

R Projects

2024-07-25

R Markdown

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When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
# READ IN CSV FILES
```

```
setwd("/Users/sarahmirza/Documents/GitHub/QBS103_Repository/") # set the working directory
genes.df <- read.csv(file = "QBS103_GSE157103_genes.csv")
head(genes.df) # see if it worked
```

```
##           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
```

```
matrix.df <- read.csv(file="QBS103_GSE157103_series_matrix.csv")
head(matrix.df)
```

```
##      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
```

```
# GENES DATA FRAME - transpose
```

```
genes.df <- as.data.frame(t(genes.df)) # transpose, convert rows to columns and columns to rows
names(genes.df) <- genes.df[1,] #set the first row in the data frame and set it to the column names for
genes.df <- genes.df[-1,] # remove the first row in the data frame so that the names are no longer a row
```

```
genes.df$participant_id <- row.names(genes.df) # make new row called participant_id and with the gene.d
merged_matrix <- merge(genes.df,matrix.df,by = "participant_id") # merge the two data frames using participant_id
head(merged_matrix) # see if it worked
```

```
##      participant_id A1BG A1CF A2M A2ML1 A3GALT2 A4GALT A4GNT
## 1 COVID_01_39y_male_NonICU 0.49 0.00 0.21 0.04 0.07 0.00 0.03
## 2 COVID_02_63y_male_NonICU 0.29 0.00 0.14 0.00 0.00 0.00 0.05
## 3 COVID_03_33y_male_NonICU 0.26 0.00 0.03 0.02 0.00 0.00 0.07
## 4 COVID_04_49y_male_NonICU 0.45 0.01 0.09 0.07 0.00 0.00 0.00
## 5 COVID_05_49y_male_NonICU 0.17 0.00 0.00 0.05 0.07 0.00 0.00
## 6 COVID_07_38y_female_NonICU 0.49 0.01 0.23 0.03 0.07 0.00 0.00
##      AAAS AACS AADAC AADACL2 AADACL3 AADACL4 AADAT AAGAB AAK1 AAMDC
## 1 18.92 4.07 0.00 0.00 0.00 0.00 0.00 22.93 7.12 17.19
## 2 18.68 3.00 0.00 0.00 0.06 0.00 0.00 21.69 6.46 13.06
## 3 13.85 1.83 0.00 0.00 0.00 0.00 0.00 18.27 3.92 13.35
## 4 22.11 4.22 0.00 0.00 0.00 0.00 0.00 26.69 8.74 17.53
## 5 8.45 1.17 0.00 0.00 0.00 0.00 0.03 17.02 7.26 10.14
## 6 28.59 4.24 0.00 0.00 0.00 0.00 0.03 26.28 12.78 12.62
##      AAMP AANAT AAR2 AARD AARS1 AARS2 AARS1 AASDH AASDHPPT AASS
## 1 61.08 0.31 21.59 0.18 13.52 2.43 9.63 6.38 19.45 0.21
## 2 54.54 0.00 19.22 0.08 13.91 2.15 11.80 4.83 12.14 0.42
## 3 25.19 0.65 8.72 0.05 5.60 1.08 4.04 2.76 7.64 0.04
## 4 67.95 0.08 20.83 0.03 15.34 2.69 14.61 8.23 18.94 0.41
## 5 18.29 1.02 7.46 0.10 6.29 0.55 5.32 5.23 11.54 0.21
```


## 6	51.35	0.13	23.90	0.12	29.47	4.35	21.09	8.90	23.49	0.63	
##	AATF	AATK	ABAT	ABCA1	ABCA10	ABCA12	ABCA13	ABCA2	ABCA3	ABCA4	ABCA5
## 1	45.83	5.60	9.63	32.30	0.32	0.00	0.49	8.47	0.37	0.01	1.86
## 2	39.37	9.79	10.36	15.84	0.37	0.00	3.36	9.49	0.71	0.00	2.81
## 3	42.35	5.34	4.59	34.38	0.29	0.00	0.26	14.24	0.17	0.00	2.17
## 4	41.92	4.73	11.02	14.24	0.31	0.00	0.13	6.37	0.94	0.00	2.94
## 5	30.56	1.50	4.42	18.39	0.19	0.00	0.16	5.90	0.17	0.00	1.38
## 6	44.16	4.16	12.02	14.66	0.55	0.00	0.23	9.16	0.75	0.00	3.60
##	ABCA6	ABCA7	ABCA8	ABCA9	ABCB1	ABCB10	ABCB11	ABCB4	ABCB5	ABCB6	ABCB7
## 1	0.19	39.31	0.00	0.27	1.61	15.59	0.38	0.01	0.04	2.77	6.42
## 2	0.11	30.42	0.00	0.20	1.68	10.98	0.25	0.19	0.04	2.52	5.80
## 3	0.07	54.85	0.00	0.33	0.59	4.04	0.14	0.09	0.15	3.14	2.59
## 4	0.02	18.91	0.01	0.30	3.14	10.00	0.18	0.74	0.11	2.11	7.42
## 5	0.03	23.28	0.00	0.21	1.66	5.69	0.07	0.21	0.04	1.14	3.40
## 6	0.05	30.95	0.00	0.23	4.20	15.09	0.18	0.81	0.11	3.99	7.33
##	ABCB8	ABCB9	ABCC1	ABCC10	ABCC11	ABCC12	ABCC2	ABCC3	ABCC4	ABCC5	ABCC6
## 1	2.95	0.20	11.20	8.85	0.04	0.00	1.65	7.19	5.96	14.83	6.62
## 2	2.35	0.51	9.39	4.46	0.01	0.00	1.31	16.21	4.49	22.21	5.87
## 3	1.57	0.05	4.74	4.08	0.09	0.00	1.72	1.44	0.58	13.02	3.13
## 4	2.71	0.31	13.05	5.75	0.02	0.01	1.55	11.11	4.09	17.49	3.37
## 5	0.71	0.12	4.29	1.91	0.02	0.00	2.56	3.13	7.37	5.53	1.66
## 6	3.51	1.11	12.24	7.33	0.02	0.00	1.57	5.34	8.10	23.46	3.61
##	ABCC8	ABCC9	ABCD1	ABCD2	ABCD3	ABCD4	ABCE1	ABCF1	ABCF2	ABCF2-H2BE1	
## 1	0.00	1.53	11.26	1.55	10.62	11.19	14.09	24.40	8.77		11.67
## 2	0.00	1.89	4.65	1.08	11.23	9.86	15.52	16.84	7.21		8.84
## 3	0.00	1.97	5.83	0.39	3.99	7.83	4.50	7.89	3.12		3.06
## 4	0.00	2.82	4.80	1.74	12.38	13.60	21.20	23.92	8.26		12.51
## 5	0.00	1.84	1.93	0.59	8.19	5.43	7.16	12.33	2.76		4.72
## 6	0.00	2.31	3.96	5.25	13.14	12.96	28.46	28.37	11.28		13.61
##	ABCF3	ABCG1	ABCG2	ABCG4	ABCG5	ABCG8	ABHD1	ABHD10	ABHD11	ABHD12	ABHD12B
## 1	23.37	32.76	0.17	0.01	0.00	0.02	0.04	14.74	8.50	14.66	0.55
## 2	18.63	23.76	0.00	0.07	0.00	0.01	0.14	10.57	8.85	9.02	1.18
## 3	11.57	41.14	0.15	0.00	0.00	0.00	0.00	6.84	8.22	4.84	0.88
## 4	23.62	15.72	0.14	0.00	0.00	0.04	0.31	16.73	9.64	13.22	0.68
## 5	9.86	9.43	0.03	0.00	0.00	0.04	0.04	6.93	4.02	3.36	0.68
## 6	25.96	14.96	0.05	0.05	0.00	0.02	0.38	18.21	8.27	13.35	0.32
##	ABHD13	ABHD14A	ABHD14A-ACY1	ABHD14B	ABHD15	ABHD16A	ABHD16B	ABHD17A	ABHD17B		
## 1	15.58	6.89		0.00	18.53	6.82	77.48	0.29	13.79	8.78	
## 2	14.33	7.08		0.00	18.78	5.76	57.11	0.19	11.89	7.38	
## 3	9.97	2.12		0.00	7.63	2.41	77.73	0.08	6.88	5.59	
## 4	16.70	9.21		0.00	28.23	8.12	56.77	0.05	12.28	9.89	
## 5	21.02	1.95		0.00	6.49	2.26	63.66	0.04	4.11	6.64	
## 6	16.37	13.20		0.17	36.75	8.38	57.29	0.18	12.89	11.82	
##	ABHD17C	ABHD18	ABHD2	ABHD3	ABHD4	ABHD5	ABHD6	ABHD8	ABI1	ABI2	
## 1	1.37	6.93	46.50	73.51	44.47	60.14	3.47	3.27	75.36	3.22	
## 2	3.34	5.10	63.70	80.70	44.43	79.17	4.54	0.99	60.41	3.68	
## 3	1.64	4.06	36.05	113.96	37.71	77.50	2.15	2.59	61.63	0.67	
## 4	1.24	6.57	54.52	106.44	41.75	69.89	7.84	1.86	66.52	4.99	
## 5	1.17	7.94	72.44	190.95	29.65	51.39	1.45	1.11	79.84	2.12	
## 6	2.60	7.49	44.91	121.66	31.88	41.47	5.11	2.22	66.89	5.82	
##	geo_accession				status	X.Sample_submission_date		last_update_date			
## 1	GSM4753021	Public	on	Aug 29 2020				Aug 28 2020		Aug 29 2020	
## 2	GSM4753022	Public	on	Aug 29 2020				Aug 28 2020		Aug 29 2020	
## 3	GSM4753023	Public	on	Aug 29 2020				Aug 28 2020		Aug 29 2020	

```

## 4    GSM4753024 Public on Aug 29 2020          Aug 28 2020      Aug 29 2020
## 5    GSM4753025 Public on Aug 29 2020          Aug 28 2020      Aug 29 2020
## 6    GSM4753027 Public on Aug 29 2020          Aug 28 2020      Aug 29 2020
##      type channel_count      source_name_ch1 organism_ch1
## 1 SRA          1 Leukocytes from whole blood Homo sapiens
## 2 SRA          1 Leukocytes from whole blood Homo sapiens
## 3 SRA          1 Leukocytes from whole blood Homo sapiens
## 4 SRA          1 Leukocytes from whole blood Homo sapiens
## 5 SRA          1 Leukocytes from whole blood Homo sapiens
## 6 SRA          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 63   male      no      unknown          2
## 3 disease state: COVID-19 33   male      no      unknown          2
## 4 disease state: COVID-19 49   male      no      unknown          1
## 5 disease state: COVID-19 49   male      no      19              1
## 6 disease state: COVID-19 38   female    no      unknown          7
##      mechanical_ventilation ventilator.free_days
## 1                yes              0
## 2                no              28
## 3                no              28
## 4                no              28
## 5                yes              23
## 6                no              28
##      hospital.free_days_post_45_day_followup ferritin.ng.ml. crp.mg.l.
## 1                0              946      73.1
## 2               39             1060    unknown
## 3               18             1335     53.2
## 4               39              583    251.1
## 5               27              800    355.8
## 6               42              366    unknown
##      ddimer.mg.l_feu. procalcitonin.ng.ml.. lactate.mmol.l. fibrinogen      sofa
## 1                1.3              36              0.9      513      8
## 2                1.03             0.37      unknown    unknown    unknown
## 3                1.48             0.07      unknown      513    unknown
## 4                1.32             0.98      0.87      949    unknown
## 5                0.69             4.92      1.48      929      7
## 6                0.87             0.06      1.17      478    unknown

```

```
# Load required package
```

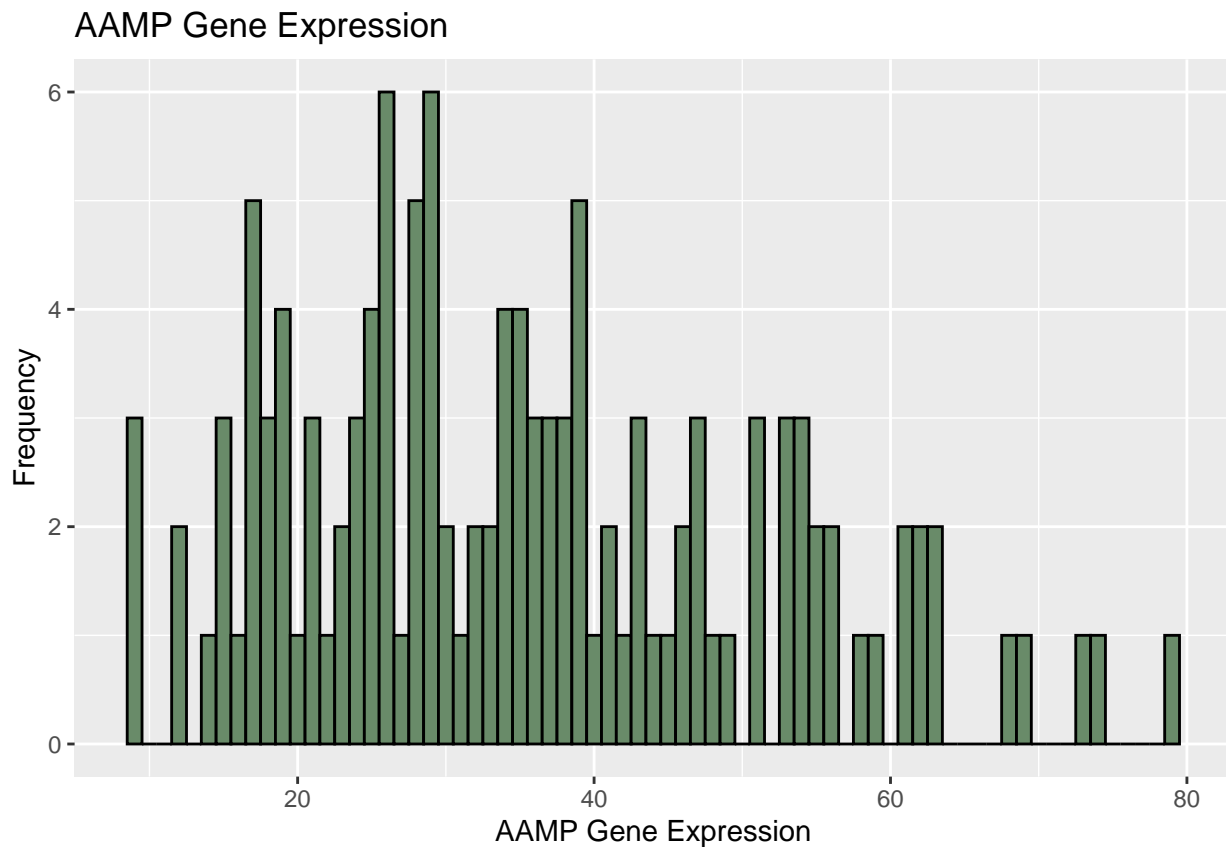
```
library(ggplot2)
```

```
# Convert AAMP to numeric to read into histogram easier
```

```
merged_matrix$AAMP <- as.numeric(merged_matrix$AAMP)
```

```
# Create histogram using the new data frame, the gene chosen was AAMP
```

```
histo <- ggplot(merged_matrix, aes(x = AAMP)) +
  geom_histogram(binwidth = 1, fill = "darkseagreen4", color = "black") +
  labs(title = "AAMP Gene Expression",
       x = "AAMP Gene Expression",
       y = "Frequency")
plot(histo)
```



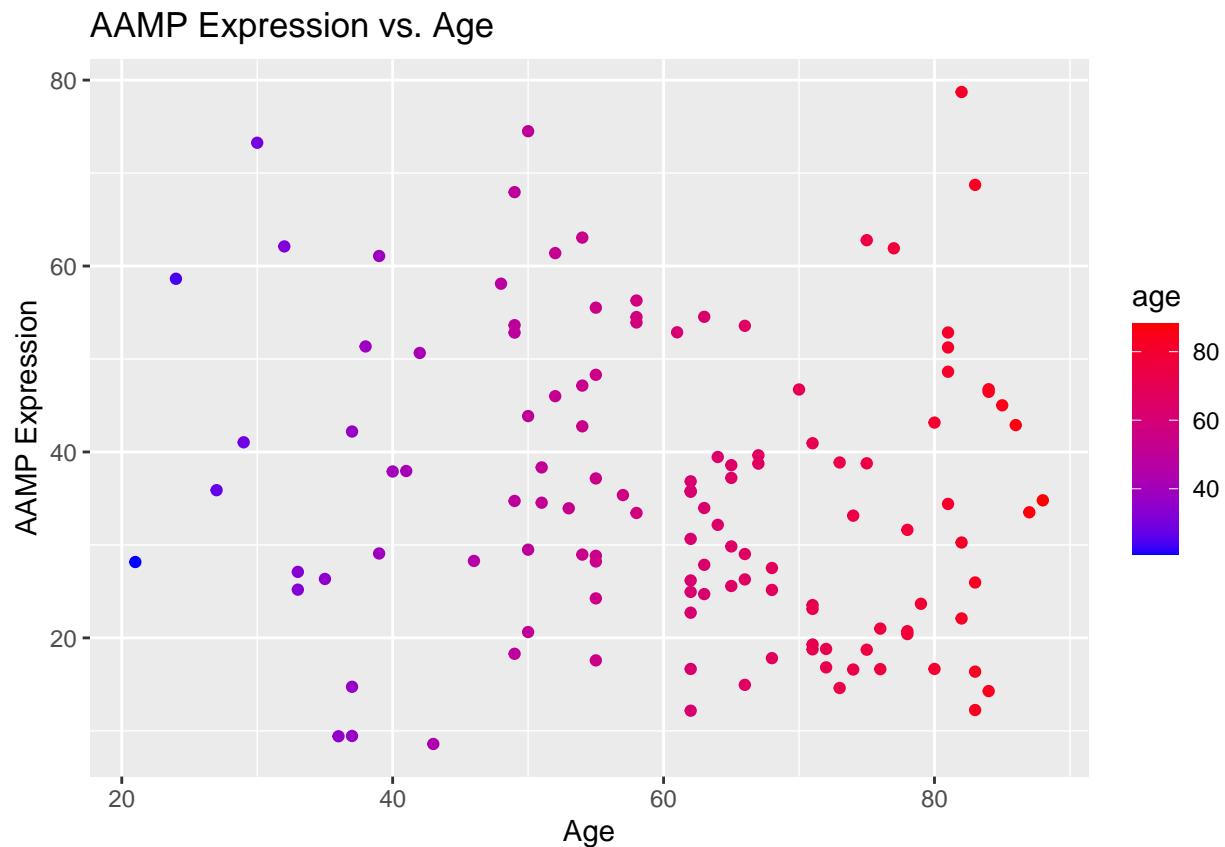
```
library(ggplot2)
setwd("/Users/sarahmirza/Documents/GitHub/QBS103_Repository/")

# Convert columns to numeric for a gradient label
merged_matrix$AAMP <- as.numeric(merged_matrix$AAMP)
merged_matrix$age <- as.numeric(merged_matrix$age)

## Warning: NAs introduced by coercion

# Create scatterplot of AAMP expression vs. age
scatter <- ggplot(merged_matrix, aes(x = age, y = AAMP, color = age)) + # color = age gives the color bar
  geom_point() +
  scale_color_gradient(low = "blue", high = "red") +
  labs(title = "AAMP Expression vs. Age",
       x = "Age",
       y = "AAMP Expression")
plot(scatter)

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

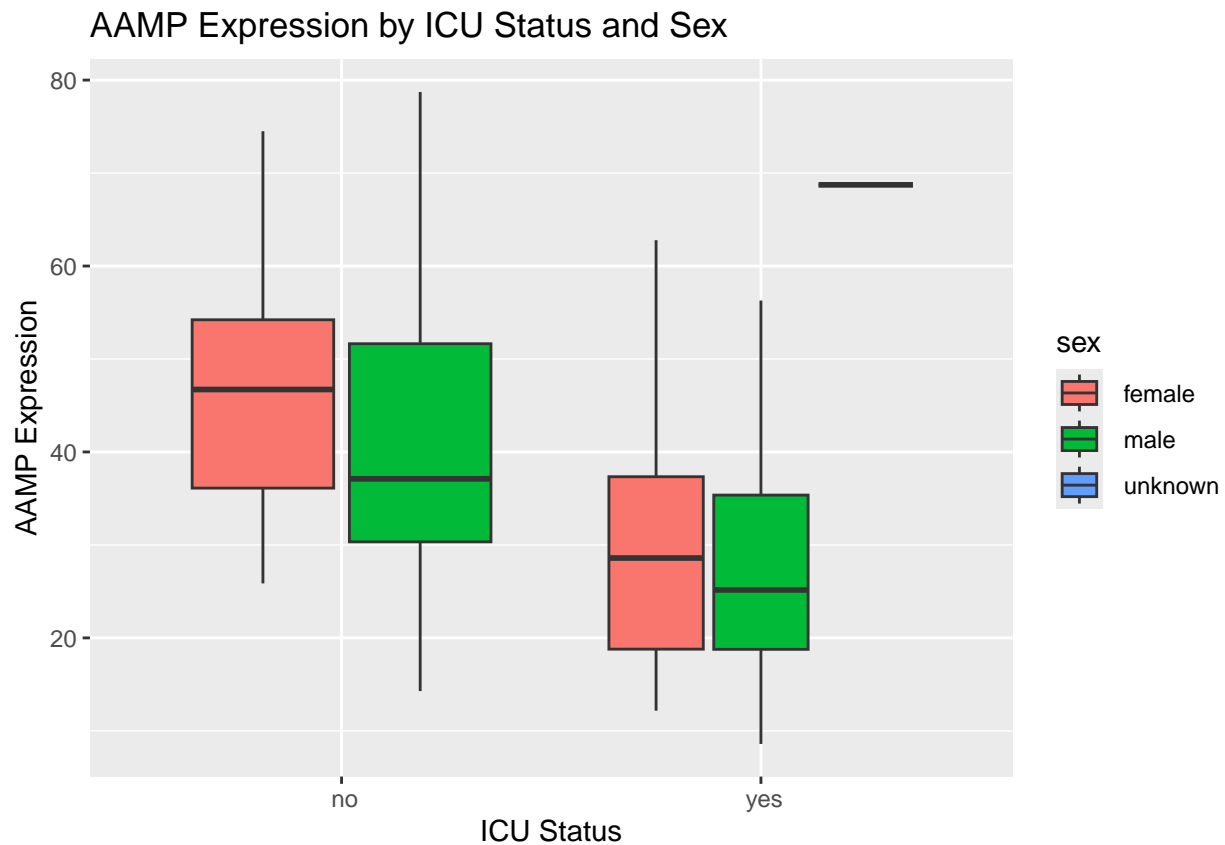


```
# Save the plot to a file
ggsave("AAMP_gene_expression_vs_age.pdf", plot = scatter, width = 8, height = 5)

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

library(ggplot2)
setwd("/Users/sarahmirza/Documents/GitHub/QBS103_Repository/")

#a boxplot of AAMP expression separated by sex and ICU Status
ggplot(merged_matrix, aes(x = icu_status, y = AAMP, fill = sex)) +
  geom_boxplot() +
  labs(title = "AAMP Expression by ICU Status and Sex",
       x = "ICU Status",
       y = "AAMP Expression",
       fill = "sex")
```



```
#merged_matrix$ferritin.ng.ml. <- as.factor(merged_matrix$ferritin.ng.ml.)
#merged_matrix$icu_status <- as.factor(merged_matrix$icu_status)

# Create a boxplot of AAMP expression separated by icu status and ferritin.ng.ml.
#ggplot(merged_matrix, aes(x = icu_status, y = AAMP, fill = ferritin.ng.ml.)) +
#  geom_boxplot() +
#  labs(title = "AAMP Expression by ICU Status and ferritin.ng.ml.",
#        x = "ICU Status",
#        y = "AAMP Expression",
#        fill = "ferritin.ng.ml.")

# Create a boxplot of AAMP expression separated by source_name_ch1 and icu status
#ggplot(merged_matrix, aes(icu_status, y = AAMP, fill = source_name_ch1)) +
#  geom_boxplot() +
#  labs(title = "AAMP Expression by ICU Status and source_name_ch1",
#        x = "icu_status",
#        y = "AAMP Expression",
#        fill = "source_name_ch1")
```