

Simulating Disease Transmission Models Via Agent Interaction Using Large Language Models

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ABSTRACT

Traditional epidemic models often fall short in capturing the complexity of human behaviors, a gap highlighted by the COVID-19 pandemic. This research explores the integration of large language models (LLMs) and agent-based modeling (ABM) with the Susceptible-Exposed-Infectious-Recovered (SEIR) framework to enhance epidemiological simulations. By leveraging LLMs, this study aims to develop a more dynamic and realistic model of disease transmission that reflects individual and community-level interactions. Our methodology utilizes the HPC-powered Mesa-Geo framework to incorporate geographically informed human agents (GeoAgents) and simulates disease spread through a detailed SEIR model, enriched by the advanced capabilities of the GPT4-XL Flan Alpaca model for generating nuanced human interactions. Preliminary results indicate that such an integration can effectively simulate complex social behaviors and adherence to public health measures, suggesting a promising direction for future epidemiological modeling. This approach not only addresses critical gaps in traditional modeling but also sets the stage for further research that could enhance public health strategies through more accurate and adaptive simulations.

Keywords: Disease Modeling, Agent-based Modeling, Large Language Models (LLMs), Public Health, Epidemiological Simulation.

I. INTRODUCTION

All The COVID-19 Pandemic has made clear the essential role of epidemiological modeling in understanding and managing infectious diseases on a global scale. Disease transmission models, specifically those incorporating the Susceptible-Exposed-Infectious-Recovered (SEIR) framework, have been used to predict the spread of disease and inform public health decisions (Novakovic & Marshall, 2022). These models simulate the contribution of individual behaviors and interactions towards the broader dynamics of disease transmission within populations.

Despite their widespread use, traditional approaches to epidemic modelling have difficulties in capturing complex human behaviors, as they typically utilize system dynamics or ordinary differential equations which incorporate aggregated variables that represent the population of interest (Miksch, Jahn et al., 2019). This level of abstraction allows for faster and more efficient model development and analysis while giving the researchers a high level of control, but in turn sacrifices some degree of realism (Jackson, Lewis et al., 2016). The COVID-19 pandemic highlighted these limitations, where traditional Susceptible-Infectious-Removed (SIR) models received

criticism for oversimplifying target phenomena (Eubank, Eckstrand et al., 2020). The oversimplification combined with the varied compliance with health guidelines across different communities raised concerns over the effectiveness of SIR models in predicting the development of a disease outbreak (Cokljat, Cruz et al., 2024).

II. RELATED WORKS

Agent-based models (ABMs) offer an alternative approach to epidemiological modeling, focusing on individual-based simulations that attempt to accurately capture agent behaviors. ABMs are designed to reproduce an epidemic as it naturally unfolds, giving insights into the mechanics underlying process of disease transmission. Perez and Dragicevic (2009) introduced an agent-based modeling approach using geographic information systems that uses individuals' interactions in a geospatial context to model the spread of disease. Since then, there has been more research on the implementation of ABMs as disease transmission models, modeling specific diseases such as dengue (Wu, Peng et al., 2023) or Covid-19 (Novakovic & Marshall, 2022). Hunter, Mac Namee and Kelleher (2018) showed that ABMs provide information that is not available using an equation-based model and the capture of agent interactions gives a better overall view of an outbreak. Though, a notable limitation of ABMs is the lack of data for unknown parameters of human behaviors such as contact patterns or frequencies, creating a risk of the model simulating the wrong dynamics (Miksch, Jahn et al., 2019).

Recent advancements in artificial intelligence (AI), specifically in the forward development of large language models, have presented a novel opportunity to address these shortcomings. Park, O'Brien et al. (2023) introduced a framework for realistic simulations of human behavior through their generation of a town populated by LLM-powered agents. While the research is text-based and agents move along a graph of nodes, the demonstration of nuanced human behavior by an LLM has significant implications for future research involving LLM-generated human interaction. Later, LLMs have been shown to have the capability to enhance ABMs by simulating complex human-like decision-making processes through Smart Agent Based Modeling (SABM) framework (Wu, Peng et al., 2023). The work therein facilitates the novel idea of agent-based modeling in natural language and an 'a priori modeling paradigm' not seen in traditional ABMs.

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III. RESEARCH MOTIVATION

This study proposes the integration of LLMs into the SEIR ABM framework to more accurately model intricate patterns of human communication and behavior. By utilizing LLMs to simulate realistic social interactions, we hope to create a more detailed and dynamic representation of individual responses to public health measures and scenarios.

The goal of this research is to develop a smart human-level model which incorporates spatial information of human agents combined with simulated dialogues and decisions generated by LLMs to allow for a more granular analysis of disease spread mechanisms. For example, understanding how individuals might react to certain disease prevention policies and how that could affect the spread of disease. Moreover, the use of LLMs within this context addresses a critical gap in traditional epidemiological models by incorporating an element of adaptive learning. As the model runs, it continually refines its generated actions based on past events, mirroring human adaptation to evolving circumstances. This capability is particularly important in the face of novel infectious diseases, where behavior and policies may change rapidly in response to new information. We hypothesize that LLM-enhanced ABMs will provide a more nuanced simulation of human interactions, leading to better alignment between model predictions and observed epidemic patterns. This research addresses a critical gap in epidemiological modelling while pioneering an interdisciplinary approach merging computational linguistics with public health modeling techniques.

IV. RESEARCH METHODOLOGY

Our project leverages the Mesa-Geo framework, a Python-based platform designed for building, visualizing, and analyzing agent-based models (ABMs) with geographical data using high performance computing tools. This enables our ABMs to incorporate GeoAgents, which are agents with geographical attributes like geometry and a coordinate reference system parameter. Our model primarily utilized the geometry aspect of GeoAgents. We further enriched our model’s capabilities by integrating DeClaRe Lab’s GPT4-XL Flan Alpaca Model’s, a large language model with 3 billion parameters accessed through the Python transformers library.

Our ABM simulates the spread of infectious diseases by implicitly utilizing the Susceptible-Exposed-Infectious-Recovered (SEIR) model shown in Perez and Dragicevic (2009), a compartmental framework in epidemiology that classifies individuals into distinct stages of disease progression: susceptible, exposed, infectious, recovered, and an additional state for deceased agents. Each agent in our model navigates these states, with transitions dictated by specific rates that define the latency period, infectious period, recovery, or death. The model parameters of our ABM consist of population size, percent of initial infected, exposure distance, incubation duration, infection duration, infection distance, death rate, and infection rate. We utilized the visualization capabilities of Mesa-Geo to give the user freedom in deciding various model parameters using sliding bars.

The model architecture comprises three classes – human GeoAgent, room GeoAgent, and Model – each integral to the dynamics of our simulation.

A. Human GeoAgents

The human GeoAgents are the main components of the model, they move around, perform generated actions, and spread disease between each other. Similar to the technique used in Park, O’Brien et al. (2023), each agent is generated with a short description of their personality which is used to inform future actions. We also defined several parameters for the agents: movement range, a memories array, and a compressed memories array. The movement range value was hard-coded to be 1 in the model to simplify the simulation process, making it easier to refine before expanding the movement capabilities. The class contains several main methods:

- 1) Move: Moves agent to specified coordinate

- 2) Update Memories: Using an LLM, generate a rating to each action the agent has performed that step and update it into their memories array. The response is parsed for the first integer by the Python re library. Based on the update memories function by.

- 3) Compress Memories: Top x number of memories by rating are saved in an array to be used when deciding actions in future steps based on the update memories function by.

- 4) Infect: Checks if the agent is infectious, and if so, determines infection probability towards neighbors using infection rate and spreads disease based on those probabilities.

- 5) Step: Runs the infect method and the compress memories method.

B. Room GeoAgents

The room GeoAgent is the space that the human agents are allowed to move around within. It also generates the interactions between agents within it. We chose to have the room agent generate the activities in a batch as it would be much more computationally expensive to have each agent generate their individual actions. The class is initialized with a room type, activity description, and an array of its occupants. The class contains one essential method, step, which has several different tasks:

- 1) Generates a list of activities for each person within the room using Flan Alpaca with the short description of each agent’s personality, each agent’s compressed memories, the room type, and activity description within the prompt.

- 2) Then, it feeds that result back into the LLM, and generates a list of who interacts with who in the room based on the activities.

- 3) The result is parsed and agents who share activities are brought together physically within the room. The LLM then generates a new coordinate within movement range for each agent that did not share an activity with another.

- 4) The memory array of each human agent is updated, and the update memories method is called for each human.

C. Model Agent

The model class is a fundamental component of the model that orchestrates the behavior of the simulation, managing the setup and execution of the model. The class initializes the human and room agents and integrates it into its system. The model class hosts a GeoSpace, which gets populated by the human and room agents that are kept track of by the model. The class also adds each agent to its scheduler, which decides the order of step function activation for each agent. We chose to use a random scheduler, where each agent’s step function is called in a random order, as it best simulates reality. Further, the class hosts an array of disease prevention techniques, designed by the user, which are taken into consideration.

At step 0 of the model, the model agent initializes the room agent then initializes the specified number of human agents, placing them within the confines of the room agent. After, the model infects the user specified number of human agents. Each step, the step method of the room agent is called, then the step methods of the human agents are called.

V. RESULTS AND DISCUSSION

The initial runs of our agent-based model, enhanced with large language models, have successfully demonstrated the integration’s potential to simulate complex social interactions that influence disease transmission dynamics. Currently, we have limited our testing to around 10 human agents, as the computational costs of more agents and their corresponding LLM calls slow down the model dramatically. This way, we can focus on the refinement of the model’s core mechanics before scaling up. Although the parameters were set arbitrarily to explore the functionality of the model, the results in Figure 1 have been promising, showing that the model can simulate nuanced agent behaviors based on dynamic interactions and health protocols.

The preliminary simulations highlight the model’s capability to simulate various hypothetical scenarios, adapting to changes in health protocols and past events that influence agent behavior. As shown in Figure 2, the LLM can generate unique personalities for each agent in the model. Figure 3 shows that it is then able to generate actions for each agent that try to follow the health protocol of ‘social distancing’ shown in Figure 2. Finally, Figure 4 shows the generated coordinates for each agent. Upon closer inspection, notice that the agents that have actions with each other from Figure 2 are brought together coordinate wise. Agents p20 and p16 share an action, and thus their resulting coordinates are (4,4) and (3,4). The same can be seen with p17 and p18, where their resulting coordinates are (7,7) and (7,8). The remaining individuals were then instructed to move while considering the health protocol of ‘social distancing’ and their movement range constraint. The results underscore the potential of LLMs to enhance the realism in simulations by generating lifelike and responsive agent behaviors, which could be crucial for more accurate public health planning and response analysis.

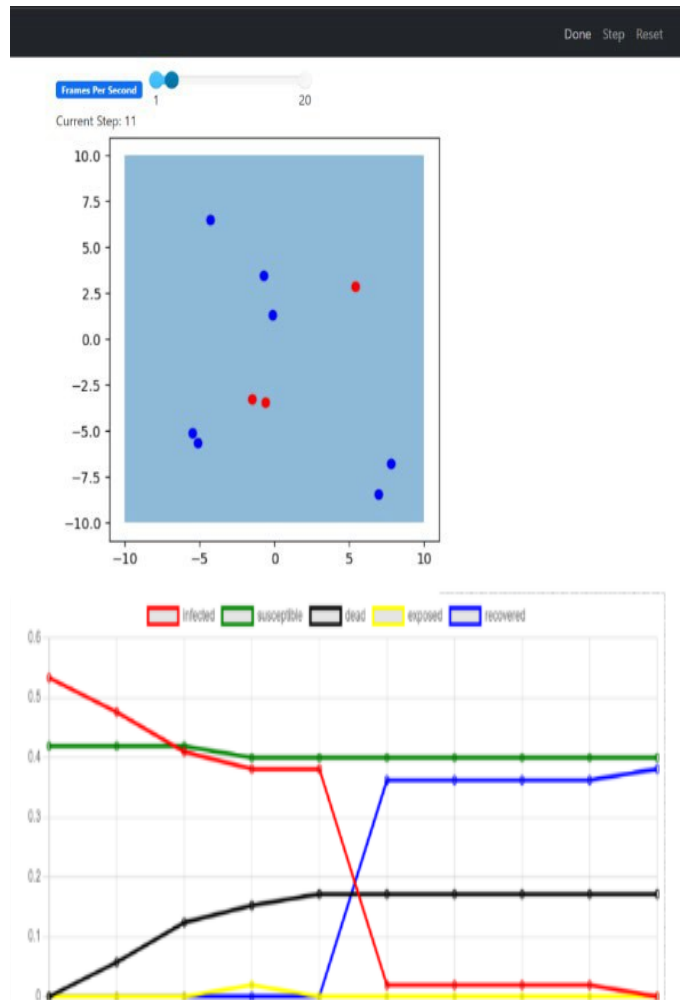


Figure 1. Disease transmission model user interface. Upper image is an example GeoSpace visualization (Blue agents are susceptible; Red agents are Infected). Lower image is an example graph of percent of each status at each step.

VI. CONCLUSION AND FUTURE WORK

In our work, we have explored the integration of large language models into SEIR agent-based models to enhance the realism of social interactions in epidemiological simulations. This approach aims to better model human-like communications and decision-making processes, which are crucial for accurately predicting disease spread dynamics. The preliminary results are promising, showing that LLM-enhanced ABMs can capture complex interaction patterns and adhere to public health measures effectively.

Given the exploratory nature of the initial simulations, the results are intended to illustrate the conceptual viability of integrating LLMs into ABMs for epidemiological research. They serve as a foundation for future research, which will involve more fine-tuning of parameters, validation against real-world data, and a detailed scenario analysis to rigorously evaluate the model’s predictive power and applicability. In an upcoming paper, we plan to scale up the model to handle larger populations and refine the integration to improve the model’s

predictive accuracy and reliability. We will extend the application of these models to diverse epidemiological scenarios and further validate the simulations with real-world data. The current research opens up new possibilities for the use of AI in public health and epidemiology, potentially leading to better disease management and intervention strategies.

This is a library study room. Currently there is a club event happening in this room. The people have been instructed to practice social distancing. There are 10 people in this location. Currently it is 10:00am. We know the following about people:

- p11: I'm p11, a 30-year-old female from Solana Beach, CA. I'm an amateur astronomer and software developer who loves discussing the latest technology trends and stargazing during clear nights.
- p12: I'm p12, a 25-year-old female from Carlsbad, CA. I enjoy surfing, yoga, and blogging about my travel adventures. I'm always eager to share stories from my journeys and learn about new cultures.
- p13: I'm p13, a 35-year-old male from San Clemente, CA. As a professional chef, I love to create fusion dishes that blend different culinary traditions. I often host cooking classes at local community centers.
- p14: I'm p14, a 22-year-old female from Oceanside, CA. I study environmental science and am passionate about wildlife conservation. I volunteer regularly at animal rescue centers and advocate for sustainable practices.

Figure 2. Generated personalities from LLM.

- p11: Engages from afar in a conversation about recent tech advancements.
- p12: Shares her travel experiences loudly from her designated spot, attracting attention but maintaining distance.
- p13: Describes his latest culinary creations, using a projector to show images.
- p14: Shows a digital presentation of wildlife she's helped conserve.
- p15: Displays recent landscape photos on a shared screen, pointing out details from a distance.
- p16: Provides ambient music by playing her violin softly, occasionally walking near p20 to coordinate on volume.
- p17: Discusses architectural designs on his laptop, inviting p18 for a closer look to discuss collaborative possibilities in design.
- p18: Explains graphic design tips using visuals, standing at a distance but projecting her voice.
- p19: Organizes a mini-seminar on entrepreneurial skills, maintaining distance as he moves around to engage with listeners.
- p20: Talks about the importance of social support, walking up to distribute printed resources to attendees.

Figure 3. Generated actions from LLM.

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- p11: (5, 4)
- p12: (2, 2)
- p13: (1, 9)
- p14: (8, 2)
- p15: (4, 3)
- p16: (4, 4)
- p17: (7, 7)
- p18: (7, 8)
- p19: (6, 7)
- p20: (3, 4)

Figure 4. Generated coordinates from LLM.

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