

Homework1_STAT515

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Question 1: The data sets here consists of applications for admission to graduate study at the University of California, Berkeley for the Fall 1973. "Admission.csv" contains university level admission status and "Original_Admissions_Data.csv" contains admissions by each department.

1. Using GGplot create an appropriate graphic to show the university-level Admissions. (Hint: Female and male applications admitted and rejected (stacked bar plot (2 bars), admitted and rejected broken down by % male/female.) (Use Admissions.csv).

```
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.2 --
## v ggplot2 3.4.0      v purrr  1.0.1
## v tibble  3.1.8      v dplyr  1.1.0
## v tidyr   1.3.0      v stringr 1.5.0
## v readr   2.1.3      v forcats 1.0.0
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

library(scales)

##
## Attaching package: 'scales'
##
## The following object is masked from 'package:purrr':
##
##     discard
##
## The following object is masked from 'package:readr':
##
##     col_factor

source("/Users/mykola/Desktop/STAT515/third_lesson/hw.R")

admission <- read_csv("Admission.csv")

## Rows: 4 Columns: 4
## -- Column specification -----
## Delimiter: ","
## chr (2): Gender, Admit
## dbl (2): Freq, Prop
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
table(is.na(admission))
```

```
##
## FALSE
##      16
```

```
summary(admission)
```

```
##      Gender      Admit      Freq      Prop
## Length:4      Length:4      Min.   : 557      Min.   :0.3240
## Class :character Class :character 1st Qu.:1008      1st Qu.:0.4268
## Mode  :character Mode  :character Median :1218      Median :0.5000
##                                     Mean  :1122      Mean   :0.4998
##                                     3rd Qu.:1332      3rd Qu.:0.5730
##                                     Max.   :1493      Max.   :0.6750
```

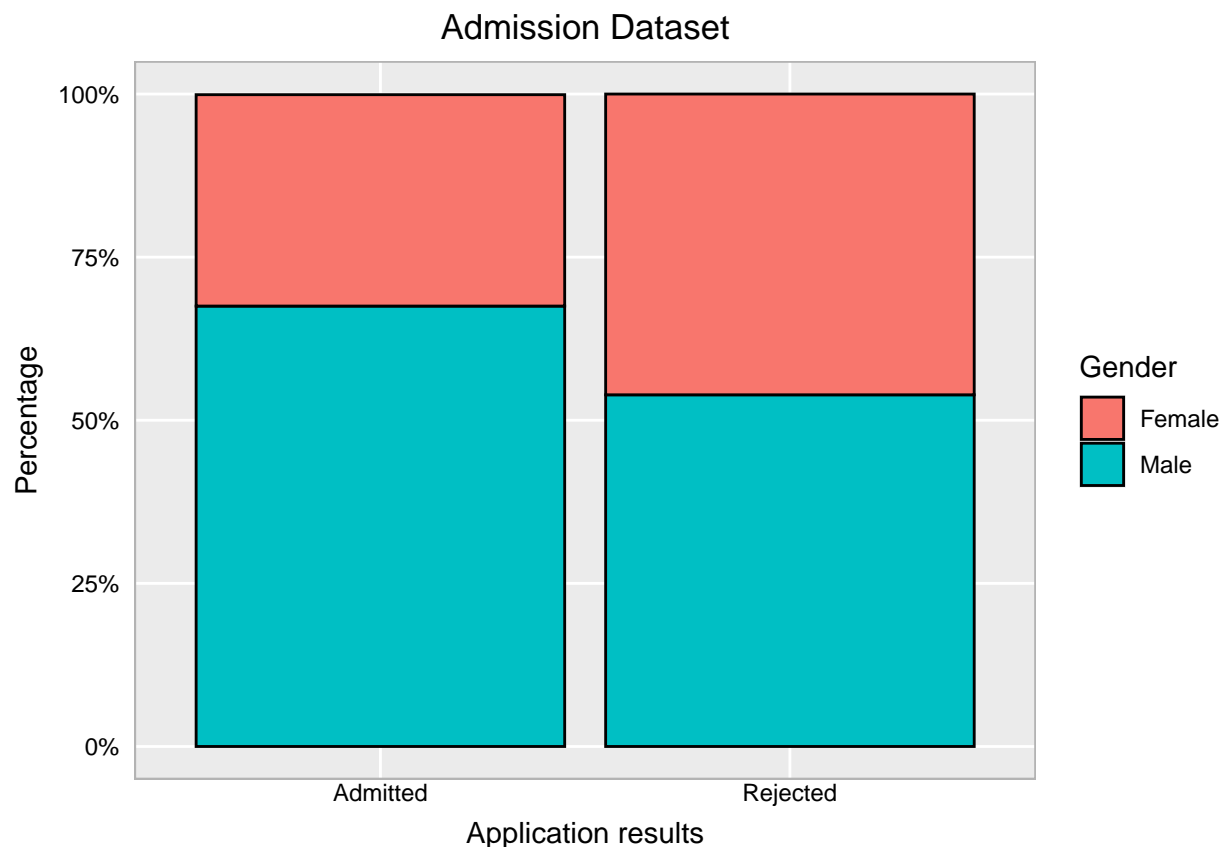
```
str(admission)
```

```
## spc_tbl_ [4 x 4] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
## $ Gender: chr [1:4] "Male" "Female" "Male" "Female"
## $ Admit : chr [1:4] "Admitted" "Admitted" "Rejected" "Rejected"
## $ Freq  : num [1:4] 1158 557 1493 1278
## $ Prop  : num [1:4] 0.675 0.324 0.539 0.461
## - attr(*, "spec")=
## .. cols(
## ..   Gender = col_character(),
## ..   Admit = col_character(),
## ..   Freq = col_double(),
## ..   Prop = col_double()
## .. )
## - attr(*, "problems")=<externalptr>
```

```
admission$Admit_gender = paste(admission$Gender, admission$Admit, sep=' ')
print(admission)
```

```
## # A tibble: 4 x 5
##   Gender Admit      Freq Prop Admit_gender
##   <chr>  <chr>    <dbl> <dbl> <chr>
## 1 Male   Admitted  1158 0.675 Male Admitted
## 2 Female Admitted   557 0.324 Female Admitted
## 3 Male   Rejected  1493 0.539 Male Rejected
## 4 Female Rejected  1278 0.461 Female Rejected
```

```
ggplot(admission) +
  geom_bar(aes(x=Admit,y=Prop,fill=Gender),stat="identity", color="black") +
  scale_y_continuous(labels = scales::percent_format(accuracy = 1)) +
  labs(x="Application results",
       y="Percentage",
       title="Admission Dataset",
       fill="Gender") + hw
```



2. Assume admissions are conducted at the department level. Create an appropriate graphic to show the department level Admissions. (use Original_Admissions_Data.csv). (Hint: Let's look at %male/female for admitted and rejected applicants by department.)

```
admission_department <- read.csv("Original_Admissions_Data.csv")
table(is.na(admission_department))
```

```
##
## FALSE
##      30
```

```
summary(admission_department)
```

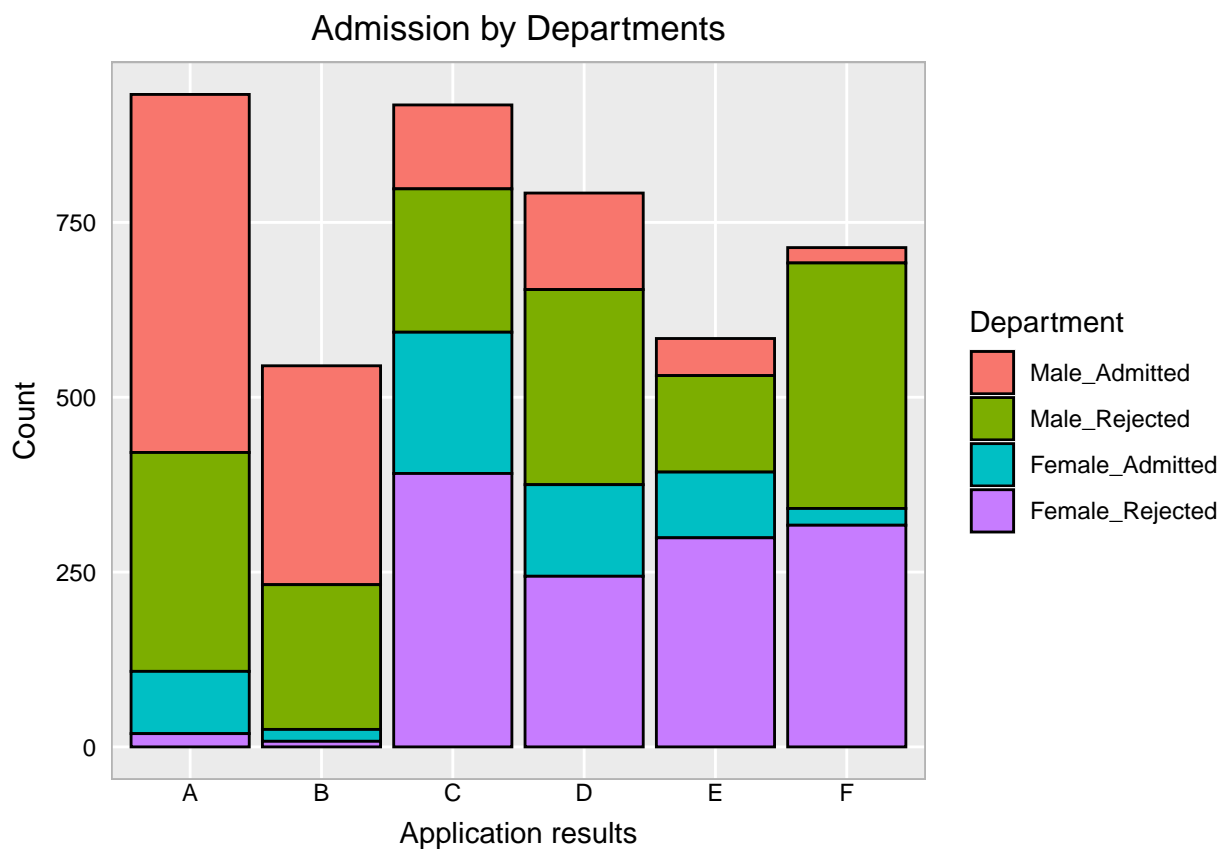
```
##      Dept      Male_Admitted  Male_Rejected  Female_Admitted
## Length:6      Min.   : 22.00    Min.   :138.0    Min.   : 17.00
## Class :character 1st Qu.: 69.75    1st Qu.:205.5    1st Qu.: 40.25
## Mode  :character Median :129.00    Median :243.0    Median : 91.50
##          Mean   :193.00    Mean   :248.8    Mean   : 92.83
##          3rd Qu.:269.25    3rd Qu.:304.5    3rd Qu.:121.75
##          Max.   :512.00    Max.   :351.0    Max.   :202.00
## Female_Rejected
## Min.   : 8.00
## 1st Qu.: 75.25
## Median :271.50
## Mean   :213.00
## 3rd Qu.:312.50
## Max.   :391.00
```

```
admission_department_sort <- gather(admission_department, key = application_result, value = amount, Male,
  factor_key = T)
```

```
head(admission_department_sort, n=10)
```

```
##   Dept application_result amount
## 1    A      Male_Admitted   512
## 2    B      Male_Admitted   313
## 3    C      Male_Admitted   120
## 4    D      Male_Admitted   138
## 5    E      Male_Admitted    53
## 6    F      Male_Admitted    22
## 7    A      Male_Rejected   313
## 8    B      Male_Rejected   207
## 9    C      Male_Rejected   205
## 10   D      Male_Rejected   279
```

```
ggplot(admission_department_sort) +
  geom_bar(aes(x=Dept,y=amount,fill=application_result),stat="identity", color="black") +
  labs(x="Application results",
    y="Count",
    title="Admission by Departments",
    fill="Department") + hw
```



3. Are admissions gender biased? What other factors could influence admission rates? Discuss.

You can see that the percentage of acceptance of different genders depends on the department. So in department A the percentage of acceptance is higher in the females, while in department C the males were

more often approved. We can also assume that the total number of applications from either gender influenced the committee's negative response to the student application (the more applications from either gender, the higher the rejection rate, but there are exceptions like Department A). And, of course, we can see that the males sent applications more often.

Question 2: The data set used, represents gene expression data for multiple samples. Use `gene expression.csv` for this question.

1. Create a scatter plot representing gene expression of "sampleB" on the X-axis and "sampleH" on the Y-axis. What kind of relationship do you observe?

```
gene <- read_csv("gene expression.csv")

## Rows: 1001 Columns: 9
## -- Column specification -----
## Delimiter: ","
## chr (1): GeneName
## dbl (8): sampleA, sampleB, sampleC, sampleD, sampleE, sampleF, sampleG, sampleH
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
table(is.na(gene))

##
## FALSE  TRUE
##  9008    1

gene = na.omit(gene)
table(is.na(gene))

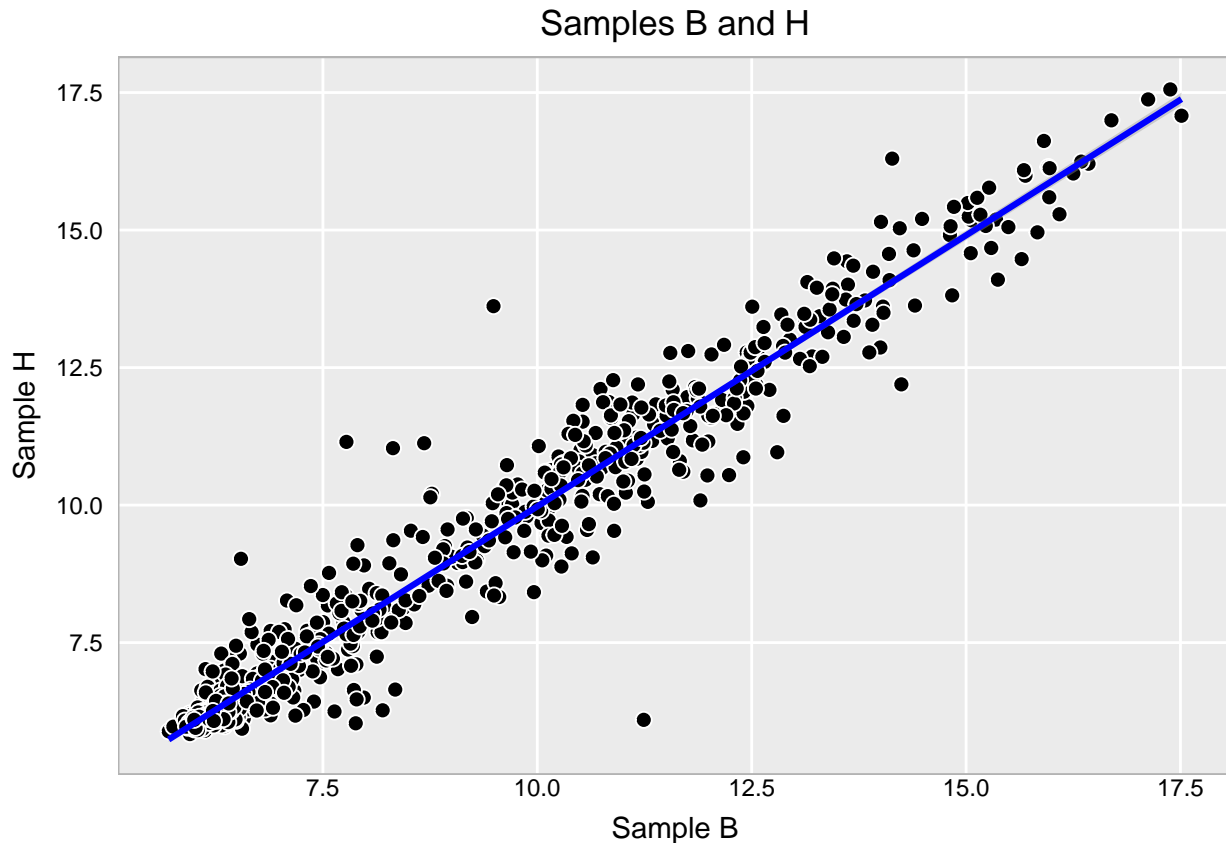
##
## FALSE
##  9000

summary(gene)

##      GeneName      sampleA      sampleB      sampleC
## Length:1000    Min.   : 5.733    Min.   : 5.702    Min.   : 5.740
## Class :character 1st Qu.: 6.198    1st Qu.: 6.223    1st Qu.: 6.216
## Mode  :character Median : 6.596    Median : 6.624    Median : 6.614
##              Mean   : 8.155    Mean   : 8.170    Mean   : 8.173
##              3rd Qu.:10.165    3rd Qu.:10.106    3rd Qu.:10.021
##              Max.   :17.453    Max.   :17.512    Max.   :17.547
##      sampleD      sampleE      sampleF      sampleG
## Min.   : 5.786    Min.   : 5.833    Min.   : 5.674    Min.   : 5.791
## 1st Qu.: 6.203    1st Qu.: 6.210    1st Qu.: 6.216    1st Qu.: 6.200
## Median : 6.635    Median : 6.672    Median : 6.613    Median : 6.601
## Mean   : 8.178    Mean   : 8.175    Mean   : 8.169    Mean   : 8.162
## 3rd Qu.:10.116    3rd Qu.:10.071    3rd Qu.: 9.991    3rd Qu.:10.148
## Max.   :17.547    Max.   :17.534    Max.   :17.538    Max.   :17.646
##      sampleH
## Min.   : 5.837
## 1st Qu.: 6.198
## Median : 6.634
## Mean   : 8.171
## 3rd Qu.:10.069
```

```
## Max.      :17.557
plt_HB <- ggplot(gene, aes(x = sampleB, y = sampleH)) +
  geom_point(shape = 21, size = 2.5, fill = "black", color = "white") +
  geom_smooth(method = lm, color = "blue", linewidth = 1.1) +
  labs(x="Sample B",
       y="Sample H",
       title="Samples B and H") + hw
plt_HB

## `geom_smooth()` using formula = 'y ~ x'
```



The graph above shows that samples B and H have pretty similar values for each gene type, with some noise exceptions.

2. Add a column to the data frame, according to the following conditions:

- Name the new column as “expre_limit”.
- If the expression of a gene is > 13 in both sampleB and sampleH, set to the value in “expre_limits” to “high”.
- If the expression of a gene is < 6 in both sampleB and sampleH, set it to “low”.
- If different, set it to “normal”.

```
gene <- gene %>%
  mutate(expre_limit = case_when((sampleB > 13 & sampleH > 13) ~ "high",
                                (sampleB < 6 & sampleH < 6) ~ "low",
                                .default = "normal")
```

```
)) #adding new column "expre_limit" with described restrictions
```

```
head(gene)
```

```
## # A tibble: 6 x 10
##   GeneName      sampleA sampleB sampleC sampleD sampleE sampleF sampleG sampleH
##   <chr>         <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>  <dbl>
## 1 A630034I12Rik  7.63   8.23   7.99   8.17   8.13   7.89   8.00   8.06
## 2 Kat6b         6.11   6.23   6.14   6.09   6.11   6.25   6.06   6.15
## 3 Hypm          7.60   7.39   7.32   7.69   7.17   7.69   7.64   6.43
## 4 A_55_P2148744 13.9    13.6   14.2   13.5   13.4   14.2   13.9   14.4
## 5 Primal        6.11   6.02   6.07   6.19   5.99   6.12   5.97   6.13
## 6 4930573021Rik  6.10   6.05   6.19   6.13   6.14   6.11   6.26   6.21
## # ... with 1 more variable: expre_limit <chr>
```

```
gene %>%
```

```
  select(sampleB, sampleH, expre_limit) %>%
```

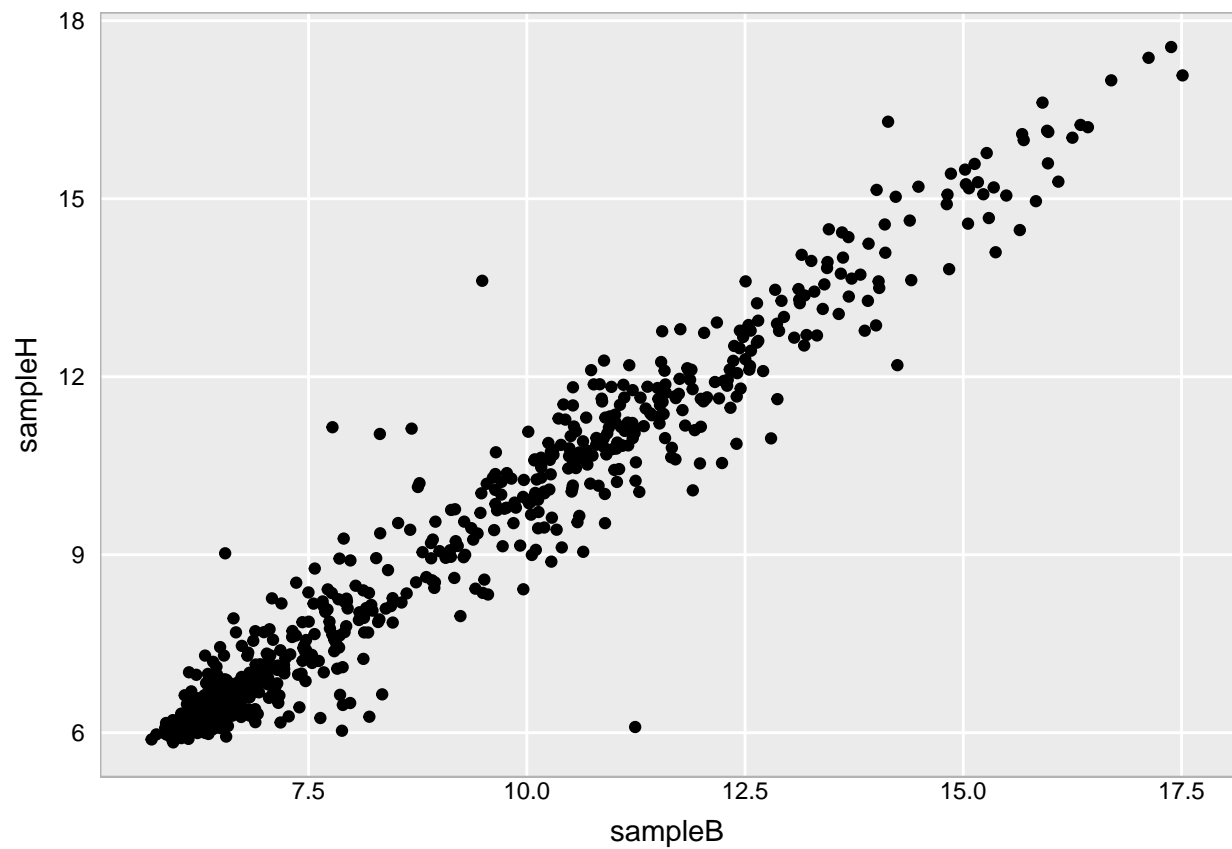
```
  head(., 10) #checking more samples to be sure everything works correctly
```

```
## # A tibble: 10 x 3
##   sampleB sampleH expre_limit
##   <dbl>   <dbl> <chr>
## 1    8.23    8.06 normal
## 2    6.23    6.15 normal
## 3    7.39    6.43 normal
## 4   13.6   14.4  high
## 5    6.02    6.13 normal
## 6    6.05    6.21 normal
## 7    7.02    6.99 normal
## 8    6.62    6.70 normal
## 9    9.41    8.43 normal
## 10   7.08    8.26 normal
```

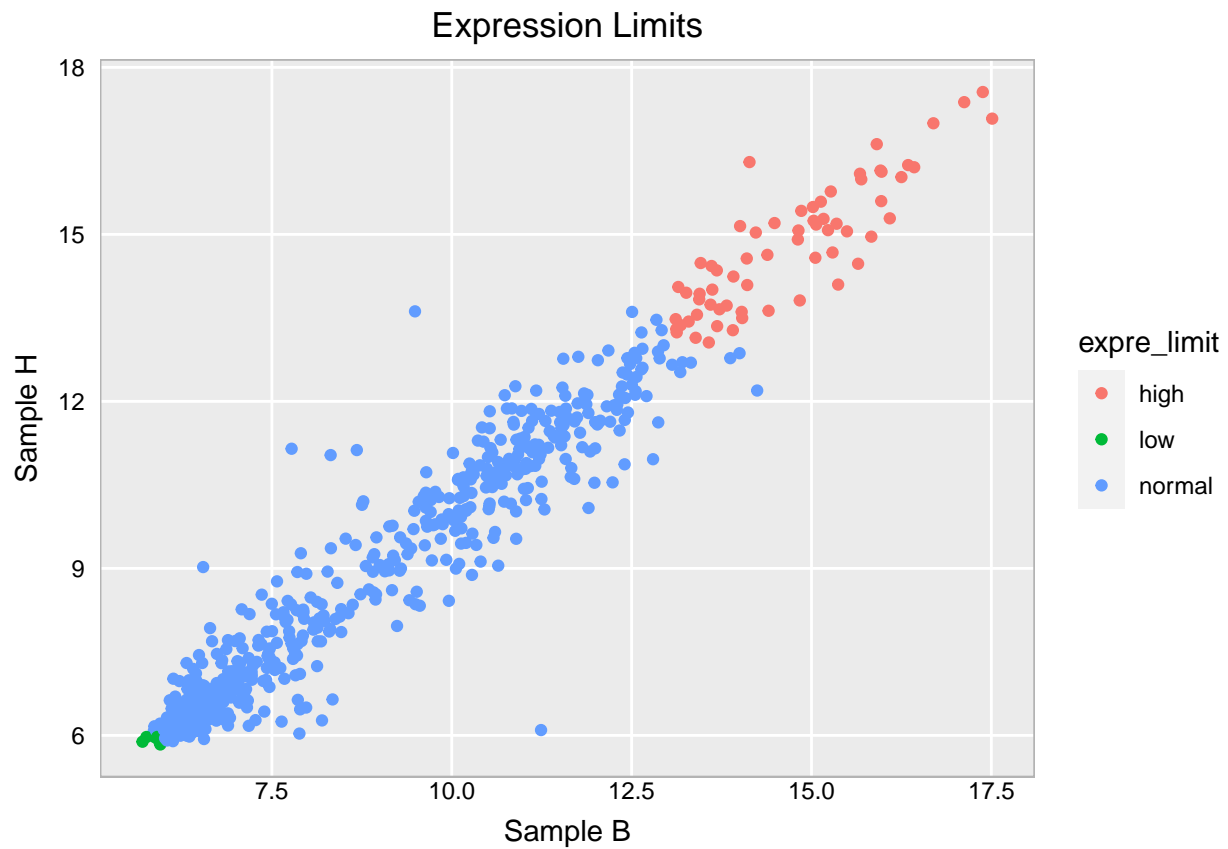
3. Color the points of the scatter plot according to the newly created column “expre_limits”. Save that plot in the object “plot1”. ### AND

4. Rename the legend title as “Expression Limits”.

```
gene2 <- ggplot(gene, aes( x=sampleB, y=sampleH))
gene2 + geom_point() + hw
```

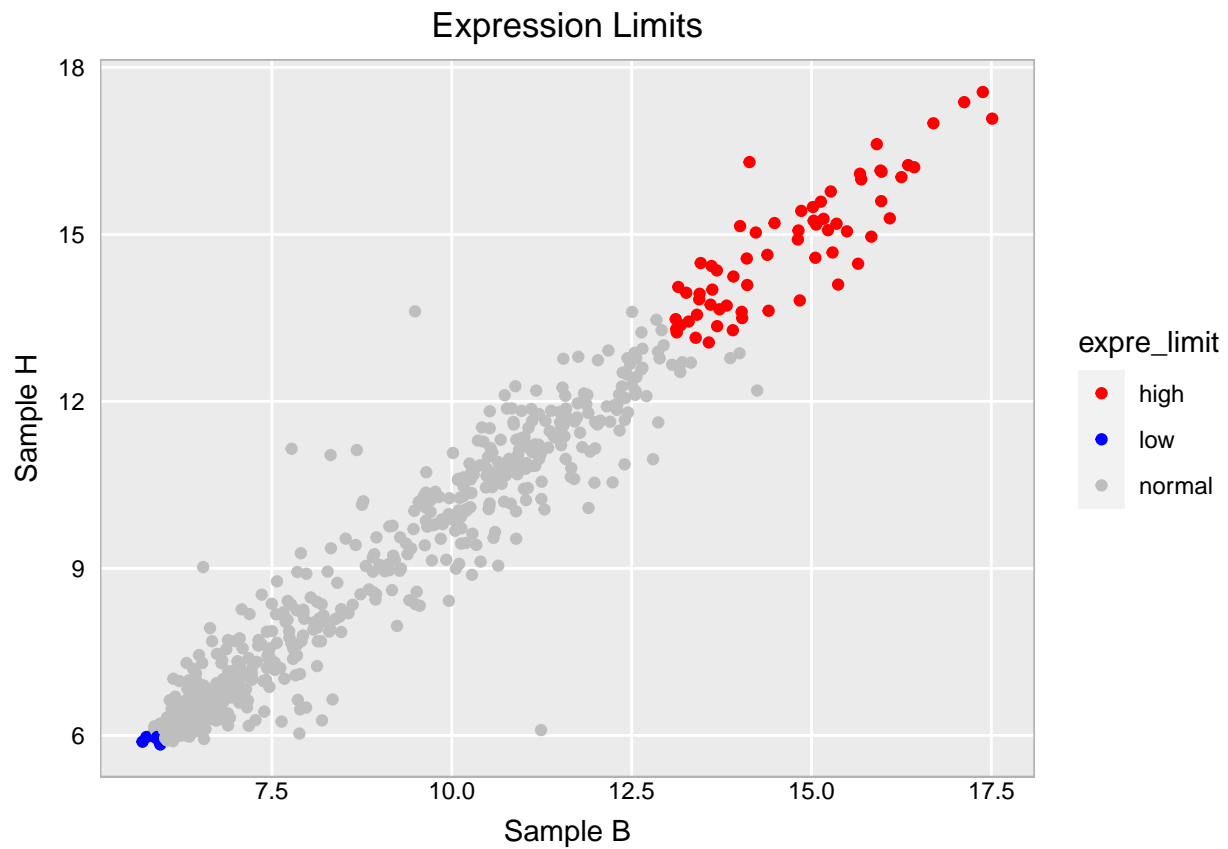


```
plot1 <- gene2 + geom_point( aes( color = expre_limit) ) +  
  labs(title = "Expression Limits",  
        x="Sample B",  
        y="Sample H") +hw  
plot1
```

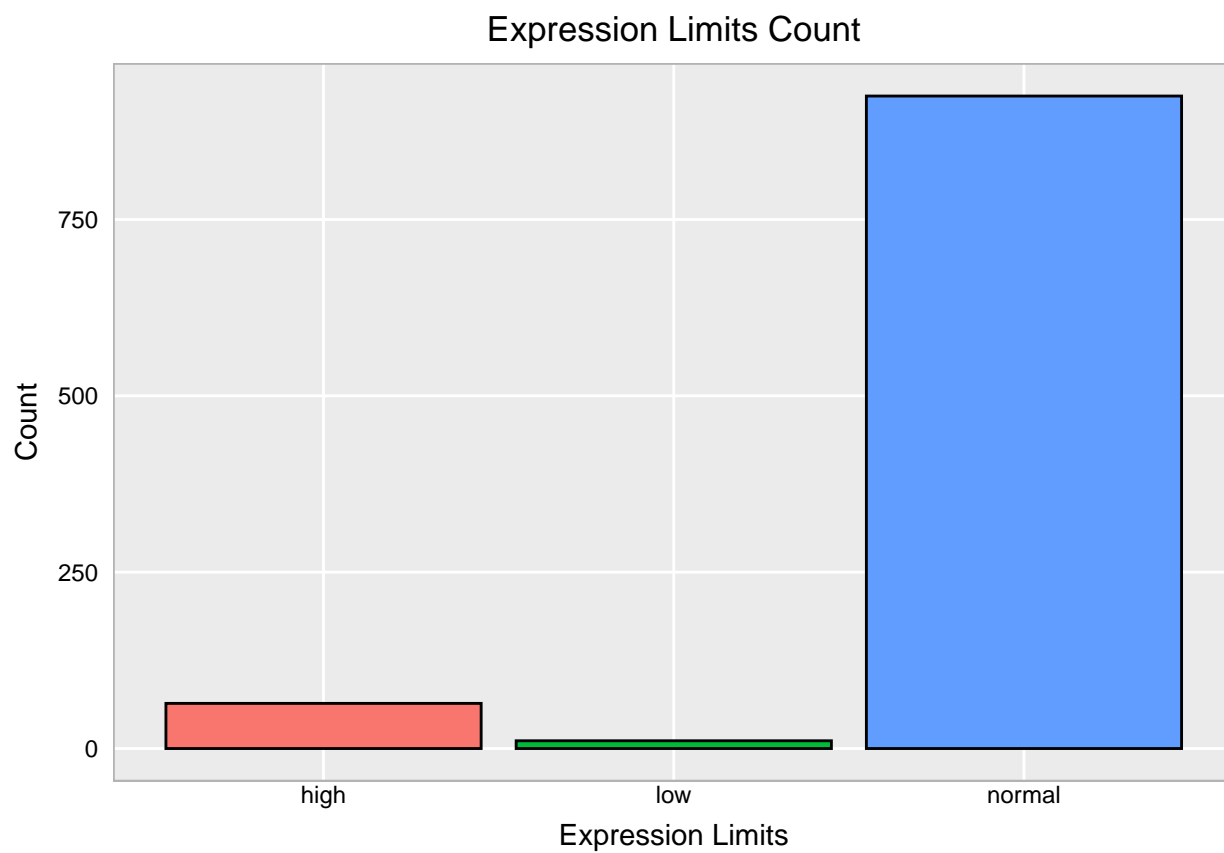
5. Add another layer to “plot1” in order to change the points colors to blue (for low), grey (for normal) and red (for high). Save this plot in the object “plot2”.

```
plot2 <- plot1 + scale_color_manual(values=c("red","blue", "grey"))+ hw
plot2
```



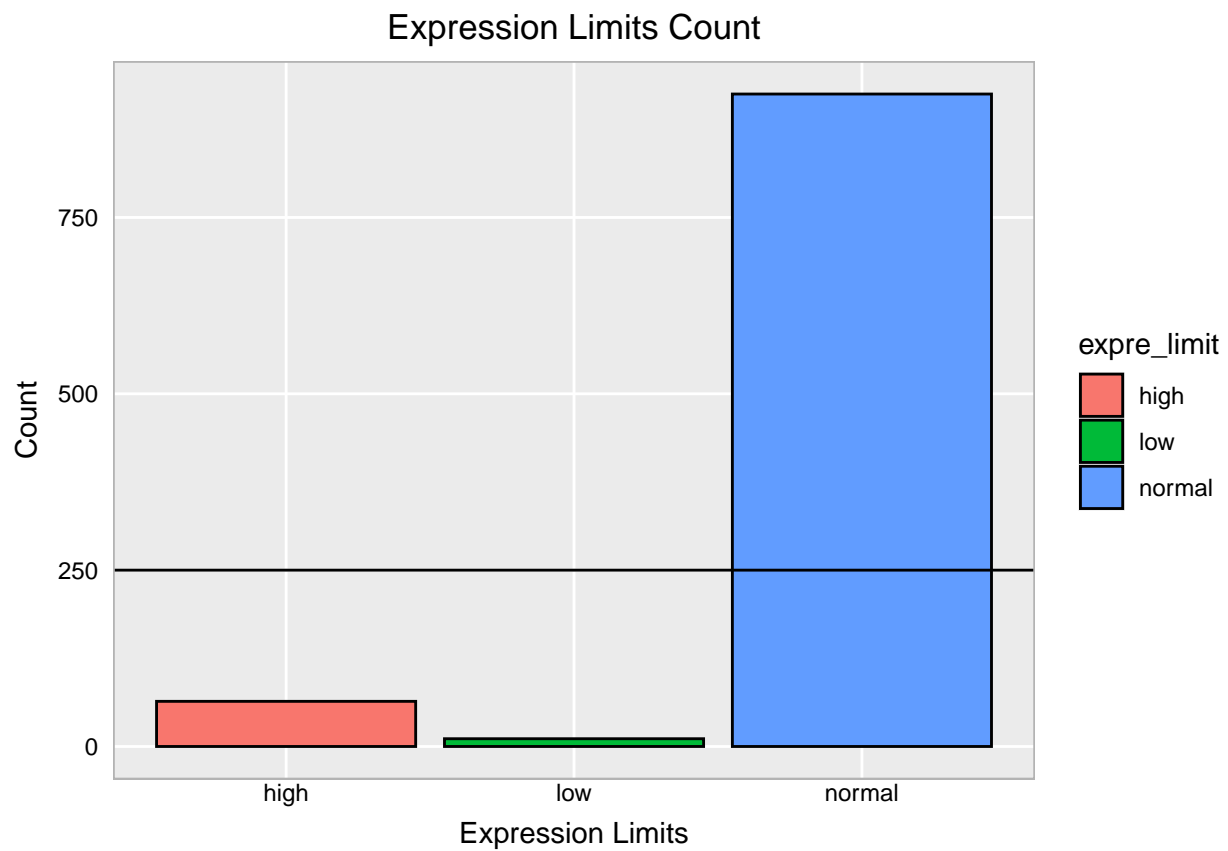
6. Produce a bar plot of how many low/normal/high genes are in the column 'expre_limits'. Save this plot as "plot3".

```
plot3 <- ggplot(gene, aes(x=expre_limit, fill=expre_limit))+
  geom_bar(color="black") +
  labs(x="Expression Limits",
       y="Count",
       title="Expression Limits Count")+ hw +
  theme(legend.position="none")
plot3
```



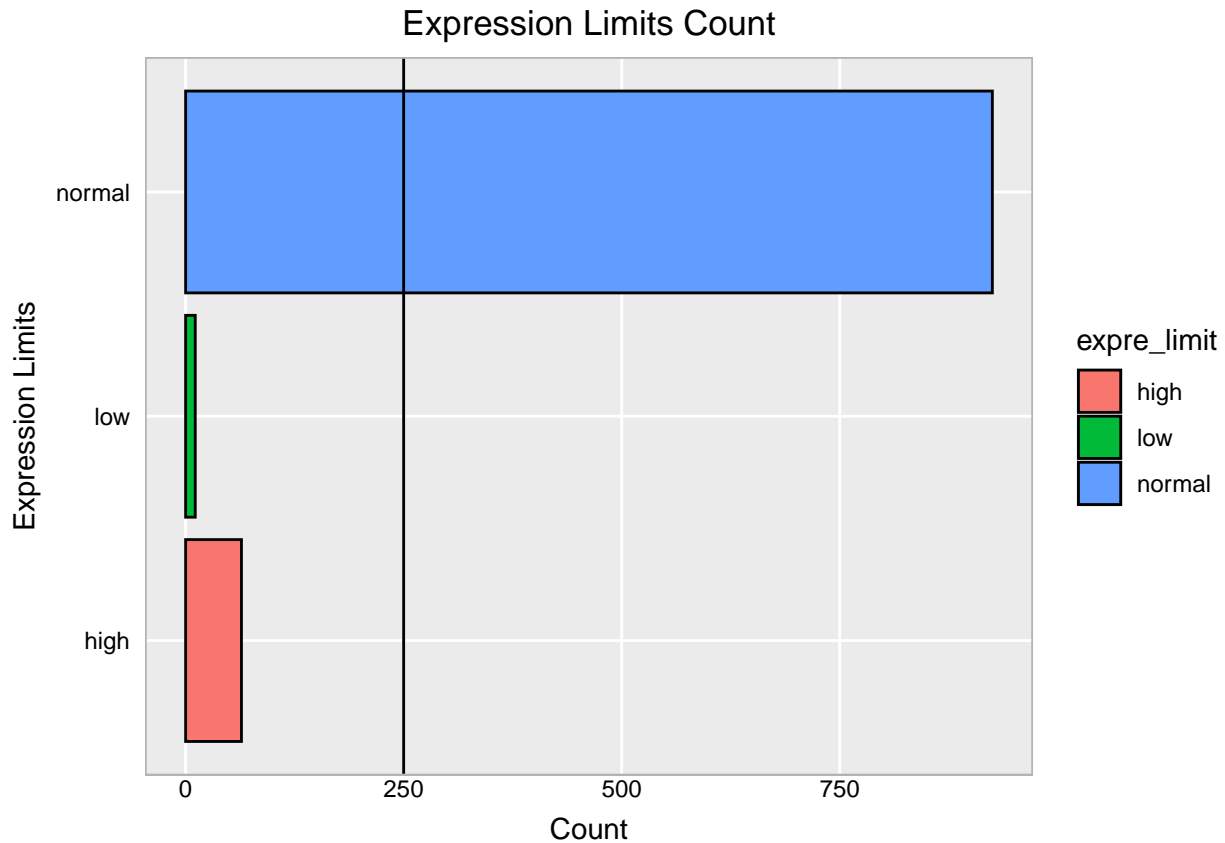
7. To plot3, add an horizontal line at counts = 250

```
plot3 <- plot3 + geom_hline(yintercept=250) + hw  
plot3
```



8. Swap the X-axis and the Y-axis of the plot from part 7).

```
plot3 + coord_flip()
```



Question 3: Titanic data set from Kaggle.com is used for this example. Please use `titanic.csv` for this question.

1. Is there a relationship between the age of the passenger and the passenger fare? Explore this by constructing a scatter plot.

```
titanic <- read_csv("titanic.csv")
```

```
## Rows: 887 Columns: 8
## -- Column specification -----
## Delimiter: ","
## chr (2): Name, Sex
## dbl (6): Survived, Pclass, Age, Siblings/Spouses Aboard, Parents/Children Ab...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
table(is.na(titanic))
```

```
##
## FALSE
## 7096
```

```
summary(titanic)
```

```
##      Survived      Pclass      Name      Sex
## Min.   :0.0000   Min.   :1.000   Length:887   Length:887
## 1st Qu.:0.0000   1st Qu.:2.000   Class :character   Class :character
## Median :0.0000   Median :3.000   Mode  :character   Mode  :character
```

```
## Mean :0.3856 Mean :2.306
## 3rd Qu.:1.0000 3rd Qu.:3.000
## Max. :1.0000 Max. :3.000
## Age Siblings/Spouses Aboard Parents/Children Aboard
## Min. : 0.42 Min. :0.0000 Min. :0.0000
## 1st Qu.:20.25 1st Qu.:0.0000 1st Qu.:0.0000
## Median :28.00 Median :0.0000 Median :0.0000
## Mean :29.47 Mean :0.5254 Mean :0.3833
## 3rd Qu.:38.00 3rd Qu.:1.0000 3rd Qu.:0.0000
## Max. :80.00 Max. :8.0000 Max. :6.0000
## Fare
## Min. : 0.000
## 1st Qu.: 7.925
## Median : 14.454
## Mean : 32.305
## 3rd Qu.: 31.137
## Max. :512.329
```

```
str(titanic)
```

```
## spc_tbl_ [887 x 8] (S3: spec_tbl_df/tbl_df/tbl/data.frame)
## $ Survived : num [1:887] 0 1 1 1 0 0 0 0 1 1 ...
## $ Pclass : num [1:887] 3 1 3 1 3 3 1 3 3 2 ...
## $ Name : chr [1:887] "Mr. Owen Harris Braund" "Mrs. John Bradley (Florence Briggs
## $ Sex : chr [1:887] "male" "female" "female" "female" ...
## $ Age : num [1:887] 22 38 26 35 35 27 54 2 27 14 ...
## $ Siblings/Spouses Aboard: num [1:887] 1 1 0 1 0 0 0 3 0 1 ...
## $ Parents/Children Aboard: num [1:887] 0 0 0 0 0 0 0 1 2 0 ...
## $ Fare : num [1:887] 7.25 71.28 7.92 53.1 8.05 ...
## - attr(*, "spec")=
## .. cols(
## .. Survived = col_double(),
## .. Pclass = col_double(),
## .. Name = col_character(),
## .. Sex = col_character(),
## .. Age = col_double(),
## .. `Siblings/Spouses Aboard` = col_double(),
## .. `Parents/Children Aboard` = col_double(),
## .. Fare = col_double()
## .. )
## - attr(*, "problems")=<externalptr>
```

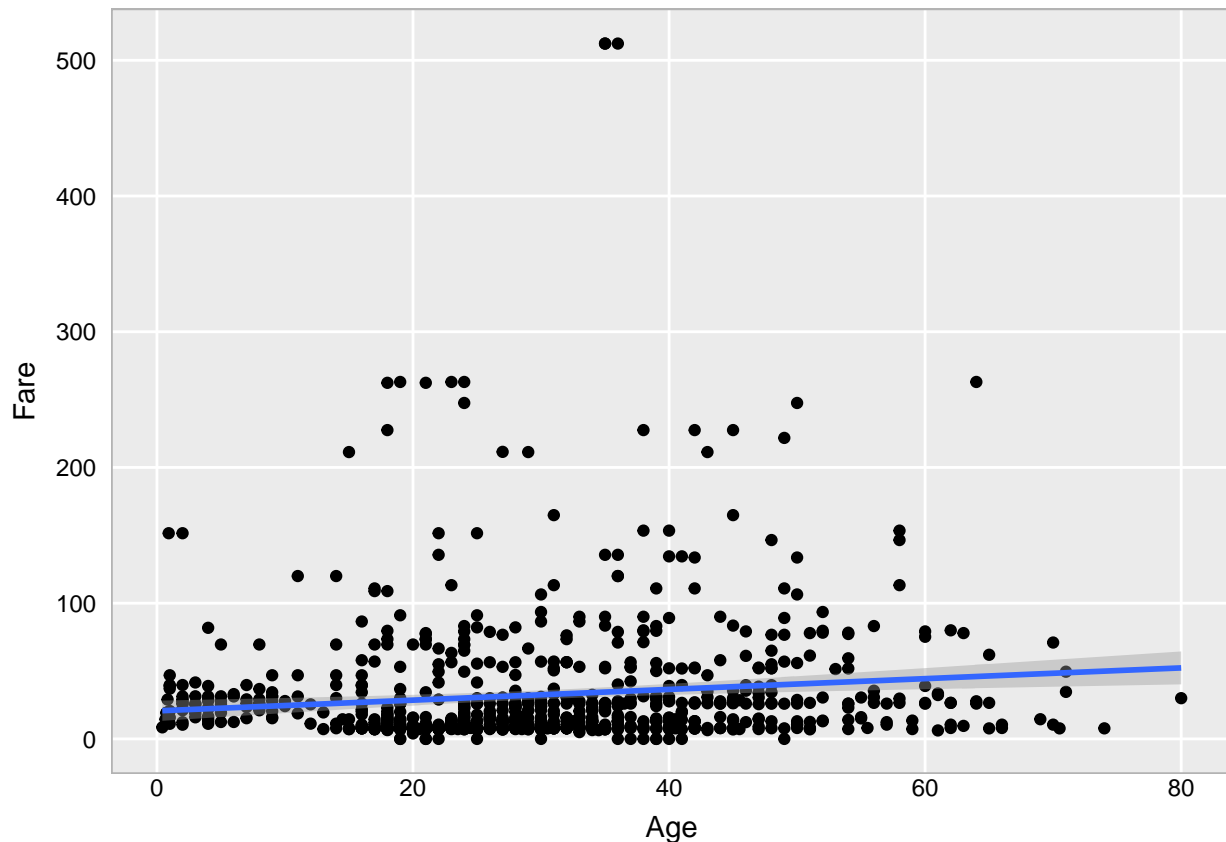
```
head(titanic, n=10)
```

```
## # A tibble: 10 x 8
## Survived Pclass Name Sex Age Sibli~1 Paren~2 Fare
## <dbl> <dbl> <chr> <chr> <dbl> <dbl> <dbl>
## 1 0 3 Mr. Owen Harris Braund male 22 1 0 7.25
## 2 1 1 Mrs. John Bradley (Florenc~ fema~ 38 1 0 71.3
## 3 1 3 Miss. Laina Heikkinen fema~ 26 0 0 7.92
## 4 1 1 Mrs. Jacques Heath (Lily M~ fema~ 35 1 0 53.1
## 5 0 3 Mr. William Henry Allen male 35 0 0 8.05
## 6 0 3 Mr. James Moran male 27 0 0 8.46
## 7 0 1 Mr. Timothy J McCarthy male 54 0 0 51.9
## 8 0 3 Master. Gosta Leonard Pals~ male 2 3 1 21.1
## 9 1 3 Mrs. Oscar W (Elisabeth Vi~ fema~ 27 0 2 11.1
```

```
## 10      1      2 Mrs. Nicholas (Adele Achem~ fema~ 14      1      0 30.1
## # ... with abbreviated variable names 1: `Siblings/Spouses Aboard`,
## # 2: `Parents/Children Aboard`
```

```
titanic_plt <- ggplot(titanic,aes(x=Age,y=Fare)) +
  geom_point() +
  geom_smooth(method="lm") + hws
titanic_plt
```

```
## `geom_smooth()` using formula = 'y ~ x'
```

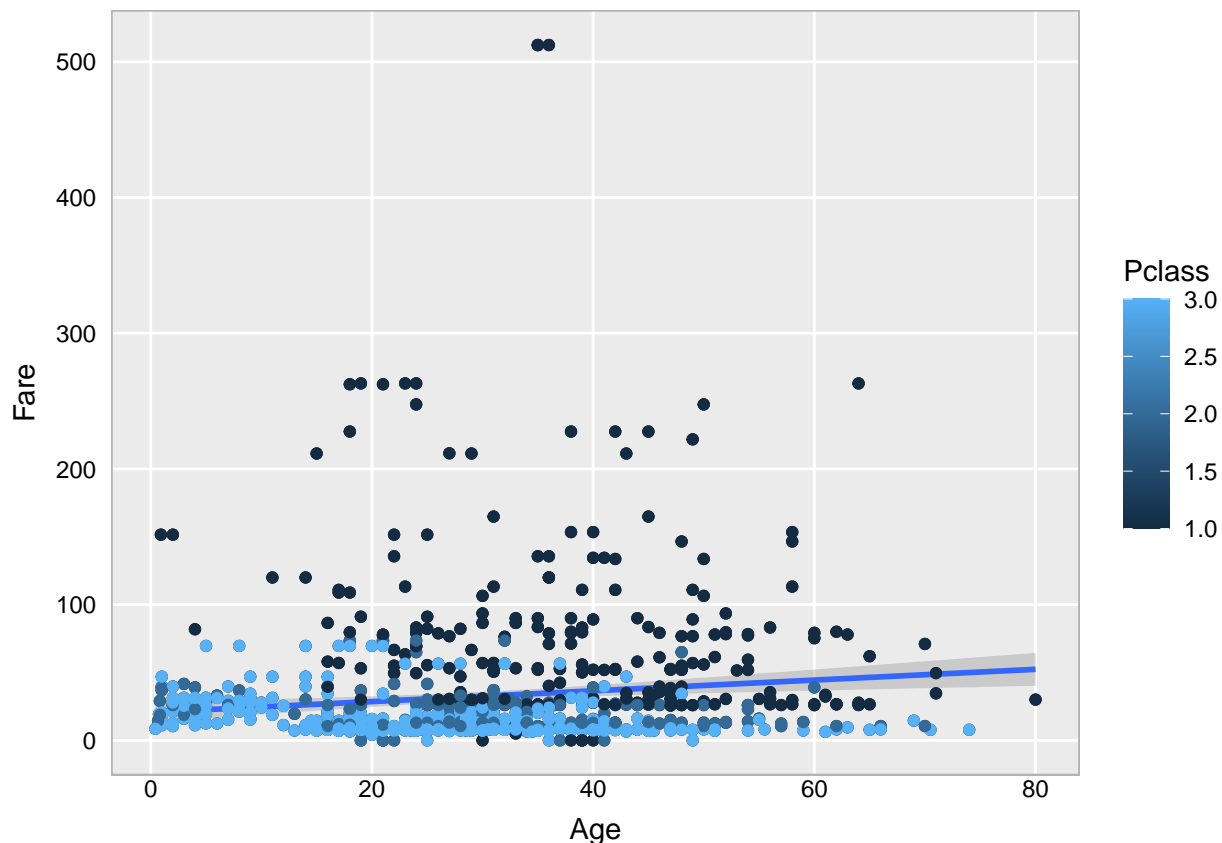


As I can see there is no significant relationship between passengers age and fare. However, I could say that the passengers who allowed themselves to buy more expensive tickets were in the age group of 20-50. Nevertheless, this is explained by the fact that there are clearly fewer children and elderly people than middle-aged passengers.

2. Color the points from question 1 by Pclass. Remember that Pclass is a proxy for socioeconomic status.

```
titanic_plt + geom_point( aes( color = Pclass) ) + hws
```

```
## `geom_smooth()` using formula = 'y ~ x'
```



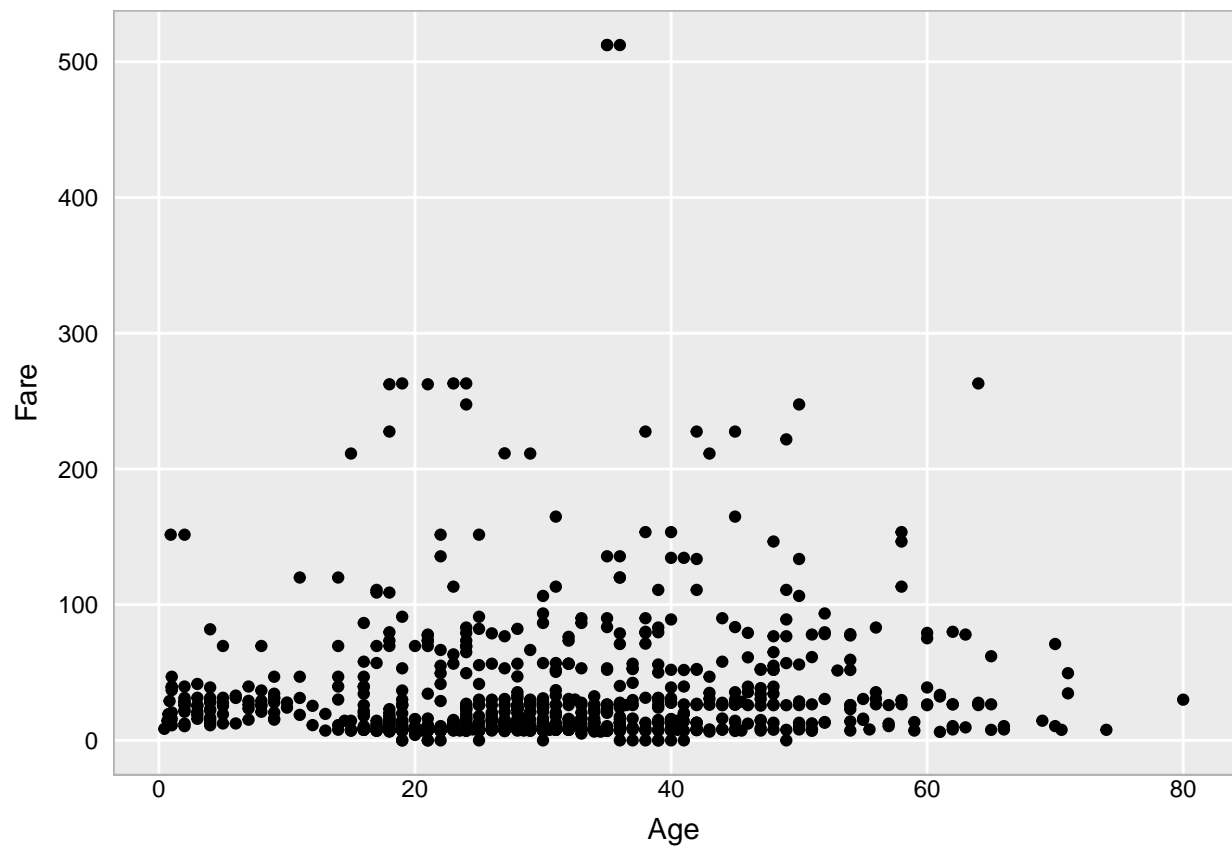
3. Manually scale the colors in question 4. 1st class = red, 2nd class = purple, 3rd class = seagreen. Also change the legend labels (1 = 1st Class, 2 = 2nd Class, 3 = 3rd Class).
4. Create Juxtaposed plots for the scatter plot made in 3 by the column 'Sex'

```
titanic_new <- titanic %>%
  mutate(Pclass_new = case_when((Pclass == 1) ~ "1st Class",
                                (Pclass == 2) ~ "2nd Class",
                                (Pclass == 3) ~ "3rd Class"
                                )) #creating a new column for better data visualization and processing p

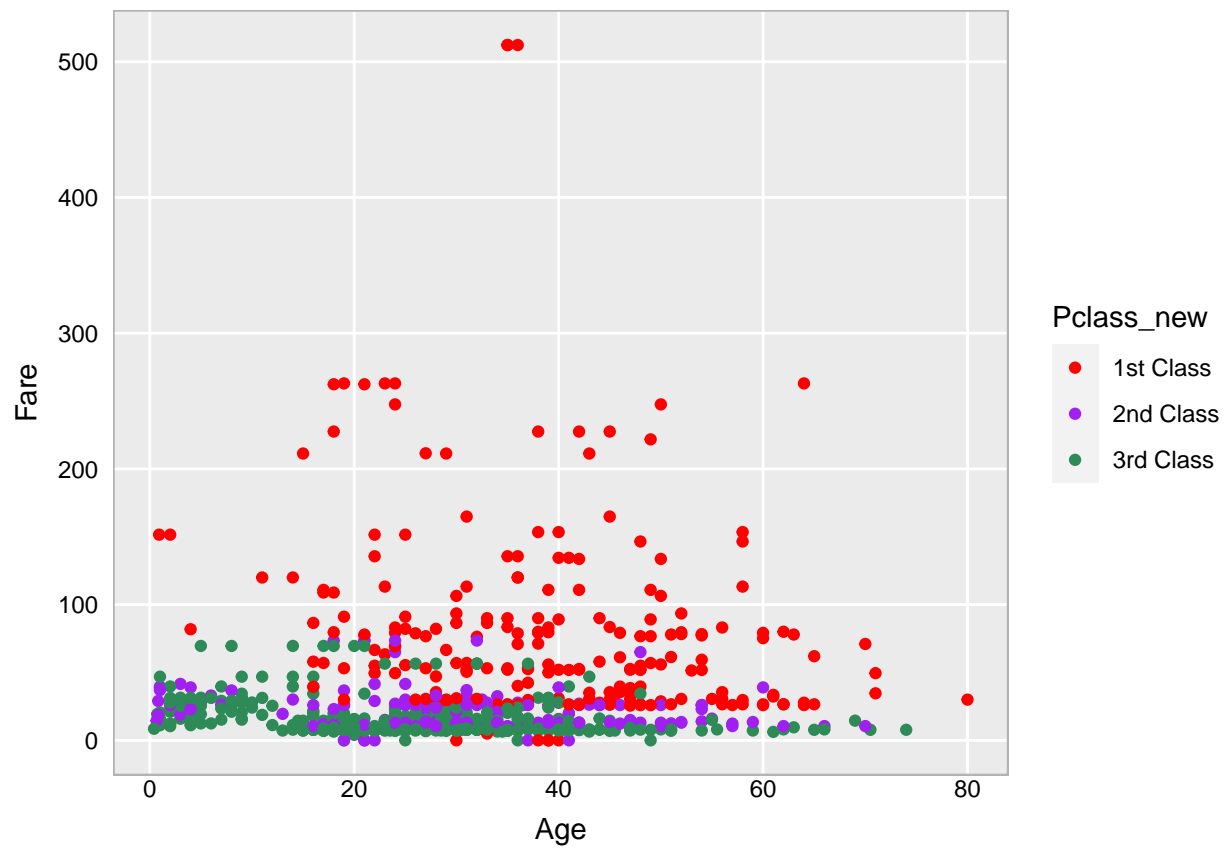
head(titanic_new)
```

```
## # A tibble: 6 x 9
##   Survived Pclass Name                Sex    Age Sibli~1 Paren~2 Fare Pclas~3
##   <dbl>   <dbl> <chr>                <chr> <dbl> <dbl> <dbl> <dbl> <chr>
## 1     0     3 Mr. Owen Harris Bra~ male    22     1     0  7.25 3rd Cl~
## 2     1     1 Mrs. John Bradley (~ fema~    38     1     0 71.3 1st Cl~
## 3     1     3 Miss. Laina Heikkin~ fema~    26     0     0  7.92 3rd Cl~
## 4     1     1 Mrs. Jacques Heath ~ fema~    35     1     0 53.1 1st Cl~
## 5     0     3 Mr. William Henry A~ male    35     0     0  8.05 3rd Cl~
## 6     0     3 Mr. James Moran      male    27     0     0  8.46 3rd Cl~
## # ... with abbreviated variable names 1: `Siblings/Spouses Aboard`,
## # 2: `Parents/Children Aboard`, 3: Pclass_new
```

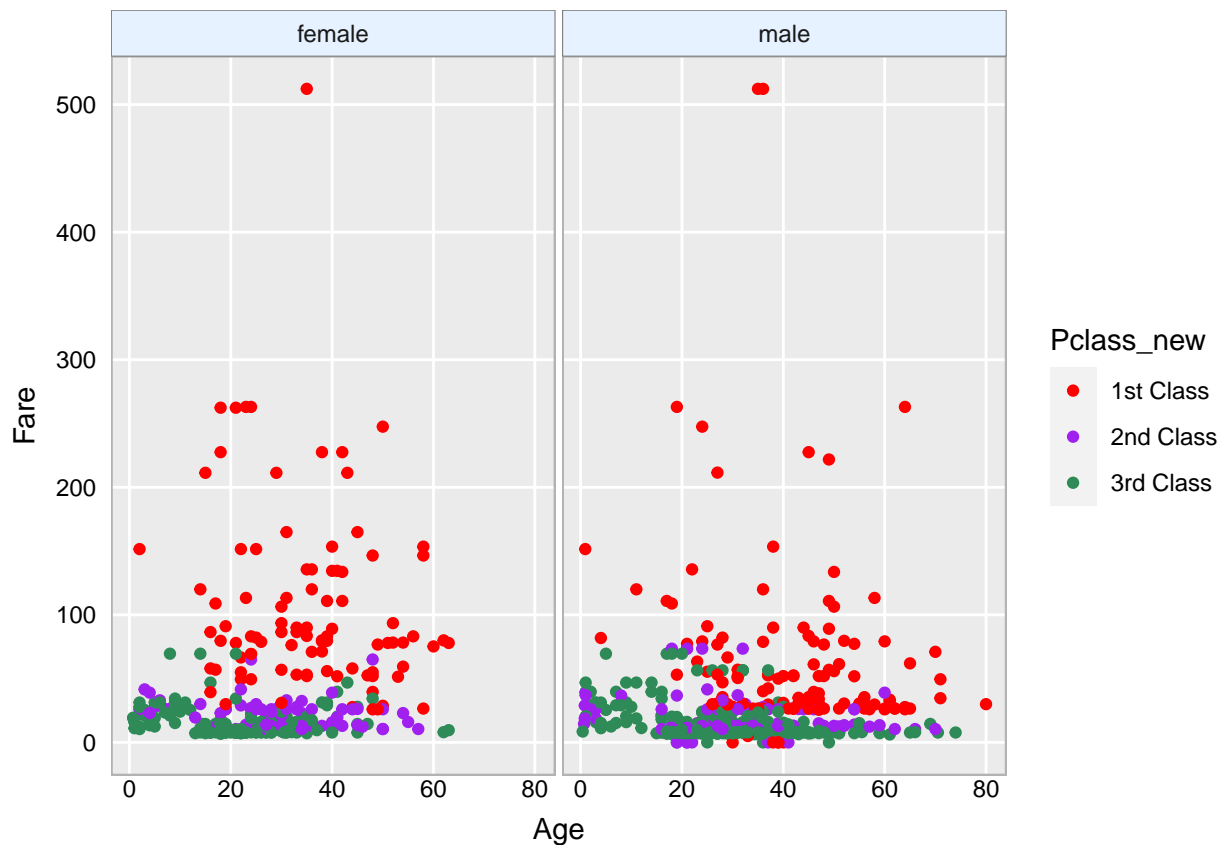
```
titanic_plt2 <- ggplot(titanic_new, aes( x=Age, y=Fare) )
titanic_plt2 + geom_point() + hw
```

```
titanic_plt3 <- titanic_plt2 + geom_point(aes(color=Pclass_new)) + scale_color_manual(values = c("red",  
titanic_plt3
```



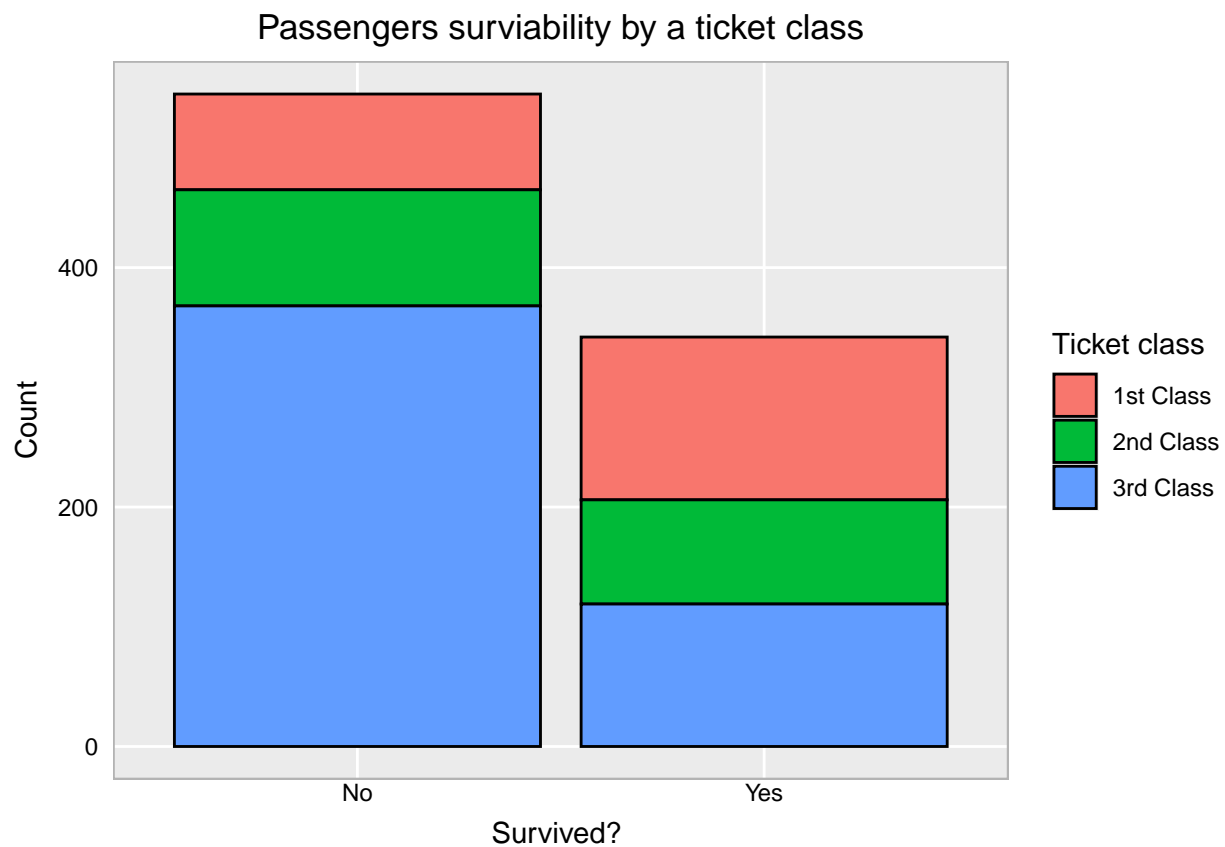
```
titanic_plt3 + facet_grid(~Sex) +hw
```



5. Plot the number of passengers (a simple count) that survived by ticket class.

```
titanic_new2 <- titanic_new %>%
  mutate(Survived_chr = case_when((Survived == 1) ~ "Yes",
                                   (Survived == 0) ~ "No"))

ggplot(titanic_new2) +
  geom_bar(aes(x=Survived_chr, fill=Pclass_new), color="black") +
  labs(x="Survived? ",
       y="Count",
       title="Passengers surviability by a ticket class",
       fill="Ticket class") + hw
```



```
count(titanic_new2, surviability=Survived_chr, TicketClass=Pclass_new)
```

```
## # A tibble: 6 x 3
##   surviability TicketClass     n
##   <chr>         <chr>    <int>
## 1 No          1st Class      80
## 2 No          2nd Class      97
## 3 No          3rd Class     368
## 4 Yes         1st Class     136
## 5 Yes         2nd Class      87
## 6 Yes         3rd Class     119
```