

Simulating the Pandemic Flu Spread in a Classroom

Group Number: 23

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Abstract:

This project simulates the spread of the flu in a classroom of 61 students to analyze how an epidemic propagates over time. The model assumes an initial infection in one student and incorporates infection spread based on 0.01 probability to susceptible students, with each infected student remaining contagious for three days. Simulations were run both on a daily basis and restricted to weekdays only to mimic realistic school days. The results show the expected number of infections per day and the typical duration until the epidemic ends. Across 1000 simulations, we find that on average, approximately half of the class becomes infected before the outbreak resolves. Additionally, the histogram of epidemic duration indicates a right-skewed distribution, with most simulations ending between 30–50 days in the weekday-only model, and a shorter span in the daily model. These findings emphasize how disease dynamics change under different time constraints and can aid in bettering health policies at schools.

Background & Problem Description:

Understanding how infectious diseases spread in small, enclosed settings like classrooms is important for predicting outbreaks and testing ways to control them. In this simulation, we model how pandemic flu could spread among 61 elementary school kids, starting with one infected student, Tommy. Tommy is contagious for three days, and each day he has a 1% ($p = 0.01$) chance of infecting any healthy classmate. If a student gets infected, they also become contagious for three days starting the next day. We assume all kids and days are independent.

Simulating disease spread is useful because it lets us explore many possible outcomes when real-world prediction is difficult. Recent research shows that simulation models, like SEIR models or individual-based simulations, help track how infections spread over time and support better public health decisions (Zhou et al., 2021; Rui et al., 2024). Simulations also help when randomness and close interactions between individuals matter, as realistic agent-based models can capture detailed spread patterns better than simple statistical models (Blanco et al., 2024). In addition, understanding transmission dynamics at both the individual and community levels is critical for improving outbreak control measures (Ryu et al., 2022).

By modeling Tommy's flu spread, we can estimate how many students are likely to get infected over time, how long the outbreak might last, and how the results might change if some students

are already immune. This mirrors how real-world researchers use simulations to better understand, predict, and manage infectious disease outbreaks.

Main Findings:

(a) Let X = the number of kids that Tommy infects on Day 1. Then $X \sim \text{Binomial}(n = 60, p = 0.01)$, because the kids and days are i.i.d. *Bernoulli*(p) trials, and we are summing the number of infections across the kids.

(b) The expected number of kids that Tommy infects on Day 1 is $E[X] = np = 60 \times 0.01 = 0.6$.

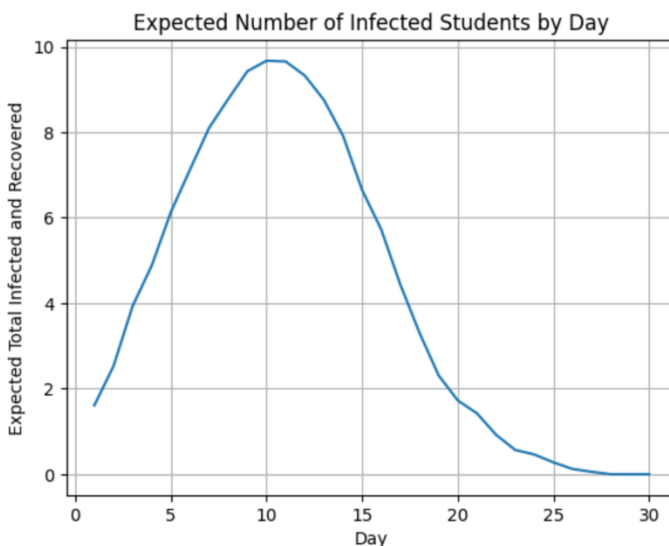
(c) Let Y = the number of new kids infected on Day 2. On Day 2, both Tommy and the kids he infected on Day 1 become infectious. Tommy attempts to infect each of the remaining

$60 - E[X] = 59.4$ susceptible kids with probability $p = 0.01$, so the expected number of infections from Tommy is $E[Y_T] = 59.4 \times 0.01 = 0.594$. Additionally, the $E[X] = 0.6$ kids infected on Day 1 also attempt to infect susceptible kids. The expected number of infections from these new infectious kids is $E[Y_{new}] = 0.6 \times 59.4 \times 0.01 = 0.3564$. Therefore, the expected total number of kids infected by Day 2 (counting Tommy) is:

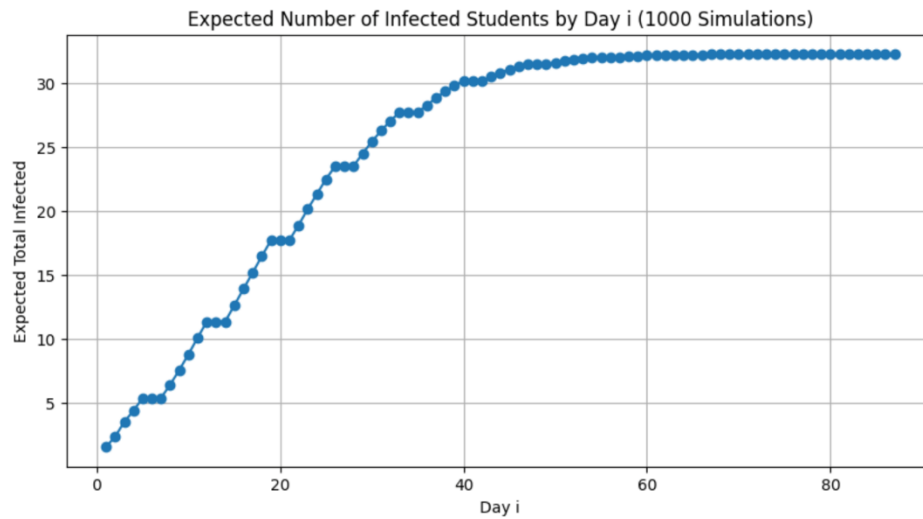
$$1(\text{Tommy}) + 0.6(\text{Day 1 infections}) + 0.594(\text{Tommy's Day 2 infections}) + 0.3564(\text{new kids' Day 2 infections}) = 2.5504.$$

(d)

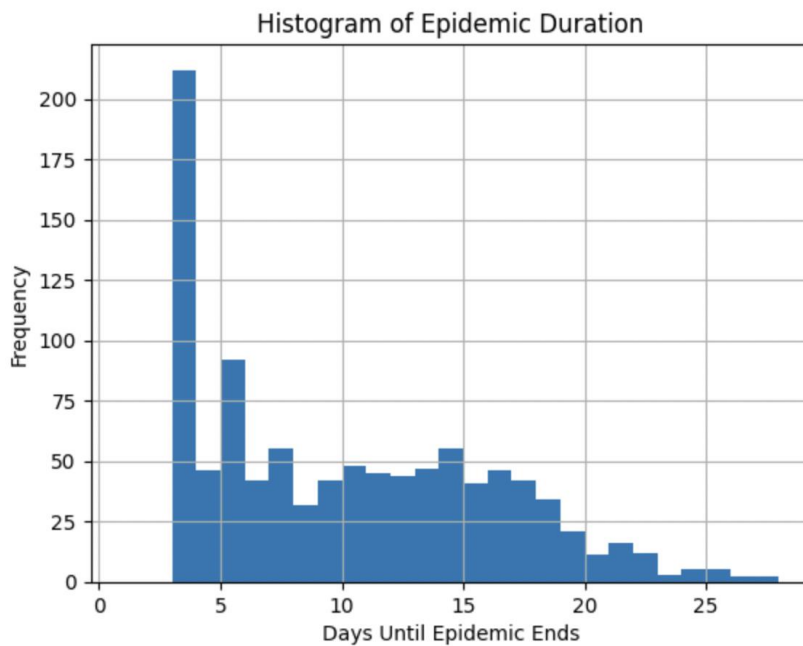
Expected Total Infections by Day: Averaging over many simulations, we found that the number of infected and recovered students typically increases steadily until it plateaus. In most cases, the epidemic reached around 30–35 total infected students, out of 61. Therefore, about half of the class is likely to be impacted in a flu outbreak.



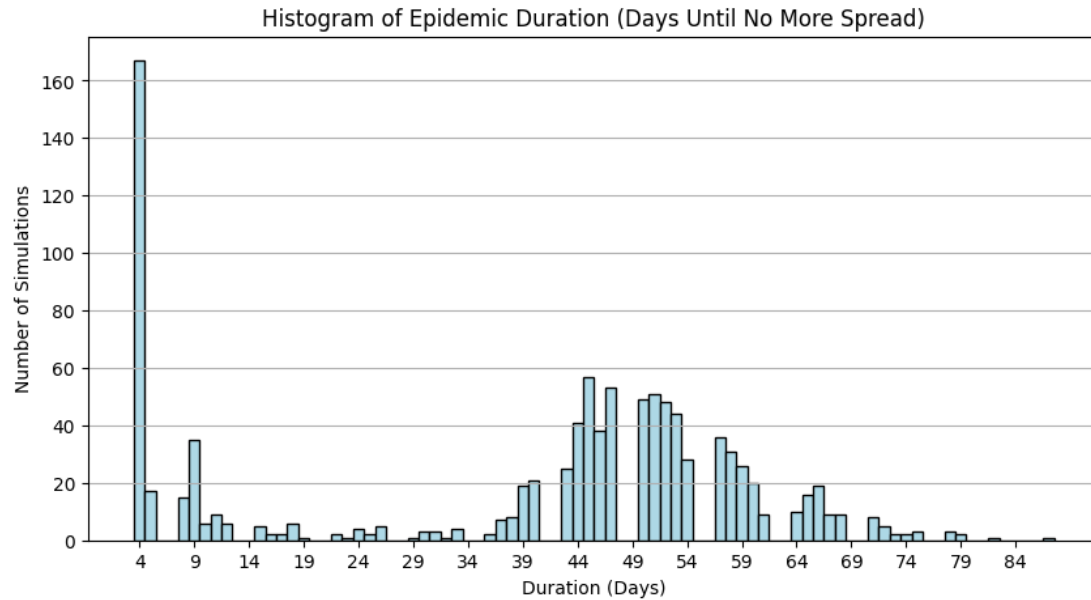
Simulating just the weekdays:



Duration of Epidemic: The histogram of epidemic durations shows a right-skewed distribution. While some simulations ended as early as 4–5 days, many extended beyond 30 days, with a long tail stretching past 80 days in some cases. This highlights that while outbreaks can sometimes die out quickly, they often persist for several weeks depending on how the infection spreads.

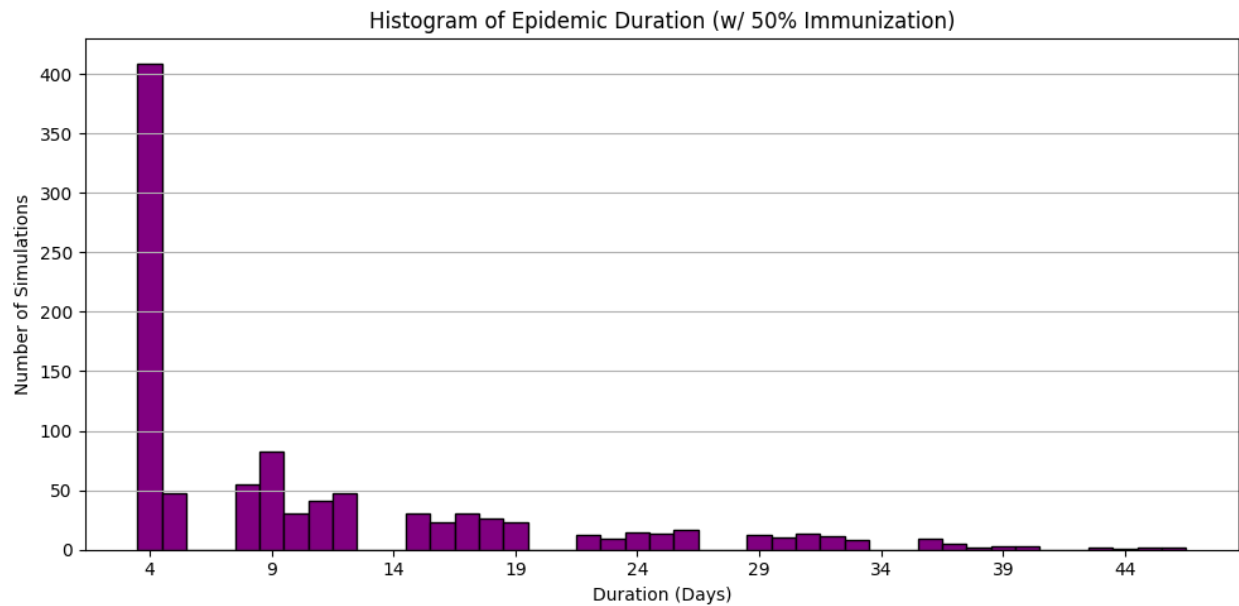
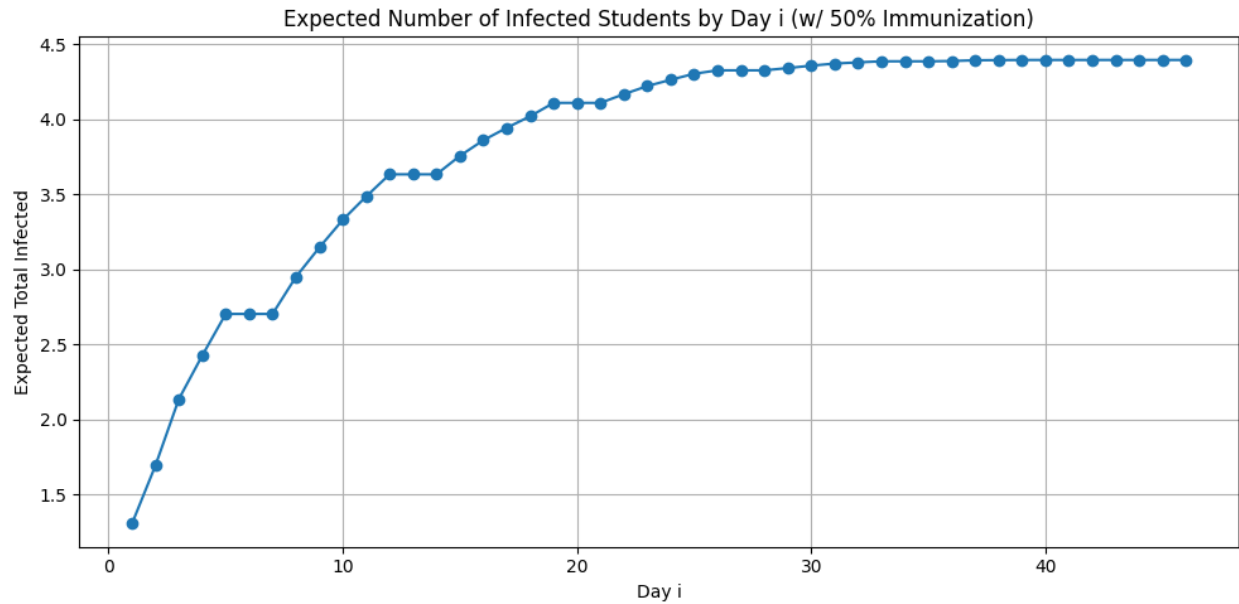


Simulating just the weekdays:



(e)

The expected number of infected students by each day remained low. Even after 45 days, the average total infected barely exceeded 5 students, compared to over 30 without immunization. The histogram of epidemic duration shows a strong left-skew. The most frequent outbreak duration was just 3–4 days. There was also not a lot of spread in the epidemic duration, and very few simulations lasted more than 30 days. Based on the histogram, we can see that smaller simulations still led to longer outbreaks; Therefore, even 50% immunity doesn't completely eliminate flu risk; Random 50% immunization dramatically flattens the infection curve and shortens the outbreak.



Conclusions:

Through this project, we gained insight into how even a single initial infection can lead to widespread transmission in a classroom setting. By simulating the flu spread over both daily and weekday-only schedules, we observed that, on average, nearly half of the class could become infected before the epidemic ends. This highlights how quickly infections can escalate in close-contact environments when no interventions are in place. We also learned how time structure (like skipping weekends) affects not just the pace of the outbreak, but also its duration and variability.

When we introduced a scenario with 50% random immunization, the impact was dramatic: the number of infected students dropped significantly, and the epidemic often ended within just a few days. However, infections were not entirely eliminated, demonstrating that even partial immunity can slow but not always stop the spread.

These results reinforce the importance of preventative health measures like vaccination and illustrate how simple simulation models can provide valuable intuition about real-world outbreaks.

For future work, this simulation can be extended in several directions. Future models could incorporate more realistic behavior such as variable infection probabilities based on proximity or exposure time, delayed onset of contagiousness, or the effect of isolating symptomatic students. The framework could also be scaled to simulate entire schools or communities and used to test school closure policies or targeted immunization strategies. Adding parameters for mask-wearing, classroom ventilation, or contact tracing could further align the model with real-life decision-making in public health.

References

1. Zhou, J., Dong, S., Ma, C., Wu, Y., & Qiu, X. (2021). Epidemic spread simulation in an area with a high-density crowd using a SEIR-based model. *PloS one*, 16(6), e0253220. <https://doi.org/10.1371/journal.pone.0253220>
2. Rui, J., Li, K., Wei, H., Guo, X., Zhao, Z., Wang, Y., Song, W., Abudunaibi, B., & Chen, T. (2024). MODELS: a six-step framework for developing an infectious disease model. *Infectious diseases of poverty*, 13(1), 30. <https://doi.org/10.1186/s40249-024-01195-3>
3. Blanco, R., Patow, G. & Pelechano, N. Simulating real-life scenarios to better understand the spread of diseases under different contexts. *Sci Rep* 14, 2694 (2024). <https://doi.org/10.1038/s41598-024-52903-w>
4. Ryu, S., Chun, J. Y., Lee, S., Yoo, D., Kim, Y., Ali, S. T., & Chun, B. C. (2022). Epidemiology and Transmission Dynamics of Infectious Diseases and Control Measures. *Viruses*, 14(11), 2510. <https://doi.org/10.3390/v14112510>