Final_Project_Step 2

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Import data sets and perform cleaning

Importing and Cleaning the data would be the fist step in data modeling. As provided in Step 1, I am going to use below CDC data set for this project.

- Provisional COVID-19 deaths by week, sex and age
  - Data as of – Date of Analysis
  - State - Jurisdiction of occurrence
  - MMWR Week – MMWR week number
  - End Week - Last week-ending date of data period
  - Sex - Sex
  - Age Group - Age group
  - Total Deaths – Deaths from all causes of deaths
  - COVID-19 Deaths - Deaths Involving COVID-19
- Conditions contributing to COVID-19 deaths, by state and age, provisional 2020-21
  - Start Date - First week-ending date of data period
  - End Date - Last week-ending date of data period
  - Group - Time-period Indicator for record: by Month, by Year, Total
  - State - Jurisdiction of occurrence
  - Condition - Condition contributing to deaths involving COVID-19
  - Age Group - Age group
  - COVID-19 Deaths - COVID 19 Deaths

The data sets contain duplicates across many columns such as state, sex and age group. So, as part of importing and cleaning step, the below filters are applied on the below columns to get the unique records in "Provisional COVID-19 deaths by week, sex and age" data set.

1. state = "United States"
2. Sex = "All Sex"
3. Age Group in ("Under 1 year","1-4 Years","5-14 Years","15-24 Years","25-34 Years","35-44 Years","45-54 Years","55-64 Years","65-74 Years","75-84 Years","85 Years and Over").
4. End Week greater than 2020-04-01

Below filters will be applied on the data set "Conditions contributing to COVID-19 deaths, by state and age, provisional 2020-21" to select unique records

1. Start Date greater than 2020-04-01 to 2021-08-01
2. Group = "By Month"

3. State = “United States”
4. Age Group in (“0-24”,“25-34”,“35-44”,“45-54”,“55-64”,“65-74”,“75-84”,85+")

Actual impact due to Covid-19 started from the Month of April 2020. So, the filter condition is applied on end week field to select the data from April 2020 to August 2021.

In addition, we are also importing vaccine and symptom data set from VARES to see if there is any impact due to vaccination.

```
knitr::opts_chunk$set(echo = TRUE)

#Importing libraries required for this project

library(readxl)
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(broom)
library(ggplot2)
library(GGally)
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```
library(coefplot)
library(knitr)
```

Data sets

Importing data sets

```
covid19_week <- read.csv("Provisional_COVID-19_Deaths_by_Week_Sex_and_Age.csv")
covid19_condition <- read.csv("COVID-19_Deaths_by_State_and_Age.csv")
data20 <- read.csv("2020VAERSDATA.csv")
data21 <- read.csv("2021VAERSDATA.csv")
symptoms20 <- read.csv("2020VAERSSYMPTOMS.csv")
symptoms21 <- read.csv("2021VAERSSYMPTOMS.csv")
vaccine20 <- read.csv("2020VAERSVAX.csv")
vaccine21 <- read.csv("2021VAERSVAX.csv")
```

Cleaning the data sets

```
#Columns present in weekly covid-19 death data set
colnames(covid19_week)
```

```
## [1] "ï..Data.as.of"   "State"           "MMWR.Week"       "End.Week"
## [5] "Sex"             "Age.Group"       "Total.Deaths"    "COVID.19.Deaths"
```

```
dim(covid19_week)
```

```
## [1] 3276    8
```

```
#Columns present in covid-19 death occurred due to underlying condition
colnames(covid19_condition)
```

```
##  [1] "ï..Data.As.Of"      "Start.Date"         "End.Date"
##  [4] "Group"              "Year"               "Month"
##  [7] "State"              "Condition.Group"    "Condition"
## [10] "ICD10_codes"        "Age.Group"          "COVID.19.Deaths"
## [13] "Number.of.Mentions" "Flag"
```

```
dim(covid19_condition)
```

```
## [1] 310500     14
```

```
#Applying filter to the data sets as defined above
covid19_week_filter <- covid19_week %>% filter(State == "United States" & Sex == "All Sex" & Age.Group
dim(covid19_week_filter)
```

```
## [1] 1001    8
```

```
covid19_cond_filter <- covid19_condition %>% filter(State == "United States" & Group == "By Month" & Ag
dim(covid19_cond_filter)
```

```
## [1] 4048   14
```

```
#Removing unwanted columns that are not required for the analysis
covid19_week_cols <- c(2,4,5,6,8)
covid19_week_final <- covid19_week_filter[,covid19_week_cols]
colnames(covid19_week_final)
```

```
## [1] "State"           "End.Week"        "Sex"             "Age.Group"
## [5] "COVID.19.Deaths"
```

```
covid19_condition_cols <- c(2,3,5,6,7,8,11,12)
covid19_condition_final <- covid19_cond_filter[,covid19_condition_cols]
colnames(covid19_condition_final)
```

```
## [1] "Start.Date"      "End.Date"        "Year"            "Month"
## [5] "State"           "Condition.Group" "Age.Group"       "COVID.19.Deaths"
```

```r
#Merge data sets by year for VARES
merged_vaccine_20 <- merge(data20, symptoms20)
merged_vaccine_20 <- merge(merged_vaccine_20, vaccine20)
dim(merged_vaccine_20)
```

```
## [1] 74253    52
```

```r
colnames(merged_vaccine_20)
```

```
##  [1] "VAERS_ID"        "RECVDATE"        "STATE"           "AGE_YRS"
##  [5] "CAGE_YR"         "CAGE_MO"         "SEX"             "RPT_DATE"
##  [9] "SYMPTOM_TEXT"    "DIED"            "DATEDIED"        "L_THREAT"
## [13] "ER_VISIT"        "HOSPITAL"        "HOSPDAYS"        "X_STAY"
## [17] "DISABLE"         "RECOVD"          "VAX_DATE"        "ONSET_DATE"
## [21] "NUMDAYS"         "LAB_DATA"        "V_ADMINBY"       "V_FUNDBY"
## [25] "OTHER_MEDS"      "CUR_ILL"         "HISTORY"         "PRIOR_VAX"
## [29] "SPLTTYPE"        "FORM_VERS"       "TODAYS_DATE"     "BIRTH_DEFECT"
## [33] "OFC_VISIT"       "ER_ED_VISIT"     "ALLERGIES"       "SYMPTOM1"
## [37] "SYMPTOMVERSION1" "SYMPTOM2"        "SYMPTOMVERSION2" "SYMPTOM3"
## [41] "SYMPTOMVERSION3" "SYMPTOM4"        "SYMPTOMVERSION4" "SYMPTOM5"
## [45] "SYMPTOMVERSION5" "VAX_TYPE"        "VAX_MANU"        "VAX_LOT"
## [49] "VAX_DOSE_SERIES" "VAX_ROUTE"       "VAX_SITE"        "VAX_NAME"
```

```r
merged_vaccine_21 <- merge(data21, symptoms21)
merged_vaccine_21 <- merge(merged_vaccine_21, vaccine21)
dim(merged_vaccine_21)
```

```
## [1] 881205     52
```

```r
colnames(merged_vaccine_21)
```

```
##  [1] "VAERS_ID"        "RECVDATE"        "STATE"           "AGE_YRS"
##  [5] "CAGE_YR"         "CAGE_MO"         "SEX"             "RPT_DATE"
##  [9] "SYMPTOM_TEXT"    "DIED"            "DATEDIED"        "L_THREAT"
## [13] "ER_VISIT"        "HOSPITAL"        "HOSPDAYS"        "X_STAY"
## [17] "DISABLE"         "RECOVD"          "VAX_DATE"        "ONSET_DATE"
## [21] "NUMDAYS"         "LAB_DATA"        "V_ADMINBY"       "V_FUNDBY"
## [25] "OTHER_MEDS"      "CUR_ILL"         "HISTORY"         "PRIOR_VAX"
## [29] "SPLTTYPE"        "FORM_VERS"       "TODAYS_DATE"     "BIRTH_DEFECT"
## [33] "OFC_VISIT"       "ER_ED_VISIT"     "ALLERGIES"       "SYMPTOM1"
## [37] "SYMPTOMVERSION1" "SYMPTOM2"        "SYMPTOMVERSION2" "SYMPTOM3"
## [41] "SYMPTOMVERSION3" "SYMPTOM4"        "SYMPTOMVERSION4" "SYMPTOM5"
## [45] "SYMPTOMVERSION5" "VAX_TYPE"        "VAX_MANU"        "VAX_LOT"
## [49] "VAX_DOSE_SERIES" "VAX_ROUTE"       "VAX_SITE"        "VAX_NAME"
```

```r
#Cleaning VARES data set. From the entire data set, We have to choose vaccines given for COVID-19 only.

filter_vaccine_20 <- filter(merged_vaccine_20, grepl("COVID19", merged_vaccine_20$VAX_TYPE))
filter_vaccine_21 <- filter(merged_vaccine_21, grepl("COVID19", merged_vaccine_21$VAX_TYPE))
```

```
#Removing unwanted columns from the data set
vaccine_cols <- c(1,3,4,7,9,10,12,21,23,28,35,36,38,40,42,44,46,47,48,49,52)

vaccine_20_final <- filter_vaccine_20[,vaccine_cols]
vaccine_21_final <- filter_vaccine_21[,vaccine_cols]
colnames(vaccine_20_final)
```

```
##  [1] "VAERS_ID"        "STATE"           "AGE_YRS"         "SEX"
##  [5] "SYMPTOM_TEXT"    "DIED"            "L_THREAT"        "NUMDAYS"
##  [9] "V_ADMINBY"       "PRIOR_VAX"       "ALLERGIES"       "SYMPTOM1"
## [13] "SYMPTOM2"        "SYMPTOM3"        "SYMPTOM4"        "SYMPTOM5"
## [17] "VAX_TYPE"        "VAX_MANU"        "VAX_LOT"         "VAX_DOSE_SERIES"
## [21] "VAX_NAME"
```

```
colnames(vaccine_21_final)
```

```
##  [1] "VAERS_ID"        "STATE"           "AGE_YRS"         "SEX"
##  [5] "SYMPTOM_TEXT"    "DIED"            "L_THREAT"        "NUMDAYS"
##  [9] "V_ADMINBY"       "PRIOR_VAX"       "ALLERGIES"       "SYMPTOM1"
## [13] "SYMPTOM2"        "SYMPTOM3"        "SYMPTOM4"        "SYMPTOM5"
## [17] "VAX_TYPE"        "VAX_MANU"        "VAX_LOT"         "VAX_DOSE_SERIES"
## [21] "VAX_NAME"
```

Final data set

```
#The final data sets after cleaning and before slicing and dicing
#covid-19 weekly death count by Age
print(str(covid19_week_final))
```

```
## 'data.frame':    1001 obs. of  5 variables:
##  $ State          : chr  "United States" "United States" "United States" "United States" ...
##  $ End.Week       : chr  "01/04/2020" "01/04/2020" "01/04/2020" "01/04/2020" ...
##  $ Sex            : chr  "All Sex" "All Sex" "All Sex" "All Sex" ...
##  $ Age.Group      : chr  "Under 1 year" "1-4 Years" "5-14 Years" "15-24 Years" ...
##  $ COVID.19.Deaths: chr  "0" "0" "0" "0" ...
## NULL
```

```
#Covid-19 monthly deaths by age with underlying condition
print(str(covid19_condition_final))
```

```
## 'data.frame':    4048 obs. of  8 variables:
##  $ Start.Date     : chr  "01/01/2020" "02/01/2020" "03/01/2020" "04/01/2020" ...
##  $ End.Date       : chr  "01/31/2020" "02/29/2020" "03/31/2020" "04/30/2020" ...
##  $ Year           : chr  "2,020" "2,020" "2,020" "2,020" ...
##  $ Month          : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ State          : chr  "United States" "United States" "United States" "United States" ...
##  $ Condition.Group: chr  "Respiratory diseases" "Respiratory diseases" "Respiratory diseases" "Respi
##  $ Age.Group      : chr  "0-24" "0-24" "0-24" "0-24" ...
##  $ COVID.19.Deaths: chr  "0" "0" "9" "27" ...
## NULL
```

```r
#Covid-19 Vaccine data for 2020 and 2021
print(str(vaccine_20_final))
```

```
## 'data.frame':    14116 obs. of  21 variables:
##  $ VAERS_ID       : int  902418 902440 902446 902464 902465 902465 902468 902468 902479 902490 ...
##  $ STATE          : chr  "NJ" "AZ" "WV" "LA" ...
##  $ AGE_YRS        : num  56 35 55 42 60 60 59 59 46 37 ...
##  $ SEX            : chr  "F" "F" "F" "M" ...
##  $ SYMPTOM_TEXT   : chr  "Patient experienced mild numbness traveling from injection site up and dow
##  $ DIED           : chr  "" "" "" "" ...
##  $ L_THREAT       : chr  "" "" "" "" ...
##  $ NUMDAYS        : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ V_ADMINBY      : chr  "PVT" "PVT" "OTH" "PVT" ...
##  $ PRIOR_VAX      : chr  "" "" "" "" ...
##  $ ALLERGIES      : chr  "none" "" "Contrast Dye IV contrast, shellfish, strawberry" "none" ...
##  $ SYMPTOM1       : chr  "Hypoaesthesia" "Headache" "Erythema" "Dizziness" ...
##  $ SYMPTOM2       : chr  "Injection site hypoaesthesia" "" "Feeling hot" "Electrocardiogram normal"
##  $ SYMPTOM3       : chr  "" "" "Flushing" "Hyperhidrosis" ...
##  $ SYMPTOM4       : chr  "" "" "" "Laboratory test normal" ...
##  $ SYMPTOM5       : chr  "" "" "" "Presyncope" ...
##  $ VAX_TYPE       : chr  "COVID19" "COVID19" "COVID19" "COVID19" ...
##  $ VAX_MANU       : chr  "PFIZER\\BIONTECH" "PFIZER\\BIONTECH" "PFIZER\\BIONTECH" "PFIZER\\BIONTECH"
##  $ VAX_LOT        : chr  "EH9899" "EH 9899" "EH9899" "EH9899" ...
##  $ VAX_DOSE_SERIES: chr  "1" "1" "1" "UNK" ...
##  $ VAX_NAME       : chr  "COVID19 (COVID19 (PFIZER-BIONTECH))" "COVID19 (COVID19 (PFIZER-BIONTECH))"
## NULL
```

```r
print(str(vaccine_21_final))
```

```
## 'data.frame':    843061 obs. of  21 variables:
##  $ VAERS_ID       : int  916600 916601 916602 916603 916604 916606 916607 916608 916609 916610 ...
##  $ STATE          : chr  "TX" "CA" "WA" "WA" ...
##  $ AGE_YRS        : num  33 73 23 58 47 44 50 33 71 18 ...
##  $ SEX            : chr  "F" "F" "F" "F" ...
##  $ SYMPTOM_TEXT   : chr  "Right side of epiglottis swelled up and hinder swallowing pictures taken Be
##  $ DIED           : chr  "" "" "" "" ...
##  $ L_THREAT       : chr  "" "" "" "" ...
##  $ NUMDAYS        : int  2 0 0 0 7 0 1 2 8 1 ...
##  $ V_ADMINBY      : chr  "PVT" "SEN" "SEN" "WRK" ...
##  $ PRIOR_VAX      : chr  "" "" "" "got measles from measel shot, mums from mumps shot, headaches and
##  $ ALLERGIES      : chr  "Pcn and bee venom" "\"Dairy\"" "Shellfish" "Diclofenac, novacaine, lidocai
##  $ SYMPTOM1       : chr  "Dysphagia" "Anxiety" "Chest discomfort" "Dizziness" ...
##  $ SYMPTOM2       : chr  "Epiglottitis" "Dyspnoea" "Dysphagia" "Fatigue" ...
##  $ SYMPTOM3       : chr  "" "" "Pain in extremity" "Mobility decreased" ...
##  $ SYMPTOM4       : chr  "" "" "Visual impairment" "" ...
##  $ SYMPTOM5       : chr  "" "" "" "" ...
##  $ VAX_TYPE       : chr  "COVID19" "COVID19" "COVID19" "COVID19" ...
##  $ VAX_MANU       : chr  "MODERNA" "MODERNA" "PFIZER\\BIONTECH" "MODERNA" ...
##  $ VAX_LOT        : chr  "037K20A" "025L20A" "EL1284" "unknown" ...
##  $ VAX_DOSE_SERIES: chr  "1" "1" "1" "UNK" ...
##  $ VAX_NAME       : chr  "COVID19 (COVID19 (MODERNA))" "COVID19 (COVID19 (MODERNA))" "COVID19 (COVID
## NULL
```

Adding additional variable to final data sets

I will be adding a variable called people to covid19_weekly data set which tells if the people is young or old based on the age. In addition, I will be adding a variable called "condition_flag" to covid19_condition data set which tells if the people had underlying conditions.

```
old <- c("55-64 Years","65-74 Years","75-84 Years","85 Years and Over")
covid19_week_final$people <- ifelse(covid19_week_final$Age.Group %in% old, "Old", "Young")
colnames(covid19_week_final)
```

```
## [1] "State"           "End.Week"        "Sex"             "Age.Group"
## [5] "COVID.19.Deaths" "people"
```

```
print(str(covid19_week_final))
```

```
## 'data.frame':    1001 obs. of  6 variables:
##  $ State          : chr  "United States" "United States" "United States" "United States" ...
##  $ End.Week       : chr  "01/04/2020" "01/04/2020" "01/04/2020" "01/04/2020" ...
##  $ Sex            : chr  "All Sex" "All Sex" "All Sex" "All Sex" ...
##  $ Age.Group      : chr  "Under 1 year" "1-4 Years" "5-14 Years" "15-24 Years" ...
##  $ COVID.19.Deaths: chr  "0" "0" "0" "0" ...
##  $ people         : chr  "Young" "Young" "Young" "Young" ...
## NULL
```

```
covid19_condition_final$condition_flag <- ifelse(covid19_condition_final$Condition.Group == "COVID-19",'
print(str(covid19_condition_final))
```

```
## 'data.frame':    4048 obs. of  9 variables:
##  $ Start.Date     : chr  "01/01/2020" "02/01/2020" "03/01/2020" "04/01/2020" ...
##  $ End.Date       : chr  "01/31/2020" "02/29/2020" "03/31/2020" "04/30/2020" ...
##  $ Year           : chr  "2,020" "2,020" "2,020" "2,020" ...
##  $ Month          : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ State          : chr  "United States" "United States" "United States" "United States" ...
##  $ Condition.Group: chr  "Respiratory diseases" "Respiratory diseases" "Respiratory diseases" "Respi
##  $ Age.Group      : chr  "0-24" "0-24" "0-24" "0-24" ...
##  $ COVID.19.Deaths: chr  "0" "0" "9" "27" ...
##  $ condition_flag : chr  "Yes" "Yes" "Yes" "Yes" ...
## NULL
```

Data sets analysis by slice and dice

Covid-19 Weekly death data set

```
covid19_week_final$COVID.19.Deaths <- as.numeric(covid19_week_final$COVID.19.Deaths)
```

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

```r
print(str(covid19_week_final,10))
```

```
## 'data.frame':    1001 obs. of  6 variables:
##  $ State          : chr  "United States" "United States" "United States" "United States" ...
##  $ End.Week       : chr  "01/04/2020" "01/04/2020" "01/04/2020" "01/04/2020" ...
##  $ Sex            : chr  "All Sex" "All Sex" "All Sex" "All Sex" ...
##  $ Age.Group      : chr  "Under 1 year" "1-4 Years" "5-14 Years" "15-24 Years" ...
##  $ COVID.19.Deaths: num  0 0 0 0 0 0 0 0 0 0 ...
##  $ people         : chr  "Young" "Young" "Young" "Young" ...
## NULL
```

```r
#Total deaths by Covid-19 for Young and old People
covid19_week_final %>% group_by(people) %>% summarise(COVID19_Deaths=sum(COVID.19.Deaths, na.rm = TRUE))
```

```
## # A tibble: 2 x 2
##   people COVID19_Deaths
##   <chr>           <dbl>
## 1 Old             67898
## 2 Young           52829
```

```r
#Slicing the data set based on People (Young and Old)
covid19_week_young <- filter(covid19_week_final, people=="Young" & COVID.19.Deaths>0)
dim(covid19_week_young)
```

```
## [1] 482   6
```

```r
covid19_week_old <- filter(covid19_week_final, people=="Old" & COVID.19.Deaths>0)
dim(covid19_week_old)
```

```
## [1] 132   6
```

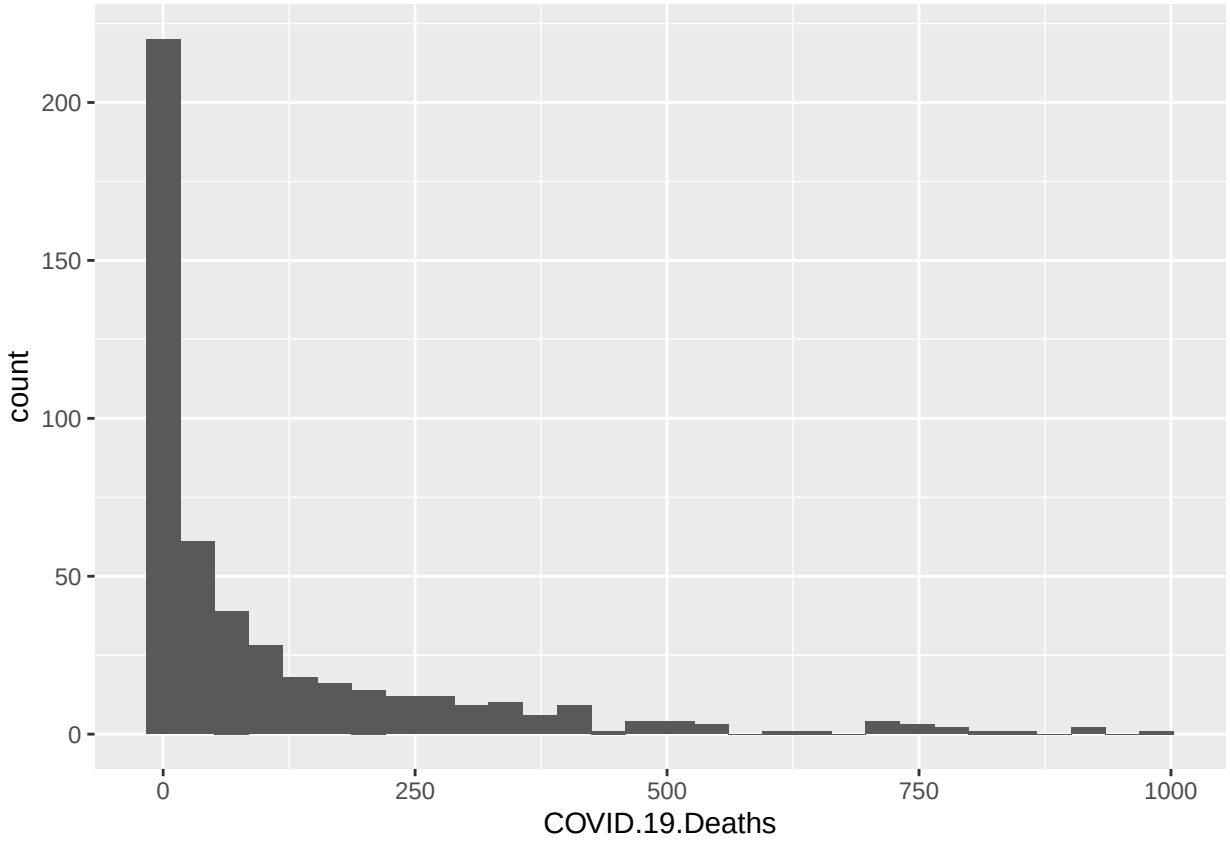
```r
#Printing the total number of deaths for young and old people
cat("Total number of covid-19 deaths for young people: ",sum(covid19_week_young$COVID.19.Deaths))
```

```
## Total number of covid-19 deaths for young people:  52829
```

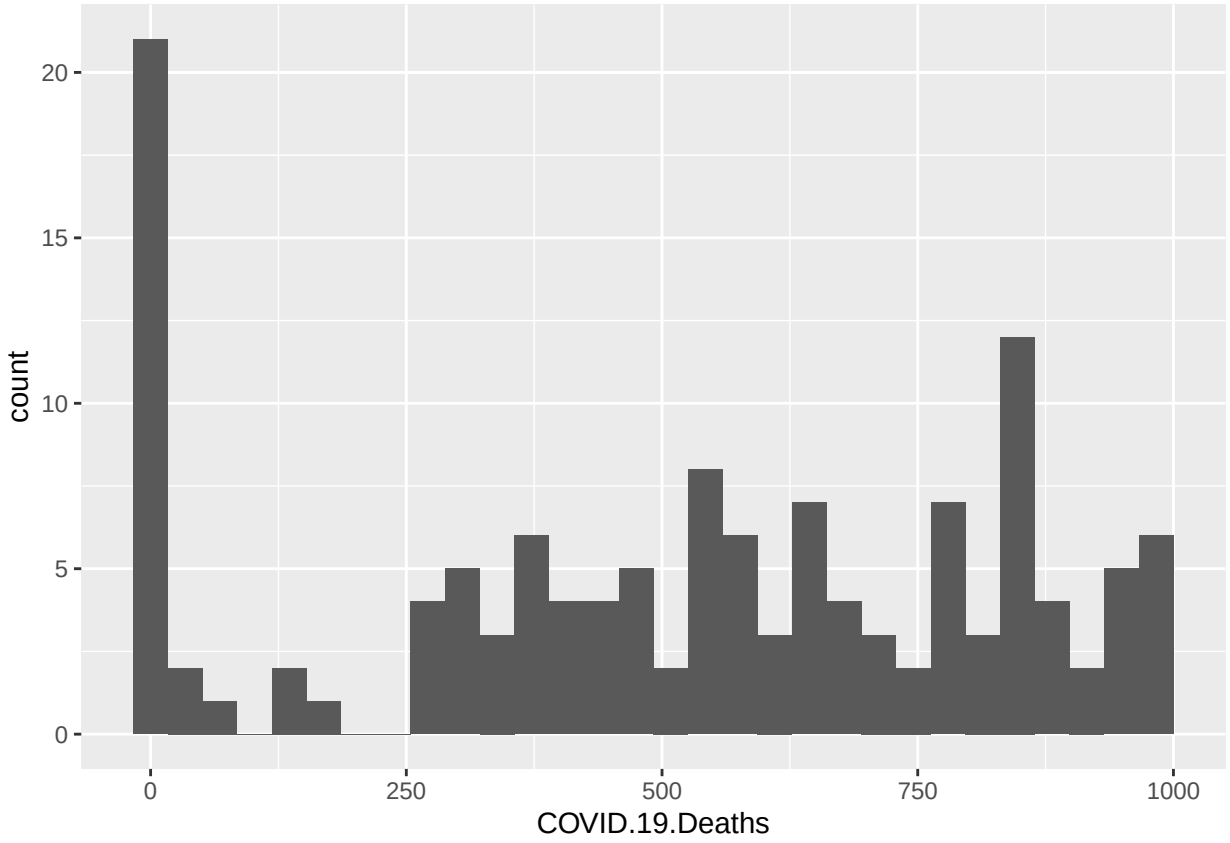
```r
cat("Total number of covid-19 deaths for old people: ",sum(covid19_week_old$COVID.19.Deaths))
```

```
## Total number of covid-19 deaths for old people:  67898
```

```r
#Histograms on covid-19 death for young and old people
ggplot(covid19_week_young, aes(COVID.19.Deaths)) + geom_histogram(bins=30)
```




```
ggplot(covid19_week_old, aes(COVID.19.Deaths)) + geom_histogram(bins=30)
```




```
#Summary of weekly covid-19 deaths data set
summary(covid19_week_young)
```

```
##     State              End.Week            Sex             Age.Group
##  Length:482         Length:482         Length:482         Length:482
##  Class :character   Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character
##
##
##
##  COVID.19.Deaths    people
##  Min.   :  1.0   Length:482
##  1st Qu.:  2.0   Class :character
##  Median : 25.5   Mode  :character
##  Mean   :109.6
##  3rd Qu.:141.5
##  Max.   :987.0
```

```
summary(covid19_week_old)
```

```
##     State              End.Week            Sex             Age.Group
##  Length:132         Length:132         Length:132         Length:132
##  Class :character   Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character
##
```

```
##
##
##  COVID.19.Deaths    people
##  Min.   :  1.0   Length:132
##  1st Qu.:310.8   Class :character
##  Median :552.5   Mode  :character
##  Mean   :514.4
##  3rd Qu.:795.2
##  Max.   :984.0
```

```
cat("The variance of death count for young people: ", var(covid19_week_young$COVID.19.Deaths))
```

```
## The variance of death count for young people:  30973.93
```

```
cat("The standard deviation of death count for young people: ", sd(covid19_week_young$COVID.19.Deaths))
```

```
## The standard deviation of death count for young people:  175.9941
```

```
cat("The variance of death count for old people: ", var(covid19_week_old$COVID.19.Deaths))
```

```
## The variance of death count for old people:  99185.96
```

```
cat("The standard deviation of death count for old people: ", sd(covid19_week_old$COVID.19.Deaths))
```

```
## The standard deviation of death count for old people:  314.938
```

Observation

The death count of young people (age < 55) is less compared to old people (age $>= 55$). The death count during the initial months were less as Covid-19 infection started spreading and peaked in the later months on 2020 and initial months of 2021, and again started going down from middle of 2021 due to vaccinations.

The histogram for the Covid-19 deaths for young people is positively skewed distribution whereas the historgram for the Covid-19 deaths for old people is also postively skewed distribution but shows some pattern for multiple distribution as well.

Covid-19 death underlying condition

```
#Converting datatype to numeric
covid19_condition_final$COVID.19.Deaths <- as.numeric(covid19_condition_final$COVID.19.Deaths)
```

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

```
print(str(covid19_condition_final))
```

```
## 'data.frame':    4048 obs. of  9 variables:
##  $ Start.Date     : chr  "01/01/2020" "02/01/2020" "03/01/2020" "04/01/2020" ...
##  $ End.Date       : chr  "01/31/2020" "02/29/2020" "03/31/2020" "04/30/2020" ...
##  $ Year           : chr  "2,020" "2,020" "2,020" "2,020" ...
##  $ Month          : int  1 2 3 4 5 6 7 8 9 10 ...
##  $ State          : chr  "United States" "United States" "United States" "United States" ...
##  $ Condition.Group: chr  "Respiratory diseases" "Respiratory diseases" "Respiratory diseases" "Respi
##  $ Age.Group      : chr  "0-24" "0-24" "0-24" "0-24" ...
##  $ COVID.19.Deaths: num  0 0 9 27 19 17 38 32 13 9 ...
##  $ condition_flag : chr  "Yes" "Yes" "Yes" "Yes" ...
## NULL
```

```
#Slicing the data set based on People with and without condition
covid19_condition_no <- filter(covid19_condition_final, condition_flag=="No" & COVID.19.Deaths>0)
dim(covid19_condition_no)
```

```
## [1] 67  9
```

```
covid19_condition_yes <- filter(covid19_condition_final, condition_flag=="Yes" & COVID.19.Deaths>0)
dim(covid19_condition_yes)
```

```
## [1] 2755    9
```

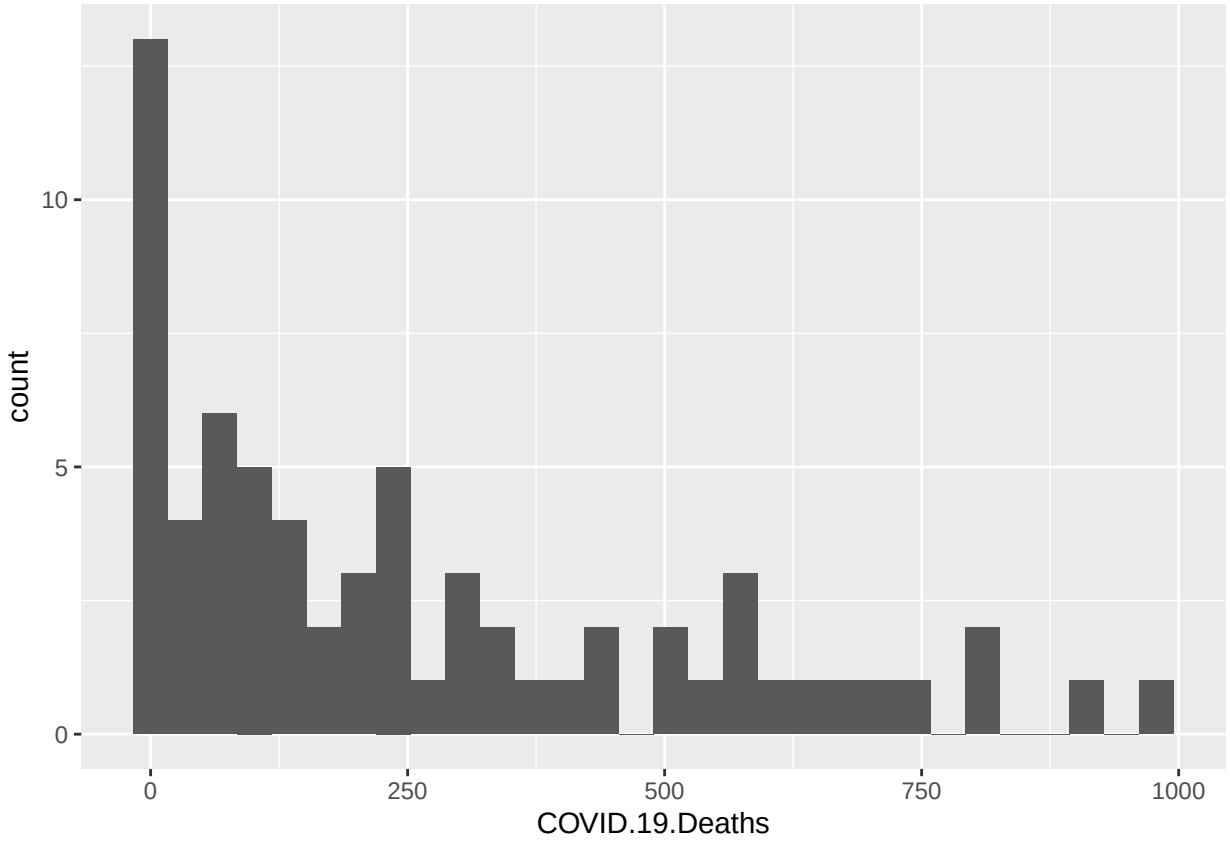
```
#Printing the total number of deaths for young and old people
cat("Total number of covid-19 deaths for the people without underlying condition: ",sum(covid19_conditi
```

```
## Total number of covid-19 deaths for the people without underlying condition:  17250
```

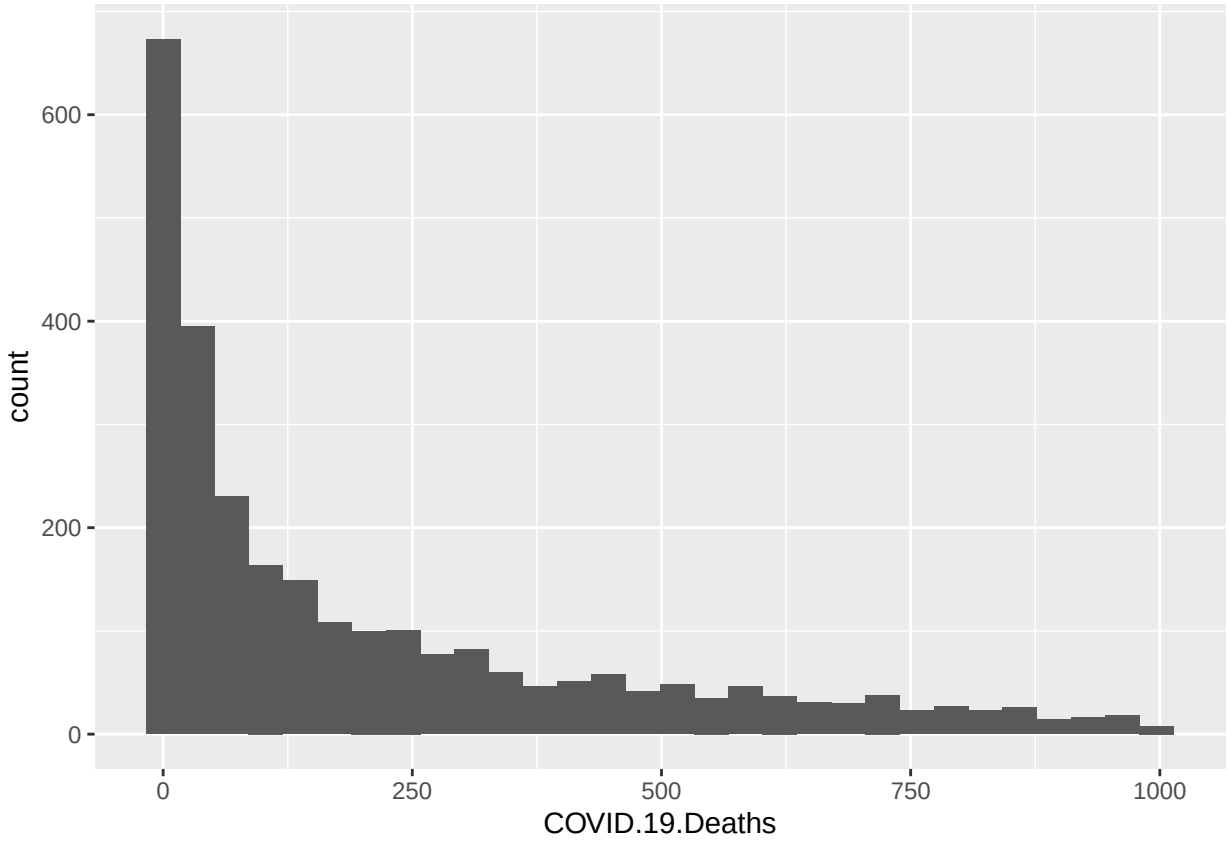
```
cat("Total number of covid-19 deaths for the people with underlying condition: ",sum(covid19_condition_y
```

```
## Total number of covid-19 deaths for the people with underlying condition:  579299
```

```
#Histograms on covid-19 death for young and old people
ggplot(covid19_condition_no, aes(COVID.19.Deaths)) + geom_histogram(bins=30)
```




```
ggplot(covid19_condition_yes, aes(COVID.19.Deaths)) + geom_histogram(bins=30)
```




```
#Summary of covid-19 deaths
summary(covid19_condition_no)
```

```
##   Start.Date          End.Date            Year             Month
##  Length:67          Length:67          Length:67          Min.   : 1.000
##  Class :character   Class :character   Class :character   1st Qu.: 3.000
##  Mode  :character   Mode  :character   Mode  :character   Median : 6.000
##                                                           Mean   : 5.701
##                                                           3rd Qu.: 8.500
##                                                           Max.   :12.000
##     State           Condition.Group     Age.Group          COVID.19.Deaths
##  Length:67          Length:67          Length:67          Min.   :  1.0
##  Class :character   Class :character   Class :character   1st Qu.: 53.0
##  Mode  :character   Mode  :character   Mode  :character   Median :164.0
##                                                           Mean   :257.5
##                                                           3rd Qu.:413.0
##                                                           Max.   :979.0
##  condition_flag
##  Length:67
##  Class :character
##  Mode  :character
##
##
##
```

```
summary(covid19_condition_yes)
```

```
##   Start.Date          End.Date             Year               Month
##  Length:2755        Length:2755        Length:2755        Min.   : 1.000
##  Class :character   Class :character   Class :character   1st Qu.: 4.000
##  Mode  :character   Mode  :character   Mode  :character   Median : 6.000
##                                                           Mean   : 6.216
##                                                           3rd Qu.: 8.000
##                                                           Max.   :12.000
##     State           Condition.Group     Age.Group          COVID.19.Deaths
##  Length:2755        Length:2755        Length:2755        Min.   :  1.0
##  Class :character   Class :character   Class :character   1st Qu.: 19.0
##  Mode  :character   Mode  :character   Mode  :character   Median : 99.0
##                                                           Mean   :210.3
##                                                           3rd Qu.:322.0
##                                                           Max.   :998.0
##  condition_flag
##  Length:2755
##  Class :character
##  Mode  :character
##
##
##
```

```
cat("The variance of death count for the people without underlying condition: ", var(covid19_condition_n
```

```
## The variance of death count for the people without underlying condition:  68582.8
```

```
cat("The standard deviation of death count for the people without underlying condition: ", sd(covid19_co
```

```
## The standard deviation of death count for the people without underlying condition:  261.8832
```

```
cat("The variance of death count for the people with underlying condition: ", var(covid19_condition_yes$
```

```
## The variance of death count for the people with underlying condition:  61526.05
```

```
cat("The standard deviation of death count for the people with underlying condition: ", sd(covid19_condi
```

```
## The standard deviation of death count for the people with underlying condition:  248.0445
```

Observation

The death count of the people without any underlying condition is less compared to those people with underlying condition.

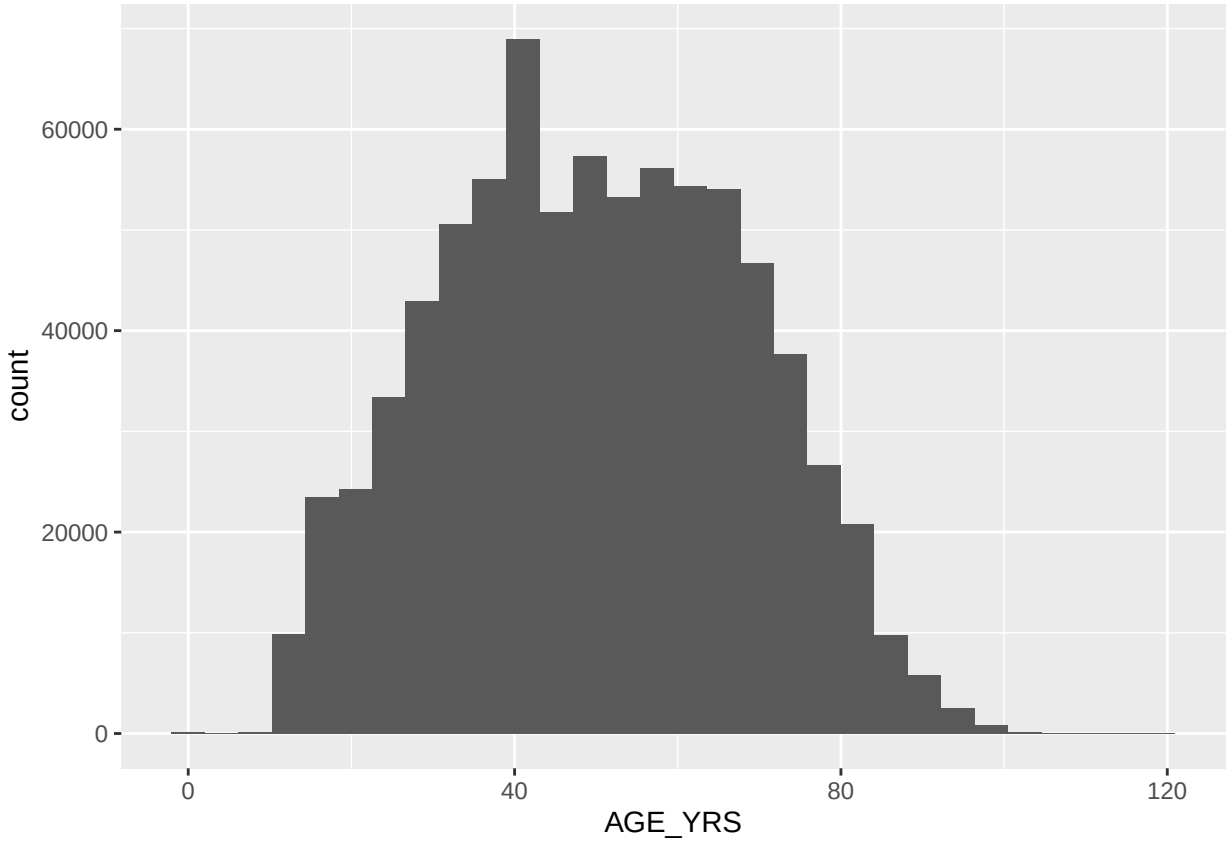
The histograms for the Covid-19 deaths for the people with and without underlying conditions are positively skewed distribution. This is because the covid-19 death count is high during 2020 and 1st quarter of 2021. From 2nd quater of 2021, the count started decreasing.

Vaccine data sets

```
#Combining vaccine data for both 2020 and 2021
vaccine_df <- union(vaccine_20_final, vaccine_21_final)

#Age Analysis
age_variable <- vaccine_df[-is.na(vaccine_df$AGE_YRS)]
age_hist <- ggplot(vaccine_df, aes(AGE_YRS)) + geom_histogram(bins=30)
age_hist
```

```
## Warning: Removed 68171 rows containing non-finite values (stat_bin).
```




```
#Death data analysis

vaccine_died <- dplyr::filter(vaccine_df, grepl("Y",vaccine_df$DIED))
colnames(vaccine_died)
```

```
##  [1] "VAERS_ID"        "STATE"           "AGE_YRS"         "SEX"
##  [5] "SYMPTOM_TEXT"    "DIED"            "L_THREAT"        "NUMDAYS"
##  [9] "V_ADMINBY"       "PRIOR_VAX"       "ALLERGIES"       "SYMPTOM1"
## [13] "SYMPTOM2"        "SYMPTOM3"        "SYMPTOM4"        "SYMPTOM5"
## [17] "VAX_TYPE"        "VAX_MANU"        "VAX_LOT"         "VAX_DOSE_SERIES"
## [21] "VAX_NAME"
```

```
vaccine_died_nodup <- vaccine_died |> dplyr::distinct(VAERS_ID, .keep_all = TRUE)
dim(vaccine_died_nodup)
```

```
## [1] 7848   21
```

```
cat("Total number of people died after taking vaccine: ", length(unique(vaccine_died$VAERS_ID)))
```

```
## Total number of people died after taking vaccine:  7848
```

```
#Splitting the data set into young and old based on age.
vaccine_died_young <- filter(vaccine_died, AGE_YRS<55)
dim(vaccine_died_young)
```

```
## [1] 1617   21
```

```
cat("Total number of young people died after taking vaccine: ", length(unique(vaccine_died_young$VAERS_
```

```
## Total number of young people died after taking vaccine:  856
```

```
vaccine_died_old <- filter(vaccine_died, AGE_YRS>=55)
dim(vaccine_died_old)
```

```
## [1] 12049    21
```

```
cat("Total number of old people died after taking vaccine: ", length(unique(vaccine_died_old$VAERS_ID)))
```

```
## Total number of old people died after taking vaccine:  6281
```

Observation

The vaccine data set also shows the death count of the people having young age (less than 54) is less compared to the old people having age greater than 55.

Information not self-evident

It is important to know that the number of covid-19 deaths reported in CDC and VAERS data sets may not be 100% correct. Only the deaths occurred in hospital and confirmed by doctors are reported.

In addition, the number of records present in data set are not necessarily the number of people affected. Looking at the number of unique VAERS_ID is the correct way to see the number of people affected by Covid-19

Different ways to look at the data

Some of the different ways to look at the data set

- Provisional COVID-19 deaths by week, sex and age
  - Age
  - Week
  - Covid-19 Deaths
  - People (derived variable based on age of the people)
- Conditions contributing to COVID-19 deaths, by state and age, provisional 2020-21
  - Age
  - Condition.Group
  - Covid-19 Deaths
  - condition_flag (derived variable based on condition.group)
- Vaccine data sets
  - Age
  - Died
  - VAERS_ID

Summarize data to answer key questions

Lot of key questions related to these data sets can be answered with simple functions and plots available in R. Below are the few questions.

What is the average death due to covid-19 for young and old people?

- Average covid-19 death count for young people: 109.6
- Average covid-19 death count for old people: 514.4

What is the variance and standard deviation of covid-19 death for young and old people?

- The variance and standard deviation of covid-19 death count for young people: 30973.93 and 175.9941
- The variance and standard deviation of covid-19 death count for old people: 99185.96 and 314.938

What is the average death due to covid-19 for the people with and without underlying condition?

- Average covid-19 death count for the people without underlying condition: 164
- Average covid-19 death count for the people with underlying condition: 210

What is the variance and standard deviation of covid-19 death for the people with and without underlying condition?

- The variance and standard deviation of covid-19 death for the people without underlying condition: 68582.8 and 261.8832
- The variance and standard deviation of covid-19 death for the people with underlying condition: 61526.05 and 248.0445

What role age played in covid-19 deaths?

```
#Calculate total deaths by age
cat("Number of covid-19 deaths by age group:\n")
```

```
## Number of covid-19 deaths by age group:
```

```
covid19_week_final %>% group_by(Age.Group) %>% summarise(COVID19_Deaths=sum(COVID.19.Deaths, na.rm = TRU
```

```
## # A tibble: 11 x 2
##    Age.Group         COVID19_Deaths
##    <chr>                      <dbl>
##  1 1-4 Years                     59
##  2 15-24 Years                 1463
##  3 25-34 Years                 6394
##  4 35-44 Years                16094
##  5 45-54 Years                28550
##  6 5-14 Years                   154
##  7 55-64 Years                27367
##  8 65-74 Years                15873
##  9 75-84 Years                11661
## 10 85 Years and Over          12997
## 11 Under 1 year                 115
```

```
#Filtering the data till Aug 2021 and applying group by to calculate total deaths by end week
cat("Number of covid-19 deaths by week:\n")
```

```
## Number of covid-19 deaths by week:
```

```
covid19_week_final %>% filter(as.Date(End.Week, format= "%m/%d/%Y") < "2021-09-01") %>% group_by(as.Dat
```

```
## # A tibble: 87 x 2
##    `as.Date(End.Week, format = "%m/%d/%Y")` COVID19_Deaths
##    <date>                                          <dbl>
##  1 2020-01-04                                          0
##  2 2020-01-11                                          1
##  3 2020-01-18                                          2
##  4 2020-01-25                                          2
##  5 2020-02-01                                          0
##  6 2020-02-08                                          2
##  7 2020-02-15                                          2
##  8 2020-02-22                                          6
##  9 2020-02-29                                          9
## 10 2020-03-07                                         37
## # ... with 77 more rows
```

What role underlying condition played in covid-19 deaths?

```
#Total deaths by Covid-19 for the people with and without underlying condition
cat("Number of deaths by underlying condition: \n")
```

```
## Number of deaths by underlying condition:
```

```
covid19_condition_final %>% group_by(condition_flag) %>% summarise(COVID19_Deaths=sum(COVID.19.Deaths, r
```

```
## # A tibble: 2 x 2
##   condition_flag COVID19_Deaths
##   <chr>                   <dbl>
## 1 No                      17250
## 2 Yes                    579299
```

```
#Death count by underlying condition
cat("Number of covid-19 deaths by underlying condition")
```

```
## Number of covid-19 deaths by underlying condition
```

```
covid19_condition_yes %>% group_by(Condition.Group) %>% summarise(COVID19_Deaths=sum(COVID.19.Deaths, na
```

```
## # A tibble: 11 x 2
##    Condition.Group                                                COVID19_Deaths
##    <chr>                                                                  <dbl>
##  1 All other conditions and causes (residual)                             26357
##  2 Alzheimer disease                                                      11834
##  3 Circulatory diseases                                                  196742
##  4 Diabetes                                                               32593
##  5 Intentional and unintentional injury, poisoning, and other ad~         14424
##  6 Malignant neoplasms                                                    25116
##  7 Obesity                                                                28579
##  8 Renal failure                                                          34375
##  9 Respiratory diseases                                                  155191
## 10 Sepsis                                                                38029
## 11 Vascular and unspecified dementia                                     16059
```

Number of covid-19 deaths after taking vaccine by age and manufacture?

```
cat("Number of covid-19 deaths after taking vaccination by age")
```

```
## Number of covid-19 deaths after taking vaccination by age
```

```
death_age <- table(vaccine_died$AGE_YRS)
print(death_age)
```

```
##
## 0.42    1 1.08   11   12   13   15   16   17   18   19   20   21   22   23   24
##    2    1    1    1    1   10    8   10    7   29    9   19   23    8    9   13
```

```
##   25   26   27   28   29   30   31   32   33   34   35   36   37   38   39   40
##    9   30   23   22   20   21   15   19   18   16   51   74   60   58   42   35
##   41   42   43   44   45   46   47   48   49   50   51   52   53   54   55   56
##   41   35   32   63   68   44   77   81   64  104  108   69   75   92  122  106
##   57   58   59   60   61   62   63   64   65   66   67   68   69   70   71   72
##  135  195  173  167  282  229  248  250  298  280  344  253  320  323  270  357
##   73   74   75   76   77   78   79   80   81   82   83   84   85   86   87   88
##  439  388  314  336  459  352  372  358  354  380  413  368  339  346  321  299
##   89   90   91   92   93   94   95   96   97   98   99  100  101  102  103  104
##  307  326  214  176  177  184   95  128  103   53   21   29   24   10    7    3
##  105  106
##    1    1
```

```
cat("Number of covid-19 deaths after taking vaccination by manufacture")
```

```
## Number of covid-19 deaths after taking vaccination by manufacture
```

```
death_type <- table(vaccine_died$VAX_MANU)
print(death_type)
```

```
##
##              JANSSEN              MODERNA     PFIZER\\BIONTECH
##                 1368                 5940                 7074
## UNKNOWN MANUFACTURER
##                   54
```

```
cat("Number of covid-19 deaths after taking vaccination by state")
```

```
## Number of covid-19 deaths after taking vaccination by state
```

```
death_state <- table(vaccine_died$STATE)
print(death_state)
```

```
##
##        AK   AL   AR   AS   AZ   CA   CO   CT   DC   DE   FL   GA   GU   HI   IA
## 2383   36  117  149    3  156  864  157   83   23   31  819  513    5   47  114
##   ID   IL   IN   KS   KY   LA   MA   MD   ME   MI   MN   MO   MP   MS   MT   NC
##   31  459  224   95  891   91  166  150   59  652  393  258   15   72   67  209
##   ND   NE   NH   NJ   NM   NV   NY   OH   OK   OR   PA   PR   RI   SC   SD   TN
##   70  111  126  266   98   47  530  351   81  127  413  155   23  112   69  440
##   TX   UT   VA   VT   WA   WI   WV   WY   XB
## 1038   45  193   16  369  320   63   39    2
```

Plots and Tables

- Histogram - Look at the distribution of data for specific variables
- Scatterplots - Identify relationships between the variables
- Residual plots - Look for outliers in the distribution
- Density plots - Observe smoothed distributions to check assumptions

- Box plots - Look for outliers in the distribution
- Tables
  - * Covid Deaths by Age
  - * Covid Deaths by underlying condition
  - * Vairables used
  - * Covid deaths by Age
  - * Covid deaths by manufacture
  - * Covid deaths by State

Machine Learning

I do not plan to use any machine learning techniques at this time

Questions

- I have done the analysis on Covid-19 deaths by age and underlying condition for Unites States as a whole. I want to do research on covid-19 deaths by age for each state present in United States, and find out which State shows high and low count.
- In addition, I would want to analyze the percentage of vaccines given across the states and check for correlations between number of vaccine and deaths. However, I am unsure of how far I will get due to limitations in data.
- I would also want to apply PMF and CDF on the data to find the distribution of discrete random variable and continuous random variables.
- I also want to apply some machine learning techniques on the data sets