

HW 1: SIR and SEIR Model Implementation for Pandemic Spread

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A. Model Implementation

The implemented SIR model can be located in BMI_Week_11.ipynb in the GitHub repository, as mentioned in Section [F](#).

B. SIR Model Simulation

The simulation of the SIR model over 150 days with the following initial conditions and parameters for a total population of $N=1000$ individuals is shown in Figure 1:

- $S(0) = 999, I(0) = 1, R(0) = 0$
- $\beta = 0.3 \times 10^{-3}$
- $\gamma = 0.1$

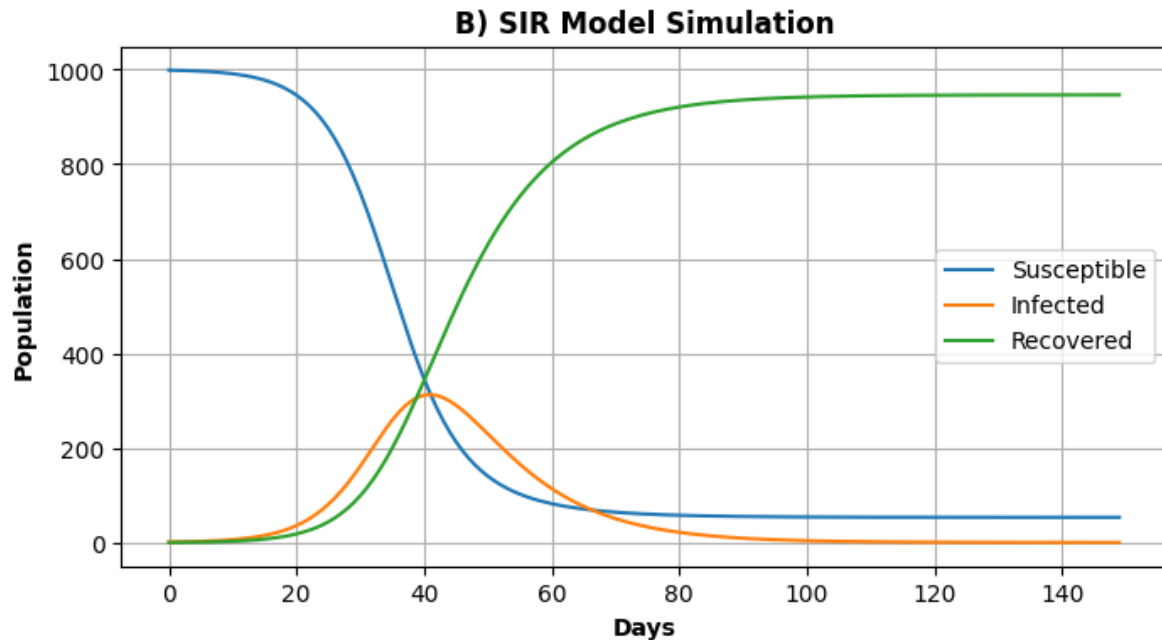


Figure 1: SIR model simulation

C. Analysis and Interpretation

i. Infection Peak

As shown in Figure 2, the infection reaches its peak on approximately day 41. The maximum number of infected individuals at this peak is around 312. The infection peak is affected due to the initial susceptible population and the transmission rate. As susceptible individuals come into contact with infected ones, the infection spreads until the recovery rate and depletion of susceptible individuals slow down the spread which causes the infection rate to decline.

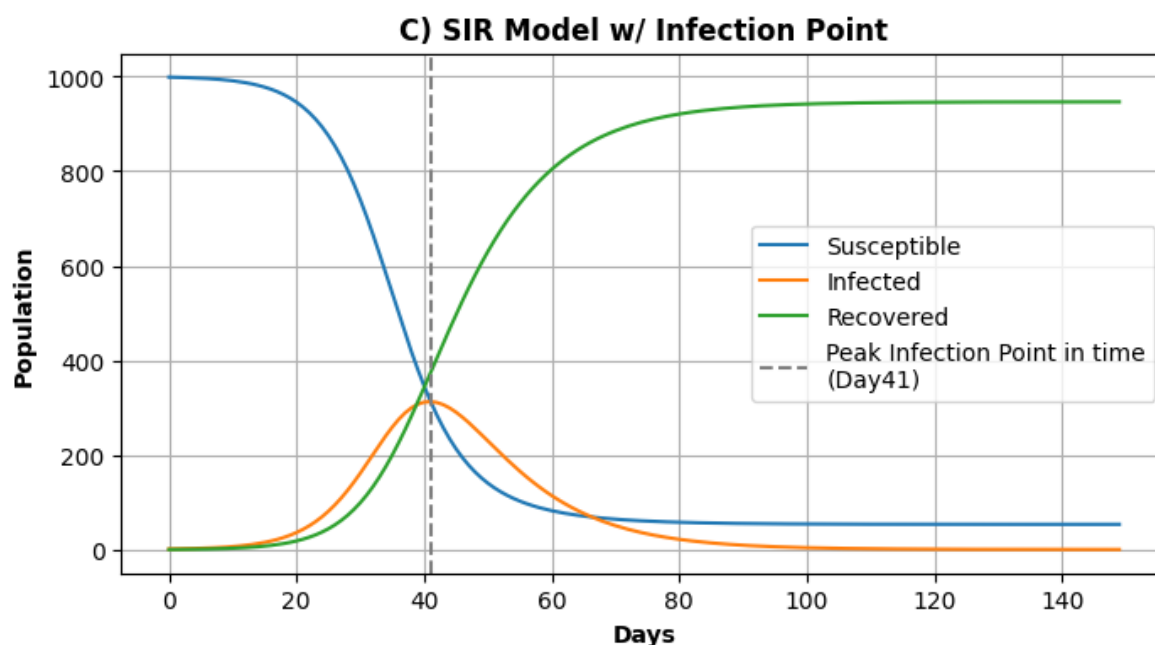


Figure 2: SIR model with infection peak point

ii. Basic reproductive number

R_0 is a measure of the average number of secondary infections produced by a single infected individual in a fully susceptible population. In this case, R_0 is quite low (0.003), which means that each infected person is expected to infect much less than one other person on average. This low R_0 means that the infection will likely spread slowly and may be controlled without extensive intervention.

iii. Pandemic dynamics

As individuals become infected, the susceptible population (S) starts high and gradually declines. The infected population (I) increases initially (reaches a peak when the infection rate is highest on day 41). After the peak, the number of infected individuals declines as more individuals recover and fewer susceptible individuals remain. The

recovered population (R) begins at zero and increases over time as infected individuals recover. Eventually, most of the population transitions to the recovered category, representing immunity or removal (expire) from the susceptible pool. This interaction between compartments illustrates the infection spread and eventual containment. This dynamic demonstrates the typical epidemic curve that has an initial rise in infections, a peak, and a gradual decline as recovery rates surpass infection rates.

D. SEIR Model with Births and Deaths

i. Implement the susceptible-exposed-infectious-recovered (SEIR)

The implemented SEIR model can be located in BMI_Week.11.ipynb in the GitHub repository, as mentioned in Section F.

ii. Simulate for 365 and 1200 days

Figure 3 and 4 shows the simulation for 365 and 1200 days, respectively.

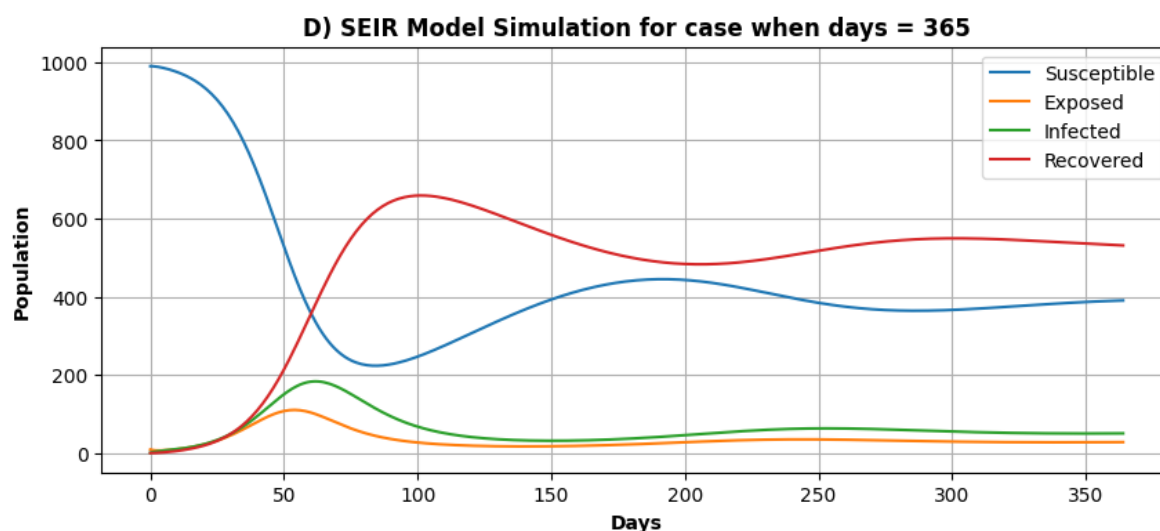


Figure 3: SEIR model simulation for 365 days

iii. Patterns observed

In both graphs, the infected compartment shows a pattern of initial peaks and then later on we see smaller waves. This pattern may be a real-world observation of pandemics, where there is an initial sharp increase in infections as the virus spreads, followed by fluctuations in infection rates as immunity builds up in the population and as susceptible individuals fluctuate over time.

The initial peak represents the first large wave of infections as the susceptible population decreases rapidly when exposed to the virus. After the initial wave, there

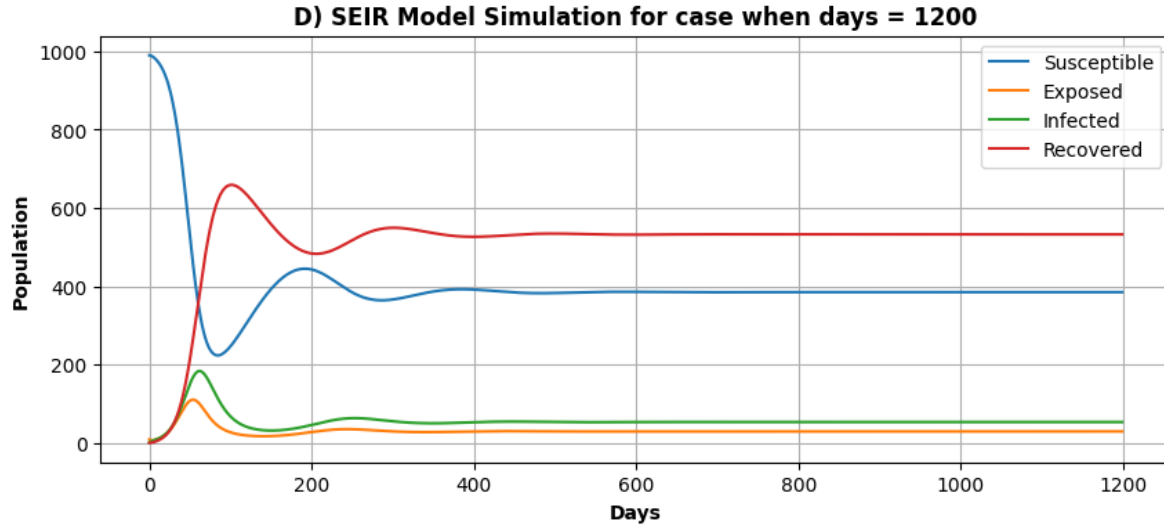


Figure 4: SEIR model simulation for 1200 days

are smaller oscillations in the infection rate. The graph for 1200 days shows more waves over a longer period, with the infection rate eventually stabilizing at a lower level. In the 365-day simulation, the waves appear to settle faster, but similar fluctuations are visible. This pattern of waves reflects the cyclical nature of disease transmission dynamics in SEIR models.

iv. Effect of Exposed Compartment & birth/death rates on pandemic dynamics

The presence of an exposed compartment shows individuals who have been exposed to the virus but are not yet infectious. The effect of birth and death rates is more visible in the longer simulation (1200 days). With a constant birth rate, new susceptible individuals are added to the population over time, which increases the number of susceptible. This increase allows for the possibility of additional waves since each new batch of susceptible individuals can be exposed and infected. Death rates also reduce the population over time, particularly affecting the infected and possibly recovered compartments, thereby reducing overall transmission potential slightly.

E. Sensitivity Analysis

i. Sensitivity analysis on SEIR model

The implemented SEIR model, along with sensitivity analysis, can be located in BML_Week_11.ipynb in the GitHub repository, as mentioned in Section F. Figure 5 shows the SEIR model simulation for 1200 days for a range of transmission rates and recovery rates.

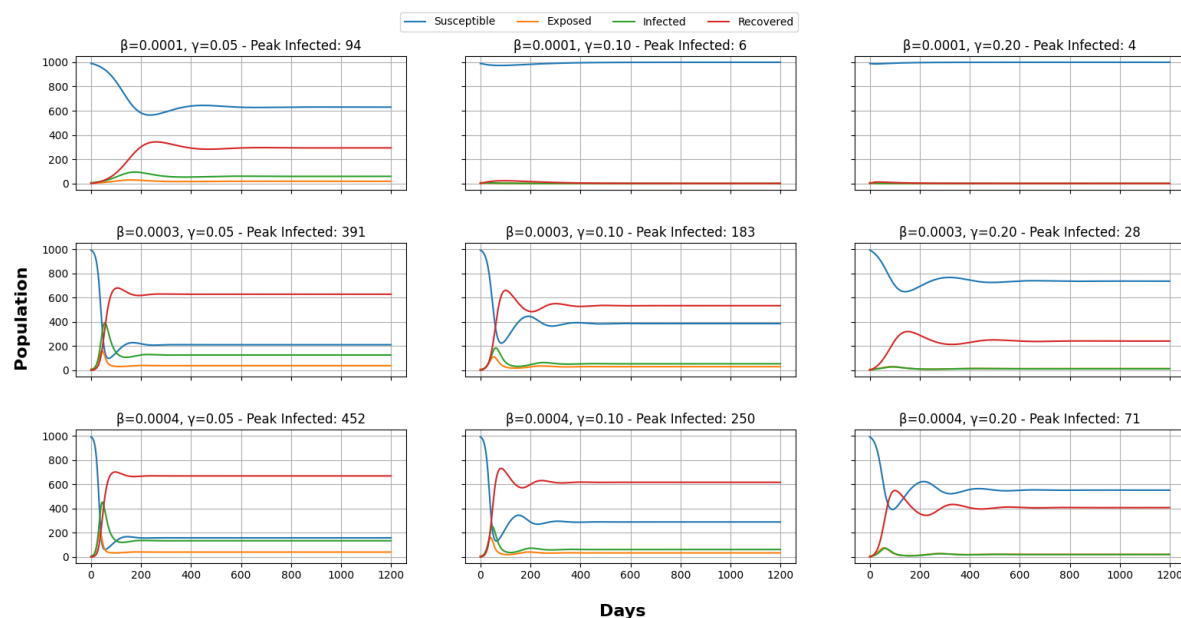


Figure 5: SEIR model simulation for 1200 days for a range of transmission rates & recovery rates.

ii. Peak and total infections over a year

Figures 6 and 7 show the peak infection and total infections over a year for each β and γ combination, respectively.

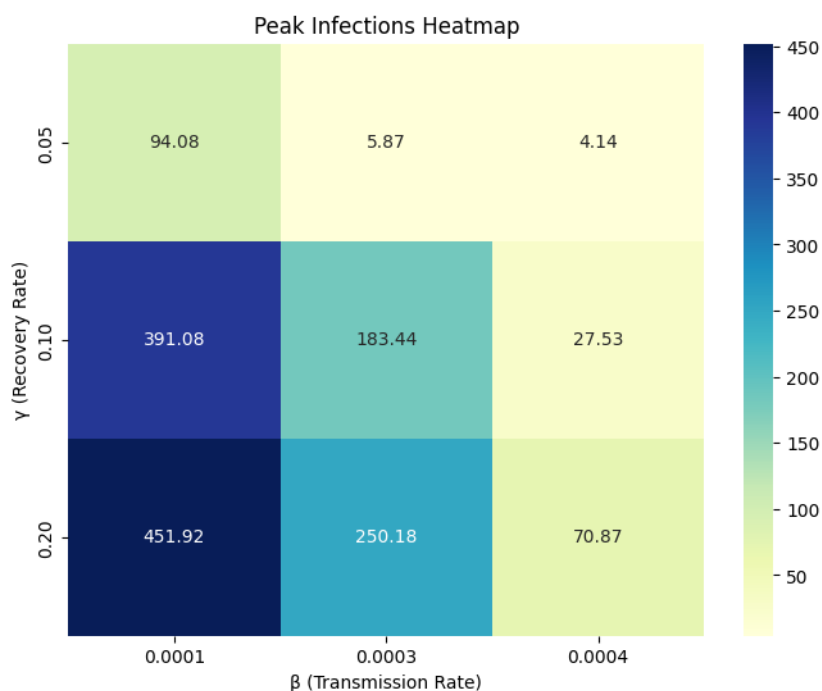


Figure 6: Peak infection over a year for each β and γ combination.

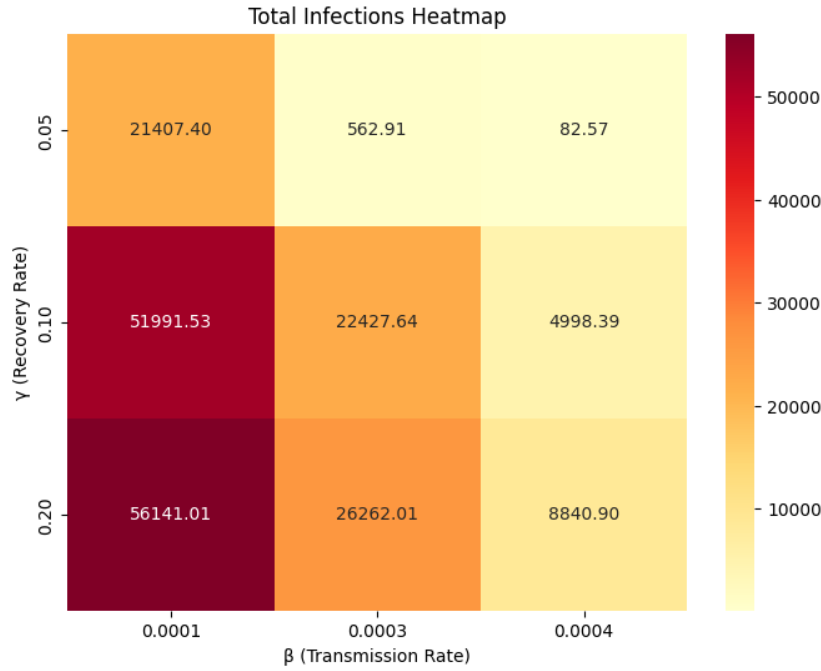


Figure 7: Total infections over a year for each β and γ combination

iii. Implications for public health interventions

Lower β values means lower transmission rates. This can be achieved through social distancing, mask-wearing, and other preventive measures. The heatmaps show that reducing β significantly lowers both total and peak infections which shows us that social distancing can reduce the pandemic's impact. For instance, moving from $\beta = 0.0001$ to $\beta = 0.0004$ decreases both infection totals and peaks when high recovery rates are higher. Higher γ values (or quick recovery) may be linked to effective medical treatments. The heatmaps show that increasing γ reduces both total and peak infections for any β value. This suggests that investing in treatments and healthcare resources that improve recovery can help control the infection burden. Combining social distancing (lower β) with improved medical treatments (higher γ) is a good strategy to minimize infection peaks and total cases during a pandemic.

F. Code Availability

The code used in this assignment can be found in this [GitHub repository](#). The code is written in Python 3.10.12 and executed in Google Colab.

References

- [1] R. Sameni, "Model-Based Prediction and Optimal Control of Pandemics by Non-Pharmaceutical Interventions," in IEEE Journal of Selected Topics in Signal

- Processing, vol. 16, no. 2, pp. 307-317, Feb. 2022, doi: [10.1109/JSTSP.2021.3129118](https://doi.org/10.1109/JSTSP.2021.3129118).
- [2] Sameni, R. (2020). Mathematical Modeling of Epidemic Diseases; A Case Study of the COVID-19 Coronavirus. ArXiv. <https://arxiv.org/abs/2003.11371>
- [3] Sameni, R., & Alphanumeric Lab. EpidemicModeling [Computer software]. GitHub. <https://github.com/alphanumericlab/EpidemicModeling>
- [4] https://en.wikipedia.org/wiki/Basic_reproduction_number
- [5] <https://www.ncbi.nlm.nih.gov/books/NBK126178/>
- [6] Hou Y, Bidkhor H. Multi-feature SEIR model for epidemic analysis and vaccine prioritization. PLoS One. 2024 Mar 1;19(3):e0298932. doi: 10.1371/journal.pone.0298932. PMID: 38427619; PMCID: PMC10906911.
- [7] Moein, S., Nickaeen, N., Roointan, A. et al. Inefficiency of SIR models in forecasting COVID-19 epidemic: a case study of Isfahan. Sci Rep 11, 4725 (2021). <https://doi.org/10.1038/s41598-021-84055-6>
- [8] A. Tasciotti, F. Urban, F. de Dea, L. Bortolussi, G. Caravagna and A. D’Onofrio, "Deep Learning-Informed Bayesian Model-Based Analysis to Estimate Superspreading Events in Epidemic Outbreaks," in IEEE Access, vol. 12, pp. 161375-161400, 2024, doi: 10.1109/ACCESS.2024.3490374.