Infectious Disease Modelling 10 (2025) 628–638

Contents lists available at ScienceDirect

Infectious Disease Modelling

journal homepage: www.keaipublishing.com/idm

Interventions for SARS-CoV-2 prevention among Jailed adults: A network-based modeling analysis

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ARTICLE INFO

Article history:
Received 1 August 2024
Received in revised form 30 October 2024
Accepted 3 February 2025
Available online 4 February 2025
Handling Editor: Dr Yijun Lou

ABSTRACT

Background: Airborne pathogens present challenges in settings like jails or prisons with a high density of contacts. The state of Georgia has the highest percentage of its citizens under correctional supervision in the United States. Yet, it had slow COVID vaccine uptake among jail residents, requiring prevention also using non-pharmaceutical interventions. Using a network-based SARS-CoV-2 transmission model parameterized with data from the Fulton County Jail, this study investigates the impact of three SARS-CoV-2 prevention strategies: vaccination, contact tracing and quarantining, and jail release to reduce jail population density.

Methods: Social contact networks were simulated at two different overlapping network layers: cell and block. Cell-level contacts represented shared confined sleeping space, whereas block-level contacts represented shared socialization space. Contact tracing and quarantining were simulated at the cell-level or both cell- and block-levels, hereafter referred to as all-level. A reference scenario and nine intervention scenarios were simulated three hundred times to estimate the median and interquartile range (IQR) of the outcome measures. Each scenario simulated a 185-day period to measure the prolonged effects of the interventions amid a potential COVID outbreak in the jail. The cumulative incidence, number of infections averted (NIA), and percentage of infections averted (PIA) were calculated comparing interventions against a base scenario without them. For the seven scenarios involving contact tracing and quarantining, total quarantines over the simulation and the number of quarantines per day were calculated to determine the quarantine requirements. Sensitivity analyses compared the impact of jointly varying vaccination rates and contact tracing rates.

Results: Cell-level contact tracing alone was an ineffective intervention (3.2% PIA), but its impact increased in combination with other interventions (i.e., vaccination or increased jail release rate). The other intervention strategies each produced a PIA over 10%, with the jail release scenario producing a PIA of nearly 20% despite only resulting in a 13% reduction in the jail population. The all-level contact tracing only scenario was effective at both 50% and 100% of contacts traced, but feasibility would be limited without a reduction in the jail population.

Conclusions: Implementing a combination intervention approach could substantially reduce the morbidity from COVID-19 and future respiratory viruses in this jail setting while providing secondary protection to the community.

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Peer review under the responsibility of KeAi Communications Co., Ltd.

https://doi.org/10.1016/j.idm.2025.02.001

1. Introduction

Controlling the spread of airborne infectious diseases in carceral settings (e.g., jails and prisons) remains challenging. Overcrowding, difficult infection control, and challenging health care delivery together produce an environment prone to disease outbreaks (Bick, 2007). During the H1N1 epidemic, this issue was compounded by the fact that over half of the jails in the United States did not receive H1N1 vaccine (Centers for Disease Control and Prevention, 2012; Lee et al., 2014). Due to continued omission of jails and prisons in pandemic preparedness and response planning, the COVID-19 pandemic presented new challenges in outbreak prevention among incarcerated persons (Akiyama et al., 2020).

Since its start in early 2020, the global COVID-19 pandemic has caused over 750 million cases globally, resulting in almost 7 million deaths (World Health Organization, 2024). In the United States specifically, there have been over 100 million cases of COVID-19 with around 1.1 million deaths (World Health Organization, 2024). After the introduction of the vaccine, states with low vaccination uptake remain especially vulnerable to future outbreaks, especially in carceral settings and other high-density social contact settings. In the state of Georgia, which experienced one of the lowest COVID vaccination rates but highest percentage of adults under correctional supervision in the country, there have been over 2.4 million confirmed COVID cases with over 36,000 confirmed COVID-related deaths (Centers for Disease Control and Prevention, 2020; Georgia Department of Public Health, 2024; Minton et al., 2021). Given the large carceral population, Georgia jails and prisons remain vulnerable to further COVID-19 and respiratory disease outbreaks, despite the impact investment in prevention interventions would have on reducing morbidity and mortality.

Infectious disease modeling studies have found that several interventions within a jail or prison could reduce COVID-19 transmission both within the jail and into the broader community. Using stochastic or deterministic compartmental modeling, these studies estimated the impact of increased testing and quarantining in prisons, reductions in new arrests, reductions in the jail or prison population sizes, and individual measures such as asymptomatic testing (Greenhalgh & Provencher, 2022; Lofgren et al., 2022; Malloy et al., 2021). These interventions have shown effectiveness alone and in combination (Greenhalgh & Provencher, 2022; Lofgren et al., 2022; Malloy et al., 2021). Even though effectiveness has been demonstrated, these studies utilized compartmental models which assumed random, homogenous mixing within compartments, and memoryless (non-persistent) contacts (Tolles & Luong, 2020). A challenge for modeling COVID within a carceral setting is the complex, dynamic, and multi-level contact network structure, which is not sufficiently represented by compartmental models (Malloy et al., 2021). Network models allow for the development of a heterogeneous contact network where transmissions occur, similar to the dynamic seen within a jail or prison (Jenness et al., 2023).

In this study, we developed a network-based transmission model for SARS-CoV-2 in a Georgia jail population that experienced challenges in responding to COVID. At baseline, the jail had a modest vaccination rate and contact tracing focused on testing cell mates. Slowing of judicial processes in courts and an effort by prisons to limit entrants stymied the release of residents (persons who are incarcerated). This study seeks to understand how vaccination, contact tracing and quarantining, as well as jail depopulation impact SARS-CoV-2 transmission. These findings may provide a possible intervention framework within jails, prisons, and other congregate settings for future respiratory viral outbreaks.

2. Methods

2.1. Study design

This analysis used a network-based transmission model of infectious disease dynamics. This model was built with the EpiModel package in R (Jenness et al., 2018). Data from the Fulton County Jail (FCJ) in Atlanta was used, and the outbreak was simulated over 185 daily time steps (roughly October 2021 to April 2022 during the height of the Omicron wave in Atlanta). Statistics were drawn from a prior descriptive analysis, where daily jail roster data was used to estimate the racial distribution, age distribution, and contact distribution within FCJ during a few periods in late 2021 and early 2022 (Jenness et al., 2023).

The FCJ structure is divided into seven floors, each containing as many as six housing blocks, and the standard block containing 19 cells (Jenness et al., 2023). During the late 2021- early 2022 observation period, FCJ housed an average daily population of three thousand residents. The open population experienced approximately 40 entrants and 40 releases each day (Jenness et al., 2023). Custody staff could reassign housing blocks and individual cells within the blocks daily. Demographically, the jail population was primarily black race (89.3%), between the ages of 20–39 (64.4%), and male (Jenness et al., 2023). Strong assortative mixing was observed by age group, with 33% of both cell- and block-level contacts occurring within defined age groups (Jenness et al., 2023). This open population had high daily rates of jail entry and exit, in addition to high daily rates of movement between cells and blocks. Cell-level changes occurred more frequently than block-level changes, and block-level changes were similar to the overall turnover rate within the jail, with lower block-level turnover than jail turnover

during the Omicron wave in January 2022 (Jenness et al., 2023). These listed statistics were used to parameterize the model for this representative population.

Contacts were dichotomized to both the cell and block levels. Cell-level contacts shared confined sleeping space, while block-level contacts shared common space. To represent vaccination prior to the model start or entry into jail, 50% of the initial jail population and 50% of individuals entering the jail were modeled as fully vaccinated, a rough estimate of vaccination in FCJ at the time. Although there was potential SARS-CoV-2 transmission to officers and other staff within the jail, the modeled population was limited to residents to analyze the effects of interventions solely on incarcerated individuals. However, residents were able to acquire SARS-CoV-2 from officers in the model through an indirectly modeled community infection mechanism. In combination with acquiring an infection from jail officers, some residents were brought into the jail with a SARS-CoV-2 infection, collectively representing the external force of infection. Sourced parameters of interest are present in Table 1. Nine intervention scenarios were developed to analyze the effect of interventions individually and jointly, compared to a base scenario with no interventions (see Table 2). For all scenarios, thirty infected individuals were introduced into the jail at the model outset.

2.2. COVID model structure

Building from the EpiModel software platform (Jenness et al., 2018), we developed a network-based model of SARS-CoV-2 transmission. This is a stochastic agent-based model (ABM), in which all major components—network evolution, disease transmission and progression, and demographic changes—are modeled stochastically at the level of individual agents (nodes). Network Dynamics: The formation and dissolution of social contacts are modeled stochastically, with individual-level contact patterns fluctuating over time according to probabilities derived from empirical data (e.g., ERGMs). Contacts are updated daily in a manner that reflects both random and structured social mixing. Disease Transmission and Progression: SARS-CoV-2 transmission between individuals occurs stochastically at each contact, with transmission probabilities dependent on factors such as the symptom status and vaccination status of the infectious agent. Similarly, disease progression from exposure to symptomatic or asymptomatic states and potential hospitalization is governed by stochastic processes based on individual-level attributes. Demographics: Births, deaths, and aging are all stochastically modeled, with individuals entering and exiting the population at daily time steps according to probabilities based on empirical mortality and birth rates. Each component contributes independently to the overall stochasticity of the model. No deterministic equations are solved in the traditional sense; rather, the entire system is evolved through stochastic processes, using Monte Carlo methods to simulate daily events over time. The model results are therefore the cumulative outcome of individual-level random events occurring over the simulation period. Further details about the stochastic implementation of network evolution, disease transmission, and demographic processes can be found in the supplementary appendix.

Natural history of COVID-19 and SARS-CoV-2 is shown in Fig. 1. Upon acquiring SARS-CoV-2, an individual moved into an exposed (latent) stage. Once an individual reached the exposed stage, they could transition to either the pre-clinical (symptomatic) or sub-clinical (asymptomatic) routes. A pre-clinical infection would lead to a clinical infection followed by either recovery, hospitalization then recovery, or hospitalization then death (Tsai et al., 2021). The subclinical infection would lead to recovery without the development of symptoms (Bartekwa et al., 2021). Individuals following the sub-clinical pathway had reduced transmission when compared to individuals with symptoms (Methi & Madslien, 2022; Tan et al., 2022). In our model, we conservatively assumed a PCR sensitivity of 80%, reflecting early estimates of test performance during the initial stages of the COVID-19 pandemic. Several studies published during this period suggested that PCR sensitivity could range from 70 to 80%, particularly due to factors such as the timing of specimen collection, improper sampling techniques, and variability in viral load detection during different stages of infection (Woloshin et al., 2020). These early

Table 1
General model parameters.

Parameter Description	Parameter Value	Source
Mean degree – cell-level	1.72	Jenness et al. (2023)
Daily contacts – cell-level	5	Fitted
Mean degree – block level	33.50	Jenness et al. (2023)
Daily contacts – block level	0.5	Fitted
Community infection rate	0.001	Fitted
Quarantine contact rate reduction	0.1	Assumed
Daily vaccination rate	See Table 2	Assumed, sensitivity analysis
Proportion traced	See Table 2	Assumed, sensitivity analysis
Proportion quarantined	See Table 2	Assumed
Arrival rate	0.014 ~40 entries per day	Jenness et al. (2023)
Jail release rate	See Table 2	Jenness et al. (2023)
Mortality rates	Stratified by race and age, see supplementary tables and figures	(Centers for Disease Control and Prevention, National Center for Health Statistics)

Table 2
Parameters adjusted for different intervention scenarios.

Scenario Description	Daily Vaccination Rate	Proportion Traced	Proportion Quarantined	Jail Release Rate
Baseline – no interventions	0	0	0	0.014 ~40 releases per day
Vaccination only	0.015 ~150 per week	0	0	0.014 ~40 releases per day
Cell-level contact tracing only (50% of contacts traced)	0	0.5	1	0.014 ~40 releases per day
Cell-level contact tracing only (100% of contacts traced)	0	1	1	0.014 ~40 releases per day
All-level contact tracing only (50% of contacts traced)	0	0.5	1	0.014 ~40 releases per day
All-level contact tracing only (100% of contacts traced)	0	1	1	0.014 ~40 releases per day
Jail release only	0	0	0	2*0.014 (until population reached 2600 – FCJ capacity)
All interventions combined (Cell-level tracing)	0.015 ~150 per week	1	1	2*0.014 (until population reached 2600 – FCJ capacity)
All interventions combined (All-level tracing – 50% quarantine capacity)	0.015 ~150 per week	1	0.5	2*0.014 (until population reached 2600 – FCJ capacity)
All interventions combined (All-level tracing – 100% quarantine capacity)	0.015 ~150 per week	1	1	2*0.014 (until population reached 2600 – FCJ capacity)

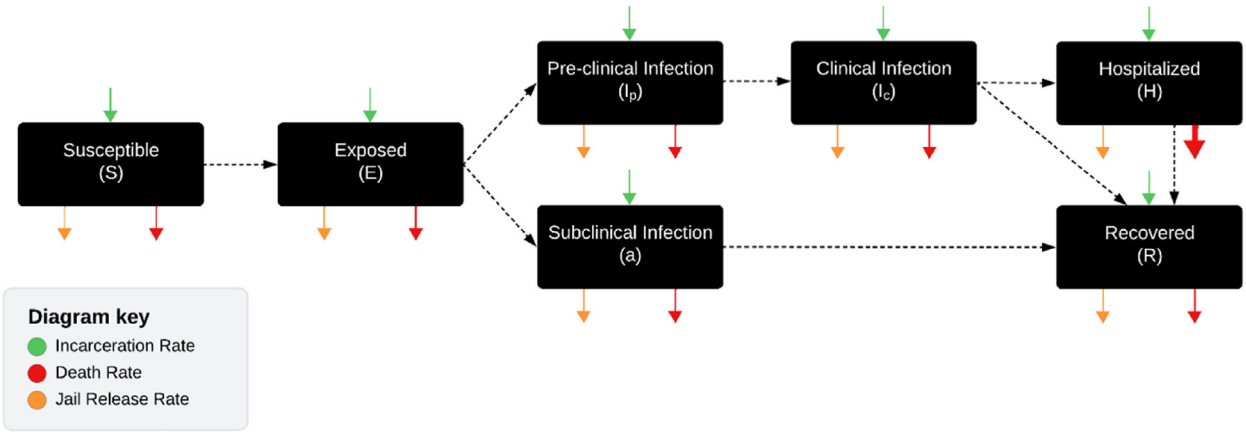

Fig. 1. Disease transmission process displaying the stages of infection, transition between stages, and entry/exit processes.

reports highlighted the potential for false-negative results, especially during the window period after infection but before peak viral shedding.

Additionally, our model focuses on a population of incarcerated persons in a jail setting, where the conditions for specimen collection and storage may not reflect those found in lab-based or clinic-based environments. The transient nature of the jail population, as well as potential limitations in specimen handling and processing, can contribute to suboptimal diagnostic conditions. Therefore, the assumption of a lower sensitivity reflects these real-world constraints in jails, where testing conditions may reduce the effectiveness of PCR diagnostics compared to controlled clinical settings.

2.3. Intervention design

Our nine modeled intervention scenarios represented three types of interventions: contact tracing and quarantining, release of residents to an established jail capacity, and COVID vaccination. Because we represented indirect transmission that would occur despite intervention effectiveness (i.e., community-acquired transmissions from jail officers), the main outcome of interest for analysis was resident cell- and block-level transmissions, the two contact layers modeled.

Contact tracing and quarantining within the jail relied on a known diagnosis status of another jail resident. In our model, we assumed that the whole block was not traced after one person was found infected and isolated. This is where the “contact tracing” part of the intervention was implemented. Our model allowed for immediate identification of close contacts through a case investigation and contact tracing process (based on the assumption that a time lag would be short due to the confined nature of the residents). Only people who were deemed close contacts of the isolated individual were eligible for quarantine,

and a certain percentage of them (depending on the parameter that we set) eventually moved to a quarantine state. Close contacts were defined as either cell-level or block-level. When the cell-level contact tracing intervention was active, only cell mates were eligible to be traced and quarantined. When the all-level contact tracing intervention was active, both cell and block mates were eligible to be traced and quarantined. Whenever someone was moved to the quarantine status, they would be placed in a cell by themselves (similar to what would happen with the isolation process) and monitored. If a quarantined individual went the full 14 days without a COVID-19 diagnosis, they were released from quarantine and their level of contact with other incarcerated persons returned to pre-quarantine levels. If an individual developed an infection that resulted in a COVID-19 diagnosis during their quarantine, they transitioned from a quarantine state to an isolation state for the full duration of their infection.

For the jail release intervention, we doubled the rate of jail release until the population reached 2600 (Jenness et al., 2023). This reduced the number of contacts between individuals and limited the opportunities for transmission. In this study, we used a deterministic value for jail release (reducing the population size from 3000 to 2600), as this was the expected population size of the Fulton County Jail during the period of analysis. This reduction in population size was determined based on policy considerations, and there was no plan to reduce the jail population below 2600, making it unnecessary to explore further variations in jail release rates. Given these constraints, our model was designed to evaluate the impact of jail release under the specific conditions reflective of the actual policy landscape. Since the goal was to align our model with real-world policy decisions, we did not include sensitivity analyses with lower jail release values, as this scenario was not considered feasible by policymakers at the time. Finally, vaccination at various rates reduced acquisition risk of SARS-CoV-2.

2.4. Model analysis

Each model scenario was simulated three hundred times. In our analysis, we chose 300 runs as this was determined to be the minimum number required to achieve numerical stability in our outcome summary measures, including means and medians, based on multiple evaluations of model outputs. We assessed this stability both in the current analysis and in previous iterations of the same agent-based model framework. Once stability in the means was reached at 300 runs, increasing the number of simulations (e.g., to 1000 or 2000 runs) did not significantly alter the results, ensuring that 300 runs provided a reliable representation of the range of possible outcomes.

This approach is standard practice in agent-based modeling (ABM), where the goal is to balance computational feasibility with statistical reliability. Several studies in the ABM literature describe using this method to select an appropriate number of simulations, emphasizing that once the variation between simulation means stabilizes, additional runs provide diminishing returns (Lorscheid et al., 2012; Lysenko & D'Souza, 2008). These evaluations are specific to each model and are influenced by factors such as the stochasticity of the system, the complexity of the model, and the range of outcomes observed. Simulations were conducted on the Emory High Performance Computing (HPC) system. Please see Appendix A for more information about the model structure. We calculated cumulative incidence across simulations over a 185-day time span. Additionally, both the number of infections averted (NIA) and percentage of infections averted (PIA) were calculated relative to a base scenario with no interventions. The median was calculated per scenario across simulations. The interventions involving contact tracing and quarantining were analyzed further to determine the number of individuals quarantined per day over the 185-day span. For sensitivity analyses, we varied the daily vaccination rate and proportion traced: both the cell-level tracing all-level tracing (i.e., both cell- and block-levels), started with twenty-five scenarios simulated one hundred times each to determine their combined effects on the PIA.

3. Results

3.1. Primary intervention results

In the base scenario without interventions, the median cumulative incidence for all transmission mechanisms across three hundred simulations was 2946 total cases (IQR: 2885, 3005) including 993 cell-level cases (IQR: 962, 1022) and 1568 block-level cases (IQR: 1523, 1601). Given that the interventions had no effect on the external forces of infection (i.e., infection from staff members or infection brought into the jail), the NIA and PIA for the intervention scenarios were calculated based on the overall cell- and block-level incidence only.

Fig. 2 displays the cell- and block-level PIA for the intervention scenarios, and Fig. 3 displays the cumulative cell- and block-level incidence for all scenarios (including reference scenario). Table 3 provides the median and IQR cumulative incidence, PIA, and NIA. When single interventions were modeled, jail release had the greatest individual impact on cell- and block-level transmissions with a median PIA of 19.5%. Cell-level contact tracing had a minimum impact on its own with median PIA of 1.8% and 3.2% for the 50% and 100% of contacts traced scenarios, respectively. With a daily vaccination rate of 0.015 (around 150 people per week, twenty-one people per day) vaccination had a median PIA of 11%. All-level contact tracing alone produced similar median PIA values of 10.4% and 16.4% when 50% and 100% of contacts were traced, respectively. Combining all interventions (either cell- or all-level tracing) resulted in the greatest decrease in cumulative incidence. Combining cell-level tracing with other interventions resulted in a ten-fold increase in PIA as the scenario using all interventions combined with cell level tracing produced a median PIA of 31.4%. Increase quarantine capacity for all-level contact tracing from 50% to 100% only had an increase in median PIA of 5.6% (36.7%–42.3%).

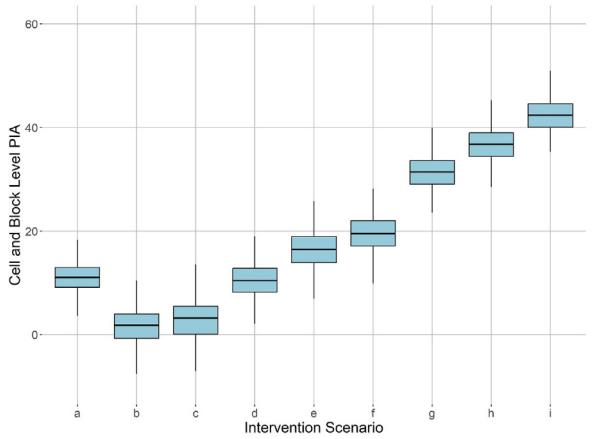

Fig. 2. Percentage of cell and block-level infections averted across 300 simulations for each of the nine scenarios – a: vaccination, b: 50% cell-level contact tracing (CT), c: 100% cell-level CT, d: 50% all-level CT, e: 100% all-level CT, f: jail release, g: all combined (cell-level CT), h: all combined (all-level CT, limited quarantine capacity), i: all combined (all-level CT, full quarantine capacity).

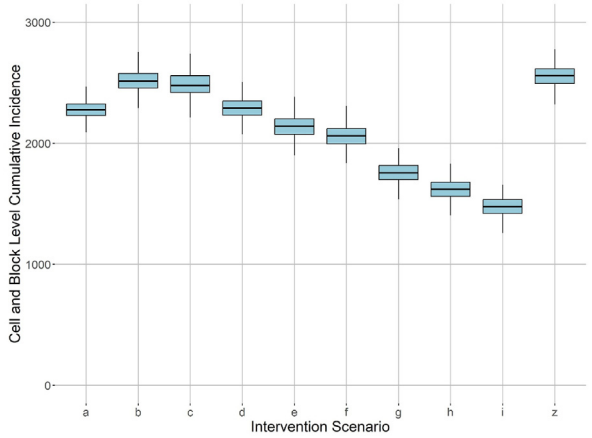

Fig. 3. Cell and block-level cumulative incidence across 300 simulations for each of the nine scenarios and a baseline scenario – a: vaccination, b: 50% cell-level contact tracing (CT), c: 100% cell-level CT, d: 50% all-level CT, e: 100% all-level CT, f: jail release, g: all combined (cell-level CT), h: all combined (all-level CT, limited quarantine capacity), i: all combined (all-level CT, full quarantine capacity), z: baseline.

Table 3
Median and IQR cumulative incidence and median and IQR number and percentage of infections averted for nine scenarios against a baseline with three hundred simulations per scenario.

Scenario Description	Label	Cumulative Incidence	Number of Infections Averted (NIA)	Percentage of Infections Averted (PIA)
		Median (IQR)	Median (IQR)	Median (IQR)
Baseline – no interventions	*z*	2560 (2496, 2616)	–	–
Vaccination only	*a*	2278 (2229, 2326)	282 (234, 331)	11.0% (9.1%, 12.9%)
Cell-level contact tracing only (50% of contacts traced)	*b*	2515 (2459, 2579)	46 (−19, 101)	1.8% (−0.7%, 4.0%)
Cell-level contact tracing only (100% of contacts traced)	*c*	2479 (2420, 2558)	82 (2, 140)	3.2% (0.1%, 5.5%)
All-level contact tracing only (50% of contacts traced)	*d*	2293 (2233, 2350)	267 (210, 327)	10.4% (8.2%, 12.8%)
All-level contact tracing only (100% of contacts traced)	*e*	2140 (2075, 2204)	420 (356, 485)	16.4% (13.9%, 18.9%)
Jail release only	*f*	2061 (1997, 2122)	499 (438, 563)	19.5% (17.1%, 22.0%)
All interventions combined (Cell-level tracing)	*g*	1757 (1700, 1816)	804 (744, 860)	31.4% (29.1%, 33.6%)
All interventions combined (All-level tracing – 50% quarantine capacity)	*h*	1621 (1562, 1679)	940 (881, 998)	36.7% (34.4%, 39.0%)
All interventions combined (All-level tracing – 100% quarantine capacity)	*i*	1476 (1420, 1536)	1084 (1024, 1140)	42.3% (40.0%, 44.5%)

3.2. Daily quarantine requirements for contact tracing

Fig. 4 displays the number of new quarantines per day for the three cell-level tracing scenarios, and Fig. 5 displays the number of new quarantines per day for the four all-level tracing scenarios. Table 4 provides the median total number of quarantines and the median number of new quarantines per day for the seven contact tracing scenarios. For the cell-level contact tracing with 50% of contacts traced, the median new quarantines per day was 0.8, meaning that around eleven residents were quarantining on average at once based on the 14-day quarantine period. Increasing this intervention to 100% of contacts traced doubled the median new quarantines per day to 1.6, meaning around twenty-two residents were quarantining on average each day. There was a higher daily new quarantine requirement for all-level tracing overall, but this resulted in a higher PIA. When 50% of contacts at all levels were traced, the resulting median quarantines per day was 9.4. On average 132 individuals were actively quarantining on a given day. Scaling this intervention up to 100% of contacts traced produces a median quarantines per day value of 14.1, equating to 197 residents quarantining on average per time step.

Combining depopulation, quarantining, and vaccination reduced the daily quarantine requirement for both cell-level and all-level tracing. All interventions combined with 100% cell-level tracing required just over one quarantine per day, equating to around fifteen residents quarantining on average per day. For the combined interventions with all-level contact tracing, the 100% quarantine capacity scenario had a median new quarantine requirement of 9.6 per day, which resulted in around 134 residents quarantining on average per time step. Reducing the quarantine capacity to 50% nearly halved the median daily quarantine requirement to 5.2, producing an average number of seventy-two residents quarantining per day. Decreasing the quarantine capacity to 50% in the all-level tracing intervention produced a more manageable new daily quarantine requirement while maintaining a higher PIA (36.7%).

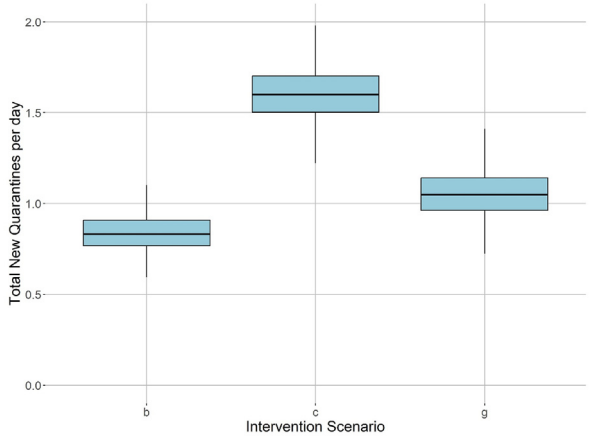

Fig. 4. Number quarantined per day across three hundred simulations for each of the three cell-level contact tracing scenarios – b: 50% cell-level contact tracing (CT), c: 100% cell-level CT, g: all combined (cell-level CT).

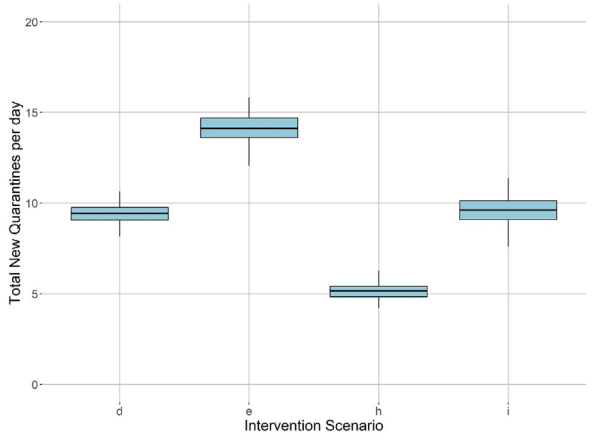

Fig. 5. Number quarantined per day across three hundred simulations for each of the four all-level contact tracing scenarios – d: 50% all-level contact tracing (CT), e: 100% all-level CT, h: all combined (all-level CT, limited quarantine capacity), i: all combined (all-level CT, full quarantine capacity).

Table 4
Median and IQR total number of quarantined individuals and median and IQR quarantined per day for seven scenarios with three hundred simulations per scenario.

Scenario Description	Label	Total Quarantined	Total Quarantined per day
		Median (IQR)	Median (IQR)
Cell-level contact tracing only (50% of contacts traced)	*b*	154 (142, 168)	0.83 (0.77, 0.91)
Cell-level contact tracing only (100% of contacts traced)	*c*	296 (278, 315)	1.60 (1.50, 1.70)
All-level contact tracing only (50% of contacts traced)	*d*	1746 (1676, 1805)	9.44 (9.06, 9.76)
All-level contact tracing only (100% of contacts traced)	*e*	2613 (2519, 2720)	14.12 (13.62, 14.70)
All interventions combined (Cell-level tracing)	*g*	194 (178, 211)	1.05 (0.96, 1.14)
All interventions combined (All-level tracing − 50% quarantine capacity)	*h*	956 (894, 1003)	5.16 (4.83, 5.42)
All interventions combined (All-level tracing − 100% quarantine capacity)	*i*	1779 (1679, 1873)	9.62 (9.08, 10.12)

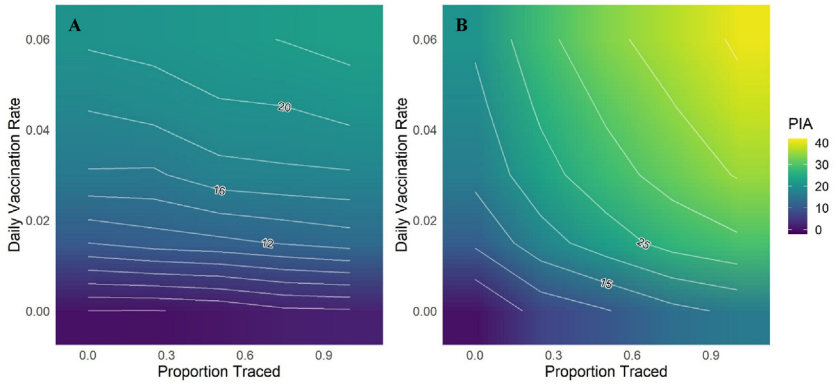

Fig. 6. Sensitivity analysis of percentage of infections averted (PIA) between (**A**) cell-level contact tracing or (**B**) all-level contact tracing and varying daily vaccination rates.

3.3. Sensitivity analyses

Fig. 6 provides the sensitivity analysis on the interaction of daily vaccination rate against proportion traced for (A) cell-level contact tracing, and (B) all-level contact tracing. For both interventions, the proportion traced ranged from 0 to 1. Additionally, daily vaccination rate varied from 0 (0 vaccines administered per day, 0 vaccines administered per week) to 0.06 (~90 vaccines administered per day, ~650 vaccines administered per week). When analyzing the cell-level tracing sensitivity analysis, we observed a low PIA across all proportions traced values at lower vaccination levels. Increases in the proportion traced at lower vaccination levels did not result in large increases in PIA. When the daily vaccinations increased significantly, higher proportions traced at the cell-level resulted in greater increases in PIA. In contrast, the proportion traced and daily vaccination rates for the all-level intervention worked additively across vaccination rates, as minimum increases in vaccination had large impacts on PIA when contacts were traced at higher proportions. All-level tracing and quarantining resulted in higher PIA overall when compared with the cell-level tracing and quarantining.

4. Discussion

4.1. Study implications

In this study modeling SARS-CoV-2 transmission in a carceral setting, none of the modeled interventions fully eliminated transmission between individuals at the cell and housing block levels. PIA for the individual interventions ranged from 1.8% to 19.5%, and combining interventions yielded PIAs ranging between 31.4% and 42.3% depending on the contact tracing intervention used. Due to the high rate of contacts between residents in this population, high rate of resident turnover, and external forces of infection, prevention of a full outbreak, with exponential increases in cases, was not obtainable in our model. Despite this, limiting the severity of COVID outbreaks is critical, and the combined interventions greatly reduced the estimated cumulative incidence over the modeled 185-day period.

Aside from recent COVID-19 modeling studies, modeling studies for other respiratory viruses in a jail and prison setting are limited. Much of the modeling previously conducted in this setting is focused on sexually transmitted infections (Ndeffo-Mbah et al., 2018). COVID models in jail settings have demonstrated that providing adequate resources such as vaccinations, increased space for quarantining, and reductions in the size of carceral populations are impactful interventions

(Greenhalgh & Provencher, 2022; Lofgren et al., 2022; Malloy et al., 2021). These interventions should be prioritized to prevent SARS-CoV-2 and other respiratory viral outbreaks.

Based on the intervention approaches taken in this study, cell-level tracing provided minimal impact on SARS-CoV-2 transmission, indicating it might be insufficient by itself. This was also evident in the sensitivity analysis at low vaccination rates. Although previous modeling studies have not analyzed the impact of quarantining cell- and block-levels separately, the quarantine functionality in our model allowed us to analyze the individual impacts of these approaches. If a resident contacted someone who was asymptomatic and released from jail prior to a positive test, they would not be traced. The high turnover and outflow present in this population had an impact on the effectiveness of contact tracing and quarantining, particularly at the jail cell-level. Another potential reason for this minimal impact was the high number of block contacts where transmissions can still occur. If a resident shared a cell with a single other individual, cell-level tracing may only result in one quarantine, despite the potential for one or more block-level contacts to acquire SARS-CoV-2. Quarantining individuals who share a cell with an infected individual was likely not sufficient to mitigate the spread of COVID-19 due to the high number of contacts occurring outside of the cell.

In contrast to the minimum effect of cell-level contact tracing on SARS-CoV-2 transmission, all-level (cells and blocks) contact tracing had a greater effect on transmission reduction. This approach to quarantining differed from the approach taken in the Greenhalgh and Provencher (2022) model, where only infected individuals were isolated instead of their contacts being quarantined. Despite this, contact tracing and quarantine produced similar reductions in cases over our modeled 185-day period to what was seen over a 2.6-year period of average incarceration in the Greenhalgh and Provencher (2022) model. Even though the structure of these interventions differed, identifying, and separating cases or contacts in this aggregate setting had the potential to reduce the impact of widespread transmission. Additionally, the effectiveness of contact tracing and quarantining can be combined with novel approaches to surveillance like wastewater sampling which could lead to quarantining cell blocks and containing transmission throughout the jail (Saber et al., 2024). Although there are modeled benefits of contact tracing at all levels, the quarantined population size may not be feasible when a jail is at or above maximum capacity. Combining this intervention with depopulation efforts maintained high PIA (36.7% or 42.3%) and provided sufficient space to quarantine people with a known exposure. All-level contact tracing was more effective than tracing at just the cell-level but combining it with other interventions may be necessary to increase its feasibility. In real-world settings, contact tracing has demonstrated effectiveness in limiting outbreaks, as it was used to identify asymptomatic infections from the contacts of a confirmed case in a Spanish prison (Vicente-Alcalde et al., 2022). Here, 15 asymptomatic cases were identified in a unit, which allowed the prison to enter a lockdown state and prevented transmission beyond the unit of interest (Vicente-Alcalde et al., 2022). Novel approaches to outbreak containment include separating or “cohorting” new admissions and vulnerable populations from the rest of the jail population (Coleman et al., 2022). Despite the clear impact of quarantining an infected resident's contacts on reducing transmission in this setting, feasibility may be limited when this approach is used independently.

Excess jail release and reducing new arrests in reference to COVID-19 have been explored in recent modeling studies (Lofgren et al., 2022; Malloy et al., 2021). In this model, excess jail release was moderate, only to reduce the population down to the level of full capacity. Specifically, the reduction in the population in the model was ~13%, from 3000 to 2600. This differs from the depopulation approaches taken by the Lofgren et al. (2022) and Malloy et al. (2021) studies. The Lofgren et al. (2022) study focused on decreasing new admissions rather than releasing excess prisoners, as conducting rapid release alone may pose a greater threat to community transmission. Coupling these approaches, such as the approach taken by Malloy et al. (2021), resulted in 83% fewer cases over an 83-day period. In the Lofgren et al. (2022) study, a blanket reduction in arrests of 90% reduced the number of incarcerated infections from 7421 at baseline to 1682. The interventions modeled in these studies resulted in greater population reductions than the reduction of approximately four hundred seen in this model, but these results demonstrate that even minimal reductions in carceral populations can potentially have a large effect on disease transmission. “Decarcerating” residents by releasing those who present the lowest risk to the community and slowing or suspending new arrests are important to limit the overcrowding in these already crowded settings (Akiyama et al., 2020). Globally, areas where decarceration was implemented did not report COVID-19 outbreaks, highlighting its real-world effectiveness as an intervention in the early stages of the pandemic (Henry, 2020). Nevertheless, one carceral facility does not exist in a void; rather, each links to the next in a chain. Decarcerating those posing little risk to community safety, and limiting entrants, cannot be a long-term strategy for community jails like FCJ. During COVID, the slowing of complex legal proceedings, combined with reluctance of prisons to accept promptly those found guilty, caused the population in jails to swell with residents facing felony charges, which comprised 93% of bed-days in FCJ during COVID (Lopez-Howard & Brown, 2022). We demonstrated for the situation at FCJ, combining interventions had an additive effect on mitigation.

Furthermore, vaccination campaigns in carceral settings have largely been unexplored in the modeling literature for COVID-19. Increasing the capacity to vaccinate residents within the jail was demonstrated to have a positive impact on PIA (11.0%), while also increasing the effectiveness of contact tracing, especially at the cell-level. This is likely because as the vaccination rate increases, the infrequent block-level contacts are less likely to result in a transmission with the provided protection from the COVID-19 vaccine. The closer, more frequent contacts at the cellular level are thus more likely to result in a transmission. Vaccination strategies in this setting, although largely underdeveloped for previous respiratory viral outbreaks, must prioritize increased access to vaccines and provision of comprehensible vaccine information to incarcerated persons and jail staff (Kronfli & Akiyama, 2020).

Given the association between incarcerated persons and COVID-19 risk factors, including "accelerated aging" taking place in these settings, some key policy and strategic changes may be warranted (Greene et al., 2018). These include prioritizing vaccine efforts towards individuals in congregate settings. Despite jails being an efficient vaccine-delivery system, this population has been historically neglected in vaccine distribution (Berk et al., 2021; Spaulding & Zawitz, 2022). By vaccinating incarcerated persons, community outbreaks may be diminished due to the high turnover rate from jails and prisons into the community (Berk et al., 2021).

4.2. Limitations

One limitation of this model was that we assumed constant community prevalence over time to represent an external force of infection. The two forces of infection from the community, infected admissions or staff transmissions, did not account for varying COVID-19 prevalence. Similarly, this model does not account for the effect of these interventions on overall community prevalence. Finally, this model used a single dose vaccination (i.e., J&J) to limit the complexity of multiple doses when using mRNA vaccines. Therefore, this model simplified the existing heterogeneity of immune response that now exists against COVID-19.

4.3. Conclusions

COVID-19 and future respiratory viruses pose challenges for high-density locations, such as jails and prisons. We found COVID-19 outbreaks in these settings were not completely avoidable due to the structured contact network and external forces of infection, but investing in a combination of interventions can have large effects within the jail or prison. Policy makers must prioritize this vulnerable population in future pandemic preparedness and response to alleviate the potential morbidity and mortality among incarcerated persons, which was higher during the COVID-19 pandemic than it was in the community (Saloner et al., 2020). Decarceration, contact tracing and quarantining, and vaccination remain the effective interventions to implement in this setting, and their effectiveness can be maximized by using multiple interventions in a single carceral setting.

CRediT authorship contribution statement

Isaac Schneider: Writing – original draft, Visualization, Resources, Methodology, Formal analysis, Data curation, Conceptualization. **Karina Wallrafen-Sam:** Writing – review & editing, Data curation. **Shanika Kennedy:** Project administration. **Matthew J. Akiyama:** Writing – review & editing, Resources, Project administration, Conceptualization. **Anne C. Spaulding:** Writing – review & editing, Resources, Funding acquisition, Data curation. **Samuel M. Jenness:** Writing – review & editing, Validation, Supervision, Software, Methodology, Data curation, Conceptualization.

Disclaimer

The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the funding agencies.

Funding

This work was supported by National Institutes of Health grant R01 AI138783 and a Bill & Melinda Gates Foundation Grant (INV-035562)

Declaration of interests

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Anne Spaulding:

In addition to funding from the NIH and Gates Foundation, Dr. Spaulding has received in the past 3 years funding through her university from HRSA and Health through Walls, and internal funding from Emory University. She has personally received consulting fees from the Medical Association of Georgia and funding for travel from the Infectious Disease Society of America.

Matthew Akiyama:

Reports grants from NIH NIDA (K99/R00 DA043011; DP2 DA053730), NIMDH (R01 MD016744), NIAID (P30 AI124414), and investigator-initiated funding paid to his institution from Gilead Sciences and Abbvie.

Acknowledgements

The research team wants to thank the Fulton County Sheriff Patrick Labat and jail staff, especially Records Manager Ms. Kielah Yancey, for their invaluable assistance.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.idm.2025.02.001.

References

Akiyama, M. J., Spaulding, A. C., & Rich, J. D. (2020). Flattening the curve for incarcerated populations—covid-19 in jails and prisons. *New England Journal of Medicine, 382*(22), 2075–2077. https://doi.org/10.1056/NEJMp2005687

Bartekwa, J. W., Abene, E. E., Luka, P. D., Yilgwan, C. S., & Shehu, N. Y. (2021). COVID-19 subclinical infection and immunity: A review. *Nigerian Journal of Medicine: Journal of the National Association of Resident Doctors of Nigeria, 30*(6), 631–636. https://doi.org/10.4103/njm.njm_85_21

Berk, J., Rich, J. D., & Brinkley-Rubinstein, L. (2021). Why we vaccinate incarcerated people first. *eClinicalMedicine, 35*. https://doi.org/10.1016/j.eclinm.2021.100864

Bick, J. A. (2007). Infection control in jails and prisons. *Clinical Infectious Diseases, 45*(8), 1047–1055. https://doi.org/10.1086/521910

Centers for Disease Control and Prevention. (2012). Receipt of A(H1N1)pdm09 vaccine by prisons and jails—United States, 2009–10 influenza season. https://www.cdc.gov/mmwr/preview/mmwrhtml/mm6051a3.htm.

Centers for Disease Control and Prevention. (2020). *COVID data tracker*. Centers for Disease Control and Prevention. https://covid.cdc.gov/covid-data-tracker.

Centers for Disease Control and Prevention, National Center for Health Statistics. (n.d.). Underlying Cause of Death, 2018-2021, Single Race Request. Retrieved April 24, 2024, from https://wonder.cdc.gov/ucd-icd10-expanded.html.

Coleman, P. C., Pailing, A., Roy, A., O'Moore, É., Chandan, J. S., Lumby, V., Newton, P., Taylor, A., Robinson, E., Swindells, J., Dowle, S., & Gajraj, R. (2022). Implementation of novel and conventional outbreak control measures in managing COVID-19 outbreaks in a large UK prison. *BMC Public Health, 22*, 677. https://doi.org/10.1186/s12889-022-12991-7

Georgia Department of Public Health. (2024). Georgia COVID-19 dashboard. https://ga-covid19.ondemand.sas.com/.

Greene, M., Ahalt, C., Stijacic-Cenzer, I., Metzger, L., & Williams, B. (2018). Older adults in jail: High rates and early onset of geriatric conditions. *Health & Justice, 6*, 3. https://doi.org/10.1186/s40352-018-0062-9

Greenhalgh, S., & Provencher, A. (2022). Inclusive health: Modeling COVID-19 in correctional facilities and communities. *BMC Public Health, 22*(1), 982. https://doi.org/10.1186/s12889-022-13313-7

Henry, B. F. (2020). Social distancing and incarceration: Policy and management strategies to reduce COVID-19 transmission and promote health equity through decarceration. *Health Education & Behavior: The Official Publication of the Society for Public Health Education, 47*(4), 536. https://doi.org/10.1177/1090198120927318

Jenness, S. M., Goodreau, S. M., & Morris, M. (2018). EpiModel: An R package for mathematical modeling of infectious disease over networks. *Journal of Statistical Software, 84*(1), 1–47.

Jenness, S. M., Wallrafen-Sam, K., Schneider, I., Kennedy, S., Akiyama, M. J., & Spaulding, A. C. (2023). Dynamic contact networks of residents of an urban jail in the era of SARS-CoV-2. *medRxiv: The Preprint Server for Health Sciences, 2023*. https://doi.org/10.1101/2023.09.29.23296359

Kronfli, N., & Akiyama, M. J. (2020). Prioritizing incarcerated populations for COVID-19 vaccination and vaccine trials. *EClinicalMedicine, 31*, Article 100659. https://doi.org/10.1016/j.eclinm.2020.100659

Lee, A. S., Berendes, D. M., Seib, K., Whitney, E. A. S., Chavez, R. S., Meyer, P. L., Berkelman, R. L., Omer, S. B., & Spaulding, A. C. (2014). Distribution of A(H1N1) pdm09 influenza vaccine: Need for greater consideration of smaller jails. *Journal of Correctional Health Care: The Official Journal of the National Commission on Correctional Health Care, 20*(3), 228–239. https://doi.org/10.1177/1078345814532223

Lofgren, E. T., Lum, K., Horowitz, A., Mabubuonwu, B., Meyers, K., & Fefferman, N. H. (2022). Carceral amplification of COVID-19: Impacts for community, corrections officer, and incarcerated population risks. *Epidemiology, 33*(4), 480–492. https://doi.org/10.1097/EDE.0000000000001476

Lopez-Howard, S., & Brown, R. (2022). Fulton county jail population review: Assessing short-and long-term jail use trends. *Justice Policy Board*. https://roughdraftatlanta.com/wp-content/uploads/2022/11/Justice-Policy-Board-Report-Nov.-18-2022.pdf.

Lorscheid, I., Heine, B.-O., & Meyer, M. (2012). Opening the 'black box' of simulations: Increased transparency and effective communication through the systematic design of experiments. *Computational & Mathematical Organization Theory, 18*(1), 22–62. https://doi.org/10.1007/s10588-011-9097-3

Lysenko, M., & D'Souza, R. M. (2008). A framework for megascale agent based model simulations on graphics processing units. *The Journal of Artificial Societies and Social Simulation, 11*(4), 1–10.

Malloy, G. S. P., Puglisi, L., Brandeau, M. L., Harvey, T. D., & Wang, E. A. (2021). Effectiveness of interventions to reduce COVID-19 transmission in a large urban jail: A model-based analysis. *BMJ Open, 11*(2), Article e042898. https://doi.org/10.1136/bmjopen-2020-042898

Methi, F., & Madslien, E. H. (2022). Lower transmissibility of SARS-CoV-2 among asymptomatic cases: Evidence from contact tracing data in Oslo, Norway. *BMC Medicine, 20*(1), 427. https://doi.org/10.1186/s12916-022-02642-4

Minton, T. D., Beatty, L. G., & Zeng, Z. (2021). *Correctional populations in the United States, 2019 — statistical tables*. Bureau of Justice Statistics. https://bjs.ojp.gov/library/publications/correctional-populations-united-states-2019-statistical-tables.

Ndeffo-Mbah, M. L., Vigliotti, V. S., Skrip, L. A., Dolan, K., & Galvani, A. P. (2018). Dynamic models of infectious disease transmission in prisons and the general population. *Epidemiologic Reviews, 40*(1), 40–57. https://doi.org/10.1093/epirev/mxx014

Saber, L. B., Kennedy, S. S., Yang, Y., Moore, K. N., Wang, Y., Hilton, S. P., Chang, T. Y., Liu, P., Phillips, V. L., Akiyama, M. J., Moe, C. L., & Spaulding, A. C. (2024). Correlation of SARS-CoV-2 in wastewater and individual testing results in a jail, Atlanta, Georgia, USA. *Emerging Infectious Diseases, 30*(13), S21–S27. https://doi.org/10.3201/eid3013.230775

Saloner, B., Parish, K., Ward, J. A., DiLaura, G., & Dolovich, S. (2020). COVID-19 cases and deaths in federal and state prisons. *JAMA, 324*(6), 602–603. https://doi.org/10.1001/jama.2020.12528

Spaulding, A. C., & Zawitz, C. (2022). Vaccination in prisons and jails: Corrections needed in future plans. *Clinical Infectious Diseases, 75*(1), e846–e848. https://doi.org/10.1093/cid/ciab1031

Tan, J., Ge, Y., Martinez, L., Sun, J., Li, C., Westbrook, A., Chen, E., Pan, J., Li, Y., Cheng, W., Ling, F., Chen, Z., Shen, Y., & Huang, H. (2022). Transmission roles of symptomatic and asymptomatic COVID-19 cases: A modelling study. *Epidemiology and Infection, 150*, e171. https://doi.org/10.1017/S0950268822001467

Tolles, J., & Luong, T. (2020). Modeling epidemics with compartmental models. *JAMA, 323*(24), 2515–2516. https://doi.org/10.1001/jama.2020.8420

Tsai, P.-H., Lai, W.-Y., Lin, Y.-Y., Luo, Y.-H., Lin, Y.-T., Chen, H.-K., Chen, Y.-M., Lai, Y.-C., Kuo, L.-C., Chen, S.-D., Chang, K.-J., Liu, C.-H., Chang, S.-C., Wang, F.-D., & Yang, Y.-P. (2021). Clinical manifestation and disease progression in COVID-19 infection. *Journal of the Chinese Medical Association, 84*(1), 3–8. https://doi.org/10.1097/JCMA.0000000000000463

Vicente-Alcalde, N., Ruescas-Escolano, E., Franco-Paredes, C., & Tuells, J. (2022). Control of a COVID-19 outbreak in a Spanish prison: Lessons learned in outbreak control. *Frontiers of Medicine, 9*, Article 806438. https://doi.org/10.3389/fmed.2022.806438

Woloshin, S., Patel, N., & Kesselheim, A. S. (2020). False negative tests for SARS-CoV-2 infection—challenges and implications. *New England Journal of Medicine, 383*(6), Article e38. https://doi.org/10.1056/NEJMp2015897

World Health Organization. (2024). *WHO COVID-19 dashboard*. Datadot. https://data.who.int/dashboards/covid19/cases.