

DE ANZA COLLEGE

Physical Sciences, Mathematics, and Engineering Division

MATH 2A Differential Equations

Instructor: Reza Shariatmadari

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Modeling and Predicting Santa Clara County Influenza Infection Rates in a Post-Pandemic Landscape

Group 9

Michael Mishkanian, Myint Shein Hein, Alex Benny, and Phillip Tran

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1 Abstract

Over the last three years of the COVID-19 pandemic, there has been a sharp decline in influenza infections. Specifically, the winter flu has been at a constant level for years, but during the pandemic there was a significant decrease in influenza cases due to quarantining, social distancing, and other safety procedures. This research models COVID-19 and influenza using two simple Susceptible, Infected, Recovered (SIR) models to predict the potential number of people that may become infected with the flu and COVID in Santa Clara County during the coming winter seasons as quarantining and other pandemic safety procedures end. The results of this research are inconclusive due to the multitude of unrealistic assumptions, oversimplifications, and estimates made in the calculations and preliminary research. Due to these findings, this research project should be seen as a case-study for a simple SIR model under strict assumptions. Suggestions are provided for future researchers about creating more accurate models.

2 Notation

This page contains a list of the notations and symbols used in this research.

Name	Notation
Basic Reproductive Number	R_0
Infected Population	I
Infection Rate	β
Recovered Population	R
Recovery Rate	γ
Susceptible Population	S
Time	t
Total Population	N

3 Purpose

This research is being conducted because there was a significant decrease in influenza cases in the last two years. Between September 2020 and April 2021, there were only about 2,000 reported cases of influenza [1]. Ordinarily, this same period averages 206,000 cases of influenza [1]. Even during “flu season,” there was not a large number of infections, creating a statistical anomaly.

The purpose of this research is to ensure that Santa Clara County is prepared to face the next wave of a major influenza outbreak. As exemplified by the early days of the COVID-19 pandemic, it is dangerous to not have safety nets to protect against large-scale health concerns. By completing this research, Santa Clara County public officials and the general public will be better informed about the dangers of a potential outbreak and prepare countermeasures against it.

4 Introduction

On January 31st, 2020, the United States declared the 2019 Novel Coronavirus as a public health emergency [2]. As the pandemic became more severe, federal and local governments began issuing “stay at home” orders, mandatory quarantining for the infected, required masking, testing enforcement, and other preventative measures. Furthermore, social distancing and frequent sanitization were strictly followed by many citizens. An unintended consequence of these actions was the steep decline of influenza infections.

Now that infections and deaths have significantly declined, American society is reverting to a pre-COVID era devoid of social distancing, lockdowns, stay at home orders, mandatory masking, and testing. Consequently, a return to normalcy would also result in an increase of influenza infections, which were artificially curbed during the COVID pandemic. It is vital that Santa Clara County public officials are aware of the potential influx of influenza infections that may swarm the medical system in the coming winter season. Using differential equations, influenza and COVID can be modeled to predict infections.

4.1 Assumptions

The model focuses on one specific location, Santa Clara County, to simplify the model and gain insightful results that affect the local community. It is also assumed that any infections will show immediately, infections are never fatal, and those who recovered from the flu or COVID will not be infected again. The effects of any vaccines are disregarded. It is assumed that it is possible to be infected by both influenza and COVID at the same time. This is largely due to the nature of the two diseases. Both are respiratory viruses, meaning they share the same medium for infection. There were enough cases of simultaneous infection to include this assumption. The observation time frame is less than one year, which allows not accounting for the birth rate and the death rate by natural causes. Furthermore, all variants of COVID-19 have been condensed into one to further simplify the model. As

a result of these assumptions, the development of the model is greatly simplified and the readability is improved as well.

5 Model

5.1 COVID-19 Transmission

Compartmental models, such as the Susceptible, Infected, Recovered (SIR) model, have been widely used to model the spread of infectious diseases. To model COVID-19 transmission, this research has opted to iterate upon a SIR model developed by Kermack and McKendrick, which was found in a paper published by Günther Bärwolff [3]. By using this model, the spread of COVID-19 can be simply modeled for Santa Clara County.

$$\frac{dS}{dt} = -\beta \frac{S}{N} I \quad (1)$$

$$\frac{dI}{dt} = \beta \frac{S}{N} I - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I \quad (3)$$

5.2 Parameters and Variables

In Equations 1, 2, and 3: β is the number of people that one infected person encounters per day, γ is the time of recovery, S is the population of susceptible individuals, I is the population of infected individuals, and R is the population of recovered individuals.

5.3 Influenza Transmission

Similar to the COVID-19 model, a SIR model is used to model the spread of influenza in Santa Clara County. However, the value of the parameters β and γ are adjusted to reflect influenza instead of COVID-19.

5.4 Determining Parameter and Constant Values

N represents the entire population of Santa Clara County, which is approximately 2,000,000 [4]. Therefore, N is the sum of all the susceptible, infected, and recovered individuals.

$$N = S + I + R \quad (4)$$

The total population of Santa Clara County is considered to be a constant number in both models, therefore:

$$N = N_{covid} = N_{flu} = 2000000 \quad (5)$$

Rearranging Equation 4 above, the population of susceptible individuals is given by:

$$S = N - I - R \quad (6)$$

The recovery rate parameter, γ , is calculated by:

$$\gamma = \frac{1}{\text{number of days to recover}} \quad (7)$$

According to current findings, it takes approximately 14 days to recover from COVID-19 [5] and 7 days to recover from influenza [6]. It can then be said that,

$$\gamma_{covid} = \frac{1}{14} \approx 0.0714 \quad (8)$$

and,

$$\gamma_{flu} = \frac{1}{7} \approx 0.14 \quad (9)$$

The number of people that one infected person encounters per day, β , is found by:

$$\beta = \frac{R_0}{\text{number of days to recover}} \quad (10)$$

In Equation 10, R_0 is the basic reproduction number, which is a value that indicates how contagious an infectious disease is. It is known that the current R_0 value for COVID in Santa Clara County is 1.10 [7] and the general R_0 for influenza is 1.28 [8]. The number of days to recover is the same as the calculations for γ in Equations 8 and 9. Therefore,

$$\beta_{\text{covid}} = \frac{1.10}{14} \approx 0.07857 \quad (11)$$

and,

$$\beta_{\text{flu}} = \frac{1.28}{7} \approx 0.1829 \quad (12)$$

5.5 Assembling the Full COVID Model

Using the parameter and constant values determined in Section 4.4, Equations 1 and 2 now become:

$$\frac{dS}{dt} = -(0.07857)\frac{S}{2000000}I \quad (13)$$

$$\frac{dI}{dt} = (0.07857)\frac{S}{2000000}I - 0.10I \quad (14)$$

Simplifying 13 and 14, and substituting the value of γ in Equation 3 yield the following set of equations:

$$\frac{dS}{dt} = -(4 \times 10^{-8})SI \quad (15)$$

$$\frac{dI}{dt} = (4 \times 10^{-8})SI - 0.10I \quad (16)$$

$$\frac{dR}{dt} = 0.10I \quad (17)$$

5.6 Assembling the Full Influenza Model

Due to the adjusted β and the shorter recovery time of influenza compared to COVID, where $\gamma_{flu} > \gamma_{covid}$, the following simplified set of equations are used to predict influenza infection rates:

$$\frac{dS}{dt} = -(9 \times 10^{-8})SI \quad (18)$$

$$\frac{dI}{dt} = (9 \times 10^{-8})SI - 0.14I \quad (19)$$

$$\frac{dR}{dt} = 0.14I \quad (20)$$

5.7 Determining Initial Conditions

Time, t , is equal to zero on March 3, 2023. This date is used because of the higher availability of relevant influenza and COVID data. More recent dates do not have all of the updated data yet. The following initial conditions are based on data gathered from the Santa Clara County Public Health Department [9] from March 3, 2023:

$$R_{covid}(0) = 477460 \quad (21)$$

$$I_{covid}(0) = 2086^\dagger \quad (22)$$

†: See "Appendix A: Sample Calculations" for the calculations of the initial COVID infected population.

Based on Equation 6, the initial population susceptible to COVID at $t = 0$ is:

$$\begin{aligned}
S_{covid}(0) &= N - I_{covid}(0) - R_{covid}(0) \\
&= 2000000 - 2086 - 477460
\end{aligned} \tag{23}$$

$$S_{covid}(0) = 1520454$$

This research is assuming that no one has recovered from the flu. Furthermore, data could not be found on the number of individuals currently infected with the flu. However, it must be true that $I_{flu}(0) > 0$ because influenza would be eradicated if $I_{flu}(0) = 0$. As a conservative estimate, is assumed that only 100 people in Santa Clara County currently have an influenza infection (This is only 0.005% of the total population). Based on these assumptions, the initial conditions for influenza are,

$$R_{flu}(0) = 0 \tag{24}$$

$$I_{flu}(0) = 100 \tag{25}$$

Again, based on Equation 6, the initial population susceptible to influenza at $t = 0$ is:

$$\begin{aligned}
S_{flu}(0) &= N - I_{flu}(0) - R_{flu}(0) \\
&= 2000000 - 100 - 0
\end{aligned} \tag{26}$$

$$S_{flu}(0) = 1999900$$

6 Results and Discussion

6.1 Predicting Influenza Infections

Using Equations 18, 19, and 20 along with the initial conditions determined in Section 5.7, the solutions curves can be graphed. Figure 1 below is generated using the Matplotlib library in Python. The solution curves on the graph are calculated using the NumPy and SciPy libraries, specifically making use of the `odeint()` function, which solves a system of ordinary differential equations.

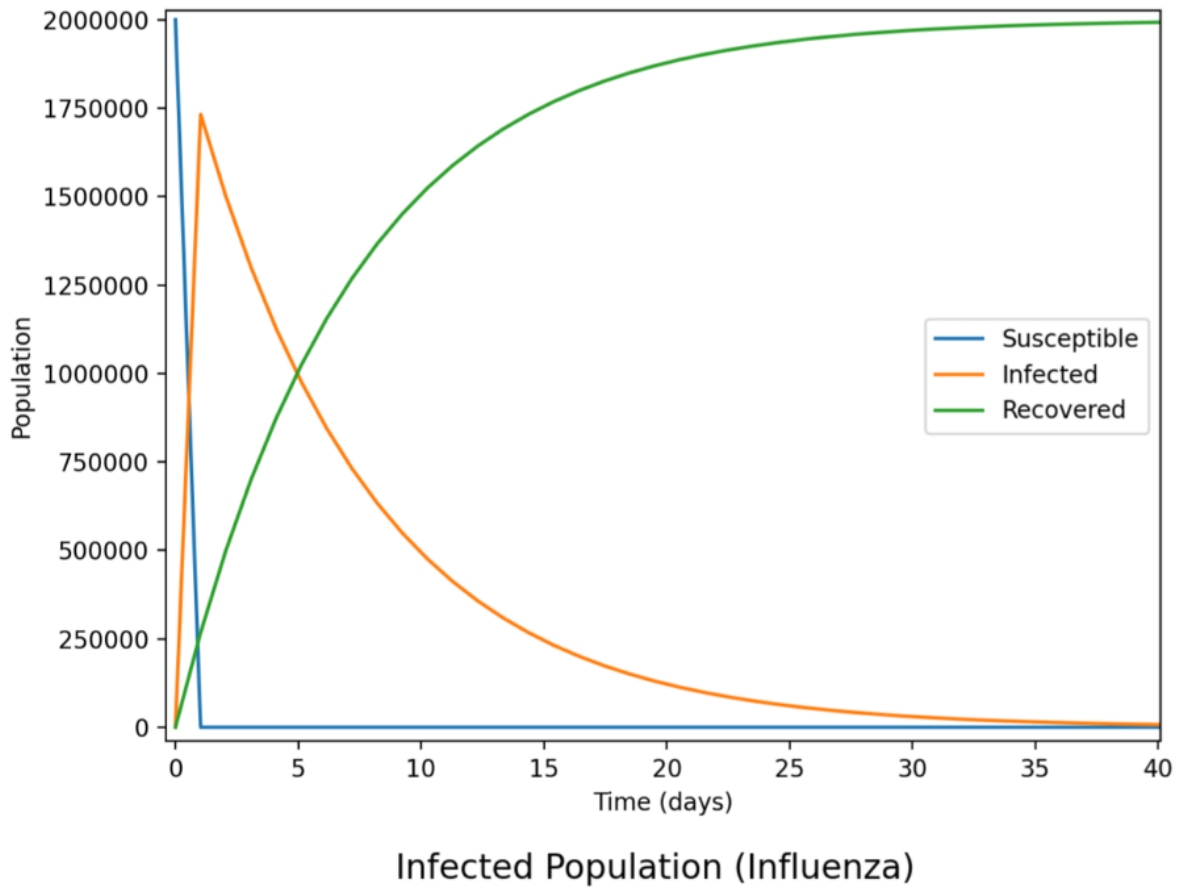


Figure 1: Solution curves of the SIR model for influenza.

In Figure 1 above, the number of infected individuals spikes up to approximately

1,750,000 in a matter of days and then quickly decays to zero. The population of susceptible individuals experiences a steep, linear drop to zero before day 3. The number of recovered individuals begins at zero and grows to 2,000,000. Interestingly, the solution curves for the Recovered and Infected population cross each other around day 6 and have an inverse relationship after that point.

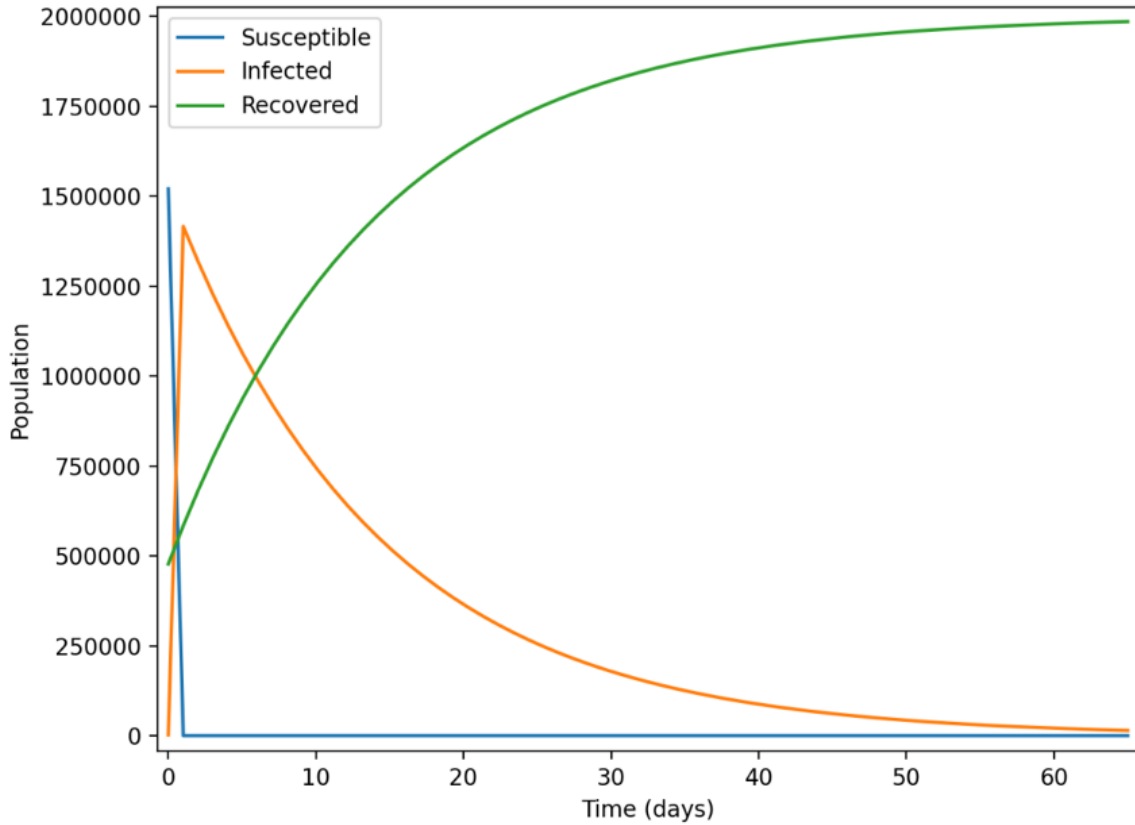
6.2 Predicting COVID-19 Infections

Using methods similar to Section 6.1, the solution curves for the SIR model of COVID-19 is generated below:

In Figure 2, there is still an initial spike in the infected population followed by a gradual decline. The susceptible population still drops to zero within days. Furthermore, there is still an inverse relationship between the Infected and recovered populations, which happens on day 6 again. One difference from the results found in Figure 1 is that the number of days to achieve a population of zero infected individuals is extended by approximately 60%. This is due to the adjusted β and γ parameters of COVID-19 (See Section 5.4).

6.3 Conclusions

The results found in Figure 1 and Figure 2 are unrealistic. Too many assumptions were made, which oversimplified the models. Despite that, what we can conclude from these simplified models is that the peak number of COVID-19 infections at any given time is approximately 1,410,000 people, whereas the peak number of influenza infections is approximately 1,750,000. We can also see that the recovery rate for influenza is faster than COVID's, despite having a higher R_0 value, showing how big an impact having a shorter recovery time frame can be. Also, we can see that on day 6 of each graph, the lines of susceptible and infected crosses but at different populations, influenza being the larger value.



Infected Population (COVID-19)

Figure 2: Solution curves of the SIR model for COVID-19.

These basic SIR models claim that the infected population will eventually reach zero. While this is mathematically true considering the assumptions, variables, and parameters—this is an unrealistic assertion. Claiming that the infected population reaches zero is equivalent to disease eradication. Influenza and, unfortunately, COVID-19 are not expected to be eliminated.

To create more accurate SIR models, parameters for reinfection and delayed-infection should be introduced. Although the addition of these parameters would increase the complexity of the models and also increase the difficulty of data gathering, it would result in more accurate and actionable results. By delaying the infections and replenishing the

susceptible population, it is expected to see graphs with fluctuating solution curves, rather than curves that reach and maintain equilibrium at the boundaries (0 and 2,000,000).

The results found in this research should be considered as qualitative examples of SIR models under a strict set of assumptions. Future researchers should read Section 7 to learn how to reduce the error of their models.

7 Error Analysis

All measurements have an inherent amount of uncertainty. Unfortunately, the lack of concrete measurements in this research have necessitated the frequent use of assumptions and estimates. Earlier in the COVID pandemic, the infection numbers were calculated via public testing sites and hospital entries. However, the rise of home testing and self-quarantining have made hospital reports inaccurate, as many people do not self-report that they have COVID. This trend is also seen with influenza, in which individuals with milder symptoms are less likely to visit the hospital. To counteract the inaccurate reporting, this research used wastewater data to estimate the initial conditions for COVID infections (See Appendix A). An attempt to replicate this method was unsuccessful for influenza infections because the data was not available. The initial condition for influenza was conservatively assumed to be 100 infections, which may have led to inaccuracies in the solution curves.

Many of the assumptions made at the beginning of this research also contributed to the inaccuracies in the models. For example, it is possible to become reinfected with the flu and COVID. However, the models in this research do not acknowledge the possibility of reinfection. As a result of this over simplistic assumption, the susceptible population immediately falls to zero and is not replenished, which is unrealistic. Deviating from reality again, the models assume that the population is stagnant, which is incorrect. The models also fail to account for the natural birthrate and death rate, as it is possible to die from COVID and the flu. Furthermore, many of the values and parameters present in the equations are estimates, not exact figures. For example, the total population of Santa Clara County was slightly overestimated to be 2,000,000 for the purpose of simplifying the calculations. Future researchers should attempt to reduce the quantity of assumptions and the magnitude of estimates to create more accurate results.

8 Literature Cited

References

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9 Appendix A: Sample Calculations

9.1 Initial COVID Infected Population in Equation 22

Using the Santa Clara County Wastewater Concentration Dashboard, COVID concentration levels are determined for March 3, 2023. The graphs provided on the Dashboard relate concentration levels to 7-Day Average COVID Case Counts from four wastewater sites within Santa Clara County. The approximate number of infected are estimated for each city and added together to determine a potential number of initial infections.

For example, in the first calculation below, the concentration of COVID-19 in San Jose's wastewater on March 3, 2023 was approximately 0.00035641. According to the graphs provided on Santa Clara County's dashboard, a concentration of 0.0002 is roughly equivalent to 1,000 COVID cases. Therefore, it is possible there were 1,782 cases of COVID in San Jose on March 3, 2023. However, it should be noted that these calculations are an approximation and add to the error of the results. Further discussion of "Error Analysis" is provided in Section 7 of this research.

San Jose	$1000 \times \frac{0.00035641}{0.0002} = 1782.05$
Sunnyvale	$100 \times \frac{0.00020131}{0.00016713} = 120.4511458$
Palo Alto	$100 \times \frac{0.00024052}{0.00024806} = 96.9604128$
Gilroy	$100 \times \frac{0.00020251}{0.00023354} = 86.71319688$
<hr/>	
$1782.05 + 120.4511458 + 96.9604128 + 86.71319688 \approx 2086$	