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Disease Spread with Mobility Heterogeneity in Campus Reopening Simulations

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Abstract

The safe reopening of educational institutions during widespread infectious disease outbreaks presents a complex challenge for public health officials and university administrators. Traditional epidemiological models often assume homogenous mixing within populations, thereby failing to capture the intricate, heterogeneous mobility patterns characteristic of a university campus. This paper investigates the explicit link between mobility heterogeneity and disease transmission dynamics using an advanced agent-based modeling framework tailored to university environments. By simulating the daily activities of thousands of autonomous agents representing students, faculty, and staff, we evaluate how varying schedules, spatial constraints, and social interactions contribute to the emergence of localized outbreaks and superspreading events. Our simulations compare a baseline scenario of unmitigated campus operations against several intervention strategies, including hybrid instructional models, targeted mobility restrictions, and staggered scheduling. The analysis reveals that transmission is disproportionately driven by a small fraction of highly connected spatial hubs, such as large lecture halls and residential dining facilities, underscoring the non-linear relationship between mobility reduction and disease containment. The findings suggest that uniform mobility restrictions are less effective and more disruptive than targeted interventions aimed at specific high-contact nodes. This research provides actionable evidence for policymakers to design nuanced reopening protocols that balance educational continuity with public health safety.

Keywords: Agent-Based Modeling; Mobility Heterogeneity; Disease Spread; Campus Reopening; Spatial Epidemiology

1. Introduction

1.1 Background and Motivation

The global disruption caused by infectious disease pandemics has starkly highlighted the vulnerabilities of high-density social environments, among which university campuses are particularly prominent. Educational institutions are unique socio-spatial ecosystems characterized by dense residential living, dynamic diurnal migration patterns, and extensive, varied social interactions. When institutions face the imperative to resume operations after a period of closure, administrators must navigate the precarious balance between restoring the academic and developmental benefits of in-person education and mitigating the inherent risks of viral transmission. Early approaches to understanding pandemic trajectories largely relied on macroscopic compartmental models, such as the classic susceptible-infectious-recovered frameworks, which aggregate populations into broad categories based on disease status. As demonstrated in initial public health assessments [1], these models are mathematically elegant and computationally efficient, providing valuable high-level forecasts of epidemic peaks and herd immunity thresholds. However, macro-level models inherently rely on the assumption of homogenous mixing, positing that any infectious individual is equally likely to contact any susceptible individual within the population.

This assumption is profoundly misaligned with the reality of human behavior, particularly within the structured environment of a university campus. Recent advances in spatial epidemiology have increasingly emphasized the critical role of mobility heterogeneity in shaping the contours of disease transmission [2]. Heterogeneity in this context refers to the unequal distribution of movement, contact rates, and spatial preferences among individuals. On a campus, an undergraduate student residing in a large dormitory and attending massive introductory lectures exhibits a fundamentally different contact network and mobility profile compared to a graduate researcher working in an isolated laboratory setting [3]. Furthermore, the physical infrastructure of a campus introduces significant spatial bottlenecks and interaction hubs, such as central cafeterias, libraries, and transit corridors, where diverse subpopulations converge [4]. Ignoring these granular, heterogeneous dynamics can lead to significant predictive errors, either overestimating the efficacy of broad lockdowns or underestimating the potential for localized superspreading events that can rapidly overwhelm institutional health resources. Recognizing this gap, researchers have increasingly turned to computational simulation techniques that can explicitly capture individual-level variations in behavior and movement [5].

1.2 Research Objectives and Scope

The primary objective of this research is to rigorously quantify the impact of mobility heterogeneity on the propagation of infectious diseases within a university setting. To achieve this, we employ agent-based modeling, a powerful computational methodology that simulates the actions and interactions of autonomous individuals, or agents, within a defined synthetic environment. By assigning empirically derived behavioral rules, daily schedules, and demographic attributes to these agents, the model generates emergent, macro-level epidemiological phenomena from the bottom up. This study seeks to construct a high-fidelity synthetic campus environment that accurately reflects the architectural and temporal constraints of a typical mid-sized university. Within this environment, we aim to map the intricate spatial-temporal contact networks that arise from routine campus life and to inject a simulated respiratory pathogen to observe its dissemination pathways.

Specifically, this paper investigates how different operational policies influence both agent mobility and subsequent disease transmission. We systematically evaluate a range of campus reopening scenarios, starting from a fully open baseline with no restrictions, to progressive interventions such as reducing classroom capacities, transitioning large lectures to online formats, and imposing localized quarantines. By tracking every simulated contact event and potential transmission vector, we intend to identify the specific environmental and behavioral factors that catalyze disproportionate disease spread. Furthermore, this research aims to provide a robust evidence base for the hypothesis that targeted interventions, which specifically disrupt high-risk mobility patterns and interaction hubs, can achieve comparable public health outcomes to campus-wide closures while preserving a significantly higher degree of educational functionality. Through this comprehensive simulation study, we contribute to the broader discourse on pandemic preparedness, offering a scalable methodology that can be adapted to various institutional contexts.

2. Literature Review and Theoretical Framework

2.1 Epidemiological Models and Mobility

The evolution of infectious disease modeling is marked by a continuous effort to incorporate greater realism into mathematical abstractions of transmission dynamics. Traditional compartmental models have served as the foundational bedrock for public health planning for nearly a century. These models, which transition individuals through various states of infection, are primarily governed by average contact rates and transmission probabilities. While early iterations provided essential insights into the basic reproduction number and the theoretical thresholds for epidemic control [6], their reliance on mean-field assumptions severely limits their applicability to highly structured populations. In environments where social networks are highly clustered and spatial constraints dictate interaction, the average contact rate becomes a poor predictor of individual risk. To address this, network-based models emerged as a significant advancement, representing individuals as nodes and their interactions as edges [7]. These models successfully captured the topological features of real-world social structures, such as degree distribution and clustering coefficients, demonstrating that pathogens spread much faster through scale-free networks where a few individuals act as highly connected hubs [8].

Despite the improvements offered by network topology, static network models often fail to capture the temporal fluidity and spatial context of human movement. Mobility is not merely a mechanism for mixing; it is a complex, environmentally constrained process driven by necessity, routine, and social preference. The integration of high-resolution mobility data into epidemiological models has revolutionized our understanding of spatial disease diffusion. Studies leveraging aggregated location data from mobile devices have unequivocally shown that restrictions on human movement strongly correlate with reductions in transmission rates [9]. However, macro-level mobility tracking often obscures the micro-level behaviors that drive indoor transmission events. For instance, the duration of exposure, the ventilation characteristics of the specific room, and the proximity of individuals within that space are critical determinants of infection risk for respiratory pathogens [10]. To bridge the gap between macroscopic mobility trends and microscopic transmission mechanics, researchers have increasingly recognized the necessity of modeling frameworks that can simulate both the physical environment and the temporal dynamics of individual schedules. This realization has catalyzed the adoption of agent-based modeling in spatial epidemiology, allowing for a synthesis of geographic information systems, transportation engineering, and infectious disease dynamics [11]. The theoretical foundation of our approach builds upon these interdisciplinary efforts, positing that disease spread is an emergent property of complex, heterogeneous, and routine human mobility [12]. Furthermore, previous investigations into superspreading phenomena suggest that biological heterogeneity in viral shedding must be coupled with environmental heterogeneity to fully explain massive outbreak clusters [13].

2.2 Agent-Based Modeling in Public Health

Agent-based modeling represents a paradigm shift in how complex systems are analyzed in public health. Unlike equation-based models that describe system-level changes over time, agent-based models define the fundamental rules of behavior for individual entities and observe the system-level patterns that arise from their collective interactions. In the context of epidemiology, an agent typically represents a single human being, endowed with specific demographic characteristics, a health state, and a behavioral profile. The environment in which these agents operate can be modeled with high spatial fidelity, incorporating the physical boundaries of buildings, rooms, and transit pathways. This methodology is particularly well-suited for simulating contained, highly structured environments like university campuses, military barracks, or long-term care facilities, where the daily routines of the population are generally predictable and spatially bound.

The application of agent-based modeling to campus health scenarios has seen substantial growth, particularly driven by the need to manage respiratory disease outbreaks safely. Earlier studies utilizing this approach focused on pandemic influenza, demonstrating how the closure of schools and universities could delay epidemic peaks [14]. However, the prolonged nature of recent global health crises has shifted the focus from simple closure to the optimization of reopening strategies. Researchers have developed sophisticated synthetic campuses to test the efficacy of non-pharmaceutical interventions such as contact tracing, asymptomatic testing regimens, and cohorting [15]. These models have consistently highlighted the outsized role of residential halls in sustaining transmission chains, given the high density and prolonged contact durations inherent to student housing [16]. Moreover, agent-based simulations have been instrumental in evaluating the logistics of resource allocation, such as determining the necessary capacity for quarantine facilities and testing centers on campus [17]. A critical advantage of this methodology is its capacity to simulate compliance heterogeneity. Real-world populations do not uniformly adhere to public health mandates; an agent-based model can assign varying levels of compliance to mask-wearing or social distancing rules, thereby testing the resilience of intervention strategies against realistic behavioral variations. By situating our research within this robust methodological lineage, we aim to extend the current literature by specifically isolating mobility heterogeneity as the primary variable of interest, systematically mapping how variations in movement intensity and spatial clustering dictate the success or failure of campus reopening protocols.

3. Methodology and Simulation Design

3.1 Agent Environment and Behavior Modeling

To rigorously investigate the dynamics of disease transmission on a university campus, we developed a high-fidelity, spatially explicit agent-based model. The simulated environment is constructed as a continuous two-dimensional plane overlaid with discrete functional zones representing a typical medium-sized residential university. The spatial architecture includes residential dormitories of varying capacities, academic buildings containing lecture halls, seminar rooms, and laboratories, as well as communal hubs such as dining halls, libraries, and recreational facilities. The structural parameters of these buildings, including square footage and maximum occupancy limits, were calibrated using architectural benchmarks standard to higher education institutions [18]. The environment is not merely a static backdrop but a dynamic constraint on agent behavior; for example, the physical dimensions of a classroom directly dictate the maximum possible distance between agents, a critical factor in respiratory transmission probability.

The synthetic population comprises ten thousand autonomous agents, proportionally divided into undergraduate students, graduate students, faculty members, and operational staff. Each agent is assigned a unique behavioral profile that dictates their daily schedule, generating a vast spectrum of mobility heterogeneity across the population. Undergraduate schedules are highly structured, characterized by cyclical movements between dense residential halls, large introductory lectures, and centralized dining facilities. Graduate students exhibit less structured mobility, often spending prolonged, continuous periods in specialized laboratory or office spaces with a smaller, more consistent set of close contacts. Faculty and staff schedules vary according to their administrative and instructional duties [19]. The movement of agents between locations is simulated in distinct temporal ticks, with each tick representing fifteen minutes of real time. To accurately model human mobility, agents utilize predefined pathways connecting the functional zones, mimicking the pedestrian traffic flows of a real campus. We employ a modified random waypoint model for intra-building movement, bounded by the specific functional constraints of the room. This granular level of spatial and temporal tracking allows the model to log every instance where two or more agents occupy the same spatial coordinate within a defined proximity threshold, thereby generating a dynamic, multi-layered contact network that evolves continuously throughout the simulated day [20].

3.2 Infection Transmission Parameters

The epidemiological component of the model operates concurrently with the behavioral simulation, calculating the probability of disease transmission during every contact event. We adopt a modified Susceptible-Exposed-Infectious-Recovered framework, applied at the individual agent level. When a susceptible agent shares a physical space with an infectious agent, a transmission algorithm is triggered. The probability of successful transmission is not a static value but is calculated dynamically based on several heterogeneous factors. Primary among these is the duration of exposure; prolonged contact in a seminar room yields a exponentially higher transmission risk than a brief, transient encounter in a campus transit corridor. Spatial proximity, calculated via the Euclidean distance between agents within the modeled environment, also heavily penalizes the transmission probability as distance increases, reflecting the dispersion mechanics of respiratory droplets and aerosols.

Furthermore, we incorporate environmental heterogeneity into the transmission equations. Different indoor environments are assigned distinct ventilation coefficients, which act as modifiers to the base transmission rate. A high-ceilinged, well-ventilated laboratory space possesses a lower environmental transmission modifier compared to a densely packed, poorly ventilated basement lecture hall. The model also accounts for biological heterogeneity in infectiousness. Rather than assuming a uniform viral shedding rate, infectious agents are assigned individual shedding profiles drawn from a log-normal distribution, thereby explicitly enabling the simulation of superspreading individuals who shed disproportionately large viral loads. To initialize a simulation run, a small, randomized seed of exposed individuals is introduced into the susceptible population, representing cases imported from outside the campus community. The model tracks the progression of the disease through the latent period, during which agents are infected but not yet infectious, into the infectious phase, which includes both presymptomatic and symptomatic stages, and finally to recovery, conferring temporary immunity.

Table 1: Simulation Parameters and Contact Probabilities

Parameter Category	Specific Variable	Assigned Value / Range	Distribution Type
Demographic	Total Agent Population	10000	Deterministic
Demographic	Student to Staff Ratio	4.0	Deterministic
Spatial	Classroom Density Limit	1.5 to 2.5 sq meters	Uniform
Behavioral	Daily Campus Dwell Time	6.0 to 14.0 hours	Normal
Epidemiological	Base Transmission Risk	0.015 to 0.045 per tick	Log-Normal
Epidemiological	Asymptomatic Fraction	0.35	Deterministic
Environmental	Ventilation Modifier	0.5 to 1.5	Categorical

4. Simulation Results and Epidemiological Analysis

4.1 Baseline Campus Reopening Scenarios

The first phase of our analysis establishes a baseline by simulating a complete, unmitigated campus reopening, mirroring operational protocols standard prior to pandemic conditions. Under this scenario, all ten thousand agents adhere to pre-pandemic schedules, with classrooms and residential halls operating at maximum capacity and no behavioral interventions such as masking or mandated social distancing in place. The results from fifty stochastic iterations of this baseline scenario demonstrate a rapid, virtually uncontained spread of the pathogen throughout the synthetic population. The infection curve typically exhibits a steep exponential growth phase within the first three weeks of the semester, rapidly depleting the susceptible pool. In these baseline runs, the peak infection rate frequently coincides with the fourth week, at which point up to thirty percent of the total campus population is concurrently in the exposed or infectious state. This massive surge in localized incidence severely overwhelms the simulated capacity of campus health services and quarantine facilities [21].

A detailed spatial analysis of the transmission events in the baseline scenario unequivocally identifies the primary drivers of the outbreak. Contrary to models assuming uniform risk, our agent-based tracking reveals that transmission is profoundly clustered in specific architectural bottlenecks and social hubs. Large introductory lecture halls, characterized by high density and prolonged occupancy durations, function as the primary engines for inter-cohort transmission. An infected student attending a three-hundred-person lecture can act as a bridge node, seeding the pathogen across multiple distinct social and residential networks simultaneously. However, while academic spaces initiate broad dissemination, residential dormitories serve as the amplifiers of the outbreak. The intense, prolonged, and largely unmonitored contacts occurring within shared living spaces and communal bathrooms facilitate extremely high secondary attack rates. The data shows that once the pathogen is introduced into a specific dormitory wing via an academic contact, it almost inevitably saturates that micro-population within days. This finding underscores the acute vulnerability of dense residential settings and confirms the hypothesis that mobility heterogeneity—specifically the cyclical movement between massive academic mixing hubs and dense residential amplifiers—is the fundamental structural vulnerability of the campus ecosystem [22].

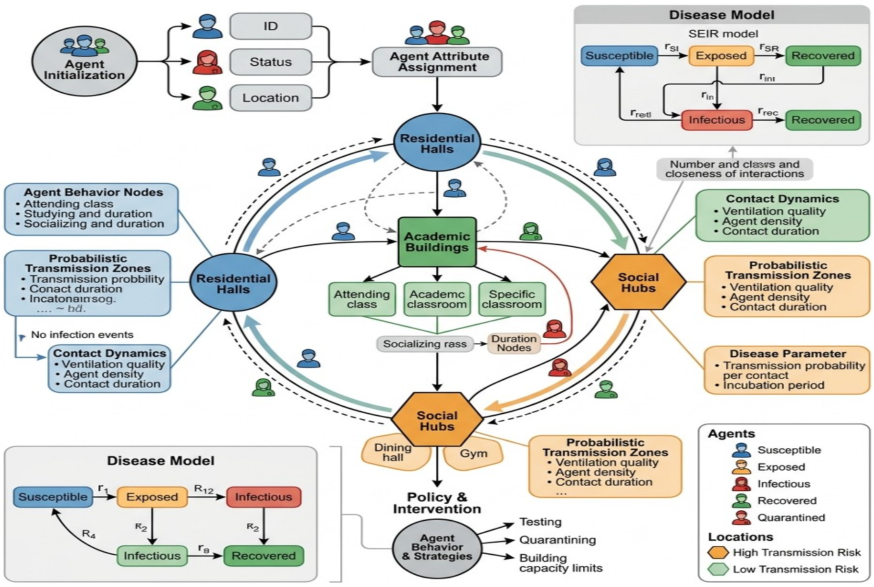

Figure 1: Comprehensive Schematic of Agent

4.2 Impact of Targeted Mobility Restrictions

Following the establishment of the baseline, we simulated the implementation of various targeted mobility restrictions to evaluate their efficacy in flattening the epidemic curve. The most prominent intervention tested was the hybrid instructional model, wherein all classes exceeding a fifty-student capacity threshold were transitioned to entirely remote formats, while smaller seminars and laboratory sessions remained in-person. This intervention fundamentally restructures the campus mobility network. By eliminating the massive, dense gatherings in large lecture halls, the intervention effectively shears the most highly connected edges from the contact graph [23]. The simulations demonstrate that this single, targeted restriction profoundly alters the epidemic trajectory. The peak concurrent infection rate drops dramatically, often by more than sixty percent compared to the baseline, and the time to peak is significantly delayed, affording institutional health systems critical lead time to manage severe cases and conduct contact tracing.

Crucially, the data reveals that the reduction in disease transmission is non-linear relative to the reduction in total campus mobility. Transitioning large classes to remote learning may only reduce the total number of daily physical interactions on campus by twenty percent, yet it curtails total infections by a vastly disproportionate margin. This non-linearity proves that all mobility is not equally hazardous; restricting the specific movements that connect disparate subpopulations yields exceptionally high returns for public health. We also simulated staggered scheduling protocols, which divide the student body into cohorts that alternate days for in-person campus access. This approach effectively halves the spatial density of all campus facilities on any given day. While effective at reducing overall transmission, the simulations indicate that staggering is less efficient than targeted hybrid models, as it disrupts the educational experience for all students uniformly without specifically neutralizing the highest-risk spatial hubs [24]. Furthermore, when examining the impact of restricting communal dining and transitioning to grab-and-go meal services, the model recorded a substantial decrease in sporadic, un-networked transmission events, further isolating the spread to known, traceable residential clusters. These comparative analyses forcefully argue against uniform, blanket campus closures in favor of precision interventions that surgically remove the structural catalysts of superspreading events while preserving lower-risk educational functions.

5. Conclusion and Policy Implications

5.1 Summary of Findings

This study utilized a highly granular agent-based modeling framework to elucidate the complex relationship between mobility heterogeneity and infectious disease transmission within the context of a university campus reopening. By simulating the intricate daily routines of thousands of diverse agents, we demonstrated that the assumption of homogenous mixing fundamentally misrepresents the epidemiological reality of structured educational environments. Our findings establish that campus outbreaks are not driven by average interactions, but rather by the specific, routine convergence of individuals at distinct spatial and temporal bottlenecks. In unmitigated scenarios, large lecture halls act as critical dissemination vectors, broadcasting the pathogen across disconnected social cohorts, while high-density residential dormitories serve as powerful amplifiers, sustaining intense, localized transmission chains. The simulations provide compelling quantitative evidence that targeted interventions aimed at restructuring these specific high-risk mobility patterns —such as shifting large classes to remote formats and decentralizing dining services—yield disproportionately large reductions in overall transmission. The non-linear relationship between mobility reduction and epidemic control confirms that strategic, data-driven modifications to campus operations can effectively mitigate major outbreaks without necessitating total institutional lockdowns [25].

5.2 Limitations and Future Directions

While the agent-based model presented in this study offers significant insights, it is subject to certain methodological and practical limitations that warrant acknowledgment. Primarily, the model's accuracy is heavily contingent on the assumption of behavioral compliance. In our simulated interventions, agents uniformly adhere to policies such as remote learning directives and isolation protocols. In reality, pandemic fatigue and varying risk perceptions lead to significant non-compliance, which can undermine the efficacy of even the most optimally designed public health strategies. Future iterations of this model must incorporate stochastic compliance parameters, allowing agents to selectively violate protocols based on psychological or demographic variables. Additionally, the synthetic environment, while detailed, relies on generalized architectural archetypes. The specific aerodynamic properties of HVAC systems in individual buildings were approximated using broad categorical modifiers rather than precise fluid dynamics calculations. Future research should seek to integrate computational fluid dynamics into the spatial transmission algorithms to more accurately reflect aerosolized viral dispersion in specific indoor micro-environments. Lastly, the model currently assumes a static pathogen profile. As viruses evolve, variations in infectiousness and immune evasion capabilities emerge rapidly. Subsequent studies must design adaptive epidemiological modules that can update transmission parameters in real-time, allowing university administrators to stress-test their operational resilience against emerging pathogenic variants [26]. Ultimately, advancing these simulation methodologies will remain critical for safeguarding public health while sustaining the core missions of educational institutions in an increasingly unpredictable global health landscape.

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