Project_part3

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DATA CLEANING AND PREP

```r
#DATA CLEANING AND PREP

# Set the working directory and read in the files
setwd("C:/Users/AlexandraTreml/Desktop/MS/QBS103/Project/QBS103_proj")
genes <- read.csv("genes_GSE157103.csv")
participant <- read.csv("series_matrix_GSE157103.csv")

# Rename the first column in genes to 'gene'
genes <- genes %>%
  rename(gene = X) %>%
  filter(gene == "A2M")

# Pivot the genes dataframe
genes_long <- genes %>%
  tidyr::pivot_longer(cols = -gene, names_to = 'id', values_to = 'expression')

#rename id column in participant, select my categorical covariates and continuous variable (+age for ed
participant <- participant %>%
  filter(icu_status == ' yes') %>%
  rename(id = participant_id)
  #filter(gene == 'A1BG')
  #select(id, age, sex, mechanical_ventilation, lactate.mmol.l.)

#join 2 dataframes
df <- left_join(participant, genes_long, by = "id")

#fill lactate unknowns with NA
df$lactate.mmol.l.[df$lactate.mmol.l. == " unknown"] <- NA
#fill sex unknowns with NA
df$sex[df$sex == " unknown"] <- NA
#remove : from age, and fill with NA
df$age[df$age == " :"] <- NA

df <- na.omit(df) #get rid of na
```

Part 1: Latex table of summary stats for all variables.

```r
# Load necessary libraries
library(dplyr)
```

```r
library(stargazer)
library(knitr)

# Convert columns to appropriate types
df$fibrinogen <- as.numeric(df$fibrinogen)
```

Warning: NAs introduced by coercion

```r
df$lactate.mmol.l. <- as.numeric(df$lactate.mmol.l.)
df$expression <- as.numeric(df$expression)
df$sex <- as.factor(df$sex)
df$mechanical_ventilation <- as.factor(df$mechanical_ventilation)
df$gene <- as.factor(df$gene)
df$crp.mg.l. <- as.numeric(df$crp.mg.l.)
```

Warning: NAs introduced by coercion

```r
# Summary of numeric variables
stargazer(df %>% select(expression, lactate.mmol.l., fibrinogen, crp.mg.l.),
          type = "text",
          summary.stat = c("mean", "sd", "n"),
          digits = 2)
```

```
## 
## ====================================
## Statistic          Mean   St. Dev. N
## ------------------------------------
## expression         0.11     0.13    54
## lactate.mmol.l.    1.64     1.39    54
## fibrinogen       501.82   216.97    45
## crp.mg.l.        144.71   102.81    48
## ------------------------------------
```

```r
sex_counts <- df %>%
  group_by(sex) %>%
  summarize(
    count = n(),
    n_percentage = (n()/nrow(df)) *100)

gene_counts <- df %>%
  group_by(gene) %>%
  summarize(
    count = n(),
    n_percentage = (n()/nrow(df)) *100)

vent_counts <- df %>%
  group_by(mechanical_ventilation) %>%
  summarize(
    count = n(),
    n_percentage = (n()/nrow(df)) *100)
```

```r
sex_counts <- sex_counts %>%
  mutate(variable = "Sex")

gene_counts <- gene_counts %>%
  mutate(variable = "Gene")

vent_counts <- vent_counts %>%
  mutate(variable = "Mechanical Ventilation")

cat_variables <- bind_rows(sex_counts, gene_counts, vent_counts)

cat_variables <- cat_variables%>%
  select(variable, count, n_percentage)

stargazer(cat_variables, type = "text", summary = FALSE, rownames = FALSE)
```

```
##
## =============================================
## variable                count    n_percentage
## ---------------------------------------------
## Sex                        17   31.4814814814815
## Sex                        37   68.5185185185185
## Gene                       54          100
## Mechanical Ventilation     17   31.4814814814815
## Mechanical Ventilation     37   68.5185185185185
## ---------------------------------------------
```

Part 2: Generate a publication quality histogram, boxplot, and scatterplot

```r
df <- na.omit(df)
df <- df %>%
  select(id, gene, sex, age, mechanical_ventilation, expression, lactate.mmol.l.)
#head(df)

df$sex <- as.factor(df$sex)
levels(df$sex)
```

```
## [1] " female" " male"
```

```r
ggplot(data = df, aes(x = expression, fill = sex)) +
  geom_histogram(binwidth = 0.05, position = 'dodge') +
  labs(x = 'Gene Expression', y = 'Frequency', title = 'A2M Gene Expression Among COVID ICU Patients') +
  scale_fill_manual(values = c("violetred", "royalblue2"))
```

A2M Gene Expression Among COVID ICU Patients
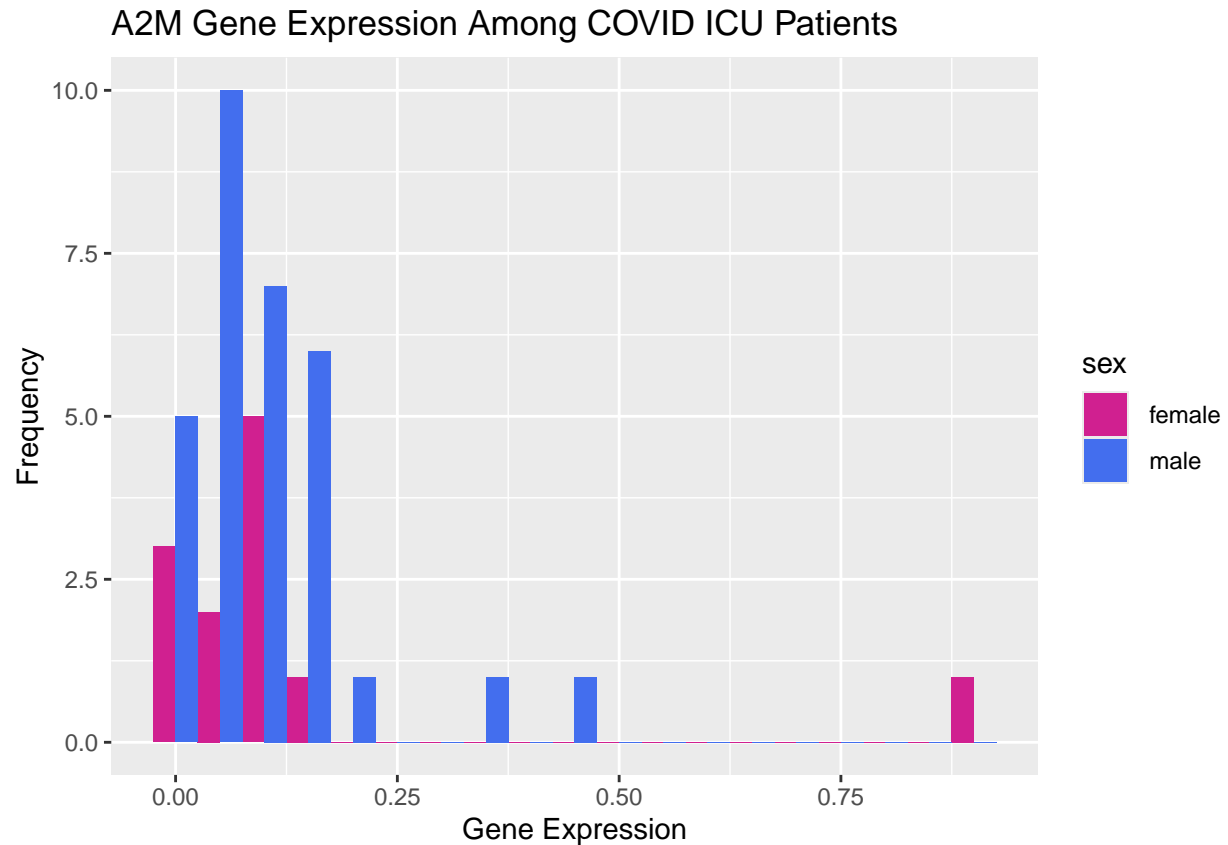

```r
# Convert lactate.mmol.l. to numeric
df$lactate.mmol.l. <- as.numeric(df$lactate.mmol.l.)

# Remove leading and trailing whitespaces from sex column
df$sex <- trimws(df$sex)
df$mechanical_ventilation <- trimws(df$mechanical_ventilation)

# Check unique levels
unique(df$sex)
```

```
## [1] "male"   "female"
```

```r
unique(df$mechanical_ventilation)
```

```
## [1] "yes" "no"
```

```r
# Set factor levels
df$sex <- factor(df$sex, levels = c("male", "female"))
df$mechanical_ventilation <- factor(df$mechanical_ventilation, levels = c("yes", "no"))


# Filter out values greater than 6.5 for the y-axis
df <- df %>% filter(lactate.mmol.l. <= 6.5)
```

```
df <- df %>% filter(expression <= 0.5)

# scatterplot vent
ggplot(df, aes(x = expression, y = lactate.mmol.l., color = mechanical_ventilation, shape = mechanical_v
  geom_point(size = 3) +
  scale_y_continuous(breaks = seq(0, ceiling(max(df$lactate.mmol.l., na.rm = TRUE)), by = 0.5)) +
  geom_smooth(method = "lm", se = TRUE) +
  labs(x = 'Gene Expression A2M', y = 'Lactate (mmol/l)', title = ' A2M Gene Expression vs Lactate for C
  theme_classic(base_size = 5) +
  scale_color_brewer(palette = 'Dark2') +
  #scale_color_manual(values = c("male" = "royalblue2", "female" = "violetred3")) +
  scale_shape_manual(values = c(16, 17)) +
  theme(
    plot.title = element_text(size = 16, face = "bold"), # Center and bold title
    axis.title = element_text(size = 12, face = "bold"), # Bold axis titles
    axis.text = element_text(size = 12), # Increase axis text size
    legend.title = element_text(size = 12),
    legend.text = element_text(size = 12)
  )
```

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


A2M Gene Expression vs Lactate for COVID ICU Patients
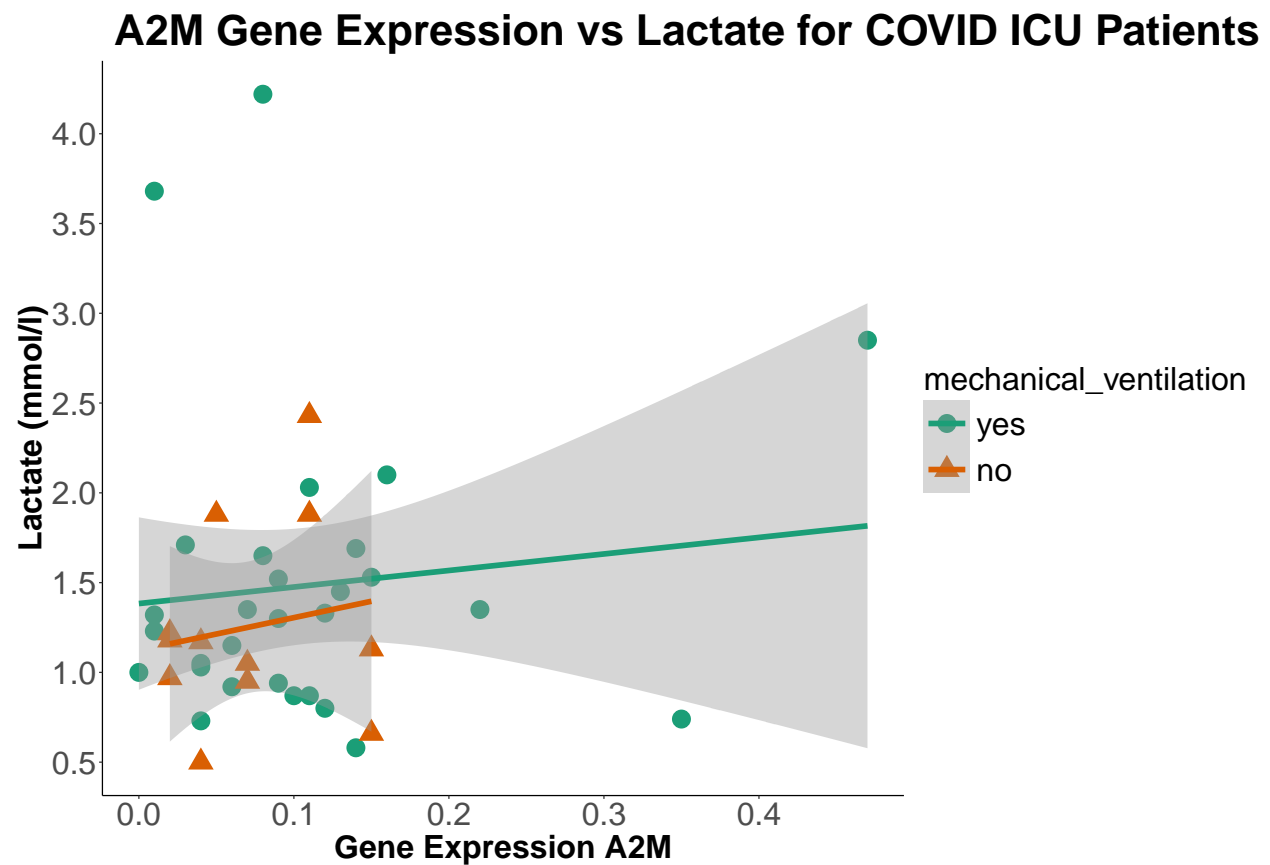
```
df$age <- as.numeric(df$age)
```

```
df$age_group <- cut(df$age,
                    breaks = c(21, 30, 50, 70, 88),
                    labels = c("21-30", "31-50", "51-70", "71-88"),
                    right = TRUE)
#head(df)


ggplot(df, aes(x = mechanical_ventilation, y = expression, color = sex)) +
  geom_boxplot() +
  scale_color_manual(values = c("male" = "royalblue1", "female" = "violetred1")) +
  labs(x = 'Mechanical Ventilation', y = 'Gene Expression', title = 'A2M Gene Expression Among Ventilate
  theme_classic()
```
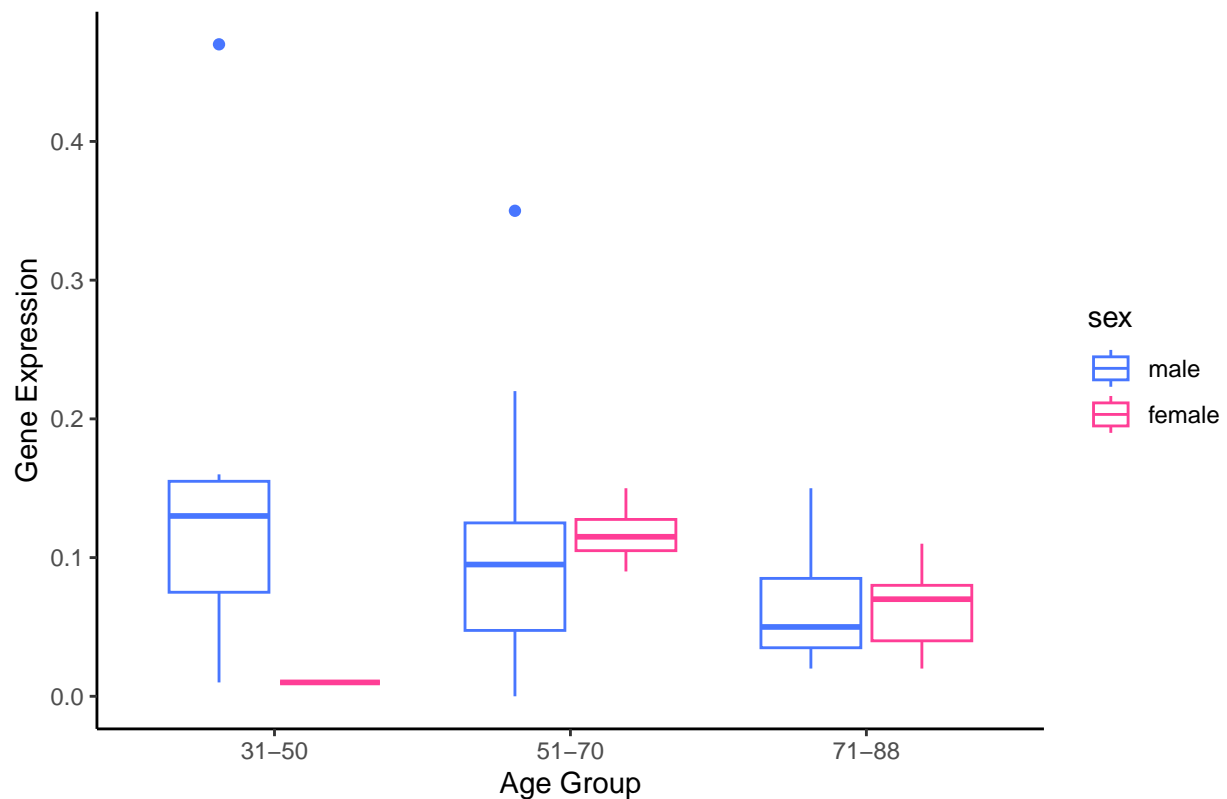
A2M Gene Expression Among Ventilated vs Non−Ventilated COVID ICU Pa
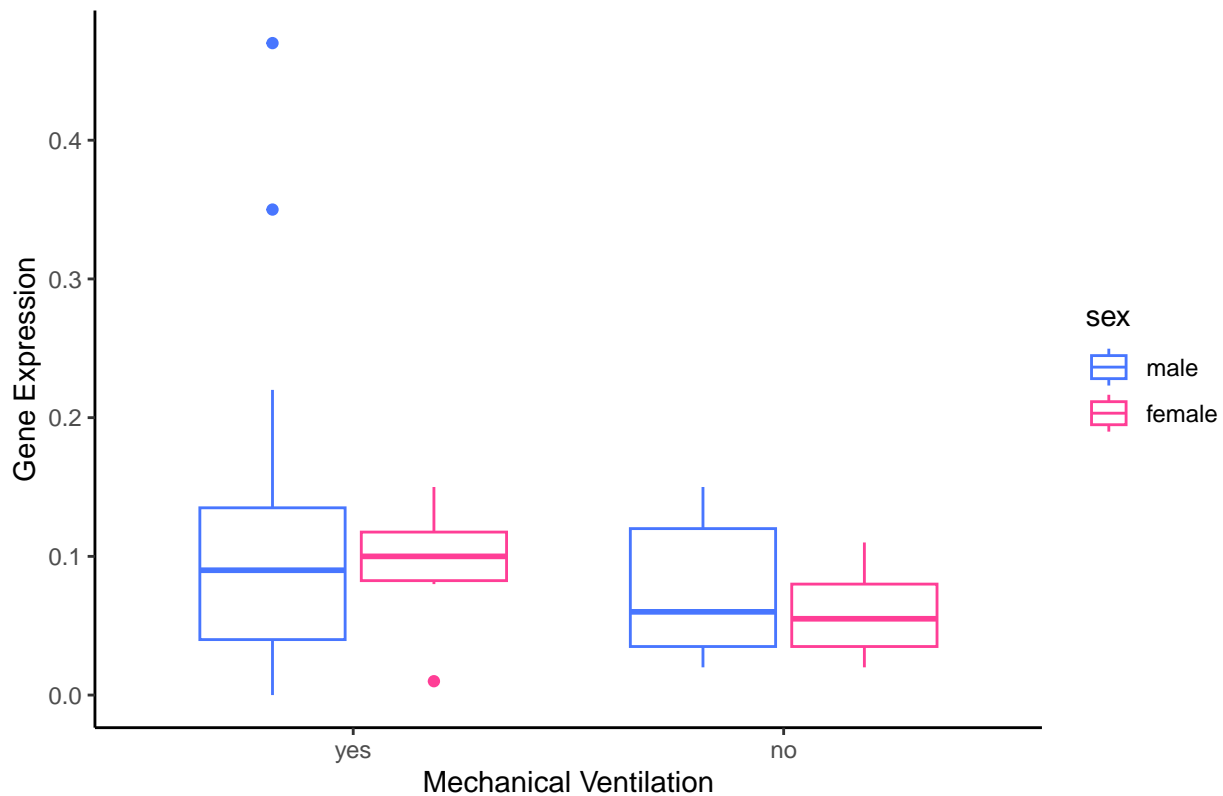

```
ggplot(df, aes(x = age_group, y = expression, color = sex)) +
  geom_boxplot() +
  scale_color_manual(values = c("male" = "royalblue1", "female" = "violetred1")) +
  labs(x = 'Age Group', y = 'Gene Expression', title = 'A2M Gene Expression Among COVID ICU Patient Age
  theme_classic()
```

A2M Gene Expression Among COVID ICU Patient Age Groups

Part 3: Generate a Heat Map

Part 4: A plot type we did not discuss in class

```r
#percent of people in the ICU on mechanical ventilation
on_vent <- df %>%
  group_by(mechanical_ventilation) %>%
  summarize(count = n())

print(on_vent)
```

```
## # A tibble: 2 x 2
##   mechanical_ventilation count
##   <fct>                  <int>
## 1 yes                       29
## 2 no                        12
```

```r
unique(df$mechanical_ventilation)
```

```
## [1] yes no
## Levels: yes no
```

```r
pie_chart <- ggplot(on_vent, aes(x = "", y = count, fill = mechanical_ventilation)) +
  geom_bar(width = 1, stat = "identity") +
  coord_polar("y") +
```

```
  labs(title = "Mechanical Ventilation Count Among ICU Patients") +
  theme_void() +
  scale_fill_manual(values = c(" yes" = "darkorange1", " no" = "cornflowerblue")) +
   geom_text(aes(label = count),
            position = position_stack(vjust = 0.5))

print(pie_chart)
```

```
## Warning: No shared levels found between 'names(values)' of the manual scale and the
## data's fill values.
## No shared levels found between 'names(values)' of the manual scale and the
## data's fill values.
## No shared levels found between 'names(values)' of the manual scale and the
## data's fill values.
```

Mechanical Ventilation Count Among ICU Patients