

ASSESSING THE IMPACTS OF HOUSEHOLD CONTACTS IN COVID-19 TRANSMISSION DYNAMIC MODELING THROUGH SMALL-WORLD NETWORKS

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ABSTRACT

In the context of the ongoing COVID-19 pandemic, understanding household transmission has become crucial for formulating effective intervention strategies. This study investigated the importance of diverse contact in transmission dynamics within household settings by leveraging the small-world network concept, characterized by high local clustering and short average path length. The methodology involved developing an agent-based simulation model with a two-layer contact network, distinguishing between household and non-household contacts. This simulation aimed to explore the impact of contact patterns on transmission dynamics and evaluates seven Non-Pharmaceutical Intervention (NPI) scenarios focusing on reducing the magnitude of different contact pattern types and timing of the intervention. The results revealed that applying the NPI for both contact types can effectively reduce peak daily case and fatalities compared to the baseline scenario (do-nothing) scenario, with varied outcomes across scenarios. Notably, a reduction in non-household contacts contributes substantially more to overall transmission compared to a reduction in household contacts, especially when assuming a non-equal or greater proportion of the two contact types. In the setting where household contacts are dominant, reducing household contacts was highly effective at mitigating transmission, particularly when the NPI leading to contact reduction was implemented before patients exhibited visible symptoms. Despite the significance of household contacts, the broader network of non-household contacts remains a crucial factor influencing overall disease transmission.

This research highlights the impact of considering heterogeneous contact patterns in household settings as well as providing insights into tailored intervention strategies.

Keywords: COVID-19, small-world network, household contact, mathematical modeling, transmission dynamics

INTRODUCTION

The coronavirus disease 2019 (COVID-19) pandemic, caused by the SARS-CoV-2 virus, has significantly impacted humanity around the world, not only in terms of physical and mental health but also in various aspects such as the economy, education, and social norms. It is possible that the long-term effects of the pandemic will continue to persist for several years and integrate as a part of one's daily life as a "new normal". In the "new normal" lifestyle, people now learn how to adjust themselves around the existence of infections; for example, mask wearing indoors becomes a norm, and social distancing is now commonly practiced at the individual, household, and community levels. Technology has helped all age range populations to have a more flexible working or studying lifestyle and be more agile in responding to future disease emergencies. It would be useful to use mathematical models to guide the design of some optimal interventions in the new era.

In the epidemiology of airborne infectious agents including influenza, common colds, and SARS, households play a critical role in disease transmission. When an infected patient is present in a household, the infection can spread quickly due to the frequent close contact that characterizes relationships between household members. There were many identified COVID-19 clusters resulting from intra-family transmission, indicating significant rates of household transmission. For example, it was noted that between 75 and 80 percent of clustered COVID-19 infections in China occurred within families (Lei et al., 2020). Omicron, the prominent SARS-CoV-2 variant, has currently replaced almost all other variants across the world (Voskarides, 2022). It is possible that new subvariants with these or other concerning traits could emerge in the future. This can raise particular concern for individuals who are at higher risk of severe illness or

complications from the disease, such as young children or older adults. Furthermore, the number of fatalities has considerably increased with age in confirmed cases (Luangasanatip et al., 2023; Wang et al., 2020). In addition, elderly adults are often more at risk from household transmission than from public transmission since they usually stay at home (Wang et al., 2020). However, there is limited data on secondary transmission within household settings (Wang et al., 2020), and few studies have explored contact networks within households (Grijalva et al., 2015), despite their significant role in the spread of diseases.

In the case of the COVID-19 pandemic, non-pharmaceutical interventions (NPI) also played a large role in disease mitigation until drugs and vaccines became available (Chowdhury et al., 2020; Davis et al., 2022; Schneiders et al., 2022). Many NPIs, such as working from home, social distancing, mask wearing, school closures, and self-isolation, would significantly alter the contact patterns in households (Canales-Romero & Hachfeld, 2022; Yamamura & Tsustsui, 2021) and affect the spread of infections within household and non-household settings. Consequently, it is necessary to consider a proactive NPI strategy and understand their impact on COVID-19 transmission, especially in households, which may be a crucial factor in overall transmission.

Therefore, this study aims to use mathematical modeling to quantify the impacts of household transmission based on the modification of simulated networks such as Small-World networks. The research will be useful for guiding intervention studies at the household level for controlling disease outbreaks, given that real data on household and non-household mixing contact patterns is limited.

MATERIALS AND METHODS

The simulation framework conducted in this study leverages the Anylogic Personal Learning Edition Software Simulation (AnyLogic 8 Personal Learning Edition 8.7.12, The AnyLogic Company, 2022), a powerful tool tailored for developing Agent-Based Modelling (ABM). To portray a nuanced disease transmission in a household setting, the introduced two-layer contact network approach offers a more fitting solution in separating household and non-household transmission into distinct layers.

1) Household Transmission Modelling:

In the first layer (Figure 1a), transmissions within households are represented using a fully connected network. This network is defined by the connectivity of all nodes, with each node connected to every other node throughout the network. Here, nodes represent household members, and the connections between nodes denote interactions among these members. This reflects the close and frequent interactions among family members within a household, which are key aspects of disease transmission in shared living spaces.

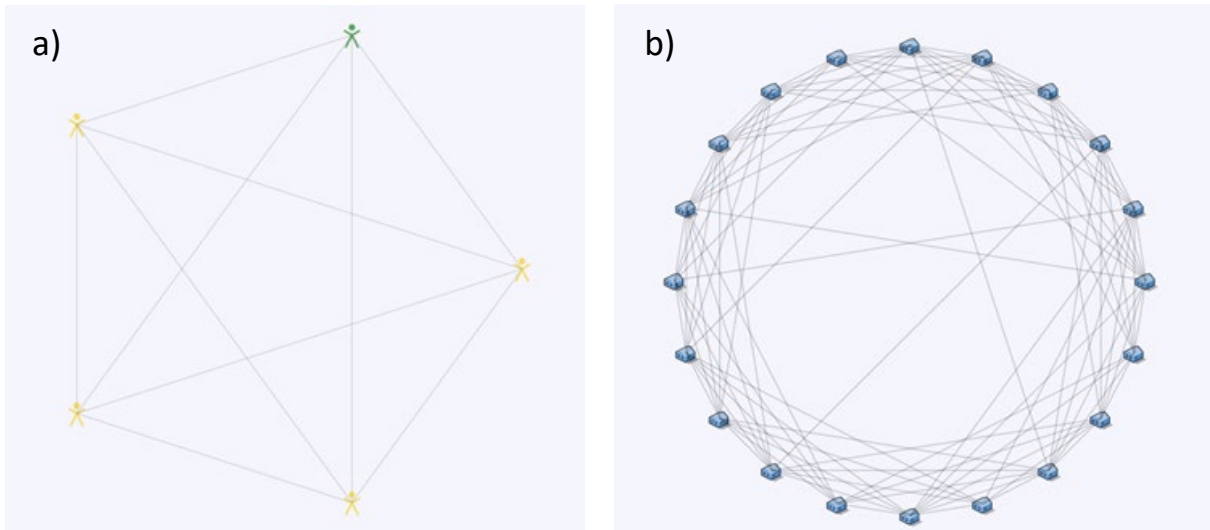


Figure 1 Contact Network Layer a) Household Contact characterized by a fully connected network, with nodes representing individuals and illustrating relationships within households b) Non-Household Contact characterized by a Small-World (SMW) network with nodes representing households, illustrating connections among households in the network.

2) Non-Household Transmission Modelling:

In addition to the within-household network, another small-world network layer is introduced to capture the dynamics of across-household transmission, representing interactions outside the household. In this second layer (Figure 1b), nodes represent individual houses, each

containing the individuals represented in the first layer. The edges in this network signify connections between households, depicting situations where individuals from distinct households come into contact with one another. The “short” links in this context represent frequent and close interactions between households, covering scenarios such as neighboring houses, where families residing nearby are more

inclined to have frequent interactions. Additionally, it includes workplaces or schools that involve larger gatherings of individuals from the same groups. Conversely, “long” links represent less frequent or more distant interactions between households that lack close social ties. These long links might account for daily random interactions in public spaces or other social community events that occur less frequently but may also involve larger gatherings of people. This approach reflects the real-life scenario where individuals are more likely to interact frequently with neighboring households while occasionally engaging with more distant ones. Therefore, integrating both types of links enables a more comprehensive representation of the diverse and intricate interaction patterns.

In each layer of the network, the nodes function as agents, which serve as the primary focus of the individual active component within the ABM, with unique attributes and behaviors. The links in the network serve as connections that facilitate interactions, representing physical or verbal contacts capable of transmitting infections. It is also crucial to define the rules governing agent behaviors, encompassing contact patterns and the adoption of Non-Pharmaceutical Interventions (NPI), which are influenced by pre-established characteristics. Key to defining these rules is the use of statecharts, which graphically represent an agent's possible health states and transitions between them based on events and conditions. The statecharts in this model represent various statuses within each compartment of the model, while also capturing their interactions with others. This model adapts the SIRS compartment-based framework to simulate COVID-19 transmission within households, incorporating specific factors related to the SARS-CoV-2 Omicron variant. A susceptible agent in the S state can transition to the I state if they come into close contact with an infected agent. In addition, an infectious agent in the I state

can transition to the R state if they recover from the disease, and an agent in the R state can transition back to the S state if they lose immunity to the disease. Notably, presymptomatic and symptomatic states are added as sub-compartments within the infectious state, representing individuals initially infected (presymptomatic) but capable of transmitting the disease and later developing symptoms. This acknowledges the potential for asymptomatic individuals to spread the disease sporadically due to a lower likelihood of taking preventative measures. Additionally, a new deceased state is introduced to account for case fatality, measuring disease severity and removing deceased individuals from the model, as they should not maintain any connections.

In order to fully capture the intricacies of diverse contact intimacy in real-world interactions, it is essential to assign distinct contact rates across the two layers of the networks. Recognizing diverse contact patterns influenced by factors like geographical setting, lifestyle, culture differences, socio-economic status, and others, contact type ratios are varied to cover a range of possible patterns. The hypothetical scenarios are introduced with varying assumptions regarding contact types, while maintaining a fixed total number of contacts at 15 per day, except for the last case where the number of contacts is varied. This number falls within the range of contact frequencies reported earlier in China (Huang et al., 2020; Zhang et al., 2020).

Assumptions around the household and non-household contacts

Assumption 1: Balanced Contact:

Both household and non-household contacts are evenly distributed, each at a rate of 7.5 per day in this scenario.

Assumption 2: Household-Dominant Contact:

Under this assumption, household contacts are elevated to 10 per day,

accompanied by a reduction in non-household contacts to 5 per day.

Assumption 3: Non-Household-Dominant Contact:

Conversely, regarding this assumption, non-household contacts are increased to 10 per day, while household contacts decrease to 5 per day.

Assumption 4: Age-Varying Contact:

The model is adapted to reflect age-dependent contact patterns in a specific setting. Given this assumption, contact proportions are adjusted based on example data from a CDC study conducted in Tokyo Prefecture, Japan (Miyahara et al., 2023), where non-household contacts are dominant for younger age groups (0-40), while household contacts are dominant for elders (above 40).

Table 1 Numbers of household and non-household contacts per day for each age range group, when assuming age-varying contacts (Miyahara et al., 2023).

Age Range (yrs)	Household Contact Rate (per day)	Non-Household Contact Rate (per day)
0-19	6.10	19.40
20-39	7.90	14.60
40-59	5.40	1.95
60-99	1.05	0.85

The simulations encompassed the seven case scenarios, involving over 400 individuals distributed across 140 households with an average of three residents per house. Over a 100-day timeframe, each scenario underwent 100 repeat iterations, contributing to more reliable results with reduced marginal error. The study explores the influence of varying contact patterns on the effectiveness of different NPI strategies, with a particular focus on two key metric outputs—Total Cases and Fatalities over a 100-day timeframe. This analysis quantifies the impacts of controlling various contact types and their timing in comparison to the baseline. The scenarios to be explored include:

Baseline scenario - Do nothing (SC0_NONE)

Scenario 1 - Restrict non-household contacts (SC1_NON_HH_CONTACT)

Scenario 2 - Restrict household contacts (SC2_HH_CONTACT)

Scenario 3 - Restrict non-household contacts ONLY IF one has visible symptoms (SC3_NON_HH_CONTACT_IF)

Scenario 4 - Restrict household contacts ONLY IF one has visible symptoms (SC4_HH_CONTACT_IF)

Scenario 5 - Restrict all contacts (SC5_ALL_CONTACT)

Scenario 6 - Restrict all contacts ONLY IF one has visible symptoms (SC6_ALL_CONTACT_IF)

To represent these NPI scenarios, the approach involves modifying the contact network by removing edges when infected individuals undergo self-quarantine, effectively cutting off their contact with others. This is achieved by adding a guard condition that blocks the transmission events from the infected node, preventing further infection spread at each network layer. This approach allows for the simulation of quarantine measures at both the household and individual levels, encompassing self-isolation and home-isolation strategies. After defining the agents, their connection, and their interactions in the environment, the simulation is run to observe the spread of the disease over time.

RESULTS

Figures 2-5 consists of visual representations include 2D histogram charts illustrating daily new infectious cases over time and bar charts depicting the total cases (total number of infected individuals) and fatalities (total number of deaths) resulting from the infectious disease under varying assumptions of contact types. These figures serve as focal points, facilitating the discernment of trends and the assessment of intervention effectiveness across diverse contact patterns and scenarios.

Assumption 1: Balanced Contact

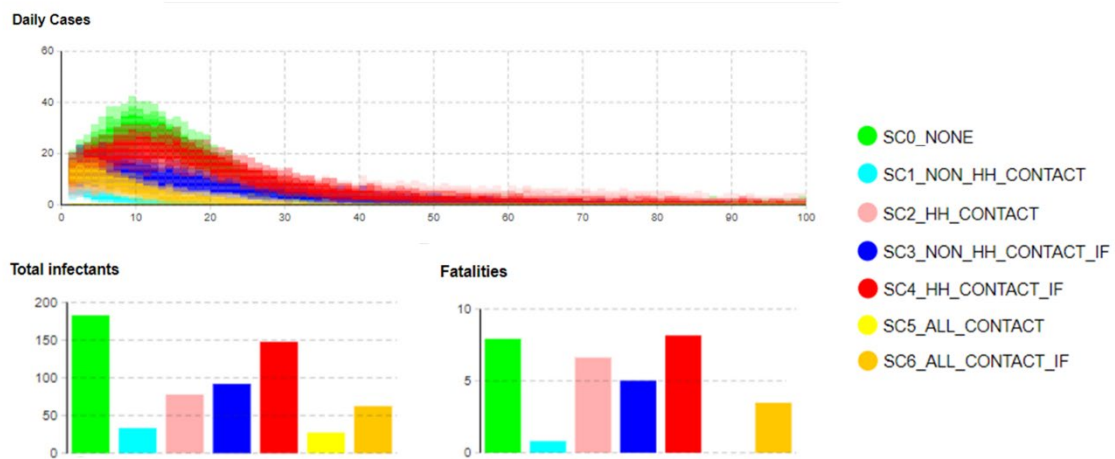


Figure 2 Model outputs from different intervention scenarios, when assuming balanced contacts a) Daily cases over time, b) Total cases, and c) Total fatalities from 100 simulations

Assumption 2: Household-Dominant Contact

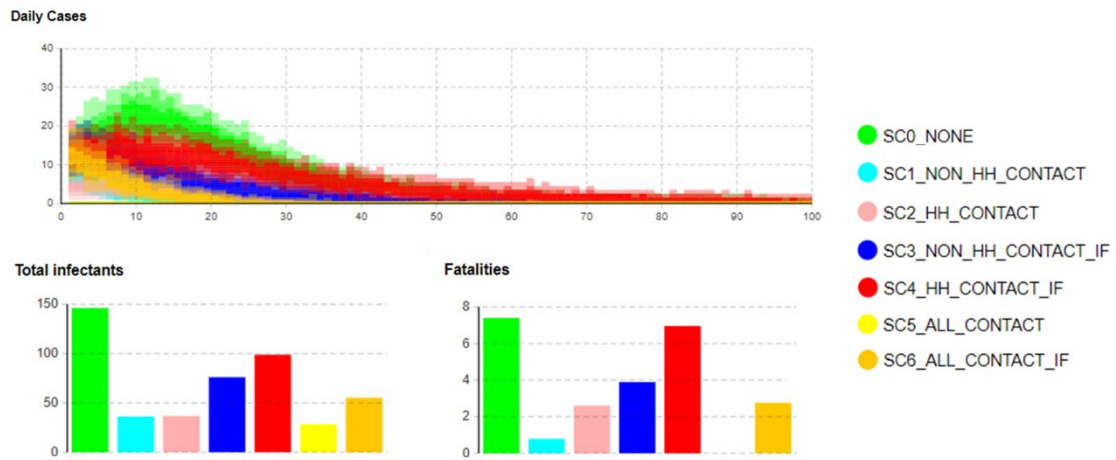


Figure 3 Model outputs from different intervention scenarios, when assuming household-dominant contacts a) Daily cases over time, b) Total cases, and c) Total fatalities from 100 simulations

Assumption 3: Non-Household-Dominant Contact

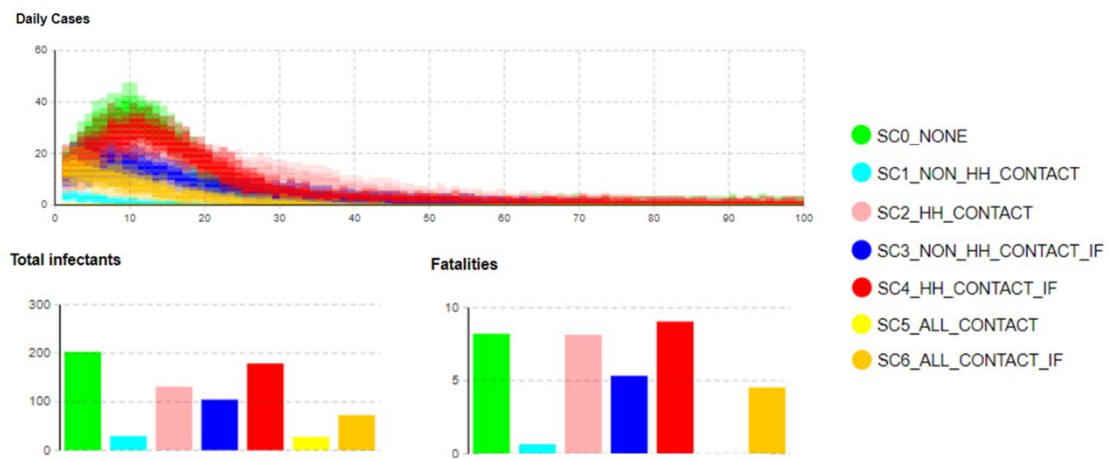


Figure 4 Model outputs from different intervention scenarios, when assuming non-household-dominant contacts a) Daily cases over time, b) Total cases, and c) Total fatalities from 100 simulations

Assumption 4: Age-Varying Contact

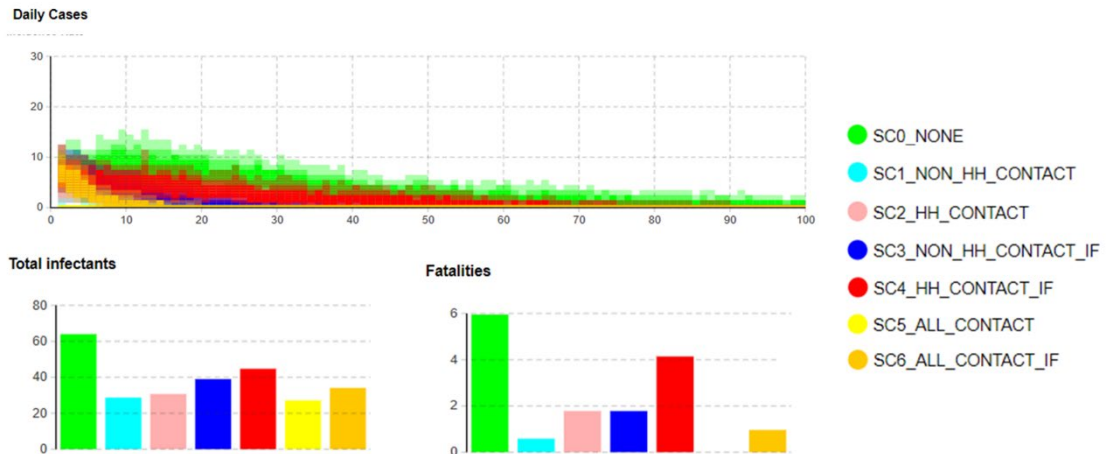


Figure 5 Model outputs from different intervention scenarios, when assuming age-varying contacts a) Daily cases over time, b) Total cases, and c) Total fatalities from 100 simulations

For more detailed numerical data, Table 2-5 below presents comprehensive results for seven NPI scenarios under various contact pattern assumptions, presenting three key outcome metrics to assess the impact of seven NPI scenarios under various contact pattern assumptions. Each result represents the mean average from 100 iterations. First, "Peak Daily Cases" represents the highest number of new confirmed cases in a single day from all over epidemic duration, providing insight into the intensity of disease spread. Second, "Total Cases" accounts for the cumulative number of infected individuals throughout the simulation, including the initially infected population. It is important to note

that this count remains non-zero even when the daily incidence is zero, as it incorporates the initially infected individuals. Finally, "Fatalities" captures the overall number of fatalities resulting from the infectious disease, offering a measure of the severity of the outbreak. All three-output metrics are presented in the table, each with the following units: "Peak Daily Cases" (cases/day), "Total Cases", and "Fatalities". Note that in all NPI scenarios, an extreme best-case assumption of 100% effectiveness is applied for simplification, representing an ideal scenario of comprehensive public health measures. Consequently, Scenario 5 exhibits zero new incidence cases across all assumptions

Table 2 Average number of peak daily cases, total cases, and fatalities (95% CI) from 100 simulations, under Assumption 1: Balanced Contact

Intervention Assumption 1	Peak Daily Cases (95% CI)	Total Cases (95% CI)	Fatalities (95% CI)
Baseline Scenario	39.48 (38.26-40.70)	182.81 (177.51-188.11)	7.93 (7.42-8.44)
Scenario1	7.34 (6.94-7.74)	33.39 (32.10-34.68)	0.81 (0.64-0.98)
Scenario2	17.06 (16.28-17.84)	77.68 (74.00-81.36)	6.62 (6.06-7.18)
Scenario3	21.24 (20.22-22.26)	91.82 (87.06-96.58)	5.02 (4.58-5.46)
Scenario4	30.91 (29.80-32.02)	147.79 (142.47-153.11)	8.16 (7.65-8.67)
Scenario5	0.00	27.29 (26.31-28.27)	0.00
Scenario6	16.87 (15.89-17.85)	62.41 (59.12-65.70)	3.48 (3.04-3.92)

Table 3 Average number of peak daily cases, total cases, and fatalities (95% CI) from 100 simulations, under Assumption 2: Household-Dominant Contact

Intervention Assumption 2	Peak Daily Cases (95% CI)	Total Cases (95% CI)	Fatalities (95% CI)
Baseline Scenario	30.60 (29.65-31.55)	146.22 (141.80-150.64)	7.40 (6.82-7.98)
Scenario1	8.87 (8.39-9.35)	36.11 (34.51-37.71)	0.79 (0.63-0.95)
Scenario2	8.78 (8.20-9.36)	36.67 (34.67-38.67)	2.60 (2.24-2.96)
Scenario3	18.97 (17.97-19.98)	76.06 (72.20-79.92)	3.89 (3.45-4.33)
Scenario4	21.90 (21.00-22.80)	98.87 (94.53-103.21)	6.96 (6.48-7.44)
Scenario5	0.00	28.31 (27.29-29.33)	0.00
Scenario6	15.58 (14.69-16.47)	55.25 (51.88-58.62)	2.76 (2.46-3.06)

Table 4 Average number of peak daily cases, total cases, and fatalities (95% CI) from 100 simulations, under Assumption 3: Non-Household-Dominant Contact

Intervention Assumption 3	Peak Daily Cases (95% CI)	Total Cases (95% CI)	Fatalities (95% CI)
Baseline Scenario	43.84 (42.70-44.98)	202.80 (199.03-206.57)	8.21 (7.67-8.75)
Scenario1	5.35 (5.03-5.67)	29.30 (28.10-30.50)	0.65 (0.50-0.81)
Scenario2	26.90 (25.92-27.88)	130.91 (126.22-135.60)	8.14 (7.49-8.79)
Scenario3	23.81 (22.65-24.97)	104.36 (99.24-109.48)	5.33 (4.86-5.80)
Scenario4	37.44 (36.32-38.56)	178.82 (174.66-182.98)	9.05 (8.43-9.67)
Scenario5	0.00	27.65 (26.71-28.59)	0.00
Scenario6	19.38 (18.24-20.52)	72.43 (68.18-76.68)	4.53 (3.97-5.09)

Table 5 Average number of peak daily cases, total cases, and fatalities (95% CI) from 100 simulations, under Assumption 4: Age-Varying Contact

Intervention Assumption 4	Peak Daily Cases (95% CI)	Total Cases (95% CI)	Fatalities (95% CI)
Baseline Scenario	14.72 (14.02-15.42)	63.96 (60.45-67.48)	5.95 (5.38-6.52)
Scenario1	4.73 (4.43-5.03)	28.71 (27.67-29.75)	0.58 (0.42-0.74)
Scenario2	6.31 (5.93-6.69)	30.71 (29.34-32.08)	1.78 (1.45-2.11)
Scenario3	9.70 (9.04-10.36)	38.97 (36.79-41.15)	1.78 (1.47-2.09)
Scenario4	10.78 (10.19-11.37)	44.70 (42.50-46.90)	4.14 (3.68-4.60)
Scenario5	0.00	27.16 (26.17-28.15)	0.00
Scenario6	8.25 (7.54-8.96)	34.06 (32.12-36.00)	0.96 (0.79-1.13)

Examining the overall results reveals that the consistent application of NPI interventions effectively controls transmission and mitigates fatality across scenarios. This leads to a reduced peak in the number of new confirmed cases per day compared to the baseline 'do nothing' scenario. The effectiveness varies based on different contact scenarios. Considering the contribution of contact types to overall transmission, non-household contact emerges as a significant factor. In the case of non-household dominant contact, the highest prevalence (202.80; 95% CI, 199.03-206.57) and considerable fatality (8.21; 95% CI, 7.67-8.75) are observed compared to other assumption cases. Restricting household contacts appears to have a less notable effect on reducing the peak of the curve, with NPI scenarios 1 and 3, focusing on restricting non-household contacts, demonstrating more visible effectiveness. Despite non-household contacts usually having a more pronounced impact on transmission dynamics, the timing of NPI implementation is also critical. Continuous application consistently outperforms post-symptomatic interventions, especially in scenarios dominated by household contacts (see Table 3). In this context, Scenario 2, consistently applying NPI measures to household contacts, achieves a substantial reduction of 71% in maximum incidence and 65% in casualties compared to the baseline scenario. In contrast, Scenario 4, which focuses on post-symptomatic NPI for household contacts, exhibits a less pronounced reduction of 28% in maximum incidence and 6% in casualties. Despite both scenarios targeting household contacts, there is a distinct difference in outcomes.

DISCUSSION

This research introduces a novel two-layer network based on Small-World Network (SMW) properties within an Agent-Based Modeling (ABM) framework, aiming to capture the heterogeneous contact patterns between household and non-household interactions. The model differentiates contact type ratios to explore the consequences of varying contact patterns, conducting simulations across diverse settings to provide insights into the effectiveness of different Non-Pharmaceutical Intervention (NPI) strategies.

In analyzing the results, NPIs exhibit a crucial role in curbing both prevalence and fatality, demonstrating varying effectiveness across different scenarios. It is also apparent that while household contacts may play a substantial role, non-household contacts significantly contribute to overall transmission due to their ability to facilitate rapid transmission across all networks. These findings align with recent research by Du (2021) suggesting that reducing long-range edges in SMW contact networks, such as restricting domestic or international travel, can effectively delay and reduce the peaks of daily new cases and fatalities. This is because removing non-household contacts isolates households, resulting in higher clustering in this layer. This observation is consistent with the findings of Volz et al. (2011), who demonstrated that clustering within households can slow transmission and reduce the final number of infected individuals. While reducing either "short" or "long" contacts can be beneficial, simultaneous reductions of both have a significantly stronger impact on intervention effectiveness, especially when implemented early to delay the peak (Du, 2021). This parallels Du (2021)'s findings on the importance of combined intervention strategies.

Moreover, the possibility of pre-symptomatic transmission underscores the limited effectiveness of interventions solely focused on applying post-symptom onset. Based on this model simulation and model assumptions, the consistent application of NPIs proves superior to post-symptomatic application in mitigating the impact. These findings correspond to those of Chen et al. (2021) and Hill et al. (2021), highlighting the importance of rapid case detection through contact tracing to effectively identify infected individuals for timely isolation strategies in containing transmission. This reinforces the need for timely interventions and comprehensive strategies to address transmission dynamics effectively.

Nevertheless, the current research model heavily relies on assumptions and simplifications based on contact rates and patterns due to limited data availability. This simplification aims to strike a balance between complexity and feasibility, preventing the model from becoming overly intricate. Despite current limitations, the flexibility of adjusting input parameters in this model allows for the exploration of more hypothetical scenarios. It enables the incorporation of new data on disease characteristics and contact patterns in various settings as more information becomes available in the future. The simulation model developed in this research can provide some ideas for designing future models to evaluate different NPI strategies, especially those involving household and non-household transmission controls for future refinements and adaptations based on evolving data. Such studies can enhance understanding of disease dynamics in relation to heterogeneities in contact patterns within and between households.

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