Assignment 1

Wanzhe Xu Laboratory of Functional Analysis in silico, Human Genome Center, The Institute of Medical Science, The University of Tokyo

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Task 1 - Literature

1. Read the research article of the hands-on working group you are assigned to (see file “Student Groups.pdf” in shared folder General course material).

2. Answer the following questions

a. What is the medically relevant insight from the article?

Answer: This paper provides an unbiased approach to integrate disparate single-cell transcriptome datasets for more accurate and reliable results. In medical research, single-cell transcriptome analysis has become an important tool for studying complex diseases and developing personalized therapeutic strategies. However, due to the high heterogeneity and technical bias of single-cell transcriptome data, there are large differences between different datasets, which makes the integration and interpretation of data difficult. With the unbiased integration approach proposed in this paper, different cellular subpopulations and differentially expressed genes can be more accurately identified while reducing batch effects and technical biases, thus deepening the understanding of disease pathogenesis and contributing to the discovery of new therapeutic targets and drugs.

b. Which genomics technology/ technologies were used?

Answer: The technique used in this study is scRNA-seq, which allows researchers to sequence the transcriptome of individual cells to gain insights into gene expression patterns and cellular heterogeneity at the single-cell level.

3. Further related research questions

a. List and explain at least three questions/ hypotheses you can think of that extend the analysis presented in the paper.

Answer: Question 1: How to deal with the effects of technical biases or batch effects? During the acquisition and processing of individual cell transcriptome data, it may be affected by various technical factors, such as sequencing depth, PCR amplification bias, etc. These technical factors may bias the integration results, so it is possible to explore how to correct the effects of these technical biases during the integration process to obtain more accurate results.

Question 2: How are differences between cell types handled when integrating individual cell transcriptomes? The approach in this paper focuses on duplicates of individual cells, but for samples with different cell types, there may be differences in gene expression levels between each cell type.

Hypotheses 3: Different integration algorithms may produce different results. Is it possible to reduce bias, such as the effect of noise, by algorithmic integration.

b. [Optional] Devise a computational analysis strategy for (some of) the listed questions under 3a.

Answer: There may be unknown batch effects in single cell transcriptome data. To avoid the influence of batch effects on integration results, some batch effect correction methods can be used, such as ComBat or Limma.

Task 4 - R basic operations

1. What is the square root of 10?

```
cat(log2(32))
```

```
output: 3.162278
```

2. What is the logarithm of 32 to the base 2?

```
cat(sum(1:1000))
```

```
output: 5
```

3. What is the sum of the numbers from 1 to 1000?

```
cat(sum(1:1000))
```

```
output:  500500
```

4. What is the sum of all even numbers from 2 to 1000?

```
sum_even <- 0

for (i in seq(2, 1000, by=2)) {  # for loop through even numbers

  sum_even <- sum_even + i  # add each even number to the sum

}
```

cat(sum_even)

5. How many pairwise comparisons are there for 100 genes?

# The seq function is used to create an equal series from 2 to 1000 with a step size of 2, so that all even numbers are obtained.

sum_even <- sum(seq(from = 2, to = 1000, by = 2))

sum_even

output: 250500

6. And how many ways to arrange 100 genes in triples?

# The NCR formula is used when some sort of ordering is done without considering the order of things. the R code is implemented as follows.

n <- 100

r <- 3

num_triplets <- factorial(n) / (factorial(r) * factorial(n - r))

print(num_triplets)

output: 161700

Task 5 - Using R example datasets

1. Use the R internal CO2 dataset (“data(CO2)”).

```
data(CO2)
help(CO2)
```

2. Describe briefly the content of the CO2 dataset using the help function.

Answer: The CO2 dataset is a time series object containing atmospheric CO2 concentration data collected at the Mauna Loa Observatory in Hawaii from 1959 to 1997. The data set has two variables, which are

CO2: atmospheric carbon dioxide concentration. Plant: the type of plant used for the experiment.

There are 468 observations in the dataset.

3. What is the average and median CO2 uptake of the plants from Quebec and Mississippi?

```
# import lib dplyr first
# install.packages("dplyr")
library(dplyr)
```

```
CO2 %>%
  # select only Quebec and Mississippi
  filter(Type %in% c("Quebec", "Mississippi")) %>%
  # group by Type
  group_by(Type) %>%
  # compute mean and median
  summarize(mean_uptake = mean(uptake), median_uptake = median(uptake))

## # A tibble: 2 × 3
##   Type        mean_uptake median_uptake
##   <fct>             <dbl>         <dbl>
## 1 Quebec             33.5          37.2
## 2 Mississippi        20.9          19.3
```

The results are shown in the table and the mean for Quebec is 33.54286 and the median is 37.15. The mean for Mississippi is 20.88333 and the median is 19.30.

4. [Optional] In the “airway” example data from Bioconductor, how many genes are expressed in each sample? How many genes are not expressed in any sample?

```
#install packge pasilla for R version 4 or more:
if (!requireNamespace("BiocManager", quietly = TRUE))
install.packages("BiocManager")
BiocManager::install("pasilla", version = "3.16")
# Install packdge airway:
if (!require("airway"))
BiocManager::install("airway")

# Load the "pasilla" package:
# library(pasilla)

# Load the "airway" dataset
data(airway)

# Extracts the data from the SingleCellExperiment object and converts i
t into a matrix
airway_mat <- as.matrix(assay(airway))

# Remove missing values
airway_mat <- na.omit(airway_mat)

# Calculate the number of expressed and non-expressed genes
expressed_genes <- sum(rowSums(airway_mat) > 0)
not_expressed_genes <- sum(rowSums(airway_mat) == 0)

# print result
cat("Number of expressed genes:", expressed_genes, "\n")
```

```
## Number of expressed genes: 33469
cat("Number of not expressed genes:", not_expressed_genes, "\n")
## Number of not expressed genes: 30633
```

Task 6 - R Functions

1. Write a function that calculates the ratio of the mean and the median of a given vector.

```
mean_median_ratio <- function(vector) {
  # Calculate mean and median
  mean <- mean(vector)
  median <- median(vector)

  # Calculate ratio
  ratio <- mean / median

  # Return ratio
  return(ratio)
}
```

2. Write a function that ignores the lowest and the highest value from a given vector and calculate the mean.

```
trimmed_mean <- function(vector) {
  # Remove lowest and highest values
  trimmed_vector <- vector[-c(which.min(vector), which.max(vector))]

  # Calculate mean of trimmed vector
  mean(trimmed_vector)
}
```

3. Read about piping from here:https://r4ds.had.co.nz/pipes.html#pipes (you don't have to learn everything, a basic understanding of the usage is enough). Write a short (max. 300 characters, no spaces) explanation of why, how, and when not to use pipes.

Pipes in R are used to chain together multiple operations, making code more readable and efficient. Pipes allow data to flow from one operation to the next, reducing the need for intermediate variables. However, pipes can be difficult to read when they become too complex or are nested too deeply. Additionally, some operations may not work well with pipes, such as functions that require multiple arguments or functions that require data to be grouped or sorted in a particular way. Therefore, pipes should be used judiciously, and not at the expense of code readability or functionality.

4. Familiarize yourself with the apply-family of functions (apply, lapply, sapply etc.) http://uc-r.github.io/apply_family Write a short explanation (max. 300 characters, no spaces) of why they could be useful in your work.

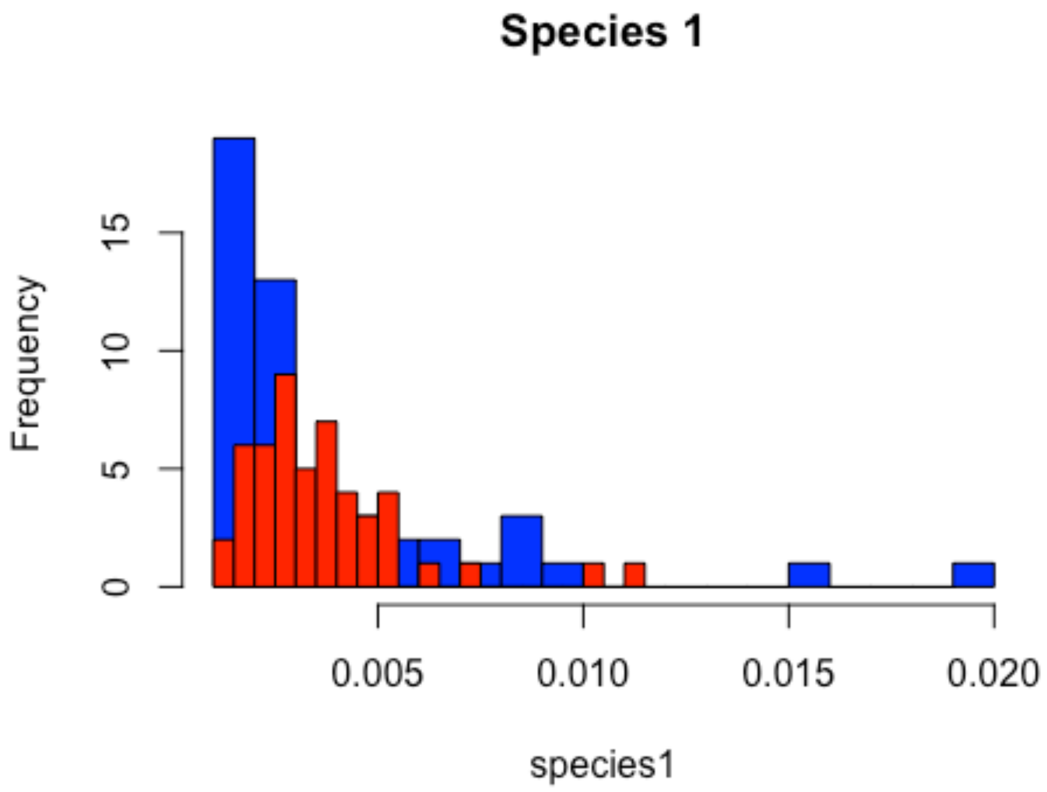
The apply-family of functions in R (apply, lapply, sapply, etc.) can be useful in my work because they allow for efficient and streamlined manipulation of data in arrays and lists. These functions provide a simpler and more concise way to apply a function to subsets of a dataset or to apply a function across multiple datasets, reducing the amount of repetitive code. The apply-family functions also allow for the output to be returned in various formats, such as a list, vector, or matrix, depending on the needs of the analysis.

Task 7 - Basic visualization with R

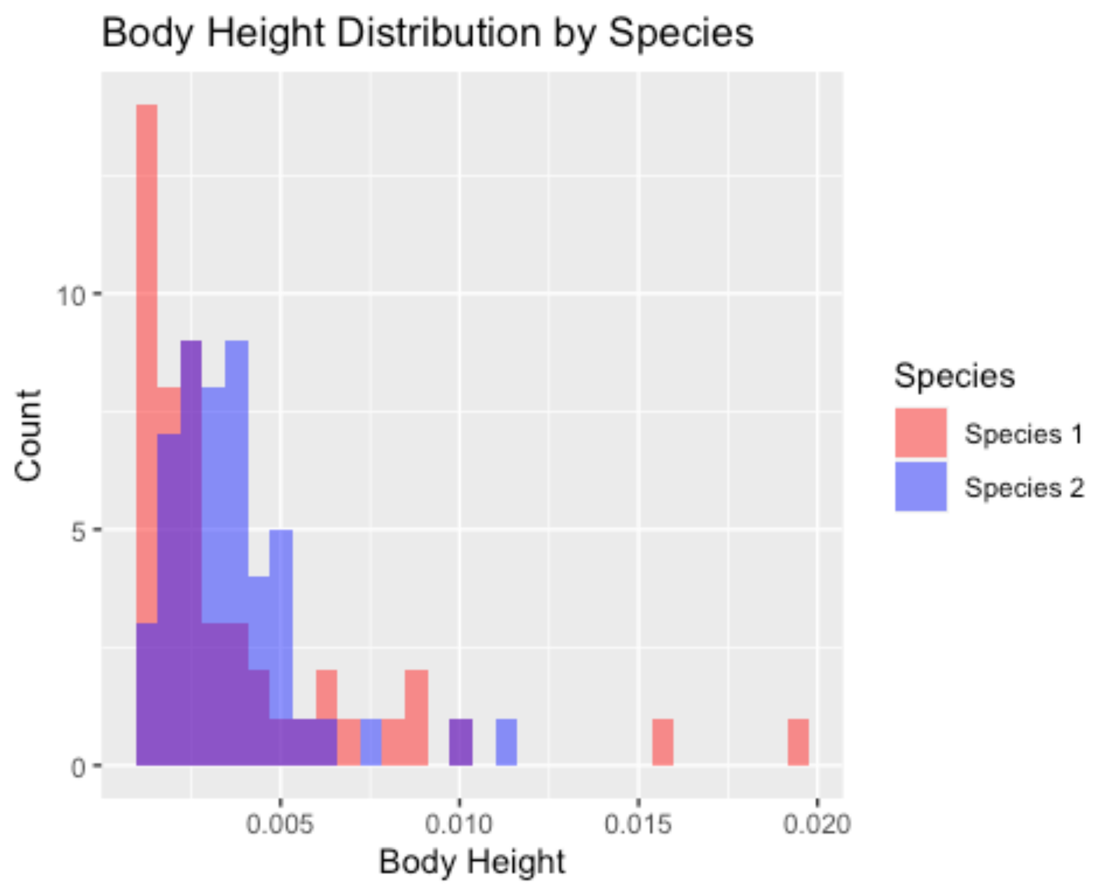
1. Compare the distributions of the body heights of the two species from the ‘magic_guys.csv’ dataset graphically

a. using the basic ‘hist’ function as well as ‘ggplot’ and ‘geom_histogram’ functions from the ggplot2 package. Optimize the plots for example by trying several different ‘breaks’. Note that ggplot2-based functions give you many more options for changing the visualization parameters, try some of them.

```
# Load the data
magic_guys <- read.csv("magic_guys.csv")
library(ggplot2)
# Calculate body height
body_height <- magic_guys$weight / magic_guys$length^2

# Subset the data by species
species1 <- subset(body_height, magic_guys$species == "jedi")
species2 <- subset(body_height, magic_guys$species == "sith")
#print(species1)
#print(species2)
type(species1)
## [1] "double"
# Use the basic hist() function to plot histograms of the body height d
ata for both species
hist(species1, breaks = 20, col = "blue", main = "Species 1")
hist(species2, breaks = 20, col = "red", add = TRUE)
```

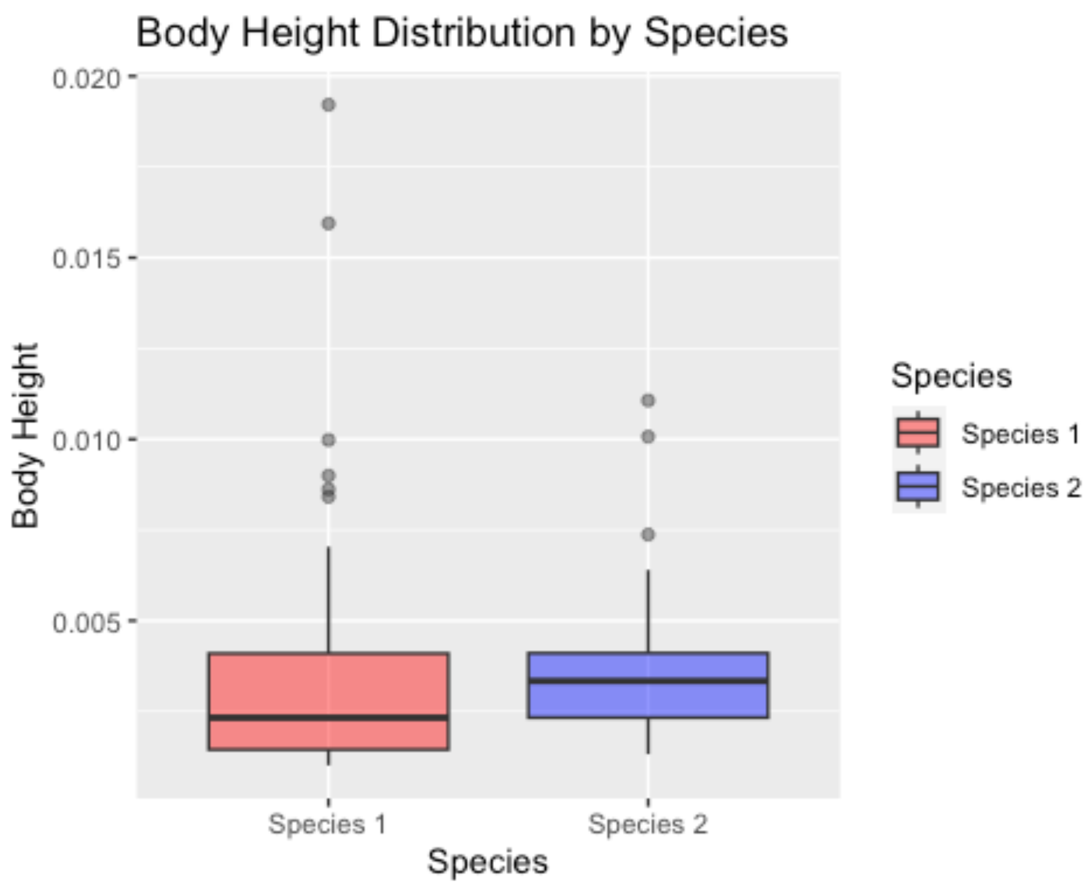


```
# Use ggplot2 and geom_histogram() to plot histograms of the body heigh
t data for both species
# Load the necessary library
library(ggplot2)

# Create a new data frame with the body heights of both species
new_df <- data.frame(Body_Height = c(species1, species2),
                     Species = factor(rep(c("Species 1", "Species 2"),
c(length(species1), length(species2)))))

# Create the histogram plot
ggplot(new_df, aes(x=Body_Height, fill=Species)) +
  geom_histogram(alpha=0.5, position="identity", bins=30) +
  labs(title="Body Height Distribution by Species", x="Body Height", y=
"Count") +
  scale_fill_manual(values=c("red", "blue"))
```



b. Do the same comparison as in a. but with boxplots. If you want to use the ggplot2-package, use the functions 'ggplot' and 'geom_boxplot'.

```
# Create the boxplot plot
ggplot(new_df, aes(x=Species, y=Body_Height, fill=Species)) +
  geom_boxplot(alpha=0.5, position="dodge") +
  labs(title="Body Height Distribution by Species", x="Species", y="Bod
y Height") +
  scale_fill_manual(values=c("red", "blue"))
```



c. Save the plots with the 'png', 'pdf', and 'svg' formats. In which situation would you use which file format?

```
# Save the plot
ggsave("temp_save.png", plot = last_plot(), width = 6, height = 4, dpi
= 300)
ggsave("temp_save.pdf", plot = last_plot(), width = 6, height = 4, dpi
= 300)
# install.packages("svglite") first
library(svglite)
ggsave("temp_save.svg", plot = last_plot(), width = 6, height = 4, dpi
= 300, device = "svg")
```

If we need a lossless, web-compatible format that supports transparency, we might choose PNG. if we need a high-quality vector format that supports CMYK colors and can be embedded in a document, we might choose PDF. if we need a scalable, web-compatible vector format, we might choose SVG. ## 2. Load the gene expression data matrix from the 'microarray_data.tab' dataset provided in the shared folder, it is a big tabular separated matrix. ### a. How big is the matrix in terms of rows and columns?

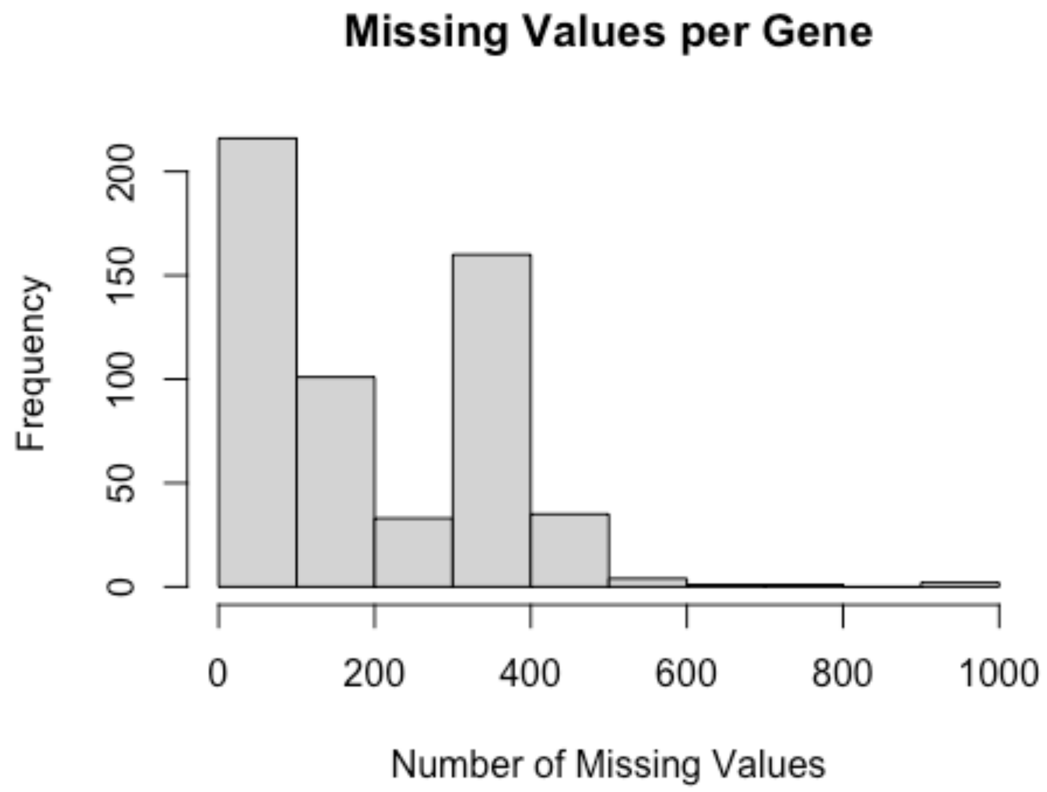
```
# Load the data
data <- read.table("microarray_data.tab", header = TRUE, sep = "\t")
```

```
# Get the dimensions of the matrix
dim(data)
## [1]  553 1000
```

As shown, the matrix has 553rows and 1000columns. ### b. Count the missing values per gene and visualize this result.

```
# Count the missing values per gene
missing_values <- apply(data, 1, function(x) sum(is.na(x)))
missing_values
##   [1]   72  226   72   74  126   87  273   95   92   85   64   56  1
03   78   66
##  [16]   74  586  455  493   67  287   85   72  329  406  397  359  3
47  355  351
##  [31]  389  375  366  348  356  355  348  358  375  359  393  346  3
67  361  353
##  [46]  352  352  494  347  396  398  357  379  347  356  382  568  3
62  366  364
##  [61]  356  371  353  352  355  381  365  350  361  353  351  349   
64   67  454
##  [76]  415  406  412  363  372  381  359  390  385  380  378  384  3
77  394  401
##  [91]  382  383  369  387  388  379  387  383  387  405  415  406  4
45  462  410
## [106]  418  407  126  409  414  116  439  433   89  430  366   67  3
93  375  403
## [121]  375  400  403  356   84  387  363  355  351  356  138  375  3
60  360  547
## [136]  379  368  377  396  379  384  383  393  375  381  390  400  3
72  391  394
## [151]  415  369  387  398  400   68  389  392  382  389  377  381  3
95  393  499
## [166]  387   83  388  368  284  385  372  393  375   98  198  329  1
70  110   68
## [181]   91  457  380   57   64   69  179   65   79   72   92   67  3
59   63  293
## [196]   97   69   81   66   62   62  115  124   90   81   68   66   
90  371   64
## [211]   69   64   67  376  375  193  103   54  122   94   69   62   
76   54   61
## [226]  183   61   52   56   58   59   56   54   64   56   57  344  1
10   93  116
## [241]  557   64  111   64   81   62   59   64  177  790  304  100   
82   61   95
## [256]   62   60   66   53  124   61  159  161  122   62   93   78   
51   69  121
## [271]   72   61  182   63   97  101  119   60   84  195   58  282   
54   65  405
## [286]  114   74  108   96  102  121   79   58  116  108   93   68
```

```
58   60   56
## [301]   63   61  112  108   62   86   62  319   60   53  127  128   
81   67   72
## [316]   81   75   72   96  122   69  106  209   60   84   85  116  2
07   85   76
## [331]  180  147  191   96  677  387  379  368  384 1000  369  420  3
73  356  349
## [346]  350  348  363  358  356  404  354  371  362  363  356  356  4
35  362  360
## [361]  367  445  358  365  357  361  376  354  360   60  291  124  3
31  109  108
## [376]  109  280   88  102   89   83  221  197   92  100  105  177  1
57  105  102
## [391]  139  109  172  106  325  275  100   85   88  105  210   89   
78   83  100
## [406]  102   88   90   81   81   76   85   82   83   79  100  101  2
81  125  104
## [421]   90   88   86  409   87   82  324  261   78   80   87  103   
93   81  242
## [436]  232  210   77  170  199  230  185  210  239  335  338  242  2
66  171  284
## [451]  219  177  121   96  302  118  112  113   96  100  426  121   
84   83  155
## [466]   95   81   87  114   83   77   87   93   80   90   76   96  1
30  102   79
## [481]   78   90  103   95   93   89   94   88  100   91   87  100  1
31   92  118
## [496]   90  100  247   80  179   97  116  165  106  109  238   99   
75  104   80
## [511]  107   97  119  472  398  117  146  132  267  238  122  324  1
01   91   79
## [526]   90  104   94  181   85  100   88   91  223   82  241  110   
82   78   92
## [541] 1000   80   78   90   99  251  103  256   90  133  104   86   
86
# Visualize the result
hist(missing_values, main = "Missing Values per Gene", xlab = "Number o
f Missing Values")
```



c. Find the genes for which there are more than X% (X=10%, 20%, 50%) missing values.

```
# Calculate the percentage of missing values for each gene
percent_missing <- apply(is.na(data), 1, mean) * 100

# Find the genes with more than X% missing values, where X is 10%, 20%,
 and 50%
X_values <- c(10, 20, 50)
for (X in X_values) {
  missing_genes <- rownames(data)[percent_missing > X]
  cat("Genes with more than", X, "% missing values:\n")
  print(missing_genes)
}
## Genes with more than 10 % missing values:
##   [1] "2"    "5"    "7"    "13"   "17"   "18"   "19"   "21"   "24"   "25"   "2
6"   "27"
##  [13] "28"   "29"   "30"   "31"   "32"   "33"   "34"   "35"   "36"   "37"   "3
8"   "39"
##  [25] "40"   "41"   "42"   "43"   "44"   "45"   "46"   "47"   "48"   "49"   "5
0"   "51"
##  [37] "52"   "53"   "54"   "55"   "56"   "57"   "58"   "59"   "60"   "61"   "6
2"   "63"
##  [49] "64"   "65"   "66"   "67"   "68"   "69"   "70"   "71"   "72"   "75"   "7
6"   "77"
```

```
##  [61] "78"  "79"  "80"  "81"  "82"  "83"  "84"  "85"  "86"  "87"  "8
8"  "89"
##  [73] "90"  "91"  "92"  "93"  "94"  "95"  "96"  "97"  "98"  "99"  "1
00" "101"
##  [85] "102" "103" "104" "105" "106" "107" "108" "109" "110" "111" "1
12" "113"
##  [97] "115" "116" "118" "119" "120" "121" "122" "123" "124" "126" "1
27" "128"
## [109] "129" "130" "131" "132" "133" "134" "135" "136" "137" "138" "1
39" "140"
## [121] "141" "142" "143" "144" "145" "146" "147" "148" "149" "150" "1
51" "152"
## [133] "153" "154" "155" "157" "158" "159" "160" "161" "162" "163" "1
64" "165"
## [145] "166" "168" "169" "170" "171" "172" "173" "174" "176" "177" "1
78" "179"
## [157] "182" "183" "187" "193" "195" "202" "203" "209" "214" "215" "2
16" "217"
## [169] "219" "226" "237" "238" "240" "241" "243" "249" "250" "251" "2
60" "262"
## [181] "263" "264" "270" "273" "276" "277" "280" "282" "285" "286" "2
88" "290"
## [193] "291" "294" "295" "303" "304" "308" "311" "312" "320" "322" "3
23" "327"
## [205] "328" "331" "332" "333" "335" "336" "337" "338" "339" "340" "3
41" "342"
## [217] "343" "344" "345" "346" "347" "348" "349" "350" "351" "352" "3
53" "354"
## [229] "355" "356" "357" "358" "359" "360" "361" "362" "363" "364" "3
65" "366"
## [241] "367" "368" "369" "371" "372" "373" "374" "375" "376" "377" "3
79" "382"
## [253] "383" "386" "387" "388" "389" "390" "391" "392" "393" "394" "3
95" "396"
## [265] "400" "401" "406" "417" "418" "419" "420" "424" "427" "428" "4
32" "435"
## [277] "436" "437" "439" "440" "441" "442" "443" "444" "445" "446" "4
47" "448"
## [289] "449" "450" "451" "452" "453" "455" "456" "457" "458" "461" "4
62" "465"
## [301] "469" "478" "479" "483" "493" "495" "498" "500" "502" "503" "5
04" "505"
## [313] "506" "509" "511" "513" "514" "515" "516" "517" "518" "519" "5
20" "521"
## [325] "522" "523" "527" "529" "534" "536" "537" "541" "546" "547" "5
48" "550"
## [337] "551"
## Genes with more than 20 % missing values:
##   [1] "2"   "7"   "17"  "18"  "19"  "21"  "24"  "25"  "26"  "27"  "2
8"  "29"
```

```
##  [13] "30"  "31"  "32"  "33"  "34"  "35"  "36"  "37"  "38"  "39"  "4
0"  "41"
##  [25] "42"  "43"  "44"  "45"  "46"  "47"  "48"  "49"  "50"  "51"  "5
2"  "53"
##  [37] "54"  "55"  "56"  "57"  "58"  "59"  "60"  "61"  "62"  "63"  "6
4"  "65"
##  [49] "66"  "67"  "68"  "69"  "70"  "71"  "72"  "75"  "76"  "77"  "7
8"  "79"
##  [61] "80"  "81"  "82"  "83"  "84"  "85"  "86"  "87"  "88"  "89"  "9
0"  "91"
##  [73] "92"  "93"  "94"  "95"  "96"  "97"  "98"  "99"  "100" "101" "1
02" "103"
##  [85] "104" "105" "106" "107" "109" "110" "112" "113" "115" "116" "1
18" "119"
##  [97] "120" "121" "122" "123" "124" "126" "127" "128" "129" "130" "1
32" "133"
## [109] "134" "135" "136" "137" "138" "139" "140" "141" "142" "143" "1
44" "145"
## [121] "146" "147" "148" "149" "150" "151" "152" "153" "154" "155" "1
57" "158"
## [133] "159" "160" "161" "162" "163" "164" "165" "166" "168" "169" "1
70" "171"
## [145] "172" "173" "174" "177" "182" "183" "193" "195" "209" "214" "2
15" "237"
## [157] "241" "250" "251" "282" "285" "308" "323" "328" "335" "336" "3
37" "338"
## [169] "339" "340" "341" "342" "343" "344" "345" "346" "347" "348" "3
49" "350"
## [181] "351" "352" "353" "354" "355" "356" "357" "358" "359" "360" "3
61" "362"
## [193] "363" "364" "365" "366" "367" "368" "369" "371" "373" "377" "3
82" "395"
## [205] "396" "401" "418" "424" "427" "428" "435" "436" "437" "441" "4
43" "444"
## [217] "445" "446" "447" "448" "450" "451" "455" "461" "498" "506" "5
14" "515"
## [229] "519" "520" "522" "534" "536" "541" "546" "548"
## Genes with more than 50 % missing values:
## [1] "17"  "57"  "135" "241" "250" "335" "340" "541"
```

d. Replace the missing values by the average expression value for the particular gene. (Note: Imputing data has to be used with caution!)

```
# Replace missing values with the average expression value for the part
icular gene
for (gene in colnames(data)) {
  gene_values <- data[,gene]
  missing_indices <- is.na(gene_values)
  if (any(missing_indices)) {
    avg_value <- mean(gene_values, na.rm=TRUE)
    gene_values[missing_indices] <- avg_value
    data[,gene] <- gene_values
  }
}
head(data)
##             g1        g2     g3          g4          g5         g6
  g7
## 1  1.80200000 0.1656927 -0.182  1.31200000  3.49700000  0.4390000  0.
777
## 2  0.02547518 0.1656927  7.693 -0.06731957  0.19300000 -1.3830000 -1.
309
## 3  1.07900000 0.1656927  1.556  1.65200000 -0.01812288  0.4600000  0.
715
## 4  3.60700000 0.1656927  1.914 -0.06731957  1.40000000  1.1090000  2.
143
## 5 -1.70000000 0.1656927  0.943 -0.06731957 -0.17000000 -0.1571338 -0.
041
```

Task 8

1. Install the Tidybiology package, which includes the data 'chromosome' and 'proteins' devtools::install_github("hirscheylab/tidybiology")

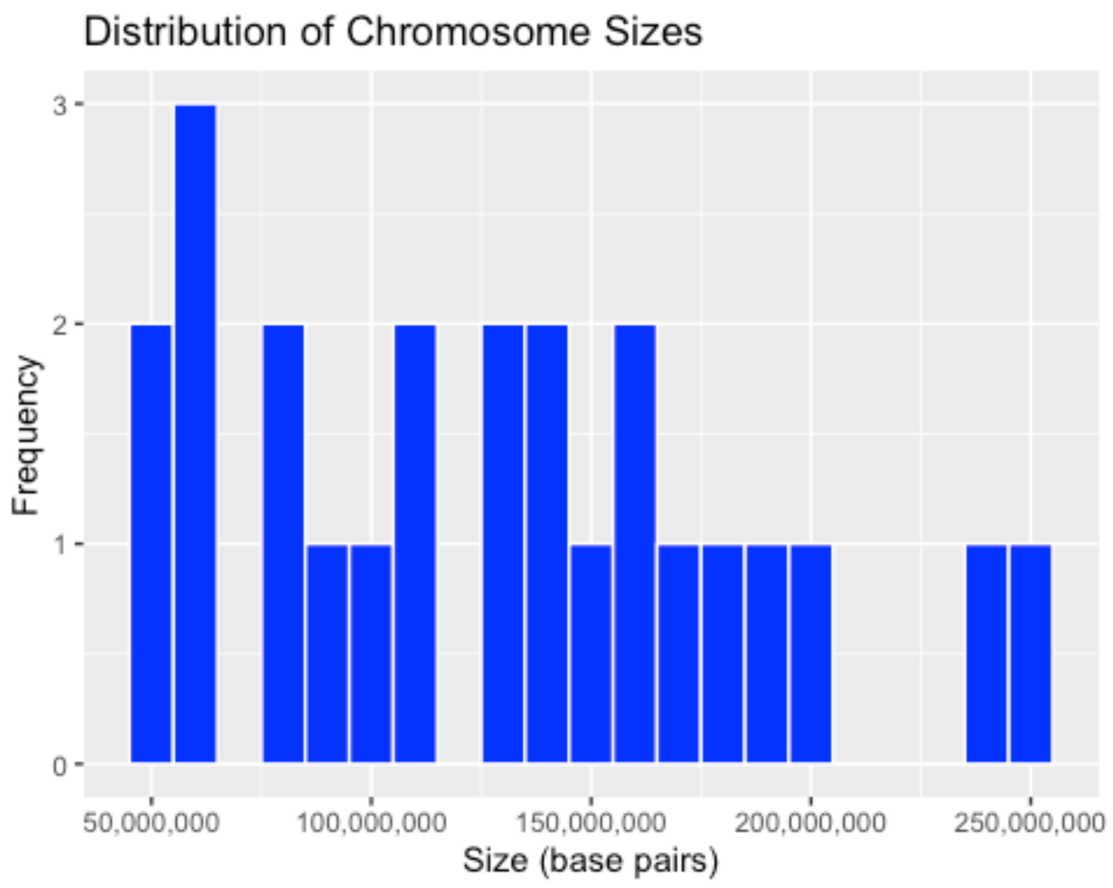
a. Extract summary statistics (mean, median and maximum) for the following variables from the 'chromosome' data: variations, protein coding genes, and miRNAs. Utilize the tidyverse functions to make this as simply as possible.

```
# Load the chromosome data
library(ggplot2)
data(chromosome)
## Warning in data(chromosome): data set 'chromosome' not found
library(tidybiology)
# Extract summary statistics for variations, protein coding genes, and
miRNAs
chromosome %>%
  summarize(
    mean_variations = mean(variations),
    median_variations = median(variations),
    max_variations = max(variations),
    mean_protein_coding_genes = mean(protein_codinggenes),
    median_protein_coding_genes = median(protein_codinggenes),
    max_protein_coding_genes = max(protein_codinggenes),
    mean_miRNAs = mean(mi_rna),
    median_miRNAs = median(mi_rna),
    max_miRNAs = max(mi_rna)
  )
## # A tibble: 1 × 9
##   mean_variati…¹ media…² max_v…³ mean_…⁴ media…⁵ max_p…⁶ mean_…⁷ med
ia…⁸ max_m…⁹
```

```
##              <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <int>    <dbl>    <
dbl>    <int>
## 1         6484572. 6172346  1.29e7     850.      836     2058     73.2
  75      134
## # … with abbreviated variable names ¹mean_variations, ²median_variat
ions,
## #   ³max_variations, ⁴mean_protein_coding_genes, ⁵median_protein_cod
ing_genes,
## #   ⁶max_protein_coding_genes, ⁷mean_miRNAs, ⁸median_miRNAs, ⁹max_mi
RNAs
```

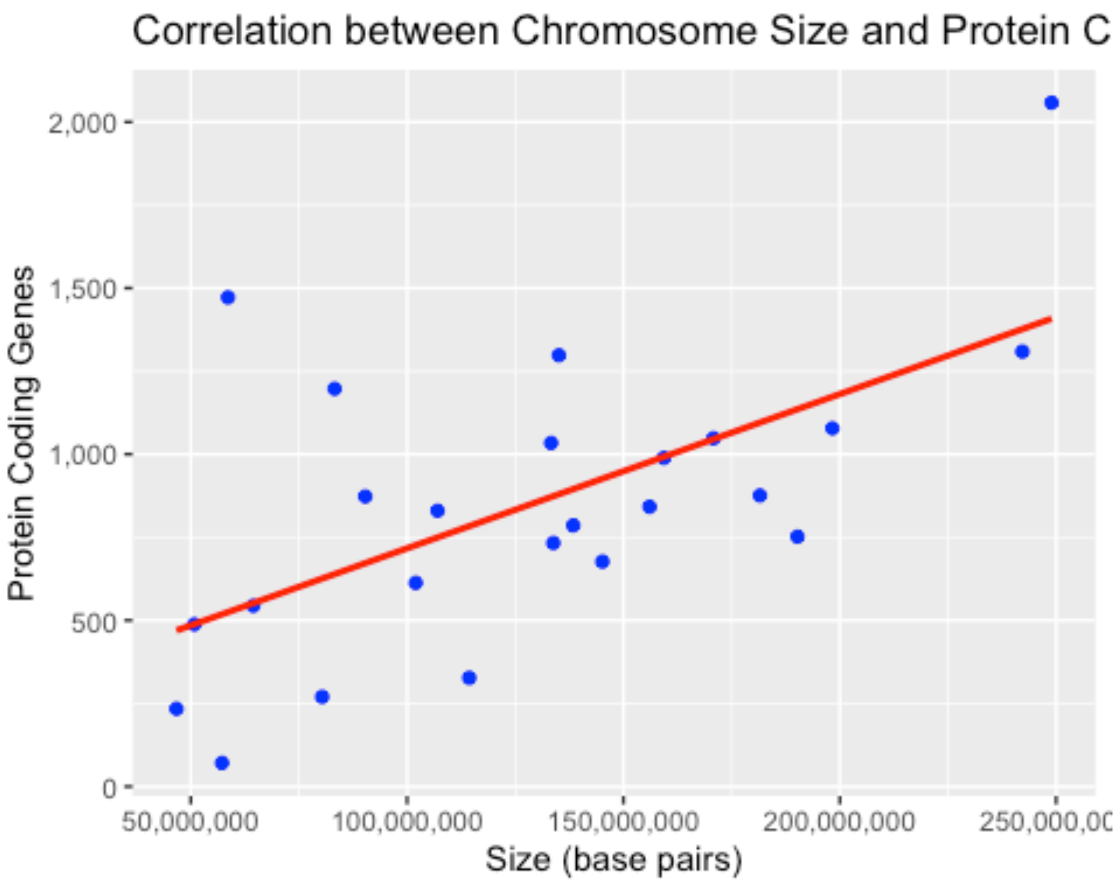
b. How does the chromosome size distribute? Plot a graph that helps to visualize this by using ggplot2 package functions.

```r
# Create a histogram of chromosome sizes
ggplot(chromosome, aes(x = basepairs)) +
  geom_histogram(binwidth = 10000000, fill = "blue", color = "white") +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(title = "Distribution of Chromosome Sizes",
       x = "Size (base pairs)", y = "Frequency")
```

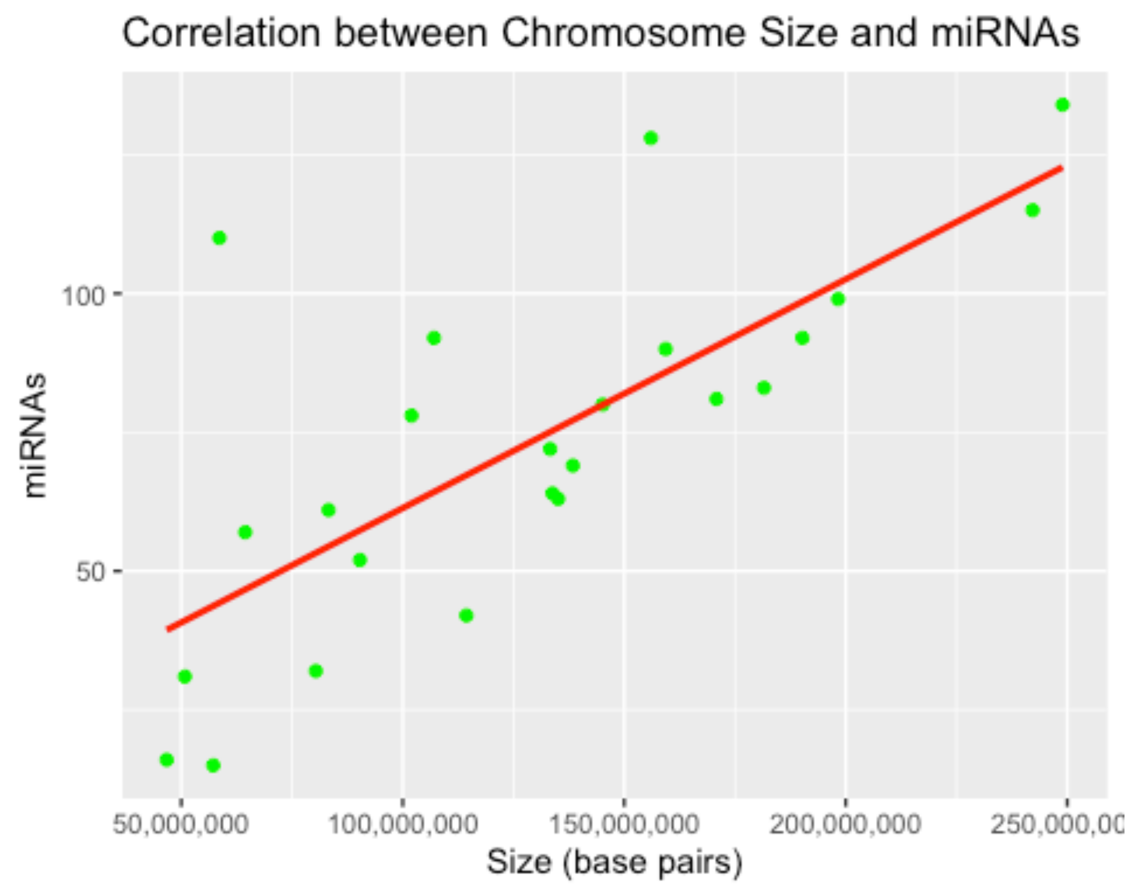


c. Does the number of protein coding genes or miRNAs correlate with the length of the chromosome? Make two separate plots to visualize these relationships.

```
# Create a scatterplot for protein coding genes
ggplot(chromosome, aes(x = basepairs, y = protein_codinggenes)) +
  geom_point(color = "blue") +
  geom_smooth(method = "lm", se = FALSE, color = "red") +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(title = "Correlation between Chromosome Size and Protein Coding
Genes",
       x = "Size (base pairs)", y = "Protein Coding Genes")
## `geom_smooth()` using formula = 'y ~ x'
```



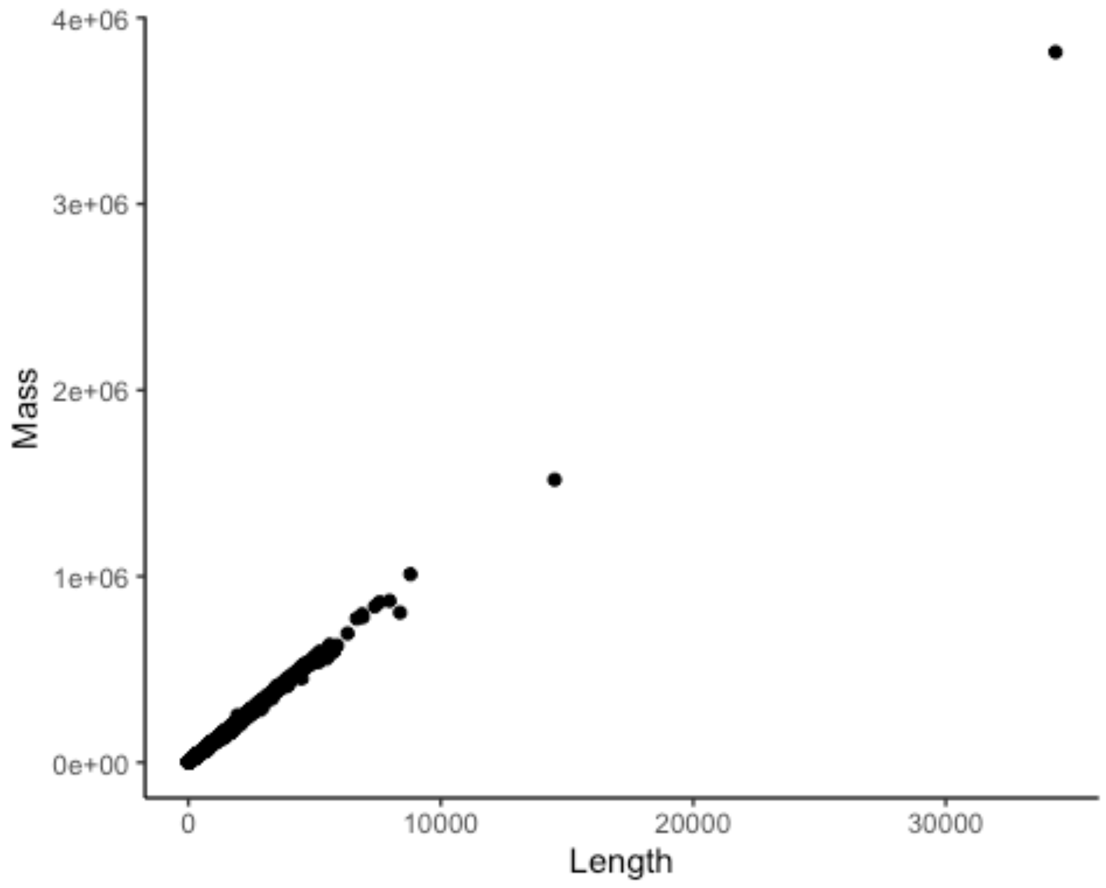
```
# Create a scatterplot for miRNAs
ggplot(chromosome, aes(x = basepairs, y = mi_rna)) +
  geom_point(color = "green") +
  geom_smooth(method = "lm", se = FALSE, color = "red") +
  scale_x_continuous(labels = scales::comma) +
  scale_y_continuous(labels = scales::comma) +
  labs(title = "Correlation between Chromosome Size and miRNAs",
       x = "Size (base pairs)", y = "miRNAs")
## `geom_smooth()` using formula = 'y ~ x'
```



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

```
# To calculate the summary statistics for the 'proteins' data variables
 length and mass, we can use the summarize() function from the dplyr pa
ckage.
proteins_summary <- proteins %>%
  summarize(mean_length = mean(length),
            median_length = median(length),
            max_length = max(length),
            mean_mass = mean(mass),
            median_mass = median(mass),
            max_mass = max(mass))

proteins_summary
## # A tibble: 1 × 6
##   mean_length median_length max_length mean_mass median_mass max_mas
s
##         <dbl>         <dbl>      <dbl>     <dbl>       <dbl>    <dbl>
## 1        557.           414      34350    62061.      46140.   381603
0
```

```r
# Use the ggplot() function to create the plot, and add geom_point() to
 add the points.
ggplot(proteins, aes(x = length, y = mass)) +
  geom_point() +
  labs(x = "Length", y = "Mass") +
  theme_classic()
```


4e+06
3e+06
2e+06
1e+06
0e+00
Mass
Length