HW1

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```
# Homework 1
# Chris Johnson
# 2/7/2025

# Load the ggplot2 library for problem 3 and tidyverse and tidyr for problem 4.
library(ggplot2)
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v readr     2.1.5
## v forcats   1.0.0     v stringr   1.5.1
## v lubridate 1.9.4     v tibble    3.2.1
## v purrr     1.0.2     v tidyr     1.3.1
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```
library(tidyr)
library(knitr)

# This assignment will need the following datasets: "Su_raw_matrix.txt",
# "diabetes_train.csv", and "titanic.csv".

# -----
# 1. Use "Su_raw_matrix.txt" for the following questions (30 points).

# First set the drive to where "Su_raw_matrix.txt" is saved.
setwd("C:/Users/Chris/OneDrive/Desktop/U of M/Winter25/CSC587/from_gdrive")

# 1a. Use read.delim function to read Su_raw_matrix.txt into a variable called su.

# Step 1: Read the "Su_raw_matrix.txt" file and turn it into a dataframe named "su".
# Use read.delim() with sep = "\t" to indicate tabs and header = TRUE
su = read.delim("Su_raw_matrix.txt", sep = '\t', header = TRUE)
# Step 2: Use View() with su to confirm the dataframe looks right.
# View(su)

# 1b. Use mean and sd functions to find mean and standard deviation of Liver_2.CEL column

# Step 1: Use the mean function in R on the "Liver_2.CEL" column of dataframe 'su'
```

```r
# to obtain the mean value of the column.
mean(su$Liver_2.CEL)
```

```
## [1] 241.8246
```

```r
# Result: Mean = 241.8246

# Step 2: Use the sd function in R on the "Liver_2.CEL" column of dataframe "su"
# to obtain the standard deviaion of the column.
sd(su$Liver_2.CEL)
```

```
## [1] 1133.352
```

```r
# Result: Standard Deviation = 1133.352

# 1c. Use colMeans and colSums functions to get the average and total values of each column.
# Step 1: Use the colMeans function to get the average of each column
colMeans(su)
```

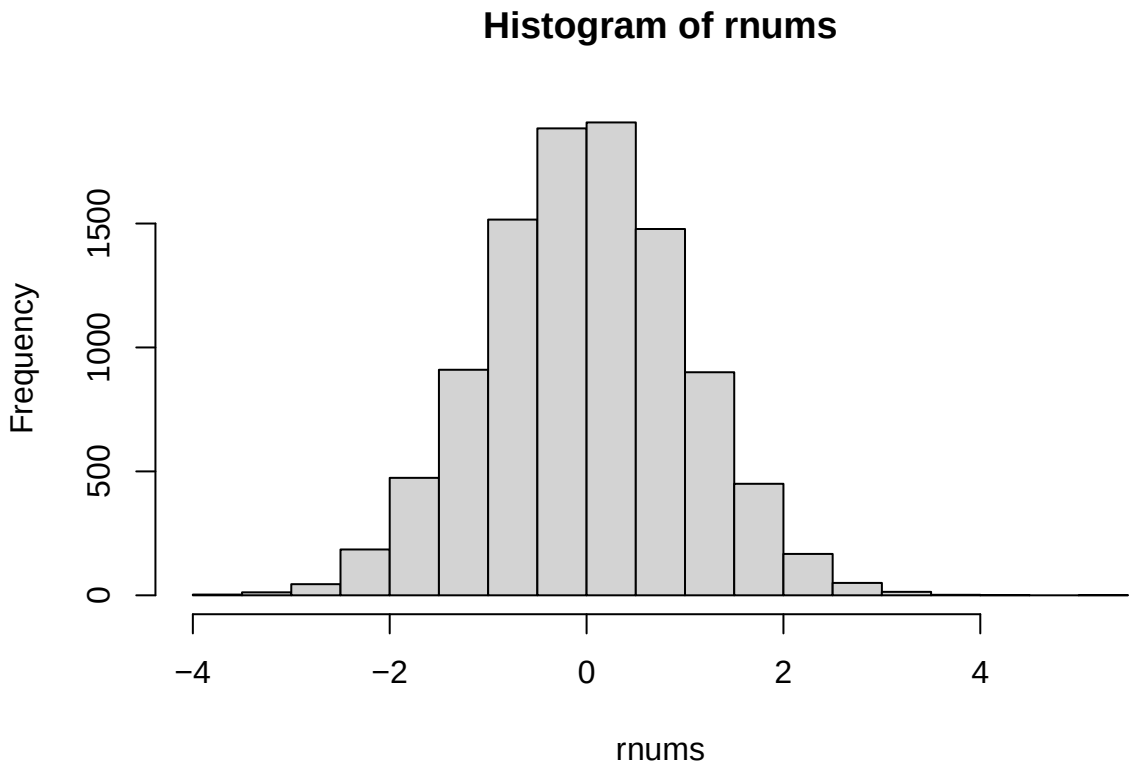
```
##       Brain_1.CEL       Brain_2.CEL Fetal_brain_1.CEL Fetal_brain_2.CEL
##          204.9763          315.0924          198.3439          267.6551
## Fetal_liver_1.CEL Fetal_liver_2.CEL       Liver_1.CEL       Liver_2.CEL
##          209.8722          399.1482          160.8558          241.8246
```

```r
# Results:  Brain_1.CEL       Brain_2.CEL Fetal_brain_1.CEL Fetal_brain_2.CEL Fetal_liver_1.CEL
#           204.9763          315.0924    198.3439          267.6551          209.8722
#           Fetal_liver_2.CEL       Liver_1.CEL       Liver_2.CEL
#           399.1482                160.8558          241.8246

# Step 2: Use the colSums function to get the sum of each column
colSums(su)
```

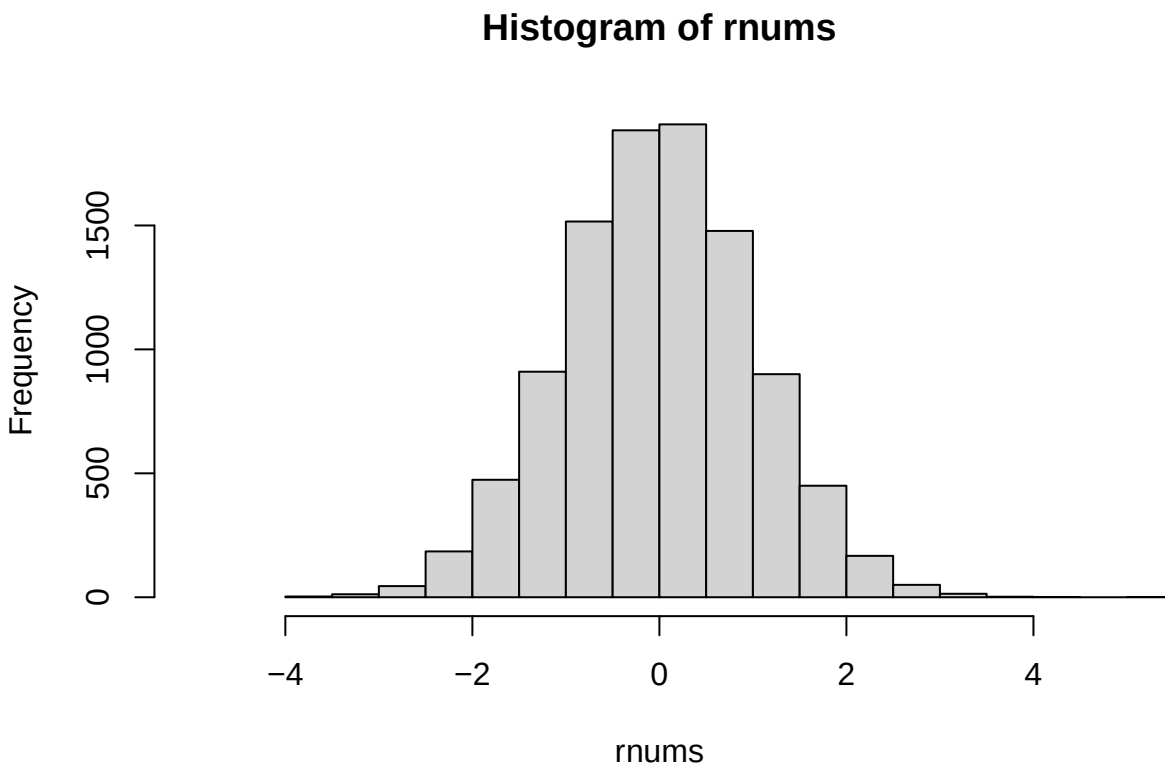
```
##       Brain_1.CEL       Brain_2.CEL Fetal_brain_1.CEL Fetal_brain_2.CEL
##           2588031           3978357           2504290           3379413
## Fetal_liver_1.CEL Fetal_liver_2.CEL       Liver_1.CEL       Liver_2.CEL
##           2649846           5039645           2030966           3053278
```

```r
# Results:  Brain_1.CEL       Brain_2.CEL Fetal_brain_1.CEL Fetal_brain_2.CEL Fetal_liver_1.CEL
#           2588031           3978357     2504290           3379413           2649846
#           Fetal_liver_2.CEL       Liver_1.CEL       Liver_2.CEL
#           5039645                 2030966           3053278

# -----
# 2.  Use rnorm(n, mean = 0, sd = 1) function in R to generate 10000 numbers for the following
# (mean, sigma) pairs and plot histogram for each, meaning you need to change the function
# parameter accordingly. Then comment on how these histograms are different from each other
# and state the reason. (20 points)

# Step 1: Generate a set of 10,000 random numbers with a mean of 0 and standard deviation of 1.
rnums = rnorm(10000, mean = 0, sd = 1)
```

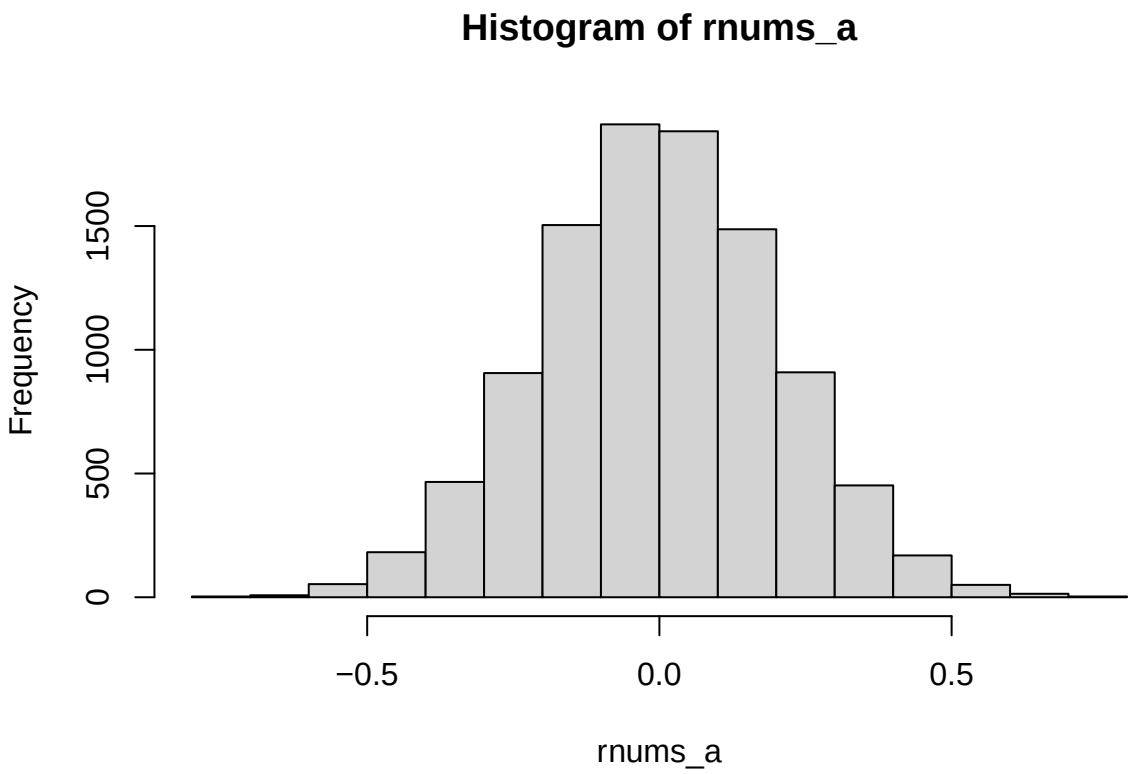
```r
# Step 2: Run it to confirm it works.
# rnums

# Step 3: Create a histogram for rnums.
hist(rnums)
```



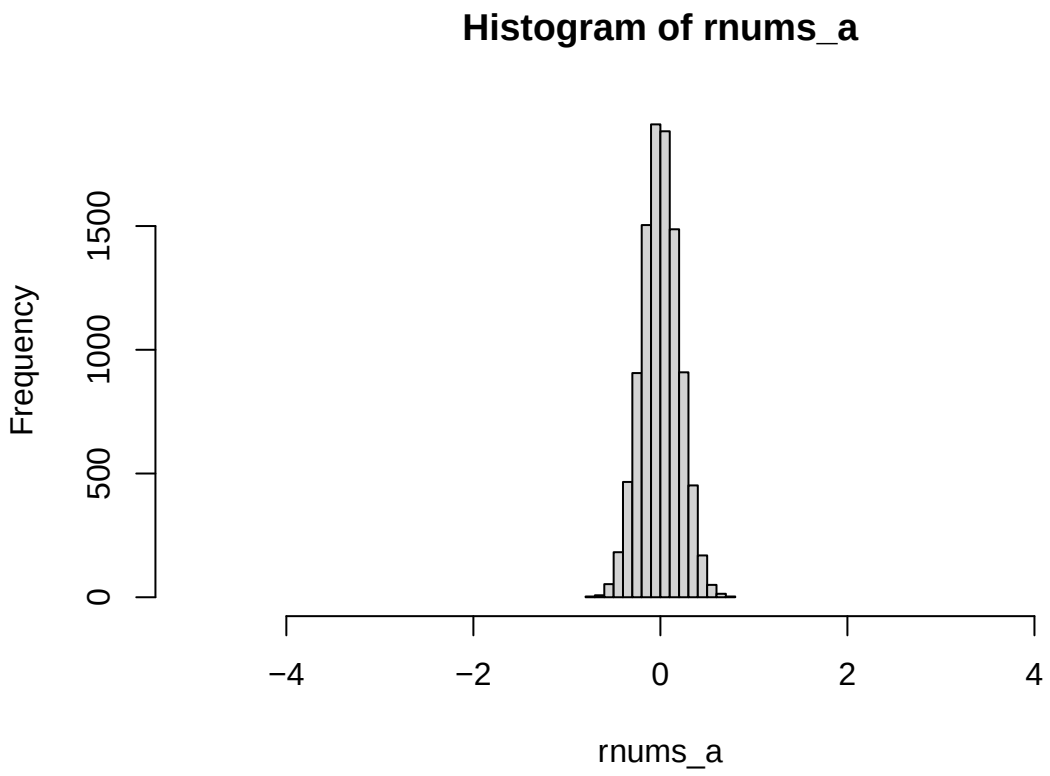

```r
# Step 4: To better see the plot differences set xlim to c(-5, 5) and plot.
hist(rnums, xlim = c(-5, 5))
```




```
# 2a. mean = 0, sigma = 0.2
# Step 1: Use rnorm function with n = 10000, mean = 0, sigma = 0.2 to create values rnums_a.
rnums_a = rnorm(10000, mean = 0, sd = 0.2)

# Step 2: Run it to confirm it works.
# rnums_a

# Step 3: Create a histogram for rnums_a using the hist function.
hist(rnums_a)
```

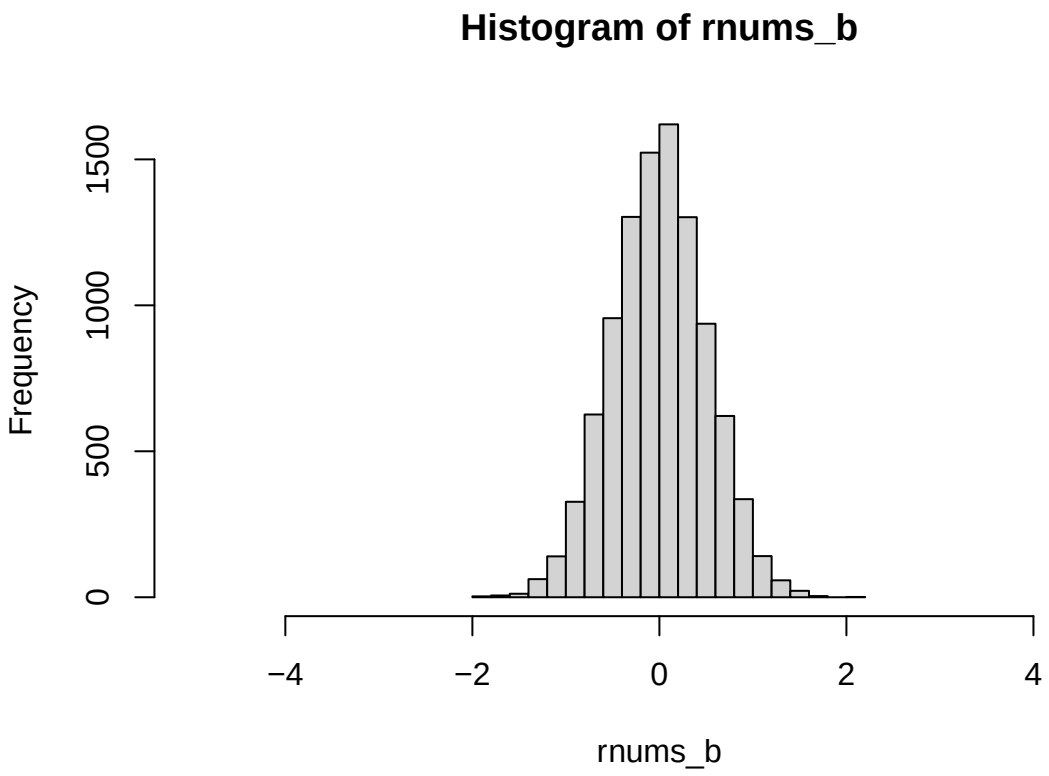



```
# Step 4: To better see the plot differences set xlim to c(-5, 5) and plot.
hist(rnums_a, xlim = c(-5, 5))
```

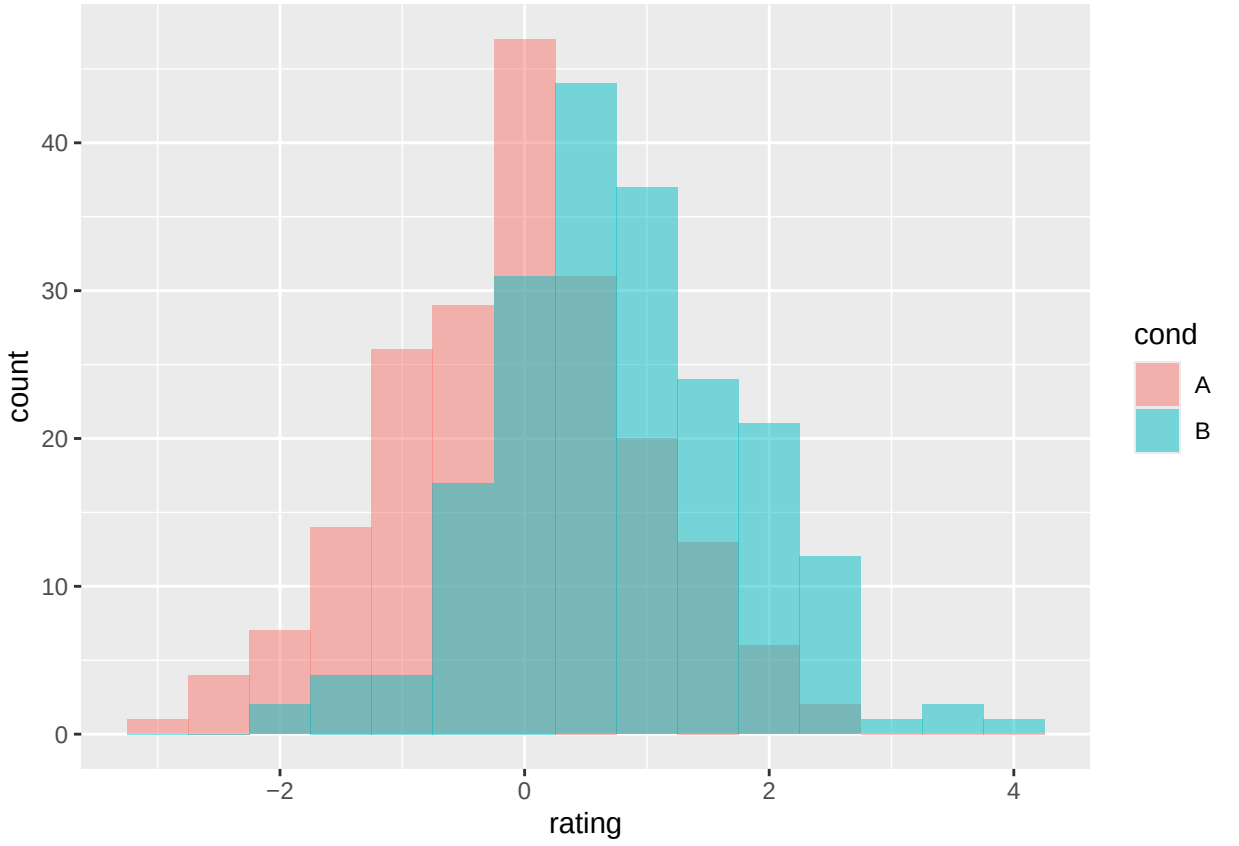



```r
# 2b. mean = 0, sigma = 0.5
# Step 1: Use rnorm function with n = 10000, mean = 0, sigma = 0.5 to create values rnums_b.
rnums_b = rnorm(10000, mean = 0, sd = 0.5)

# Step 2: Run it to confirm it works.
# rnums_b

# Step 3: Create a histogram for rnums_b using the hist function.
hist(rnums_b)
```

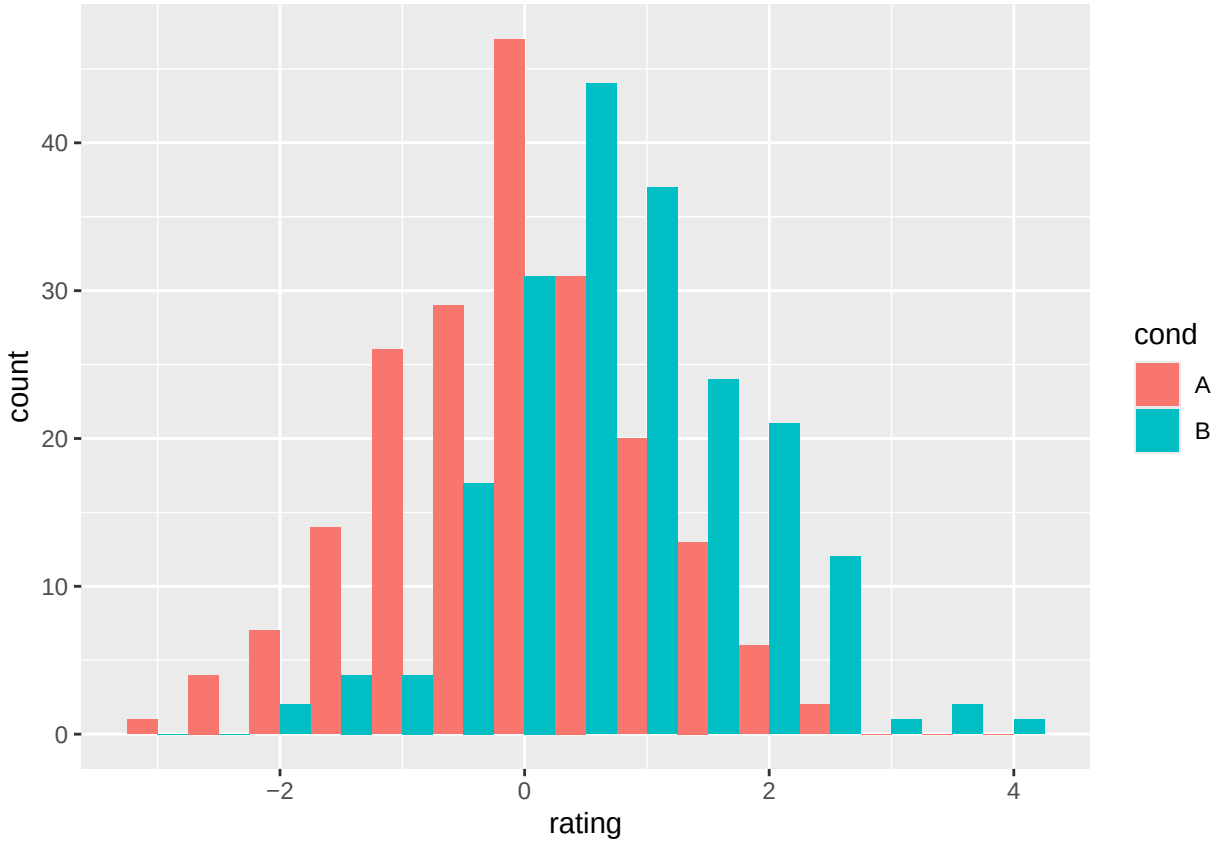

```
# Step 4: To better see the plot differences set xlim to c(-5, 5) and plot.
hist(rnums_b, xlim = c(-5, 5))
```



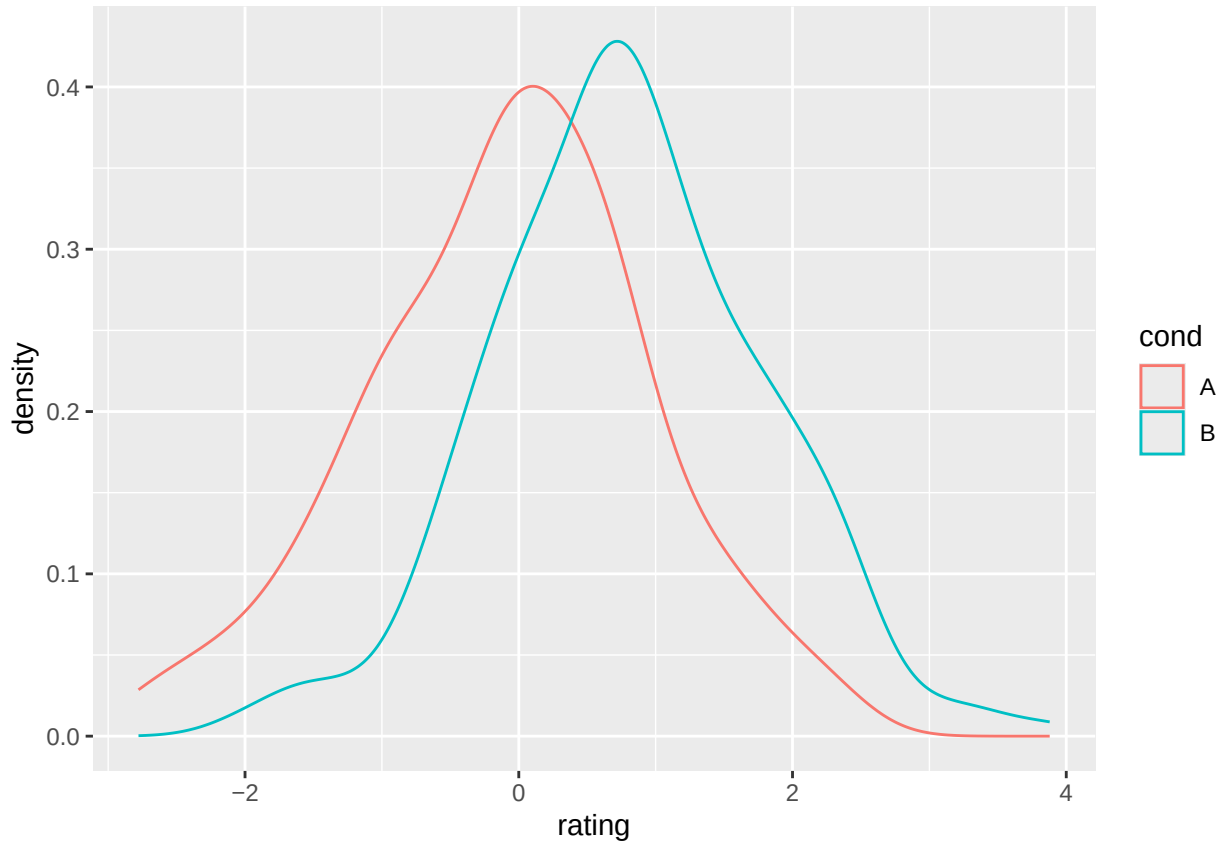

```
# -----
# 3. Perform the steps below with "dat" dataframe which is just a sample data for you
# to observe how each plot function ( 3b through 3e ) works. Notice that you need to
# have ggplot2 library installed on your system. Please refer slides how to install
# and import a library. Installation is done only once, but you need to import the
# library every time you need it by saying library(ggplot2). Then run the following
# commands for questions from 3a through 3e and observe how the plots are generated
# first. (20 points)

# 3a.
# Step 1: Create a dataframe named dat.
dat = data.frame(cond = factor(rep(c("A", "B"), each = 200)),
                 rating = c(rnorm(200), rnorm(200, mean = .8)))
# Step 2: View it to confirm it looks right.
# View(dat)

# 3b.
# Create overlaid histograms for dat.
ggplot(dat, aes(x = rating, fill = cond)) +
  geom_histogram(binwidth = .5, alpha = .5, position = "identity")
```



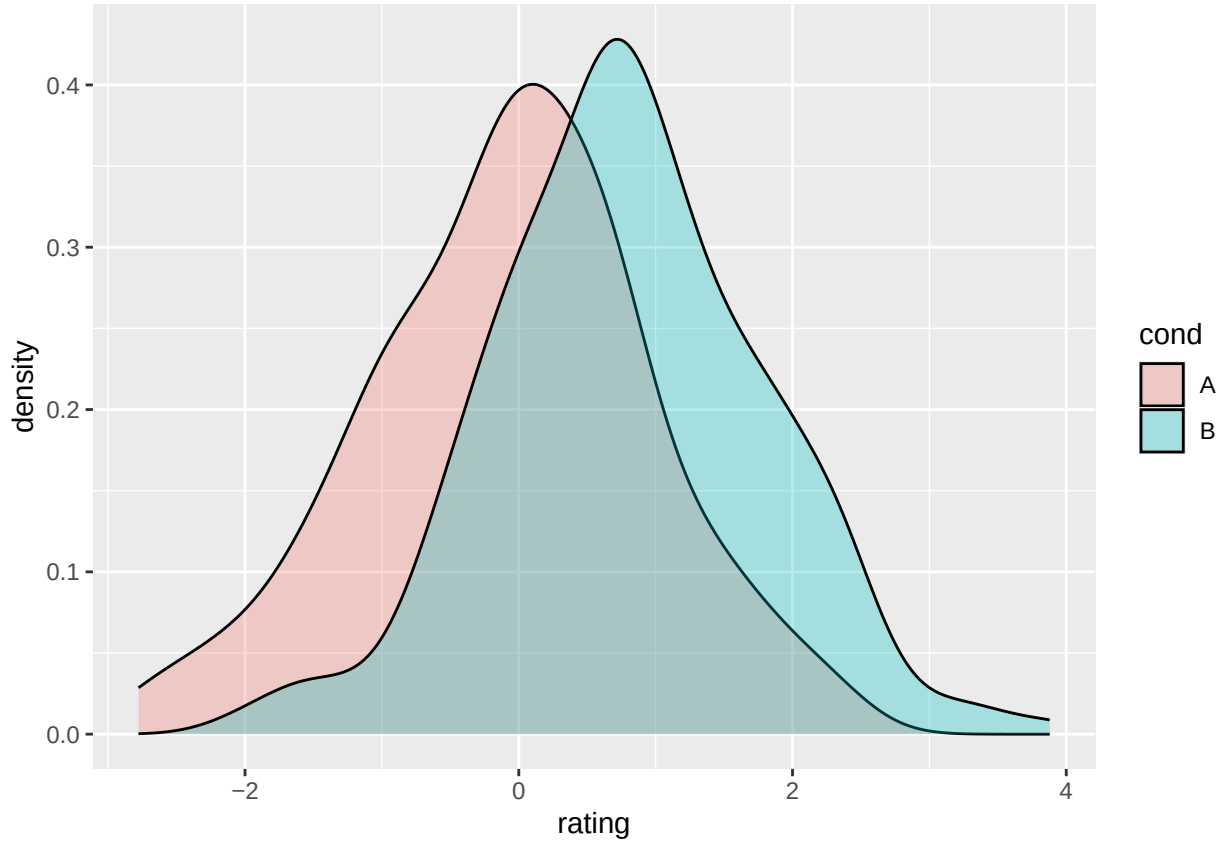

```
# 3c.
# Create an interleaved histogram for dat.
ggplot(dat, aes(x = rating, fill = cond)) + geom_histogram(binwidth = .5, position = "dodge")
```



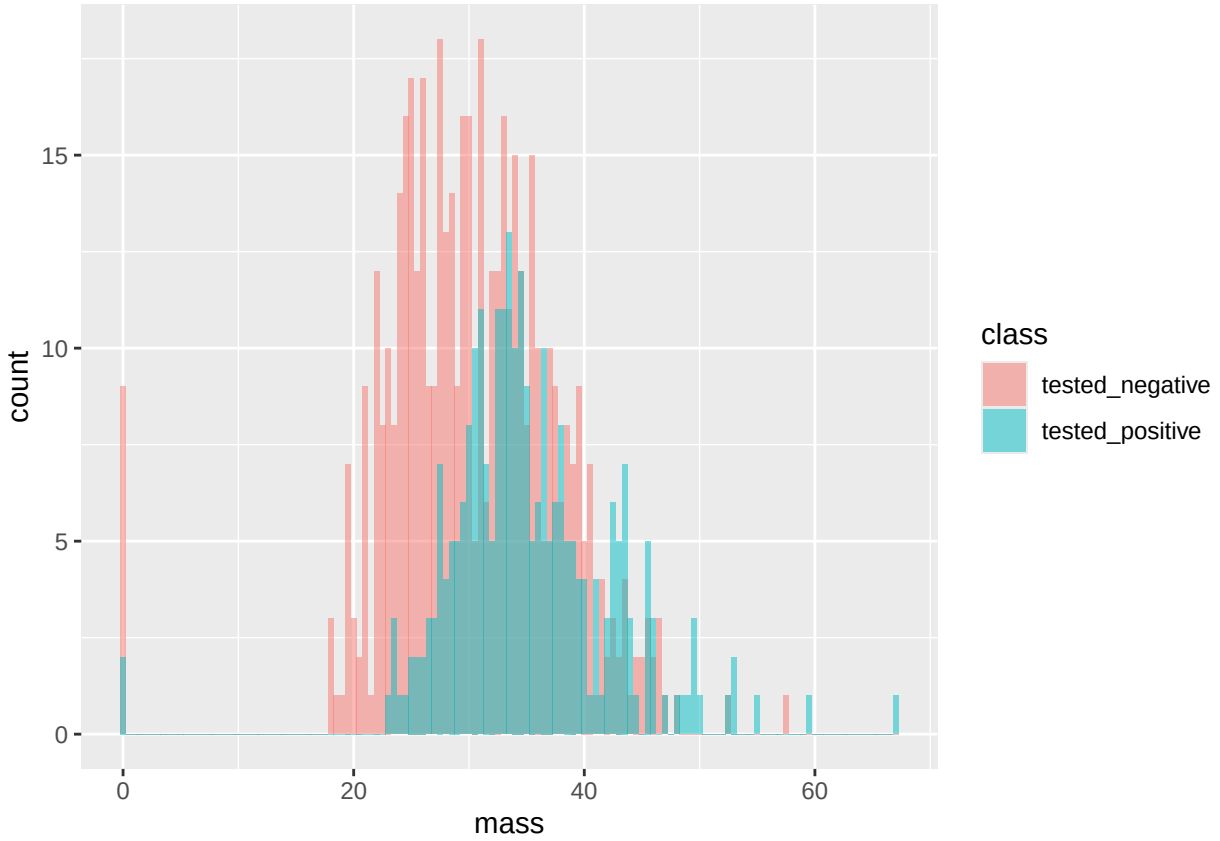

```
# 3d.
# Create density plots for dat.
ggplot(dat, aes(x = rating, colour = cond)) + geom_density()
```



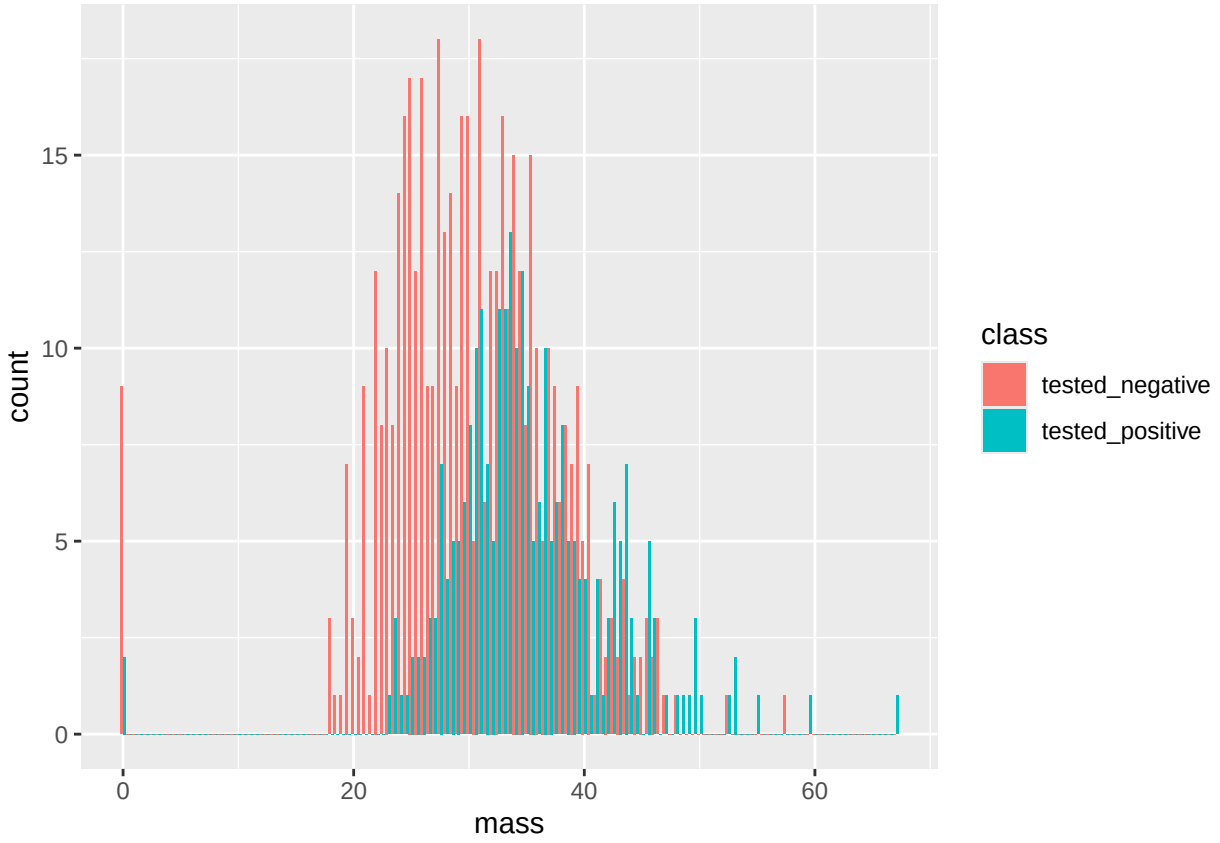

```
# 3e.
# Create density plots with semitransparent fill for dat.
ggplot(dat, aes(x = rating, fill = cond)) + geom_density(alpha = .3)
```



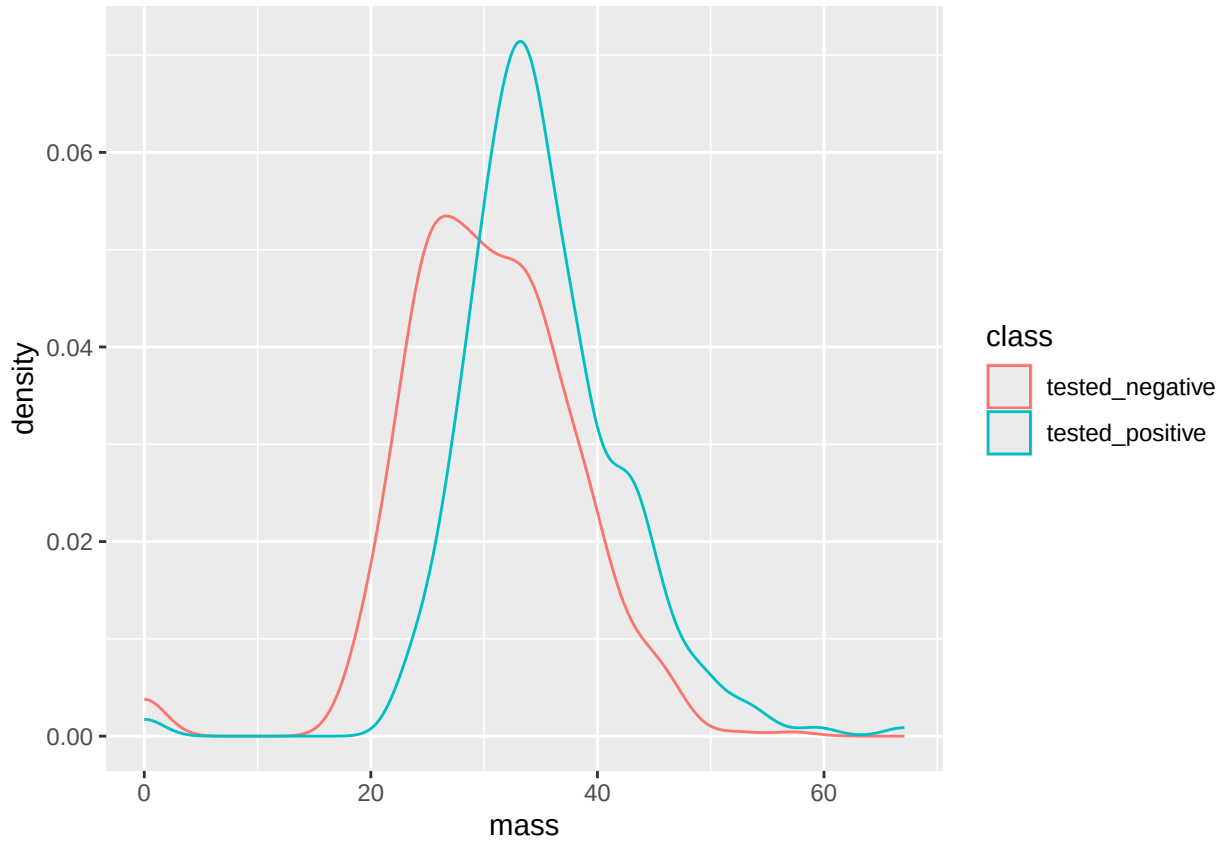

```
# 3f.
# Set the drive to where "diabetes_train.csv" is saved.
setwd("C:/Users/Chris/OneDrive/Desktop/U of M/Winter25/CSC587/from_gdrive")

# Step 1: Read the "diabetes_train.csv" file and create a dataframe named 'diabetes'
# use commas for sep and true for header.
diabetes = read.csv("diabetes_train.csv", sep = ',', header = TRUE)

# Step 2: View it to confirm it looks right.
# View(diabetes)

# 3f(b).
# Create overlaid histograms for diabetes.
ggplot(diabetes, aes(x = mass, fill = class)) +
  geom_histogram(binwidth = .5, alpha = .5, position = "identity")
```



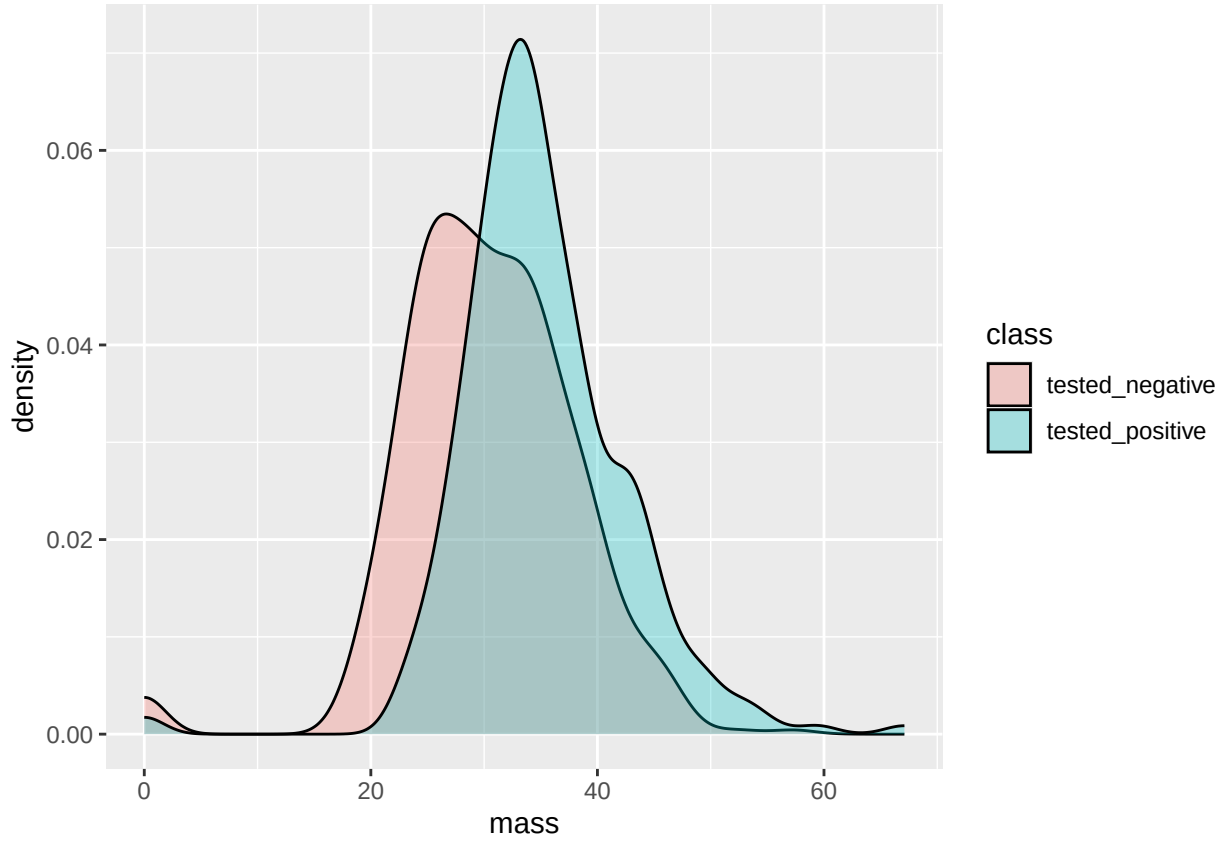

```
# 3f(c).
# Create an interleaved histogram for diabetes.
ggplot(diabetes, aes(x = mass, fill = class)) + geom_histogram(binwidth = .5, position = "dodge")
```




```
# 3f(d).
# Create density plots for diabetes.
ggplot(diabetes, aes(x = mass, colour = class)) + geom_density()
```




```
# 3f(e).
# Create density plots with semitransparent fill for diabetes.
ggplot(diabetes, aes(x = mass, fill = class)) + geom_density(alpha = .3)
```




```
# -----
# 4. Read the titanic.csv file from DATA folderto a variable named passengers and
# perform the following steps and explain the operation very briefly. Please make
# sure you have tidyverse installed on your system and you may specifically need
# to import the tidyr library. Otherwise, the chain of operations through "piping"
# won't work. (20 points):

# Set the drive to where "titanic.csv" is saved.
setwd("C:/Users/Chris/OneDrive/Desktop/U of M/Winter25/CSC587/from_gdrive")

# Step 1:  Read the "titanic.csv" file and create a dataframe named passengers.
passengers = read.csv("titanic.csv", sep = ',', header = TRUE)
# Step 2: View it to confirm it looks right.
# View(passengers)

# 4a.
# Pass the passengers values and drop the rows with NA values and then summarize
# the Min, 1st Qu., Median, Mean, 3rd Qu., and Max of each column. .
passengers %>% drop_na() %>% summary()
```

```
##        X          PassengerId       Survived         Pclass
##  Min.   :  0.0   Min.   :  1.0   Min.   :0.0000   Length:714
##  1st Qu.:221.2   1st Qu.:222.2   1st Qu.:0.0000   Class :character
##  Median :444.0   Median :445.0   Median :0.0000   Mode  :character
##  Mean   :447.6   Mean   :448.6   Mean   :0.4062
##  3rd Qu.:676.8   3rd Qu.:677.8   3rd Qu.:1.0000
```

```
##  Max.   :890.0   Max.   :891.0   Max.   :1.0000
##      Name               Sex                 Age            SibSp
##  Length:714         Length:714         Min.   : 0.42   Min.   :0.0000
##  Class :character   Class :character   1st Qu.:20.12   1st Qu.:0.0000
##  Mode  :character   Mode  :character   Median :28.00   Median :0.0000
##                                        Mean   :29.70   Mean   :0.5126
##                                        3rd Qu.:38.00   3rd Qu.:1.0000
##                                        Max.   :80.00   Max.   :5.0000
##      Parch           Ticket               Fare           Cabin
##  Min.   :0.0000   Length:714         Min.   :  0.00   Length:714
##  1st Qu.:0.0000   Class :character   1st Qu.:  8.05   Class :character
##  Median :0.0000   Mode  :character   Median : 15.74   Mode  :character
##  Mean   :0.4314                      Mean   : 34.69
##  3rd Qu.:1.0000                      3rd Qu.: 33.38
##  Max.   :6.0000                      Max.   :512.33
##    Embarked
##  Length:714
##  Class :character
##  Mode  :character
##
##
##
```

```
# 4b.
# Pass the passengers values and filter the values so it only displays the rows with
# male passengers.
head(passengers %>% filter(Sex == "male"))
```

```
##    X PassengerId Survived Pclass                            Name  Sex Age SibSp
## 1  0           1        0      3         Braund, Mr. Owen Harris male  22     1
## 2  4           5        0      3        Allen, Mr. William Henry male  35     0
## 3  5           6        0      3                Moran, Mr. James male  NA     0
## 4  6           7        0      1         McCarthy, Mr. Timothy J male  54     0
## 5  7           8        0      3 Palsson, Master. Gosta Leonard male   2     3
## 6 12          13        0      3 Saundercock, Mr. William Henry male  20     0
##   Parch    Ticket    Fare Cabin Embarked
## 1     0 A/5 21171  7.2500              S
## 2     0    373450  8.0500              S
## 3     0    330877  8.4583              Q
## 4     0     17463 51.8625   E46        S
## 5     1    349909 21.0750              S
## 6     0 A/5. 2151  8.0500              S
```

```
# 4c.
# Pass the passengers values and arrange them by Fare price in descending order.
head(passengers %>% arrange(desc(Fare)))
```

```
##     X PassengerId Survived Pclass                                Name    Sex Age
## 1 258         259        1      1                    Ward, Miss. Anna female  35
## 2 679         680        1      1 Cardeza, Mr. Thomas Drake Martinez   male  36
## 3 737         738        1      1              Lesurer, Mr. Gustave J   male  35
## 4  27          28        0      1     Fortune, Mr. Charles Alexander   male  19
## 5  88          89        1      1         Fortune, Miss. Mabel Helen female  23
```

```
## 6 341         342        1      1     Fortune, Miss. Alice Elizabeth female  24
##   SibSp Parch   Ticket     Fare       Cabin Embarked
## 1     0     0 PC 17755 512.3292                   C
## 2     0     1 PC 17755 512.3292 B51 B53 B55       C
## 3     0     0 PC 17755 512.3292        B101       C
## 4     3     2    19950 263.0000 C23 C25 C27       S
## 5     3     2    19950 263.0000 C23 C25 C27       S
## 6     3     2    19950 263.0000 C23 C25 C27       S
```

```
# 4d.
# Pass the passengers values and create a column named FamSize which is the sum
# of the columns Parch and SibSp.
head(passengers %>% mutate(FamSize = Parch + SibSp))
```

```
##   X PassengerId Survived Pclass
## 1 0           1        0      3
## 2 1           2        1      1
## 3 2           3        1      3
## 4 3           4        1      1
## 5 4           5        0      3
## 6 5           6        0      3
##                                                 Name    Sex Age SibSp Parch
## 1                             Braund, Mr. Owen Harris   male  22     1     0
## 2 Cumings, Mrs. John Bradley (Florence Briggs Thayer) female  38     1     0
## 3                              Heikkinen, Miss. Laina female  26     0     0
## 4        Futrelle, Mrs. Jacques Heath (Lily May Peel) female  35     1     0
## 5                            Allen, Mr. William Henry   male  35     0     0
## 6                                    Moran, Mr. James   male  NA     0     0
##             Ticket    Fare Cabin Embarked FamSize
## 1        A/5 21171  7.2500              S       1
## 2         PC 17599 71.2833   C85        C       1
## 3 STON/O2. 3101282  7.9250              S       0
## 4           113803 53.1000  C123        S       1
## 5           373450  8.0500              S       0
## 6           330877  8.4583              Q       0
```

```
# 4e.
# Pass the passengers values and create a column for mean Fare amount and another
# for the sum of survivors from Survived and grouped by the sex of the passengers.
head(passengers%>% group_by(Sex) %>% summarise(meanFare = mean(Fare), numSurv = sum(Survived)))
```

```
## # A tibble: 2 x 3
##   Sex    meanFare numSurv
##   <chr>     <dbl>   <int>
## 1 female     44.5     233
## 2 male       25.5     109
```

```
# -----
# 5. By using quantile(), calculate 10th, 30th, 50th, 60th percentiles of skin
# attribute of diabetes data. (10 points)

# Use the quantile function with x = diabetes$skin and c(10, 30, 50 , 60 / 100)
```

```r
# to see the 10th, 30th, 50th, and 60th percentiles.
quantile(x = diabetes$skin, probs = c(10, 30, 50, 60)/100)
```

```
## 10% 30% 50% 60%
##   0  10  23  27
```

```r
# Results: 10% 30% 50% 60%
#           0  10  23  27
```