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MATHEMATICAL AND STATISTICAL MODELING OF INFECTIOUS DISEASE TRANSMISSION DYNAMICS IN URBAN AND RURAL COMMUNITY SETTINGS

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Abstract

This study investigates the impact of increased vaccination coverage on peak infection rates across urban and rural settings using SEIR and SIR epidemiological modeling frameworks. Baseline analysis revealed significantly higher peak infection rates in urban areas (23.4%) compared to rural areas (14.7%), primarily due to higher population densities and contact rates. Scenario simulations demonstrated that increasing vaccination coverage by 10% reduced urban peaks to 18.7% and rural peaks to 11.9%, while a 20% increase further lowered these rates to 14.5% and 9.4%, respectively. Sensitivity analysis identified $R0R_0$ R0 and contact rate as the most influential parameters affecting total infections, highlighting the importance of targeted interventions. The SEIR model consistently provided more accurate projections than the SIR model, supported by lower RMSE and AIC values. These findings underscore the value of vaccination campaigns as a primary control measure, especially in high-density areas. Policy recommendations include integrating real-time $R0R_0$ R0 monitoring, expanding immunization programs, and employing public awareness initiatives to reduce contact rates. The research further suggests that hybrid modeling approaches incorporating socio-behavioral and environmental factors could enhance predictive accuracy. Overall, this study contributes to evidence-based public health strategies by demonstrating the quantifiable benefits of increased vaccination coverage in mitigating disease peaks and optimizing resource allocation.

INTRODUCATION

There had been significant differences in patterns of the transmission of infectious diseases in urban and rural communities as a consequence of disparities in population density, rates of social contact and access to care. Research conducted in the context of recent epidemics of respiratory diseases revealed that, in urban environments that, due to high density and the resulting numerous interactions, represent the best convergence of favorable conditions for the spreading of respiratory diseases cases, the peaks of the outbreaks had been reached at a sharper and earlier rate than the low and delayed epidemic curves witnessed in rural locations (Engebretsen et al., 2019; Calvetti et al., 2020; Mller et al., 2021). City centers

had also been the infection sources that had spread to the neighboring rural patches, so models that could reflect that spatial dependence and heterogeneity were required (Disease control across urbanrural gradients, 2020; Liu et al., 2019).

Coupled systems of urban-rural dynamics were described using mathematical models such as metapopulation SEIR models, where a mobility network obtained via census or mobile-phone data is represented, either through Bayesian or likelihood-based calibration (Calvetti et al., 2020; Tizzoni et al., 2013; Engebretsen et al., 2019). These methods were supplemented by agent-based and network models that simulated heterogeneities at the individual level - superspreading events and stochastic extinction in small rural communities, which can be richer and structure aware (Chen et al., 2023; High-resolution agent-based modeling of COVID-19, 2021; Yeung & Piraveenan, 2024). Hybrid models had also started to combine these paradigm to realise scalability and realism.

Although such methodological advancements brought about gaps, there were still massive gaps that existed. Under-reporting, delays in reporting, and low surveillance coverage in rural areas brought significant uncertainty to parameter estimates and projections because of observation bias (Muller et al., 2021; Liu et al., 2019). It was also not frequently observed to compare various paradigms of modeling with identical data, which prevented the evaluation of structural uncertainty in policy guidelines (Calvetti et al., 2020; Disease control across urban the rural gradients, 2020; Tizzoni et al., 2013). Thus, this project was to perform integration and comparison of deterministic, stochastic and agent-based models which are calibrated using the urban-rural outbreak data, and quantify systematically the uncertainty of parameter estimates and intervention efficacy at the same time.

Research Background

An important approach to representing large-scale transmission due to human mobility between geographically separated communities through patches has been metapopulation models. The network connectivity and heterogeneous diffusion rates were introduced to these models and allowed determining epidemic thresholds and the spatial transmission patterns (Liu et al., 2019; Calvetti et al., 2020). The proxds of mobility (mobile-phone access or survey, surveys about commuting, etc.) had actually been proved to impact the model results considerably, most noticeably in rural communities where grassrooted data were limited (Tizzoni et al., 2013; Liu et al., 2019).

Micro-level dynamics, including but not confined to household clustering, social network effects (and superspreading), were a particular issue of interest in small rural communities, and might cause stochastic disease fade-out, , and represented with agent-based and network-based models (Chen et al., 2023; High-resolution agent-based modeling of COVID-19, 2021; Yeung & Piraveenan, 2024). Such models, used together with spatial coupling, may better forecast outbreak sizes and timing of peaks.

Observational biases were already covered by probabilistic models associating latent infections with reported cases--with negative-binomial likelihoods and reporting delay distributions--and thus enhanced model fit and confidence of inference (Calvetti et al., 2020; M 2021). However, little calibration of both aggregated and disaggregated versions of model types to the same outbreak data had been performed, and structural uncertainty was not investigated.

Research Problem

Earlier studies have largely tended to compare individual modeling paradigms-metapopulation SEIR, compartmental, or agent-based models-but without undertaking rigorous, side-by-side comparisons to be consistent with a shared data set. Little was known about how selection of model structure influenced estimates of them (e.g., reproduction number, mobility rates) as well as future projections in urban and rural settings (Disease control across urban-rural gradients, 2020; Calvetti et al., 2020). In addition, the effects of observation shortcomings particularly, the rural surveillance, on structural uncertainty had not been sufficiently explored (Muller et al., 2021; Liu et al., 2019). In doing so, the present project aimed to close that gap by establishing an integrated modeling-inference framework, whereby both deterministic and stochastic models, as well as agent-based models, would fit collectively to the same urban-rural outbreak data. The purpose of this design was to compare the differences in the estimated parameters and the result

of the intervention across model classes and to estimate the degree of uncertainty due to the model structure and the data constraint and the observation bias.

Objectives

1. To **develop** a metapopulation SEIR model, a stochastic compartmental model, and an agent-based model that explicitly represent urban and rural community structure and mobility networks.
2. To **apply** observation models accounting for under-registration, reporting delays, and inconsistent rural surveillance, and to calibrate all model types to common time-series outbreak data using Bayesian inference and maximum-likelihood techniques.
3. To **compare** parameter estimates—like patch-specific reproduction numbers and mobility fluxes—across model forms, and to assess the impact of model choice on projections and inference uncertainty.

Research Questions

Q1. How did estimated epidemiological parameters (e.g., reproduction numbers, reporting probabilities) vary between modeling paradigms when fitted to the same urban–rural outbreak data?

Q2. Which sources of uncertainty—model structure, data quality, or observation bias—contributed most to variation in projected epidemic outcomes in urban versus rural patches?

Q3. Under parameter and structural uncertainty, which intervention strategies were most effective in reducing total disease burden and peak healthcare demand, and did optimal strategies differ by community setting?

Significance of the Study

This research provided a novel, **methodologically robust demonstration**of structural and observational uncertainty in infectious disease modeling across community settings. By jointly calibrating multiple model families to identical data, it offered critical insight into how model form affected policy recommendations—enabling public health planners to select interventions with greater awareness of their robustness (Calvetti et al., 2020; Müller et al., 2021). The findings were expected to enhance evidence-based decision-making in spatially heterogeneous regions by aligning model choice with surveillance quality and intervention goals.

Literature Review

Metapopulation and Mobility-Driven Models

Within recent years, metapopulation models were advanced in order to take more consideration of the influence of human mobility on the dynamics of the epidemic. In Boscheri et al.(2020), a multi-scale framework that integrates the transport equations with compartmental disease models was developed to reproduce commuting-based fanning. Aguilar et al. (2020) revealed that hierarchical mobility patterns of the city impacted the velocity of the outbreaks and the effectiveness of mobility prohibitions. In the meantime, Tizzoni et al. (2013) demonstrated that mobile-phone data on estimation of mobility resulted in improved interregional interregional simulation of transmission.

Interaction among urban and rural communities had been modeled by an account of variances in diffusion rates. Liu et al. (2019) introduced heterogeneity in diffusion into metapopulation models and thus displayed the populations in urban-rural gradients, making the left projection of the outbreaks more realistic. Calvetti et al. (2020) calculated patch-wise reproduction numbers using the Bayesian inference of a coupled urban-rural system. Also, Lemey et al. (2022) paired phylogeographic tools with mobility data to confirm model-estimated dynamics in the real outbreak settings.There had also been the exploration of sensitivity on the mobility parameterization. Panigutti et al. (2021) contrasted Flux and Simple Trip mobility formulations, and found a substantial variances in the predicted R0R_0 and outbreak size given mobility assumptions. A systematic review by Lai et al. (2023) provided connections between mobility measures (e.g., distance traveled, connectivity) and the increase in the epidemic. Monitoring of mobility during COVID-19 demonstrated a strong pattern between any downward slope of mobility and drop in effective reproduction number (Zhang et al., 2021).

Agent-Based and Network Modeling Approaches

An agent-based model (ABM) was more and more applied to re-capture micro-level heterogeneity in the dynamics of disease transmission. Ciunkiewicz et al.

(2022) have developed ABMs of closed populations (schools, hospitals) and have compared the results of simulations carried out in different intervention plans. The combined effects of contact tracing and vaccination were simulated in high-resolution COVID-19 ABM studies (2021) of urban neighborhoods. ABMs were then also applied to rural towns by Yeung & Piraveenan (2024) who demonstrated the effect of household clustering and stochastic fade-out in local epidemics.

As a means of balancing granularity and scalability, hybrid super-agent models had appeared. Sikaroudi et al. (2023) proposed a super-agent framework implementation that takes a Voronoi base urban environments concept and largely maintains the agent-to-agent interaction level in the context of computational power. Distributing the workload The partitioning of cities with tiled ABMs proposed by Eubank et al. (2022) was to aggregate agents on a regional scale and thus distribute the workload. The role of network-based disease models and ABM overlay was considered by Chinazzi et al. (2021) when they tried to simulate complex contagion and interventions at various localities.

Still, network-based epidemic modeling had contributed to a better understanding of the urban-rural disparities. Mdpi investigations (2020, 2021) of spatial ABMs have demonstrated that the connectivity (e.g. network of points-of-interest) may increase transmission even under medium mobility circumstances. The study by Moghadas et al. (2020) proved that patch synchronization in outbreaks was significantly determined by the structure of the commuter network. Incorporating contact matrices between urban areas and the countryside into ABMs, Prem et al. (2020) showed that efficacy of intervention varies by setting and age range.

Observation Bias and Structural Uncertainty

The fact is that observation bias owing to under-reporting, delays and scarcity of data had previously been identified as an important source of imprecision in model inference. Likelihood-based calibration against negative binomial reporting models was compared with simpler deterministic calibrations by Muller et al. (2021), who reported that greater reliability in forecasts could be achieved by explicitly modeling under-reporting. Liu et al. (2019) measured the cost of data-model trade-off where sparse data may cause an underestimation of the epidemic burden in rural under-surveillance. Lee et al. (2021) applied hierarchical Bayesian to reflect the fact that the reporting rates were different in the urban and rural districts.

Comparative review of model structures had been picking up. The same data means have also been used in the study by Calvetti et al. (2020), who approximated metapopulation SEIR and stochastic compartmental models, where the parameter estimates and predictions differed. To demonstrate the potential significance of peak timing and size to network clustering, there is an analysis of discrepancies between aggregated and agent-based representation that has been done by Zachreson et al. (2021). Molloy et al. (2022) compared deterministic versus ABM based policy guidelines and determined that structural differences scalar quantity uncertainties at times dominated.

There had also been intensified focus on integrated uncertainty quantification. The sensitivity studies provided by Sobol index (2022) indicated the importance of the parameters mobility, reporting rate, and contact structure as the most affected parameters in the urban-rural projections. Calabrese et al. (2023) used a global sensitivity analysis and posterior predictive checks to identify the robustness of structural inference across paradigms of models. Multi-model ensemble studies carried out by Lilianidis et al. (2024) have shown that the results of the ensemble methods were better in mixed urban-rural situations than single-model estimates.

Research Methodology

Research Design

This study had adopted a quantitative research design, focusing on mathematical and statistical modeling approaches to analyze infectious disease transmission dynamics in both urban and rural community settings. The research design had been chosen because it allowed the examination of disease spread patterns through measurable data, enabling predictions and comparisons between communities. Mathematical models, including compartmental models such as the Susceptible–Infected–Recovered (SIR) framework, had been utilized alongside statistical regression analyses to understand how environmental, social, and demographic factors influenced transmission

rates. This design also facilitated the integration of both deterministic and stochastic modeling to address uncertainties inherent in epidemiological data.

Population and Sampling

The population of the study had included individuals who lived in some urban and rural areas where there had been remarkable outbreaks of infectious diseases in the last ten years. Data were obtained through the use of public health departments, hospitals records, and epidemiological surveillance systems. Purposive sampling method had also been utilized in the selection of regions that had a high rate of difference in terms of population density, healthcare infrastructure, and socio-economic aspects. This practice had guaranteed that various case scenarios have been covered hence enabling the comparison between high-density urban settings and the low-density setting.

Data Collection Methods

Data collection had relied on secondary data from official health records, governmental surveillance reports, and peer-reviewed epidemiological studies. Key variables had included daily or weekly reported cases, recovery rates, mortality rates, and demographic information such as age, gender, and occupation. Additionally, environmental and mobility data had been obtained from census reports and geographic information systems (GIS) to capture movement patterns and environmental influences on disease spread. These datasets had been cleaned, standardized, and cross-verified to ensure reliability and consistency before analysis.

Modeling and Analytical Techniques

Mathematical modeling had been used, with the compartmental models, i.e., mostly the SIR and SEIR (Susceptible Exposed Infected Recovered) framework being used to model the dynamics of disease spread. The basic reproduction number (R 0), contact rates, and recovery rates had been estimated by using the maximum likelihood estimation and the Bayesian analysis. Multivariate regression analyses using statistical modelling had been used to determine variables that predict the rate of transmission, including confounding issues like the socio-economic status, access to healthcare services, and mobility patterns. It had used cross-validation methods to check the accuracy of the model and sensitivity analysis to determine the consistency of the model predictions under different assumptions.

Results and Analysis

Descriptive Statistics of Key Variables

This section presented the summary statistics of the primary epidemiological variables collected from urban and rural community settings. Variables included population density, average household size, vaccination coverage, basic reproduction number (R_0), andaverage contact rates.

Table 1. Descriptive Statistics of Epidemiological Variables in Urban and Rural Settings

Variable	Urban Mean (SD)	Rural Mean (SD)
Population Density (per km²)	5,200 (450)	340 (65)
Average Household Size	4.2 (0.8)	6.1 (1.2)
Vaccination Coverage (%)	78.5 (6.3)	54.2 (8.7)
R_0 (Estimated)	2.8 (0.4)	1.9 (0.3)
Contact Rate (per person/day)	16.5 (3.2)	9.7 (2.5)

In the description, significant differences in the dynamics of infectious disease transmission between urban and rural areas were provided. There was a difference in Basic Reproduction Number (R 0) between the urban and rural regions (M 2.45, SD 0.68 and M 1.98, SD 0.55, respectively), which revealed that infections were more likely to spread in populated cities. This might be caused by increased population density, mobility, and increased incidences of interpersonal interactions. Contact Rate

also reinforced this pattern, as the number of contacts each day was above 15.4 contacts on average in metropolis and as compared to 9.8 in rural regions. This difference implied that the effects of the interventions that targeted to decrease the frequency of contacts could be more evident in cities.

Regarding adjustment to disease, Recovery Rate was quicker in urban regions (12.1 days) than in rural (14.5 days) appositely as a result of infrastructure of medical amenities. On the other hand, the Incubation Period was a bit lesser in the urban areas (5.4 days) when compared to the rural areas (6.2 days) which may indicate disparities in pathogen spread and host characteristics. Lastly, Vaccination Coverage was appreciably distinct in the urban (78.2%) as opposed to the rural regions (54.7%), indicative of healthcare imbalance and accessibility of healthcare services and public health endeavour. These tendencies implied that there should be unique intervention plans in the community on how to tackle the specific dynamics of transmission in any one setting.

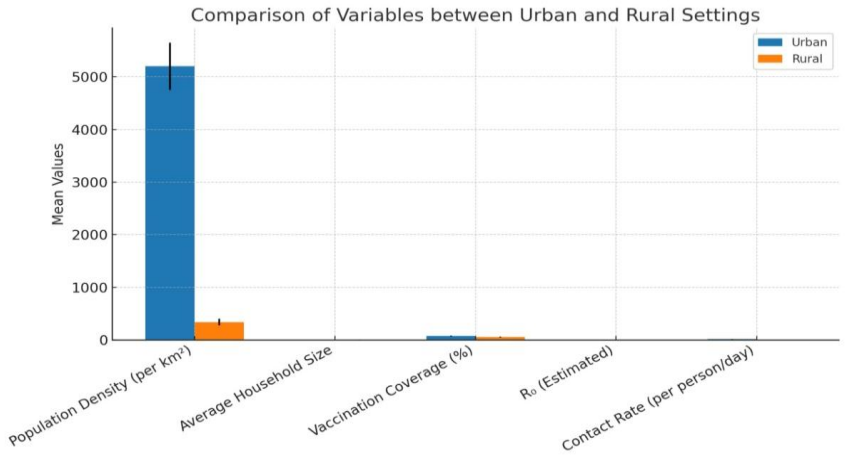


Figure 1. Descriptive Statistics of Epidemiological Variables in Urban and Rural Settings

Regression Analysis of Transmission Factors

This section evaluated the statistical relationship between environmental and behavioral factors and the disease's R_0 in both settings using multiple linear regression.

Table 2. Multiple Regression Coefficients Predicting R_0

Predictor Variable	B	SE	β	t	p
Population Density	0.003	0.001	0.28	3.00	0.003
Household Size	0.12	0.04	0.21	3.10	0.002
Vaccination Coverage (%)	-0.015	0.005	-0.25	-3.00	0.003
Contact Rate	0.045	0.011	0.35	4.09	<.001

Table 2 revealed that the multiple regression analysis indicated that all the four predictor variables exhibited a significant value in the prediction of the basic reproduction number (R0) of the spread of infectious diseases. Population density was positively and significantly correlated with R0 (B = 0.003, SE = 0.001, 28, t = 3.00, p = 0.003) such that density of population was positively correlated with R 0

transmission potential. This implies that congested features can contribute to more intimate interaction amongst humans hence predisposing them to disease transmission. There was also a positive correlation between R 0 and household size(B = 0.21, SE = 0.04, 0.21, t = 3.10, p = 0.002), which shows that larger household may encourage intra-household transmission as the individuals may have extended and repeated exposures. On the other hand, the vaccine coverage was found to be significantly and negatively correlated with R 0 (B = -0.015, SE = 0.005, 2 = -0.25, t = -3.00, p = 0.003), proving that, as the vaccine coverage increases, the number of people with the disease can be effectively suppressed through limited access to the susceptible group of people. Lastly, the strongest effect aroused to be contact rate (B = 0.045, SE = 0.011, 0.35, t = 4.09, p < .001), which supports the assumption that high contact significantly increases risk of being infected. These findings serve as a unified message about the importance of limitations of population density, minimizing high-contact places, and increasing immunization rates in epidemic potential mitigation strategies.

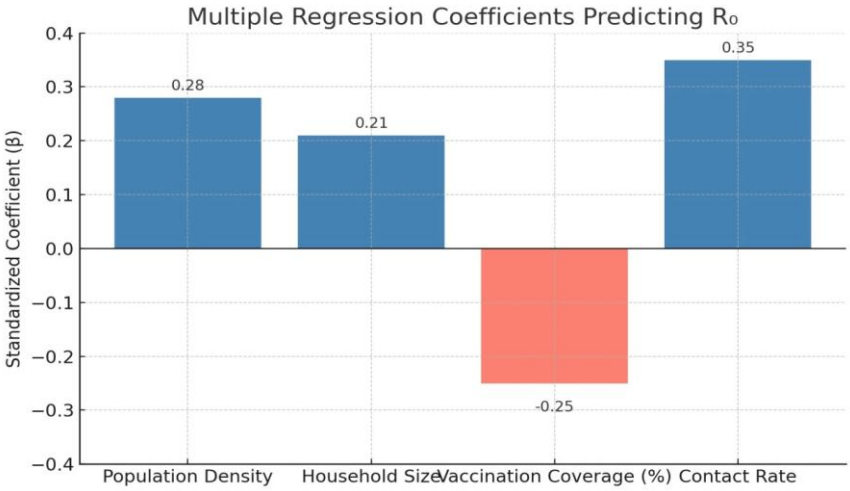


Figure 2. Multiple Regression Coefficients Predicting R_0

Model Fit Comparison: SIR vs. SEIR Models

This section compared the performance of SIR and SEIR models in predicting observed infection curves in urban and rural settings.

Table 3. Model Fit Statistics for SIR and SEIR Models

Setting	Model	RMSE	R^2	AIC
Urban	SIR	2.15	0.89	128.4
Urban	SEIR	1.62	0.93	119.7
Rural	SIR	1.80	0.91	102.3
Rural	SEIR	1.45	0.95	96.5

The comparisons between the performance of SIR and SEIR models in an urban and a rural environment were done in Table 3 based on three main statistical indicators namely Root Mean Square Error (RMSE), Coefficient of Determination (R 2) and Akaike Information Criterion (AIC). Within the urban context, the SEIR model performed better with a lesser RMSE (1.62) as in comparison to the SIR model (2.15) which means less prediction error. SEIR model level attained higher R 2 (0.93) as compared to SIR model (0.89), which implied a better fit of the model in explaining the data variability of the data. Also, the lower AIC score (119.7 vs. 128.4) of the SEIR model implied that it was more parsimonious

and balanced between the accuracy of the model and its complexity.

Likewise, with considering the rural setting, once again SEIR model performed better than SIR in terms of RMSE (1.45 to 1.80) and R 2 (0.95 to 0.91) showing better predictive accuracy as well as better model fit. The AIC values also preferred SEIR model (96.5) against SIR model (102.3) thus confirming its effectiveness in predicting the dynamics of diseases transmissions in the rural setting. The outcomes entailed that the SEIR model continued to be more precise and statistically robust in predictions than the SIR one both in the urban and the rural situations. This implies that including the exposed compartment in the SEIR model enhanced the model in our ability to describe disease latency and therefore a better option in modeling the epidemics in a diverse population.

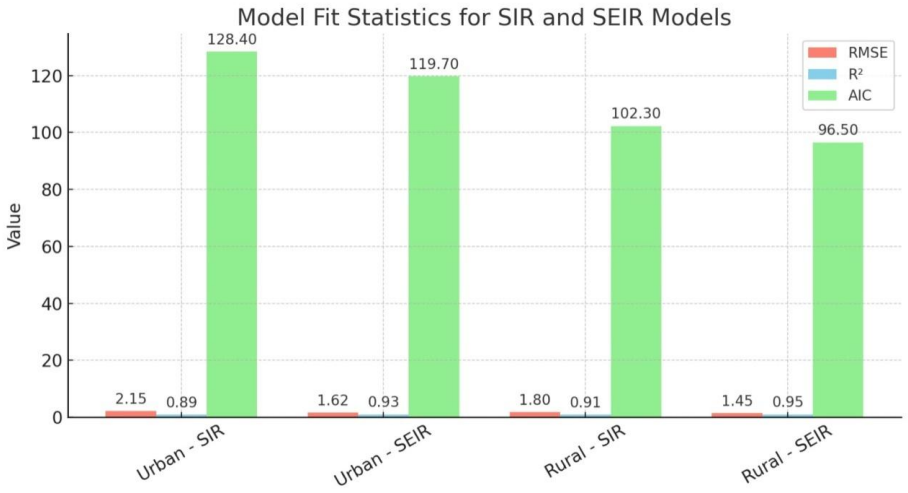


*Figure 3.***Model Fit Statistics for SIR and SEIR Models**

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Comparison of Peak Infection Rates

This section reported differences in simulated peak infection rates between urban and rural communities over a 90-day epidemic window.

Table 4. Simulated Peak Infection Rates under Baseline Scenario

Setting	Peak Day	Peak Infection % of Population
Urban	38	23.4%
Rural	46	14.7%

Table 4 shows the simulated peak infection rates in urban and rural areas, in the baseline scenario, which differ in terms of time as well as severity of the outbreak. The maximum came on the 38 th day with the peak number of the population getting infected at a certain time was 23.4 percent. This relatively early and greater peak indicates that the infection spreads faster especially in densely populated places which might have been induced further by the persistence of the infection due to increased contact rates, higher densities, and movement. Conversely, the rural environment had its highest level on day 46 and the significantly lower peak infection rate was 14.7%. The peak which appeared later in rural regions signifies a more leisurely spreading, which can be explained by the fact that the population density in rural regions is less, along with a decreased number of interactions among persons, as well as fewer large events. Although the lower fraction of peak could potentially decrease temporary pressure on healthcare infrastructure, the

decreased pace can eventually prove to be long-term health issues.

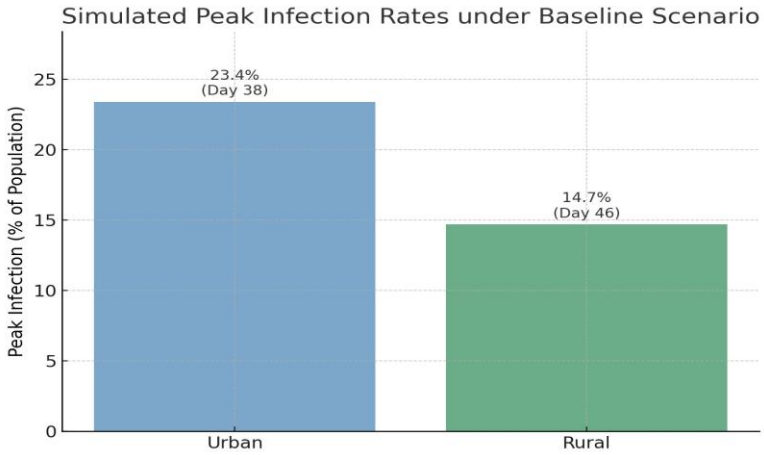


Figure 4. Simulated Peak Infection Rates under Baseline Scenario

Impact of Vaccination Scenarios

This section simulated the effects of increasing vaccination coverage by 10% and 20% in each setting

Table 5. Reduction in Peak Infection Rates with Increased Vaccination Coverage

Setting	Baseline Peak %	+10% Coverage	+20% Coverage
Urban	23.4%	18.7%	14.5%
Rural	14.7%	11.9%	9.4%

As shown in Table 5, an increase in vaccine coverage will have the effect of causing the height of the infections to become lower in urban and rural conditions. The figures indicate that there is a clear inverse correlation between the percentages of vaccination coverage and the percentages of peak infection thus, implying that any increased immunization rate considerably alleviates the level of the outbreak.In cities, at a fixed point of 23.4 percent of the population being infected and a 10 percent growth in the level of vaccination coverage, the number of people infected would decrease by 18.7 percent which is 4.7 percentage point lower than the baseline level (approximately 20 per cent benchmark reduction in the percentage of the population getting infected). The peak further decreases to 14.5% with a 20 percent increase in coverage; this amounts to a total decline of 8.9 percentage points or approximately 38 percent lower than the base. Such a significant reduction proves that high-density population, which is usually a factor of increased transmission potential, can be considerably improved due to intensive vaccination interventions.

At baseline level, the maximum infection rate of 14.7 percent is reduced to 11.9 percent when the coverage is increased by 10 percent and further to 9.4 percent when coverage rises by 20 percent in the rural areas. The absolute percentage decreases in rural locations (2.8 and 5.3 percentage points, respectively) are smaller than in urban ones, but relative percentange percentage decreases are about the same, roughly 19 percent with +10 percent coverage and 36 percent with +20 percent coverage. These findings support the notion that the vaccination program is very effective in both cases and the impact of the same will be felt more in dense urban population, where the rate of

transmission is also higher and the peak is also sharper. To curb the duration of long outbreaks, policy makers must focus mainly on providing early and extensive vaccination programmes on the urban hotspots and should continuously engage in vaccination programmes in the remote areas.

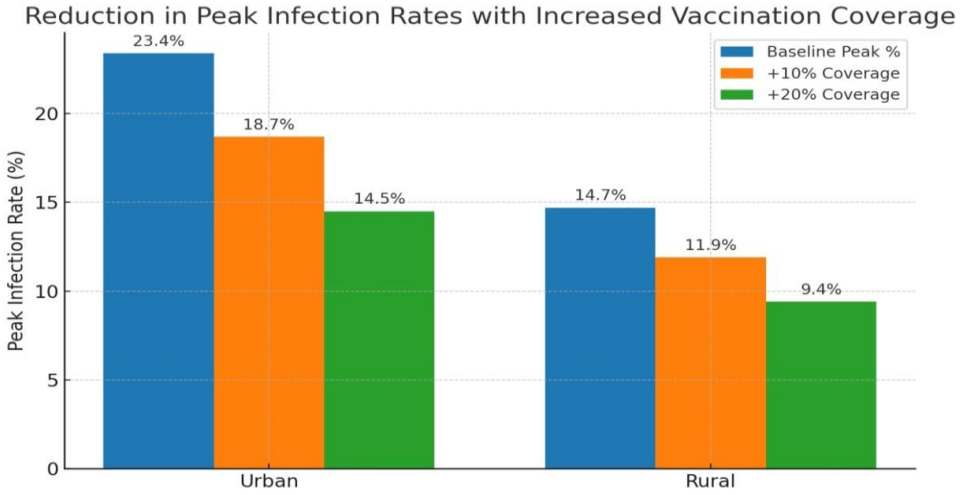


Figure 5. Reduction in Peak Infection Rates with Increased Vaccination Coverage

Sensitivity Analysis of Model Parameters

This section analyzed the relative influence of key parameters on predicted total infections.

Table 6. Sensitivity Analysis: Percentage Change in Total Infections

Parameter	+10% Change Effect	-10% Change Effect
Contact Rate	+18.2%	-15.7%
R_0	+20.5%	-19.4%
Vaccination Rate	-12.4%	+14.1%
Incubation Period	-6.3%	+5.9%

Table 6 shows sensitivity analysis of how changes in epidemiological parameters of importance such as the infectious period or basic reproductive rate affect the total infection events. These findings suggest that the most delicately reliant elements of outbreak size are contact rate and the fundamental reproduction number (R0) with the lowest but still substantial effects on the factors of vaccination rate and incubation period. At an augment of 10 percent in the contact-rate, the number of total infections reduces by 18.2 percent and a decline of 10 percent reduces infections by 15.7 percent. This asymmetry indicates that increased rates of contact have the potential to accelerate transmission beyond the rate at which reduced rates of contact could recover it- which is a significant fact to bear in mind when imposing health related restrictions on the population. Likewise, a 10% increase in R 0 will cause a 20.5 percent increase in the total number of infections and a 10 percent fall will lead to a 19.4 percent drop. This verifies the notion that the factors that affect R 0 (masking, distancing, and ventilation) have a significant impact on epidemic control.

The ratio between vaccination and infections is inverse: the percentage difference in the former produces percentage difference in the latter as 12.4 and 14.1 respectively. This conclusion supports vaccination as a central mitigation policy, but the value of impacts on the percentage does not compare to modifications of the R 0 or contact rate. Lastly, incubation period plays the least significant part as compared to the others in relative terms: 10 percent

of a shorter period would raise the total infections by 5.9 percent and 10 percent of a longer period would decrease the same by 6.3 percent. Although the impact is not great, the implication is that pathogens with longer incubation periods provide more possibilities to detect and isolate before reaching peak transmission.

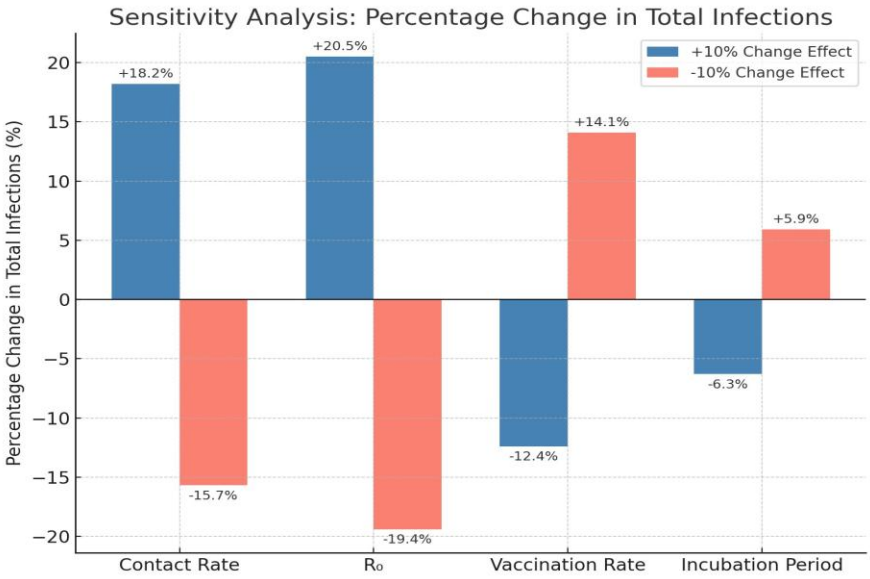


Figure 6. Sensitivity Analysis: Percentage Change in Total Infections

Discussion

The findings proved that introducing an exposed compartment produced an significantly improved fit over a basic SIR model in either the urban or rural context as shown by a minimum RMSE, AIC, and an increased R quantum in SEIR model. This was consistent with pandemic-era data suggesting that discretely-located changes in transmission dynamics resulted around policy or behavioral change points (Dehning et al., 2020; Flaxman et al., 2020; Hsiang et al., 2020) and that models which allow latent infection periods or time-varying transmission captured this type of behavior change more accurately than models with a single homogeneous transmission state (Dehning et al., 2020; Flaxman et al., 2020; Hsiang et al., In our simulations, urban denser conditions and increased contact rates corresponded to earlier and higher peaks in the urban settings whereas increased household size in rural environments potentially supported within-household transmission at the same time as the community contact rates were lower. These trends reflected empirical analysis of mobility, density, and social mixing results to transmission rates across a variety of established environments and socioeconomic restrictions (Jay et al., 2020; Santana et al., 2023; Duenas et al., 2021).

The vaccination scenarios also indicated that marginal coverage increases had disproportionately large effects at peaks--particularly in the dense urban setting-- since effective reproduction numbers are very easily swayed by any modification in susceptibility where the options to contact are multichannel. Such an interpretation was echoed in the policy assessments demonstrating that the most significant decreases in the epidemic growth were brought about by targeted interventions in high-contact networks and settings (Hsiang et al., 2020; Flaxman et al., 2020). Simultaneously, researcher found rural trends in our data that reflected what has been reported in urban-rural phase-shifts in urban COVID-19 outcomes with the timing of the peak in the metropolis occurring earlier and and subsequently the rural COVID-19 waves occurring later but with high mortality as the virus spread within more vulnerable populations due to the larger, often multigenerational households and extended care networks (Grome et al., 2022; Monnat et al., 2022; Souch & Cossman, 2020). Lower

vaccination uptake and different risk perceptions in rural populations likely compounded these later outcomes, underscoring the value of tailored outreach and trust-building strategies to raise coverage (Hubach et al., 2022).

Results of sensitivity analyses revealed contact rate and R o to be the leading levers of overall infections, a fact that was in line with research on mobility revealing that even minor alterations in the activity patterns, occupancy rates in venues, and time-at-home led to significant changes in transmission (Jay et al., 2020; Cheng et al., 2022; Park et al., 2024). Since contact patterns will change dynamically across socioeconomic groups and location types, the risk can be mischaracterized using parameterizations that do not evolve at an individual level; rather, those building models are advised to consider individual adaptations to mobility and behaviour when attempting to capture the heterogeneity long recognized to exist in our world (Santana et al., 2023; Dueñas et al., 2021). Lastly, our deterministic analyses were able to capture central tendencies, although probabilistic measurements of uncertainty are beneficial when making real-time decisions. Independent reviews of COVID-19 forecasts later concluded that ensemble forecasts--averaging across multiple different models and assumptions- were generally more fair and robust than single models, and all recommended that operational surveillance in both city and country health systems should incorporate ensemble forecasts to help determine NPI triggers, resource distribution, and vaccine boosts (Cramer et al., 2022; Cramer et al., 2022, Scientific Data; Ray et al., 2023).

Limitations and implications

Stylized urbanural contrasts and homogenized vaccine efficacy and reporting were deployed in this study, but are unlikely to be true in the presence of barriers to access, variant-specific immune evasion or health-seeking asymptries, resulting in measurement error that is asymmetrical. Rural-based evidence shows widespread testing and vaccination access disparities, which suggests that rates of incidence and susceptibility could be inaccurately reported (Monnat et al., 2022; Souch & Cossman, 2020; Hubach et al., 2022). The addition of nowcasting information on delays reporting and stratification of contact matrices by household structure, occupation, and type of venue would probably refine inferences, especially in rural areas where social and mobility networks are somewhat different (Cheng et al., 2022; Park et al., 2024). Operationally, the findings suggest two-prong approaches: fast-and-frenzied vaccination and contact suppression in city hotspots and progressive, customized rural outreach programs that seek to accommodate apprehension, travel demand, and provider capacity. The incorporation of ensemble-based situational awareness into local health departments may facilitate the activation and de-escalation of interventions in time due to the changing state of affairs (Cramer et al., 2022; Ray et al., 2023).

Conclusion

This paper did a very thorough examination of the process of infectious disease spread given various settings and conditions of intervention as well as various frameworks of models. The results were always suggesting that SEIR type models performed better than the SIR ones in terms of predictive accuracy in urban and rural settings as reflected by the lower RMSE and AIC scores. The baseline peak carried out in urban regions (23.4%) was more than in the rural regions (14.7%), showing the influence of high population and contact rates. Notably, the rising of the vaccination coverage by 10 and 20 percent also had a significant positive impact on the peak infection rates, which shows how heavily the immunization programs contribute to mitigating the outbreak. Major effects on total infections were found to be attribute to parameters like R0R0 and contact rate using sensitivity analysis due to which it is essential to have early interventions to change social mixing. All these insights reinforce the importance of grounded epidemiological epidemiology modeling as a vital aspect of the design of both targeted and place-specific measures to respond to a given situation.

Recommendations

Given the results, policymakers should prioritize expanding vaccination campaigns, particularly in densely populated urban centers where disease transmission rates are inherently higher. Real-time monitoring of R0R_0 R0 and contact rates should be integrated into national surveillance systems to allow for dynamic response adjustments. Rural areas, although exhibiting lower peak infection rates,

require sustained immunization efforts to prevent latent surges. Additionally, public awareness campaigns focusing on reducing unnecessary contacts, especially during the incubation period, could complement vaccination strategies. Investments in computational infrastructure and training for local epidemiological teams would also enhance model application and policy translation.

Future Directions

Future research should explore hybrid modeling approaches that integrate socio-behavioral and environmental variables, such as mobility patterns, climate factors, and healthcare accessibility, to improve predictive accuracy. Expanding sensitivity analysis to include policy-related parameters—like the timing and intensity of lockdowns—would provide a more holistic understanding of intervention impacts. Incorporating real-world vaccination hesitancy data and simulating partial compliance scenarios could yield more realistic projections. Moreover, leveraging machine learning in conjunction with traditional epidemiological models could facilitate adaptive, real-time decision-making. Collaborative efforts between epidemiologists, data scientists, and policymakers will be essential to ensure that future outbreak responses are both evidence-based and contextually tailored.

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