# **COVID-19 Excess Mortality Analysis**



# Background

Course: BUS4469 - Competing with Analytics - Group Project

Topic: COVID-19 Excess Mortality Analysis

Description: What was the impact of COVID-19 on causes of death in Ontario and our recommendations for the

future

Submission: December 8th, 2021

Project Team: 9 (Adam Miller, Anna Larkin, Dalton McPhaden, Justin Voronoff, Nir Oyberman)

## Introduction

The team will be investigating excess mortality in Ontario during the 2020-2021 COVID-19 pandemic. We will utilize a Statistics Canada dataset of weekly causes of mortality. We hope to understand how many additional deaths COVID-19 has caused directly and indirectly, and how it affected mortality due to other causes. Analyzing this data could provide interesting implications regarding the severity of COVID-19. For example, we may find that a strained healthcare system dealing with the pandemic resulted in higher deaths in other causes, or perhaps lockdowns due to COVID-19 decreased deaths due to accidents. This pandemic has been the greatest, most damaging public health crisis to impact people globally in the 21st century. By understanding how COVID-19 affected mortality, we can get a better idea of the true impact of the pandemic.

Questions we would like to understand:

- How many people were expected to die in the province of Ontario during the COVID-19 time period?
- How many people actually died in the province of Ontario during the COVID-19 time period?
- How many extra people died during the COVID-19 time period? (i.e. actual deaths compared to forecast for that period)
- How many of these deaths are due to the COVID-19 virus itself?
- How many of these deaths are due to other causes; did COVID-19 affect mortality by other causes?
- How effective were restrictions at lowering excess deaths during the COVID-19 time period?

We will be training and testing various models on pre-COVID deaths. Once we find the model with the lowest error, we will re-train the model with the entire pre-COVID dataset. This model will forecast expected deaths assuming COVID did not occur. We can then compare actual deaths to expected deaths to understand excess mortality as a result of COVID-19, directly or indirectly, and the impact of COVID-19 on other causes of death.

There are three objectives in this project:

- Impact of COVID-19 on total mortality
- Impact of COVID-19 on non-COVID causes of death
- · Evaluate efficacy of lockdowns

# **Loading Data**

Load Libraries

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```
# time series forecasting
library(forecast)

# neural Networks
library(nnfor)

# errors
library(Metrics)

# time series manipulation
library(xts)

#plotting tools with expanded functionality
library(ggplot2)
```

Data Source: Statistics Canada - Provisionaly Weekly Death Counts by Cause (https://www150.statcan.gc.ca/t1/tbl1/en/tv.action?pid=1310081001&cubeTimeFrame.startDaily=2010-01-09&cubeTimeFrame.endDaily=2021-06-30&referencePeriods=20100109%2C20210630)

Load Data and Observe

Hide

DeathData = read.csv("data/ontario\_covid\_2010\_2021.csv", fileEncoding = "UTF-8-BOM")
head(DeathData)

Totalall.causes.of.death	Malignant.neoplasms	Diseases.of.heart
<int></int>	<int></int>	<int></int>
1905	500	380
1860	495	365
1840	545	360
1705	500	355
1720	490	340
1810	510	400
	<int> <int> 1905 1860 1840 1705 1720</int></int>	<int> <int>         1905       500         1860       495         1840       545         1705       500         1720       490</int></int>

This dataset displays weekly death counts in Ontario, organized by cause of death. The first column 'Date' is the first day of each week and ranges from 2010/01/09 to 2021/06/26 (YY/MM/DD), giving us 599 data points. The original dataset had values for all provinces, but had significant amounts of missing data for provinces other than Ontario. For this reason, we preprocessed the data to remove provinces other than Ontario. As we would expect from StatsCan data, there are no missing values, null values, or values that are extreme outliers. As such, no further data cleaning is required. The data range goes back to 2010. As we will show below, there was a large spike in deaths in 2018, likely due to a particularly bad North American flu season.

(https://www.cdc.gov/flu/about/season/flu-season-2017-2018.htm). We selected data back to 2010 so that models will not overemphasize 2018, which had an unusually large number of deaths.

Hide

### summary(DeathData)

Date	Total.	.all.caus	es.of.de	eath	Maligna	ant.neoplasms	Dise	ases.of.hear	t Cer
ebrovascular.diseas	ses								
Length:599	Min.	:1510			Min.	:425.0	Min.	:260.0	Mi
n. : 60.00									
Class :character	1st Qu	:1745			1st Qu.	:520.0	1st	Qu.:340.0	1st
Qu.: 90.00									
Mode :character	Median	:1890			Median	:545.0	Medi	an :360.0	Med
ian : 95.00									
	Mean	:1913			Mean	:543.7	Mean	:366.2	Mea
n : 96.94									
	3rd Qu	:2045			3rd Qu.	:565.0	3rd	Qu.:390.0	3rd
Qu.:105.00									
	Max.	:2645			Max.	:635.0	Max.	:510.0	Ma
x. :135.00									
Chronic.lower.resp	oiratory.	.diseases	Acciden	nts	uninter	ntional.injur	ies.	COVID.19	
Information.unavail	Lable								
Min. : 45.0			Min.	: 55	.0			Min. : 0.0	0.0
Min. : 0.000									
1st Qu.: 65.0			1st Qu.	.: 85	.0			1st Qu.: 0.0	0.0
1st Qu.: 0.000									
Median : 75.0			Median	: 95	.0			Median: 0.	00
Median : 0.000									
Mean : 78.4			Mean	: 98	.9			Mean : 15.	98
Mean : 6.269									
3rd Qu.: 85.0			3rd Qu.	:110	.0			3rd Qu.: 0.	0.0
3rd Qu.: 0.000									
Max. :140.0			Max.	:180	.0			Max. :490.	0.0
Max. :355.000									

The above summary shows the descriptive statistics of the "Total..all.causes.of.death" and all other causes of death included in this dataset.

To create the time series, we will have to create year and week columns.

Data Clean Up: Add Year, Month and Day Columns

```
# number of weeks
numData = dim(DeathData)[1]
DateSplit = c(0,0,0)
for (i in 1:numData){
 DateSplit = unlist(strsplit(DeathData$Date[i],"-"))
 DeathData$Year[i] = as.numeric(DateSplit[1])
 DeathData$Month[i] = as.numeric(DateSplit[2])
 DeathData$Day[i] = as.numeric(DateSplit[3])
 DeathData$Total_named_causes_of_death[i] = sum(DeathData[i,3:8])
 DeathData$Other[i] = DeathData$Total..all.causes.of.death[i] - DeathData$Total_named_c
auses_of_death[i] # adds column which captures all unclassified deaths
}
DeathData$Year = sapply(DeathData$Year, as.numeric)
DeathData$Day = sapply(DeathData$Day, as.numeric)
startYear = DeathData$Year[1]
# display new columns
head(DeathData)
```

Date	Totalall.causes.of.death	Malignant.neoplasms	Diseases.of.heart
<chr></chr>	<int></int>	<int></int>	<int></int>
1 2010-01-09	1905	500	380
22010-01-16	1860	495	365
32010-01-23	1840	545	360
12010-01-30	1705	500	355
52010-02-06	1720	490	340
62010-02-13	1810	510	400

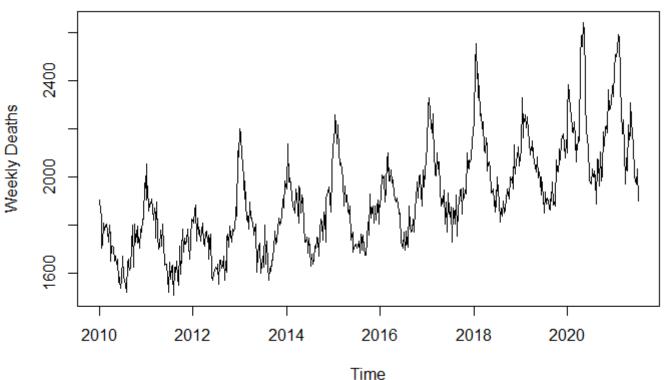
The dataset now has new columns for Year, Month and Day. Additionally, since the selected causes of death do not add up to the total deaths, a column titled "Other" was added, representing the difference between total deaths and deaths belonging to one of the causes included in the dataset.

## **Initial Observations**

Create a Time Series of Total..all.causes.of.death

DeathData.ts <- ts(DeathData\$Total..all.causes.of.death, start=c(startYear), frequency=5
2)
plot(DeathData.ts, main = "Total Deaths in Ontario between 2010 and 2021", ylab = "Weekl
y Deaths")</pre>

### Total Deaths in Ontario between 2010 and 2021



#### Observations:

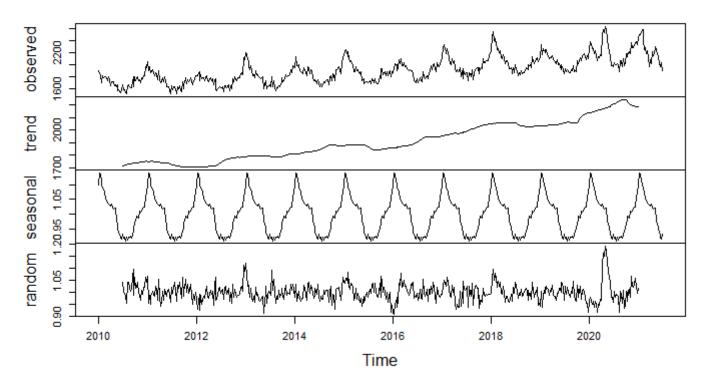
- We can observe that the total deaths in Ontario displays seasonality and an increasing trend over time
- This points us to models such as Holts-Winter, neural networks, ARIMA and other potential non-course models such as TBATS because they account for trend and seasonality
- The relative seasonal amplitudes seem to increase, indicating that this is a multiplicative time series
- There is a spike in total deaths around January 2018, likely due to the unusually bad flu season
- The pattern changes from 2020 onwards. It is difficult to tell if it increases or decreases but there is a definite shift in the pattern due to COVID-19

### View Decomposed Data

Hide

DeathData.ts.decomposed = decompose(DeathData.ts, type = "multiplicative")
plot(DeathData.ts.decomposed)

### Decomposition of multiplicative time series



#### Observations:

- There is an increasing trend over time, which makes sense as the population increases over time and thus mortality should too
- There is seasonality evident in the data. This will be observed further in the non-COVID data to ensure the impact of the pandemic is removed
- The randomness is relatively constant around 1, therefore the multiplicative model is appropriate. There is a spike in randomness in 2020 which is the impact of COVID-19

## Objective 1: What was the impact of COVID-19 on "Total..all.causes.of.death":

Process to answer Objective 1:

- 1. Split into pre-COVID and COVID data, and perform exploratory analysis
- 2. Test various models using pre-COVID data to find the lowest error
- 3. Rebuild best model and forecast what mortality should have been if COVID did not happen
- 4. Compare expected deaths without COVID to actual deaths during COVID to determine excess mortality

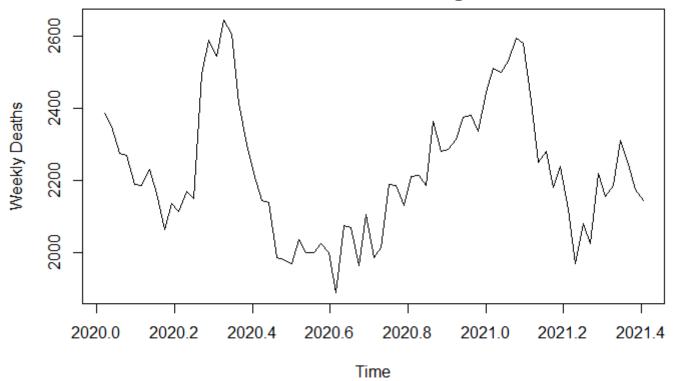
# 1) Subset Data into Pre-COVID and COVID data; exploratory analysis

```
# define data points
numDataPoints = length(DeathData.ts)
start2020 = numDataPoints-(52+26)

# subset
DeathData.pre2020 = subset(DeathData.ts, start = 1, end = start2020)
DeathData.2020_2021 = subset(DeathData.ts, start = start2020+1 , end = numDataPoints-5)
#COVID set is from 2020 onwards
DeathData.predict.csv = subset(DeathData.ts, start = numDataPoints-5+1, end = numDataPoints)
# write the last 2020-2021 subset to csv; this is the data that we will compare our pred ictions to to determine excess deaths
write.csv(DeathData.predict.csv, 'data/predict.csv')

# plot subset data
plot(DeathData.2020_2021, main = "Total Deaths in Ontario during Pandemic", ylab = "Week ly Deaths")
```

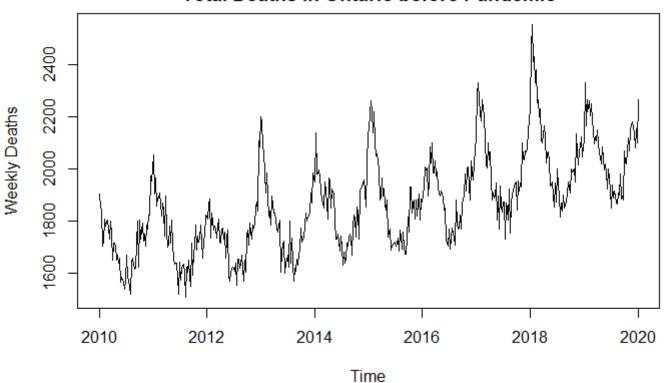
## **Total Deaths in Ontario during Pandemic**



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plot(DeathData.pre2020, main = "Total Deaths in Ontario before Pandemic", ylab = "Weekly
Deaths")

### **Total Deaths in Ontario before Pandemic**

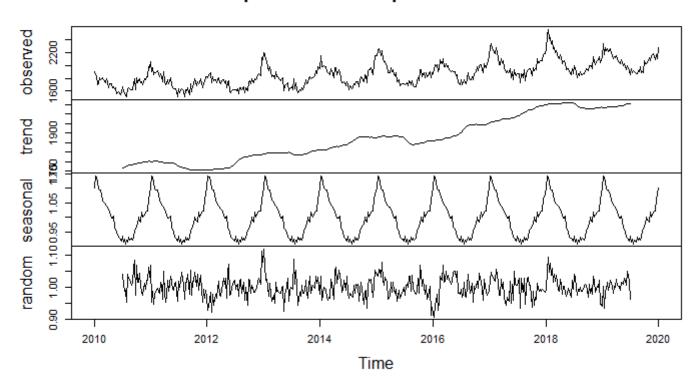


### 1.1.1) Decomposition of Pre-COVID

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DeathData.pre2020.decomposed = decompose(DeathData.pre2020, type = "multiplicative")
plot(DeathData.pre2020.decomposed)

### Decomposition of multiplicative time series



Hide

order(DeathData.pre2020.decomposed\$figure)

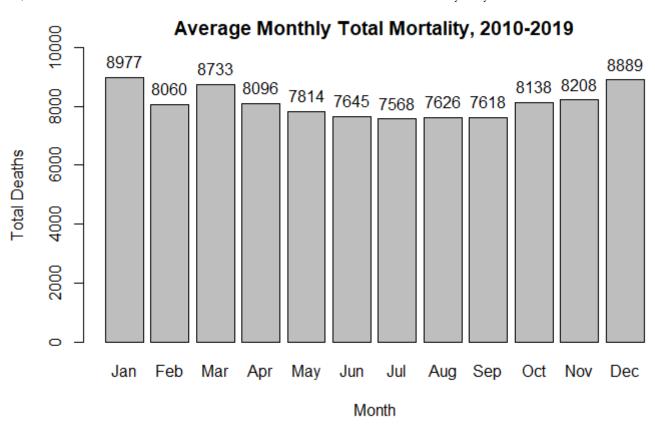
[1] 30 32 28 26 36 34 31 25 29 35 24 37 23 33 27 22 38 39 21 20 40 41 44 43 18 17 42 46 19 16 47 45 48 50 49 15 14 13 12 [40] 11 10 9 51 8 52 7 6 1 5 4 3 2

### Observations of the non-COVID Total Deaths Data:

- The seasonality is ordered from lowest to highest, therefore the most deaths in Ontario occur from around weeks 1 7 (January March) and least occur around weeks 25 35 (June August)
- In the United States, death rates are generally 8-12% higher in winter months than in summer months due
  to various factors related to colder temperatures. (https://www.epa.gov/climate-indicators/climate-changeindicators-cold-related-deaths) It is unsurprising to see a similar pattern in Canada; we will explore below
  differences in mortality between seasons. We can also visually represent this in the section below by
  aggregating weekly data into months, and finding the average for that month over the years.

## 1.1.2) Monthly Total Deaths

```
# retrieve the dates that we need
dates = DeathData$Date[1:length(DeathData.pre2020)]
# convert the time series object to an xts for manipulation
DeathData.pre2020.xts = xts(x = DeathData.pre2020,
                            order.by = as.POSIXct(dates))
# aggregate months into a year/month matrix
monthMatrix = matrix(0, 10, 12)
for(i in 1:10){
  year = paste('20', as.character(i+9), sep = '')
  for(j in 1:12){
    month = as.character(j)
    index = paste(year, month, sep='-')
    monthMatrix[i,j] = sum(DeathData.pre2020.xts[index])
  }
}
# find the average of each month
monthlyAverage = matrix(0, 0, 12)
for(i in 1:12){
  # note: we divide by 10 because there are 10 years (2010 - 2019)
  # therefore there are 10 months worth of deaths
  # dividing by 10 gives average deaths in that month in this timeframe
  monthlyAverage[i] = sum(monthMatrix[,i]) / 10
}
# generate months for x-axis
months = seq(1, 12, 1)
months = month.abb[months]
# plot
plot = barplot(monthlyAverage,
                main = "Average Monthly Total Mortality, 2010-2019",
                ylab = "Total Deaths",
                xlab = "Month",
                names.arg = months,
                ylim = c(0, 10000)
# data labels
text(plot, monthlyAverage, round(monthlyAverage, 0), cex = 1, pos = 3)
```



Validating what we observed from the decomposition, we can see that over the years, typically there are more deaths in the winter months and fewer in the summer months. To see how much higher deaths are in the winter than the summer:

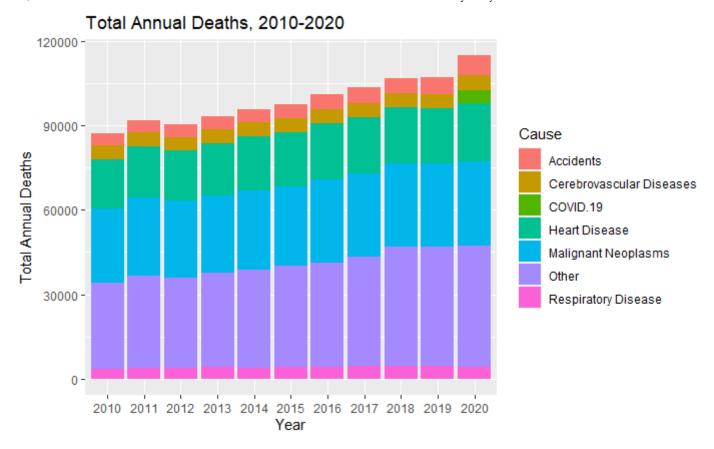
```
Hide
DeathsOrdered = order(monthlyAverage)
print(DeathsOrdered)
                     2
                       4 10 11 3 12
 [1]
            8
                  5
                                                                                        Hide
# this ranks deaths by month. Deaths are highest in January and lowest in July. By how m
uch is January higher than July?
HighestAverage = monthlyAverage[DeathsOrdered[12]]
LowestAverage = monthlyAverage[DeathsOrdered[1]]
SeasonalDiff = HighestAverage/LowestAverage-1
print(SeasonalDiff)
[1] 0.1861003
```

Deaths are higher in the winter by 18.6%, significantly higher than the 8-12% figure cited by the U.S. EPA report discussed above. This is likely due to Canada having an overall colder climate during the winter, with more parts of the country experiencing winter conditions. This increases the magnitude of the seasonality.

## 1.1.3) Total Annual Deaths by Cause

```
# create Empty Data Frame:
DeathsPerYear = data.frame(
  "Year" = c(2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020)
  "Malignant Neoplasms" = c(0),
  "Heart Disease" = c(0),
  "Cerebrovascular Diseases" = c(0),
  "Respiratory Disease" = c(0),
  "Accidents" = c(0),
  "COVID.19" = c(0),
  "Other" = c(0))
# shrink dataset from Deaths/Week into Deaths/Year:
index = 1
baseyear = 2010
neoplasmTotal <- heartTotal <- vascularTotal <- respiratoryTotal <- accidentsTotal <- co
vidTotal <- otherTotal <- 0
# repeat from 2010 to 2020
for (i in 1:11){
  # sum deaths in a given year
 while (DeathData$Year[index] == baseyear){
    neoplasmTotal = neoplasmTotal + DeathData$Malignant.neoplasms[index]
    heartTotal = heartTotal + DeathData$Diseases.of.heart[index]
    vascularTotal = vascularTotal + DeathData$Cerebrovascular.diseases[index]
    respiratoryTotal = respiratoryTotal + DeathData$Chronic.lower.respiratory.diseases[i
ndex]
    accidentsTotal = accidentsTotal + DeathData$Accidents..unintentional.injuries.[inde
x ]
    covidTotal = covidTotal + DeathData$COVID.19[index]
    otherTotal = otherTotal + DeathData$Other[index]
    index = index + 1
  }
  # fill in the empty data frame
  DeathsPerYear[i, 2] = neoplasmTotal
  DeathsPerYear[i, 3] = heartTotal
  DeathsPerYear[i, 4] = vascularTotal
  DeathsPerYear[i, 5] = respiratoryTotal
 DeathsPerYear[i, 6] = accidentsTotal
  DeathsPerYear[i, 7] = covidTotal
  DeathsPerYear[i, 8] = otherTotal
  neoplasmTotal <- heartTotal <- vascularTotal <- respiratoryTotal <- accidentsTotal <-
 covidTotal <- otherTotal <- 0</pre>
  baseyear = baseyear + 1
# re-arrange data for plotting
causesNum = 7
year = c(
  rep("2010", causesNum),
```

```
rep("2011", causesNum),
  rep("2012", causesNum),
  rep("2013", causesNum),
  rep("2014", causesNum),
 rep("2015", causesNum),
 rep("2016", causesNum),
 rep("2017", causesNum),
  rep("2018", causesNum),
  rep("2019", causesNum),
  rep("2020" , causesNum))
condition = rep(c(
    "Malignant Neoplasms",
    "Heart Disease",
    "Cerebrovascular Diseases",
    "Respiratory Disease",
    "Accidents",
    "COVID.19",
    "Other"
  ), 11)
value = data.frame(77)
index = 1
for (i in 1:11) {
 for (j in 1:causesNum) {
    value[index] = DeathsPerYear[i, j + 1]
    index = index + 1
 }
}
value <- as.data.frame(t(value))</pre>
# create dataframe
dea = data.frame("Year" = year, "Cause" = condition, "Deaths" = value)
# plot
ggplot(data = dea, aes(x = Year, y = V1, fill = Cause)) +
       geom col() +
       ylab("Total Annual Deaths") +
       ggtitle("Total Annual Deaths, 2010-2020")
```



Although there was a clear increase in deaths in 2020 due to COVID-19, COVID-19 is actually a relatively small contributor to the total annual deaths, with Accidents, Malignant Neoplasms, Heart Disease, and "other" causes of death being clearly more. This shows that we must investigate the impact of COVID-19 on all causes of death, as the second-order impacts of COVID and policy responses to the pandemic may have influenced other causes of death.

## 2) Model Selection

## 2.1) Split non-COVID data into Training and Testing time series

```
training.percent = .75

nTrain = round(length(DeathData.pre2020)*training.percent)
nTest = round(length(DeathData.pre2020)-nTrain)

train.ts = subset(DeathData.pre2020, start = 1, end = nTrain)
testing.ts = subset(DeathData.pre2020, start = nTrain + 1, end = nTrain + nTest)

# check
originalLength = length(DeathData.pre2020)
originalLength == (nTrain + nTest)
```

[1] TRUE

Pass: originalLength == nTrain + nTest

## 2.2) Try different models

We will test the following three models for the lowest error, then re-train the best model with the entire dataset.

### Models:

- 2.2.1 Feed Forward Neural Network
- 2.2.2 ARIMA
- 2.2.3 TBATS

We chose not to do Drift, Mean, or (S)Naive, and other models which do not capture trend/seasonality, as they will not appropriately handle our data, which has trend and seasonality. Holt-Winters doesn't suffice as the frequency of our data is greater than 48 seasonal patterns. We rejected linear regression as it does not handle multiplicative seasonality.

### 2.2.1 Feed Forward Neural Network

Model Description: A neural network is a collection of connected nodes in which the connections between nodes do not form a cycle. Neural networks are trained by modifying the weights of the connections, resulting in a model that can approximate complicated functions. Neural networks are effective because unlike other models they make no assumptions about the trend. The following implementation uses the elm() function in the 'nnfor' package, which fits Extreme Learning Machine (ELM) neural networks for time series forecasting.

Train the Neural Network and Forecast

```
Hide
```

```
defaultW <- getOption("warn")
options(warn = -1)

DeathData.ts.pre2020.training.elm = elm(train.ts)
summary(DeathData.ts.pre2020.training.elm)</pre>
```

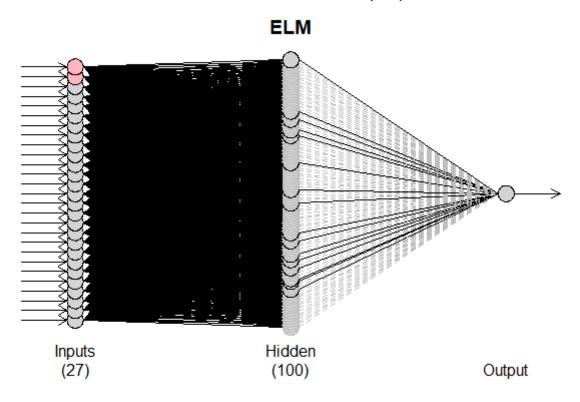
	Length	Class	Mode
net	14	nn	list
hd	1	-none-	numeric
W.in	0	-none-	NULL
W	20	-none-	list
b	20	-none-	numeric
W.dct	20	-none-	list
lags	25	-none-	numeric
xreg.lags	0	-none-	NULL
difforder	1	-none-	numeric
sdummy	1	-none-	logical
ff.det	1	-none-	numeric
det.type	1	-none-	character
У	391	ts	numeric
minmax	4	-none-	list
xreg.minmax	0	-none-	NULL
comb	1	-none-	character
type	1	-none-	character
direct	1	-none-	logical
fitted	341	ts	numeric
MSE	1	-none-	numeric

Hide

```
DeathData.ts.pre2020.training.elm.fcast = forecast(DeathData.ts.pre2020.training.elm, h
= nTest)
options(warn = defaultW)
```

### Plot the NN and Display Statistics

```
plot(DeathData.ts.pre2020.training.elm)
```



Hide

print(DeathData.ts.pre2020.training.elm)

```
ELM fit with 100 hidden nodes and 20 repetitions.

Series modelled in differences: D1.

Univariate lags: (1,2,3,4,5,6,7,8,9,10,11,12,14,15,16,17,18,19,21,24,26,39,41,48,49)

Deterministic seasonal dummies included.

Forecast combined using the median operator.

Output weight estimation using: lasso.

MSE: 3963.7809.
```

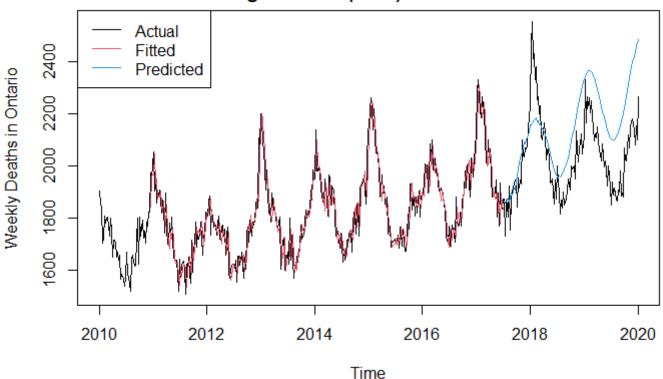
### Display Model Fit and Predictions

Hide

```
plot(DeathData.pre2020, main = "Extreme Learning Machine (ELM) Model Fit and Prediction
s", ylab = "Weekly Deaths in Ontario")
lines(DeathData.ts.pre2020.training.elm.fcast$fitted, col = 2)
```

```
lines(DeathData.ts.pre2020.training.elm.fcast$mean, col = 4)
legend("topleft", lty = 1, col = c(1,2,4), legend = c("Actual", "Fitted", "Predicted"))
```

## Extreme Learning Machine (ELM) Model Fit and Predictions



### NN RMSE

Hide

```
elm.rmse = rmse(testing.ts[1:length(testing.ts)], DeathData.ts.pre2020.training.elm.fcas
t$mean)
elm.rmse
```

[1] 166.8074

### NN MAPE

Hide

```
elm.mape = mape(testing.ts[1:length(testing.ts)], DeathData.ts.pre2020.training.elm.fcas
t$mean)
elm.mape
```

[1] 0.06928313

### 2.2.2 **ARIMA**

Model Description: Autoregressive integrated moving average (ARIMA) is the most used approach for time series data and is composed of three parts: 1. auto regressive part which is a regression model that includes lag (past observations). 2. a differencing part that makes the data stationary by using a constant mean and variance over time, and 3. a moving average part that takes the average of the last N observations. Seasonality can be

incorporated into ARIMA by using SARIMA, which adds additional parameters for seasonality. The following implementation uses auto.arima() which automates the process of finding the parameters that generate the least error.

Train the ARIMA model

```
Hide
```

```
# create the model and view summary
arima.model = auto.arima(train.ts)
```

Test the Model

Hide

```
# print the summary
summary(arima.model)
```

```
Series: train.ts
ARIMA(1,0,2)(2,1,0)[52] with drift
Coefficients:
         ar1
                  ma1
                          ma2
                                  sar1
                                           sar2
                                                  drift
      0.8668 -0.5398 0.0294 -0.6803 -0.1848 0.6953
s.e. 0.0435
               0.0695 0.0645
                                0.0571
                                         0.0651 0.1473
sigma^2 estimated as 4458: log likelihood=-1914.68
AIC=3843.36
             AICc=3843.69
                             BIC=3870.14
Training set error measures:
                    ME
                           RMSE
                                     MAE
                                                MPE
                                                       MAPE
                                                                 MASE
                                                                              ACF1
Training set -0.456487 61.61973 44.87435 -0.1260478 2.45313 0.5028894 0.0004267557
```

Hide

```
# create the forecast
arima.fcast = forecast(arima.model, h = nTest)

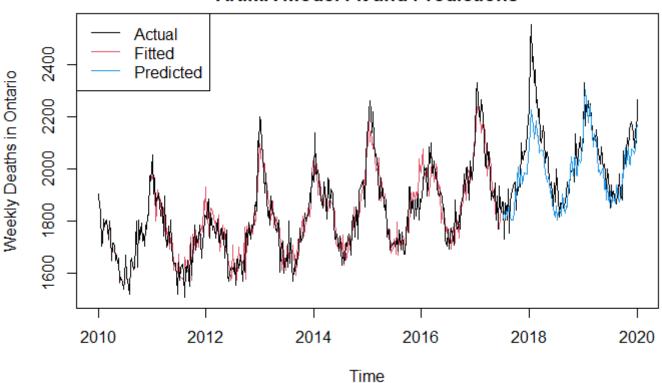
# plot
plot(DeathData.pre2020, col = 1, main = "ARIMA Model Fit and Predictions", ylab = "Weekl
y Deaths in Ontario")
lines(arima.fcast$fitted, col = 2)
```

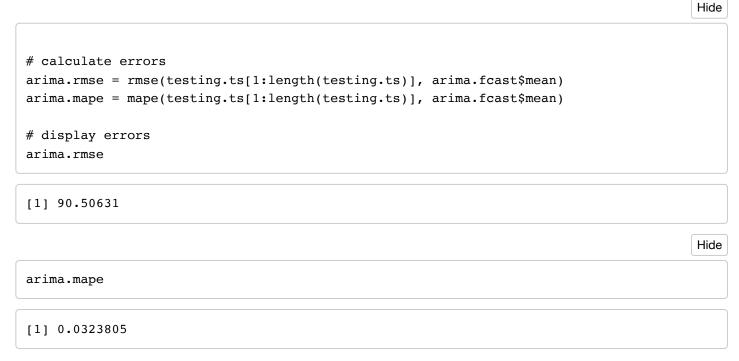
Hide

```
lines(DeathData.pre2020, col = 1)
lines(arima.fcast$mean, col = 4)
```

```
legend("topleft", lty = 1, col = c(1,2,4), legend = c("Actual", "Fitted", "Predicted"))
```

### ARIMA Model Fit and Predictions





### Observations:

- The constants from the auto.arima are as follows: ARIMA(1,0,2)(2,1,0)[52] with drift
- The display of ARIMA constants for both trend and seasonality confirms our above assumption that there is clear trend and seasonality in this data

### **2.2.3 TBATS**

Model Description: TBATS is an advanced time series forecasting method that consists of the following features: trigonometric seasonality, box-cox transformation, ARMA errors, trend and seasonal components. The following implementation uses the tbats() function from the 'forecast' library, as described by De Llevra, Hyndman & Snyder in 2011 (https://www.rdocumentation.org/packages/forecast/versions/8.15/topics/tbats). Since we were unable to implement Holts-winter, TBATS is an effective substitute as it incorporates exponential smoothing.

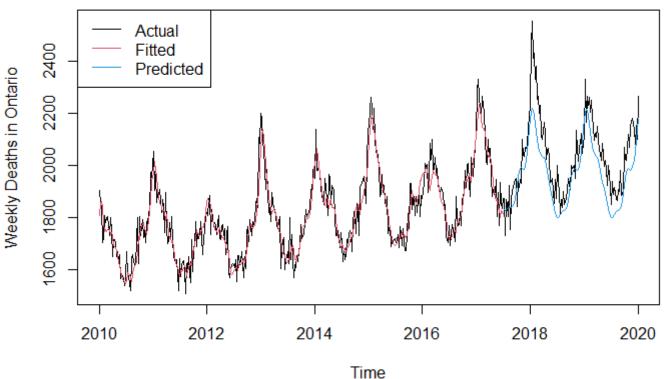
```
# train and forecast TBATS
trainTBATS <- tbats(train.ts)
trainTBATS.fcast <- forecast(trainTBATS, h = nTest)

Hide

# display TBATS Model Fit and Predictions
plot(DeathData.pre2020, main = "TBATS Model Fit and Predictions", ylab = "Weekly Deaths in Ontario")
lines(trainTBATS.fcast$fitted, col = 2)</pre>
```

```
lines(trainTBATS.fcast$mean, col = 4)
legend("topleft", lty = 1, col = c(1,2,4), legend = c("Actual", "Fitted", "Predicted"))
```

### **TBATS Model Fit and Predictions**



Hide

```
# calculate Errors
tbats.rmse = rmse(testing.ts[1:length(testing.ts)], trainTBATS.fcast$mean)
tbats.mape = mape(testing.ts[1:length(testing.ts)], trainTBATS.fcast$mean)

# display Errors
tbats.rmse

[1] 101.9873

Hide
tbats.mape
```

### 2.3 Select the best model

We create a table that displays the MAPE and RMSE of each model that we have tested.

```
errors = matrix(c(elm.mape,elm.rmse,arima.mape,arima.rmse,tbats.mape,tbats.rmse),ncol =
2,byrow = TRUE)
colnames(errors) = c("MAPE","RMSE")
rownames(errors) = c("ELM","ARIMA","TBATS")
print(errors)
```

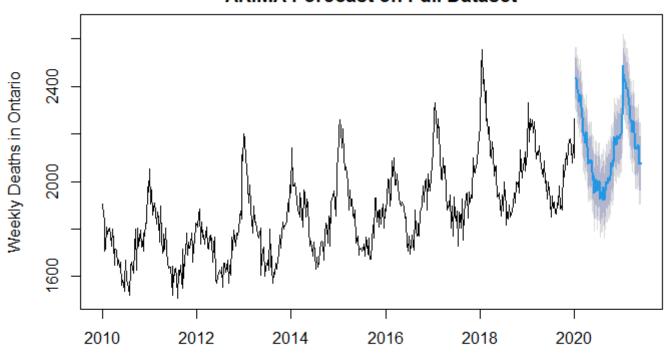
```
MAPE RMSE
ELM 0.06928313 166.80741
ARIMA 0.03238050 90.50631
TBATS 0.04059625 101.98727
```

All models have MAPE below ~6% indicating that the models selected for testing are appropriate for the data. ARIMA has lowest MAPE and lowest RMSE and is selected as our final model.

# 3) Rebuild model with full dataset, and use it to predict excess deaths.

```
# re-create the ARIMA model with the entirety of the 2020 data
actualArima <- auto.arima(DeathData.pre2020)
actualArima.fcast <- forecast(actualArima, h = length(DeathData.2020_2021))
plot(actualArima.fcast, main = "ARIMA Forecast on Full Dataset", ylab = "Weekly Deaths i
n Ontario")</pre>
```

### **ARIMA Forecast on Full Dataset**



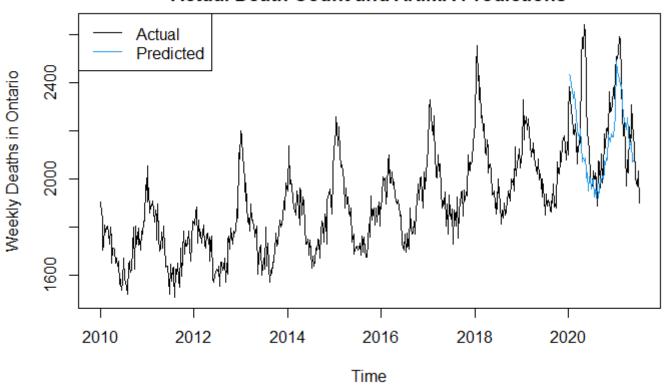
# 4) Compare predicted deaths to actual deaths during COVID

```
plot(DeathData.ts, main = "Actual Death Count and ARIMA Predictions", ylab = "Weekly Dea
ths in Ontario")
lines(actualArima.fcast$mean, col=4)
```

legend("topleft", lty=1, col=c(1,4), legend = c("Actual", "Predicted"))

file:///Users/justinvoronoff/Desktop/5th Year/1st Sem/Ivey/Competing with Analytics/Final Assignment/FINAL/Submission/Markdown.nb.html#

### **Actual Death Count and ARIMA Predictions**



The ARIMA prediction does not align with actual deaths during the COVID time period. This does not indicate that our prediction is poor, rather, it demonstrates the impact of COVID-19 on mortality.

```
PredictedDeaths = sum(actualArima.fcast$mean)
paste("Predicted Deaths:", round(PredictedDeaths, digits=0))

[1] "Predicted Deaths: 157496"

Hide

ActualDeaths = sum(DeathData.2020_2021)
paste("Actual Deaths:", ActualDeaths)

[1] "Actual Deaths: 162495"

Hide

ExcessDeaths = ActualDeaths - PredictedDeaths
paste("Excess Deaths:", round(ExcessDeaths, digits=0))

[1] "Excess Deaths: 4999"
```

```
COVIDDeaths = sum(DeathData$COVID.19)
paste("COVID Deaths:", round(COVIDDeaths, digits=0))
```

```
[1] "COVID Deaths: 9575"
```

Our model forecasts that approximately 167,629 deaths were expected, while 172,390 actually occurred. The COVID-19 pandemic resulted in approximately 4,761 more deaths than expected. There have been 9,575 COVID-19 deaths, which indicates other causes of death decreased.

We now know that COVID-19 decreased the amount of other death causes in Ontario over 2020 and 2021. This could be for a number of reasons, for example, less people are going outside, more people wearing masks, misdiagnosis of other causes, etc. For further analysis, we need to observe the impact of COVID-19 on each respective cause of death.

# Objective 2: What was the impact of COVID-19 on other causes of death

Review summary of causes of death

Hide

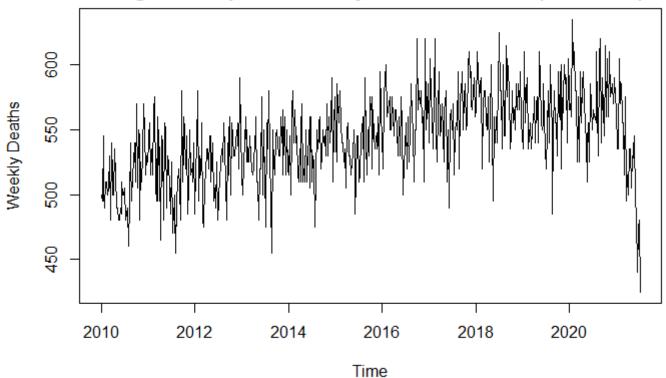
summary(DeathData)

Date		all.cause	s.of.death	Malignar	nt.neoplasms	Diseas	es.of.heart	Cer
ebrovascular.dise								
Length:599	Min.	:1510		Min. :	:425.0	Min.	:260.0	Mi
n. : 60.00								
Class :character	1st Qu.	:1745		1st Qu.:	:520.0	1st Qu	.:340.0	1st
Qu.: 90.00								
Mode :character	Median	:1890		Median :	:545.0	Median	:360.0	Med
ian : 95.00								
	Mean	:1913		Mean :	:543.7	Mean	:366.2	Mea
n : 96.94								
	3rd Qu.	:2045		3rd Qu.:	:565.0	3rd Qu	.:390.0	3rd
Qu.:105.00								
	Max.	:2645		Max. :	:635.0	Max.	:510.0	Ma
x. :135.00								
Chronic.lower.re	spiratory.	diseases .	Accidents.	.unintent	tional.injuri	ies.	COVID.19	
Information.unava	ilable							
Min. : 45.0		:	Min. : 55	5.0		Mi	n. : 0.0	0
Min. : 0.000								
1st Qu.: 65.0			1st Qu.: 85	5.0		1s	t Qu.: 0.0	0
1st Qu.: 0.000								
Median: 75.0			Median : 95	5.0		Ме	dian : 0.0	00
Median : 0.000								
Mean : 78.4			Mean : 98	3.9		Ме	an : 15.9	8
Mean : 6.269								
3rd Qu.: 85.0			3rd Qu.:110	0.0		3re	d Qu.: 0.0	0
3rd Qu.: 0.000								
Max. :140.0			Max. :180	0.0		Ma	x. :490.0	00
Max. :355.000								
Year	Month		Day	Total	_named_causes	of dea	ath Oth	ner
	Min. : 1.	000 Min	. : 1.00		- <u>-</u> : 935		Min.	: 50
0.0								
1st Qu.:2012 1	st Qu.: 3.	000 1st	Qu.: 8.00	1st Ou	1.:1130		1st Qu.	: 61
5.0	~		_		•		~ ~ ~	_
	Median : 6.	000 Med	ian :16.00	Median	n :1185		Median	: 70
0.0					•			
	Mean : 6.	404 Mea	n :15.76	Mean	:1200		Mean	<b>:</b> 71
3.3				- <del></del>				
	rd Qu.: 9.	000 3rd	Qu.:23.00	3rd O	1.:1255		3rd Qu.	. 79
5.0		JIW	201120100	u gu			J_u gu	, ,
	lax. :12.	000 Max	. :31.00	Max.	:1800		Max.	:109
		JJU HUA		iiun.	• 1000		iiun.	• ± U J

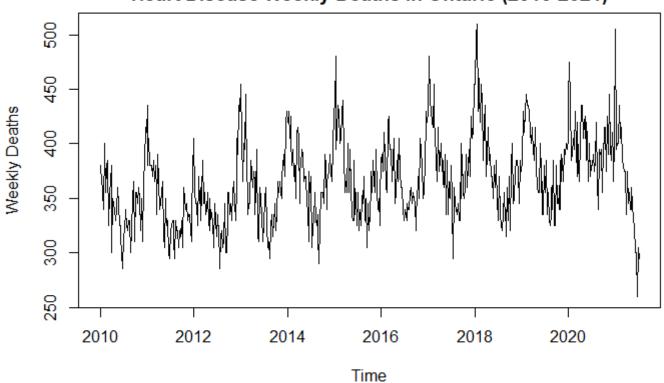
Create time series for all death causes:

```
Malignant.neoplasms.ts = ts(DeathData$Malignant.neoplasms[1:numDataPoints],
                            start = startYear,
                            frequency = 52)
Diseases.of.heart.ts = ts(DeathData$Diseases.of.heart[1:numDataPoints],
                          start = startYear,
                          frequency = 52)
Cerebrovascular.diseases.ts = ts(DeathData$Cerebrovascular.diseases[1:numDataPoints],
                                  start = startYear,
                                  frequency = 52)
resp.ts = ts(DeathData$Chronic.lower.respiratory.diseases[1:numDataPoints],
             start = startYear,
             frequency = 52)
Accidents.ts = ts(DeathData$Accidents..unintentional.injuries.[1:numDataPoints],
                  start = startYear,
                  frequency = 52)
noInfo.ts = ts(DeathData$Information.unavailable[1:numDataPoints],
               start = startYear,
               frequency = 52)
other.ts = ts(DeathData$Other[1:numDataPoints],
              start = startYear,
              frequency = 52)
causes.ts = list(
            list("Malignant Neoplasms", Malignant.neoplasms.ts),
            list("Heart Disease", Diseases.of.heart.ts),
            list("Cerebrovascular Diseases", Cerebrovascular.diseases.ts),
            list("Chronic Respiratory Diseases", resp.ts),
            list("Accidents", Accidents.ts),
            list("No Information", noInfo.ts),
            list("Other",other.ts)
)
numCauses = 7
# plot the time series
for (i in 1:numCauses){
  plot(causes.ts[[i]][[2]], main = paste(causes.ts[[i]][[1]], "Weekly Deaths in Ontario
 (2010-2021)"), ylab = "Weekly Deaths")
}
```

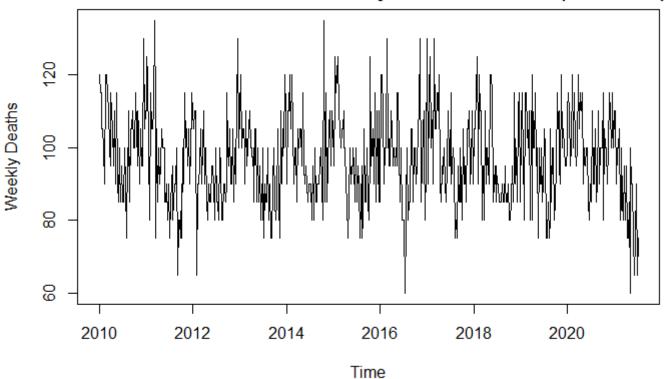
## Malignant Neoplasms Weekly Deaths in Ontario (2010-2021)



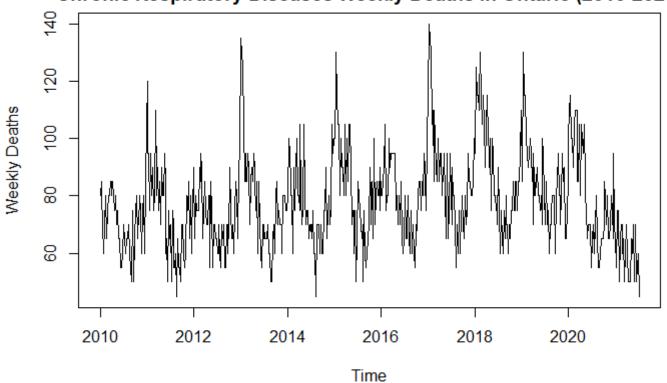
## Heart Disease Weekly Deaths in Ontario (2010-2021)



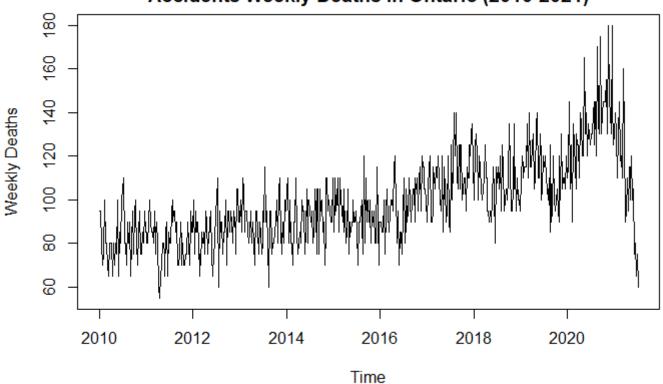
## Cerebrovascular Diseases Weekly Deaths in Ontario (2010-2021)



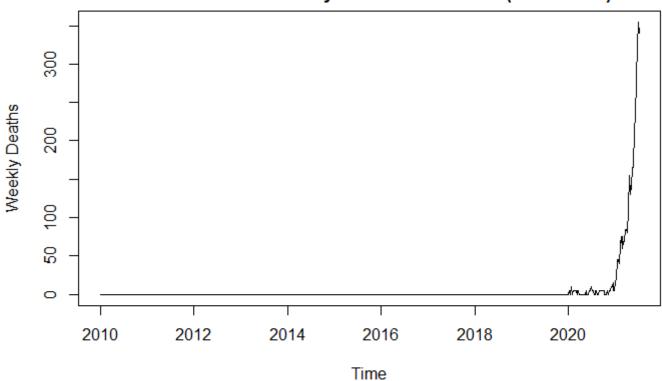
## Chronic Respiratory Diseases Weekly Deaths in Ontario (2010-2021)



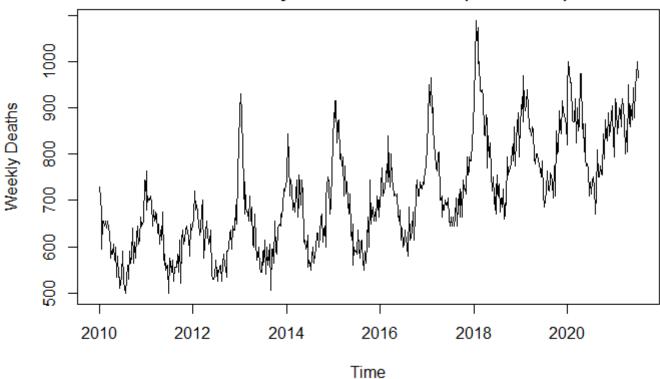
## Accidents Weekly Deaths in Ontario (2010-2021)



## No Information Weekly Deaths in Ontario (2010-2021)



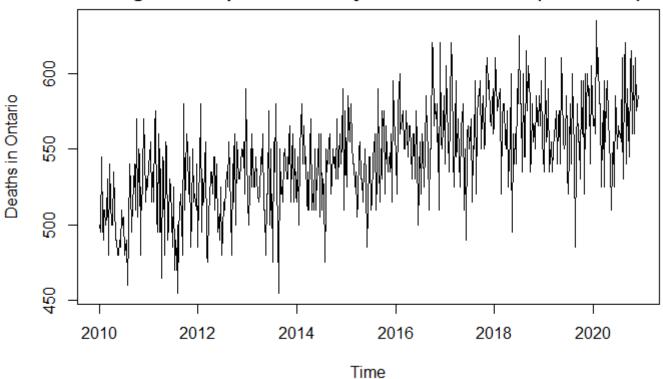
### Other Weekly Deaths in Ontario (2010-2021)



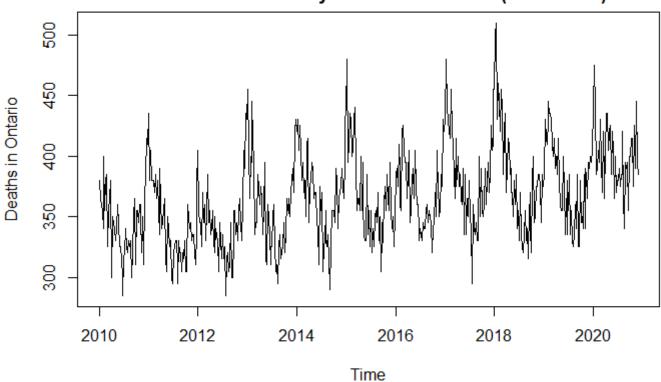
In 2021, there is a clear increase in cause "no information". This makes sense; the more recent a death, the less likely that a coroner's report has been completed. Therefore, for a fair analysis, we will restrict these causes of death to 2020.

```
Malignant.neoplasms.ts = ts(DeathData$Malignant.neoplasms[1:(numDataPoints-26-5)],
                            start = startYear,
                            frequency = 52)
Diseases.of.heart.ts = ts(DeathData$Diseases.of.heart[1:(numDataPoints-26-5)],
                          start = startYear,
                          frequency = 52)
Cerebrovascular.diseases.ts = ts(DeathData$Cerebrovascular.diseases[1:(numDataPoints-26-
5)1,
                                 start = startYear,
                                 frequency = 52)
resp.ts = ts(DeathData$Chronic.lower.respiratory.diseases[1:(numDataPoints-26-5)],
             start = startYear,
             frequency = 52
)
Accidents.ts = ts(DeathData$Accidents..unintentional.injuries.[1:(numDataPoints-26-5)],
               start = startYear,
               frequency = 52
)
#no information doesn't have enough data to be decomposed, and is therefore excluded
other.ts = ts(DeathData$Other[1:(numDataPoints-26-5)],
              start = startYear,
              frequency = 52)
causes.ts = list(
            list("Malignant Neoplasms", Malignant.neoplasms.ts),
            list("Heart Disease", Diseases.of.heart.ts),
            list("Cerebrovascular Diseases", Cerebrovascular.diseases.ts),
            list("Chronic Respiratory Diseases", resp.ts),
            list("Accidents", Accidents.ts),
            list("Other",other.ts)
)
numCauses = 6
# plot the time series
for (i in 1:numCauses){
  plot(causes.ts[[i]][[2]], main = paste(causes.ts[[i]][[1]], "Weekly Deaths in Ontario
 (2010-2020)"), ylab = "Deaths in Ontario")
}
```

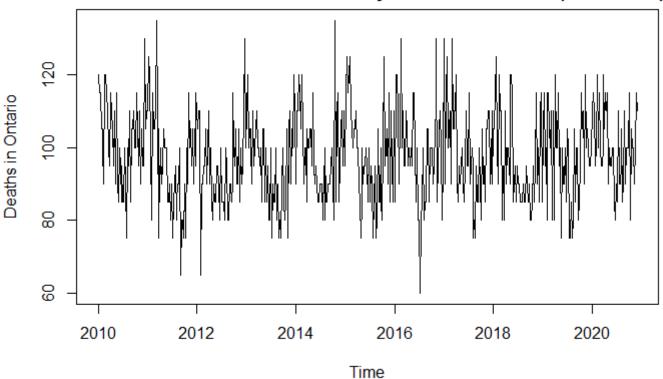
## Malignant Neoplasms Weekly Deaths in Ontario (2010-2020)



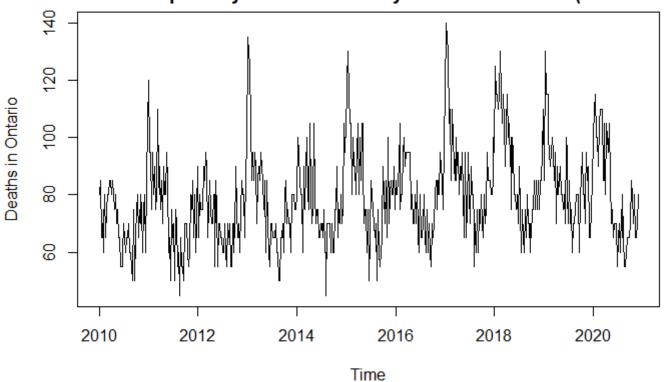
## Heart Disease Weekly Deaths in Ontario (2010-2020)



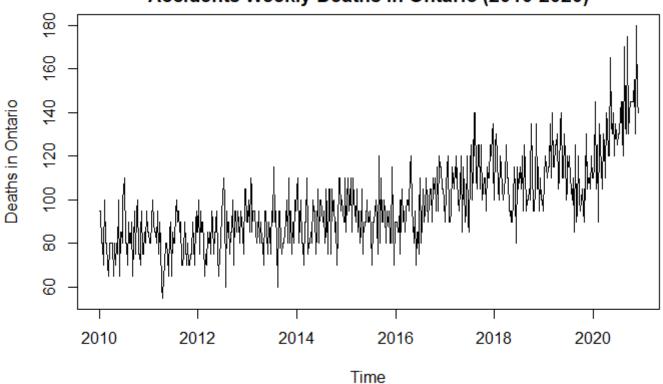
## Cerebrovascular Diseases Weekly Deaths in Ontario (2010-2020)



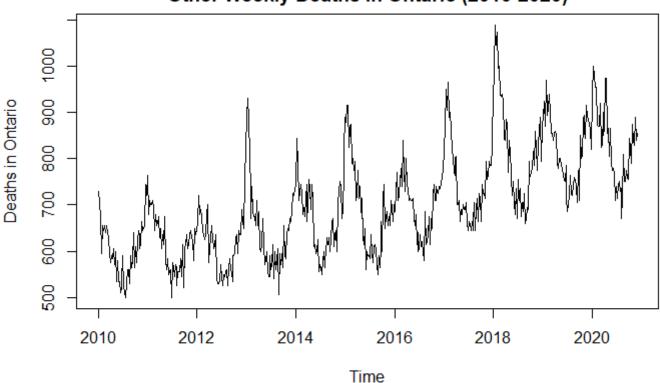
## Chronic Respiratory Diseases Weekly Deaths in Ontario (2010-2020)



### Accidents Weekly Deaths in Ontario (2010-2020)



## Other Weekly Deaths in Ontario (2010-2020)



All causes of death seem to have trend and seasonality, except for Accidents, which seems to have trend but no seasonality, and cerebrovascular deseases, which don't appear to have trend (this may indicate that their prevalence is decreasing at the rate of population increase). Interestingly, there is a clear trend and seasonality in the "Other" cause of death.

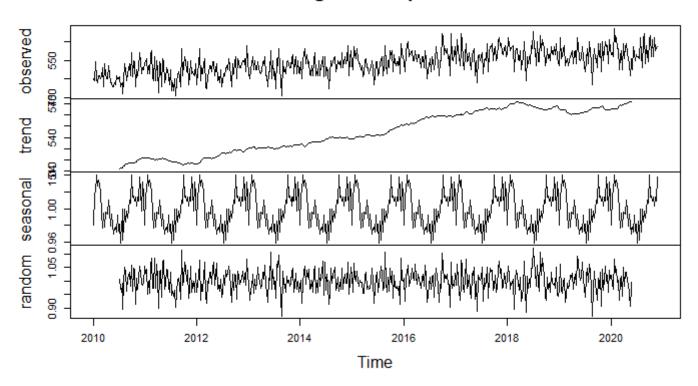
For confirmation, we will decompose each time series

Hide

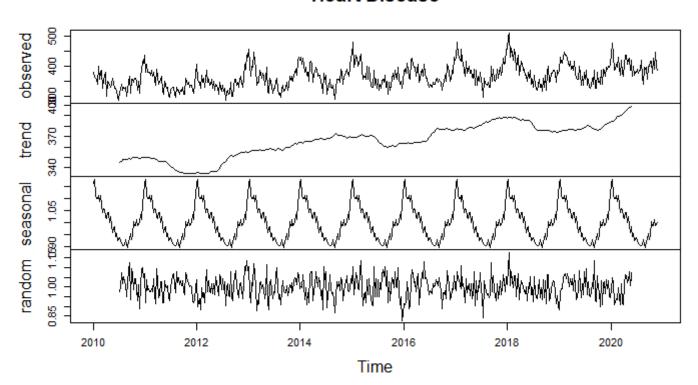
```
# helper function
customTitleDecompPlot = function (x, title = "", ...)
  xx <- x$x
  if (is.null(xx))
    xx <- with(x, if (type == "additive")</pre>
      random + trend + seasonal
      else
        random * trend * seasonal)
 plot(
    cbind(
      observed = xx,
      trend = x\$trend,
      seasonal = x$seasonal,
      random = x$random
    ),
    main = title,
  )
}
```

```
# plot the time series
decomposed = list()
for (i in 1:numCauses){
  decomposedCause = decompose(causes.ts[[i]][[2]], type = "multiplicative")
  decomposed[[i]]=decomposedCause
  customTitleDecompPlot(decomposed[[i]],causes.ts[[i]][[1]])
}
```

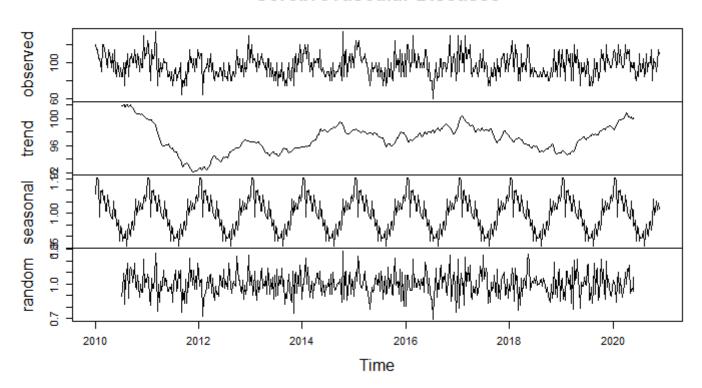
## **Malignant Neoplasms**



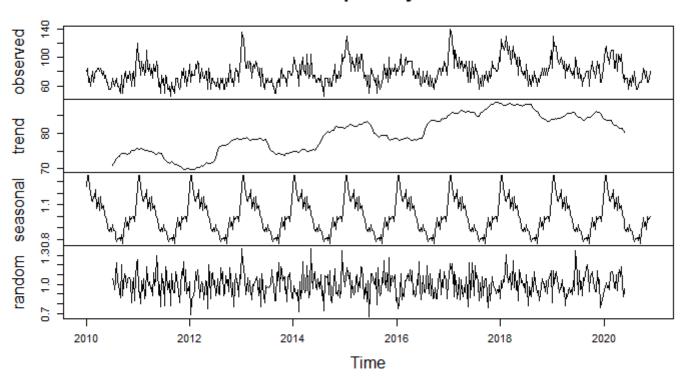
### **Heart Disease**



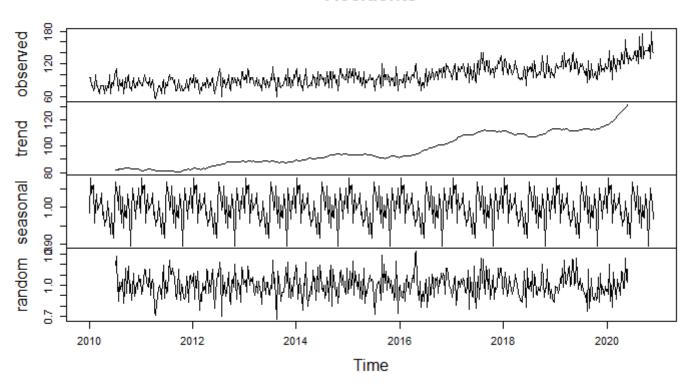
### Cerebrovascular Diseases

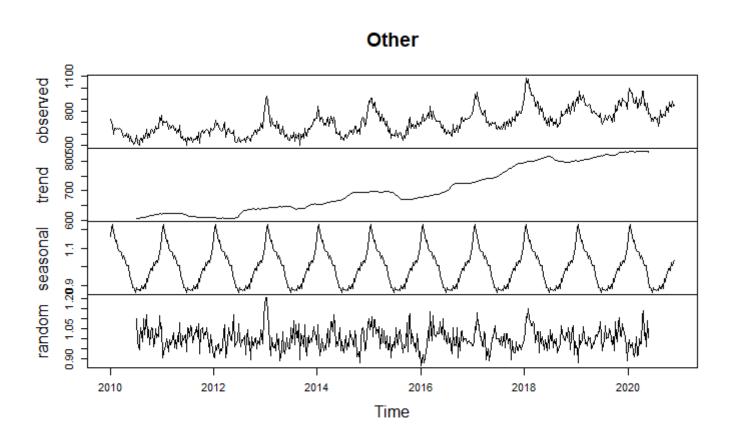


## **Chronic Respiratory Diseases**



### **Accidents**





### Implications:

• Some causes of death did not see a significant difference when COVID started. For example, malignant neoplasms did not see significant changes in their trendlines when COVID began

- Some causes of death, especially those that are due to acute episodes that must be treated immediately, increased, likely because people were not getting needed treatment due to hospital strain or fear of contracting COVID at the hospital. For example, Heart disease and accidents, both of which are likely to result in death from sudden acute episodes (physical trauma, heart attacks), saw increases in deaths
- Chronic respiratory deaths saw a marked decrease. This was likely due to COVID outcompeting other
  respiratory viruses, as well as people with existing respiratory conditions dying of COVID due to their
  weakened respiratory systems
- A final, interesting implication is the trendline in "other" deaths became flat with the onset of COVID.
   Considering that generally the trend of weekly deaths should be increasing as population increases, this may indicate that there is another cause of death that was decreasing, but that is not visible, in the "other" category. This may be acute respiratory diseases such as the flu, which were clearly less prevalent during the COVID-19 pandemic

# Objective 3: Evaluate Efficacy of Lockdowns

In this section, we evaluate the effectiveness of lockdowns by comparing lockdown stringency in Ontario to deaths, and analyzing potential correlation.

Create excess deaths data frame to use with stringency index data

```
DeathData.COVID = DeathData[c(522:(599-5)),c(10:11)]  # take only COVID data rownames(DeathData.COVID) <- 1:73  # re-index row names

DeathData.COVID$Actual <- DeathData.2020_2021

DeathData.COVID$Predicted <- actualArima.fcast$mean

DeathData.COVID$Excess <- DeathData.2020_2021 - actualArima.fcast$mean

colnames(DeathData.COVID) <- c("Year", "Month", "Actual Deaths", "Predicted Deaths", "Excess Deaths")

DeathData.COVID
```

	Year <dbl></dbl>	Month <dbl></dbl>	Actual Deaths <int></int>	Predicted Deaths <dbl></dbl>	Excess Deaths <dbl></dbl>
1	2020	1	2385	2435.396	-50.395693
2	2020	1	2350	2431.162	-81.161871
3	2020	1	2275	2390.894	-115.893784
4	2020	1	2270	2373.437	-103.437163
5	2020	2	2190	2336.339	-146.338855
6	2020	2	2185	2363.662	-178.661560
7	2020	2	2230	2313.134	-83.134363
8	2020	2	2165	2270.707	-105.707337
9	2020	2	2065	2204.479	-139.478951
10	2020	3	2135	2196.371	-61.370725
1-10	of 73 rov	ws		Previous <b>1</b> 2 3 4	5 6 8 Next

Stringency index is a a measurement created by the Centre of Excellence on the Canadian Federation used to "measure the relative stringency of policy responses" to the COVID-19 pandemic. The index captures 13 measures by imposed by governments, including travel and gathering restrictions, mask mandates, amongst others.

Data Source: Centre of Excellence on the Canadian Federation - COVID-19 Stringency Index (https://centre.irpp.org/data/covid-19-provincial-policies/)

Load stringency index data and observe

Hide

```
StringencyData = read.csv("data/ontario_stringency_index_2020_2021.csv", fileEncoding =
"UTF-8-BOM") # get data
StringencyData.weekly = StringencyData[seq(1,nrow(StringencyData),7),] # select weekly d
ata
# create lagged stringencyIndex data
# lag by three weeks as 18.5 is the average number of days between first symptoms of COV
ID and death
# source: https://www.drugs.com/medical-answers/covid-19-symptoms-progress-death-353626
4/
laggedStringencyData.weekly <- StringencyData.weekly[c(rep(NA,3), 1:(nrow(StringencyDat</pre>
a.weekly)-3)),
StringencyData.weekly$`Stringency Index -3 Weeks` <- laggedStringencyData.weekly$stringe
ncyIndex # add lagged data to df
StringencyData.weekly = StringencyData.weekly[c(1:73),]
                                                               # only take data with corr
esponding COVID data
rownames(StringencyData.weekly) <- 1:73</pre>
                                                               # re-index row names
tail(StringencyData.weekly)
```

date <chr></chr>	stringencyIndex <dbl></dbl>	Stringency Index -3 Weeks <dbl></dbl>
68 2021-04-17	58.9	47.1
69 2021-04-24	73.2	54.2
70 2021-05-01	73.2	58.9
71 2021-05-08	73.2	58.9
72 2021-05-15	73.2	73.2
73 2021-05-22	73.2	73.2
6 rows		

Add stringency index to the data frame

```
DeathData.COVID$`Stringency Index` <- StringencyData.weekly$stringencyIndex

DeathData.COVID$`Stringency Index -3 Weeks` <- StringencyData.weekly$`Stringency Index -

3 Weeks`
colnames(DeathData.COVID) <- c("Year", "Month", "Actual Deaths", "Predicted Deaths", "Excess
Deaths", "Stringency Index", "Stringency Index -3 Weeks")

DeathData.COVID = DeathData.COVID[c(14:73),]  # take data from the beginning of lockdowns
rownames(DeathData.COVID) <- 1:60  # re-index row names

tail(DeathData.COVID)
```

	Actual Deaths <int></int>	Predicted Deaths <dbl></dbl>	Excess Deaths <dbl></dbl>	Stringency Index <dbl></dbl>
4	2155	2147.235	7.764682	58.9
4	2185	2135.352	49.647802	73.2
5	2310	2154.541	155.459015	73.2
5	2245	2073.980	171.019512	73.2
5	2175	2074.545	100.455385	73.2
5	2145	2073.167	71.833340	73.2
	4 5 5 5	dbl> <int>       4     2155       4     2185       5     2310       5     2245       5     2175</int>	dbl> <int> <dbl>       4     2155     2147.235       4     2185     2135.352       5     2310     2154.541       5     2245     2073.980       5     2175     2074.545</dbl></int>	dbl> <int> <dbl>           4         2155         2147.235         7.764682           4         2185         2135.352         49.647802           5         2310         2154.541         155.459015           5         2245         2073.980         171.019512           5         2175         2074.545         100.455385</dbl></int>

Hide

```
startYear = DeathData.COVID$Year[1]
startMonth = DeathData.COVID$Month[1]

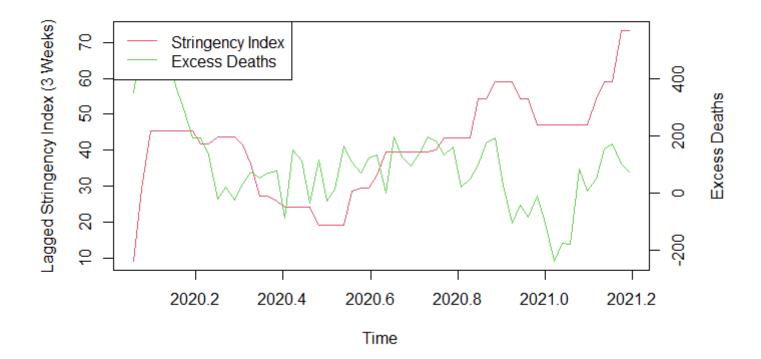
ExcessDeaths.ts <- ts(DeathData.COVID$`Excess Deaths`, start=c(startYear, startMonth), fr
equency=52)
StringencyIndex.ts <- ts(DeathData.COVID$`Stringency Index -3 Weeks`, start=c(startYear, startMonth), frequency=52)

par(mar = c(5, 4, 4, 4) + 0.3)  # additional space for second y-axis
plot(StringencyIndex.ts, col = 2,ylab = "Lagged Stringency Index (3 Weeks)") # create
first plot
par(new = TRUE)  # add new
plot</pre>
```

```
plot(ExcessDeaths.ts, col = 3,  # create
  second plot without axes
    axes = FALSE, xlab = "", ylab = "")
axis(side = 4, at = pretty(range(ExcessDeaths.ts)))  # add sec
ond axis
```

Hide

```
mtext("Excess Deaths", side = 4, line = 3)
                                                                                # add sec
ond axis label
legend("topleft", lty = 1, col = c(2,3), legend = c("Stringency Index", "Excess Deaths"
))
```

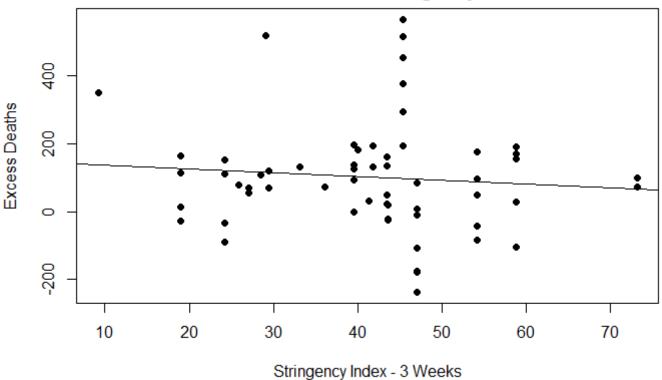


Visually, it appears that there is a negative correlation between the stringency of government measures and excess deaths.

Create correlation between stringency index and excess deaths

```
# plot correlation between variables
plot(DeathData.COVID$`Stringency Index -3 Weeks`,DeathData.COVID$`Excess Deaths`,
    main="Excess Deaths vs. Stringency Index",
    xlab="Stringency Index - 3 Weeks",
    ylab="Excess Deaths")
# fit line
abline(lm(DeathData.COVID$`Excess Deaths` ~ DeathData.COVID$`Stringency Index -3 Weeks
`))
```

### Excess Deaths vs. Stringency Index



#### Observations:

• Scatter plot shows negative line of best fit but it does not appear to be a strong correlation.

Hide

```
cor.test(DeathData.COVID$`Excess Deaths`,DeathData.COVID$`Stringency Index -3 Weeks`, me
thod="pearson") # get correlation between variables
```

```
Pearson's product-moment correlation

data: DeathData.COVID$`Excess Deaths` and DeathData.COVID$`Stringency Index -3 Weeks`
t = -0.7033, df = 58, p-value = 0.4847
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
    -0.3379895    0.1658402
sample estimates:
        cor
    -0.09195691
```

### Observations:

### P-value of correlation: ~.5

• As the p-value of the correlation is greater than 0.05, we can conclude that the relationship between excess deaths and stringency index is not statistically significant

### Correlation coefficient: -0.09

- There is a negative correlation between the two variables meaning a higher stringency index results in less excess deaths
- The correlation coefficient can be anywhere between -1 and 1 and therefore, a correlation coefficient of -0.09 shows a weak relationship

In conclusion, stringency index and excess deaths on their own are not a good measure of lockdown effectiveness. However, the limited dataset, absence of other variables that significantly impact excess deaths, makes it difficult to determine the true relationship between the variables.

## Conclusion

In conclusion, COVID-19 has caused a significant impact on mortality in the province of Ontario, including other causes of death. Notably, excess mortality was lower than the number of COVID deaths, indicating that the virus directly affected other causes of death. Analysis investigating the correlation between stringency of government response to the pandemic and excess deaths was inconclusive. Preliminary findings indicated a negative correlation, though the result was statistically insignificant. In the future, as data becomes more readily available post-pandemic, the team would like to re-visit this analysis as a next step.

Implications for the long term:

- Although the data for lockdown efficacy was inconclusive due to a high p-value, it still showed a negative
  correlation between excess deaths and lockdowns. With more data as the pandemic continues, this may
  be able to provide strong evidence either for or against the effectiveness of lockdowns.
- The decompositions in objective 2 show the importance of ensuring there is sufficient hospital capacity, and the importance of ensuring that people continue to seek medical care, even during periods of lockdown. This can inform public health decision making going forward
- Lastly, the decrease in deaths from other (inc. flu) and chronic respiratory diseases may show that
  measures like social distancing and masking are effective in slowing the spread of non-COVID respiratory
  viruses; this can be used as evidence to encourage their localized use in high-risk settings in the future.