A Validated Framework for Modelling Infectious Disease Spread in Long-term Healthcare

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***Abstract*—This study presents a real-world validation of localized epidemiological modelling techniques using long-term care data, focusing on COVID-19 spread in a complex multi-floor facility. We adapt an advanced agent-based model framework, previously developed for highly localized settings, to address the unique challenges of smart healthcare in long-term care environments. The validation process incorporates quantitative analysis against real-world outbreak data using statistical tests to compare probability distributions. Qualitative This is a change is further performed on randomly sampled animations. Our methodology addresses computational challenges of simulating large, multi-floor environments by implementing optimized pathfinding algorithms and considering complex disease transmission dynamics. The model accounts for heterogeneous populations of residents, staff, and visitors, each with distinct behavioural patterns and epidemiological responses. Our results found that all simulated outbreak metrics were statistically likely to have been sampled from the same distribution as the validation data. This outcome demonstrates the model's accuracy in predicting disease spread and its practical relevance in guiding interventions. This study bridges the gap between theoretical modelling and practical application in long-term care settings, providing a validated framework for understanding and managing pandemic scenarios in complex healthcare environments. Our findings have implications beyond the current COVID-19 pandemic and long-term care environments, offering a robust methodology for modelling and managing future infectious disease outbreaks in various healthcare settings.**

***Index Terms*—Smart healthcare, agent-based simulation, long-term care, validation, decision support, machine reasoning, risk, epidemiological model, COVID-19, causal network, Bayesian network**

I. Introduction

Previous research laid the foundation for understanding the intricate dynamics of COVID-19 spread within localized environments [1], [2]. These studies emphasized the significance of agent-based models (ABMs) in simulating the disease's transmission, incorporating various factors such as social behaviours, preventive measures, and environmental characteristics [3]. The integration of these models with smart healthcare approaches has enabled more precise monitoring and management of disease spread, particularly in vulnerable settings where data-driven decision-making is crucial.

This paper introduces a novel validation approach for the developed ABM framework. The validation process is crucial, as it ensures the reliability and accuracy of the model in predicting and analyzing the spread of COVID-19 under different scenarios. We aim to bridge the gap between theoretical modelling and practical application, ensuring that the model can be a valuable tool for policymakers and healthcare administrators.

The ongoing COVID-19 pandemic has highlighted the variability of virus spread in different settings, necessitating models that can adapt to these variations [4], [5]. The developed ABM framework, previously applied to university research labs and elderly care facilities, demonstrated the effectiveness of various interventions, including mask-wearing and vaccination [1], [2]. However, to enhance the model's utility and relevance, validation against real-world data is critical. This paper aims to validate the model using data from long-term care facilities operated by our partner, the Brenda Strafford Foundation (BSF).

The modelling of COVID-19 spread in long-term care facilities presents unique challenges that distinguish it from other environments. These facilities house a particularly vulnerable population, with residents often having multiple comorbidities and weakened immune systems, making them more susceptible to severe outcomes from COVID-19 infection [6]. The close-quarters living arrangements and high-touch care required in these settings create conditions conducive to rapid disease spread [7]. Additionally, the frequent rotation of staff members and the potential introduction of the virus from visitors adds complexity to the modelling process. The cognitive impairment of some residents may also impact their ability to adhere to infection control measures, further complicating containment efforts [8]. These factors necessitate highly specialized and adaptable models that can account for the unique dynamics of long-term care environments.

Simulation validation techniques are complex and highly application-specific. These techniques can be utilized in both subjective (qualitative) and objective (quantitative) manners, with notable examples itemized below [9].

- **Animation:** Graphically display the model's operational behaviour over time.
- **Degenerate tests:** Assess model behaviour under extreme or boundary conditions.
- **Event validity:** Compare the occurrences within the

simulation model to those in the real system.
- **Extreme condition tests:** Examine the model's plausibility under extreme conditions.
- **Face validity:** Involve expert opinion on the model's reasonableness.
- **Historical data validation:** Utilize historical data not used in model development to test model behaviour.

These techniques aim to explore various facets of model behaviour and output. Ensuring model components agree closely with real-world data and behaviours validates the simulation's accuracy and reliability for its intended application [9], [10].

Given these challenges and the critical importance of protecting vulnerable populations in long-term care settings, this study aims to address the following research questions:

1) How accurately can the agent-based model predict the spread of COVID-19 in a real-world long-term care facility?
2) To what extent does the model capture the unique dynamics and challenges of disease transmission in long-term care environments?

This research contributes to the broader field of epidemiological modelling by offering a validated tool for understanding and managing infectious disease outbreaks. The implications of this study extend beyond COVID-19, providing insights and methodologies applicable to future infectious disease outbreaks in arbitrary local environments. The paper is structured as follows: the proposed methodology is described in Section II, experimental results, observations, and discussion are provided in Section III, and Section IV summarizes our findings and future directions.

II. Methodology

This study employs a comprehensive methodology for epidemiological simulation validation using real-world disease outbreak data. Our approach integrates data acquisition and analysis from the BSF's Bow View Manor long-term care facility, scenario configuration for this complex multi-floor environment, ensemble simulation to capture stochastic variation, and rigorous validation techniques. We use quantitative and qualitative methods, including statistical tests and expert review, to assess the model's accuracy and practical utility. The methodology aims to bridge the gap between theoretical modelling and real-world application, providing a validated tool for understanding and managing infectious disease outbreaks in arbitrary localized environments.

A. Data Acquisition and Analysis

The BSF facility provides the data we use for this validation study from its Bow View Manor location. The BSF is involved in various scientific and medical research studies with multiple research institutions. This experience in research makes the BSF facility a suitable candidate for performing real-world validation on the simulation framework. Bow View Manor is a long-term care facility in Calgary, Alberta, with a maximum occupancy of 237 residents. The scope of this data includes time-series infection tracking, resident and staff demographics, population schedules, and facility occupancy statistics.

For time-series outbreak tracking, BSF staff record the resident unit, symptoms experienced, date of initial COVID-19 test, date of subsequent COVID-19 test, and test outcomes. For facility staff, the organizational position and last-worked date were additionally recorded. Due to the nature of long-term care, many of the residents in Bow View Manor are immunocompromised, increasing the risk of disease transmission and more severe infection outcomes. Isolation protocols for infected individuals are implemented as a risk mitigation strategy, and staff track daily disease progression. Resident schedules are altered during disease outbreaks to minimize group activities and mitigate further infection risk.

Disease tracking and statistics have been provided for all outbreaks from October 2022 to June 2024. BSF staff recorded eight outbreak events during this period. Summary statistics detailing key outbreak metrics, including duration, frequency, and severity of epidemiological outcomes, are calculated. The distributions of these metrics are computed for quantitative analysis. Individual patient disease progression and outcome statistics are also explored.

B. Scenario Configuration

Previous studies introducing the localized simulation framework and integrating decision support utilized the Biometric Technologies Lab space at the University of Calgary as the scenario map [1], [2]. This space is $\sim 100m^2$, significantly smaller than the 237-resident Bow View Manor. Agent pathing through the environment is achieved using computational optimization techniques such as the bi-directional A* (A-star) algorithm [11]. This algorithm experiences complexity scaling given by $O(b^d)$ where d represents the length of the shortest path and b is the branching factor [12]. This results in complexity that is exponential with respect to graph size, becoming computationally intractable for large graphs [13]. Comparing the graph size of Bow View Manor to the proof of concept, the number of nodes increases from $\sim$10,000 to $\sim$720,000. The algorithm scales linearly with the number of agents, which increases to $\sim$400 compared to $\sim$10. Techniques for simplifying this problem into smaller sub-problems, such as transit node routing or hub labelling, allow the problem to be computationally tractable with larger graphs [14], [15]. Parallelism addresses the computational load introduced by adding agents to scenarios. Bow View Manor is additionally structured as a multi-floor complex. This structure requires special consideration when simulating ventilation, airborne disease spread, agent pathing, and environmental interactions. Graph construction for multi-floor environments introduces node branching beyond the standard two-dimensional rectilinear pathing.

The scenario map required for simulation is created based on the floor plan of the respective facility, illustrated in Fig. 1. BSF staff provided floor plan documents for all six (five plus basement) Bow View Manor facility floors. The facility is split into neighbourhood blocks comprised of resident rooms. Hallways and common areas connect these neighbourhoods,

with stairwells and elevators between floors. The west wing of the building spans five floors of resident neighbourhoods above the basement. The east, central, and north wings span two floors of resident neighbourhoods above the basement. The basement contains common areas, offices, and services for staff and residents.

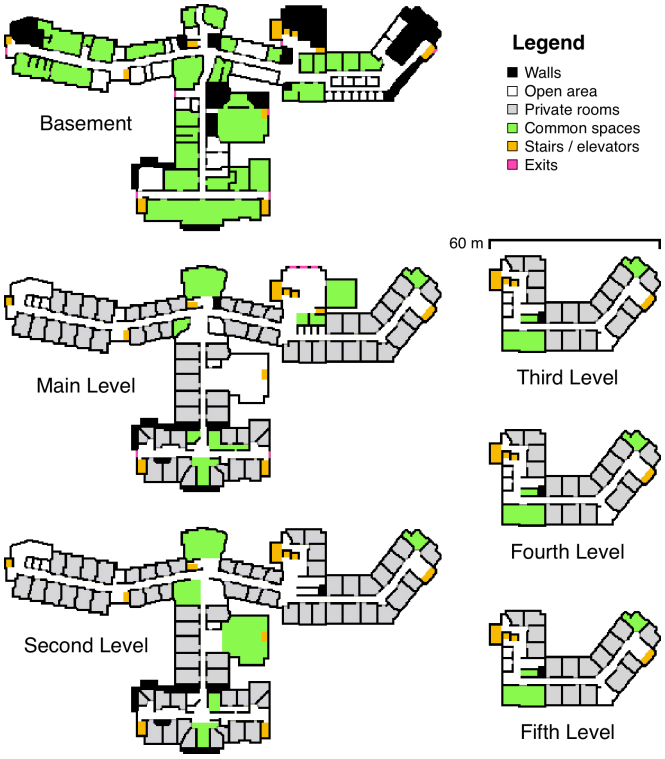

Fig. 1. Bow View Manor facility scenario map for simulation. Note that "common spaces" include professional offices, nursing stations, and other shared environments.

Agent population composition in Bow View Manor is heterogeneous, comprising 236 residents, 98 nursing staff across all positions and shifts, and 64 randomized visitors for simulation. Each agent archetype follows a different daily schedule and exhibits different behavioural patterns. This heterogeneity extends to the epidemiological response for each group.

C. Ensemble Simulation

Ensemble results are critical for generating meaningful statistics and distributions in simulated environments. The inherent stochasticity of ABMs arising from the probabilistic nature of disease transmission, individual behaviours, and environmental interactions necessitates ensembling to capture result frequencies, variance, and extreme outcomes. Statistical summary measures for key epidemiological indicators like infections, outbreak durations, and outbreak frequencies can be directly computed. These measures and underlying probability distributions enable inference for the likelihood of different epidemiological outcomes and their associated risk. For this validation study, we simulated a single scenario with 10,000 ensemble runs informed by data acquired from the BSF.

D. Transit Node Routing

The requirement for ensemble simulations necessitates significant computational efficiency improvements. In previous work, graph traversal for pathfinding accounted for over 90% of simulation runtime on average. This overhead becomes problematic when scaling up to more complex graphs, such as for the Bow View Manor facility. We implemented several optimization strategies to address these limitations. A transit node routing approach was designed to reduce the complexity of pathfinding. A total of 551 transit nodes were identified and placed manually on the graph based on known traffic patterns in the environment. These transit nodes comprise a sub-graph which enables coarse pathfinding within the facility, with an example illustrated in Figure 2. We further employed path pre-computation and caching techniques, allowing frequently used routes to be stored and quickly retrieved rather than recalculated. Implementing these changes resulted in a $\sim$1500$\times$ average reduction in agent pathing computation time. This efficiency allowed for more extensive ensemble simulations, enhancing the statistical robustness and reliability of the modelling results.

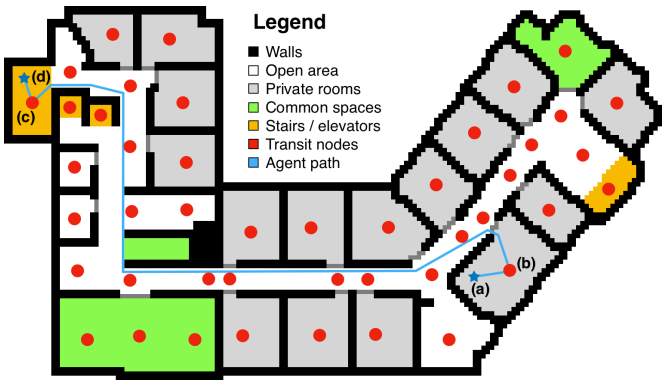

Fig. 2. Transit node routing example using Bow View Manor third floor. Red dots represent vertices in the transit node sub-graph. Blue stars, labelled (a) and (d), represent the start- and end-points of the agent's path, respectively. The nearest proximity transit nodes to each start- and end-point, labelled (b) and (c), are first identified. Path segments (a)→(b) and (c)→(d) are computed along with a coarse path segment between the two transit nodes (b)→(c). These three segments are concatenated to form the full path.

E. Validation and Verification

For the quantitative validation, we compare distributions at the outbreak level, focusing on key epidemiological indicators that capture the overall dynamics of COVID-19 spread in the long-term care facility. Data provided by the BSF includes eight distinct outbreak events characterized by a minimum of two coinciding infections following one or more days with zero active infections. The selected metrics include outbreak duration, outbreak frequency (number of days between outbreaks), and infections per outbreak. These metrics provide a comprehensive view of the disease's behaviour, encompassing outbreak severity and temporal characteristics. We employ two well-established statistical tests to quantitatify the similarity between the simulated and observed distributions: the Kolmogorov-Smirnov (KS)

test and the Anderson-Darling (AD) test [16], [17]. The KS test is sensitive to differences in the location and shape of cumulative distribution functions. The AD test gives more weight to the tails of distributions, making it particularly useful for detecting differences in extreme values. We calculate both the test statistics and their associated p-values for each metric. This approach evaluates the model's ability to reproduce the observed outbreak characteristics, providing a robust foundation for assessing the model's validity and predictive power. We additionally explored Kullback–Leibler (KL) divergence but did not include it in the results for this study.

Qualitative validation of the model involved reviewing animations generated from randomly sampled simulation results. This process allowed for a visual assessment of key simulation elements, including agent pathing, behaviour, interactions, and disease transmission mechanics. Observers examined these animations to verify that agents moved realistically through the multi-floor environment, following expected routes and respecting physical barriers. Agent behaviour was scrutinized to ensure it matched the typical routines of residents, staff, and visitors in the facility. Interactions between agents and disease transmission events were closely monitored to ensure they adhered to epidemiological rules such as proximity-based transmission and intervention measures. This review helped identify any discrepancies or unexpected behaviours that might require further refinement.

F. Causal Analysis and Risk Assessment

Preliminary results for the simulated scenario used in this validation study were analyzed using decision support tools and protocols developed in previous studies [2]. Risk assessment for various epidemiological outcomes was conducted, and the results were contextualized against previous studies. These results are briefly discussed in Section IV but are reserved for further investigation.

III. Results

Validation results for this study are presented as Quantitative Analysis, which compares simulated outbreak metrics to real-world data using statistical tests, and Qualitative Analysis, which summarizes observer feedback on the model's operation and accuracy. These analyses collectively evaluate the model's predictive accuracy, practical relevance, and potential for guiding intervention strategies. Study limitations are also discussed.

A. Quantitative Analysis

The quantitative analysis of our validation results showed a statistically significant alignment between the simulated results and real-world data from the Bow View Manor facility. Figure 3 presents a timeline of outbreak events, differentiating staff and resident infections, along with fatality and hospitalization events. This visualization provides an overview of outbreak characteristics within the facility.

Figures 4 to 6 graphically compare simulated and real-world distributions for outbreak duration, frequency, and

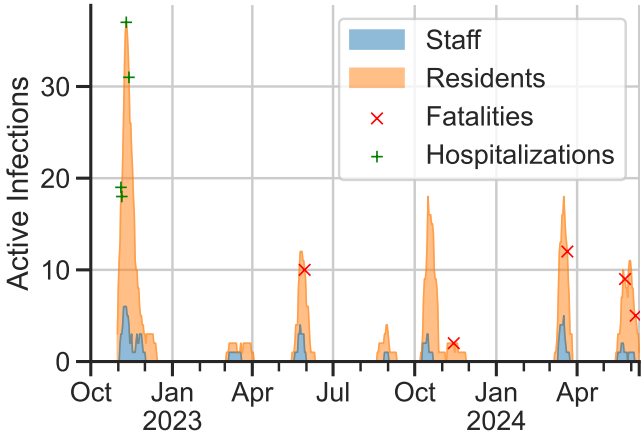

Fig. 3. Real-world outbreak data collected from the Brenda Strafford Foundation (BSF) Bow View Manor long-term care facility. Staff and resident infections are delineated and stacked in the area chart. Fatality and hospitalization events are overlaid.

infections per outbreak, respectively. Each of these quantities has a defined minimum "physical" threshold. These thresholds are seven days for outbreak duration, one day for outbreak frequency, and two active coinciding infections. Visualizations use kernel density estimation with threshold constraints to approximate probability densities for each distribution. The KS and AD tests were applied to assess the similarity of these distributions, reporting both the statistic and corresponding p-value. A statistic value of 0.0 and a p-value of 1.0 denote identical sample distributions. The null hypothesis states that both BSF data and simulated results were sampled from the same underlying distribution.

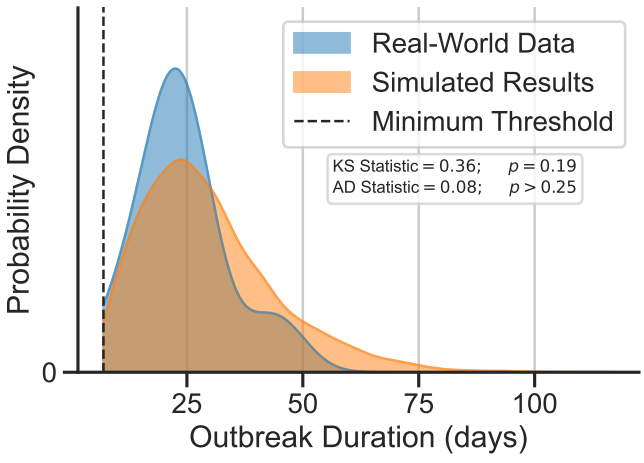

Fig. 4. Comparison of outbreak duration distributions. Kolmogorov-Smirnov (KS) and Anderson-Darling (AD) statistics are reported.

For outbreak duration, the KS test returned a statistic of 0.36 with $p = 0.19$, while the AD test returned a statistic of 0.08 with $p > 0.25$. These results suggest that there is no significant difference between the simulated and real-world distributions, and the null hypothesis can be accepted.

For outbreak frequency, the KS test returned a statistic of

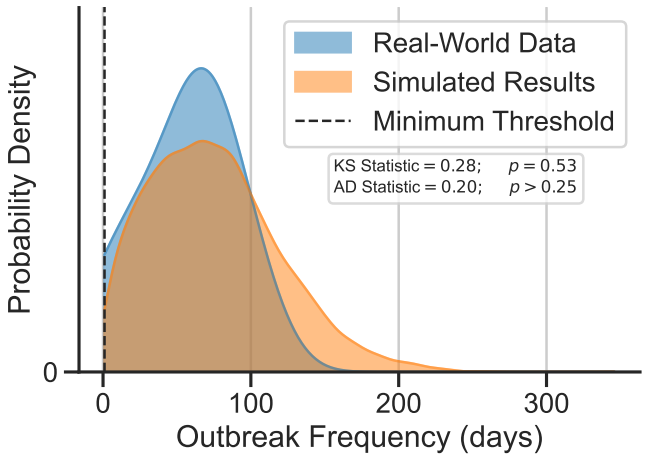

Fig. 5. Comparison of outbreak frequency distributions. Kolmogorov-Smirnov (KS) and Anderson-Darling (AD) statistics are reported.

0.28 with $p = 0.53$, while the AD test returned a statistic of 0.20 with $p > 0.25$. These high p-values indicate a strong similarity between the simulated and observed distributions of time intervals between outbreaks and again allow for the null hypothesis to be accepted.

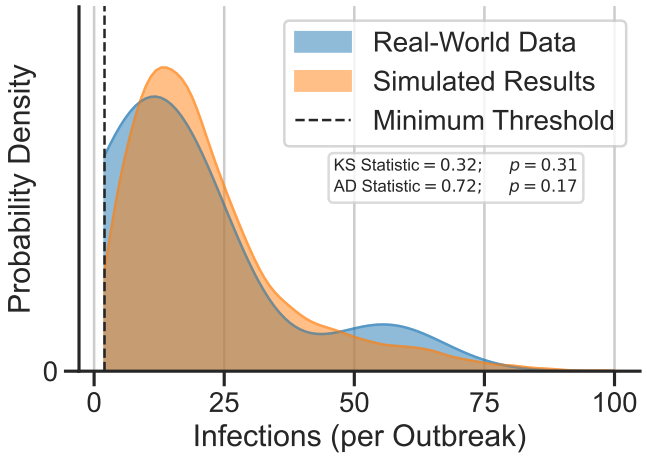

Fig. 6. Comparison of infections-per-outbreak distributions. Kolmogorov-Smirnov (KS) and Anderson-Darling (AD) statistics are reported.

For the number of infections per outbreak, the KS test returned a statistic of 0.32 with $p = 0.31$, while the AD test returned a statistic of 0.72 with $p = 0.15$. Although the AD statistic is higher for this metric, the p-values for both tests remain above the conventional significance threshold of $p = 0.05$, suggesting that the null hypothesis can again be accepted.

These results demonstrate that the simulation successfully captures key epidemiological characteristics of infectious disease outbreaks in the long-term care setting. The consistently high p-values across all metrics imply that the simulated outcomes are statistically similar to the real-world data and likely to be sampled from the same underlying distributions.

B. Qualitative Analysis

Qualitative analysis of randomly sampled simulation animations revealed that the model accurately captured the complex dynamics of epidemiological outbreaks in the Bow View Manor facility. Reviewers observed that agents (residents, staff, and visitors) moved realistically through the multi-floor environment. All agents consistently adhered to physical constraints and followed expected paths. Disease transmission mechanisms functioned as intended, with proximity-based infections occurring in line with implemented epidemiological rules. Agent behaviours and interactions represented those expected in a long-term care setting, including distinct patterns for residents, staff, and visitors. Importantly, even in extreme outbreak scenarios, the model maintained high fidelity without breakdown in its core dynamics. This qualitative assessment complements the quantitative validation, providing confidence that the simulation accurately represents the nuanced realities of disease spread in a long-term care environment.

C. Limitations

This validation study presents results for a simulated scenario; however, the environment scope is limited to the Bow View Manor long-term care facility. Similarities between long-term care facilities operated by the BSF or other organizations allow a straightforward translation of these validation results. These similarities further extend to clinical settings such as hospitals and clinics. The subject behaviour, transmission mechanics, visibility, and degree of control will differ in educational institutions or public facilities. This variability proves challenging to validate due to the extensive assumptions required for unknown parameters in each simulated scenario. Applying this simulation framework to facilities with improved visibility and control over their occupants will provide results with lower uncertainty and more explicit methods for validation.

No analytical solution is available to generate risk distributions associated with simulation outcomes. As such, large-scale validation exercises across arbitrary environments are not feasible due to the explicit requirement of real-world comparison data. This simulation framework will benefit from continued validation exercises following the protocol proposed by this study.

IV. Conclusion and Future Work

This study presents a validated smart healthcare framework for modelling infectious disease spread in long-term care facilities, focusing on COVID-19. The agent-based model, adapted for the complex multi-floor environment of Bow View Manor, demonstrated strong alignment with real-world outbreak data. Quantitative analysis using Kolmogorov-Smirnov and Anderson-Darling tests showed no significant differences between simulated and observed distributions for key epidemiological indicators, including outbreak duration, outbreak frequency, and infections per outbreak. Qualitative analysis confirmed the model's fidelity in representing agent behaviours and disease transmission dynamics. These

findings validate the model's accuracy in predicting disease spread and its practical relevance in guiding interventions. By bridging the gap between theoretical modelling and practical application, this framework offers a robust methodology for understanding and managing infectious disease outbreaks in long-term care settings, with potential applications to various healthcare environments beyond the current COVID-19 pandemic.

Applying decision support protocols defined in previous studies yielded promising preliminary results. Increased pharmacological and non-pharmacological intervention measures resulted in a proportionally decreased excess risk of infection. Due to the larger number of agents in the scenario used for this validation study, a disproportionate reduction in outbreak severity as measured by duration and total infections was observed. Hospitalization and fatality events were also strongly correlated with total infection numbers. These results can be attributed to the increased exposure arising from cohabitation in the environment, as they were not observed when capacity reduction schemes were enforced to reduce agent population density. Further investigation is currently being conducted.

Future directions for improving computational performance and efficiency in agent-based epidemiological simulations include synthesizing results using machine learning (ML) techniques. ML approaches such as Graph Neural Networks have shown promise in modelling epidemic dynamics and predicting outcomes more efficiently than traditional mechanistic models [18]. Large language models could potentially enhance agent-based simulations by enabling more nuanced modelling of agent behaviours and interactions [19]. Leveraging advanced ML methods to learn patterns from simulation results may enable rapid synthesis of epidemiological projections and insights. These ML-based data synthesis techniques represent a promising direction for improving scalability and real-time capabilities in epidemiological modelling tools.

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This research was conducted following the ethical standards of the Conjoint Health Research Ethics Board (CHREB) at the University of Calgary and received approval (Ethics ID: REB22-1159). All data used in this study was aggregated and anonymized by trained staff at the Brenda Strafford Foundation. AI-assisted writing tools (Grammarly and Perplexity AI) were used for grammatical correctness and editing purposes.

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