Applications-Oriented Problems
Pandemic Flu Spread (Differential Equation Version)

Group 420
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Abstract

This project explores the effect of the flu within a confined setting using a continuous-time SEIR (Susceptible Exposed Infectious Recovered) model. In this project, I use real world data to generate the parameters needed for the model to simulate the 2023-2024 flu season in the USA. The model is then used to simulate the spread of the flu in a classroom setting with and without vaccination. The results show that the flu spreads rapidly in a close-contact environment like a classroom, with the entire class becoming infected and removed within 20 days. The model with vaccination shows a slower spread of the flu, with only a portion of the class becoming infected. The project provides insights into the dynamics of disease transmission and the impact of vaccination on disease spread. The Python widget allows users to explore different scenarios and gain insights into the dynamics of disease spread in a classroom setting.

1. Introduction

In this project, I address the problem of modeling the spread of a pandemic flu within a confined setting using a continuous-time SEIR (Susceptible Exposed Infectious Recovered) model. Specifically, I simulate a scenario with 60 healthy children and one infected child to observe the dynamics of infection spread in a close-contact environment. The model is implemented in Python, and I modify the equation to include vaccination rates and vaccination efficacy. This parameter will allow me to analyze how varying vaccination rates and efficacy influence the infectious rate and the overall spread of disease.

Modeling disease spread in close-contact environments, like a classroom, has practical real-world implications. In settings such as kindergartens, children are often in close proximity, leading to a high risk of infection transmission. Based on conversations with a professional in the field (my girlfriend, who is a kindergarten teacher), I learned that illnesses spread quickly, with nearly all children in a class sometimes becoming infected within a day. The SEIR model is well-suited for this context, as it allows me to predict the progression of disease transmission under various conditions, including different vaccination rates. [5]

2. Methodology

To model the spread of a pandemic flu, I implemented two continuous SEIR (Susceptible-Exposed-Infectious-Removed) models. The SEIR model is a compartmental model that divides the population into four groups: susceptible, exposed, infectious, and removed. Each compartment in the SEIR model represents a different stage of disease progression. People move between compartments at rates determined by the model parameters.

1. Susceptible (S)

This group consists of individuals who are vulnerable to infection but have not been exposed yet. individuals in this group have no immunity and can potentially get infected if exposed to the disease.

$$\frac{dS}{dt} = -\beta \cdot S(t) \cdot I(t)$$

Params:

- β: Transmission rate of disease per day
- $S(t)$: Number of susceptible individuals at time t
- $I(t)$: Number of infectious individuals at time t

β will be derived using two methods:

- **Method 1:** Using the basic reproduction number R_0 and the recovery rate γ.
- **Method 2:** Iteratively fit β values to the data using the SEIR model.

Once both methods are complete, I will compare the results to determine the best β value for the model.

S $\rightarrow$ E:
Susceptible individuals become exposed when they come into contact with an infectious individual. Rate at which this happens is dictated by the transmission rate β and the number of infectious individuals in the population.

2. Exposed (E)

Exposed individuals are those who have been infected but are not yet infectious due to the incubation period of the disease. During this time, exposed individuals cannot transmit the disease to others.

$$\frac{dE}{dt} = \beta \cdot S(t) \cdot I(t) - \sigma \cdot E(t)$$

Params:

- σ: Rate at which exposed individuals become infectious per day. This is the inverse of the incubation period of the disease.
- $E(t)$: Number of exposed individuals at time t

E $\rightarrow$ I:
After the incubation period, exposed individuals become infectious and can transmit the disease to others.

3. Infectious (I)

This group consists of individuals who are actively spreading the disease. Over time the infectious individuals will either recover or die.

$$\frac{dI}{dt} = \sigma \cdot E(t) - \gamma \cdot I(t)$$

Params:

- γ: Recovery rate of the disease per day. This is the inverse of the average infectious period.
- $I(t)$: Number of infectious individuals at time t

I $\rightarrow$ R:
Infectious individuals will recover or be removed at a rate determined by the recovery rate γ. Recovered individuals are assumed to be immune to the disease and cannot be reinfected.

4. Removed (R)

This group consists of individuals who have either recovered or died from the disease. Recovered individuals are assumed to be immune to the disease and cannot be reinfected. We know that with diseases like the flu, immunity is not always permanent, but for the purposes of this model, we assume that recovered individuals are immune for the duration of the simulation.

$$\frac{dR}{dt} = \gamma \cdot I(t)$$

5. Basic Reproduction Number (R_0)

The basic reproduction number will tell us how many people an infected person will infect in a fully susceptible population.

$$R_0 = \frac{\beta}{\gamma}$$

Interpretation:

- If $R_0 > 1$, the disease will spread in the population. Each infection will cause more than one new infection. [6]
- If $R_0 < 1$, the disease will die out. Each infection will cause less than one new infection.
- If $R_0 = 1$, each infection will cause one new infection.

6. Vaccination Rate and Efficacy

To account for vaccination, I added a vaccination rate parameter, v, which moves individuals from the susceptible compartment to the removed compartment. I am treating the vaccination rate as a constant value that is applied before the model starts.

$$\frac{dS}{dt} = -\beta \cdot S(t) \cdot I(t) - v \cdot S(t)$$

$$\frac{dR}{dt} = \gamma \cdot I(t) + v \cdot S(t)$$

Params:

- v: Vaccination rate before model starts

The vaccine efficacy is not being included in the model. Since vaccines are not 100% effective, some vaccinated individuals may still get infected. The efficacy of the vaccine is included in the model by creating 3 groups.

- **Protected Population:** This is the population that is immune to the disease due to vaccination. This is captured by the equation:

  $$\text{Population Size} \cdot v \cdot \text{vaccine efficacy}$$

- **Partially Susceptible Population:** This is the population that received the vaccine but are not fully immune. This is captured by the equation:

  $$\text{Population Size} \cdot v \cdot (1 - \text{vaccine efficacy})$$

  For simplicity, I am assuming that partially susceptible individuals have the same transmission rate as fully susceptible individuals.

- **Fully Susceptible Population:** This is the population that did not receive the vaccine and is fully susceptible to the disease. This is captured by the equation:

  $$\text{Population Size} \cdot (1 - v)$$

The Susceptible compartment will be a mixture of the fully susceptible and partially susceptible populations.

To simulate as close to the real world as possible, I created two continuous SEIR models: one without vaccination and one with vaccination. The model without vaccination is the basic SEIR model, while the model with vaccination includes a vaccination rate parameter that moves individuals from the susceptible compartment to the removed compartment.

3. Exploratory Data Analysis

I gathered various metrics for the flu from the CDC and other websites to estimate the parameters needed for the SEIR model. The initial data used for the parameter estimation is as follows:

Parameter	Value
Flu Season Duration	16 weeks
Initial Flu Cases	1.5% of total flu tests
Total Flu Tests	3,910,204
Total Positive Flu Tests	351,460
USA Population	334,900,000
Vaccination Rate	48%
Vaccine Efficacy	36.5%
R_0	1.47
Infectious period	3 days
Incubation period	2 days

Table 1: Key Data Points and Assumptions gathered for the SEIR model [1] [4] [6] [3]

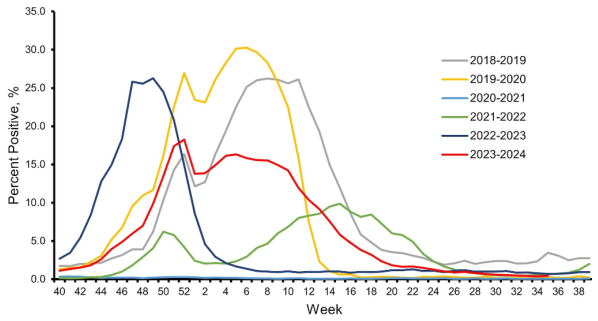

Figure 1: Positive Percentage of Flu tests from 2018-2024

3.1. Estimating Beta from R_0

This method uses the basic reproduction number R_0 and the recovery rate γ to estimate the transmission rate β. As shown in the Methodology section above, the relationship between R_0, β, and γ is given by:

$$R_0 = \frac{\beta}{\gamma}$$

Reworking the equation we can solve for β:

$$\beta = R_0 \cdot \gamma$$

$$\beta_0 = 1.47 \cdot \frac{1}{3} = 0.49$$

To differentiate between β values, I am calling this initial estimate β_0.

3.2. Estimating Beta using iteration

For this method, I used the β_0 as a starting point and fitted various different β values to the 2023-2024 flu season data that got close to the target number of daily infections. This was derived by the following:

$$\text{Target Daily Infections} = \frac{\text{Total Positive Flu Tests}}{\text{Flu Season Duration}}$$

To find the best β, I calculated the mean squared error between the model's daily infections and the target daily infections. The error was calculated using the formula:

$$\text{Error} = \frac{(\text{Model Daily Infections} - \text{Target Daily Infections})^2}{112}$$

The best β was the value that minimized the error. Below are the parameters and results for the model without vaccination:

Parameter	Value
γ	1/3
σ	1/2
S	334,841,347
E	351,460
I	58,653
R	0
R_0	1.47
β_0	0.49
β	0.27

Table 2: Initial Parameters and Results for the SEIR model without vaccination

The model starts off with 58,653 infectious individuals. This coincides with the initial flu cases of 1.5% of total flu tests. I decided to use this number for the initial number of infectious individuals instead of exposed individuals because when you test positive for the flu you are already infectious. This amount is also removed from the susceptible compartment.

This iterative approach resulted in a β value of 0.27. This value is a lot lower than the initial estimate from R_0 and will be used for the model without vaccination.

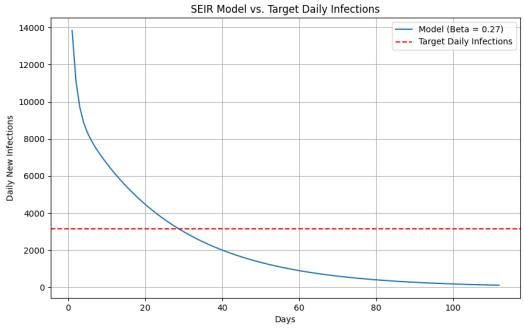

Figure 2: Daily Infections β 0.24

As seen in the graph above, this beta values causes the model to follow an exponential decay curve. This is because the model is overpredicting the number of daily infections for the first 30 days. After that, the model levels out towards 0. This doesn't match the data from the CDC, which shows a more parabolic type curve.

I believe this is happening due to the simplicity of the model. A lot of people get the flu vaccine every year and this model isn't accounting for that. This model is also assuming that everyone in the Removed compartment has gained immunity to the flu, which isn't true.

3.3. Estimating Beta with Vaccination

In an effort to mimick the real world, I created a model that included a vaccination rate parameter v and took into account vaccine efficacy.

Below are the parameters and results for the model with vaccination:

Parameter	Value
γ	1/3
σ	1/2
S	276,166,867
E	351,460
I	58,653
R	58,674,480
R_0	1.47
β_0	0.49
Partially Susceptible	102,077,520
Protected	58,674,480
Fully Susceptible	174,148,000
β	0.48

Table 3: Initial Parameters and Results for the SEIR model with vaccination

Just like above, we're starting off with 58,653 infectious individuals. The model also starts off with 58,674,480 protected individuals, 102,077,520 partially susceptible individuals, and 174,148,000 fully susceptible individuals. For simplicity we're assuming that partially susceptible individuals have the same transmission rate as fully susceptible individuals so they both get combined into the susceptible compartment.

This iterative approach resulted in a β value of 0.48. This value is closer to the initial estimate from R_0.

As we can see from the graph in figure 3, this beta value takes about 90 days to reach the daily infection target, and then proceeds to exceed it for the rest of the flu season. When looking at the CDC graph, the curve starts leveling out at around 16 weeks before ultimately coming down at around week 24.

I was curious to see how the model would look if I extended the flu season to 52 weeks (365 days) to see if the model would eventually level out. The graph in figure 4 shows that the model does eventually level out at 150 days (21 weeks) and then starts to come down to 0 for the remainder of the year. While this is still a bit off from the CDC data, it's a lot closer than the model without vaccination.

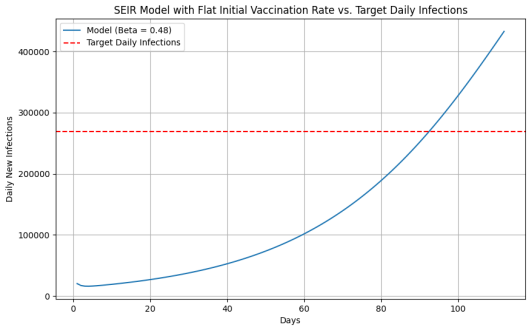

Figure 3: Daily Infections β 0.48

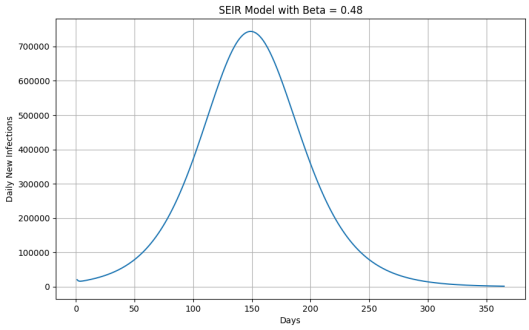

Figure 4: Daily Infections β 0.48 for 365 days

3.4. Beta Comparison and Selection

After comparing the estimated, I chose to go with the β value of 0.48 for the actual project. My reasoning for this is that daily infection graph for the vaccine model is a lot closer to the CDC data than the model without vaccination and its a closer to the initial estimate from R_0.

4. Evaluation

Using the following values, I was able to create two models for a school classroom where 1 child is infected with the flu and 60 children are healthy. The first model is without vaccination and the second model is with vaccination.

Parameter	Value
γ	1/3
σ	1/2
S	60
E	0
I	1
R	0
R_0	1.47
β	0.48

Table 4: Initial Parameters for SEIR Model Without Vaccination

Some assumptions that were made for the first model:

- The flu season lasts 16 weeks.
- Kids only get exposed to the flu at school. On weekends, the β value is set to 0.
- The initial number of infectious individuals is 1.
- No one has gotten a vaccine.
- Sick kids are still going to school.
- Exposure can happen once a day.

The last assumption is important due to computational restraints. Realistically kids can have multiple exposures in a day, but that would cause the model to run for a long time. The model is set to run for 16 weeks, so the assumption was made that kids can only get exposed once a day.

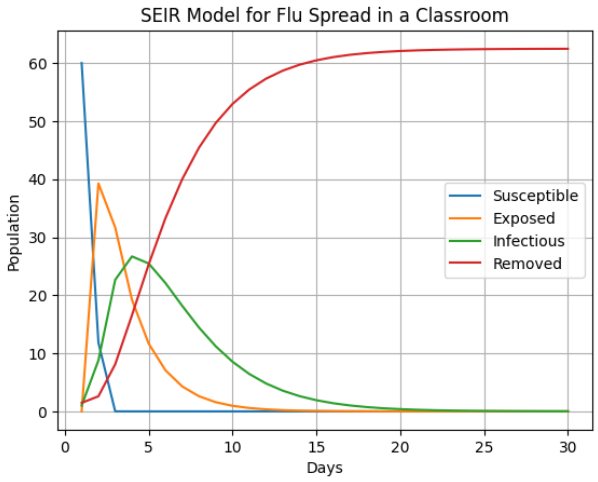

Figure 5: Daily Infections β 0.48 and 1 exposure a day

Figure 5 shows the daily infections for the model without vaccination and 1 exposure a day. You can see that the curves are a bit sharp and that is due to the 1 exposure limit. Here we see that by day 5, the end of the school week, the entire susceptible population has been exposed. By day 20th, the entire class is in the Removed compartment. This makes sense based on the assumptions we gathered where kids are still going to school sick. These findings are consistent with the real-world observations that illnesses spread quickly in close-contact environments like schools. [2]

When we consider multiple exposures a day, we see a smoother graph as seen in figure 6. This is because the model is now able to spread out the exposures over the course of the day. This is more realistic as kids can get exposed multiple times a day in a school setting. The resulting graph is smoother and we see some increases in the number of daily exposures, with values exceeding 40 exposed individuals at once. The results are still the same as the model with 1 exposure a day. By day 20th, the entire class has been moved to the Removed compartment.

This is pretty interesting since it suggests that the number of exposures doesn't affect the end results too much. This is due to the fact that the flu is very contagious and can spread quickly in close-contact environments. One thing it did show is that the initial hypothesis of the industry professional was correct. The kids will become infected within one day.

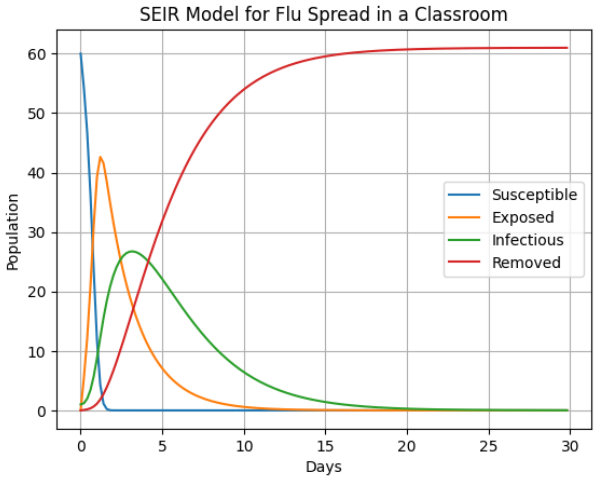

Figure 6: Daily Infections β 0.48 and 5 exposures a day

The second model is with vaccination. The following values were used to create the model:

Parameter	Value
γ	1/3
σ	1/2
S	49
E	0
I	1
R	11
R_0	1.47
β	0.48
Vaccination Rate	48%
Vaccine Efficacy	36.5%

Table 5: Initial Parameters for SEIR Model Without Vaccination

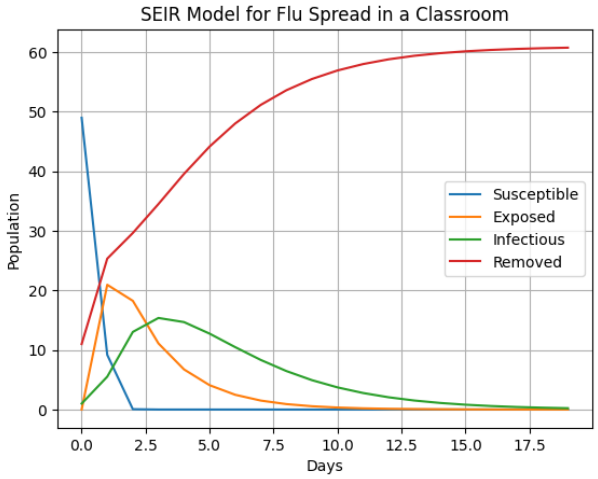

Figure 7: Daily Infections β 0.48 and Vaccination Rate 48%

As we can see in figure 7, the curves are a lot shorter than without vaccination. This is due to the fact that the model is now accounting for the 48% of the class that is vaccinated with a 36.5% efficacy. This is a more realistic model as roughly half of the population is vaccinated every year. The model is also able to account for the fact that the vaccine isn't 100% effective. This model is only accounting for 1 exposure throughout the day, but as seen in figure 6, the number of exposures doesn't affect the results too much because of how contagious the flu is.

The main class of the project provides a Python widget that will allow users to interact with the model and explore different scenarios by adjusting the parameters. For example, having a fully vaccinated class and halving the flu transmission rate. The widget allows users to see how these changes affect the spread of the flu in the classroom.

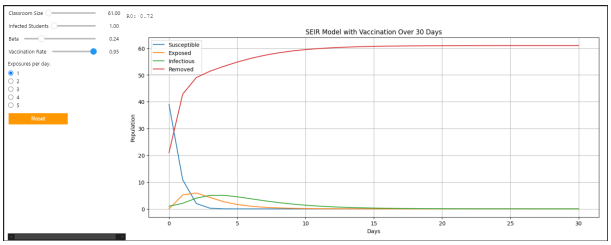

Figure 8: The entire class is vaccinated and the flu transmission rate is halved

5. Conclusion

In this project, I used a continuous-time SEIR model to simulate the spread of a pandemic flu in a classroom setting. I estimated the transmission rate β using two methods:

- One based on the basic reproduction number R_0 and the recovery rate γ.
- The other based on iterative fitting to the data.

I compared the results from both methods and selected the best β value for the model.

I then created two models:

- One without vaccination.
- One with vaccination.

The model without vaccination showed rapid spread of the flu in the classroom, with the entire class becoming infected within 20 days. This result remained true whether the model assumed 1 exposure per day or multiple exposures per day. This is consistent with the flu's high transmission rate in close-contact environments like schools. The important change that we saw was that the model with multiple exposures proved that the initial hypothesis of the industry professional of the kids will become infected within one day was correct.

The model with vaccination showed a slower spread of the flu, with only a portion of the class becoming infected. The model provides insights into the dynamics of disease transmission and the impact of vaccination on disease spread. Future work could involve extending the model to include more complex interactions and parameters, such as allowing for reinfection or adding a variable for the efficacy of the vaccine over time.

I hope this project provides a useful framework for understanding the spread of infectious diseases in close-contact environments and the potential impact of vaccination on disease transmission. The Python widget allows users to explore different scenarios and gain insights into the dynamics of disease spread in a classroom setting.

6. Acknowledgements

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ChatGPT was used in the following manner:

- Help understand the SEIR model.
- Help make an outline of the process for the project.
- Proofread and grade the report based on the rubric.
- Help with the LaTeX formatting, including writing the math equations.
- Debugging code and helping with the Python Widgets implementation.
- Help generate bib file and references.

References

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[2] K. K. Coleman and W. V. Sigler. Airborne influenza a virus exposure in an elementary school. *Scientific Reports*, 10(1):1859, February 2020. Published February 5, 2020.

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