

```
#Jaini Shah  
#QBS 103 Final Project  
#Summer 2024
```

```
#Submission #1
```

```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'  
  
## The following objects are masked from 'package:stats':  
##  
## filter, lag  
  
## The following objects are masked from 'package:base':  
##  
## intersect, setdiff, setequal, union
```

```
library(tidyr)  
# set the working directory to where my csv file is located  
getwd()
```

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

```
setwd("/Users/jainishah/Desktop/final_project_data")
```

```
#reading gene expression data and metadata files  
gene_expression <- read.csv("genes.csv")  
metadata <- read.csv("metadata.csv")
```

```
head(gene_expression)
```

```
##           X COVID_01_39y_male_NonICU COVID_02_63y_male_NonICU  
## 1      A1BG                      0.49                      0.29  
## 2      A1CF                      0.00                      0.00  
## 3      A2M                       0.21                      0.14  
## 4     A2ML1                      0.04                      0.00  
## 5 A3GALT2                      0.07                      0.00  
## 6     A4GALT                      0.00                      0.00  
## COVID_03_33y_male_NonICU COVID_04_49y_male_NonICU COVID_05_49y_male_NonICU  
## 1                      0.26                      0.45                      0.17  
## 2                      0.00                      0.01                      0.00  
## 3                      0.03                      0.09                      0.00  
## 4                      0.02                      0.07                      0.05  
## 5                      0.00                      0.00                      0.07  
## 6                      0.00                      0.00                      0.00  
## COVID_06_.y_male_NonICU COVID_07_38y_female_NonICU COVID_08_78y_male_ICU  
## 1                      0.21                      0.49                      0.12  
## 2                      0.00                      0.01                      0.00  
## 3                      0.08                      0.23                      0.08
```

## 4	0.04	0.03	0.01
## 5	0.00	0.07	0.00
## 6	0.00	0.00	0.00
## COVID_09_64y_female_ICU COVID_10_62y_male_ICU COVID_11_52y_female_NonICU			
## 1	0.51	0.10	0.38
## 2	0.01	0.00	0.02
## 3	0.88	0.13	0.47
## 4	0.02	0.01	0.03
## 5	0.79	0.15	0.08
## 6	0.00	0.00	0.00
## COVID_12_50y_male_ICU COVID_13_37y_male_NonICU COVID_14_55y_male_ICU			
## 1	0.45	0.18	0.23
## 2	0.00	0.00	0.00
## 3	0.16	0.07	0.22
## 4	0.00	0.01	0.04
## 5	1.75	0.00	0.93
## 6	0.00	0.00	0.00
## COVID_15_68y_male_ICU COVID_16_48y_male_NonICU COVID_17_54y_male_NonICU			
## 1	0.42	0.41	0.63
## 2	0.00	0.01	0.02
## 3	0.07	0.58	0.15
## 4	0.00	0.00	0.02
## 5	0.15	0.19	0.00
## 6	0.03	0.00	0.00
## COVID_18_70y_female_NonICU COVID_19_51y_male_NonICU COVID_20_62y_male_ICU			
## 1	0.47	0.33	0.32
## 2	0.00	0.02	0.00
## 3	0.30	0.11	0.07
## 4	0.02	0.02	0.00
## 5	0.06	0.00	0.22
## 6	0.03	0.00	0.00
## COVID_21_66y_male_ICU COVID_22_43y_male_ICU COVID_23_76y_male_ICU			
## 1	0.18	0.09	0.18
## 2	0.00	0.00	0.01
## 3	0.00	0.06	0.03
## 4	0.00	0.00	0.00
## 5	0.37	0.06	0.07
## 6	0.03	0.00	0.03
## COVID_24_55y_male_ICU COVID_25_55y_male_ICU COVID_26_41y_female_ICU			
## 1	0.22	0.29	0.42
## 2	0.01	0.00	0.00
## 3	0.11	0.09	0.18
## 4	0.02	0.03	0.00
## 5	0.15	0.00	0.87
## 6	0.00	0.00	0.00
## COVID_27_71y_female_ICU COVID_28_63y_male_ICU COVID_29_63y_female_ICU			
## 1	0.16	0.18	0.35
## 2	0.01	0.00	0.00
## 3	0.23	0.18	0.03
## 4	0.01	0.05	0.03
## 5	0.18	0.45	0.15
## 6	0.00	0.00	0.03
## COVID_30_54y_male_ICU COVID_31_50y_male_ICU COVID_32_72y_male_ICU			
## 1	0.23	0.15	0.34

## 2	0.00	0.00	0.01
## 3	0.11	0.47	0.04
## 4	0.01	0.00	0.00
## 5	0.00	0.00	0.29
## 6	0.00	0.03	0.00
## COVID_33_81y_male_NonICU	COVID_34_64y_female_NonICU		
## 1	0.35	0.36	
## 2	0.00	0.00	
## 3	0.30	0.11	
## 4	0.06	0.00	
## 5	0.26	0.12	
## 6	0.00	0.00	
## COVID_35_58y_female_NonICU	COVID_36_68y_male_NonICU	COVID_37_87y_male_NonICU	
## 1	0.26	0.18	0.20
## 2	0.00	0.01	0.00
## 3	0.51	0.09	0.09
## 4	0.02	0.00	0.07
## 5	0.16	0.08	0.31
## 6	0.00	0.00	0.00
## COVID_38_68y_male_ICU	COVID_39_80y_female_ICU	COVID_40_66y_male_ICU	
## 1	0.29	0.19	0.22
## 2	0.00	0.00	0.00
## 3	0.10	0.27	0.17
## 4	0.02	0.00	0.00
## 5	0.35	0.00	0.08
## 6	0.00	0.07	0.00
## COVID_41_74y_male_ICU	COVID_42_21y_female_ICU	COVID_43_83y_female_ICU	
## 1	0.19	0.24	0.29
## 2	0.00	0.01	0.00
## 3	0.14	0.33	0.00
## 4	0.00	0.01	0.00
## 5	0.19	0.39	0.11
## 6	0.00	0.00	0.00
## COVID_44_46y_male_ICU	COVID_45_62y_female_ICU	COVID_46_62y_male_ICU	
## 1	0.22	0.14	0.53
## 2	0.00	0.00	0.01
## 3	0.14	0.15	0.10
## 4	0.00	0.03	0.00
## 5	0.00	0.19	0.06
## 6	0.04	0.00	0.00
## COVID_47_78y_male_ICU	COVID_48_72y_female_ICU	COVID_49_73y_male_ICU	
## 1	0.08	0.19	0.48
## 2	0.01	0.00	0.00
## 3	0.04	0.06	0.09
## 4	0.03	0.01	0.03
## 5	0.60	0.23	0.00
## 6	0.00	0.06	0.00
## COVID_50_37y_male_ICU	COVID_51_58y_female_NonICU	COVID_52_71y_male_NonICU	
## 1	0.08	0.21	0.25
## 2	0.00	0.00	0.01
## 3	0.01	0.13	0.00
## 4	0.00	0.00	0.03
## 5	0.00	0.00	0.00
## 6	0.72	0.00	0.00

##	COVID_53_35y_female_NonICU	COVID_55_62y_female_ICU	COVID_56_33y_female_NonICU
## 1	0.25	0.09	0.28
## 2	0.00	0.00	0.00
## 3	0.64	0.09	0.16
## 4	0.10	0.01	0.09
## 5	0.00	0.00	0.23
## 6	0.00	0.00	0.00
##	COVID_57_30y_female_NonICU	COVID_58_62y_male_NonICU	COVID_59_55y_male_NonICU
## 1	0.42	0.39	0.33
## 2	0.00	0.00	0.00
## 3	0.27	0.08	0.10
## 4	0.01	0.00	0.00
## 5	0.19	0.00	0.07
## 6	0.05	0.00	0.00
##	COVID_60_49y_male_NonICU	COVID_61_54y_female_NonICU	COVID_62_78y_female_ICU
## 1	0.22	0.25	0.21
## 2	0.00	0.00	0.00
## 3	0.14	0.10	0.04
## 4	0.00	0.03	0.00
## 5	0.00	0.13	0.05
## 6	0.02	0.00	0.00
##	COVID_63_39y_female_ICU	COVID_64_65y_male_ICU	COVID_65_84y_male_NonICU
## 1	0.29	0.38	0.40
## 2	0.00	0.01	0.01
## 3	0.01	0.04	0.07
## 4	0.00	0.02	0.00
## 5	0.14	0.56	0.58
## 6	0.00	0.00	0.00
##	COVID_66_66y_female_NonICU	COVID_67_57y_male_ICU	COVID_68_79y_male_ICU
## 1	0.64	0.37	0.58
## 2	0.00	0.00	0.00
## 3	0.00	0.35	0.15
## 4	0.00	0.00	0.01
## 5	0.00	0.00	0.00
## 6	0.00	0.00	0.05
##	COVID_69_77y_female_NonICU	COVID_70_81y_male_NonICU	COVID_71_37y_male_ICU
## 1	0.52	0.27	0.07
## 2	0.00	0.00	0.01
## 3	0.29	0.07	0.12
## 4	0.02	0.00	0.01
## 5	0.00	0.00	0.00
## 6	0.00	0.06	0.00
##	COVID_72_50y_female_NonICU	COVID_73_82y_male_NonICU	COVID_74_55y_female_ICU
## 1	0.52	0.46	0.24
## 2	0.00	0.01	0.00
## 3	0.10	0.02	0.12
## 4	0.01	0.02	0.02
## 5	0.00	0.17	0.26
## 6	0.00	0.04	0.00
##	COVID_75_55y_male_NonICU	COVID_76_73y_female_ICU	COVID_77_55y_female_ICU
## 1	0.23	0.17	0.05
## 2	0.01	0.00	0.00
## 3	0.14	0.09	0.01
## 4	0.00	0.01	0.00

## 5	0.00	0.04	0.00
## 6	0.00	0.00	0.00
## COVID_78_80y_male_NonICU	COVID_79_27y_male_NonICU	COVID_80_71y_male_ICU	
## 1	0.19	0.08	0.28
## 2	0.00	0.01	0.00
## 3	0.20	0.03	0.05
## 4	0.00	0.00	0.00
## 5	0.00	0.00	0.05
## 6	0.00	0.00	0.00
## COVID_82_67y_male_NonICU	COVID_83_85y_female_NonICU		
## 1	0.39	0.47	
## 2	0.01	0.00	
## 3	0.10	0.18	
## 4	0.00	0.05	
## 5	0.00	0.00	
## 6	0.00	0.00	
## COVID_84_75y_female_NonICU	COVID_85_62y_male_ICU	COVID_86_52y_female_NonICU	
## 1	0.35	0.29	0.60
## 2	0.00	0.00	0.00
## 3	0.03	0.04	0.27
## 4	0.00	0.00	0.02
## 5	0.17	0.00	0.00
## 6	0.00	0.00	0.00
## COVID_87_61y_male_ICU	COVID_89_90y_female_NonICU	COVID_90_86y_female_NonICU	
## 1	0.65	0.20	0.40
## 2	0.00	0.00	0.00
## 3	0.15	0.07	0.05
## 4	0.00	0.03	0.01
## 5	0.00	0.14	0.31
## 6	0.00	0.00	0.02
## COVID_91_29y_female_NonICU	COVID_92_82y_female_ICU	COVID_93_81y_female_ICU	
## 1	0.60	0.34	0.37
## 2	0.00	0.00	0.00
## 3	0.03	0.02	0.11
## 4	0.02	0.04	0.00
## 5	0.05	0.58	0.05
## 6	0.00	0.00	0.00
## COVID_94_24y_female_NonICU	COVID_95_49y_male_NonICU	COVID_96_51y_male_NonICU	
## 1	0.81	0.37	1.61
## 2	0.00	0.01	0.00
## 3	0.17	0.20	0.02
## 4	0.02	0.02	0.00
## 5	0.00	0.15	0.00
## 6	0.06	0.00	0.00
## COVID_97_76y_male_ICU	COVID_98_81y_male_NonICU	COVID_99_71y_male_ICU	
## 1	0.19	0.78	0.33
## 2	0.00	0.00	0.00
## 3	0.02	0.26	0.02
## 4	0.05	0.00	0.00
## 5	0.12	0.37	0.04
## 6	0.03	0.00	0.00
## COVID_100_74y_female_NonICU	COVID_101_58y_male_ICU	COVID_102_84y_male_NonICU	
## 1	0.30	0.33	0.12
## 2	0.00	0.00	0.00

## 3	0.09	0.11	0.01
## 4	0.00	0.03	0.01
## 5	0.04	0.05	0.00
## 6	0.00	0.00	0.07
## COVID_103_83y_male_NonICU	NONCOVID_01_54y_female_NonICU		
## 1	0.20	0.89	
## 2	0.00	0.00	
## 3	0.03	0.04	
## 4	0.03	0.00	
## 5	0.04	0.00	
## 6	0.00	0.00	
## NONCOVID_02_65y_male_ICU	NONCOVID_03_65y_male_ICU	NONCOVID_04_90y_male_NonICU	
## 1	0.32	0.44	0.21
## 2	0.00	0.00	0.00
## 3	0.01	0.05	0.05
## 4	0.00	0.02	0.00
## 5	0.04	0.04	0.21
## 6	0.00	0.00	0.00
## NONCOVID_05_83y_female_NonICU	NONCOVID_06_75y_female_ICU		
## 1	0.31	0.89	
## 2	0.00	0.00	
## 3	0.01	0.14	
## 4	0.01	0.01	
## 5	0.00	0.00	
## 6	0.00	0.06	
## NONCOVID_07_50y_male_ICU	NONCOVID_08_53y_female_ICU		
## 1	0.45	0.47	
## 2	0.00	0.01	
## 3	0.07	0.04	
## 4	0.02	0.00	
## 5	0.00	0.15	
## 6	0.00	0.00	
## NONCOVID_09_49y_female_NonICU	NONCOVID_10_67y_male_ICU		
## 1	0.40	0.33	
## 2	0.00	0.00	
## 3	0.04	0.05	
## 4	0.00	0.01	
## 5	0.00	0.23	
## 6	0.00	0.08	
## NONCOVID_11_58y_female_NonICU	NONCOVID_12_82y_male_ICU		
## 1	0.58	0.12	
## 2	0.00	0.00	
## 3	0.03	0.02	
## 4	0.00	0.00	
## 5	0.00	0.00	
## 6	0.00	0.02	
## NONCOVID_13_65y_male_ICU	NONCOVID_14_75y_female_ICU		
## 1	0.31	0.16	
## 2	0.00	0.00	
## 3	0.04	0.08	
## 4	0.01	0.00	
## 5	0.32	0.05	
## 6	0.02	0.02	
## NONCOVID_15_83y_unknown_ICU	NONCOVID_16_40y_female_ICU		

## 1	0.59	0.34
## 2	0.00	0.00
## 3	0.03	0.07
## 4	0.04	0.00
## 5	0.00	0.13
## 6	0.19	0.00
##	NONCOVID_17_84y_female_ICU	NONCOVID_18_88y_male_ICU
## 1	0.37	0.33
## 2	0.00	0.00
## 3	0.07	0.06
## 4	0.01	0.00
## 5	0.18	0.00
## 6	0.00	0.00
##	NONCOVID_19_66y_female_ICU	NONCOVID_20_62y_female_ICU
## 1	0.25	0.20
## 2	0.00	0.00
## 3	0.11	0.01
## 4	0.00	0.02
## 5	0.04	0.00
## 6	0.03	0.07
##	NONCOVID_21_71y_male_NonICU	NONCOVID_22_63y_male_NonICU
## 1	0.40	0.30
## 2	0.00	0.00
## 3	0.04	0.02
## 4	0.02	0.02
## 5	0.00	0.00
## 6	0.00	0.00
##	NONCOVID_23_42y_female_NonICU	NONCOVID_24_32y_female_NonICU
## 1	0.70	0.75
## 2	0.00	0.00
## 3	0.02	0.27
## 4	0.01	0.00
## 5	0.00	0.06
## 6	0.00	0.00
##	NONCOVID_25_62y_male_NonICU	NONCOVID_26_36y_male_ICU
## 1	2.80	0.22
## 2	0.00	0.00
## 3	0.04	0.28
## 4	0.00	0.00
## 5	0.00	0.00
## 6	0.00	0.00

```
head(metadata)
```

##	participant_id	geo_accession	status
## 1	COVID_01_39y_male_NonICU	GSM4753021	Public on Aug 29 2020
## 2	COVID_02_63y_male_NonICU	GSM4753022	Public on Aug 29 2020
## 3	COVID_03_33y_male_NonICU	GSM4753023	Public on Aug 29 2020
## 4	COVID_04_49y_male_NonICU	GSM4753024	Public on Aug 29 2020
## 5	COVID_05_49y_male_NonICU	GSM4753025	Public on Aug 29 2020
## 6	COVID_06_:y_male_NonICU	GSM4753026	Public on Aug 29 2020
##	X.Sample_submission_date	last_update_date	type channel_count
## 1	Aug 28 2020	Aug 29 2020	SRA 1
## 2	Aug 28 2020	Aug 29 2020	SRA 1

```

## 3          Aug 28 2020      Aug 29 2020  SRA          1
## 4          Aug 28 2020      Aug 29 2020  SRA          1
## 5          Aug 28 2020      Aug 29 2020  SRA          1
## 6          Aug 28 2020      Aug 29 2020  SRA          1
##          source_name_ch1 organism_ch1      disease_status age  sex
## 1 Leukocytes from whole blood Homo sapiens disease state: COVID-19 39 male
## 2 Leukocytes from whole blood Homo sapiens disease state: COVID-19 63 male
## 3 Leukocytes from whole blood Homo sapiens disease state: COVID-19 33 male
## 4 Leukocytes from whole blood Homo sapiens disease state: COVID-19 49 male
## 5 Leukocytes from whole blood Homo sapiens disease state: COVID-19 49 male
## 6 Leukocytes from whole blood Homo sapiens disease state: COVID-19 : male
##      icu_status apacheii charlson_score mechanical_ventilation
## 1          no          15              0              yes
## 2          no unknown              2              no
## 3          no unknown              2              no
## 4          no unknown              1              no
## 5          no          19              1              yes
## 6          no unknown              1              no
## ventilator.free_days hospital.free_days_post_45_day_followup ferritin.ng.ml.
## 1              0              0              946
## 2              28              39             1060
## 3              28              18             1335
## 4              28              39              583
## 5              23              27              800
## 6              28              36              563
##      crp.mg.l. ddimer.mg.l_feu. procalcitonin.ng.ml.. lactate.mmol.l. fibrinogen
## 1       73.1          1.3          36          0.9          513
## 2    unknown          1.03          0.37      unknown      unknown
## 3       53.2          1.48          0.07      unknown          513
## 4      251.1          1.32          0.98          0.87          949
## 5      355.8          0.69          4.92          1.48          929
## 6      129.1      unknown          0.67          0.86          769
##      sofa
## 1         8
## 2    unknown
## 3    unknown
## 4    unknown
## 5         7
## 6    unknown

```

```

# checking structure of gene expression data and metadata data
#str(gene_expression)
#str(metadata)

```

```

# melting gene_expression data (using Tidyverse) from wide data to long data so the two files can be merged
gene_long <- gene_expression %>%
  tidyr::gather(key = "ParticipantID", value = "Expression", -X)

```

```

# renaming the gene column to "Gene"
names(gene_long)[names(gene_long) == "X"] <- "Gene"

```

```

# checking the first 6 rows of the melted data
head(gene_long)

```



```
##      Gene      ParticipantID Expression
## 1   A1BG COVID_01_39y_male_NonICU      0.49
## 2   A1CF COVID_01_39y_male_NonICU      0.00
## 3   A2M  COVID_01_39y_male_NonICU      0.21
## 4  A2ML1 COVID_01_39y_male_NonICU      0.04
## 5 A3GALT2 COVID_01_39y_male_NonICU      0.07
## 6  A4GALT COVID_01_39y_male_NonICU      0.00
```

```
# merging the melted gene expression data with the metadata using the shared column of "ParticipantID"
merged_data <- merge(gene_long, metadata, by.x = "ParticipantID", by.y = "participant_id")
head(merged_data)
```

```
##      ParticipantID      Gene Expression geo_accession
## 1 COVID_01_39y_male_NonICU  A1CF      0.00    GSM4753021
## 2 COVID_01_39y_male_NonICU  A1BG      0.49    GSM4753021
## 3 COVID_01_39y_male_NonICU  AADAC      0.00    GSM4753021
## 4 COVID_01_39y_male_NonICU AADACL2      0.00    GSM4753021
## 5 COVID_01_39y_male_NonICU AADACL3      0.00    GSM4753021
## 6 COVID_01_39y_male_NonICU AADACL4      0.00    GSM4753021
##      status X.Sample_submission_date last_update_date type
## 1 Public on Aug 29 2020      Aug 28 2020      Aug 29 2020 SRA
## 2 Public on Aug 29 2020      Aug 28 2020      Aug 29 2020 SRA
## 3 Public on Aug 29 2020      Aug 28 2020      Aug 29 2020 SRA
## 4 Public on Aug 29 2020      Aug 28 2020      Aug 29 2020 SRA
## 5 Public on Aug 29 2020      Aug 28 2020      Aug 29 2020 SRA
## 6 Public on Aug 29 2020      Aug 28 2020      Aug 29 2020 SRA
##      channel_count      source_name_ch1 organism_ch1
## 1      1 Leukocytes from whole blood Homo sapiens
## 2      1 Leukocytes from whole blood Homo sapiens
## 3      1 Leukocytes from whole blood Homo sapiens
## 4      1 Leukocytes from whole blood Homo sapiens
## 5      1 Leukocytes from whole blood Homo sapiens
## 6      1 Leukocytes from whole blood Homo sapiens
##      disease_status age sex icu_status apacheii charlson_score
## 1 disease state: COVID-19 39 male      no      15      0
## 2 disease state: COVID-19 39 male      no      15      0
## 3 disease state: COVID-19 39 male      no      15      0
## 4 disease state: COVID-19 39 male      no      15      0
## 5 disease state: COVID-19 39 male      no      15      0
## 6 disease state: COVID-19 39 male      no      15      0
##      mechanical_ventilation ventilator.free_days
## 1      yes      0
## 2      yes      0
## 3      yes      0
## 4      yes      0
## 5      yes      0
## 6      yes      0
##      hospital.free_days_post_45_day_followup ferritin.ng.ml. crp.mg.l.
## 1      0      946      73.1
## 2      0      946      73.1
## 3      0      946      73.1
## 4      0      946      73.1
## 5      0      946      73.1
## 6      0      946      73.1
```

```
##      ddimer.mg.l_feu.  procalcitonin.ng.ml.. lactate.mmol.l.  fibrinogen sofa
## 1          1.3              36              0.9          513      8
## 2          1.3              36              0.9          513      8
## 3          1.3              36              0.9          513      8
## 4          1.3              36              0.9          513      8
## 5          1.3              36              0.9          513      8
## 6          1.3              36              0.9          513      8
```

```
# filtered data using 'filter(Gene == A1CF)' to only extract rows for where the gene is A1CF
# selecting columns for the covariate variables that I picked
```

```
clean_data <- merged_data %>%
  filter(Gene == "ABCA1") %>%
  select(Gene, ParticipantID, Expression, age, sex, icu_status)

head(clean_data)
```

```
##      Gene      ParticipantID Expression age      sex icu_status
## 1 ABCA1  COVID_01_39y_male_NonICU    32.30  39    male      no
## 2 ABCA1  COVID_02_63y_male_NonICU    15.84  63    male      no
## 3 ABCA1  COVID_03_33y_male_NonICU    34.38  33    male      no
## 4 ABCA1  COVID_04_49y_male_NonICU    14.24  49    male      no
## 5 ABCA1  COVID_05_49y_male_NonICU    18.39  49    male      no
## 6 ABCA1  COVID_07_38y_female_NonICU   14.66  38  female      no
```

```
# checking data types of the columns
str(clean_data)
```

```
## 'data.frame': 125 obs. of 6 variables:
## $ Gene : chr "ABCA1" "ABCA1" "ABCA1" "ABCA1" ...
## $ ParticipantID: chr "COVID_01_39y_male_NonICU" "COVID_02_63y_male_NonICU" "COVID_03_33y_male_NonICU" ...
## $ Expression : num 32.3 15.8 34.4 14.2 18.4 ...
## $ age : chr "39" "63" "33" "49" ...
## $ sex : chr " male" " male" " male" " male" ...
## $ icu_status : chr " no" " no" " no" " no" ...
```

```
# converting age data to numeric - if not already
clean_data$age <- as.numeric(clean_data$age)
```

```
## Warning: NAs introduced by coercion
```

```
# converting sex and icu_status to factors - if not already
clean_data$sex <- as.factor(clean_data$sex)
clean_data$icu_status <- as.factor(clean_data$icu_status)
```

```
# confirming conversions
str(clean_data)
```

```
## 'data.frame': 125 obs. of 6 variables:
## $ Gene : chr "ABCA1" "ABCA1" "ABCA1" "ABCA1" ...
## $ ParticipantID: chr "COVID_01_39y_male_NonICU" "COVID_02_63y_male_NonICU" "COVID_03_33y_male_NonICU" ...
## $ Expression : num 32.3 15.8 34.4 14.2 18.4 ...
```

```
## $ age      : num  39 63 33 49 49 38 78 64 62 74 ...
## $ sex      : Factor w/ 3 levels " female"," male",...: 2 2 2 2 2 1 2 1 2 1 ...
## $ icu_status : Factor w/ 2 levels " no"," yes": 1 1 1 1 1 1 2 2 2 1 ...
```

```
# removing rows with missing values to 'final_data' which will be utilized for data visualization
final_data <- clean_data %>%
```

```
  filter(!is.na(sex) & sex != " unknown",
         !is.na(icu_status) & icu_status != " unknown")
```

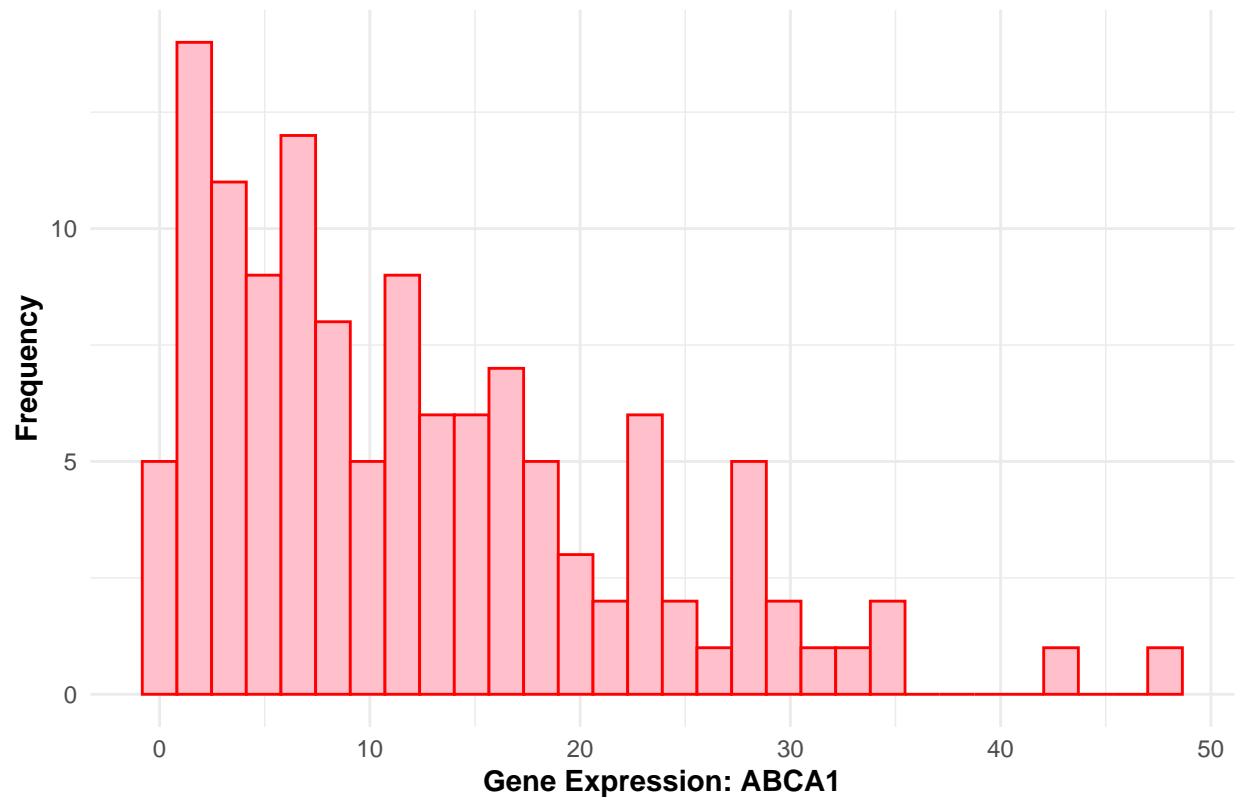
```
#Histogram for Gene Expression
```

```
library(ggplot2)
```

```
# initializes the plot with 'final_data' and maps all 'Expression' values to the x-axis
ggplot(final_data, aes(x = Expression)) +
  geom_histogram(fill = "pink", color = "red") +
  # plots the histogram with bars outlined and filled
  labs(title = "Histogram of Gene Expression for ABCA1", # adds title and axis labels
        x = "Gene Expression: ABCA1",
        y = "Frequency") +
  theme_minimal() + # applied minimal theme for appearance
  theme( # making the titles of plot and axis bold
        plot.title = element_text(hjust = 0.5, face = "bold"),
        axis.title = element_text(face = "bold"),
        legend.title = element_text(face = "bold")
  )
```

```
## 'stat_bin()' using 'bins = 30'. Pick better value with 'binwidth'.
```

**Histogram of Gene Expression for ABCA1**



```
# Scatterplot for gene expression and continuous covariate (Age)
```

```
library(ggplot2)
```

```
# initializes the plot with 'final_data' and maps all 'age' values to x-axis 'Expression' values to the
```

```
ggplot(final_data,aes(x = age,y = Expression ,color = age)) +
```

```
  geom_point() +
```

```
  scale_color_gradient(low = "green", high = "blue") + # color gradient for age
```

```
  labs(title = "Scatterplot of Gene Expression for ABCA1 vs. Age (yrs.)", # title for plot and axis
```

```
        subtitle = "Color indicates age, ranging from green (young) to blue (old)",
```

```
        x = "Age (yrs.)",
```

```
        y = "Gene Expression: ABCA1",
```

```
        color = "Age") +
```

```
  theme_minimal() +
```

```
  theme( # making the titles of axis and plot bold
```

```
    plot.title = element_text(hjust = 0.5, face = "bold"),
```

```
    plot.subtitle = element_text(hjust = 0.5),
```

```
    axis.title = element_text(face = "bold"),
```

```
    legend.title = element_text(face = "bold")
```

```
  ) +
```

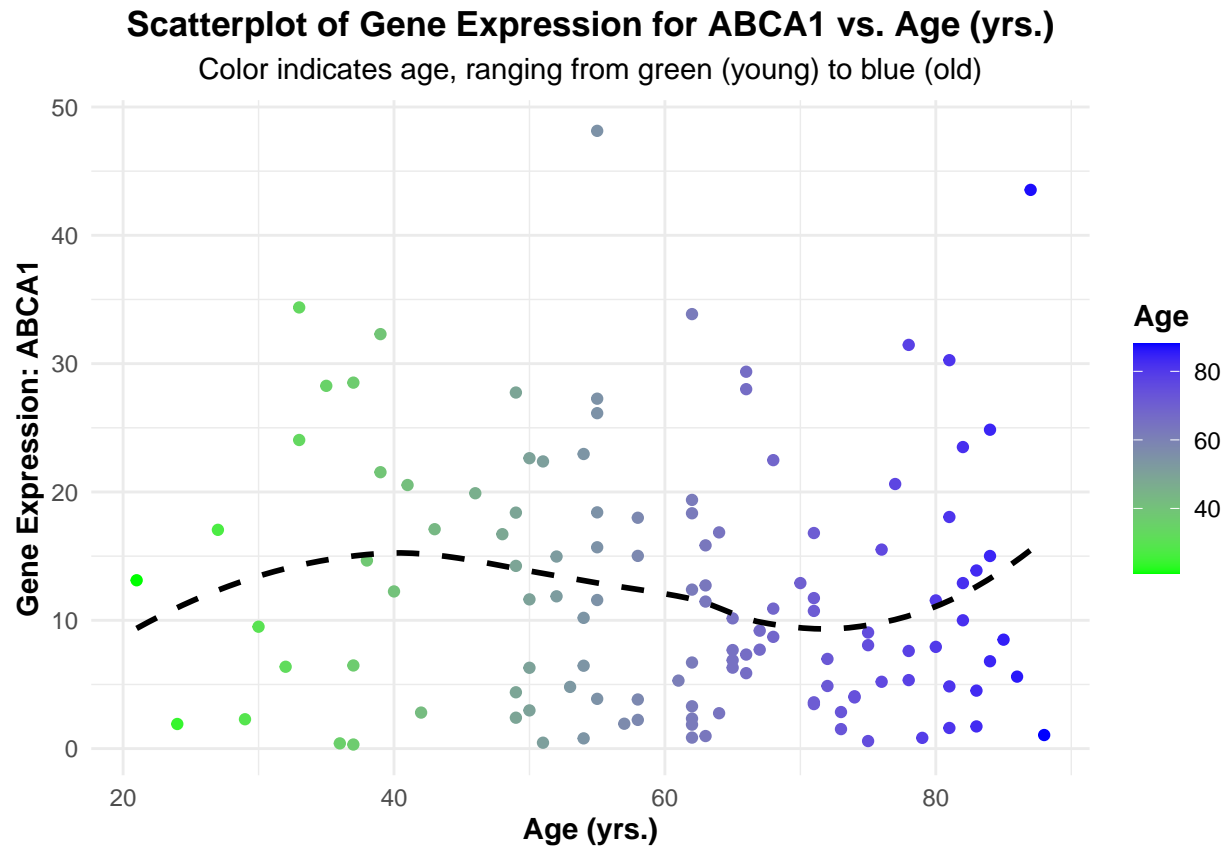
```
# adding a smooth line to show trend in data
```

```
geom_smooth(method = "loess", se = FALSE, color = "black", linetype = "dashed")
```

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

```
## Warning: Removed 2 rows containing non-finite outside the scale range
## ('stat_smooth()').
```

```
## Warning: Removed 2 rows containing missing values or values outside the scale range
## ('geom_point()').
```



```
# Boxplot of gene expression separated by both categorical covariates (Sex and ICU Status)

library(ggplot2)
library(harrypotter)

# create boxplot with categorical covariates
ggplot(final_data, aes(x = sex, y = Expression, fill = icu_status)) +
  geom_boxplot(outlier.shape = 12, outlier.size = 2, color = "darkgray", lwd = 0.8, alpha = 0.7) +
  scale_fill_hp_d(option = "ronweasley") + # change border color and box details
  facet_wrap(~ icu_status) + # separate plots by ICU status
  labs(title = "Boxplot of Gene Expression by Sex and ICU Status", # assigned titles for axis and plot
       x = "Sex",
       y = "Gene Expression",
       fill = "ICU Status") +
  theme_minimal(base_size = 15) + # minimal theme with font size
  theme( # making the titles of axis and plot bold, changing placement of titles
        plot.title = element_text(hjust = 0.125, face = "bold"),
        axis.title = element_text(face = "bold"),
        legend.title = element_text(face = "bold"))
)
```

## Boxplot of Gene Expression by Sex and ICU Status

