

Simulating the Spread of an Infectious Disease in a Small Community

Edmund Sayson (30047166)
Department of Computer Science
University of Calgary
Calgary, AB, Canada
edmund.sayson1@ucalgary.ca

Khanh Do (30104044)
Department of Computer Science
University of Calgary
Calgary, AB, Canada
khanh.do@ucalgary.ca

Jessica Tran (30089544)
Department of Computer Science
University of Calgary
Calgary, AB, Canada
jessica.tran3@ucalgary.ca

Abstract— Infectious diseases remain a formidable challenge to public health, requiring comprehensive understanding of transmission dynamics for effective mitigation and containment. Drawing inspiration from the pivotal lessons learned during the COVID-19 pandemic, this research aims to address the pressing need for localized disease spread modeling within small communities. Motivated by the profound impacts of COVID-19 on global health and societal stability, our research seeks to extend existing methodologies to enhance comprehension of disease transmission patterns, speed, and intervention impacts. Our focus lies in leveraging Agent-Based Simulation (ABS) to capture individual-level interactions and behaviors within the community. Each agent represents an individual, allowing for the manipulation of starting characteristics to compare their results. Furthermore, we plan to incorporate human behavior details to agents and geographic details to increase the accuracy of disease spread predictions by introducing a mix of homogeneous and heterogeneous agents. By computer simulation, our research hopes to provide practical insights for the development of targeted mitigation plans and containment strategies tailored to small community settings.

Keywords— *Agent-Based Modeling, Geographic Information Systems, Infectious Disease, Simulation, Human Behavior, COVID-19*

I. INTRODUCTION

In the wake of recent global health crises, understanding the mechanisms of infectious disease spread within small communities has emerged as a critical area of study. Infectious diseases, characterized by their ability to traverse through populations, pose significant challenges to public health systems, particularly in localized settings where interactions are dense and frequent [1]. The recent COVID-19 pandemic has underscored the necessity for

robust epidemiological models that can accurately simulate and predict disease transmission dynamics, facilitating the implementation of effective containment and mitigation strategies.

Agent-Based Models (ABMs) have increasingly become crucial in the epidemiological toolkit, offering important insights into the spread of infectious diseases by accounting for individual behaviors, interactions, and spatial dynamics within a community [5]. ABMs, by their very nature, enable the representation of heterogeneous agents, each with distinct attributes and behaviors, interacting within a defined environment. This approach contrasts with traditional equation-based epidemiological models, which, while useful, often assume homogeneity within the population and may overlook crucial spatial and social interactions that significantly impact disease transmission [1].

The integration of Geographic Information Systems (GIS) with ABMs represents a significant advancement in the field, enhancing the explicitness of simulations and thereby providing a more detailed and realistic depiction of how diseases spread across varied geographical landscapes [5]. This integration is particularly crucial in small communities where geographical features, population density, and local behaviors can markedly influence transmission patterns.

Furthermore, by integrating human behavior models, such as those based on occupation and daily routines, into the ABM, the simulator provides insights into how personal and collective actions can influence the trajectory of a disease outbreak. The inclusion of realistic mobility patterns, such as random walks within specific locations and decision-driven movements between locations, contributes significantly to the depth of the simulation. It allows for a better understanding of the interaction between human behavior and disease spread, emphasizing the importance of considering these factors in pandemic preparedness and response [7].

Our research is motivated by the profound impacts of the COVID-19 pandemic on small communities,

highlighting the urgent need for localized disease spread modeling to better understand and combat infectious diseases. By leveraging ABM, GIS, and human behavior models, we aim to simulate the spread of an infectious disease within a small community, capturing the complex interaction between individual behaviors and disease transmission. This approach allows for analysis of how various factors, such as human mobility, social networks, and geographical attributes, contribute to the spread and containment of infectious diseases [5, 7].

In this study, we seek to explore the potential impacts of different interventions on disease spread within a small community setting. Overall, we aim to provide valuable insights into the effectiveness of different strategies for controlling disease spread.

II. RELATED WORKS

A. A Comparison of Agent-Based Models and Equation Based Models for Infectious Disease Epidemiology

Hunter et al. [1] compares agent-based (ABM) and equation-based (EBM) models for simulating measles outbreaks in Irish towns. ABMs simulate individual behaviors and interactions within a detailed virtual environment, providing nuanced outbreak scenarios, while EBMs use compartmental equations to model population segments, offering quicker but less detailed insights. The study utilized real-world demographic and health data to create realistic simulation settings for both models. Findings revealed that ABMs, despite being resource-intensive, offered more detailed insights into the dynamics of disease spread and the impact of public health interventions, whereas EBMs were faster and less resource-intensive but provided a more generalized view of outbreaks. The research highlights the trade-offs between the detailed, individual-level insights provided by ABMs and the broader, less detailed perspectives offered by EBMs, suggesting a complementary use of both models in public health planning and response.

B. A Hybrid Agent-Based and Equation Based Model for the Spread of Infectious Diseases

Hunter et al. [2] proposes a modeling approach that merges both agent-based (ABM) and equation-based (EBM) modeling into a hybrid model. Although ABMs are able to capture the heterogeneous characteristics that cause the spread of an outbreak, they are computationally intensive. On the other hand, EBMs can capture the overall dynamics and homogeneous characteristics at very little computational cost. The proposed methodology involves switching between ABM and EDM depending on the number of agents infected. After testing multiple runs of different percentages of infected agents before switching models, findings revealed that the hybrid model is able to switch between ABM and EDM for the majority of runs when 35% of agents

or below were infected. It was also shown that at all percentages that the switch took place, there were significant time savings when running the hybrid model over just the purely agent-based model.

C. A Model for the Spread of Infectious Diseases in a Region

Hunter et al. [3] introduces the importance of how a town's location within a network of other towns in the same region will impact a disease's circulation. Using an already existing agent-based model that simulates the spread of measles through an Irish town, the model is scaled up to simulate a region containing multiple towns. Four main assumptions (environment, society, transportation, disease) are considered when scaling up as they may reduce the fidelity of the existing model. When testing, each component is validated by checking to see if simulation results are somewhat different, but not drastically so. Results show that scaling up an agent-based model using validated assumptions does not show significant influence on the results and allows for a country or region to be better modeled.

D. Adapting an Agent-Based Model of Infectious Disease Spread in an Irish County to COVID-19

Hunter et al. [4] discusses adapting an existing agent-based model for the spread of measles in Ireland to simulate the spread of COVID-19. As the model already captures the structure of populations and commuting patterns of the Irish population, the only parameters that need to be adjusted are the disease parameters. Different values of the basic reproductive number are tested, along with intervention strategies, such as vaccinations. Findings show that in the same town or city, the different disease components lead to different results for both measles and COVID-19. It is concluded that agent-based modeling is a powerful tool that can be used to simulate how a specific society experiences different outbreaks.

E. An agent-based approach for modeling dynamics of contagious disease spread

Perez et al. [5] introduces an agent-based (ABM) modeling strategy that combines geographic information systems (GIS) to simulate the spread of a disease in an urban environment. The model is implemented using measles outbreak as a case study where individuals are represented as agents that have mobility to move between places within the urban environment. Data from georeferenced land use datasets are used to show specific areas where agents move around in. Results demonstrate that the dynamic spatial interactions within the population of Burnaby, BC, lead to a high number of exposed individuals in geographical locations such as schools and universities.

F. Modeling the spread of infectious diseases through influence maximization

Yao et al. [6] adapts the influence maximization problem to model the spreading process of a disease. It is mentioned that agent-based modeling does not consider the role of social network structures for transmission of diseases. In this model, network structures are analyzed and connections among individuals with infection probabilities are modeled. Results found that sparse and clustered networks, and precautionary actions play a role in the prevention of disease spread.

G. Pandemic Simulator: An Agent-Based Framework with Human Behavior Modeling for Pandemic-Impact Assessment to Build Sustainable Communities

Weligampola et al [7]. introduce an innovative Agent-Based Model (ABM) named PDSIM. This model is designed to provide an in-depth simulation of pandemic spread through the integration of human behavior modeling and environmental interactions. PDSIM's framework includes a unique motion model that emulates realistic human movement and an environment builder that facilitates the creation of complex simulated environments. The simulator allows for the evaluation of various pandemic management strategies, including social distancing, hygiene practices, and vaccination protocols, by simulating disease transmission among different demographic groups and settings. Results from the study highlight the tool's capability in modeling the dynamics of disease spread and assessing the impact of containment measures. This contributes significantly to the field by offering insights that can assist policymakers and healthcare professionals in developing more informed strategies for building resilient and sustainable communities in the face of pandemics.

III. PROPOSED METHODOLOGY

This paper proposes an extension of the existing agent-based modeling methodology by incorporating human behaviour patterns to the agents and adding geographic details into the model.

The first enhancement involves integrating human behaviour patterns into the agents' algorithms. This will include realistic schedules such as going to school or work during weekdays, and common free time activities during weekends or evenings. By capturing these daily activity patterns, the aim is to simulate more accurate interactions within the model.

The second enhancement entails incorporating geographic details into the models. This will include integrating land use data to model a real town's environment so that the agents' movements will be reflected more realistically.

This proposed methodology seeks to progress the accuracy of agent-based modeling in capturing the socio-geographic systems in a small community, and therefore provide a better understanding of how a disease will spread through.

IV. DATASET

A. Canmore Land Use Districts

This dataset contains information about the polygons that show the boundary of Land Use Districts, also known as zoning, in the town of Canmore. The polygons are determined by the Town of Canmore Land Use Bylaw [9].

- Type of Data: Table
- Statistics: 300 records of land use districts
- Weblink:
https://opendata-canmore.opendata.arcgis.com/data-sets/a0117c599e95492e97d67a8a26e60e13_0/explore?location=51.067260%2C-115.326743%2C12.74

B. 2021 Census Profile for Canmore

This dataset from Statistics Canada contains demographic and socio-economic information for the population of Canmore, Alberta. There are details about the population's age, sex, language, education, income, housing, and other socio-economic indicators [10].

- Type of Data: Table
- Statistics: 53 topics
- Weblink:
<https://www12.statcan.gc.ca/census-recensement/2021/dp-pd/prof/details/page.cfm?Lang=E&SearchText=Canmore%20&DGUIDlist=2021S0504828&GENDERlist=1&STATISTIClist=1&HEADERlist=0>

C. Epidemiology for Diseases and Conditions

The government of Canada provides epidemiology data for a number of diseases. We are planning on creating a dataset with the information in this web source by gathering the transmission rate, incubation period, and infectious period of COVID-19, measles, and influenza [11].

- Type of Data: Text
- Statistics: 3 diseases that we plan on using
- Weblink:
<https://www.canada.ca/en/public-health/services/diseases.html>

V. IMPLEMENTATION

We will simulate the spread of an infectious disease by leveraging Python, and Mesa. Mesa is an open-source Python library for agent-based modeling, ideal for simulating complex systems and exploring emergent behaviors [8]. We also use a GIS extension of Mesa called Mesa-Geo in order to host GIS-based GeoAgents [15] and

use a basic template off of the Project Mesa Github examples [18].

Specifically, we will be simulating the spread of different diseases in the community of Canmore, Alberta. This will be done by using the census profile data of Canmore from Statistics Canada [10] to create a population of agents that will be used in our Agent-Based Model. Furthermore, datasets that contain the polygons of the city's land use districts [9] and buildings [17] are used in order to allow the agents' movements to accurately reflect the location of homes, schools, and workplaces.

Our model starts off with an adjustable number of infected individuals in the community and follows the SEIR [17] model where agents are one of four statuses: Susceptible, Exposed, Infected, and Recovered. If a susceptible agent is in the same vicinity as an infected agent, then there will be a probability of converting the susceptible agent to an exposed one depending on the transmission rate of the specific disease and whether the infected individual is a household contact or stranger. If an agent does become exposed, then they will go through an incubation period before becoming infected for the duration of infectiousness of the disease. Finally, they will become recovered and in this model, they cannot be reinfected. Each step in the model would represent a period in the current day, either morning, afternoon, or evening. Our model would keep track of the current day of the week to determine if it is a weekday or weekend in order to vary the routine of each agent.

With data from sources such as the Public Health Agency of Canada [11], we simulated three different diseases: measles, COVID-19, and influenza. For each disease, the infection risk, incubation period, and infectious period parameters for the models are changed accordingly. Although the parameters for each disease can vary in real-life due to many factors, we used averages to have one value for each. For measles, the basic reproductive number is 12–18 [19], the transmission rate is 90%, incubation period is about 10 days, and infectious period is 8 days [13]. For COVID-19, the basic reproductive number is 2–4 people [21, 22] and duration of infectiousness is 10 days for those with mild or moderate symptoms and 20 days for severe [23]. Using the average of these numbers, we can calculate the transmission rate using (1) to get 0.2 or 20% [24]. The incubation period for COVID-19 is about 11.5 days [12]. For influenza, the transmission rate is 9.3% for those ages 0–17 years old, 8.8% for those 18–64 years old, and 3.9% for those 65 years old and over [20]. The incubation period is 2 days and the infectious period is 5 days [14]. In the case that the infected individual is in the same household as the susceptible, transmission rates are 5–10 times higher than non-household contacts [25].

$$R_0 = \frac{\beta}{\gamma} \quad (1)$$

VI. SUMMARY AND CONCLUSIONS

After running through our models starting with 5 infected individuals of a population of 15,000, these are the results after one month without intervention.

Measles

Week#	Susceptible	Exposed	Infected	Recovered
0	14995	0	5	0
1	14664	331	5	0
2	11594	3204	197	5
3	5589	7849	1368	194
4	2460	8850	3138	552

Covid-19

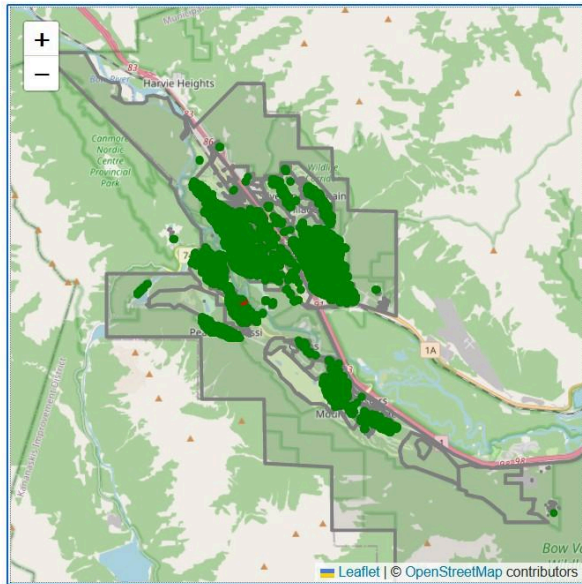
Week#	Susceptible	Exposed	Infected	Recovered
0	14995	0	5	0
1	14839	156	5	0
2	14109	820	71	0
3	13061	1765	169	5
4	9257	4538	1147	58

Influenza

Week#	Susceptible	Exposed	Infected	Recovered
0	14995	0	5	0
1	14211	443	327	19
2	9424	2031	2756	789
3	3994	1496	3934	5576
4	1556	551	1887	11006

Measles

Current Step: 0

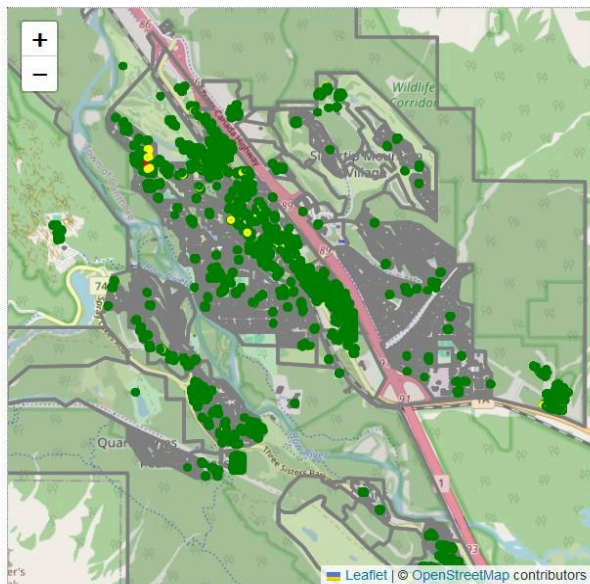


Schedule: Mon Morning

Susceptible: 14995 Exposed: 0 Infected: 5 Recovered 0

Figure(1): Measles spread at week 0

Current Step: 24

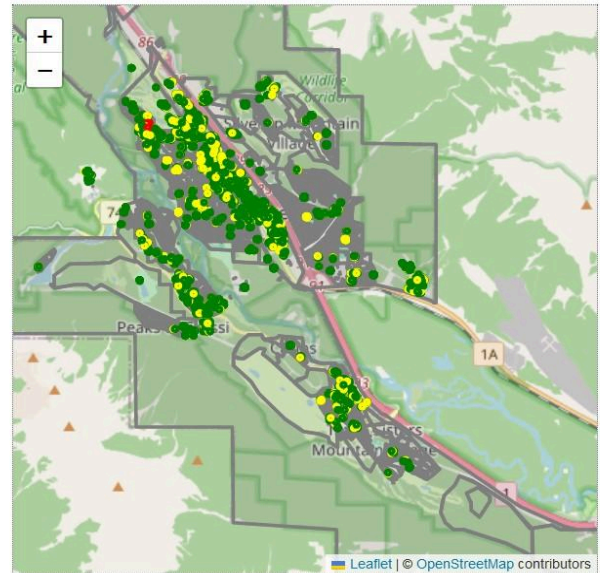


Schedule: Mon Morning

Susceptible: 14664 Exposed: 331 Infected: 5 Recovered 0

Figure(2): Measles spread at week 1

Current Step: 42

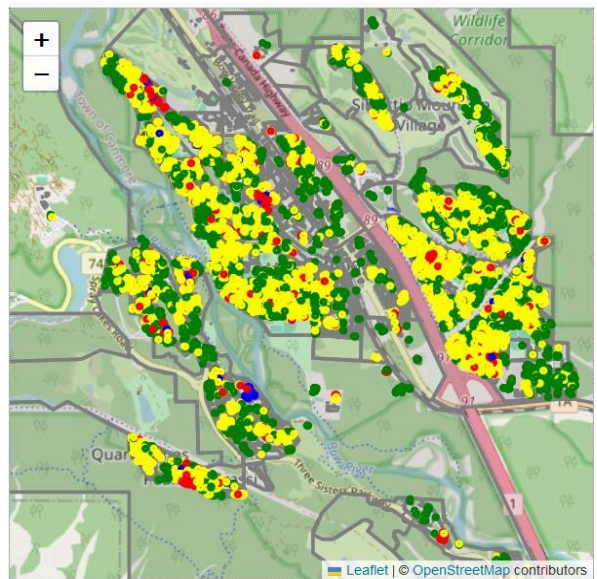


Schedule: Mon Morning

Susceptible: 11594 Exposed: 3204 Infected: 197 Recovered 5

Figure(3): Measles spread at week 2

Current Step: 65

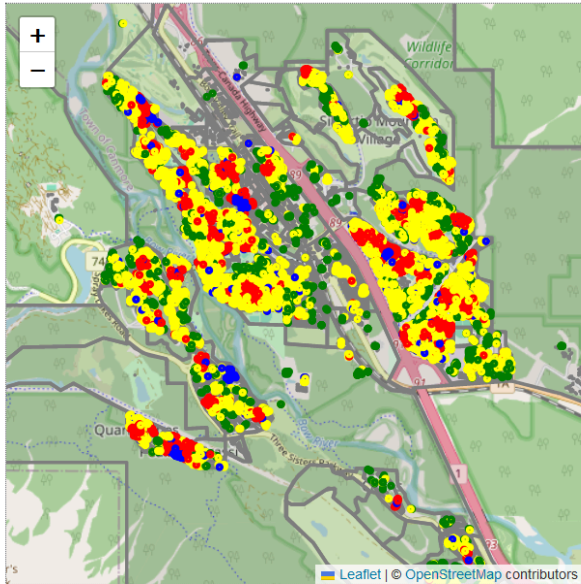


Schedule: Mon Evening

Susceptible: 5589 Exposed: 7849 Infected: 1368 Recovered 194

Figure(4): Measles spread at week 3

Current Step: 86



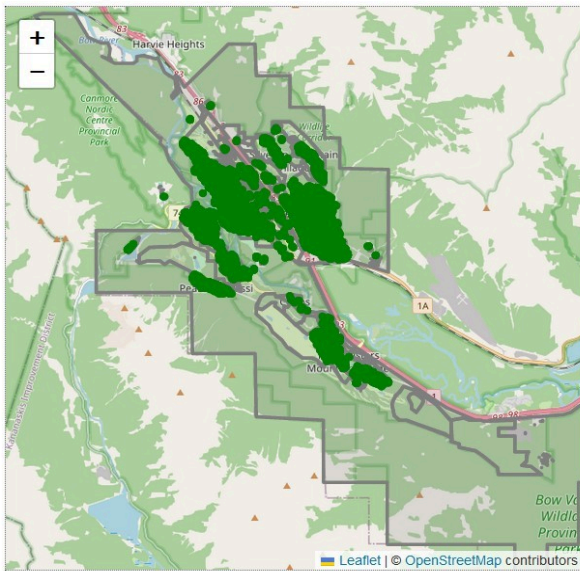
Schedule: Mon Evening

Susceptible: 2460 Exposed: 8850 Infected: 3138 Recovered 552

Figure(5): Measles spread after a month

Covid-19

Current Step: 0

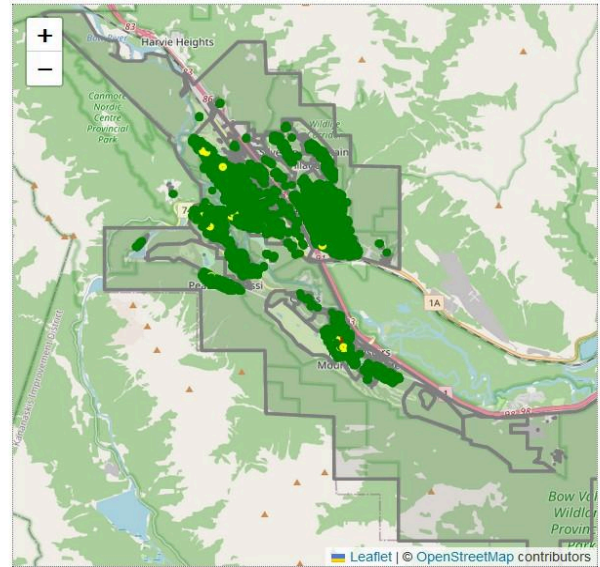


Schedule: Mon Morning

Susceptible: 14995 Exposed: 0 Infected: 5 Recovered 0

Figure(6): Covid-19 spread at week 0

Current Step: 23

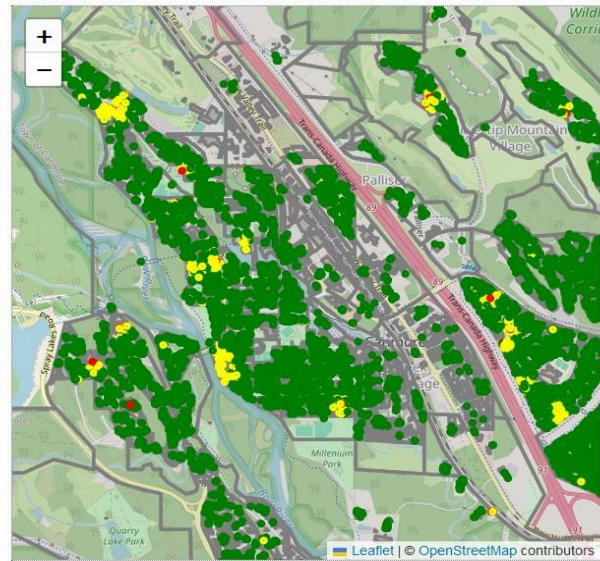


Schedule: Mon Evening

Susceptible: 14839 Exposed: 156 Infected: 5 Recovered 0

Figure(7): Covid-19 spread at week 1

Current Step: 44

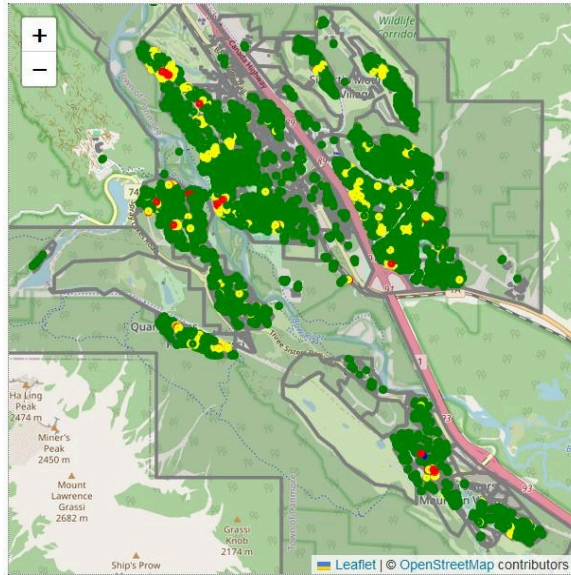


Schedule: Mon Evening

Susceptible: 14109 Exposed: 820 Infected: 71 Recovered 0

Figure(8): Covid-19 spread at week 2

Current Step: 65

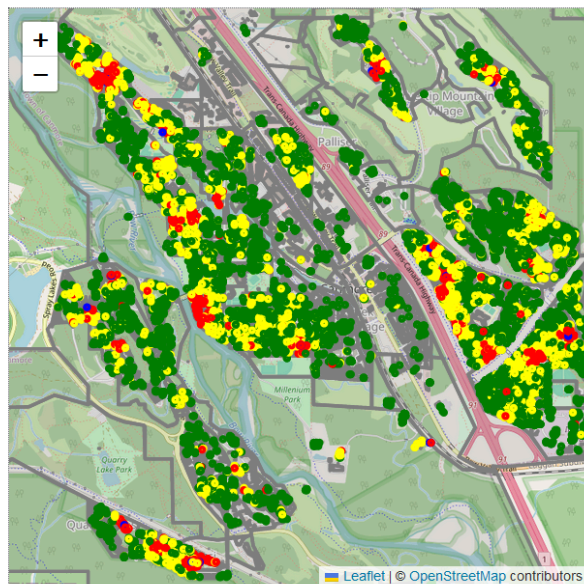


Schedule: Mon Evening

Susceptible: 13061 Exposed: 1765 Infected: 169 Recovered 5

Figure(9): Covid-19 spread at week 3

Current Step: 86



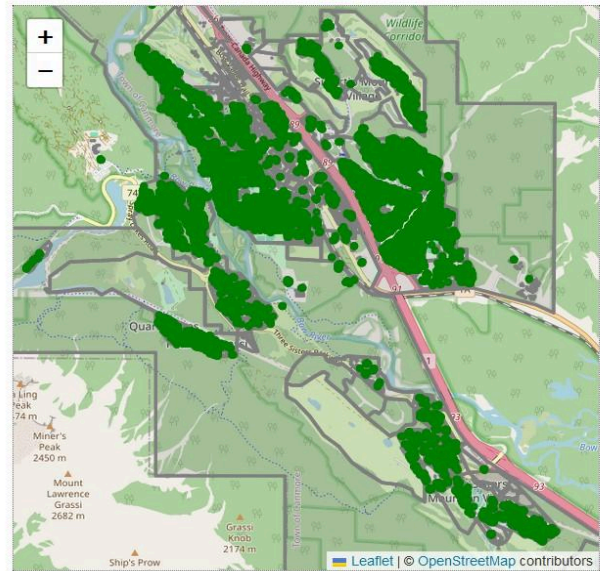
Schedule: Mon Evening

Susceptible: 9257 Exposed: 4538 Infected: 1147 Recovered 58

Figure(10): Covid-19 spread after a month

Influenza

Current Step: 0

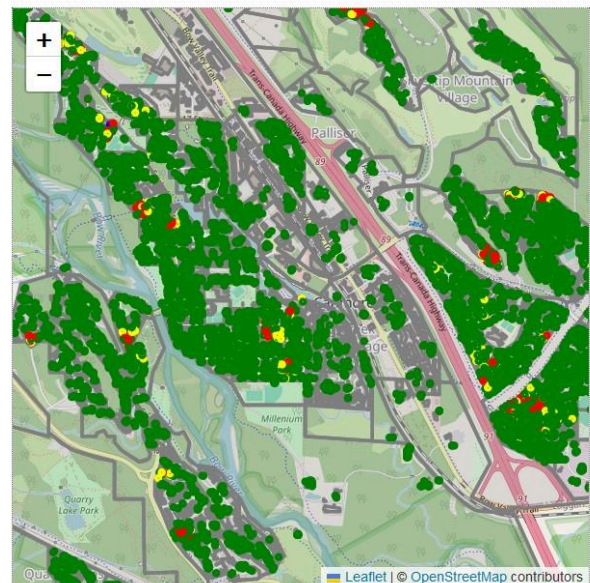


Schedule: Mon Morning

Susceptible: 14995 Exposed: 0 Infected: 5 Recovered 0

Figure(11): Influenza spread at week 0

Current Step: 23

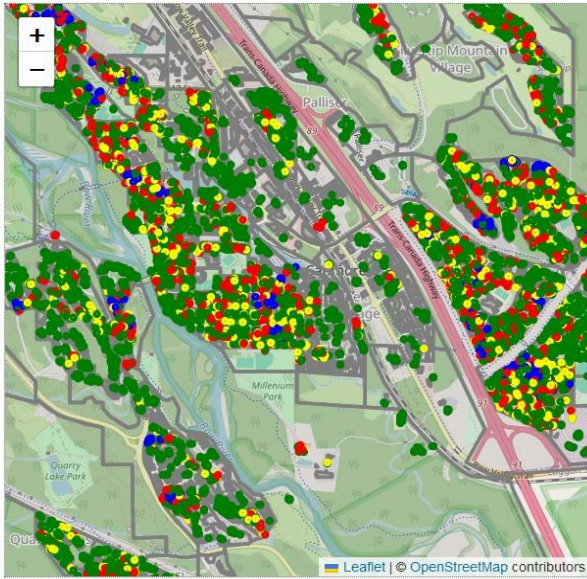


Schedule: Mon Evening

Susceptible: 14211 Exposed: 443 Infected: 327 Recovered 19

Figure(12): Influenza spread at week 1

Current Step: 44

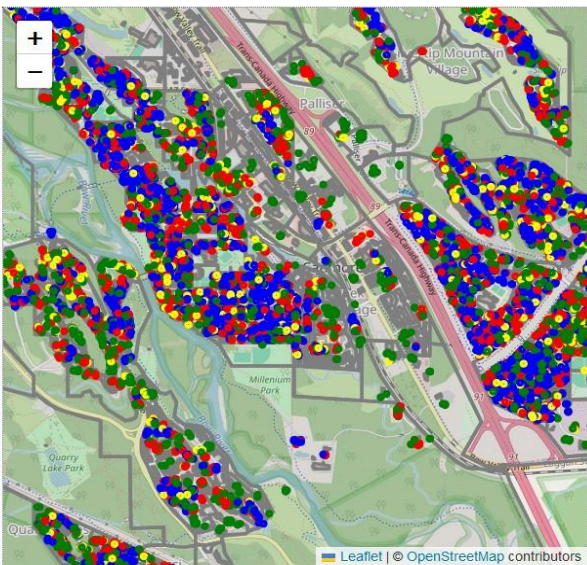


Schedule: Mon Evening

Susceptible: 9424 Exposed: 2031 Infected: 2756 Recovered 789

Figure(13): Influenza spread at week 2

Current Step: 65

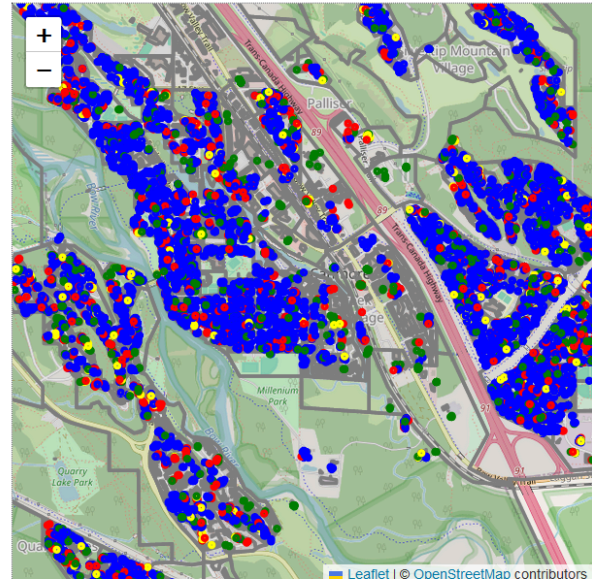


Schedule: Mon Evening

Susceptible: 3994 Exposed: 1496 Infected: 3934 Recovered 5576

Figure(14): Influenza spread at week 3

Current Step: 86



Schedule: Mon Evening

Susceptible: 1556 Exposed: 551 Infected: 1887 Recovered 11006

Figure(15): Influenza spread after a month

Measles: Although measles has an extremely high transmission risk of 90%, its incubation period lasts for 10 days on average. Additionally, infection duration is shorter than the incubation period on average. Thus, the initial spread is slow compared to a disease like Influenza. In the first two weeks only 197 individuals were infected and showed symptoms while 3204 individuals were still in the incubation period. If actions were taken to limit the spread within the first 2 weeks, 2/3rds of the initial susceptible agents would be safe.

Covid-19: Covid-19's transmission rate of 20% and incubation period of 11 days also results in a slow initial spread. After 2 weeks, only 71 individuals were infected and could transmit the disease to others. While 820 agents were exposed. After an entire month, around 2/3rds of the population were never exposed.

Influenza: The transmission rate of influenza is the lowest of the 3 diseases we chose. It sits at 7.3% on average. However, due to its extremely short incubation period of 2 days and infection duration of 5 days it has spread the fastest out of the 3. Within the first week, 327 agents were infected and could spread it further. 443 agents were exposed and would shortly turn infectious. This exponentially grew to 2756 infected and 2031 exposed in week 2. More than 4x the amount in week 1. By the end of the month, 90% of the population had contracted and/or been exposed to Influenza. Even with a short infection duration of 5 days it spread rapidly. However, due to this 5 day duration, 70% of the population recovered by the end.

Our research has successfully demonstrated the capabilities of Agent-Based Modeling (ABM) enhanced with human behavior and geographic information systems to simulate the transmission dynamics of infectious diseases in a small community. By integrating realistic human movement and environmental interactions, we have provided a nuanced understanding of how individual behaviors and local geographic details can significantly influence disease spread.

Key Findings:

1. **Disease-specific Dynamics:** Our simulations revealed distinct spread patterns for measles, COVID-19, and influenza, highlighting the critical role of disease characteristics such as incubation period and transmission rate in shaping epidemiological outcomes.
2. **Impact of Interventions:** The simulation outcomes underscore the importance of timely interventions. For example, early containment measures could potentially have halted the rapid spread of measles, as demonstrated in the initial slow spread due to its longer incubation period.
3. **Utility of ABS:** The flexibility of ABS allowed us to model complex interactions within the community, showing how various factors such as population density, mobility patterns, and local connectivity play a role in disease propagation.

Implications:

Our findings advocate for the use of localized, detailed epidemiological models in public health planning, especially for preparing and responding to infectious disease outbreaks. The ability of ABS to incorporate heterogeneous agents and detailed geographic data makes it an invaluable tool in designing targeted interventions that are tailored to specific community settings.

Future Directions:

To further enhance the model's predictive power and utility, future research should focus on:

- Integrating more detailed behavioral data: Including more granular data regarding individual daily activities could improve the accuracy of transmission dynamics.
- Cross-model validation: Comparing the results from our ABM with real-world disease outbreak data can help in refining the model and increasing its reliability.
- Exploring scalability: Testing the model in larger or interconnected communities could provide insights into the spread of diseases in more complex environments.

By continuing to refine these models, we can better understand infectious disease dynamics and improve our preparedness and response strategies. This research not only advances our knowledge in the field of computational

epidemiology but also serves as a critical tool for public health officials in managing future pandemics.

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