1. Use "Su_raw_matrix.txt" for the following questions (30 points). setwd("C:\\Users\\DELL\\Desktop\\CSC587\\Week2\\datamining-main\\Rscripts") getwd()

(a) Use read.delim function to read Su_raw_matrix.txt into a variable called su. data.file <- file.path('data', 'Su_raw_matrix.txt')

su <- read.delim(data.file, header = TRUE)</pre>

(b) Use mean and sd functions to find mean and standard deviation of Liver_2.CEL column

```
mean(su[["Liver_2.CEL"]])
sd(su[["Liver_2.CEL"]])
```

(c) Use colMeans and colSums functions to get the average and total values of each column.

colMeans(su)

colSums(su)

- 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)
- (a) mean=0, sigma=0.2

```
sigma1 \leftarrow data.frame(X = rnorm(10000, mean = 0, sd = 0.2))
```

(b) mean=0, sigma=0.5

```
sigma2 < -data.frame(X = rnorm(10000, mean = 0, sd = 0.5))
```

Please save your figures as image from RStudio. (Hint: to see the difference in plots you may need to set the xlim parameter in plot function to c(-5,5)) #Start visualizing data using the ggplot2 package.

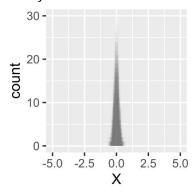
```
library('ggplot2')
```

```
sigma1ggpot = ggplot(sigma1, aes(x = X)) + geom\_histogram(binwidth = 0.001) + xlim(c(-5, 5))
```

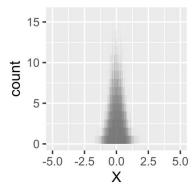
 $sigma2ggpot = ggplot(sigma2, aes(x = X)) + geom_histogram(binwidth = 0.001) + xlim(c(-5, 5))$

ggsave("histogram_sigma1.png", plot = sigma1ggpot, width = 2, height = 2, dpi = 5000)

ggsave("histogram_sigma2.png", plot = sigma2ggpot, width = 2, height = 2, dpi = 5000)



(a) mean=0, sigma=0.2

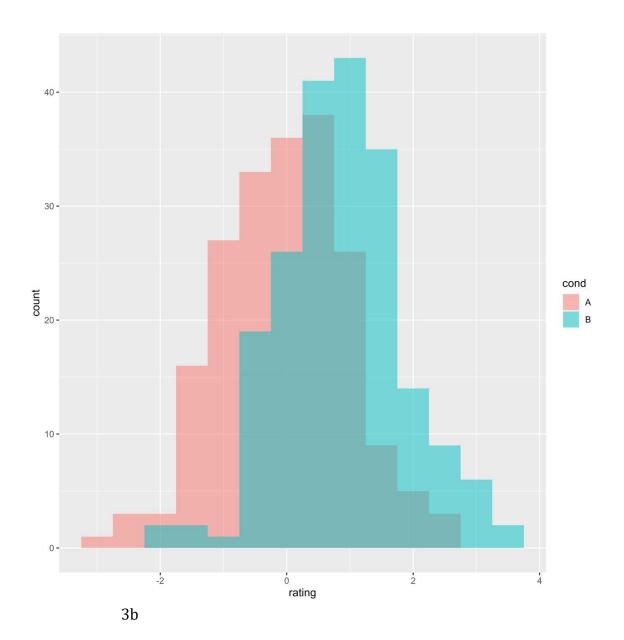


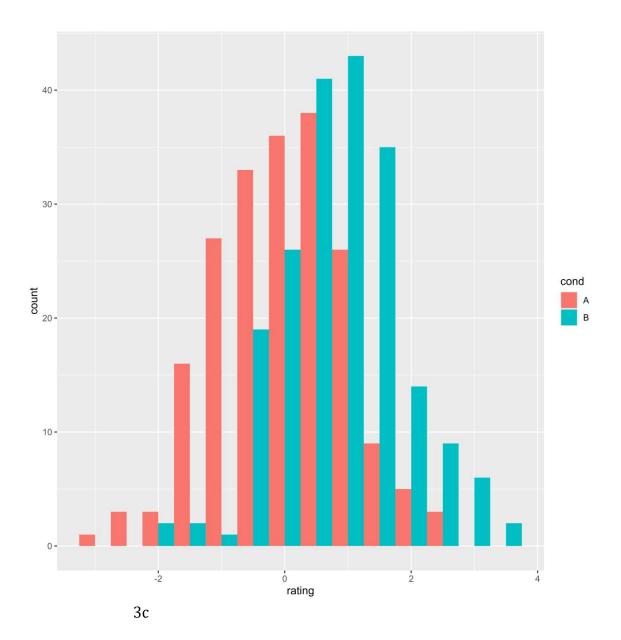
(b) mean=0, sigma=0.5

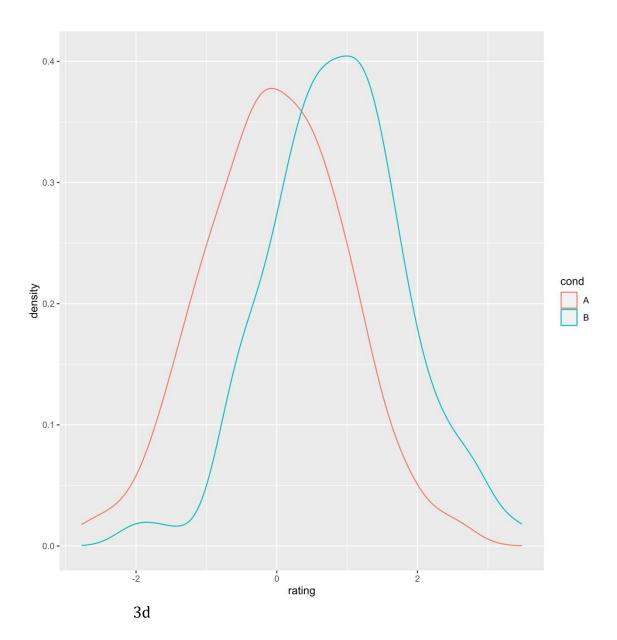
The sigma 0.5 is lower/shorter and wider. The reason for these differences is that the standard deviation (sigma) controls the spread of the distribution. A smaller sigma results in a narrower distribution, while a larger sigma leads to a wider distribution.

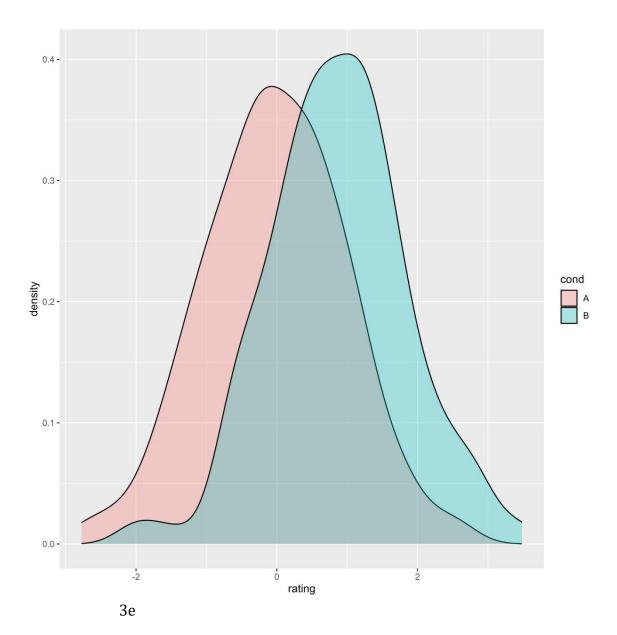
- 3. Perform the steps below with "dat" dataframe which is just a sample data for you to observe how each plot function (3b through 3e) works. Notice that you need to have ggplot2 library installed on your system. Please refer slides how to install and import a library. Installation is done only once, 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)
- (a) dat <- data.frame(cond = factor(rep(c("A","B"), each=200)), rating = c(rnorm(200), rnorm(200, mean=.8)))
- dat <- data.frame(cond = factor(rep(c("A","B"), each=200)), rating = c(rnorm(200),rnorm(200, mean=.8)))
- (b) # Overlaid histograms

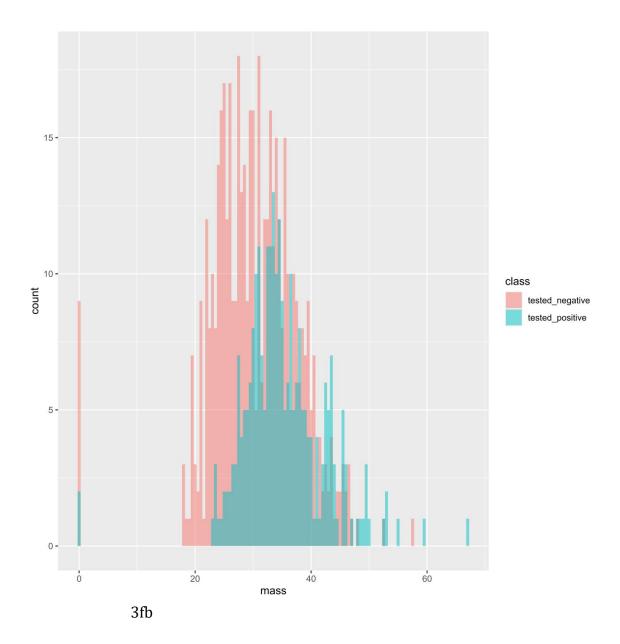
```
ggplot(dat, aes(x=rating, fill=cond)) + geom_histogram(binwidth=.5, alpha=.5,
position="identity")
t1 = ggplot(dat, aes(x=rating, fill=cond)) + geom_histogram(binwidth=.5, alpha=.5,
position="identity")
(c) # Interleaved histograms
ggplot(dat, aes(x=rating, fill=cond)) + geom histogram(binwidth=.5,
position="dodge")
t2 = ggplot(dat, aes(x=rating, fill=cond)) + geom histogram(binwidth=.5,
position="dodge")
(d) # Density plots
ggplot(dat, aes(x=rating, colour=cond)) + geom density()
t3 = ggplot(dat, aes(x=rating, colour=cond)) + geom_density()
(e) # Density plots with semitransparent fill
ggplot(dat, aes(x=rating, fill=cond)) + geom density(alpha=.3)
t4 = ggplot(dat, aes(x=rating, fill=cond)) + geom_densitv(alpha=.3)
(f) Read "diabetes_train.csv" into a variable called diabetes and apply the same
functions 3b through 3e for the mass attribute of diabetes and save the images.
(Hint: instead of cond above, use the class attribute to color your groups. When you
have fill option, your plots should show same type of chart for both groups in
different colors on the same figure. Keep in mind that diabetes and dat are both
DataFrames)
data.file <- file.path('data', 'diabetes train.csv')</pre>
diabetes <- read.csv(data.file, header = TRUE, sep = ',')
p1 = ggplot(diabetes, aes(x=mass, fill=class)) + geom histogram(binwidth=.5,
alpha=.5, position="identity")
p2 = ggplot(diabetes, aes(x=mass, fill=class)) + geom histogram(binwidth=.5,
position="dodge")
p3 = ggplot(diabetes, aes(x=mass, colour=class)) + geom_density()
p4 = ggplot(diabetes, aes(x=mass, fill=class)) + geom_density(alpha=.3)
ggsave("histogram_3fb.png", plot = p1, width = 8, height = 8, dpi = 1000)
ggsave("histogram_3fc.png", plot = p2, width = 8, height = 8, dpi = 1000)
ggsave("histogram_3fd.png", plot = p3, width = 8, height = 8, dpi = 1000)
ggsave("histogram_3fe.png", plot = p4, width = 8, height = 8, dpi = 1000)
ggsave("histogram_3b.png", plot = t1, width = 8, height = 8, dpi = 1000)
ggsave("histogram_3c.png", plot = t2, width = 8, height = 8, dpi = 1000)
ggsave("histogram_3d.png", plot = t3, width = 8, height = 8, dpi = 1000)
ggsave("histogram_3e.png", plot = t4, width = 8, height = 8, dpi = 1000)
```

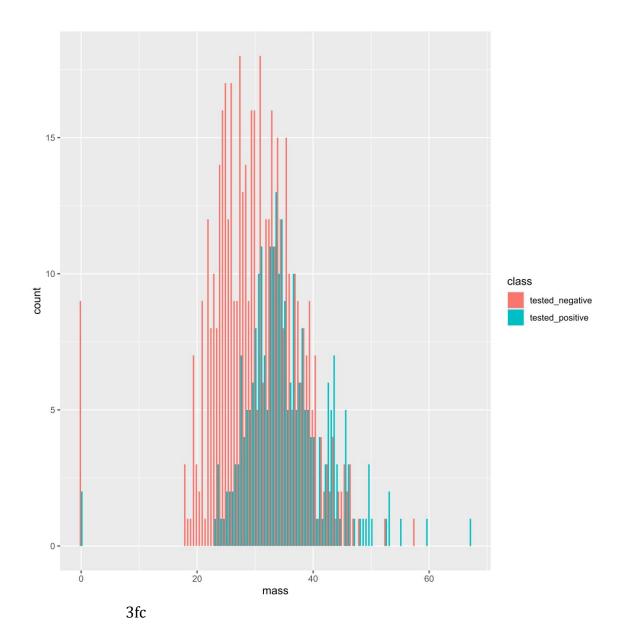


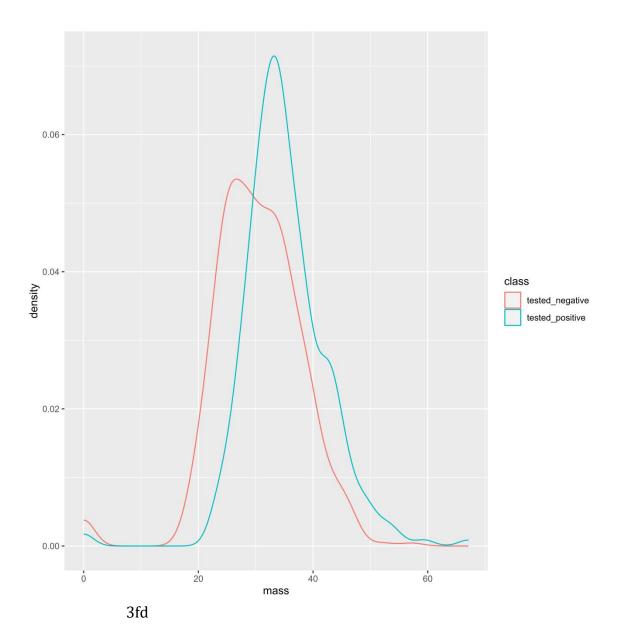


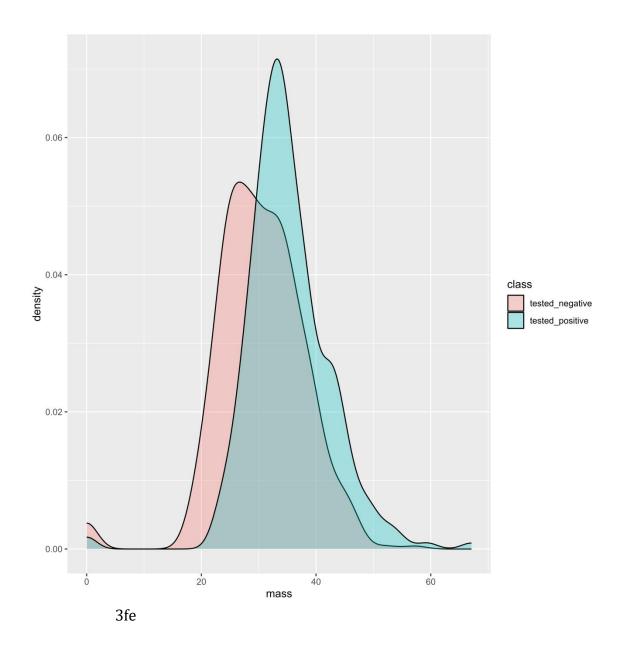






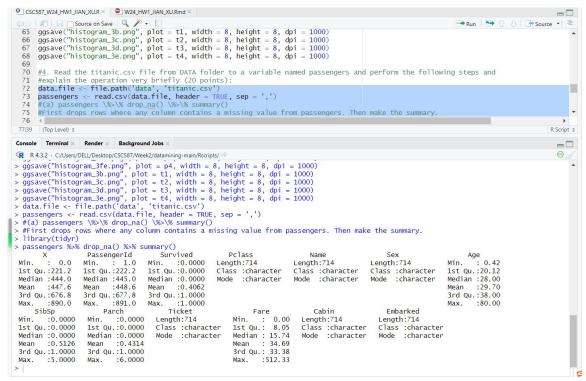






4. Read the titanic.csv file from DATA folder to a variable named passengers and perform the following steps and explain the operation very briefly (20 points):

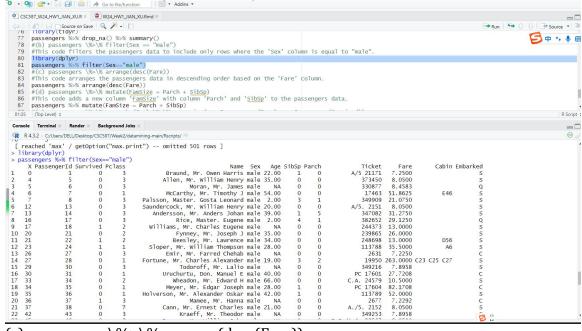
```
data.file <- file.path('data', 'titanic.csv')
passengers <- read.csv(data.file, header = TRUE, sep = ',')
library(tidyr)
library(dplyr)
(a) passengers \%>\% drop_na() \%>\% summary()
First drops rows where any column contains a missing value from passengers. Then make the summary.
passengers %>% drop_na() %>% summary()
```



(b) passengers \%>\% filter(Sex == "male")

This code filters the passengers data to include only rows where the 'Sex' column is equal to "male".

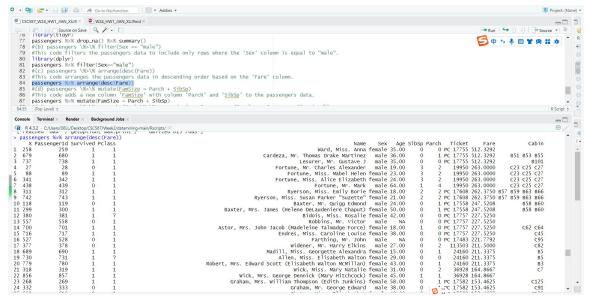
passengers %>% filter(Sex=="male")



(c) passengers \%>\% arrange(desc(Fare))

This code arranges the passengers data in descending order based on the 'Fare' column.

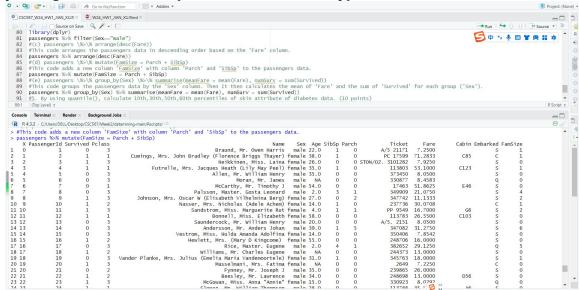
passengers %>% arrange(desc(Fare))



(d) passengers \%>\% mutate(FamSize = Parch + SibSp)

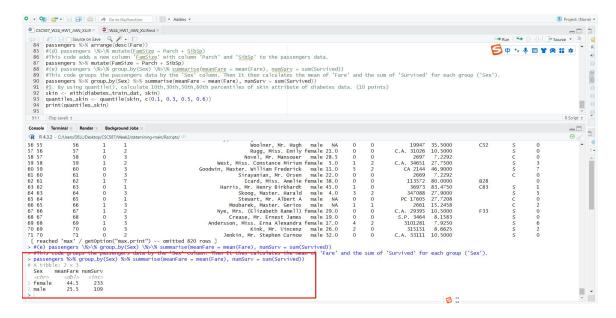
This code adds a new column 'FamSize' with the value of column 'Parch' plus the value of column 'SibSp' to the passengers data.

passengers %>% mutate(FamSize = Parch + SibSp)



(e) passengers \%>\% group_by(Sex) \%>\% summarise(meanFare = mean(Fare),
numSurv = sum(Survived))

This code groups the passengers data by the 'Sex' column. Then It then calculates the mean of 'Fare' and the sum of 'Survived' for each group ('Sex'). passengers %>% group_by(Sex) %>% summarise(meanFare = mean(Fare), numSurv = sum(Survived))



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

quantiles_skin <- quantile(skin, c(0.1, 0.3, 0.5, 0.6))

