Corkran *et al. BMC Infectious Diseases* (2025) 25:635
https://doi.org/10.1186/s12879-025-10786-w

BMC Infectious Diseases

RESEARCH

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An agent-based model to assess the impact of shared staff and occupancy rate on infectious disease burden in nursing homes

Kiel Corkran[1], Jose Pablo Gómez-Vázquez[2], Arash Arjmand[1], Miriam Nuño[3] and Majid Bani-Yaghoub[1*]

Abstract

Infectious diseases can propagate between nursing homes through asymptomatic staff members who are employed at multiple facilities. However, the transmission dynamics of infections, both within individual nursing homes and across facilities, has been less investigated. To fill this gap, we developed an agent-based model of two nursing homes extendible to a network of n nursing homes connected with different percentages of shared staff. Focusing on the outbreaks of COVID-19 in U.S. nursing homes, we calibrated the model according to the COVID-19 prevalence data and estimated levels of shared staff for each State. The model simulations indicate that reducing the percentage of shared staff below 5% plays a significant role in controlling the spread of infection from one nursing home to another through personal protective equipment usage, rapid testing, and vaccination. As the percentage of shared staff increases to more than 30%, these measures become less effective, and the mean prevalence of infection reaches a steady state in both nursing homes. The hazard ratios for infection and mortality indicate that nursing homes with higher occupancy rates are more significantly affected by increased staff-sharing percentages. In conclusion, the burden of infection significantly increases with greater staff sharing between nursing homes, particularly in high-occupancy facilities, where transmission dynamics are amplified due to greater resident density and staff interactions.

Keywords Agent-based model, Nursing home, Shared staff, COVID-19, Infection, GAMA

Introduction

The emergence of the SARS-CoV-2 pandemic has left a lasting impact on the world since it began spreading across the world in early 2020. The pandemic strained healthcare services and personnel to their limits in many regions of the world, including the US [3, 4, 45]. It also resulted in stressful states of loneliness, anxiety, depression, and many other issues that impact the life of the individual and collective society [38, 40, 48, 49].

On March 13, 2020, the Centers for Medicare & Medicaid Services (CMS) imposed substantial limitations on entry to nursing homes, essentially imposing a lockdown that restricted access exclusively to residents, staff, and contractors [14]. Despite these regulations, research indicates that COVID-19 mortality rates among nursing home residents were much higher compared to other communities and age groups [27, 36, 46]. There are nearly 44,736 long-term care facilities in the US, of which 15,116 of them are nursing homes and roughly make up 33% of the facility's population [26]. These facilities

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*Correspondence:
Majid Bani-Yaghoub
baniyaghoubm@umkc.edu
[1] Division of Computing, Analytics and Mathematics, School of Science and Engineering, University of Missouri-Kansas City, Kansas City, MO 64110, USA
[2] Department of Veterinary Medicine and Epidemiology, University of California Davis, Davis, CA 95616, USA
[3] Department of Public Health Sciences, University of California Davis, Davis, CA 95616, USA

have more than 1.2 million staff and host approximately 2.1 million residents [26]. During the initial six-month period of the pandemic, nursing homes accounted for over 40% of COVID-19-related fatalities in the United States [24]. In a study of 5,256 US nursing home residents diagnosed with COVID-19, older age, male gender, and the presence of compromised cognitive and physical abilities were identified as risk factors for 30-day mortality [44]. Other risk factors for mortality included facility size, urban location, and a greater percentage of African American residents [25]. Another study revealed that lower health inspection ratings in nursing homes and private ownership were associated with higher COVID-19-related deaths [39]; however, the study did not identify significant variations in COVID-19 deaths among nursing home residents based on race or ethnicity [35]. Nursing homes with higher rates of SARS-CoV-2 infections also experienced higher SARS-CoV-2-related mortality in residents [9]. In contrast to individuals residing in the community at large, nursing home residents exhibit a significantly higher vulnerability to COVID-19 [2, 3, 7, 38, 39]. This can be due to limited mobility and frequent interaction with the same individuals within the nursing home setting and, therefore, transmitting the infection at an elevated rate [51, 54]. In addition to the above-mentioned factors, there have been apparent inequalities in the healthcare (e.g., testing and vaccination) provided for the staff versus the nursing home residents. For instance, it was reported that at the end of January 2021, vaccination levels had a 77.8% median first dose rate among residents, but the median was only 37.5% among staff [24]. In addition, frequent transmission of infection from caregivers or residents who never developed symptoms (i.e., asymptomatic COVID-19 carriers) showed that universal and frequent testing has its own limitations [9, 10]. For instance, a study published in Annals of Internal Medicine revealed that Rapid COVID-19 tests miss 90% of asymptomatic cases [59].

In addition to vaccination rates and vaccine efficacy [7], research shows that staffing levels in nursing homes can directly impact the prevalence and incidence of infections in these facilities [15]. A comprehensive analysis involving 50 million smartphones' geolocation data explored connections between nursing homes [15]. The study revealed that 5.1% of smartphone users who spent at least one hour in a nursing home also visited another facility after nationwide visitor restrictions were enacted in March 2020. This potentially pertains to smartphone users who were staff members rather than visitors. Using cross-sectional regressions, the study showed that staff linkages between nursing homes are a significant predictor of infection outbreaks in nursing homes. Other studies show that the risk of infection is significantly higher among staff working across different care homes than those who were working in the same care home [16], [68]. Nguyen et al. [17] used hybrid system dynamics and agent-based modeling to show that the infection risk is significantly increased both in shared staff and the residents of those nursing homes. They also found that filling vacant positions with staff can lead to more infections and outbreaks than leaving these positions unfilled. Baister et al. [68] use a compartmental modeling approach to study the effects of staff sharing. Using sensitivity analysis, they show that limiting staff sharing between facilities and reducing staff interactions with the general public would greatly reduce the disease burden. Building on the studies mentioned above, the main objective of the present study is to further increase our understanding of the impact of the shared staff on the spread of disease in nursing homes. The occupancy rate, defined as the percentage of occupied beds in a facility, has been positively correlated with higher infection rates due to increased crowding [62, 63]. By developing, validating, and simulating an agent-based disease model, we seek to quantify the impact of varying levels of staff sharing on disease dynamics in two nursing homes with different occupancy rates, one of which is overcrowded relative to the other.

An extensive review of agent-based modeling studies of COVID-19 disease transmission in a nursing home shows that routing testing and vaccination are the most effective control and preventive methods. This includes assessing the effectiveness of routine testing for COVID-19 on both staff and residents [18, 29, 30]. One study found that an optimal strategy to control rapid COVID-19 transmission scenario would be daily testing and immunization of at least one-third of the population or weekly testing and immunizing half of the population combined with a 10-day isolation period for positive cases [26]. Previous research has also suggested that the effectiveness of testing is highly dependent on factors such as test turnaround time, detection thresholds, and the frequency of mitigation testing [37]. Another study found that encouraging staff to vaccinate is not sufficient but may significantly reduce symptomatic cases in residents if a vaccine confers at least some protection against infection or infectiousness [30]. Other model simulations on the transmission dynamic of COVID-19 explore the use of non-pharmacal interventions (NPI), such as personal protective equipment (PPE), in combination with other prevention strategies, such as achieving optimal vaccination levels and testing frequencies. It has been shown that the most common form of NPI prevention strategy, PPE, can substantially reduce mortality in residents if the effectiveness of PPE is above 50% [7, 18]. Another study found that NPI can significantly reduce the spread of COVID-19 and the risk of outbreaks in nursing homes [13]. Summarizing the findings from these prior studies reveals that the transmission dynamics of infectious diseases in nursing homes cannot be attributed to a fixed set of predictors.

Considering the challenges associated with implementing an effective anti-infection program in nursing homes—such as reluctance towards vaccination among staff and residents and the potential for the spread of new strains of infection—the disease modeling can become even more complex when there is a network of two or more nursing homes with caregivers frequently commuting between them to interact with different pools of residents. To address this, we have developed an agent-based model (ABM) that measures the significance of shared staff between two nursing homes. Furthermore, this study takes into account the testing frequency and vaccination levels among residents and caregivers in two nursing homes designed to represent the average conditions found in such facilities in the United States. Our objective behind the creation of this model is to quantify the effect of a limited shared caregiver pool split between two nursing homes using a case study of COVID-19. From there, we want to use simulations of the calibrated model to assess the effects of shared staff on policies that are supposed to effectively reduce the spread of infectious disease among nursing home residents.

The rest of this paper is organized as follows. Sect. "Materials and Methods" provides the details of the model, including the model structure, model parameters and progression of infection. Sect. "Results" provides the details of model validations and simulations, and Sect. "Discussion" presents the primary findings and conclusions.

Materials and methods

Model structure

To simulate the transmission of COVID-19 within a network of two nursing homes where caregivers are employed in multiple facilities, we developed a stochastic agent-based model using two synthetic nursing homes as the basis. These two nursing homes are called Nursing Home 1 (or NH1 for short) and Nursing Home 2 (or NH2 for short). NH1 was given a resident size of 56 people with a staff size of 25 caregivers, and NH2 was given a resident size of 82 people with a staff size of 40. The rationale for choosing specific resident sizes is rooted in the mean number of residents per nursing home in the United States, accounting for variations in resident size across states. The distribution of residents per state was derived from demographic information sourced from the Long-Term Care Community Coalition [41] and [42]. For the fitted gamma probability distribution of residents, see Figure S1 and Table S1 in the supplementary document.

Tables S2 and S3 of the supplementary document provide the number of staff and shifts used for baseline model simulation. The calculation of specific staff sizes for NH1 and NH2 was based on hours per resident per day (HPRD) values. We assumed 3.50 HPRD for NH1 (196 h of care per day for 56 residents) and 3.56 HPRD for NH2 (292 h of care per day for 82 residents). Note that the minimum HPRD requirement for US nursing homes is 3.50 [31]. For a full breakdown of HRPD, staff and resident sizes, number of workers, and type for each shift used in the agent-based model, see Table S4. We set the number of workers for each type of shift and then divided the total number of hours for each worker type by the total number of hours that are needed to be covered to get HRPD for each worker type. Minimal care standards recommended by researchers indicate that for registered nurses (RN), their total HPRD should be 0.75; for licensed practical nurses (LPN), their HPRD should be 0.55; and that registered nursing aids (RNA) should be set at 2.8 [30]. However, research studies indicate that most nursing homes fall short of meeting these standards [19]. The District of Columbia is the only region that mandates this overall staffing level, and merely six states require the presence of a registered nurse 24 h a day, irrespective of facility size [19]. Therefore, we applied staff sizes that were less than or equal to the recommended levels for each staff type.

The constructed model takes account of day-to-day operations within and between two nursing homes (NH1 and NH2) in a period of three months. Figure 1 illustrates a schematic representation of the location of bedrooms with up to three residents per room and quarantine rooms reserved for residents. Other locations include recreation areas, which, for the purposes of our model, are currently off-limits to residents and staff interactions. Both nursing homes have the same layout to reduce the variability that could arise from structural differences between nursing homes.

Agents in the model include nursing home residents and caregivers divided into three different types of caregivers: RN, LPN, and RNA. Services that caregivers provide include basic medical care, ensuring patient comfort, helping with activities of daily living, discussing health care and treatment plans, and reporting vital patient information [53]. Note that RNs differ from the LPN and NRA as their duties are more administrative based rather than duties that involve directly working with residents. For example, typical duties that an RN would include administering medication and treatment to residents, working with doctors to coordinate care

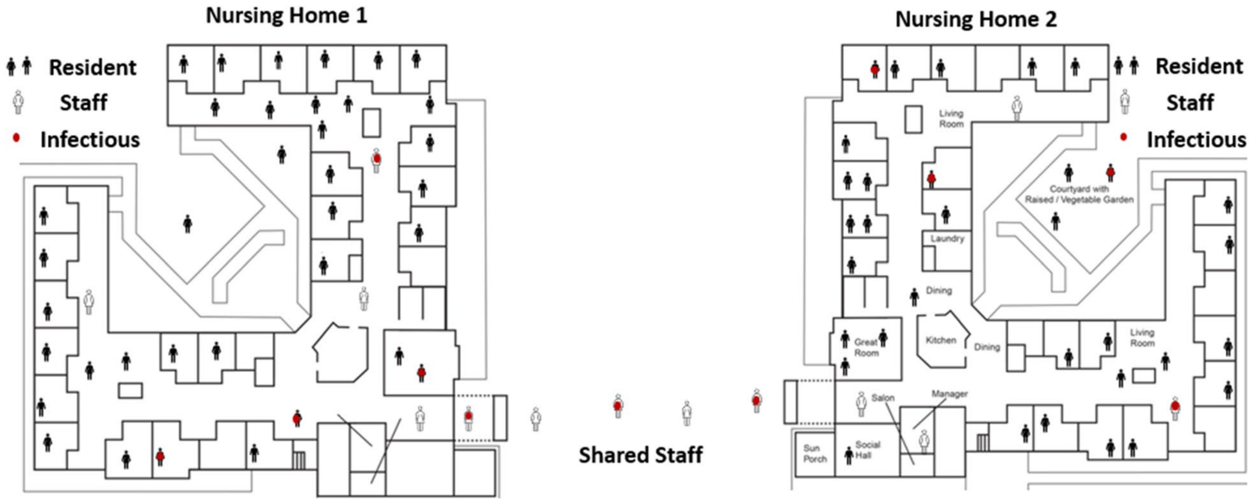


Fig. 1 The floor plan for two nursing homes (NH1 and NH2) considered in the agent-based model. Agents can be susceptible, infectious, or recovered. For each simulation, a certain percentage of staff is shared in both nursing homes. Staff are divided into three different types: registered nurses (RN), licensed practical nurses (LPN), and registered nursing aids (RNA)

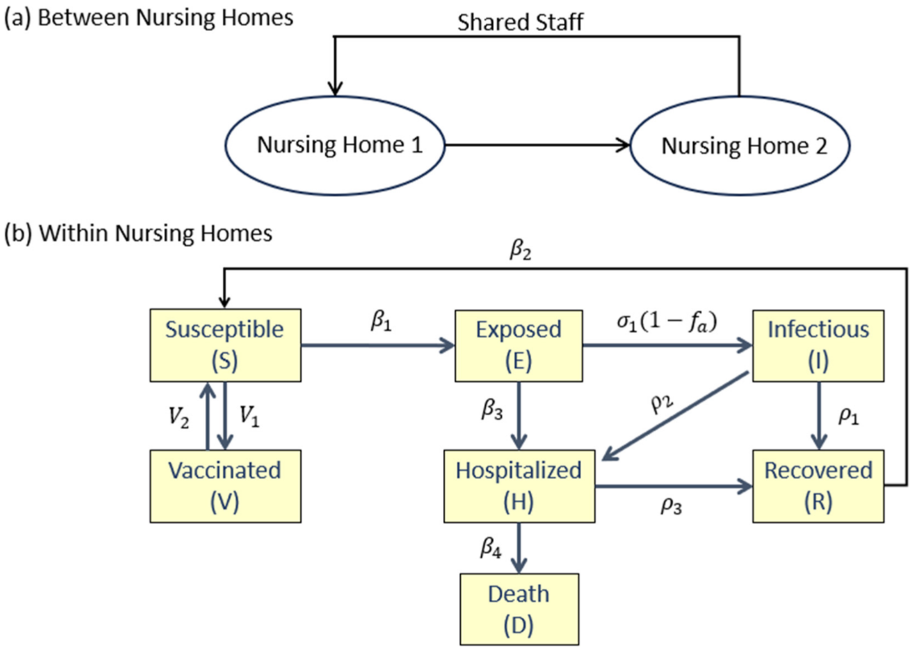


Fig. 2 Schematic diagrams of the proposed Agent-Based model. **a** COVID-19 infection can spread within each nursing home by infectious residents and staff. It can also spread from one nursing home to another by asymptomatic staff members working in both nursing homes, (**b**) Residents of each nursing home can enter each state according to their vaccination and health status

plans, performing diagnostic tests, and overseeing other nursing staff [53].

Figure 2a shows that the infection can be transmitted from one nursing home to another by asymptomatic staff members working in both nursing homes. The disease transmission dynamics associated within and between the two nursing homes were assumed to follow the Susceptible-Exposed-Infectious-Recovered (SEIR) compartmental framework. This SEIR model consists of seven different compartments of susceptible, exposed, infectious, vaccinated, hospitalized, recovered, and deceased residents. We assume that staff members who show COVID-19 symptoms will stop working immediately. Figure 2b shows the compartmental SEIR diagram within each nursing home.

Our agent-based model assumes that infected residents are not replaced by new residents during the simulation. They either remain quarantined within the facility or are transferred to a healthcare facility. Caregivers who become infected with SARS-CoV-2 are replaced with susceptible staff members. Recovered agents remain immune from infection over the course of 120 days with an assumed exposed period of a logarithmic normal distribution [33]. A complete summary of baseline parameters and corresponding references can be found in Table 1.

Disease dynamics

When an infectious agent comes in contact with a susceptible agent, the transmission of the virus between the two is assumed to follow a Bernoulli probability distribution (i.e.,$P(y_i = 1|x_j = 1) \equiv p_t$ with $y_i = 1$ representing susceptible agent (y_i) becoming infectious, given the agent x_j being in an infectious state. The variable p_t of the ABM is calculated per agent at each time step of the simulation using the following formula.

$$p_t = \frac{e^{\ln(OR_\omega X_\omega)+\ln(OR_\pi X_\pi)+\ln(OR_\nu X_\nu)}}{1+e^{\ln(OR_\omega X_\omega)+\ln(OR_\pi X_\pi)+\ln(OR_\nu X_\nu)}} \tag{1}$$

where the odds ratio $\omega(OR_w)$ stands for the model's global baseline transmission probability of both caregivers and resident's agents, the variable $\pi(OR_\pi)$ is a value that represents the odds of transmission reduction due to PPE use, and X_π represent the effect upon transmission caused by the presence of PPE. The term ν (O R_ν) represents the odds of transmission reduction due to vaccination and X_ν represent the effect upon transmission caused by the vaccine status.

As suggested by research [40, 47], we assumed that p_t for asymptomatic, presymptomatic, and atypical manifestations of COVID-19 in staff and residents is much higher than p_t for symptomatic individuals. For the preventive strategies, we assumed that testing and isolation measures were already in place. Therefore, infectious agents can transmit COVID-19 only if they have not been detected by a test or isolated from other agents. We assumed a exposed period modeled by a lognormal distribution characterized by a mean duration of 7 days [33]. After the end of the exposed period, an agent will enter the infectious state where, on average, 39% of agents will remain in an asymptomatic state until recovery [21]. After the exposed period, on average, 23% of the infectious agents need hospitalization [6, 20]. The average time spent in a hospital was considered about six days [20].

Agents who were asymptomatic yet never needed hospitalization were set to an average of 15 days for their recovery period [22]. Since we assume that caregivers are replaced once they become infectious with non-infectious replacement, their ability to transmit the infection was no longer considered in the model simulations. We also assumed that when residents contract their primary infection, it will provide them with sufficient immunity throughout the remainder of the time left in our 91-day simulations.

Table 1 A list of the model parameters values and descriptions that reflect disease transmission dynamics within and between nursing homes[f]

Symbol	Parameter description	Mean value	Refs
$\boldsymbol{f_a}$	Proportion of asymptomatic individuals	0.39	[21]
$\boldsymbol{\sigma}_1$	Probability of shedding	0.38	[33]
$\boldsymbol{\beta}_1$	Infection transmission rate for residents	0.15[a]	[25, 33]
$\boldsymbol{\rho}_{\mathbf{h}}$	Proportion of hospitalized residents	0.23	[6, 20]
$\boldsymbol{\beta}_4$	Mortality rate among hospitalized residents	0.26[b]	[43, 56]
$\boldsymbol{\rho}_1$	Recovery rate = 1/duration of infection	1/15 days[c]	[12]
$\boldsymbol{\rho}_3$	Percent recovery among hospitalized residents	40.7%[b]	[43, 56]
$\boldsymbol{V}_1$	Percent vaccinated for residents (and staff)	70.5%, (40.1%)[d]	[57]
$\boldsymbol{V}_2$	The period until vaccine-induced immunity wanes	87 days[e]	[58]

[a] The transmission rate in Nursing Home 1 was assumed to be slightly lower than that of Nursing Home 2, reflecting differences in management practices and quality of care (mean value of 0.14 versus 0.15)

[b] Hospitalization and mortality rates vary greatly among nursing homes [38]

[c] In most Nursing homes, residents were classified as recovered after a minimum of 14 days from the symptom onset and provided that two consecutive tests for SARS-CoV-2 were negative [12]

[d] Percent values greatly fluctuate across states and time periods. For instance, as of January 2024, only 38% of residents and 15% of staff have received the new vaccine. Meanwhile, 50% of residents and 22% of staff received their vaccination series in 2022 [57]

[e] This is the estimated value for the Omicron variant

[f] Values of $\boldsymbol{\beta}_2$ and $\boldsymbol{\beta}_3$ are assumed to be zero. Parameter values for $\boldsymbol{f_a}$, $\boldsymbol{\sigma}_1$, $\boldsymbol{\rho}_1$ and $\boldsymbol{V}_2$ are both for staff and residents

Staff and resident interactions

Our agent-based model consists of two main types of agents: the residents and the caregivers. We assumed that nursing homes follow strict visitor restrictions and, therefore, the transmission of infection from visitors to staff or residents is negligible. For each nursing home, we limit resident size per room to three while assigning separate rooms for the quarantine of infected residents or for residents to be isolated for specialized care. The number of residents per quarantine room is limited to one at a time, with a total of 10 rooms split evenly between NH1 and NH2.

Individual nursing home parameters are described in Table 1, and a description of the combined distribution of staff types can be found in Table 2. Each simulation assigns a percentage level of shared staff between NH1 and NH2 by taking the total number of shared staff found in Table 2. The percentage value is then used to determine how many of each type of staff will be distributed among the agents who make the shared staff group.

Since our staff consists of three different types of nurses (i.e., RN, LPN, and NRA), we assumed different daily contact patterns with residents (see Table 2). To translate these patterns into simulations, we parameterized them by establishing a set of contact-per-hour probabilities delineated through the Poisson distribution. For RNA, the mean value Y_1 is equal to 75, suggesting that they interact with an estimated average of 7.5 residents per hour (Table 2). Similarly, for RN, we considered an average value of 6, and LPN our mean value was equal to 10. These parameters were derived by exploring data on the hours of care received per resident/day (HRD) from CMS nursing home databases [13, 41]. For RNs, LPNs, and RNA, who work in both nursing homes, we assumed a Poisson distribution with differing rates to capture the number of weekly interactions with residents and non-shared staff.

All residents were assumed to have a uniform probability of contacting any of the three staff types. Uniform probability was also assumed for the case of a virus being introduced by any of the three staff types. The simulation also assigns the staff to one of three different work schedules that factor in length and time of day as follows. We assumed that 41% work full-time (40 h a week), 37% work part-time (hours worked ≤ 32), and 22% work overtime (hours worked ≥ 40). Also, 40% of staff work the morning shift (7 am to 3 pm), 40% of staff work the evening shift (3 pm to 11 pm), and the remaining 20% of staff work the overnight shift (11 am to 7 am). For simplicity, these assumptions were the same for both nursing homes. When staff are not working at either of the two nursing homes, they are assumed to be spending time in the community. Staff type and shift length are based on a sample of two nursing homes that match the total combined staff multinomial distribution found in Table S3 of the supplementary document.

Interventions

To simplify our model, we only parameterized the most practical interventions to control transmission of SARS-COV-2. These parametrized interventions consist of PPE usage, rapid testing, and vaccination. We considered that staff receive a test every 14 days, while only one resident per room is tested every 14 days. This means that it takes longer than a month for all residents to be tested. PPE's effect in reducing COVID-19 transmission correlates with the shedding rate and disease infection probability parameters. Since our primary objective was to investigate the impact of shared staff on disease transmission, we only used the results of phase 3 clinical test results for

Table 2 Range of parameters used in global sensitivity analysis

Parameter	Description	Range of values
G_p	Global SARS-CoV-2 virus shedding for agents	[0.27, 0.49]
P_{or}	Odds ratio for PPE use in a nursing home	[0.07, 0.20]
T_s	Sensitivity of COVID-19 test	[0.70, 0.90]
R_h	Percent of agents who are hospitalized	[0.15, 0.30]
B_m	Percent of agents who die from the infection	[0.20, 0.40]
A_p	Percent of asymptomatic agents	[0.25, 0.53]
V_1	Percent vaccinated	[15, 90]
V_2	Number of days until vaccine-induced immunity wanes	[67, 129]
Y_1	Number of contacts per hour for RNA agents[a]	[6, 9]
Y_2	Number of contacts per hour for RN agents[a]	[3, 9]
Y_3	Number of contacts per hour for LPN agents[a]	[5, 15]
S_p	Percent of staff who work in both nursing homes	0, 5, 10, 20, 30, 50

[a] These numbers were used to estimate the infection transmission rates associated with staff members

the Pfizer and Moderna vaccines to give an approximation of the vaccination effect (the value was set to 0.043 for the baseline scenario). We considered a vaccination schedule with a 21-day gap between the first and second doses, along with a moderate level of efficacy before the second dose.

For the baseline scenario, we assumed policies for residents, such as limiting resident contact with the community, daily screening of residents, and some use of PPE in nursing homes. For cyclic testing of residents and staff, we increased the time from the standard week to bi-weekly as we wanted to study the impact of shared staff more than interventions. Residents who tested positive were not removed but rather isolated from their roommates.

Shared staff

We used data from existing literature to guide our assumption about the percentage of shared staff [9–11]. Variables captured in the dataset include the number of facilities, number of certified beds, average number of beds per facility per state, total patients' days, number of residents, HPRD, number of COVID-19 cases per state, mean degree, mean strength, total number of cases per state, and average registered nurse. Some studies have estimated the mean degree and mean strength of nursing home networks was estimated using cell phone signals to track staff activity [15]. Specifically, the mean strength value refers to the average total number of smartphones that appear in a nursing home and some other nursing homes, and the mean degree refers to the average number of neighbors that are connected to a nursing home [15]. From this specific dataset, we estimated the distribution of shared staff percentage levels per state. (i.e., assuming a mean degree of one, we divided the total amount of shared staff connections per nursing home by the total nursing staff in a nursing home). From the estimated distribution, we observed that most states have an estimated percentage level of less than 20% and that a large portion of states have less than 10% estimated level of shared staff. Our highest estimated shared staff percentage was about 50%, while roughly four states had shared staff levels estimated between 20 to 35%. The complete breakdown of the estimated shared staff percentage probability distribution can be seen in Fig. 3.

Model implementation, outcomes and reproducibility

We followed the Design Concepts and Details (ODD) protocol for model description and replication [28]. To run simulations for our ABM, we used version 1.9 of the GIS Agent-Based Modeling Architecture or GAMA [50]. For analysis of our simulations, we mainly used the software package MATLAB [26]. Model reproducibility is a crucial aspect of scientific research and computational modeling, emphasizing the ability to recreate and validate results obtained from a given model. To replicate our study, researchers can download and run the source codes at the following GitHub link: https://github.com/Corkran1/NH_COVID Detailed instructions on how to run the codes and how to interpret the outputs can be found in the supplementary document entitled "Instructions to Run Simulations." Simulations were run at 20,000 per shared staff level at a length of 91 days with 3 different controlled seeds for each day. For each of those seeds, the simulation took data points every 3 h with a time series of 720 observations accounting for each simulation. The reason behind the increase in the level of shared staff was based on trends found in the estimated probability distribution of shared staff throughout the United States. Key output variables from our simulation that were measured are prevalence, death rates, individual and basic reproduction numbers, hazard ratios of infection and

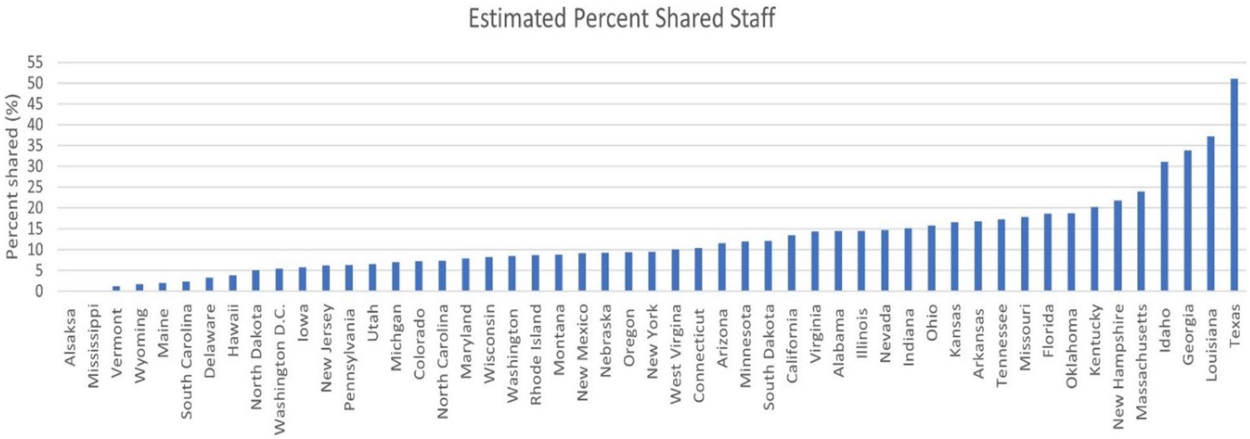


Fig. 3 Estimated percentage of staff working in more than one nursing home facility according to each state

mortality, cumulative number of infected, and number of hospitalizations. In a broad sense, the basic reproduction number (R_0) can be best described as a measure of the transmissibility fitness of an infection in a totally susceptible population [3, 8, 29]. Specifically, R_0 is defined as the average number of secondary infections generated by a single infected individual in a completely susceptible population. If $R_0 > 1$, it indicates that the disease has the capacity to spread within the population, potentially leading to an epidemic. Conversely, if $R_0 < 1$, the disease is likely to die out over time. Similarly, the individual reproduction number (IR_0) is the average number of secondary infections caused by a specific individual over the course of infection [23]. We used this definition to calculate the basic reproduction number as the average number of a specific group (e.g., nurse or resident) at different time steps for infection over the course of each simulation. Applying these definitions to our model, we see that IR_0 deals with how many new infections each agent can cause on its own, while the basic reproduction number represents the average number of infections caused by staff or residents over the course of infection.

Our model was calibrated and validated with data on positive COVID-19 cases reported between May 2021, and January 2023, reported by CMS [13].

Analysis of outcomes and sensitivity analysis

We performed hypothesis testing to determine if simulated outcomes, such as daily prevalence rates, were significantly different from our baseline using parametric and non-parametric methods. This was done to evaluate the qualitative impact of the increasing percentage of shared staff prevalence and incidence of infection. We used MATLAB to generate descriptive statistics and figures on the key variables listed in Table 1 and the prevalence of COVID-19 infection within the nursing home population.

To conduct the global sensitivity analysis, we initially converted the model outputs pertaining to infection prevalence into a binary format. Specifically, instances where the prevalence at a given time fell below the overall average were assigned to a value of zero; otherwise, a value of one was assigned. This binary transformation was performed separately for the prevalence of COVID-19 in the staff population and the resident population. Subsequently, we employed classification and regression tree (CRT) modeling [52] to discern the most influential parameters with respect to residents and staff being infected (coded as 1) and not infected (coded as zero). These analyses were conducted across 50,000 simulations. We used the IBM SPSS statistical software [5] to generate regression trees and obtained a rank of the model's most sensitive parameters. Details of the global sensitivity analysis can be found in the supplementary document Table S5.

Results

Global sensitivity analysis

The results of our CRT analysis showed that model predictions on prevalence percentage are sensitive to complex combinations of existing parameters. As shown in Fig. 4, for both analyses, the number of residents (N) and the number of available beds (B) were the top two important model parameters. This aligns with previous research findings indicating that residents in nursing homes situated in socially deprived areas exhibited an elevated incidence of COVID-19 infection, partly because of a lack of resources and crowdedness and occupancy rate [20, 34]. As demonstrated in the subsequent sections, the prevalence of infection and hazard

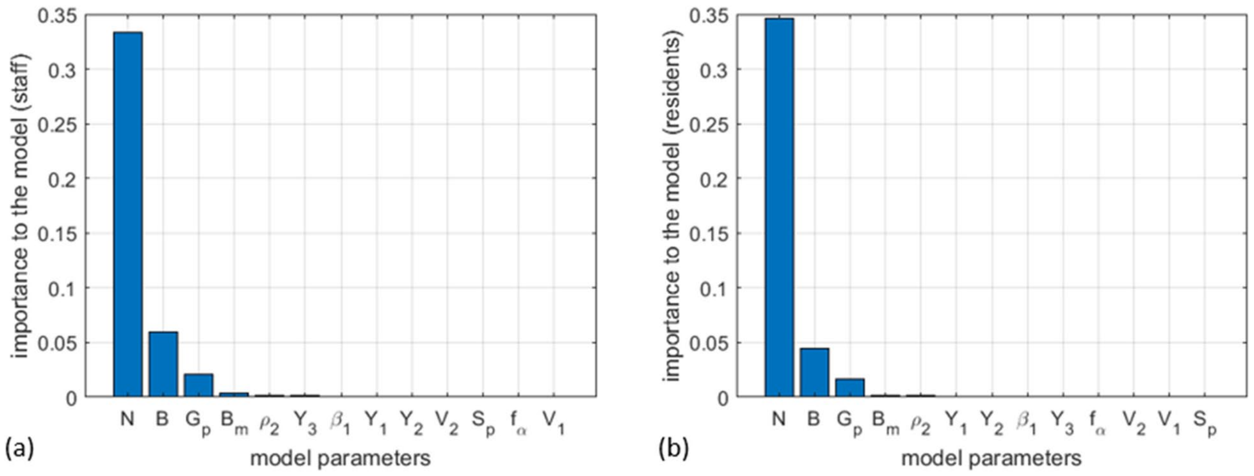


Fig. 4 The independent variable significance ranking based on the (**a**) staff and (**b**) resident COVID-19 prevalence

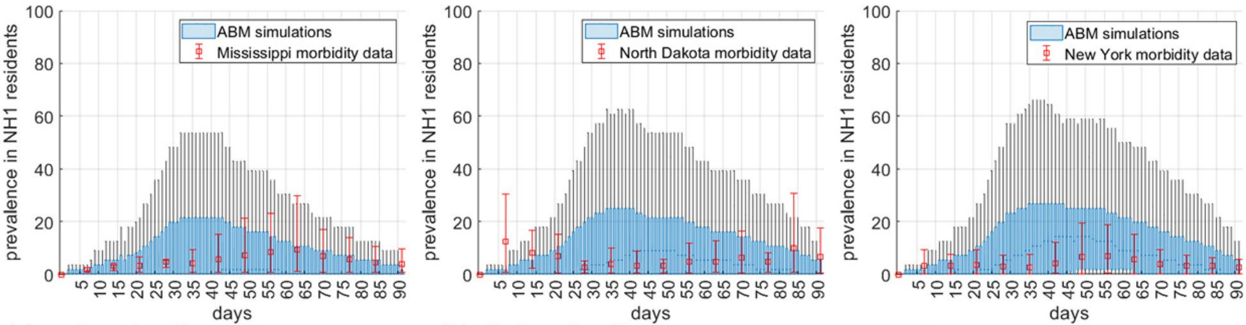
ratios in NH1 are significantly higher, which can be partially attributed to its higher occupancy rate, expressed as $N/(N+B)$. The next three important parameters were the virus-shedding rate (G_p), percent mortality among hospitalized residents (B_{m}), and Percent recovery among hospitalized residents (ρ_2), which is consistent in both CRT models. See Fig. 4 for bar charts associated with the global sensitivity analysis. Also, the overall accuracies of the CRT models (i.e., the proportion of correctly classified cases out of the total cases) were more than 90% (see Table S5b in the supplementary document).

Model validation

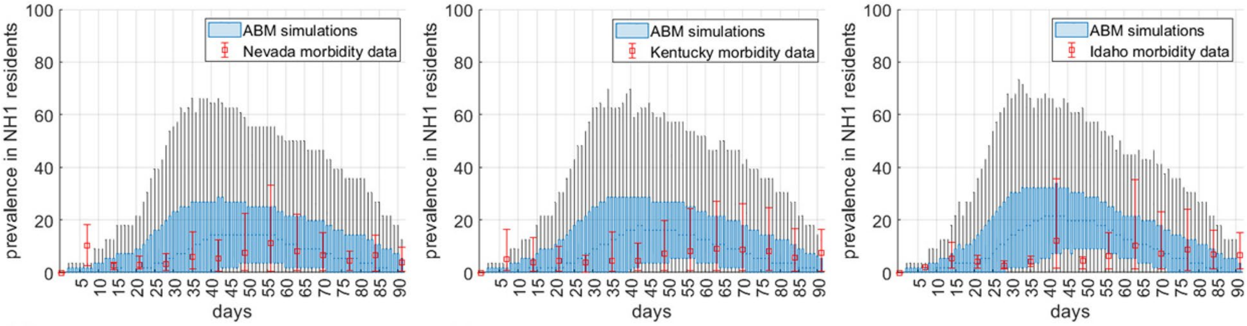
To evaluate the validity of the model, we adopted a broad approach by using data from nursing homes across multiple states rather than focusing on two specific facilities. Extensive simulations demonstrated that the model is generalizable to various pairs of nursing homes that adhere to its core assumptions. Namely, we employed the time series data of COVID-19 prevalence among staff and residents in nursing homes across six different States during the omicron phase of the pandemic (i.e., weeks from November 28, 2021, to February 27, 2022, encompassing a total of 14 weeks). The selection of these States was based on their respective estimated average percentages of shared staff (see Fig. 3). The model simulations were fitted to the time series prevalence nursing home data from Mississippi, North Dakota, New York, Nevada, Kentucky, and Idaho with corresponding 0.15%, 5.13%, 9.50%, 14.73%, 20.15%, and 31.09% estimates of shared staff, respectively. See Figures S2-S4 in the supplementary document for the estimated probability density functions and boxplots of the prevalence data.

The process of model fitting was completed in two steps. First, the prevalence values were iteratively simulated using the GAMA simulation platform, and then Matlab was employed to test the validity and generate the boxplots. Figure 5 presents a comparative visualization of box plots for the model simulations (depicted in blue and gray) alongside the weekly box plots of the prevalence data (depicted in red). While the model fails to capture certain spikes, there is a substantial level of agreement between the box plots of the model simulations and the observed weekly prevalence data. Similar behavior was observed for NH2, as shown in Figure S5 of the supplementary material.

Focusing on the middle 50% of values, represented by the interquartile range (IQR), we employed three metrics to further assess the validity of the model as follows. The Overlap Coefficient (OP), also referred to as the Szymkiewicz–Simpson coefficient [65], quantifies the agreement



(a) no shared staff (b) 5% shared staff (c) 10% shared staff



(d) 15% shared staff (e) 20% shared staff (f) 30% shared staff

Fig. 5 Simulated prevalence boxplots of COVID-19 infection in NH1 residents were fitted to weekly prevalence data of six different states (shown with red bars) associated with the emergence of Omicron variant (weeks from November 28, 2021, to February 27, 2022). There is a fair amount of agreement between the model simulations and the prevalence data between the IQRs of the model simulations and the observations. It is defined as the ratio of the intersection length of the two IQRs to the length of the smaller IQR:

$$OP = \frac{IQR_{Observed} \cap IQR_{Model}}{\min\left(IQR_{Observed}, IQR_{Model}\right)} \tag{2}$$

To evaluate the alignment between the model and the observations, we also calculated the Modified Overlap Coefficient (MOP), which prioritizes the observed data by measuring the proportion of the observed IQR that overlaps with the model IQR. This asymmetrical metric is given by

$$MOP = \frac{IQR_{Observed} \cap IQR_{Model}}{IQR_{Observed}} \tag{3}$$

Unlike the OP, which provides a balanced measure of agreement, the MOP emphasizes alignment with the observed data. Building upon the principles of penalty functions [66, 67] and overlap-based similarity measures [65], we also incorporated a dynamic penalty into the MOP to account for excessively wide model intervals, while still quantifying the overlap. Specifically, the Penalty-Adjusted Overlap Coefficient is given by

$$OC_{PA} = \frac{IQR_{Observed} \cap IQR_{Model}}{IQR_{Observed}} \times \min\left(1, \frac{1}{\gamma\left|\frac{IQR_{Observed}}{IQR_{Model}} - 1\right|}\right), \tag{4}$$

where γ is a positive value that controls the influence of penalty.

Table 3 summarizes the goodness-of-fit results for the ABM, based on the mean values of OP, MOP and OC_{PA}, where values corresponding to NH2 are shown inside the parentheses. For NH1, the model demonstrated high accuracy across states, with $mean(OP)$ values ranging from 0.70 (Idaho) to 0.97 (New York). The $mean(MOP)$ values were slightly lower, ranging from 0.68 (Idaho) to 0.95 (New York). The $mean(OC_{PA})$ values, which account for observed case adjustments, were lower overall but maintained a reasonable range, with the highest value of 0.84 observed in New York and the lowest of 0.63 in Idaho. For NH2, the model showed similar trends, though accuracy was slightly lower in most cases. $mean(OP)$ ranged from 0.69 (Idaho) to 0.95 (New York), while $mean(MOP)$ ranged from 0.65 (Idaho) to 0.94 (New York). The $mean(OC_{PA})$ values for NH2 were slightly higher than those for NH1 in some states, such as New York (0.86) and Nevada (0.84). Overall, the results suggest that the ABM is robust in estimating prevalence for both nursing homes, with some variations influenced by state-specific factors. The higher accuracy in states like New York indicates that the model performs better in environments with more comprehensive prevalence data.

Prevalence of infection

Baseline scenario

In the baseline scenario, we assumed that vaccination was equally distributed, PPE use was low, there was bi-weekly testing, and most importantly, there was no shared staff between the two homes. Under these assumptions, the mean prevalence for 91 days was 6.71% (SD 11.36) and 4.58% (SD 7.76) for nursing homes 1 and 2, respectively (see Table 4). The ABM was initialized with a single infection originating from a caregiver, who was part of the shared staff pool and initially transmitted the infection in NH1 or NH2.

Relation between prevalence and shared staff percentages

Increasing the shared staff levels from 0 to 30% resulted in a significant rise in COVID-19 infection rates in both nursing homes. Thereafter, the rate of increase slowed down, and the prevalence of infection reached an equilibrium for each nursing home (about 79% and 51% for NH1 and NH2, respectively). For instance, as shown in Table 4, an increase of 5% shared staff from the baseline results in a slight increase in mean prevalence to 8.40% from the baseline value of 6.71% in NH1 and a gradual

Table 3 Mean values of the Overlap Coefficient (OC)[a], Modified Overlap Coefficient (MOP) and Penalty-Adjusted Overlap Coefficient OC_{PA} [b] for measuring model performance using the prevalence data from six different states[b]. The values inside the parentheses correspond to model estimations for NH2

[c]Metric/State	Mississippi	North Dakota	New York	Nevada	Kentucky	Idaho
$mean(OP)$	0.89 (0.80)	0.85 (0.80)	0.97 (0.95)	0.91 (0.90)	0.85 (0.84)	0.70 (0.69)
$mean(MOP)$	0.89 (0.79)	0.82 (0.75)	0.95 (0.94)	0.91 (0.90)	0.84 (0.82)	0.68 (0.65)
$mean(OC_{PA})$	0.81 (0.74)	0.72 (0.69)	0.84 (0.86)	0.81 (0.84)	0.77 (0.77)	0.63 (0.61)

[a] The maximum Overlap Coefficient (OC) across all the states is equal to 1

[b] We chose $\gamma = 0.20$ and $\gamma = 0.15$ for NH1 and NH2, respectively

[c] The estimated percentage of shared staff in each state is as follows: Mississippi (0.15%), North Dakota (5.13%), New York (9.50%), Nevada (14.73%), Kentucky (20.15%), and Idaho (31.09%)

Table 4 Descriptive statistics of daily prevalence of COVID-19 infection among residents of nursing homes 1 and 2

Percent of shared Staff	Mean prevalence	Median prevalence	Maximum prevalence	Std of prevalence
Nursing Home 1				
0	6.71%	1.62%	73.21%	11.36
5	8.40%	1.79%	73.21%	12.21
10	9.63%	4.45%	75.36%	12.56
15	9.98%	3.57%	78.57%	12.65
20	10.46%	5.36%	79.21%	12.84
30	11.57%	5.36%	79.21%	13.29
50	11.57%	5.35%	79.22%	13.29
Nursing Home 2				
0	4.58%	1.04%	50.14%	7.76
5	5.74%	1.22%	50.89%	8.34
10	6.58%	2.44%	54.88%	8.58
15	6.82%	2. 44%	53.66%	8.64
20	7.15%	3.66%	50.5%	8.77
30	7.90%	3.66%	50.8%	9.08
50	7.91%	3.66%	51.2%	9.08

increase in mean prevalence from 4.58% to 5.74% in NH2. This pattern of small increases in the daily mean prevalence rates was observed for both nursing homes. After a threshold value near 30%, both nursing homes retained almost the same levels of mean prevalence as before (i.e., mean prevalence of 11.57% and 7.90% for nursing homes 1 and 2, respectively).

Cumulative prevalence refers to the proportion of new infections among the residents or staff population over the course of the study, which spans 91 days. Figure 6 illustrates the time series of mean cumulative prevalence of COVID-19 in residents and staff members for NH1 and NH2. Increasing the level of shared staff significantly increased the mean cumulative prevalence of the infection. For instance, at the level of 30 percent shared staff, the cumulative prevalence among both NH1 and NH2 residents was 60% from days 55 to 90. As the proportion of shared staff increased from 0 to 30%, the mean communicative prevalence among NH1 residents increases, but that of NH2 seems to reach a steady state near 80%. The main reason for such patterns is that NH1 is overcrowded (82 residents with zero vacant beds), and the infection spreads much faster. NH2 is not crowded (56 residents with 26 vacant beds), and therefore, it responds to the increased percentage of shared staff at a slower rate. We also simulated the prevalence of COVID-19 for up to 180 days, where the time series reached endemic values in all cases of shared staff.

Infection and mortality hazard ratios

The increased levels of shared staff directly resulted in increased hazard of death for individuals residing in the

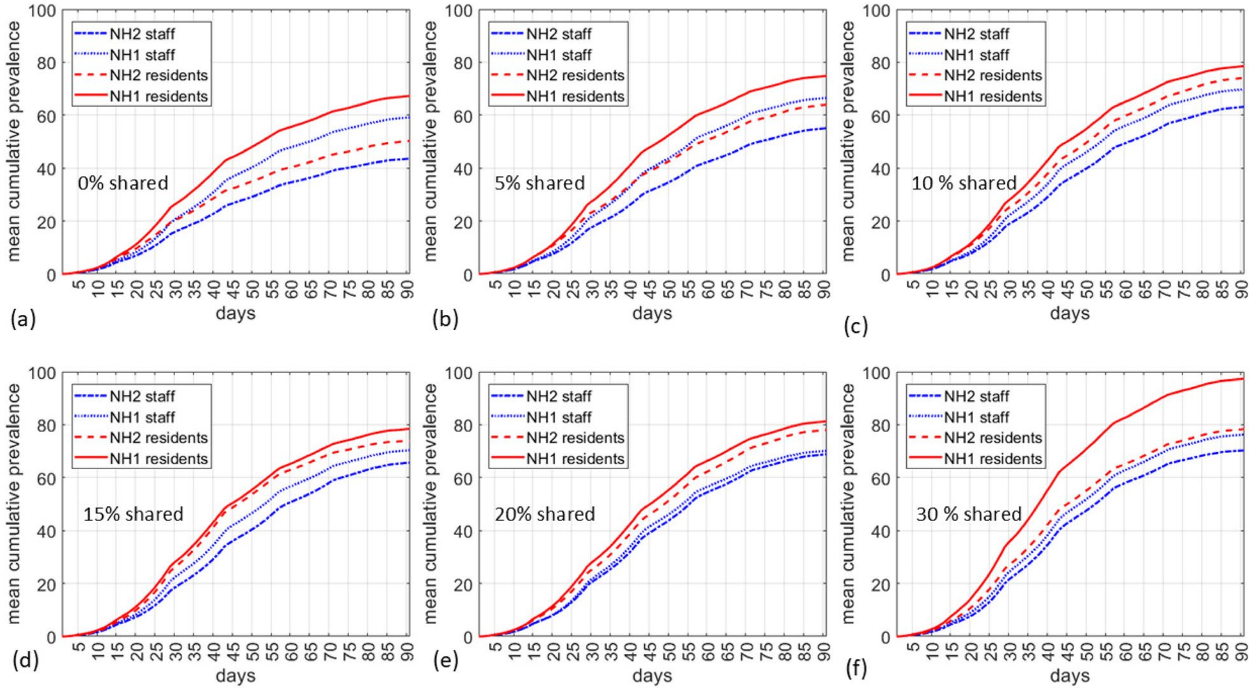


Fig. 6 Simulated cumulative prevalence of COVID-19 among staff and residents of nursing homes 1 and 2. Increasing the shared staff results in an increase in the cumulative prevalence

nursing homes. For instance, at a 5% shared staff level, we observed relatively low values for mortality hazard ratios, with NH1 exhibiting a ratio value of 1.6 and NH2 a value of 1.39 (see Fig. 7a). As the shared staff percentage increased beyond 5%, a pattern emerged, indicating an incremental rise in death hazard ratios for each nursing home. Upon reaching a 50% shared staff level, the mortality hazard ratio for NH1 reached 2.5, while NH2 had a hazard ratio of 1.52. Hence, based on our simulations, individuals—whether residents or caregivers are more prone to mortality due to the increased level of shared staff. This is important because the assumed levels of vaccination could not control the hazard ratios, and it suggests that increasing shared staff can neutralize disease control and preventive measures. Further details on specific mortality hazard ratio values for our shared staff scenarios and Cox regression statistics can be found in the supplementary document, particularly in Tables S8 and S9.

Furthermore, the escalation of shared staff levels also yielded a substantial increase in the likelihood for residents and caregivers in both nursing homes to experience the hazardous event of COVID-19 infection. To illustrate, at the 5% shared staff level, NH1 exhibited an initial hazard ratio of 2.24, while NH2 demonstrated an infection hazard ratio of approximately 1.57 (see Fig. 7b). Analogous to the mortality hazard ratios, an ascending trend is visible in the odds as the level of shared staff percentages increased across our simulations (Fig. 7). In comparison to the mortality hazard ratios, it is noteworthy that at the 30% and 50% levels of shared staff, no significant alterations occurred in the ratio values within our simulations. Consequently, a threshold level of 30% for shared staff was identified as the point at which significant changes ceased to transpire for infection hazards and reached an equilibrium.

Discussion

The present study employs agent-based modeling and simulation to assess the impact of asymptomatic spreaders on nursing home staff and residents. The adverse effects of staff sharing are amplified in high-occupancy facilities, as evidenced by NH1's higher prevalence and hazard ratios compared to those of NH2 (Table 4, Figs. 6 and 7). The study's key contributions are twofold: first, the proposed model is validated using state-level data, enhancing its generalizability and reproducibility; second, it quantifies the impact of critical factors, including staff sharing and occupancy rates, on the burden of infection across nursing homes. Hence, the present work differs from the previous studies that employed modeling strategies to assess the dynamics of infection in a single nursing home. These studies investigate the behavior of individuals through a defined set of rules [35] or investigate the effects of various interventions in a single nursing home facility [18, 22, 29, 30, 37]. Other studies that include more than one nursing home [16, 17] demonstrate that the risk of infection increases as the number of shared staff is increased. The referenced study by Ryskina et al. [64] highlights a correlation between infected residents and staff, which aligns with our findings (see Fig. 6). It also notes that higher occupancy is linked to increased infections in staff, consistent with the higher prevalence of infection observed in NH1 staff compared to NH2 staff. Our simulations indicate that facilities with 5% or more shared staff experience significantly higher hazard

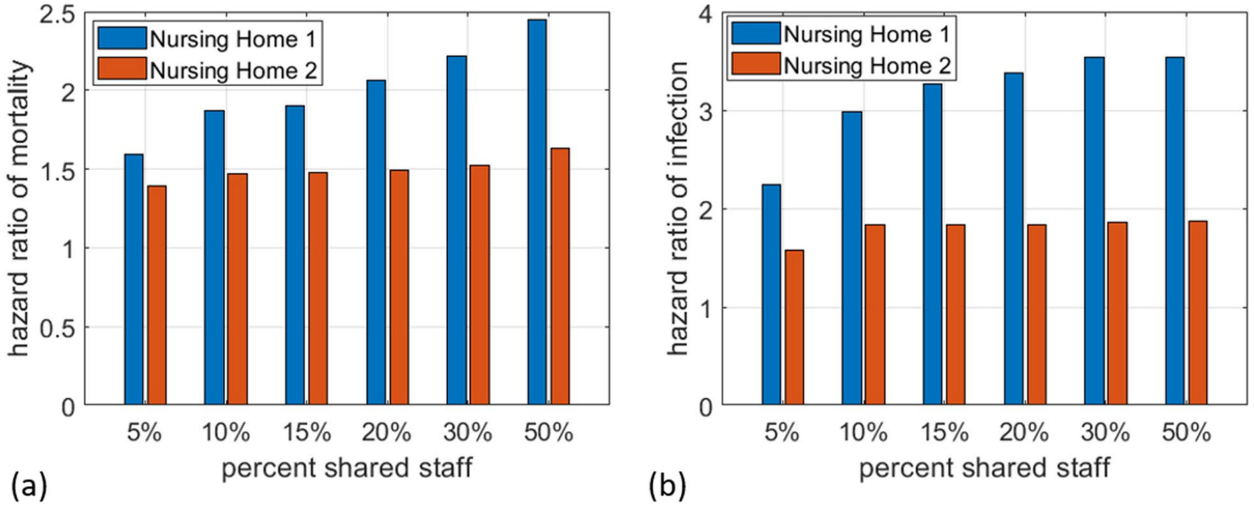


Fig. 7 Hazard ratios of infection and mortality as a function of percent shared staff. The escalation of shared staff levels results in a substantial increase in (**a**) the hazard ratio of mortality and (**b**) the likelihood for residents of both nursing homes to contract COVID-19 infection

ratios for mortality and infection, with the effect being more pronounced in NH1 due to its higher occupancy rate.

The present study lays out the foundations for investigating the global epidemiology of infection in a network of nursing homes connected by shared staff. However, it should be noted that the proposed model has several limitations as follows. We have assumed restricted visitor access in our model, making asymptomatic staff the only external source of infection for residents. This was not the case at the beginning of the COVID-19 pandemic. Hence, the model cannot be applied to cases where visitor restriction is not in place. The model assumes connections only between two nursing homes, despite the potential for multiple nursing homes to be interconnected. Although extending the model to networks of n nursing homes is possible, we anticipate that the computational cost will exponentially increase with the value of n. Also, the calculated reproduction numbers can be divided into four categories resident-to- resident, resident-to-staff, staff-to-resident, and staff-to-staff reproduction numbers. This can enable researchers and decision-makers to identify the most effective control and preventive measures according to each reproduction number. Another limitation of the model is that other staff (such as cleaners, cooks, gardeners, physiotherapists, and administrators) have not been included. These individuals could also contribute to the transmission of infection in nursing homes [15]. We assumed identical layouts for both nursing homes to minimize variability from structural differences. However, real-world nursing homes may have diverse layouts. Another limitation of this study is the assumption of a Poisson distribution for contact patterns within the agent-based model, which does not fully capture the heterogeneity of real-world contact networks.

Health equity refers to fairness and justice in healthcare, ensuring all individuals receive the care they need regardless of circumstances [55]. Sharing staff between nursing homes, especially given minimal HPRPD, can create health equity issues by leading to uneven distribution of care. When staff are stretched thin across two nursing homes, staff burnout can increase, leading to higher turnover and reduced care quality [60, 61]. Tired or overworked staff are less able to provide high-quality, attentive care, particularly for residents with complex needs if staff are constantly moving between two nursing homes. The present study highlights the adverse effects of shared staff in relation to the transmission of infectious diseases, especially during an outbreak in a nursing home with a high occupancy rate (see Sect. "Infection and mortality hazard ratios"). Addressing issues related to inadequate wages and the absence of financial incentives is the first step in enhancing the recruitment and retention of employees [1, 32]. This can mitigate the prevalent staff shortages in nursing homes and reduce the occurrence of staff members working across multiple facilities. While some nurses are actively promoting health equity through educational efforts and advocacy within their professional associations, fostering a more widespread commitment among all nurses can further propel the nationwide advancement of health equity [36, 38]. Therefore, it is imperative for nursing organizations to collaboratively formulate a comprehensive agenda aimed at addressing the social determinants of health and realizing health equity goals [55]. In addition, there is a need for a more nuanced approach to quarantine protocols in nursing homes that balances infection prevention and control with the overall health and quality of life of residents.

In conclusion, limiting the allocation of personnel across multiple nursing home facilities can significantly reduce transmission risks during outbreaks of highly infectious diseases. Further research is needed to fully understand the trade-offs between such restrictions and the operational flexibility during periods of lower outbreak risk.

Supplementary Information

The online version contains supplementary material available at https://doi.org/10.1186/s12879-025-10786-w.

Supplementary Material 1

Acknowledgements
The authors would like to express their sincere gratitude for the thoughtful and constructive feedback provided by the anonymous reviewers.

Authors' contributions
Kiel Corkran was responsible for data acquisition and preprocessing. He performed the primary model analysis and simulations, including statistical validation and parameter estimation. He is the one who actually wrote the paper. Jose Pablo Gómez-Vázquez contributed to the coding and implementation of the disease model in Python/R. He was also involved in the sensitivity analysis and conducted robustness checks on the model's predictions. He also contributed to the interpretation of the model's results and assisted in revising the manuscript for intellectual content. Arash Arjmand reviewed and revised the article. He also helped with the coding and some simulations. Miriam Aracely Nuño contributed to the study's methodology by refining the model's assumptions and reviewing the article. She was responsible for drafting some sections of the discussion, focusing on the implications of the findings for public health policy. Majid Bani-Yaghoub led the conceptualization of the study and developed the mathematical model for disease transmission. He was responsible for the initial design of the computational simulations and wrote the first draft of the manuscript. He also supervised the overall research process and made significant contributions to revising the manuscript.

Funding
This study was supported by the Center for Disease Control and Prevention under grant number 1U01CK000671-01.

Data availability
GitHub: https://github.com/Corkran1/NH_COVID/tree/master/models
The guide to run code is in a separate file called "Instructions to Run Simulations."

Declarations

Ethics approval and consent to participate
The UMKC Institutional Review Boards approved this study on 14 June 2023 (IRB #2094337 KC). All study participants provided informed consent. Participants did not receive any incentives. This research was conducted in accordance with the Declaration of Helsinki and relevant ethical guidelines.

Consent for publication
Not applicable.

Competing interests
The authors declare no competing interests.

Received: 26 September 2024 Accepted: 11 March 2025

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