Final Project

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```
getwd() # finding my working directory
```

```
## [1] "/Users/annieglenning/Documents/GitHub/QBS103"
```

```
setwd("/Users/annieglenning/Documents/Dartmouth/SU24/QBS_103/Data") # set my working directory to where
original_gene_data <- read.table("QBS103_GSE157103_genes.csv", header = TRUE, sep = ",") # reading in t
series_data <- read.table("QBS103_GSE157103_series_matrix.csv", header = TRUE, sep = ",") # reading in
```

```
# transposing the gene data
original_gene_data <- as.data.frame(original_gene_data)
if (is.character(original_gene_data[1, 1])) {
  gene_data <- t(original_gene_data)
  colnames(gene_data) <- gene_data[1, ]
  gene_data <- gene_data[-1, ]
  gene_data <- as.data.frame(gene_data)
}
```

Identify one gene, one continuous covariate, and two categorical covariates

```
AAGAB <- as.numeric(gene_data$AAGAB) # one gene
AAGAB
```

```
##   [1] 22.93 21.69 18.27 26.69 17.02 17.50 26.28 13.91 13.57 12.54 30.25 17.97
##  [13] 28.07 17.66 12.84 26.42 21.98 17.65 27.72 14.54 14.36 10.10 13.21 12.63
##  [25] 19.75 16.05 17.29 14.19 10.18 14.40 14.90 12.41 17.23 13.30 18.66 21.90
##  [37] 19.03 11.82  8.11 18.47  6.29 19.75  8.36 21.71 13.75 13.21 17.74  6.42
##  [49]  8.70  4.55 18.97 22.00 30.85 18.12 18.17 24.32  9.09 20.36 18.09 27.68
##  [61] 15.57 25.64 10.35 27.70 16.26 11.61  6.83 28.83 27.37 15.33 21.83 30.10
##  [73] 11.88 28.81 11.65 15.04 24.31 17.14 14.70 14.86 22.38 17.84  9.97 18.84
##  [85] 17.95 10.35 12.82 14.99 12.69 15.17 16.91 17.93 11.85  7.37  7.84  6.05
##  [97] 14.77 16.32 15.23 11.55 12.03 10.13  6.43 13.69 10.22 11.82 14.58  9.00
## [109] 16.94 14.67 16.96 17.49 13.35  8.18 16.21 10.70 17.78  9.43  8.33 11.42
## [121] 12.57  7.48 10.35 14.06  9.49  5.24
```

```
series_data$age # one continuous covariate
```

```
##   [1] "39"   "63"   "33"   "49"   "49"   " :"   "38"   "78"   "64"   "62"
```

```
##  [11] "52"   "50"   "37"   "55"   "68"   "48"   "54"   "70"   "51"   "62"
##  [21] "66"   "43"   "76"   "55"   "55"   "41"   "71"   "63"   "63"   "54"
##  [31] "50"   "72"   "81"   "64"   "58"   "68"   "87"   "68"   "80"   "66"
##  [41] "74"   "21"   "83"   "46"   "62"   "62"   "78"   "72"   "73"   "37"
##  [51] "58"   "71"   "35"   "62"   "33"   "30"   "62"   "55"   "49"   "54"
##  [61] "78"   "39"   "65"   "84"   "66"   "57"   "79"   "77"   "81"   "37"
##  [71] "50"   "82"   "55"   "55"   "73"   "55"   "80"   "27"   "71"   "67"
##  [81] "85"   "75"   "62"   "52"   "61"   " >89" "86"   "29"   "82"   "81"
##  [91] "24"   "49"   "51"   "76"   "81"   "71"   "74"   "58"   "84"   "83"
## [101] "54"   "65"   "65"   " >89" "83"   "75"   "50"   "53"   "49"   "67"
## [111] "58"   "82"   "65"   "75"   "83"   "40"   "84"   "88"   "66"   "62"
## [121] "71"   "63"   "42"   "32"   "62"   "36"
```

```
series_data$sex # first categorical covariate
```

```
##   [1] " male"    " male"    " male"    " male"    " male"    " male"
##   [7] " female"  " male"    " female"  " male"    " female"  " male"
##  [13] " male"    " male"    " male"    " male"    " male"    " female"
##  [19] " male"    " male"    " male"    " male"    " male"    " male"
##  [25] " male"    " female"  " female"  " male"    " female"  " male"
##  [31] " male"    " male"    " male"    " female"  " female"  " male"
##  [37] " male"    " male"    " female"  " male"    " male"    " female"
##  [43] " female"  " male"    " female"  " male"    " male"    " female"
##  [49] " male"    " male"    " female"  " male"    " female"  " female"
##  [55] " female"  " female"  " male"    " male"    " male"    " female"
##  [61] " female"  " female"  " male"    " male"    " female"  " male"
##  [67] " male"    " female"  " male"    " male"    " female"  " male"
##  [73] " female"  " male"    " female"  " female"  " male"    " male"
##  [79] " male"    " male"    " female"  " female"  " male"    " female"
##  [85] " male"    " female"  " female"  " female"  " female"  " female"
##  [91] " female"  " male"    " male"    " male"    " male"    " male"
##  [97] " female"  " male"    " male"    " male"    " female"  " male"
## [103] " male"    " male"    " female"  " female"  " male"    " female"
## [109] " female"  " male"    " female"  " male"    " male"    " female"
## [115] " unknown" " female"  " female"  " male"    " female"  " female"
## [121] " male"    " male"    " female"  " female"  " male"    " male"
```

```
series_data$icu_status # second categorical covariate
```

```
##   [1] " no"  " no"  " no"  " no"  " no"  " no"  " no"  " yes" " yes" " yes"
##  [11] " no"  " yes" " no"  " yes" " yes" " no"  " no"  " no"  " no"  " yes"
##  [21] " yes" " yes" " yes" " yes" " yes" " yes" " yes" " yes" " yes" " yes"
##  [31] " yes" " yes" " no"  " no"  " no"  " no"  " no"  " yes" " yes" " yes"
##  [41] " yes" " yes" " yes" " yes" " yes" " yes" " yes" " yes" " yes" " yes"
##  [51] " no"  " no"  " no"  " yes" " no"  " no"  " no"  " no"  " no"  " no"
##  [61] " yes" " yes" " yes" " no"  " no"  " yes" " yes" " no"  " no"  " yes"
##  [71] " no"  " no"  " yes" " no"  " yes" " yes" " no"  " no"  " yes" " no"
##  [81] " no"  " no"  " yes" " no"  " yes" " no"  " no"  " no"  " yes" " yes"
##  [91] " no"  " no"  " no"  " yes" " no"  " yes" " no"  " yes" " no"  " no"
## [101] " no"  " yes" " yes" " no"  " no"  " yes" " yes" " yes" " no"  " yes"
## [111] " no"  " yes" " yes" " yes" " yes" " yes" " yes" " yes" " yes" " yes"
## [121] " no"  " no"  " no"  " no"  " no"  " yes"
```

Generate the following three plots using ggplot2

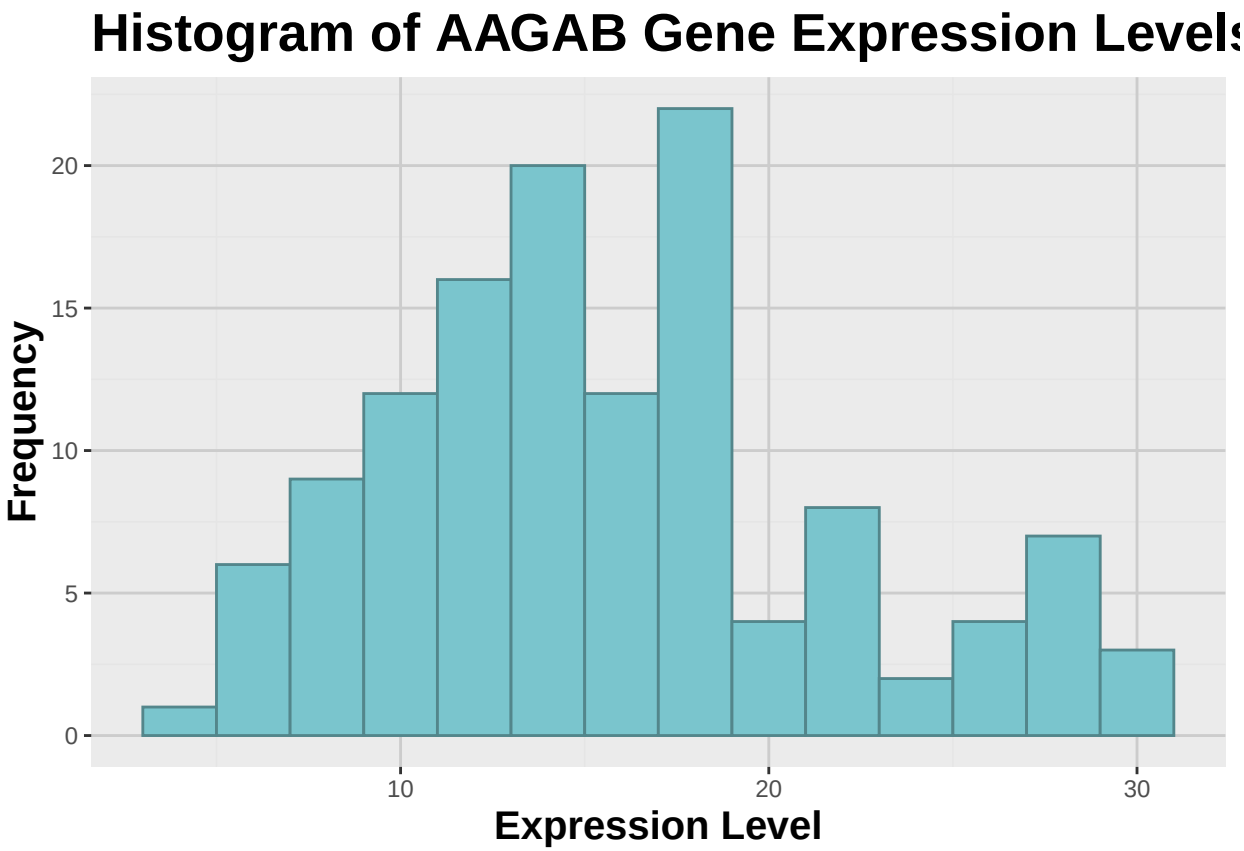
```
library(tidyverse)
```

```
## -- 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 ggplot2   3.5.1     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.1
## v purrr     1.0.2
## -- 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 error
```

```
library(ggplot2)
```

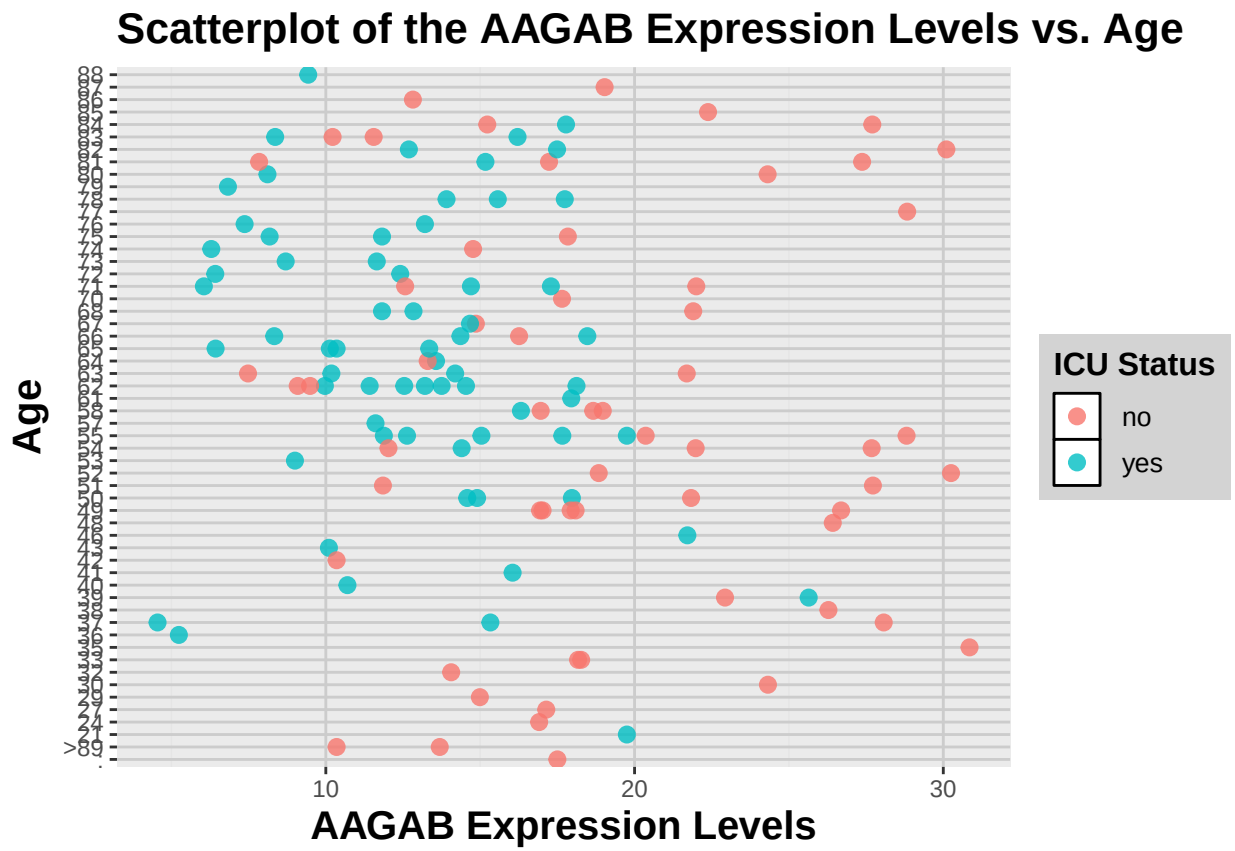
Histogram for my Gene selected

```
ggplot(gene_data, aes(x = as.numeric(AAGAB))) +
  geom_histogram(binwidth = 2, fill = "cadetblue3", color = "cadetblue4") +
  labs( # labeling the title and axis
    title = "Histogram of AAGAB Gene Expression Levels",
    x = "Expression Level",
    y = "Frequency"
  ) +
  theme(
    plot.title = element_text(size = 20, face = "bold"), # title
    axis.title = element_text(size = 15, face = "bold"), # axis
    panel.grid.major = element_line(color = "grey80"), # background
    panel.grid.minor = element_line(color = "grey90")
    )
```



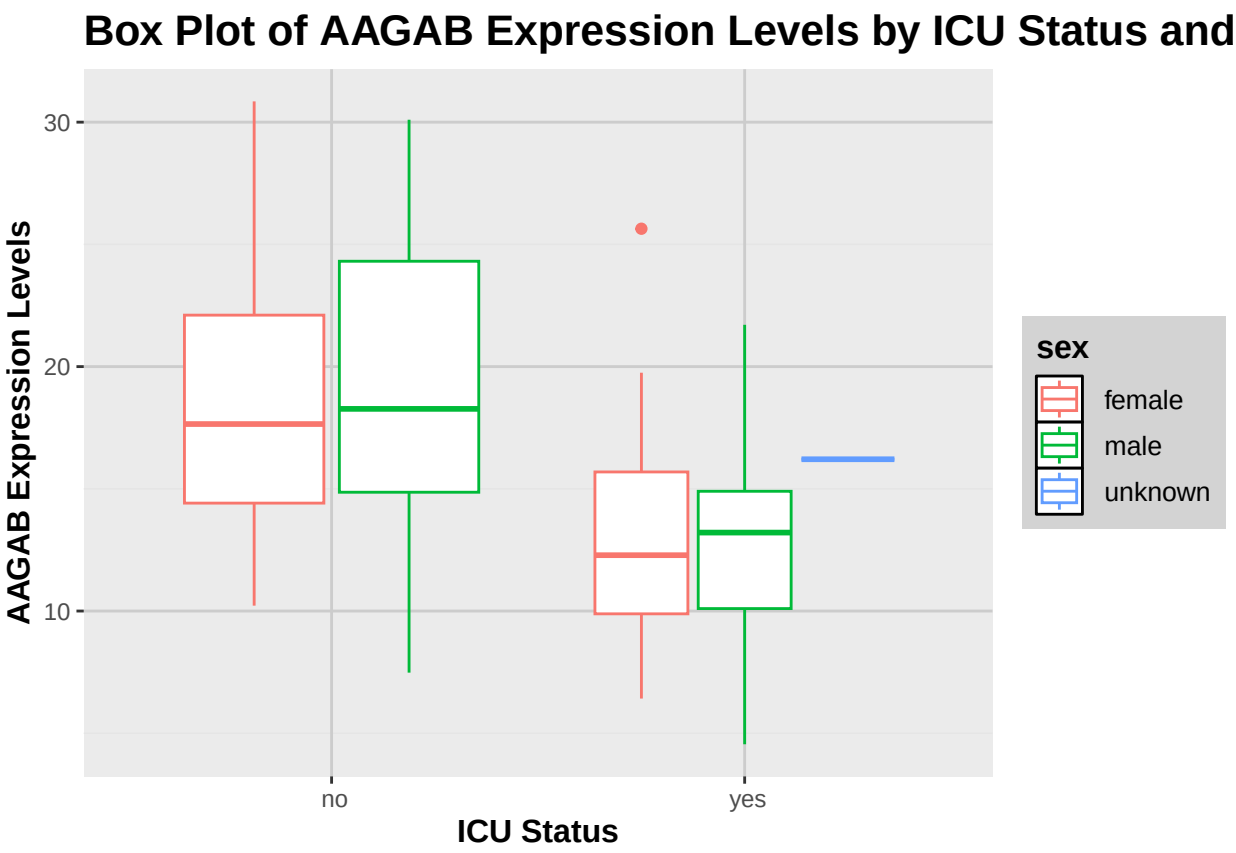
Scatterplot

```
ggplot(series_data, aes(x = as.numeric(AAGAB), y = age,
                        color = factor(icu_status))) + # seperarting the points by icu status
  geom_point(size = 2.5, alpha = 0.8) + # size and transparency of the point
  labs( # labeling the title and axis
    title = "Scatterplot of the AAGAB Expression Levels vs. Age",
    x = "AAGAB Expression Levels",
    y = "Age",
    color = "ICU Status" # legend title
    ) +
  theme(
    plot.title = element_text(size = 16, face = "bold"),
    axis.title = element_text(size = 15, face = "bold"),
    legend.title = element_text(size = 12, face = "bold"),  # editing the legend
    legend.text = element_text(size = 10),
    legend.background = element_rect(fill = "lightgray", color = NA),
    legend.key = element_rect(fill = "white", color = "black"),
    panel.grid.major = element_line(color = "grey80"), # background
    panel.grid.minor = element_line(color = "grey90")
    )
```



Box Plot

```
ggplot(series_data,aes(x = icu_status, y = as.numeric(AAGAB), color = sex)) +
  geom_boxplot() +
  labs( # labeling the title and axis
    title = "Box Plot of AAGAB Expression Levels by ICU Status and Sex",
    x = "ICU Status",
    y = "AAGAB Expression Levels"
  ) +
  theme(
    plot.title = element_text(size = 16, face = "bold"),
    axis.title = element_text(size = 12, face = "bold"),
    legend.title = element_text(size = 12, face = "bold"), # editing the legend
    legend.text = element_text(size = 10),
    legend.background = element_rect(fill = "lightgray", color = NA),
    legend.key = element_rect(fill = "white", color = "black"),
    panel.grid.major = element_line(color = "grey80"), # background
    panel.grid.minor = element_line(color = "grey90")
  )
```


Box Plot of AAGAB Expression Levels by ICU Status and
AAGAB Expression Levels
30
20
10
no
yes
ICU Status
sex
female
male
unknown