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Interventions for SARS-CoV-2 Prevention among Incarcerated Adults: A Network-Based Modeling Analysis

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2020

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An abstract of
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Abstract

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Background. COVID-19 presents challenges in settings like jails or prisons with a high density of contacts. The state of Georgia has seen limited COVID vaccine uptake with one of the highest incarceration rates in the United States. 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.

Methods. 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 common space. Contact tracing and quarantining were simulated at the cell-level or both the cell- and block-levels. A reference scenario and nine intervention scenarios were simulated 300 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 in the midst of a potential COVID outbreak in the jail. The cumulative incidence, number of infections averted (NIA), and percentage of infections averted (PIA) were calculated for all scenarios. 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. Additionally, a sensitivity analysis was conducted to compare the interaction between vaccination rates and contact tracing rates.

Results. We found that cell-level contact tracing was a relatively ineffective intervention by itself (3.2% PIA), but its effectiveness increased when combining it with other interventions (i.e., vaccination or increased jail release rate). The other intervention strategies each produced a PIA of 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 is limited without a reduction in the jail population.

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

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INTRODUCTION.

Controlling the spread of infectious diseases in carceral settings remains challenging. Overcrowding, limited infection control, and inefficient health care delivery together produce an environment prone to disease outbreaks.[1] During the H1N1 epidemic, this issue was confounded by the fact that over half of the jails in the United States did not receive H1N1 vaccine.[2] Due to continued apathy towards jails and prisons in pandemic preparedness and response, the COVID-19 pandemic has presented new challenges in outbreak prevention among incarcerated persons.

Since its start in early 2020, the global COVID-19 pandemic has caused over 750 million cases globally, resulting in almost 7 million deaths.[3] In the United States specifically, there have been over 100 million cases of COVID-19 with around 1.1 million deaths.[3] 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 locations. In the state of Georgia, which has one of the lowest fully vaccinated rates but highest incarceration rates in the country, there have been over 2.3 million confirmed COVID cases with over 35,000 confirmed COVID-related deaths.[4-6] Given the large carceral population, Georgia jails and prisons remain vulnerable to further COVID-19 outbreaks, despite the large impact that an investment in minor interventions would have on disease transmission.

Infectious disease modeling studies have found that a variety of interventions within a jail or prison reduce COVID-19 transmission both within the jail and into the broader community. Previous studies have used stochastic or deterministic compartmental modeling to analyze 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.[7-9] These interventions have shown effectiveness alone and in combination, highlighting the high return on

investment these interventions would bring.[7-9] Even though effectiveness has been demonstrated, these studies utilize compartmental models which assume random, homogenous mixing within compartments, and memoryless contacts.[10] A major challenge for infectious disease modeling within a carceral setting is the complexity of the contact network structure, which may not be sufficiently represented by compartmental models.[9] Network models allow for the development of a heterogeneous contact network where transmissions occur, similar to the dynamic seen within a jail or prison.[9]

In this study, we developed a network-based transmission model for SARS-CoV-2 in a Georgia jail population that represents common challenges in infectious disease response. This study seeks to understand how vaccination, contact tracing and quarantining, and jail depopulation impact SARS-CoV-2 transmission. These findings may provide a possible intervention framework within jails/prisons for future respiratory viral outbreaks.

METHODS.

Study design. This analysis used a network-based transmission model of infectious disease dynamics. This model was built with the EpiModel package in R.[11] Fulton County Jail (FCJ) was used as a representative population, and the outbreak was simulated over 185 daily time steps. Statistics were drawn from a prior descriptive analysis, where daily 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.[12] 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 brought into the jail population were modeled as fully vaccinated.

Although there was potential SARS-CoV-2 transmission to officers and other staff within the jail, the modeled population was limited to residents (persons who are incarcerated) to analyze the effects of interventions solely on the population living in these settings. However, residents were able to acquire SARS-CoV-2 from officers in the model through an indirectly modeled community infection mechanism. Sourced parameters of interest are present in **Table 1**. Nine intervention scenarios were developed (and a baseline scenario) to analyze the effect of various interventions working both individually and in conjunction with other interventions (see **Table 2**). For all scenarios, 30 infected individuals were introduced into the jail at time step 1.

COVID model structure. Building from the EpiModel software platform, we developed new features in the EpiModelCOVID package, which provides an existing structure to analyze situations regarding SARS-CoV-2 transmission. This model utilized an SEIR disease stage structure, resulting in individual, stochastic transitions between stages (see **Figure 1**). After acquiring SARS-CoV-2, an individual moved into an exposed (latent) stage. When the quarantine intervention was active, an individual was placed in quarantine if they had contact with someone known to be positive for COVID-19. If a quarantined individual went the full 14 days without developing infection, they were released from quarantine. Once an individual reaches the exposed stage, they can transition to either the pre-clinical (symptomatic) or sub-clinical (asymptomatic) routes. A pre-clinical infection would lead to a clinical infection followed by hospitalization and death, recovery, or hospitalization and recovery. The subclinical infection would lead to recovery without the development of symptoms. Individuals following the sub-clinical pathway had reduced transmission when compared to individuals with symptoms. PCR testing was conducted throughout the simulations with a sensitivity of 80%.

Intervention design. The nine intervention scenarios were built around three types of interventions: contact tracing and quarantining, release of persons who are incarcerated to an established capacity, and vaccination. Because we represented modes of transmission that would occur regardless of intervention effectiveness (i.e., community-acquired transmissions from officers), the main outcome of interest for analysis was based solely on 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 person within the jail. Since contacts would be easy to narrow down for existing people within the jail, once an individual received a positive diagnosis their contacts were able to be traced and quarantined at the same time step. Although this may not be a realistic assumption outside of this setting, we perceive the existence of a time lag between a close contact and contact tracing as not necessary in this setting due to the lack of need to spend resources tracking down contacts needed within the broader community. Additionally, any lag resulted in missing contacts due to the high rate of turnover within this population. Quarantining reduced the contact intensity for both the cell and block networks by 90%. The next major intervention involved doubling the rate of jail release until the population reaches 2600, a target closer to the maximum capacity of the representative jail.[12] Inherently this reduced the number of contacts between individuals and limit the opportunities for transmission. Lastly, vaccination sought to reduce acquisition of SARS-CoV-2 while reducing transmission. In addition to scenarios where each intervention was working independently, scenarios using combinations of these interventions were simulated.

Model analysis. Each of the model scenarios was simulated 300 times, and cumulative incidence was calculated per simulation to produce boxplots for general analysis. Additionally, both the number of infections averted (NIA) and percentage of infections averted (PIA) were calculated per simulation relative to the base scenario with no interventions. The median was calculated per

scenario across simulations to conduct analyses between interventions. 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 the sensitivity analysis between the proportion traced and daily vaccination rate, both the cell-level tracing and all-level tracing started with 25 scenarios simulated 100 times each to determine their combined effects on the outcome of interest – PIA.

RESULTS.

Descriptive statistics. The jail is divided into seven floors, with each containing as many as six blocks, and the standard block containing 19 cells.[12] Demographically, the jail population was primarily black (89.3%), between the ages of 20-39 (64.4%) and male (100%).[12] Strong assortative mixing was noted within age groups, with 33% of both cell- and block-level contacts occurring within defined age groups.[12] Generally, 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.[12] These listed statistics were used to parameterize the model for this representative population.

Primary intervention results. Prior to simulating the different scenarios, the baseline without interventions was simulated. The median cumulative incidence for all transmission mechanisms across 300 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 have no effect on the external forces of infection (i.e., infection from staff member 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.

Figure 2 displays the cell- and block-level PIA for the nine intervention scenarios, and **Figure 3** displays the cumulative cell- and block-level incidence for the nine intervention scenarios plus the baseline scenario. **Table 3** displays the median and IQR cumulative incidence, PIA, and NIA for the ten scenarios. When single interventions were used, 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 values 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) vaccination alone as an intervention 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. The interventions appeared to work additively. Combining cell-level tracing with other interventions increased its effectiveness ten-fold as the scenario using all interventions combined with cell level tracing produced a median PIA of 31.4%. Reducing quarantine capacity for all-level contact tracing from 100% to 50% only had a reduction in median PIA of 5.6% (42.3% to 36.7%).

Daily quarantine requirements for contact tracing. **Figure 4** displays the number of new quarantines per day for the three cell-level tracing scenarios, and **Figure 5** displays the number of new quarantines per day for the four all-level tracing scenarios. **Table 4** displays 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 is 0.8, meaning that around 11 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 22 residents were quarantining on

average each day. When looking at the intervention outputs, there is a higher daily new quarantine requirement for all-level tracing overall, but this results in a higher PIA. When 50% of contacts at all levels were traced, the resulting median quarantines per day was 9.4. The 14-day average was 132, meaning that 132 individuals were 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 reduces the daily quarantine requirement for both cell-level and all-level tracing. All interventions combined with 100% cell-level tracing required just over 1 quarantine per day, equating to around 15 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 halves the median daily quarantine requirement to 5.2, producing an average number of 72 residents quarantining per day. Decreasing the quarantine capacity to 50% in the all-level tracing intervention produces a more manageable new daily quarantine requirement while maintaining a higher PIA (36.7%).

Bivariate scenario analyses. **Figure 6** provides the sensitivity analysis output displaying daily vaccination rate against proportion traced for (A) cell-level contact tracing, and (B) all-level contact tracing. For both interventions, the proportion traced varied 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, it is important to note the 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 were ramped up significantly, increases in the proportion 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. Like the results presented above, all-level tracing and quarantining resulted in higher PIA overall when compared with the cell-level tracing and quarantining.

DISCUSSION.

When modeling SARS-CoV-2 transmission in a carceral setting, none of the proposed interventions could fully eliminate transmission between individuals at the cell and block levels. PIA for the individual interventions ranged from 1.8% to 19.5%, and combining interventions worked additively with PIA values 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 turnover, and other mechanisms of infection, full outbreak prevention in our model was not obtainable with the listed parameters and starting conditions. Despite this, limiting the severity of these outbreaks is still important, and the combined interventions were able to greatly reduce cumulative incidence over a 185-day period. Aside from recent COVID-19 modeling studies, modeling studies for other respiratory viruses in a jail and prison setting are scarce or nonexistent in the literature. Much of the modeling previously conducted in this setting is focused on STDs or STIs.[14] With modeling studies demonstrating the in-jail and community impact of transmission in carceral settings, there is enough evidence that providing adequate resources such as vaccinations, increased space for quarantining, and reductions in the size of carceral populations are all effective

interventions.[7-9] These interventions should be prioritized to prevent SARS-CoV-2 outbreaks now and to prevent other respiratory viral outbreaks in the future.

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 is also evident in the sensitivity analysis at low vaccination rates. Although previous modeling studies did not analyze the impact of quarantining at the cell-level, the quarantine functionality in this model likely plays a role on this intervention's individual impact. If an individual contacted someone who was asymptomatic and released 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, especially at the cellular level. Another potential reason for this minimal impact is the high number of block contacts where infections can still occur. If a resident shares a cell with a single other individual, cell-level tracing may only result in one quarantine, but the high number of block-level contacts may have also acquired SARS-CoV-2. Quarantining individuals who share a cell with an infected individual is likely not sufficient to mitigate the spread of COVID-19 due to the high degree 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 contact tracing had a greater effect on transmission reduction. This approach to quarantining differed from the approach taken in the Greenhalgh and Provencher model, where only infected individuals were quarantined instead of their contacts.[7] Despite this, testing and quarantine produced similar reductions in cases over a 185-day period in this model to what was seen over a 2.6-year period of average incarceration in the Greenhalgh and Provencher model.[7] Even though the structure of these interventions differed, identifying, and separating cases or contacts in this aggregate setting has 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 to quarantine blocks and contain transmission throughout the jail.[12] 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 is more effective than tracing at just the cell-level but combining it with other interventions may be necessary to increase its feasibility.

Excess jail release and reducing new arrests in reference to COVID-19 have been explored in recent modeling studies.[8,9] In this model, excess jail release occurred until the jail population was closer to the jail capacity from a starting population size of 3000 to 2600. This differs from the depopulation approaches taken by the Lofgren et al. and Malloy et al. studies.[8,9] The Lofgren et al. study focused on decreasing new admissions rather than releasing excess prisoners, as conducting rapid release alone may pose a greater threat to community transmission.[8] Coupling these approaches, such as the approach taken by Malloy et al. resulted in 83% fewer cases over an 83-day period.[9] In the Lofgren et al. study, a blanket reduction in arrests of 90% reduced the number of incarcerated infections from 7421 at baseline to 1682.[8] The interventions modeled in these studies resulted in greater population reductions than the reduction of approximately 400 seen in this model, but these results demonstrate that even minimal reductions in carceral populations can potentially have a large effect on respiratory viral transmission.

Conversely, vaccination campaigns have largely been unexplored in the modeling literature for COVID-19, but vaccination remains paramount to the reduction in transmission of respiratory viruses. 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 more people are vaccinated, the infrequent block-level contacts are less likely to result in a transmission with the provided protection from the COVID-19 vaccines. 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.

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 should be enacted.[15] These include prioritizing vaccine efforts towards individuals in congregate settings, especially for future respiratory viruses. Despite surpluses existing within communities, and jails being an efficient vaccine-delivery system, this population has been historically neglected vaccines.[16,17] By vaccinating incarcerated persons, community outbreaks are diminished due to the high turnover rate from jails and prisons into the community.[17] Also, "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.[18] Globally, areas where decarceration was implemented did not report COVID-19 outbreaks, highlighting its effectiveness as an intervention.[19] Contact tracing has also demonstrated effectiveness in limiting outbreaks, as it was used to identify asymptomatic infections from the contacts of a confirmed case in a Spanish prison.[20] 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.[20] Novel approaches to outbreak containment include separating or "cohorting" new admissions and vulnerable populations from the rest of the jail population.[21] Combining various interventions in a

multi-faceted or combination approach should be the policy focus moving forward to protect this vulnerable population from COVID-19 and other respiratory pathogens.

Limitations. The main limitation of this model was that the cell- and block-level layers were not represented hierarchically, meaning that a resident's cell-level contacts were not included as block-level contacts. The inherent structure of jails and prisons results in all cell-level contacts being block-level contacts, given that cellmates always share a common space or block. Future iterations of this model will include the hierarchical structure that is more representative of contact networks within this setting. Another limitation was an assumed constant community prevalence over time. The two forces of infection from the community, infected admissions or staff transmissions, did not account for varying COVID-19 prevalence. Finally, this model used a single dose vaccination (i.e., J&J) to limit the complexity of 4+ doses when using mRNA vaccines. With updated boosters and additional doses now available, this model simplified the existing heterogeneity of immune response that now exists against COVID-19.

Conclusions. COVID-19 and future respiratory viruses pose challenges for high-density locations, such as jails and prisons. This study finds that outbreaks in these settings are 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.[22] Decarceration, contact tracing and quarantining, and vaccination remain the most effect interventions to implement in this setting.

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TABLES AND FIGURES

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	Calibrated parameter
Mean degree – block level	33.50	Jenness et. al, 2023
Daily contacts – block level	0.5	Calibrated parameter
Community infection rate	0.001	Calibrated parameter
Quarantine contact rate reduction	0.1	Calibrated parameter
Daily vaccination rate	See **Table 2**	Calibrated parameter, sensitivity analysis
Proportion traced	See **Table 2**	Calibrated parameter, sensitivity analysis
Proportion quarantined	See **Table 2**	Calibrated parameter
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	CDC WONDER Database

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 reaches 2600 – FCJ capacity)
All interventions combined (Cell-level tracing)	0.015 ~150 per week	1	1	2*0.014 (until population reaches 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 reaches 2600 – FCJ capacity)
All interventions combined (All-level tracing – 100% quarantine capacity)	0.015 ~150 per week	1	1	2*0.014 (until population reaches 2600 – FCJ capacity)

Table 3. *Median and IQR cumulative incidence and median and IQR number and percentage of infections averted for nine scenarios against a baseline with 300 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%)

Table 4. *Median and IQR total number of quarantined individuals and median and IQR quarantined per day for seven scenarios with 300 simulations per scenario*

Scenario Description	Label	Total Quarantined Median (IQR)	Total Quarantined per day 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)

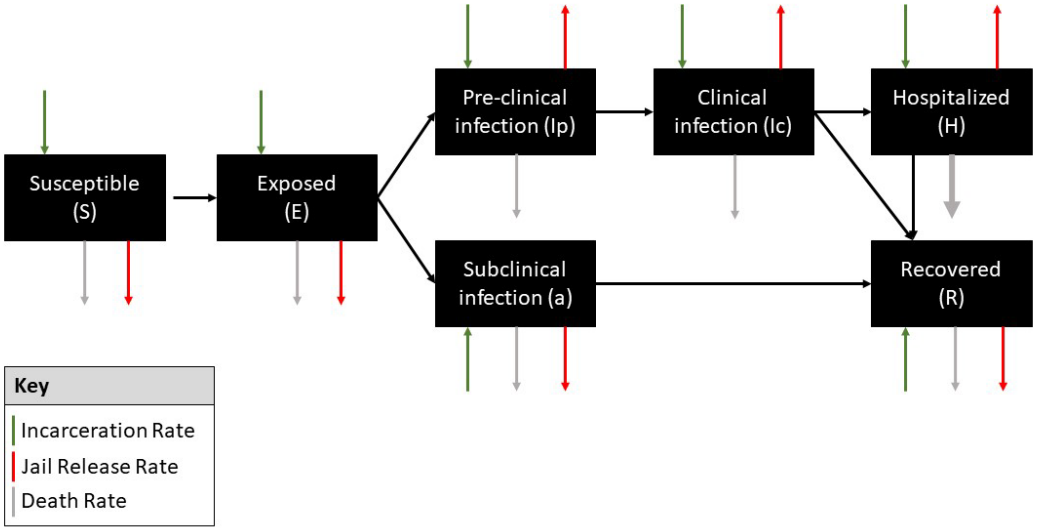

Figure 1. *Disease transmission process displaying the stages of infection, transition between stages, and entry/exit processes*

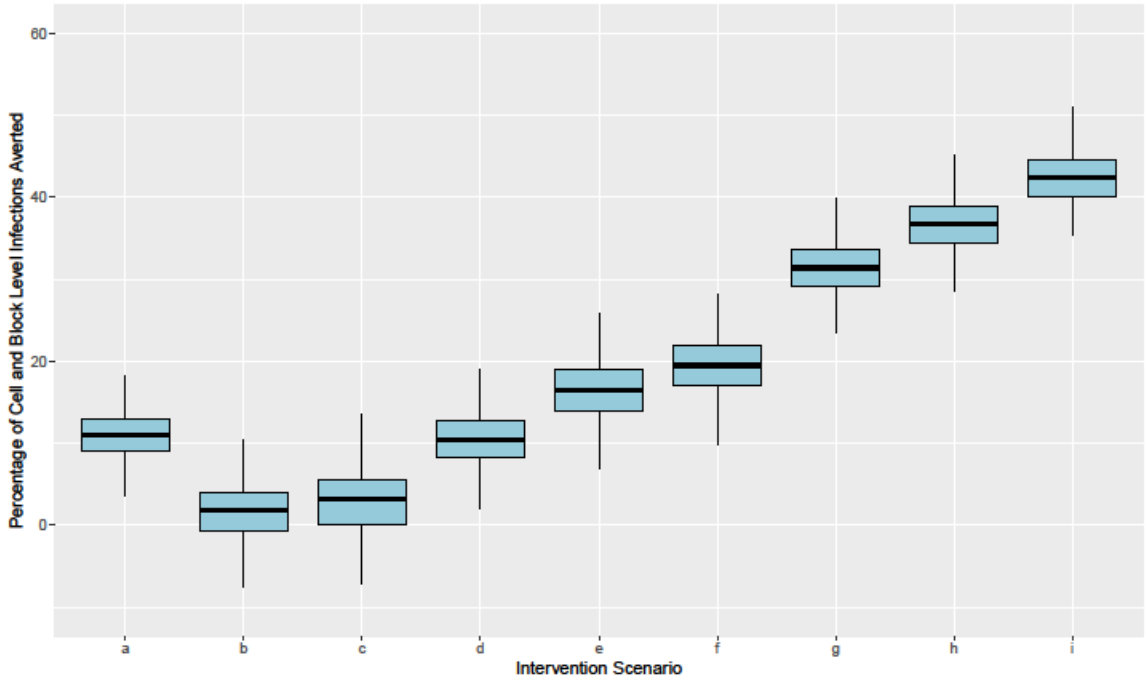

Figure 2. *Percentage of cell and block-level infections averted across 300 simulations for each of the nine scenarios – a: vaccination, b: 50% cell-level contact tracing (CT), c: 100% cell-level CT, d: 50% all-level CT, e: 100% all-level CT, f: jail release, g: all combined (cell-level CT), h: all combined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

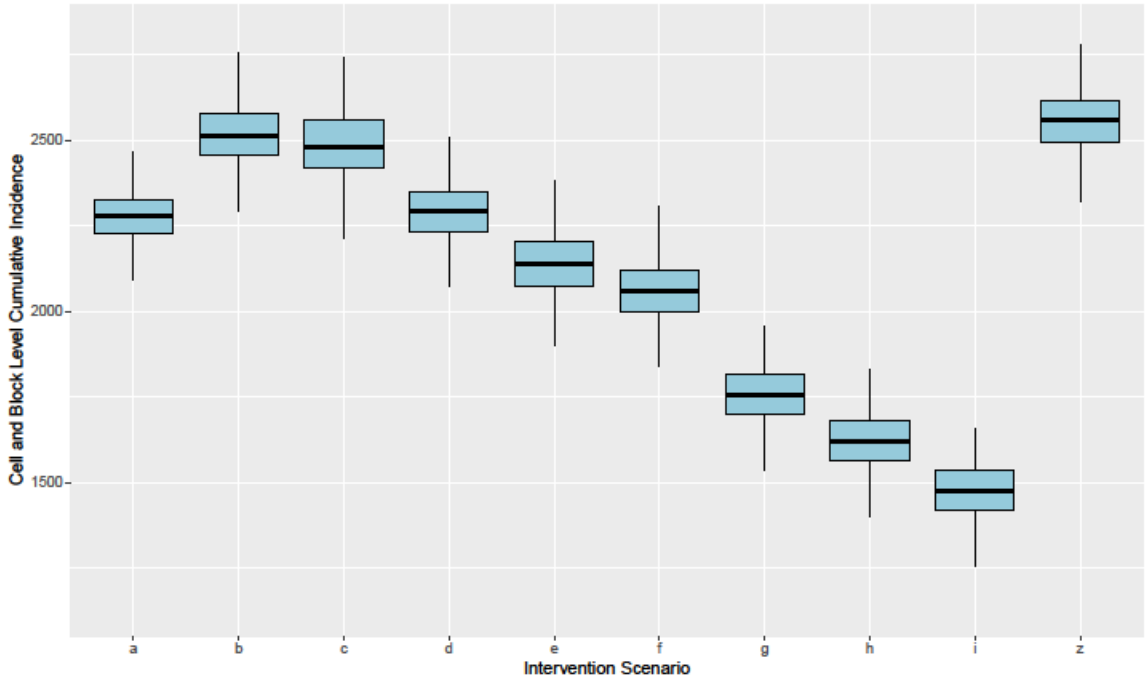

Figure 3. *Cell and block-level cumulative incidence across 300 simulations for each of the nine scenarios and a baseline scenario – a: vaccination, b: 50% cell-level contact tracing (CT), c: 100% cell-level CT, d: 50% all-level CT, e: 100% all-level CT, f: jail release, g: all combined (cell-level CT),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

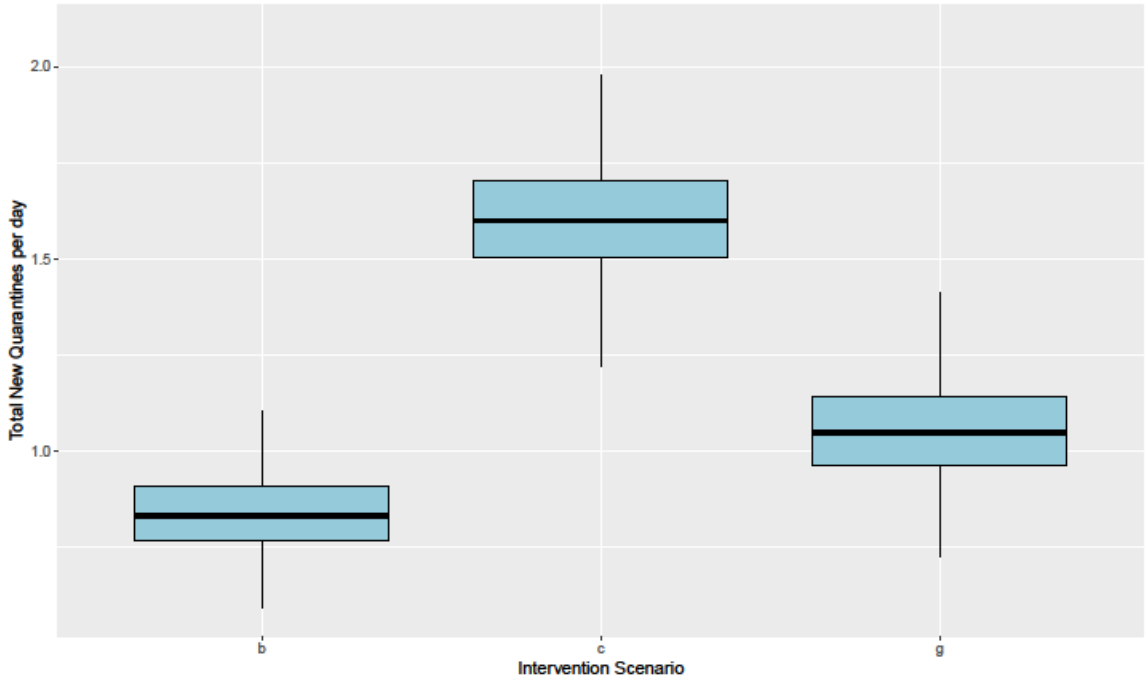

Figure 4. *Number quarantined per day across 300 simulations for each of the three cell-level contact tracing scenarios – b: 50% cell-level contact tracing (CT), c: 100% cell-level CT, g: all combined (cell-level CT)*

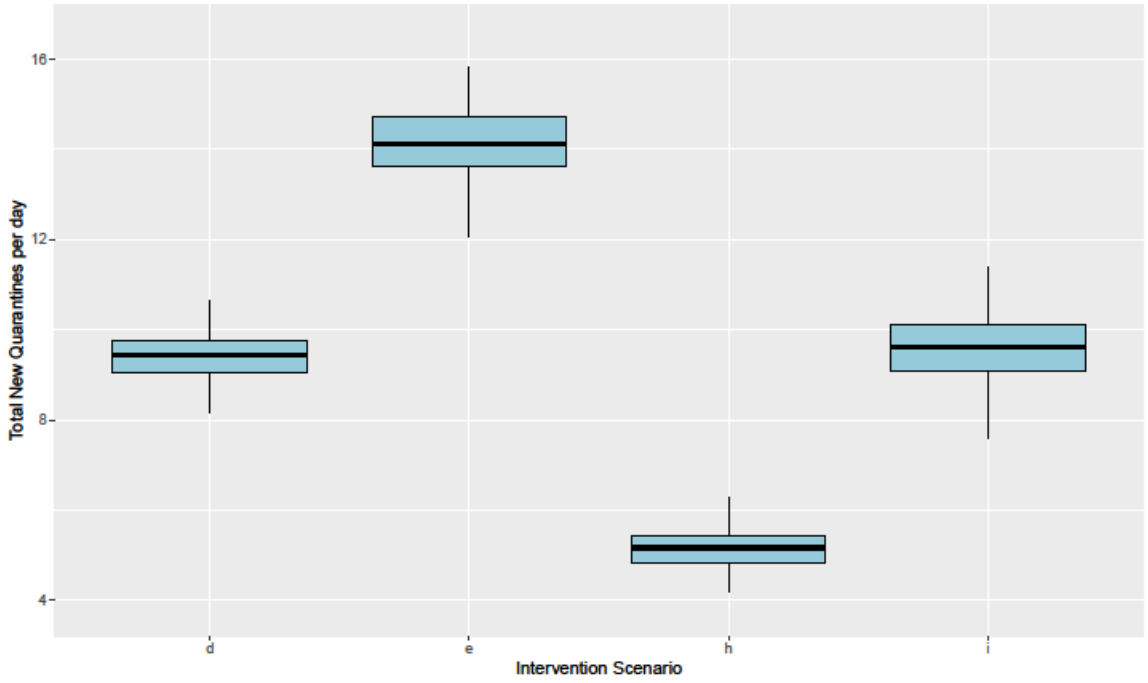

Figure 5. *Number quarantined per day across 300 simulations for each of the four all-level contact tracing scenarios – d: 50% all-level contact tracing (CT), e: 100% all-level CT, h: all combined (all-level CT, limited quarantine capacity), i: all combined (all-level CT, full quarantine capacity)*

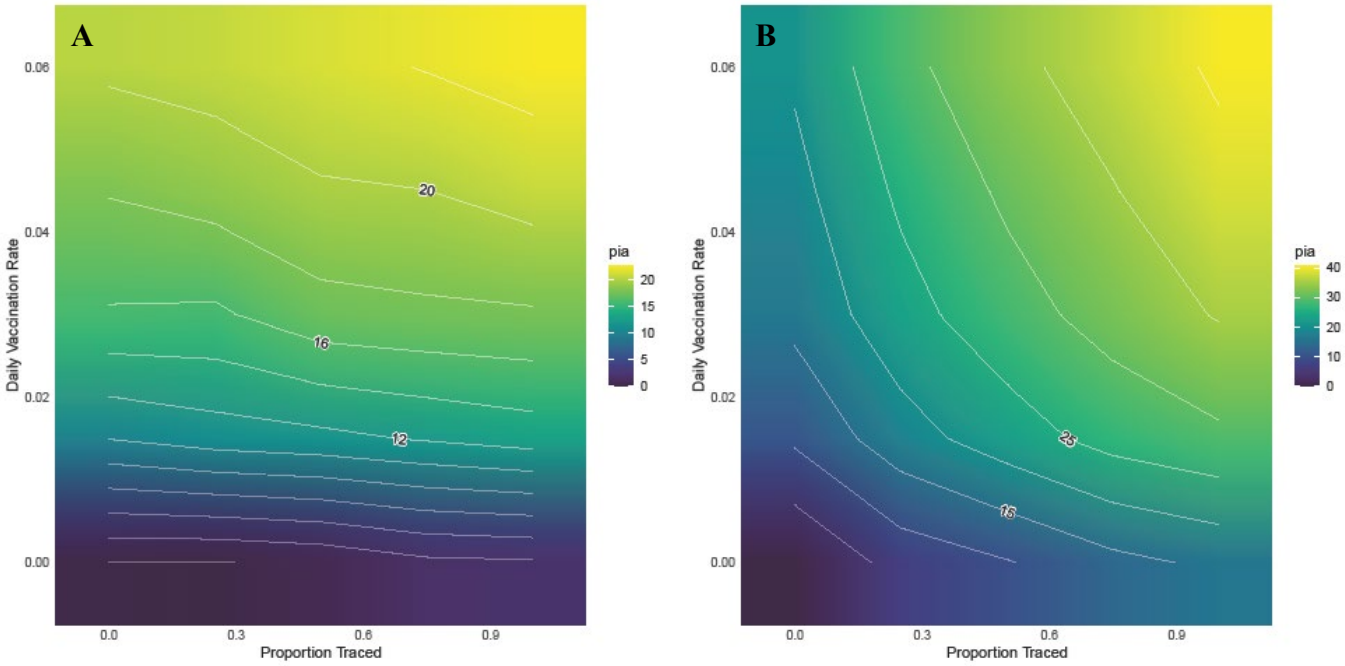

Figure 6. *Sensitivity analysis of percentage of infections averted (PIA) between (**A**) cell-level contact tracing or (**B**) all-level contact tracing and varying daily vaccination rates*