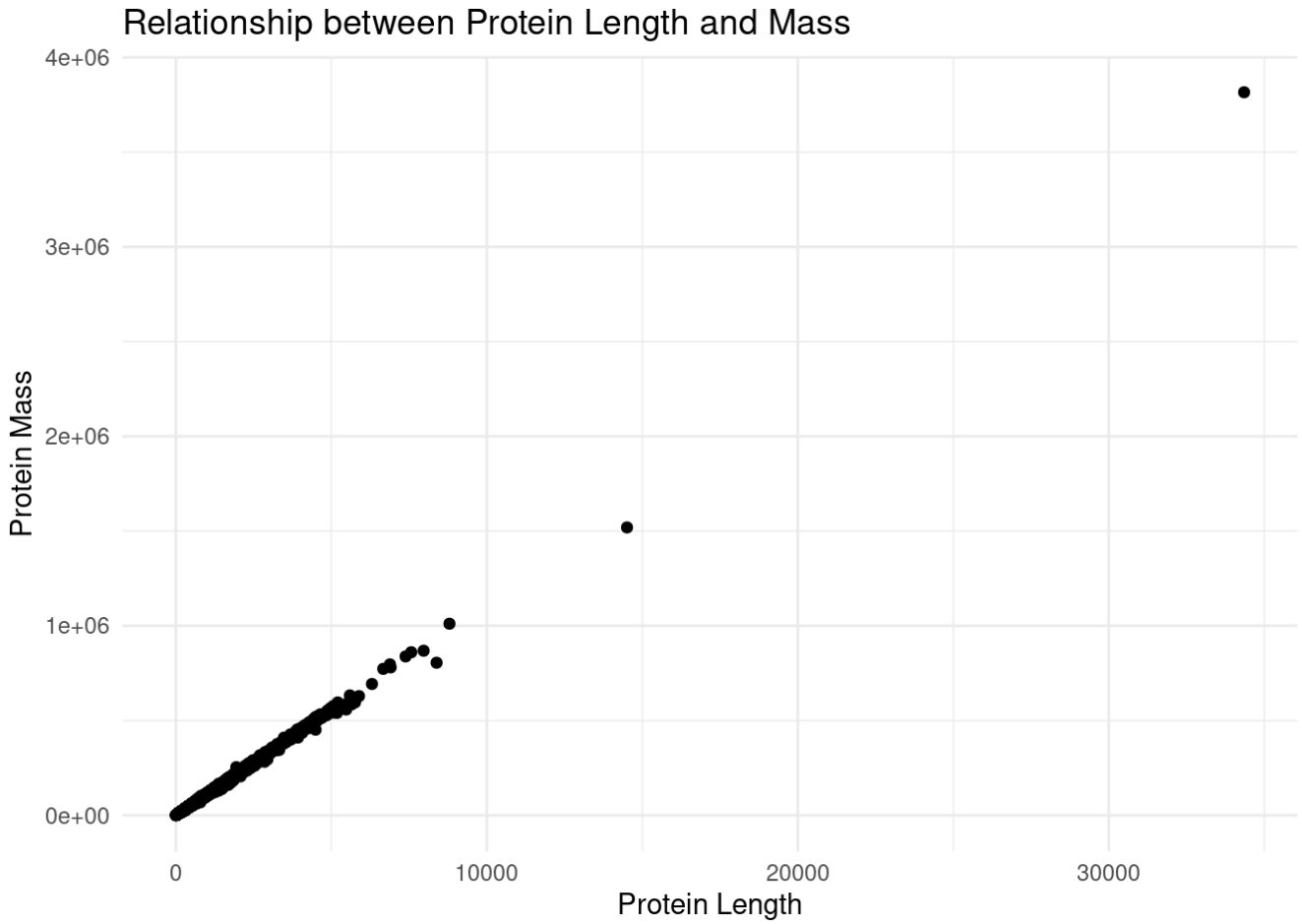

```
# Scatter plot to visualize correlation between miRNAs and chromosome length
ggplot(chromosome, aes(x = basepairs, y = mi_rna)) +
  geom_point() +
  labs(title = "Correlation between miRNAs and Chromosome Length",
       x = "Chromosome_size",
       y = "miRNAs") +
  theme_minimal()
```




```
## d. Calculate the same summary statistics for the 'proteins' data variables leng
th and mass.
# Create a meaningful visualization of the relationship between these two variable
s by
# utilizing the ggplot2 package functions. Play with the colors, theme- and
# other visualization parameters to create a plot that pleases you.

data("proteins")
# Summary statistics for 'length' and 'mass' variables
summary_stats_proteins <- proteins %>%
  summarise(
    Mean_Length = mean(length, na.rm = TRUE),
    Median_Length = median(length, na.rm = TRUE),
    Max_Length = max(length, na.rm = TRUE),
    Mean_Mass = mean(mass, na.rm = TRUE),
    Median_Mass = median(mass, na.rm = TRUE),
    Max_Mass = max(mass, na.rm = TRUE)
  )

summary_stats_proteins
```

```
## # A tibble: 1 × 6
##   Mean_Length Median_Length Max_Length Mean_Mass Median_Mass Max_Mass
##         <dbl>         <dbl>      <dbl>     <dbl>       <dbl>    <dbl>
## 1        557.           414      34350    62061.      46140.  3816030
```

```
# Scatter plot to visualize the relationship between 'length' and 'mass'
ggplot(proteins, aes(x = length, y = mass)) +
  geom_point() +
  labs(title = "Relationship between Protein Length and Mass",
       x = "Protein Length",
       y = "Protein Mass") +
  theme_minimal()
```



Waiting for your comments and suggestions~

Best

xufeng SHU