STA 104: Take Home Project

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Question 1: K or more groups

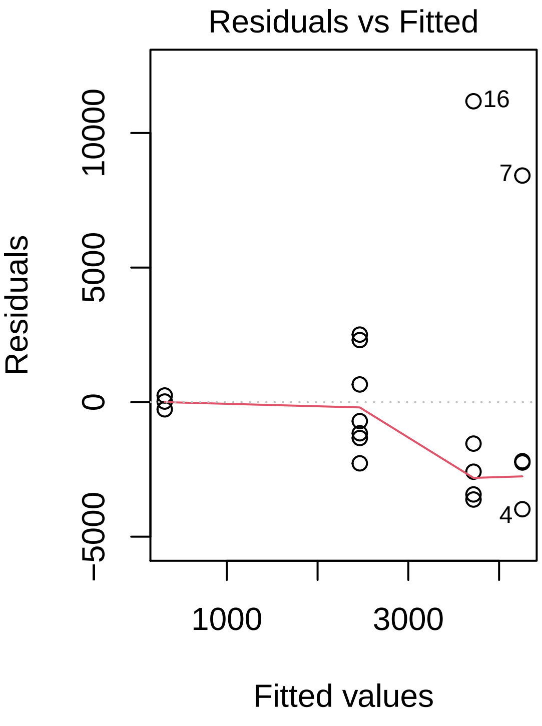
I Introduction

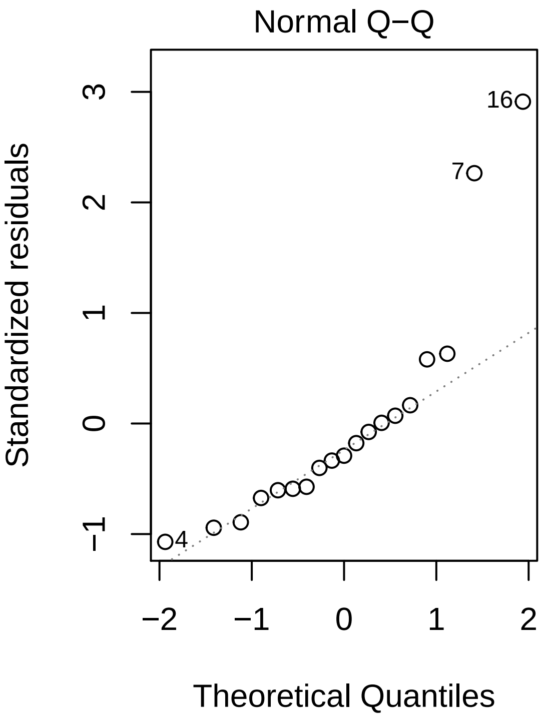
Covid-19 has vastly changed the way of how the world works. Millions of people in America are all unable to do their work properly and have been forced to work at home. We are currently analyzing a data set called `CovidA`. which has 4 columns. The 4 columns are `Year` (The year the data was taken), `Month`(The month the data was reported),`State` (The state where the deaths are being counted), and `Death` (Cumulative deaths of the month). Instead of working with the whole dataset,we chose to instead subset the dataset and work with 4 states. We chose California, New York City, Florida, and Alabama. We chose California because that is where my partner and I are located and we would like to know more about California compared to other states. We chose New York City because NYC is a typically very popular spot for visitors and we were curious on how the analysis will work with a heavily populated city with Corona. Both of those states listed are also heavily Democratic. We chose Alabama because they are an republican state that is widely known for not believing in the Coronavirus. We also chose Florida largely because it is one of the only states where nobody ever believed in the Coronavirus. All the bars, indoor dining and tourism is rampant over there with the state not caring if anyone wears a mask. We are curious on how Florida and Alabama is doing in terms of the virus compared to states that are very progressive and strict on guidelines such as California and NYC. We also picked these states mainly because we really wanted to see if the Democratic way or the Republican way ultimately ends up in an different result or not. Since we want to compare multiple groups, we will be using the K- sample method which is very useful in analyzing groups. We will be using multiple tests such as the Shapiro - Wilks Test and the Levene Test to determine whether to use the Permutation Test or the Kruskal-Wallis Test.

II Summary of Data

Table 1: Summary Statistics

	California	**Florida**	**Alabama**	**New York City**
Group Mean	4256.750	2465.00000	315.666667	3718.200
Group SD	5673.232	1863.53750	257.663217	6302.866
Rank Mean	11.750	11.42857	4.666667	9.800
Sample Size	4.000	7.00000	3.00000	5.000

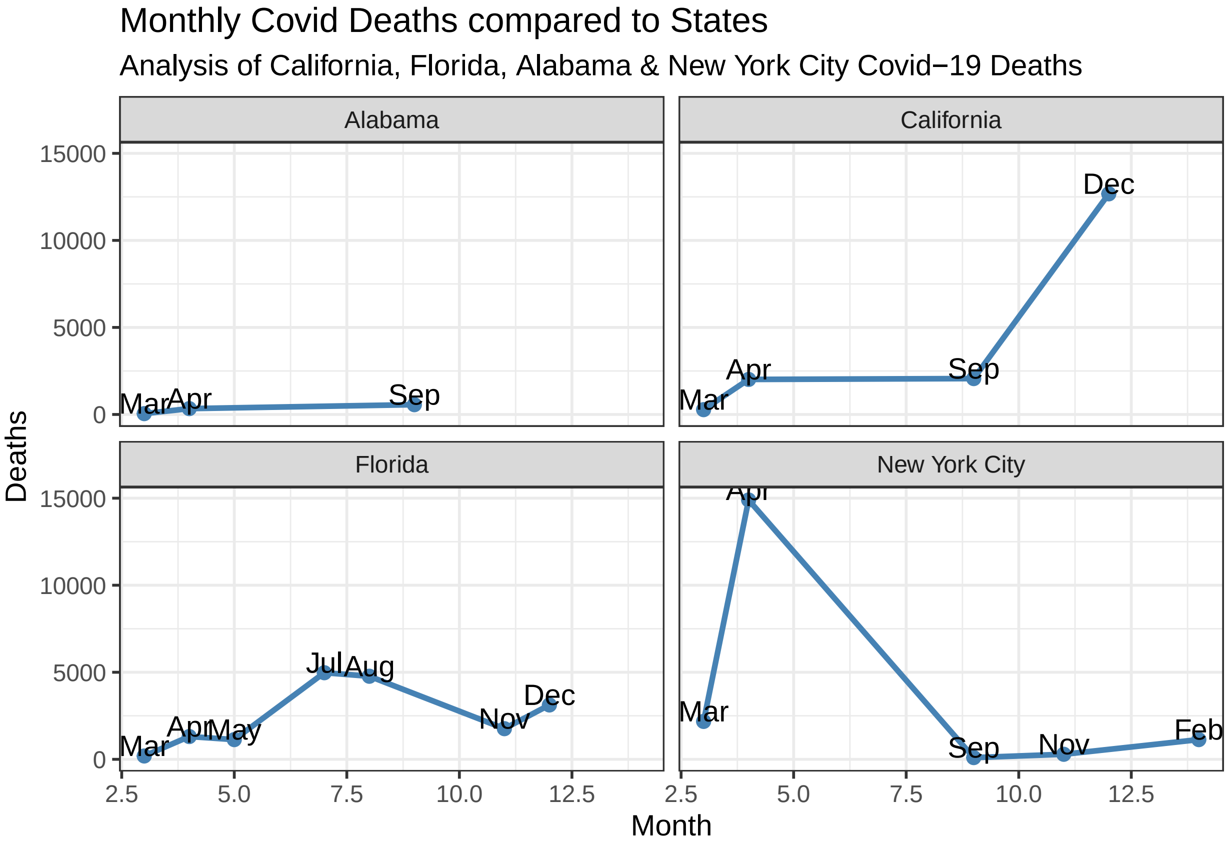




Looking at the summary statistics, it seems as though that the average number of deaths in significantly higher in New York City as well as California, compared to Florida and Alabama. This might be due to the fact of the population and the tourism that the 2 democratic states get attracted to such as the beautiful beaches in California to the famous Times Squared in New York City.

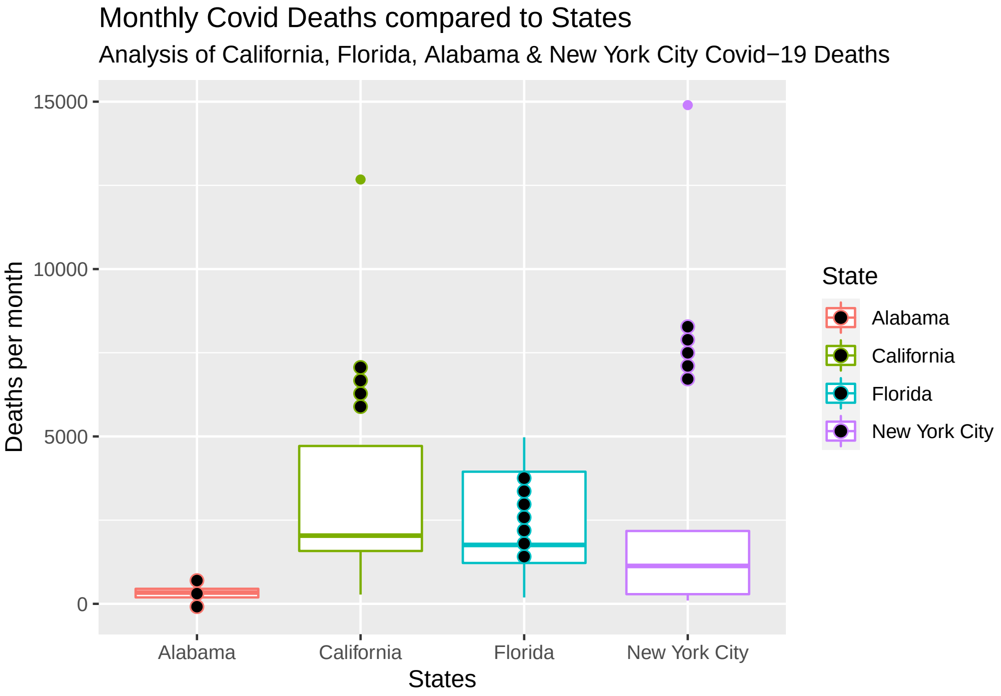
We see from the Shapiro- Wilks test based on the hypothesis that the variable is normally distributed in the dataset. We see that since the p-value is really low, we reject the null hypothesis and confirm that that the variable is not normally distributed. We also use the Levene test to test if K samples have equal variances and find that we fail to reject the null hypothesis thus concluding that no violations of any assumptions have happened.

In this forthcoming graph, I purposely ended up changing a dataset column where I made a replica of the subsetted graph that we had from the `CovidA` dataset. I then changed the months to where month 1 was January of 2020 and month 14 was February of 2021. This helped in viewing the graphs as there was no data for every month and when I first did the graph, specifically for NYC, there was no data of February of 2020 but there was of February 2021. This confused GGplot and instead of skipping February of 2020, it displayed the plot of February 2021 instead, which changes the whole graph. I also added another column in the dataset which has the abbreviation names for the months for aesthetically pleasing graphs using GGplot. This graph really helps visualize the whole dataset and understand what we will be doing in this analysis.



We see here that surprisingly, there were a lot of deaths in California, despite it being a much more Democratic and very progressive state. While they had it mostly low, the sudden increase in deaths was due to the fact that it was December, and people were probably visiting their friends and loved ones regardless which led to an increase in deaths. Florida, in this case, is very surprising how they have managed to keep their deaths down despite the fact that everything is open there and nobody believes in the virus. However, there have been multiple stories of Florida faking their death count as they want to remain open and not face criticism. Infact, during the beginning of the pandemic and data scientist was fired because she refused to fib the numbers of the death count. Alabama is not too surprising because it's not a popular spot to travel to and is not known for tourism. However, it is a shock that not too many deaths happened there as it is a republican state and indoor dining has been going on regardless of the pandemic. I would not be surprised if Alabama might be lying in its death count as well. NYC it seems like had the most death earlier on in 2020, which makes sense as a lot of people still weren't the processing the fact of how serious the pandemic was and so people were still traveling and doing work as well as flights being very active which shows in the graph as to why NYC had too many deaths in April of 2020. People also weren't walking around with masks and were enjoying their life as well. New York City is also known for a lot of consulting jobs as well which is why it makes me think that led to can increase in cases as consulting companies require its employees to travel to meet clients which leads to more deaths and further rampant spreading.

Lastly we also graph the distribution of deaths in order to analyze which test we would be using, the F-test or the Kruskal-Wallis Test.



Looking at this graph, we see that there are outliers in multiple groups as well as skewed distributions as well. This leads us to believe to use the Kruskal - Wallis Test in order to understand the results a bit more. We also use Kruskal - Wallis as it has more power than a permutation test when exposed to outliers, or a skewed distribution in 1 or more of the groups. We will be using the regular Kruskal - Wallis Test as the Large Sample Approximation requires the sample size to be n ≥ 30 which in this case the dataset has only 19.

(III) Analysis

Since we have seen that we will be using the Kruskal - Wallis Test, we will be using ranks instead of the actual X_{ij} values.Our null hypothesis in using the Kruskal - Wallis Test is:

$$H_0 : F_1(x) = F_2(x) = F_3(x) = F_4(x)$$

$$H_A : F_i(x) \geq F_j(x) \text{ or } F_i(x) \leq F_j(x) \text{ for some i} \neq \text{j}$$

We than perform the test and find that using the KW test with 4000 permutations gives an p-value of .3395.

(IV) Interpretation

Since the P-value was larger than α, we conclude that we fail to reject the null hypothesis thus meaning that all the groups are similar and that none of any 2 groups are statistically significant from each other. Since we fail to reject the null hypothesis we find that there is no point in finding out which groups are significantly different from each other which results in us ending our test.

Ⓥ Conclusion

We conclude thus that all the 4 groups are all similar with none of them being statistically significant. This comes to us as shocking as Democrats being California & NYC have been enforcing very serious covid restrictions. I also expected the Republican states being Alabama and Florida groups to differ. However, we should also not take this conclusion as an definite answer as there are many other confounding variables in play such as the fact that the population size in California and NYC combined is almost 60 million people. On the other side, Alabama and Florida have a combined of only 25 million. Thus it is more likely to result in more deaths in California and NYC compared to Alabama and Florida. There are also many other confounding variables that we should account for in our analysis such as weather, amount of people traveling between states, age of the population, and even how all the data was collected and arranged. There has been a lot of fake data spread around such as mentioned earlier with the data scientist. We might never be able to get an accurate depiction on whether the states are statistically significant or not due to misconception of data.

Question 2: Tests for Independence

Ⓘ Introduction

In this section of our report, we test the given data set (`CovidB.csv`) to see if there are any dependencies between any of the variables in the given data set. Our data set consists of the following variables: Year (the year in which the death occurred), Month (the month in which the death occurred), Sex (whether the deceased was male or female), Age Group (the age of the deceased at the time of their death), and Death (the number of deaths within each of the previous categories). We will test for independence between each of these variables using the techniques learned in Lecture, such as the Parametric χ^2 test and Permutation test for independence.

For our project, we have filtered the given data into a smaller subset that concentrates around the 2020 holiday season; particularly October - December of 2020. This will give us insight as to whether or not the holiday season has an impact on the number of deaths.

(II) Summary of Data

Below we have the first 4 lines of our altered data set:

Table 2: First 4 rows:

Year	**Month**	**Sex**	**Age group**	**Death**
2020	10	Male	0-17 years	6
2020	10	Male	18-29 years	41
2020	10	Male	45-54 years	667
2020	10	Male	55-64 years	1689

Next, we will find the average number of deaths for each variable, along with its standard deviation. We will start with the variable `Months`:

Table 3: Average and SD of Month

Month	**Average Mean**	**Standard Deviation**
10	471.500	611.002
11	908.875	1188.628
12	1745.250	2290.832

As we can see above, the average number of deaths increases as we progress into the holiday season. This time period is also known for colder weather and is typically the Flu season. These factors may also play a role in the increased number of deaths.

Next, we have the variable `Age Group`:

Table 4: Average and SD of Age Group

Age Group	**Average Mean**	**Standard Deviation**
0-17 years	10.33333	3.204164
18-29 years	75.50000	42.378060
45-54 years	1104.83333	761.362310
55-64 years	2976.83333	1926.509841

When looking at the groups that are most affected by Covid-19, we notice that as the age range of the subject increases, so does the death count.

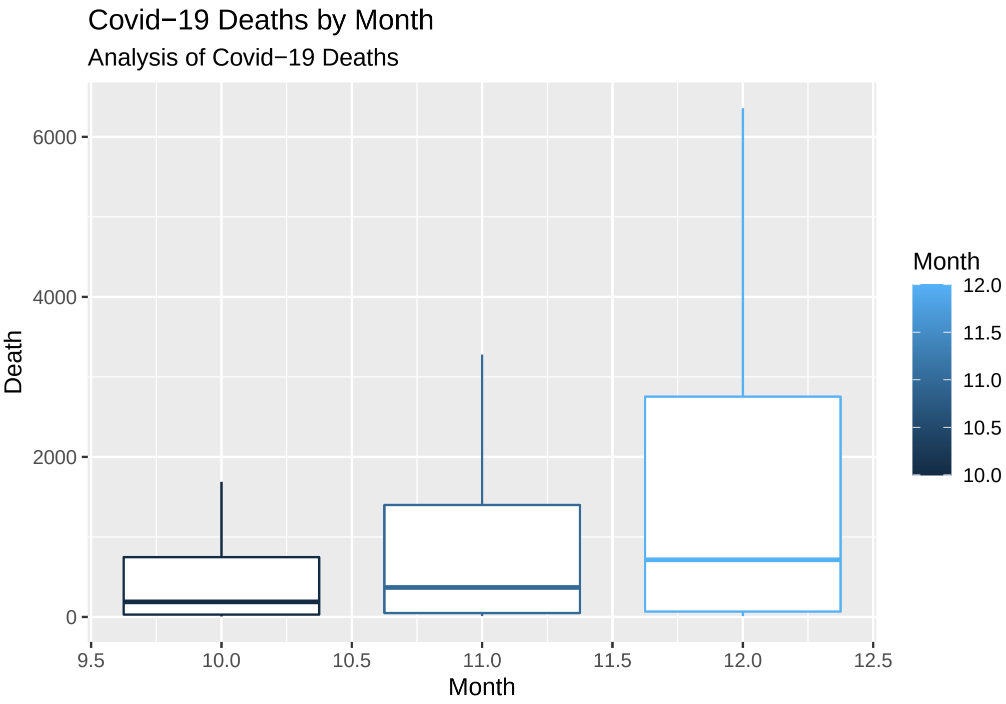
Finally, we have the variable `Sex`:

Table 5: Average and SD of Sex

Sex	**Average Mean**	**Standard Deviation**
Female	751.5833	1091.165
Male	1332.1667	1926.396

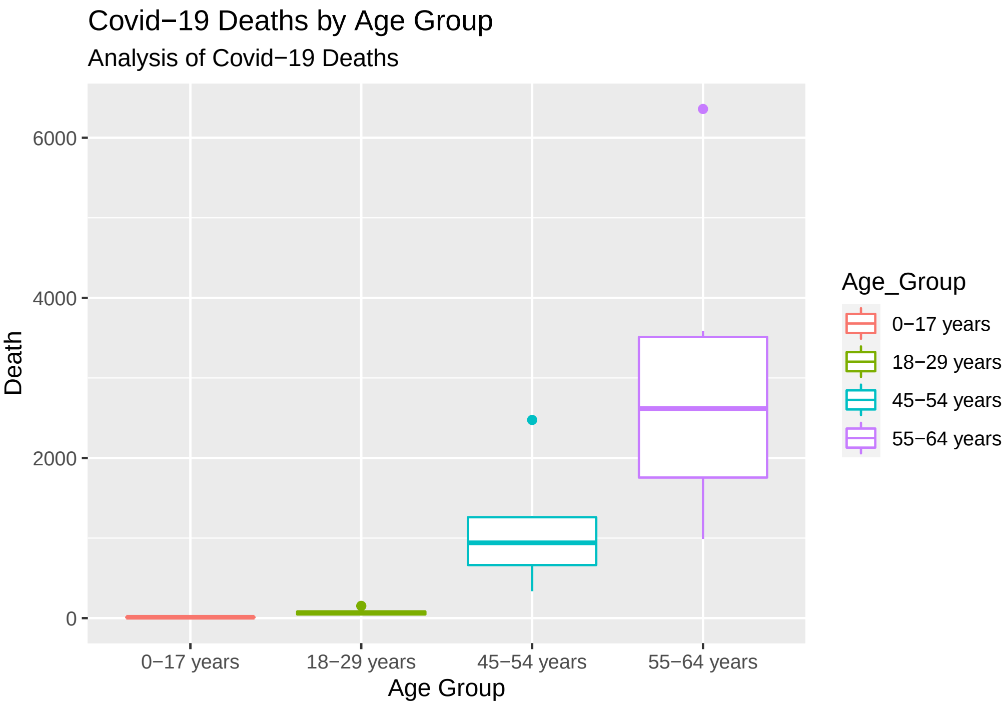
As we can see above, there are far more male deaths than female deaths, almost by a factor of 2. This can be interpreted very widely, so we will conduct further analysis later in the report.

Below we have a box-plot for each month in our selected range:



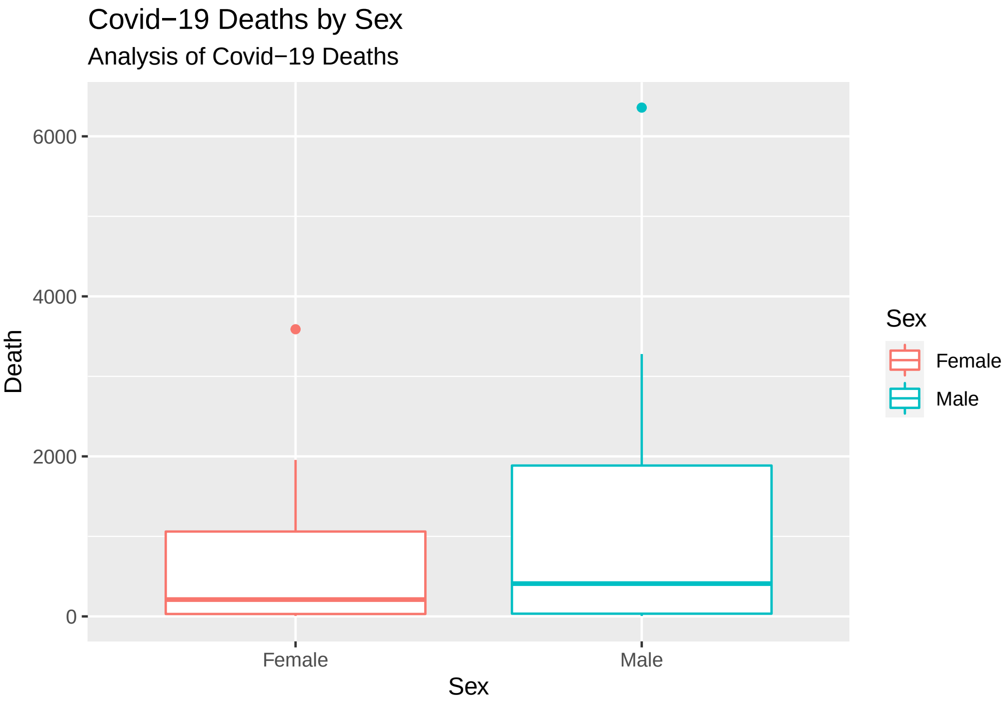
As we can see from the above plot, the deaths increase as we get closer to the holiday season.

Below we have a box-plot for each age group in our selected range:



As we can see above, there is a large difference in deaths between age groups. This makes sense, as those who are older have weaker immune systems, and are therefore less able to fight off the virus once infected.

Below we have a box-plot for each sex:



Here we see that males account for a much larger portion of those who die from the Covid-19 virus.

(III) Analysis

In this section of the report we will be analyzing our data to answer the following question: Are Sex and Age Group independent in relation to Covid-19 deaths? We will use two tests to help determine the answer. The first test we will use is the Parametric χ^2 test and the second is the Permutation test for independence.

We will start our analysis by looking at the contingency table formed from our filtered data:

Table 6: Contingency Table

Sex	**0-17 years**	**18-29 years**	**45-54 years**	**55-64 years**
Female	29	183	2273	6534
Male	33	270	4356	11327

Now that we have our table, we will form a null and alternative hypothesis:

H_o : The sex and age group of a patient regarding Covid-19 deaths is independent.

H_A : The sex and age group of a patient regarding Covid-19 deaths is dependent.

Now we can calculate our test statistic, χ^2. We than proceed to do the permutation test after obtaining the χ^2. We use 4000 permutations for the test. We also than find the Tukey-Inspired cutoff value. All the results are included in the following table for ease.

Table 7: Tests

χ^2	**Permutation Test P-value**	**Tukey cutoff value**
17.91532	1	3.520652

Lastly, we have our observed values:

Table 8: Observed Values

	0-17 years	**18-29 years**	**45-54 years**	**55-64 years**
Males vs. Females	1.757583	1.936158	-3.520652	2.67481

IV Interpretation

In our analysis, we started with the following null and alternative hypothesis:

H_o : The sex and age group of a patient regarding Covid-19 deaths is independent.

H_A : The sex and age group of a patient regarding Covid-19 deaths is dependent.

Using the above test statistics and p-values, and by testing at a significance level $\alpha = 0.05$, we can conclude that since the p-value of 1 is larger than our significance level, we fail to reject H_o and conclude that the sex and age group of a given patient are independent in relation to Covid-19 death rates.

This tells us that the likelihood of a male dying from Covid-19 is the same regardless of what age group he is in. As we can see from the averages in the Summary section, males are almost twice as likely to die from the Covid-19 virus than females are. This could be due to the fact that males are more likely to take risks and are usually less attentive to rules than females are.

From our observed values, we can see that the greatest difference in the death rate between age groups was between the age group $45 - 54$ years and $55 - 64$ years, with a difference in observed values of 6.195. This is well above the Tukey-Inspired Cutoff value of 3.521, meaning that this difference is significant. There was also a significant difference between the age group $45 - 54$ years and the other two groups as well, with their differences coming in at 5.278 for the age group $0 - 17$ years and 5.457 for the age group $18 - 29$ years. This indicates that the biggest jump in deaths occurred between the age group $45 - 54$ years and the other groups. As the data suggested in the Summary section, the gap in the death rate between age groups increased significantly as the age increased.

Ⓥ Conclusion

In conclusion, what we learned in this report is that gender and age are independent when it comes to Covid-19 death rates. We also saw that males have a higher recorded death rate than females, that the death rate increases with age, and that the death rates spiked during the winter months of 2020. The spike in the death rate in the later months of the year could be from a variety of factors.

Firstly, the winter months are known as the flu season. If a person's immune system is fighting the flu, then it is weaker, giving Covid-19 a better fighting chance. Second, the winter months contain the holiday season. This influences people to ignore safety protocols due to their adherence to traditions such as Halloween, Thanksgiving, Christmas/Hanukka/Kwanza, and the New Year celebration. These events usually require family and/or friends to gather, which helps the virus spread and infect more people. This is a catalyst for the virus to take more lives.

I'd like to note that these are observations, and we should never take correlation of data to have a causal relationship. This is a mere extrapolation of the data, and should be taken as such. However, there is a trend that is hard to ignore. Thank you for your time, and your attention throughout this report!

VI

Code Appendix

```
# cuttingoffcode
library(knitr)
opts_chunk$set(tidy.opts = list(width.cutoff = 70), tidy = TRUE)
# importing dataset
library(readr)
CovidA <- read_csv("CovidA.csv")
# subsetting data
CovidA_sub = subset(CovidA, CovidA$State == "California" | CovidA$State ==
    "New York City" | CovidA$State == "Florida" | CovidA$State == "Alabama")
# summary of data with mean,sd, rank,sample size
CovidA_sub$Rank = rank(CovidA_sub$Death, ties = "average")
Group.order = aggregate(Death ~ State, data = CovidA_sub, mean)$State
Xi = aggregate(Death ~ State, data = CovidA_sub, mean)$Death
si = aggregate(Death ~ State, data = CovidA_sub, sd)$Death
Ri = aggregate(Rank ~ State, data = CovidA_sub, mean)$Rank
ni = aggregate(Death ~ State, data = CovidA_sub, length)$Death
results = rbind(Xi, si, Ri, ni)
rownames(results) = c("Group Mean", "Group SD", "Rank Mean", "Sample Size")
colnames(results) = as.character(Group.order)
SR.2 = var(CovidA_sub$Rank)
# Anova Test
Ano = aov(Death ~ State, data = CovidA_sub)
par(mfrow = c(1, 2))
plot(Ano, 1)
plot(Ano, 2)
# shapiro test and levene test
shapiro.test(CovidA_sub$Death)
library(lawstat)
levene.test(CovidA_sub$Death, as.factor(CovidA_sub$State))
library(ggplot2)
library(dplyr)
# line graph converting months as to not get confused by year so month
# 1 is January 2020 and month 14 is February 2021
CovidA_sub_graph = CovidA_sub
CovidA_sub_graph$Month[19] = 14
CovidA_sub_graph$month.name = month.abb[CovidA_sub$Month]
# ggplot graph with facetwrap
ggplot(data = CovidA_sub_graph, aes(Month, Death)) + geom_line(color = "steelblue",
    size = 1) + geom_point(color = "steelblue", size = 2) + labs(title = "Monthly Covid Deaths compared
    subtitle = "Analysis of California, Florida, Alabama & New York City Covid-19 Deaths",
    y = "Deaths", x = "Month") + facet_wrap(~State) + theme_bw() + geom_text(aes(label = month.name),
    hjust = 0.5, vjust = 0)
# Boxplot
ggplot(CovidA_sub, aes(x = Death, y = State, color = State)) + geom_boxplot() +
    coord_flip() + geom_dotplot(binaxis = "y", stackdir = "center", dotsize = 0.8) +
    labs(title = "Monthly Covid Deaths compared to States", subtitle = "Analysis of California, Florida
        y = "States", x = "Deaths per month")
# KW Test
set.seed(1)
N = nrow(CovidA_sub)
```

```
KW.OBS = 1/SR.2 * sum(ni * (Ri - (N + 1)/2)^2)  #Note, this assumes you calculate ni and Ri above
R = 4000
many.perms.KW = sapply(1:R, function(i) {
    permuted.data = CovidA_sub  #So we don't overwrite the original data
    permuted.data$Group = sample(permuted.data$State, nrow(permuted.data),
        replace = FALSE)  #Permuting the groups
    SR.2 = var(permuted.data$Rank)
    ni = aggregate(Rank ~ Group, data = permuted.data, length)$Rank
    Ri = aggregate(Rank ~ Group, data = permuted.data, mean)$Rank
    KW.i = 1/SR.2 * sum(ni * (Ri - (N + 1)/2)^2)
    return(KW.i)
})
p.value = mean(many.perms.KW > KW.OBS)
# End of 1st part of Project code
library(readr)
CovidB <- read_csv("CovidB.csv")


Covid_B_sub = subset(CovidB, CovidB$Month == 10 & CovidB$Age_Group == "0-17 years" |
    CovidB$Month == 10 & CovidB$Age_Group == "18-29 years" | CovidB$Month ==
    10 & CovidB$Age_Group == "45-54 years" | CovidB$Month == 10 & CovidB$Age_Group ==
    "55-64 years" | CovidB$Month == 11 & CovidB$Age_Group == "0-17 years" |
    CovidB$Month == 11 & CovidB$Age_Group == "18-29 years" | CovidB$Month ==
    11 & CovidB$Age_Group == "45-54 years" | CovidB$Month == 11 & CovidB$Age_Group ==
    "55-64 years" | CovidB$Month == 12 & CovidB$Age_Group == "0-17 years" |
    CovidB$Month == 12 & CovidB$Age_Group == "18-29 years" | CovidB$Month ==
    12 & CovidB$Age_Group == "45-54 years" | CovidB$Month == 12 & CovidB$Age_Group ==
    "55-64 years")
head(Covid_B_sub, 4)

average_death_by_month = aggregate(Death ~ Month, data = Covid_B_sub, mean)
average_death_by_month

sd_death_by_month = aggregate(Death ~ Month, data = Covid_B_sub, sd)
sd_death_by_month

average_death_by_age = aggregate(Death ~ Age_Group, data = Covid_B_sub,
    mean)
average_death_by_age

sd_death_by_age = aggregate(Death ~ Age_Group, data = Covid_B_sub, sd)
sd_death_by_age

average_death_by_sex = aggregate(Death ~ Sex, data = Covid_B_sub, mean)
average_death_by_sex

sd_death_by_sex = aggregate(Death ~ Sex, data = Covid_B_sub, sd)
sd_death_by_sex
ggplot(Covid_B_sub, aes(x = Month, y = Death, group = Month, color = Month)) +
    geom_boxplot() + labs(title = "Covid-19 Deaths by Month", subtitle = "Analysis of Covid-19 Deaths",
    y = "Death", x = "Month")
ggplot(Covid_B_sub, aes(x = Age_Group, y = Death, group = Age_Group, color = Age_Group)) +
    geom_boxplot() + labs(title = "Covid-19 Deaths by Age Group", subtitle = "Analysis of Covid-19 Deat
    y = "Death", x = "Age Group")
ggplot(Covid_B_sub, aes(x = Sex, y = Death, group = Sex, color = Sex)) +
    geom_boxplot() + labs(title = "Covid-19 Deaths by Sex", subtitle = "Analysis of Covid-19 Deaths",
    y = "Death", x = "Sex")

contingency_table = xtabs(Death ~ Sex + Age_Group, data = Covid_B_sub)
contingency_table

ni. = rowSums(contingency_table)
n.j = colSums(contingency_table)

the.test = chisq.test(contingency_table, correct = FALSE)
eij = the.test$expected
chi.sq.obs = as.numeric(the.test$statistic)

set.seed(3223)
R = 4000
r.perms = sapply(1:R, function(i) {
    perm.data = Covid_B_sub
    perm.data$Age_Group = sample(perm.data$Age_Group, nrow(perm.data),
        replace = FALSE)
    chi.sq.i = chisq.test(contingency_table, correct = FALSE)$stat
    return(chi.sq.i)
})
perm.pval = mean(r.perms >= chi.sq.obs)

n = sum(contingency_table)
ni. = rowSums(contingency_table)
n.j = colSums(contingency_table)
all.pjG1 = contingency_table[1, ]/ni.[1]
all.pjG2 = contingency_table[2, ]/ni.[2]
all.pbar = n.j/n
all.Zij = c(all.pjG1 - all.pjG2)/sqrt(all.pbar * (1 - all.pbar) * (1/ni.[1] +
    1/ni.[2]))

r.perms.cutoff = sapply(1:R, function(i) {
    perm.data = Covid_B_sub
    perm.data$Sex = sample(perm.data$Sex, nrow(perm.data), replace = FALSE)
    row.sum = rowSums(contingency_table)
    col.sum = colSums(contingency_table)
    all.pji = contingency_table[1, ]/row.sum[1]
    all.pji. = contingency_table[2, ]/row.sum[2]
    all.pbar = col.sum/sum(row.sum)
    all.Zij = c(all.pji - all.pji.)/sqrt(all.pbar * (1 - all.pbar) * (1/row.sum[1] +
        1/row.sum[2]))
    Q.r = max(abs(all.Zij))
    return(Q.r)
})
alpha = 0.05
cutoff.q = as.numeric(quantile(r.perms.cutoff, (1 - alpha)))
all.Zij_2 = matrix(all.Zij, nrow = 1)
colnames(all.Zij_2) = c("0-17 Years", "18-29 Years", "45-54 Years", "55-64 Years")
rownames(all.Zij_2) = c("Males vs. Females")
```

```
all.Zij_2
```