

CSC487: Data Mining - Homework #1

Cason Konzer

1. Use `Su_raw_matrix.txt` for the following questions (30 points).

- (a) Use `read.delim` function to read `Su_raw_matrix.txt` into a variable called `su`. (Notice that `su` has become a data frame

```
su <- read.delim(file = "Su_raw_matrix.txt")
```

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

```
m_sd <- function(col)
{
  m <- mean(col)
  sd <- sd(col)
  return <- rbind(m, sd)
  colnames(return) <- ""
  print(return)
  return
}
p_1_b <- m_sd(col = su$Liver_2.CEL)
```

```
##
## m    241.8246
## sd 1133.3523
```

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

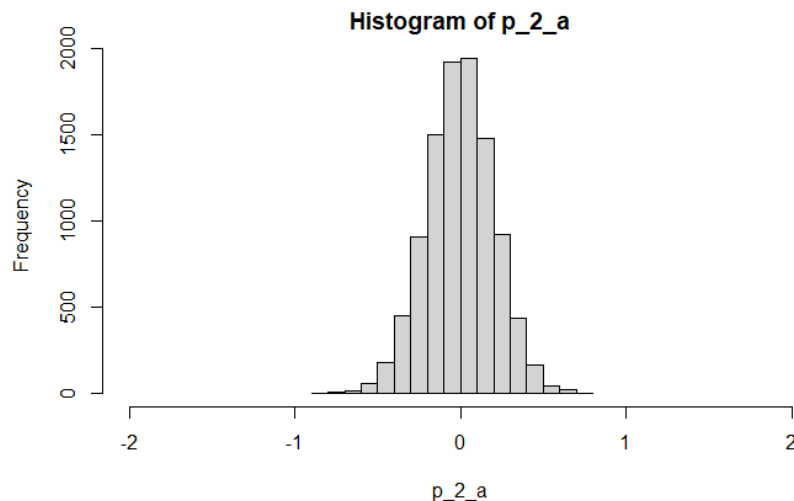
```
cm_cs <- function(df)
{
  cm <- colMeans(df)
  cs <- colSums(df)
  return <- rbind(t(cm), t(cs))
  rownames(return) <- c("m", "sd")
  print(return)
  return
}
p_1_c <- cm_cs(df = su)
```

```
##      Brain_1.CEL Brain_2.CEL Fetal_brain_1.CEL Fetal_brain_2.CEL
## m      204.9763      315.0924      198.3439      267.6551
## sd 2588031.1500 3978356.6500      2504289.5500      3379413.0500
##      Fetal_liver_1.CEL Fetal_liver_2.CEL Liver_1.CEL Liver_2.CEL
## m      209.8722      399.1482      160.8558      241.8246
## sd      2649846.0000      5039644.7500 2030965.7500 3053277.5500
```

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).

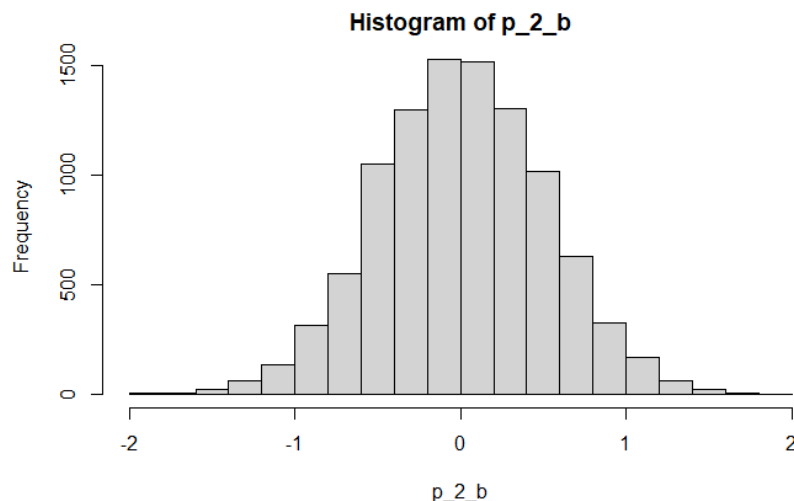
(a) mean=0, sigma=0.2

```
p_2_a <- rnorm(n = 10000, mean = 0, sd = 0.2)
hist(p_2_a, xlim = c(-2,2))
```



(b) mean=0, sigma=0.5

```
p_2_b <- rnorm(n = 10000, mean = 0, sd = 0.5)
hist(p_2_b, xlim = c(-2,2))
```



We can clearly see that `p_2_a` has a much tighter distribution than `p_2_b`. Note: this is because it has a smaller standard deviation. We also can see both samples have sample mean 0 as they were drawn from a random normal distribution with population mean 0.

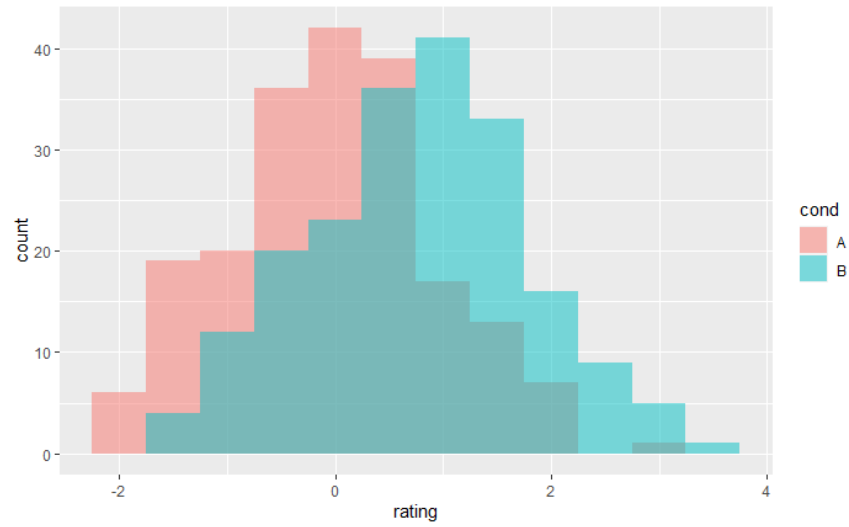
3. Perform the steps below with "dat" dataframe which is just a sample data for you to observe how each plot function (3b through 3e) works. Notice that you need to have `ggplot2` library installed on your system. Please refer slides how to install and import a library. Installation is done only once, but you need to import the library every time you need it by saying `library(ggplot2)`. Then Run the following commands and observe how the plots are generated. (40 points).

(a)

```
dat <- data.frame(cond = factor(rep(c("A", "B"), each = 200)),
                  rating = c(rnorm(200), rnorm(200, mean = 0.8)))
```

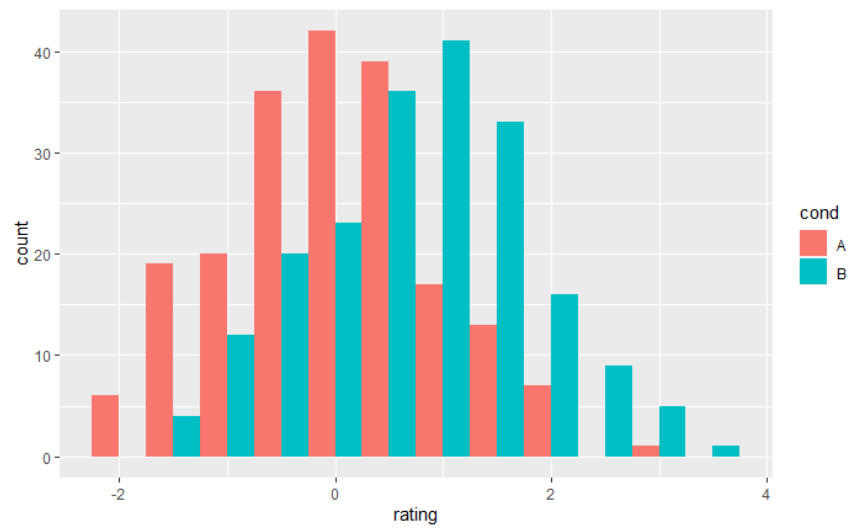
(b)

```
plot(ggplot(dat, aes(x = rating, fill = cond)) +
     geom_histogram(binwidth = 0.5, alpha = 0.5, position = "identity"))
```



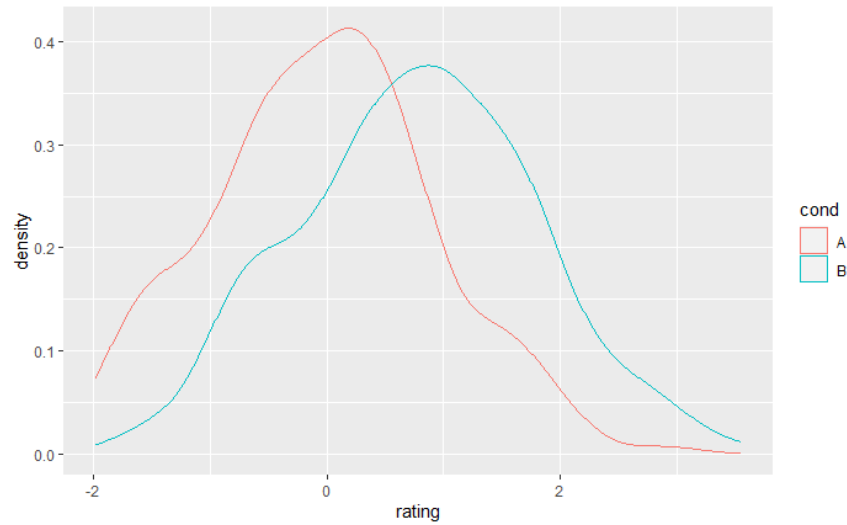
(c)

```
plot(ggplot(dat, aes(x = rating, fill = cond)) +  
  geom_histogram(binwidth = 0.5, position = "dodge"))
```



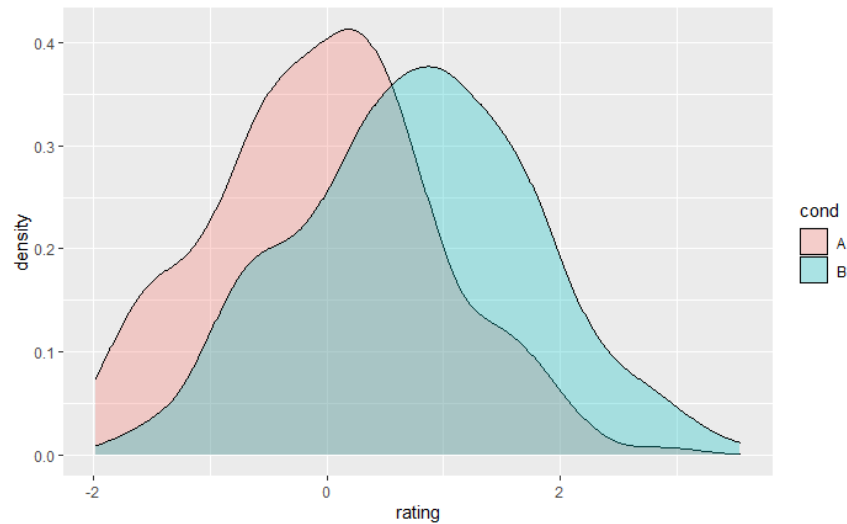
(d)

```
plot(ggplot(dat, aes(x = rating, colour = cond)) +  
  geom_density())
```



(e)

```
plot(ggplot(dat, aes(x = rating, fill = cond)) +  
  geom_density(alpha = 0.3))
```



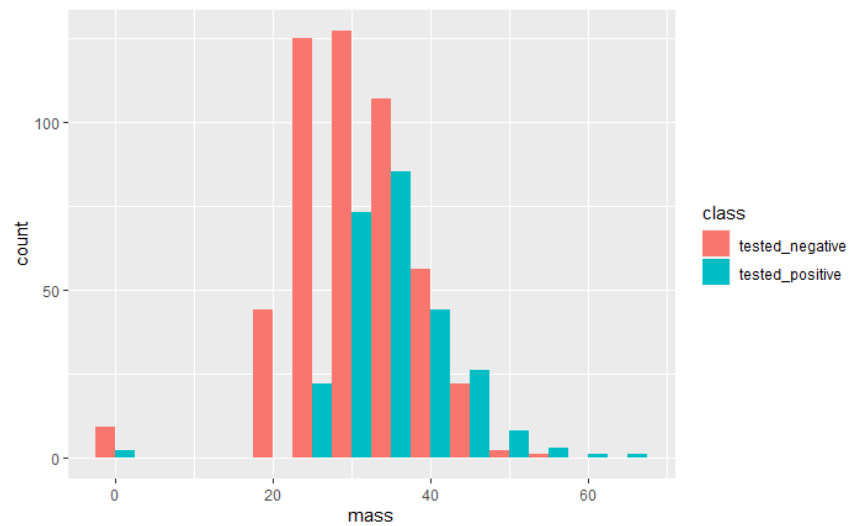
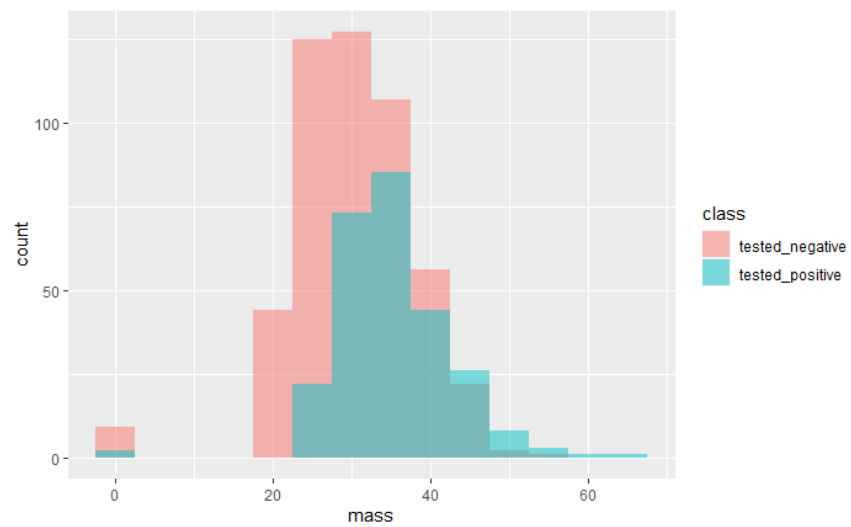
(f)

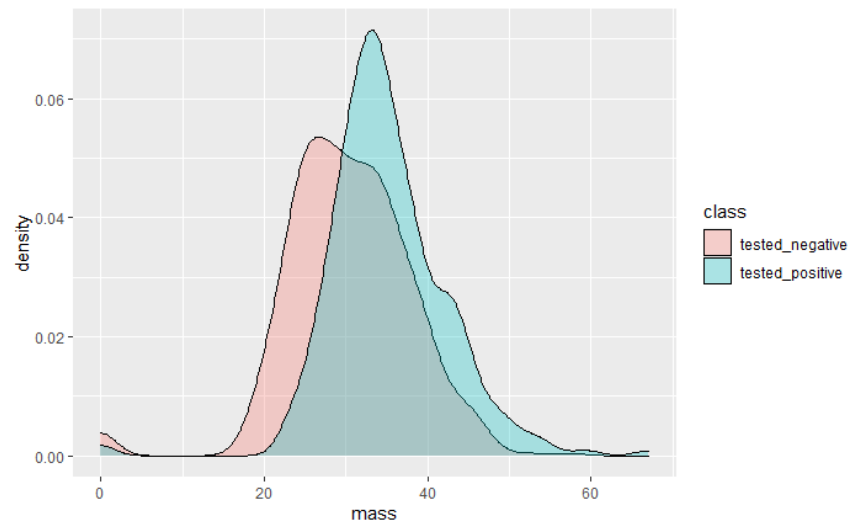
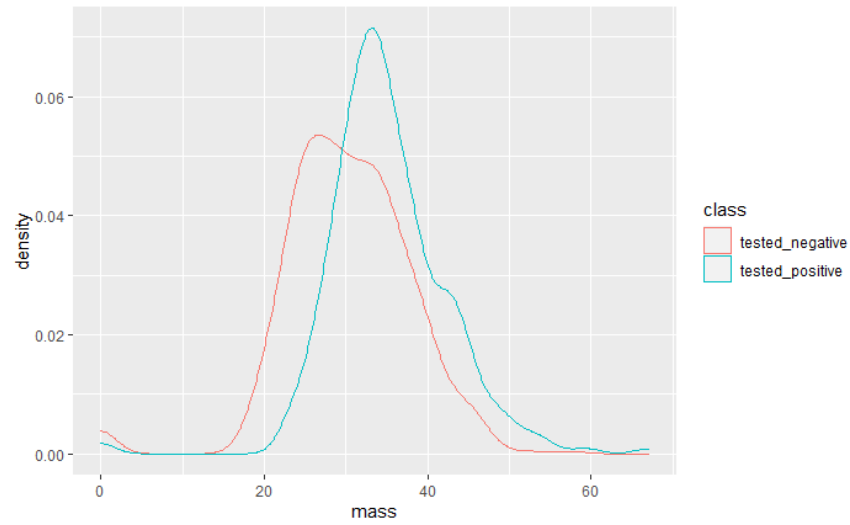
```
diabetes <- read.csv("diabetes_train.csv")  
plot(ggplot(diabetes, aes(x = mass, fill = class)) +  
  geom_histogram(binwidth = 5, alpha = 0.5, position = "identity"))
```

```
plot(ggplot(diabetes, aes(x = mass, fill = class)) +  
  geom_histogram(binwidth = 5, position = "dodge"))
```

```
plot(ggplot(diabetes, aes(x = mass, color = class)) +  
  geom_density())
```

```
plot(ggplot(diabetes, aes(x = mass, fill = class)) +  
  geom_density(alpha = 0.3))
```





4. By using `quantile()`, calculate 10th,30th,50th,60thpercentiles of skin attribute of diabetes data. (10 points).

```
print(quantile(diabetes$skin, probs = c(0.10, 0.30, 0.50, 0.60)))
```

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