Final_Project_Presentation_1

Sai_Lakkireddy

2023-07-24

Importing and combining the Data from two csv files

Steps:
1. Import both the csv files
2. Convert the gene expression into long format
3. Inner join it with meta data

```
#set current working directory to the previous folder
setwd("../")

#import the geneExpression and metaData csv from the data folder
data_gene_Expression <- read.csv("data/QBS103_finalProject_geneExpression.csv", header=TRUE)
data_meta <- read.csv("data/QBS103_finalProject_metadata.csv", header=TRUE)


#We convert the geneExpression data from wide form into long form
data_gene_Expression.longForm <- data_gene_Expression %>%
  pivot_longer(cols = starts_with(c("COVID_","NONCOVID_")),
  names_to = "participant_id",
  values_to = "gene_expression_value"
  )

#make a final data frame by combining the two data sets and making it a data frame
final_df <- as.data.frame(data_gene_Expression.longForm %>% inner_join( data_meta,
           by=c('participant_id')))
```

Pre-processing the data

Steps:
1. Remove “unknown” strings and prefixes
2. Convert the class the columns to their appropriate type

```
#rename with x column with gene
final_df <- rename(final_df, gene = X)

#remove all unknown strings and substitute it with NAs
final_df[, 16:27][final_df[, 16:27] == ' unknown' | final_df[, 16:27] == 'unknown'] <- NA
```

```r
#format the disease status column to just include the status
final_df$disease_status <- sub('disease state: ', '', final_df$disease_status)

#convert the column type of disease_status, sex, icu_status and mechanical_ventilation to factor
final_df <- final_df %>%
  mutate_at(vars(disease_status, sex, icu_status, mechanical_ventilation), as.factor)

#convert the class of age, charlson_score
final_df <- final_df %>%
  mutate_at(vars(age, apacheii,ferritin.ng.ml., crp.mg.l., ddimer.mg.l_feu., procalcitonin.ng.ml.., lac
```

Optional - handle missing values

```r
# check all the numeric colums
num_cols <- names(select_if(final_df, is.numeric))

# Create an imputation model
imputation_model <- mice(final_df[num_cols], method = "pmm", printFlag = FALSE)

# Perform the imputation
imputed_data_final <- complete(imputation_model)
# update the final data frame with the imputed values
final_df[num_cols] <- imputed_data_final[num_cols]
```

Create a sub set with a chosen continous covariate and 2 categorical covariates

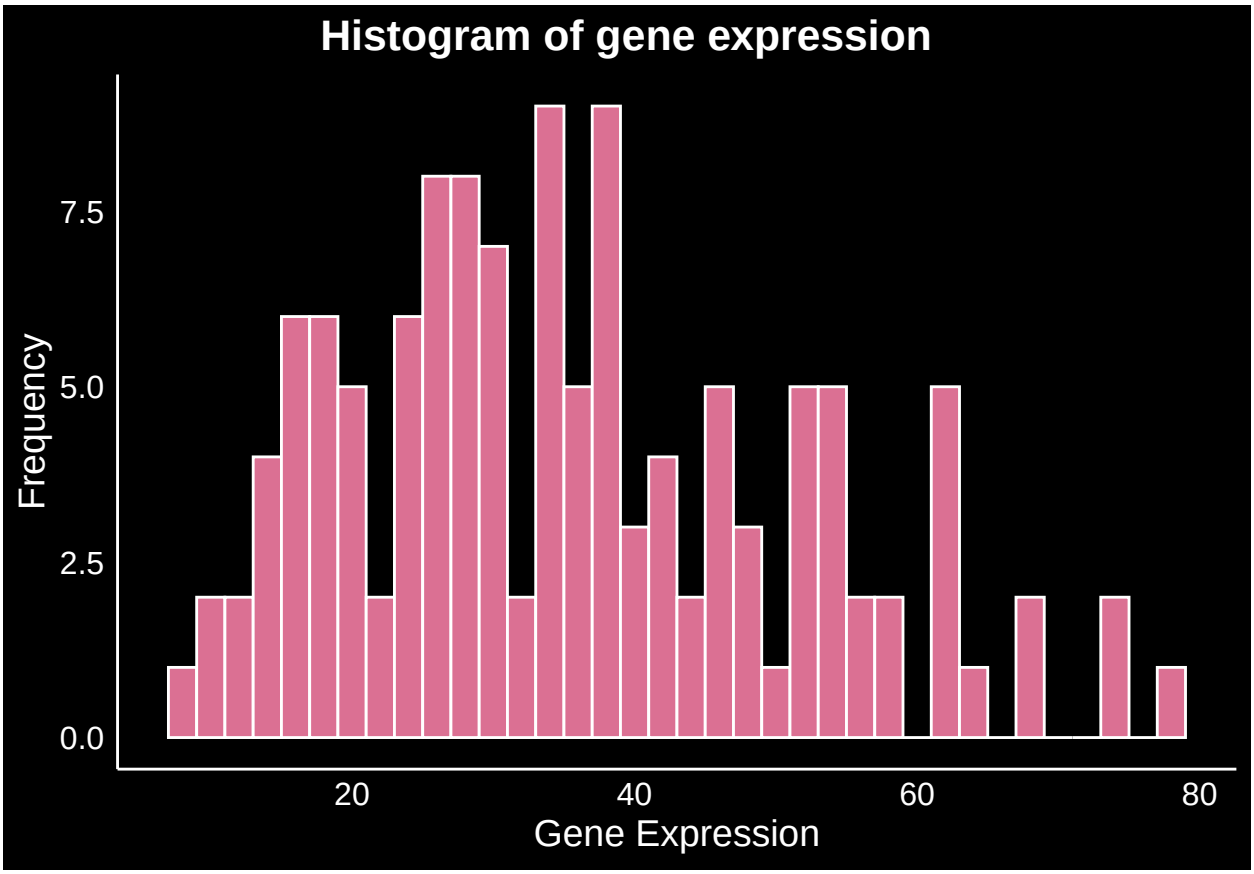
```r
final_subset <- final_df[final_df$gene == 'AAMP', c('gene','gene_expression_value','age', 'icu_status',

head(final_subset)
```

```
##      gene gene_expression_value age icu_status disease_status
## 4501 AAMP                61.08  39         no       COVID-19
## 4502 AAMP                54.54  63         no       COVID-19
## 4503 AAMP                25.19  33         no       COVID-19
## 4504 AAMP                67.95  49         no       COVID-19
## 4505 AAMP                18.29  49         no       COVID-19
## 4506 AAMP                51.35  38         no       COVID-19
```

Histogram for Gene Expression

```r
ggplot(final_subset, aes(x = gene_expression_value)) +
  geom_histogram(binwidth = 2, color = "white", fill = "#DB7093") +
  theme_minimal() +
  theme(
    panel.background = element_rect(fill = "black"),
    plot.background = element_rect(fill = "black"),
    axis.line = element_line(color = "white"),
```

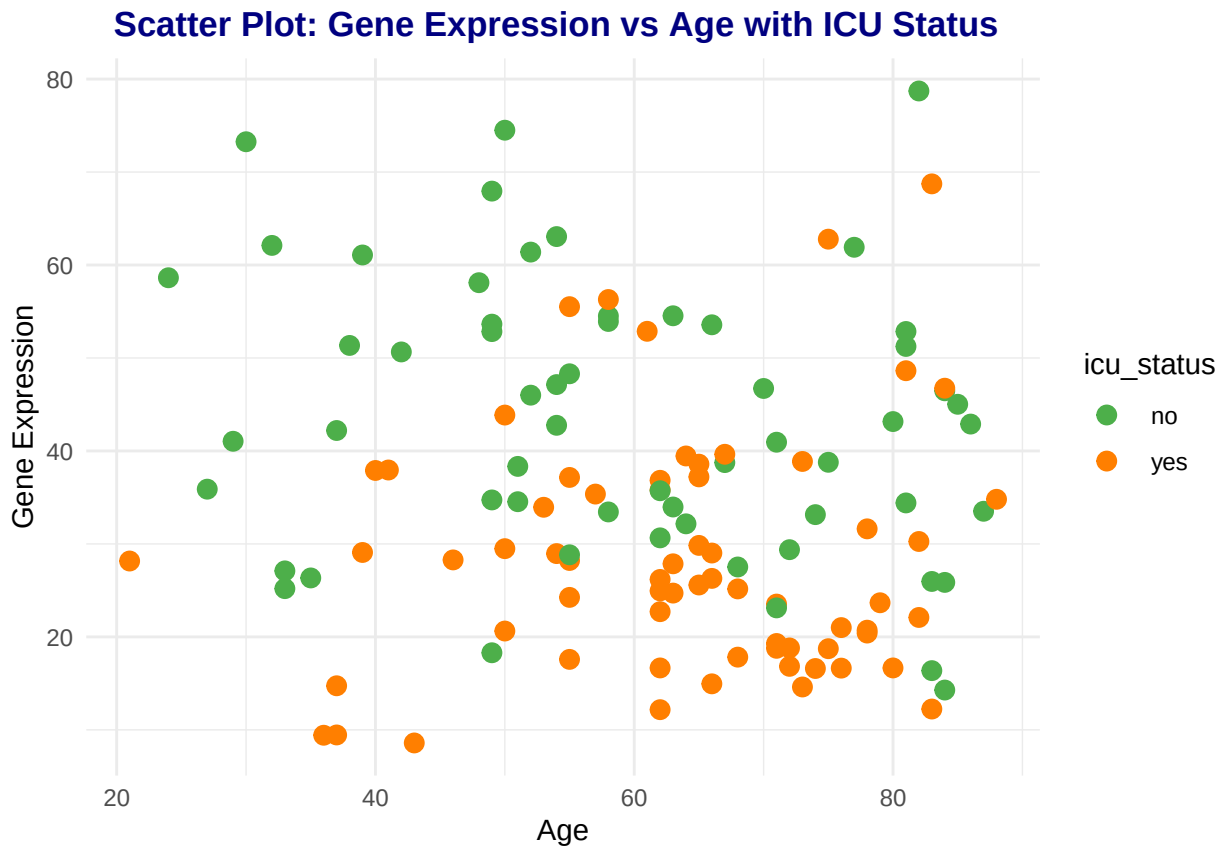
```
    axis.text = element_text(color = "white", size = 12),
    axis.title = element_text(color = "white", size = 14),
    panel.grid = element_blank(),
    plot.title = element_text(color = "white", size = 16, face = "bold", hjust = 0.4),
  ) +
  ggtitle("Histogram of gene expression") +
  xlab("Gene Expression") +
  ylab("Frequency")
```



Scatter plot: Age vs Gene Expression factoring for ICU status

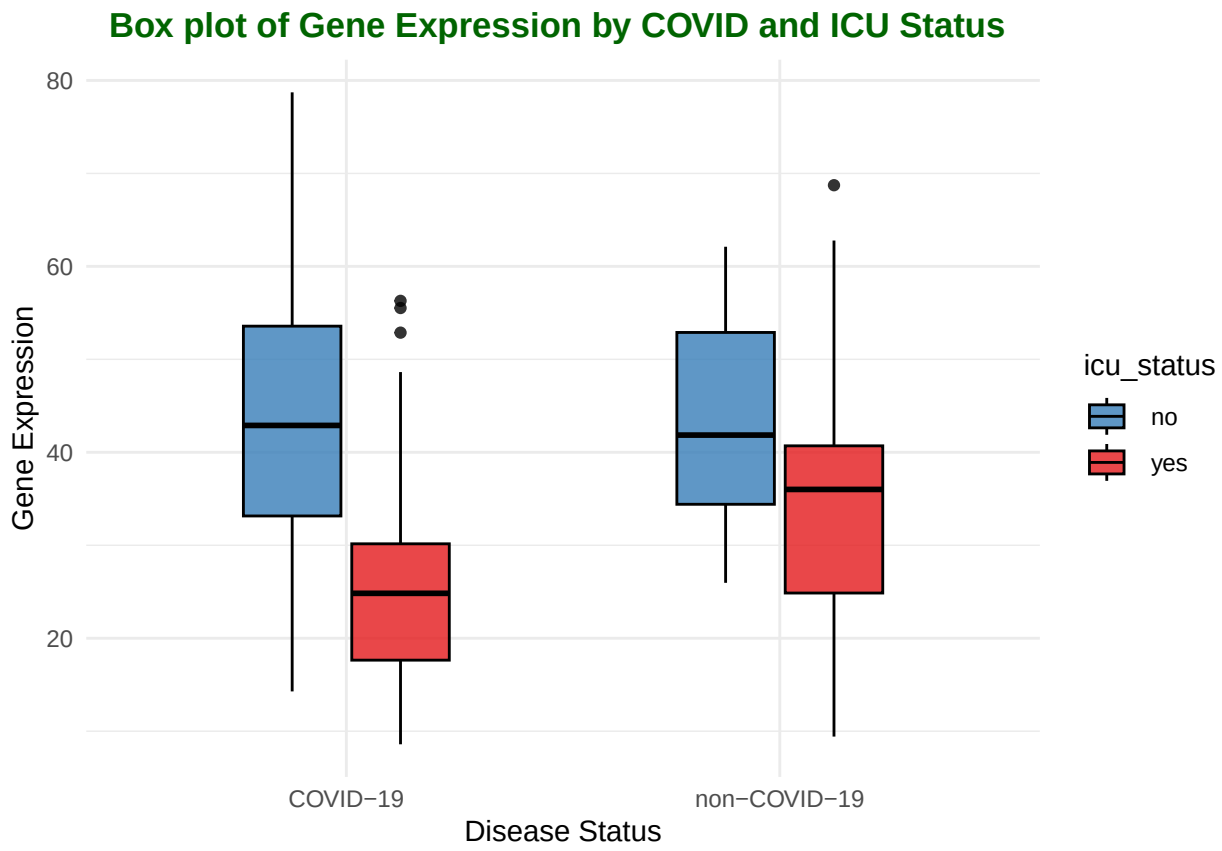
```
my_colors_1 <- c("#4DAF4A", "#FF7F00")


# Create the scatter plot with custom color scheme
ggplot(final_subset, aes(x = age, y = gene_expression_value, color = icu_status)) +
  geom_point(size = 3) +
  scale_color_manual(values = my_colors_1) +
  theme_minimal() +
      theme(
    plot.title = element_text(color = "navy", size = 13, face = "bold", hjust = 0.4)
  ) +
  ggtitle("Scatter Plot: Gene Expression vs Age with ICU Status") +
```

```
  xlab("Age") +
  ylab("Gene Expression")
```



Box plot: Gene Expression by COVID and ICU Status

```
my_colors_2 <- c("#377eb8", "#e41a1c")
ggplot(final_subset, aes(x = disease_status, y = gene_expression_value, fill = icu_status)) +
  geom_boxplot(color = "black", width = 0.5, alpha = 0.8) +
  scale_fill_manual(values = my_colors_2) +
  theme_minimal() +
    theme_minimal() +
      theme(
    plot.title = element_text(color = "darkgreen", size = 13, face = "bold", hjust = 0.4)
  )+
  ggtitle("Box plot of Gene Expression by COVID and ICU Status") +
  xlab("Disease Status") +
  ylab("Gene Expression")
```


Box plot of Gene Expression by COVID and ICU Status
80
60
40
20
Gene Expression
COVID−19
non−COVID−19
Disease Status
icu_status
no
yes