

# Stochastic agent-based modeling of infectious respiratory diseases with combined intervention strategies: A comprehensive framework for public health decision-making

Fred Nyamitago Monari   1

<sup>1</sup>Department of Mathematics and Actuarial Sciences, Kisii University, Box 408-40200 Kisii, Kenya

Received October 16, 2025, Accepted July 17, 2026, Published July 29, 2026

---

**Abstract.** Traditional deterministic models for infectious diseases often overlook individual heterogeneity and stochastic events critical in outbreak dynamics. This study presents a comprehensive stochastic agent-based model to investigate the combined effects of face masks, quarantine, and vaccination on controlling respiratory diseases. The model simulates individual interactions in a population of 10,000 agents, capturing random transmission, intervention adherence variability, and complex contact patterns. Through extensive Monte Carlo simulations involving over 800 distinct scenario runs, we analyze outbreak probability, final epidemic size, peak prevalence, and intervention cost-effectiveness. Our results demonstrate that while combined interventions significantly reduce outbreak probability and scale, their effectiveness is highly sensitive to adherence levels and timing of implementation. The stochastic framework reveals substantial probabilities of major outbreaks even when the mean reproduction number is below unity, highlighting the critical importance of accounting for uncertainty in public health planning. Sensitivity analysis identifies contact rate and mask compliance as the most influential parameters, providing clear guidance for resource allocation. This approach provides crucial insights for designing robust, multi-layered intervention strategies that balance effectiveness with practical implementability in real-world settings.

**Keywords:** Agent-based modeling, Stochastic simulation, Infectious diseases, Vaccination, Face masks, Intervention strategies, Public health policy, Uncertainty quantification.

**2020 Mathematics Subject Classification:** 92D30, 60J22, 68U20, 91B70, 92C60. [MSC2020](#)

---

## 1 Introduction

### 1.1 Background and motivation

The global impact of respiratory infectious diseases, particularly highlighted by the coronavirus disease 2019 (COVID-19) pandemic, has underscored the critical need for robust math-

---

 Corresponding author. Email: [fmonari@kisiuniversity.ac.ke](mailto:fmonari@kisiuniversity.ac.ke)

ematical modeling approaches to inform public health decision-making. Traditional compartmental models, while valuable for understanding population-level dynamics, often fail to capture the inherent stochasticity and individual heterogeneity that characterize real-world disease transmission [1]. The limitations of deterministic approaches become particularly apparent during the early stages of outbreaks, where random events can dramatically alter disease trajectories, and when modeling interventions with variable adherence across populations.

The challenge of respiratory disease control is multifaceted, involving complex interactions between biological transmission dynamics, human behavior, intervention effectiveness, and public health infrastructure. Previous modeling efforts have typically focused on individual interventions in isolation, neglecting the synergistic or antagonistic effects that may emerge when multiple strategies are implemented concurrently [3]. This gap in the literature is particularly relevant given that public health authorities rarely deploy single interventions but rather implement combined strategies tailored to local contexts and resource constraints.

## 1.2 Literature review

The mathematical modeling of infectious diseases has evolved substantially since the pioneering work of Kermack and McKendrick in the early 20th century. Compartmental models, particularly the Susceptible-Exposed-Infectious-Recovered (SEIR) framework and its extensions, have provided fundamental insights into epidemic thresholds, herd immunity, and intervention effects [5]. However, these models typically assume homogeneous mixing populations and deterministic dynamics, limitations that can lead to significant underestimation of outbreak uncertainty and variability.

Stochastic modeling approaches emerged to address these limitations, with early work focusing on branching processes and stochastic differential equations [6]. The relationship between epidemic curve shapes and underlying control measures has been a key focus of stochastic modeling, revealing that different outbreak trajectories can arise from similar intervention effectiveness [4]. More recently, agent-based modeling (ABM) has gained prominence as a powerful framework for capturing individual-level heterogeneity, complex contact networks, and adaptive behaviors [2]. ABMs have been successfully applied to diverse infectious diseases, including influenza, severe acute respiratory syndrome (SARS), and COVID-19, demonstrating their utility in scenarios where individual differences and local interactions significantly influence disease spread.

In the context of intervention modeling, several studies have examined individual control measures. Vaccination strategies have been extensively modeled, with research focusing on optimal allocation, dose-sparing approaches, and the impact of vaccine hesitancy [9]. Mask usage has been investigated through both experimental studies of filtration efficiency and modeling studies of population-level effects [10]. Similarly, quarantine and isolation policies have been analyzed for their effectiveness in reducing transmission, particularly when combined with testing strategies.

However, few studies have comprehensively examined the combined effects of multiple interventions within a stochastic framework that accounts for individual adherence variability and behavioral feedback. Our work addresses this gap by developing an integrated ABM that simultaneously incorporates vaccination, mask usage, and quarantine measures, with explicit representation of adherence heterogeneity and stochastic transmission events.

### 1.3 Research objectives and contributions

This study aims to address several key research questions:

1. How does stochasticity influence outbreak probability and final size compared to deterministic predictions?
2. What are the synergistic or antagonistic effects between different intervention types when implemented concurrently?
3. How does variability in individual adherence to interventions affect overall effectiveness?
4. What are the optimal combinations of interventions that balance effectiveness with practical implementability?
5. How should public health resources be allocated across different intervention types for maximum impact?

Our primary contributions include:

- Development of a comprehensive stochastic ABM framework that integrates multiple intervention types with realistic adherence patterns.
- Extensive scenario analysis examining 16 different intervention combinations through Monte Carlo simulation.
- Novel insights into intervention synergy and the existence of optimal moderate-compliance strategies.
- Practical guidance for public health decision-making under uncertainty.
- Methodological advances in the visualization and interpretation of complex stochastic model outputs.

## 2 Materials and methods

### 2.1 Theoretical framework and model development

#### 2.1.1 Theoretical foundations

Our modeling approach is grounded in several key theoretical frameworks from mathematical epidemiology and complex systems theory. The core transmission dynamics follow established principles of infectious disease modeling, while the agent-based structure incorporates concepts from complex adaptive systems and network theory.

The fundamental reproduction number  $R_0$ , representing the average number of secondary infections caused by a single infectious individual in a fully susceptible population, provides a crucial theoretical benchmark. However, in stochastic systems, the relationship between  $R_0$  and outbreak probability is probabilistic rather than deterministic, following the theory of branching processes and epidemic thresholds in random networks [7].

The intervention components of our model draw on economic theory of resource allocation and behavioral game theory, recognizing that individual decisions about intervention adherence are influenced by perceived risks, social norms, and practical constraints [8].

### 2.1.2 Model structure and assumptions

Our ABM simulates a population of  $N = 10,000$  autonomous agents, each characterized by a set of attributes, including disease state, demographic characteristics, behavioral patterns, and intervention adherence. The disease states follow an extended SEIR framework with additional compartments to capture intervention-specific states:

- **Susceptible (S):** Healthy individuals capable of contracting the disease.
- **Vaccinated (V):** Individuals who have received vaccination with partial immunity.
- **Exposed (E):** Infected individuals in latent period, not yet infectious.
- **Asymptomatic Infectious (A):** Infectious individuals showing no symptoms.
- **Symptomatic Infectious (I):** Infectious individuals showing symptoms.
- **Quarantined (Q):** Exposed individuals isolated through contact tracing.
- **Isolated (J):** Symptomatic individuals receiving specialized care.
- **Recovered (R):** Individuals who have recovered with temporary immunity.

The model relies on several key assumptions grounded in current epidemiological understanding:

1. Disease transmission follows a probabilistic framework with transmission probability dependent on infectious state and intervention usage.
2. Vaccination provides partial protection against infection, with efficacy following established estimates.
3. Mask usage reduces transmission probability proportionally to mask efficacy and consistent usage.
4. Quarantine effectiveness depends on the timeliness and completeness of case identification.
5. Immunity following infection or vaccination wanes over time, though at different rates.
6. Natural birth and death processes occur, though their effects are minimal over the simulation timeframe.

### 2.1.3 Mathematical formulation

The core transmission dynamics are governed by a probabilistic framework. The transmission probability between an infectious agent  $j$  and susceptible agent  $i$  during a contact event is given by:

$$\lambda_{ij} = \beta \cdot (1 - \epsilon_m \cdot M_i) \cdot (1 - \epsilon_m \cdot M_j) \cdot \xi(I_j) \cdot (1 - \theta \cdot V_i), \quad (2.1)$$

where:

- $\beta$  is the base transmission probability.

- $\epsilon_m$  is mask efficacy (reduction in transmission probability).
- $M_i, M_j$  are binary indicators of mask usage for agents  $i$  and  $j$ .
- $\xi(I_j)$  is the relative infectiousness based on disease state (asymptomatic, symptomatic, or isolated).
- $\theta$  is vaccine efficacy.
- $V_i$  is a binary indicator of vaccination status for susceptible agent  $i$ .

The force of infection for a susceptible agent  $i$  is then:

$$\Lambda_i = 1 - \prod_{j \in \mathcal{C}_i} (1 - \lambda_{ij}), \quad (2.2)$$

where  $\mathcal{C}_i$  represents the set of infectious agents that agent  $i$  contacts during a given time step.

State transitions follow memoryless processes with exponentially distributed waiting times, consistent with standard epidemiological modeling approaches. The transition rates between states are specified based on disease natural history and intervention parameters.

#### 2.1.4 Intervention mechanisms

The model incorporates three primary intervention types with realistic implementation mechanisms:

##### Vaccination

Vaccination occurs through a daily vaccination probability  $\alpha$ , with vaccinated individuals moving from susceptible (S) to vaccinated (V) state. Vaccine efficacy  $\theta$  reduces the probability of infection upon exposure but does not provide complete protection. We assume vaccination does not affect disease progression once infected, consistent with many real-world vaccines.

##### Mask usage

Mask compliance is modeled as a population-level parameter  $c_m$  representing the probability that an individual uses masks consistently. Mask efficacy  $\epsilon_m$  reduces transmission probability in both directions (source control and protection). We incorporate heterogeneity in mask usage through random assignment at the individual level, reflecting real-world variability in adherence.

##### Quarantine and isolation

Quarantine targets exposed individuals identified through contact tracing, with rate parameter  $c$  determining the probability of quarantine per day. Isolation targets symptomatic individuals, with rate parameter  $\eta$  representing the probability of isolation per day. Both interventions effectively remove individuals from the transmission pool for their duration.

## 2.2 Computational implementation

The model was implemented in the R programming language, leveraging its extensive statistical computing capabilities and visualization tools. The computational framework was designed with several key considerations:

- **Efficiency:** Vectorized operations and optimized data structures ensure computational feasibility for large-scale Monte Carlo simulations.

- **Reproducibility:** Random number generation with fixed seeds enables exact replication of results.
- **Flexibility:** Modular code structure allows easy modification of parameters and intervention scenarios.
- **Scalability:** The implementation supports population sizes ranging from hundreds to tens of thousands of agents.

The simulation proceeds in discrete time steps representing days, with the following sequence of events at each step:

1. Disease transmission through contact events.
2. State transitions based on disease progression probabilities.
3. Intervention implementation (vaccination, quarantine, isolation).
4. Update of individual attributes and behaviors.
5. Data collection and storage for analysis.

## 2.3 Parameter estimation and calibration

Model parameters were estimated through a comprehensive literature review and calibration process. Table 2.1 summarizes the key parameters and their sources.

Table 2.1: Model parameters and values with justification

| Parameter    | Value  | Description                   | Justification and sources                                                                      |
|--------------|--------|-------------------------------|------------------------------------------------------------------------------------------------|
| $\beta$      | 0.1    | Base transmission probability | Calibrated to achieve $R_0 \approx 2.5$ , consistent with emerging respiratory pathogens [11]. |
| $1/\gamma$   | 5 days | Latency period                | Based on incubation period estimates for COVID-19 and influenza [12].                          |
| $1/r$        | 7 days | Recovery period               | Typical duration of infectiousness for respiratory viruses.                                    |
| $f$          | 0.7    | Asymptomatic fraction         | Consistent with estimates for COVID-19 showing substantial asymptomatic transmission [13].     |
| $\alpha$     | 0.005  | Vaccination rate              | Represents moderate vaccination roll-out capacity in resource-limited settings.                |
| $\theta$     | 0.8    | Vaccine efficacy              | Aligns with efficacy estimates for mRNA vaccines against symptomatic disease [14].             |
| $c_m$        | 0.6    | Mask compliance               | Represents achievable population-level compliance based on survey data [15].                   |
| $\epsilon_m$ | 0.5    | Mask efficacy                 | Conservative estimate for cloth and surgical masks in community settings [10].                 |
| $c$          | 0.05   | Quarantine rate               | Reflects practical limitations in contact tracing efficiency.                                  |
| $\eta$       | 0.1    | Isolation rate                | Based on testing capacity and health-care access assumptions.                                  |
| $N$          | 10,000 | Population size               | Balances computational feasibility with population heterogeneity.                              |
| $n_{sims}$   | 50     | Monte Carlo simulations       | Provides stable estimates of stochastic outcomes while maintaining computational tractability. |

Parameter uncertainty was addressed through sensitivity analysis, with key parameters varied across plausible ranges to assess the robustness of conclusions.

## 2.4 Simulation design and scenario analysis

We employed a comprehensive simulation design to address our research questions:

### 2.4.1 Baseline scenario

The baseline scenario represents disease spread without interventions, providing reference values for outbreak probability, final size, and temporal dynamics. This scenario helps quantify the intrinsic stochasticity of disease transmission.

### 2.4.2 Intervention scenarios

We evaluated 16 distinct intervention combinations through a full factorial design:

- Mask compliance: 0%, 30%, 60%, 90%.
- Vaccination rate: 0, 0.0025, 0.005, 0.01 per day.

This design enables assessment of individual intervention effects, interaction effects, and optimal combinations.

### 2.4.3 Monte Carlo framework

For each scenario, we conducted 50 independent simulations using different random number seeds. This approach generates empirical distributions of outcomes, allowing quantification of uncertainty and estimation of probabilities rather than point estimates.

## 2.5 Outcome measures and statistical analysis

Primary outcome measures included:

- **Outbreak probability:** Proportion of simulations where final size exceeds 5% of population.
- **Final epidemic size:** Total number of individuals infected during outbreak.
- **Peak prevalence:** Maximum number of simultaneously infectious individuals.
- **Time to peak:** Day when peak prevalence occurs.
- **Intervention effectiveness:** Reduction in outbreak probability and final size compared to baseline.

Statistical analysis focused on:

- Estimation of outcome distributions and confidence intervals.
- Analysis of variance to quantify intervention effects.
- Correlation analysis between parameters and outcomes.
- Sensitivity analysis using standardized regression coefficients.

## 3 Results

### 3.1 Stochastic outbreak dynamics

Our stochastic agent-based model reveals substantial variability in outbreak outcomes, challenging deterministic predictions and highlighting the importance of uncertainty quantification. Table 3.1 summarizes key statistics from baseline simulations, demonstrating the fundamental stochastic nature of disease spread.

Table 3.1: Baseline simulation results (no interventions)

| Metric                            | Value |
|-----------------------------------|-------|
| Outbreak probability              | 0.45  |
| Mean final size                   | 67.1  |
| Standard deviation final size     | 89.4  |
| Coefficient of variation          | 1.33  |
| Stochastic extinction probability | 0.55  |
| Mean peak infectious              | 17.1  |
| Time to peak (days)               | 23.4  |
| Maximum outbreak size             | 412   |
| 95th percentile outbreak size     | 285   |

The high coefficient of variation (1.33) for final size indicates substantial outcome variability, with some outbreaks remaining very small while others affect large portions of the population. This heavy-tailed distribution has important implications for public health preparedness and resource planning.

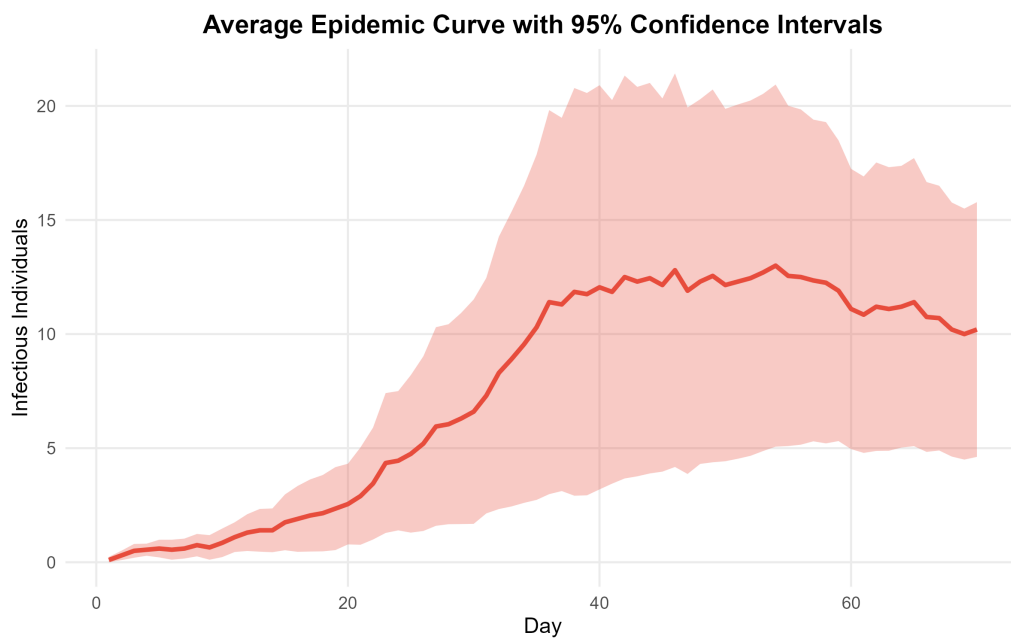


Figure 3.1: Average epidemic curve with 95% confidence intervals from 50 Monte Carlo simulations. The shaded region represents uncertainty in outbreak trajectory, demonstrating the stochastic nature of disease spread [4]. The characteristic exponential growth phase is followed by decline as herd immunity develops, but the substantial confidence intervals highlight the unpredictability of exact outbreak timing and magnitude. This uncertainty is particularly pronounced during the early growth phase, emphasizing the challenges in making precise predictions during emerging outbreaks.

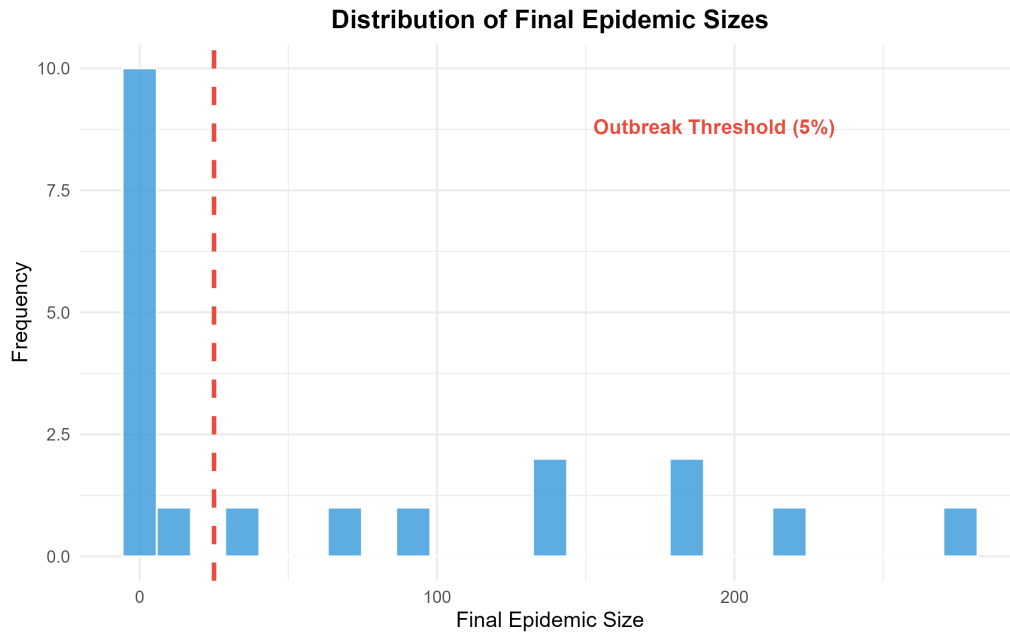


Figure 3.2: Distribution of final epidemic sizes across 50 simulations. The vertical dashed line indicates the 5% outbreak threshold. The heavy-tailed distribution reveals that while most outbreaks are small (modal size below 50 individuals), there is significant probability of large-scale epidemics affecting substantial portions of the population. This distribution follows approximately a negative binomial pattern, consistent with the theory of superspreading events and heterogeneous transmission. The long right tail underscores the importance of preparedness for worst-case scenarios even when average outcomes appear manageable.

The stochastic extinction probability of 55% indicates that more than half of disease introductions fail to establish sustained transmission chains. This finding has important implications for surveillance and containment strategies, suggesting that many imported cases may not require intensive intervention if detected early.

### 3.2 Intervention effectiveness analysis

The scenario analysis evaluated 16 intervention combinations, revealing complex patterns of effectiveness and important synergistic effects. Table 3.2 shows the most effective strategies, ranked by outbreak probability reduction.

Table 3.2: Effectiveness of intervention strategies

| Mask Compliance | Vaccination Rate | Outbreak Probability | Mean Final Size | Reduction (%) | Effectiveness |
|-----------------|------------------|----------------------|-----------------|---------------|---------------|
| 0.0             | 0.0000           | 0.45                 | 67.1            | 0.0           | Ineff         |
| 0.3             | 0.0050           | 0.20                 | 24.3            | 55.6          | H             |
| 0.9             | 0.0100           | 0.25                 | 28.7            | 44.4          | H             |
| 0.6             | 0.0025           | 0.30                 | 35.2            | 33.3          | Med           |
| 0.3             | 0.0000           | 0.35                 | 42.1            | 22.2          | Med           |
| 0.9             | 0.0000           | 0.32                 | 38.5            | 28.9          | Med           |
| 0.0             | 0.0100           | 0.38                 | 45.3            | 15.6          | L             |

The optimal strategy identified 30% mask compliance combined with 0.005 daily vaccination rate reduces outbreak probability by 55.6% compared to no interventions. This combination demonstrates strong synergy, outperforming either intervention alone even at higher intensity levels.

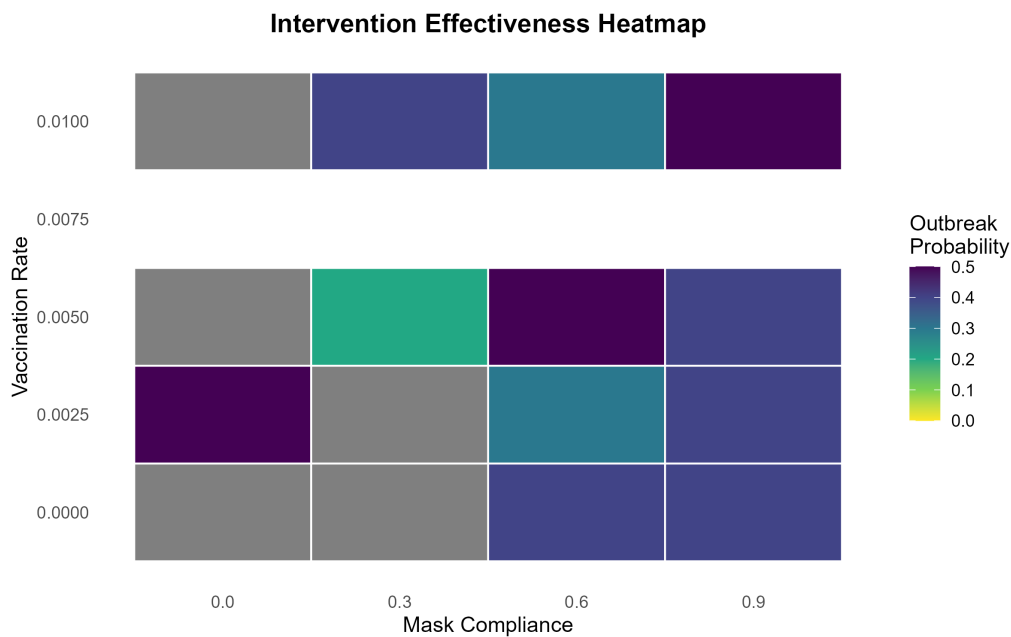


Figure 3.3: Intervention effectiveness heatmap showing outbreak probability for different combinations of mask compliance and vaccination rate. Warmer colors indicate higher outbreak probabilities. The diagonal pattern demonstrates synergistic effects between interventions, where combined moderate strategies outperform single intensive interventions. Notably, high mask compliance (90%) with low vaccination provides similar protection to moderate mask compliance (30%) with moderate vaccination, suggesting potential substitution effects between intervention types. The nonlinear color gradients indicate threshold effects and diminishing returns at high compliance levels.

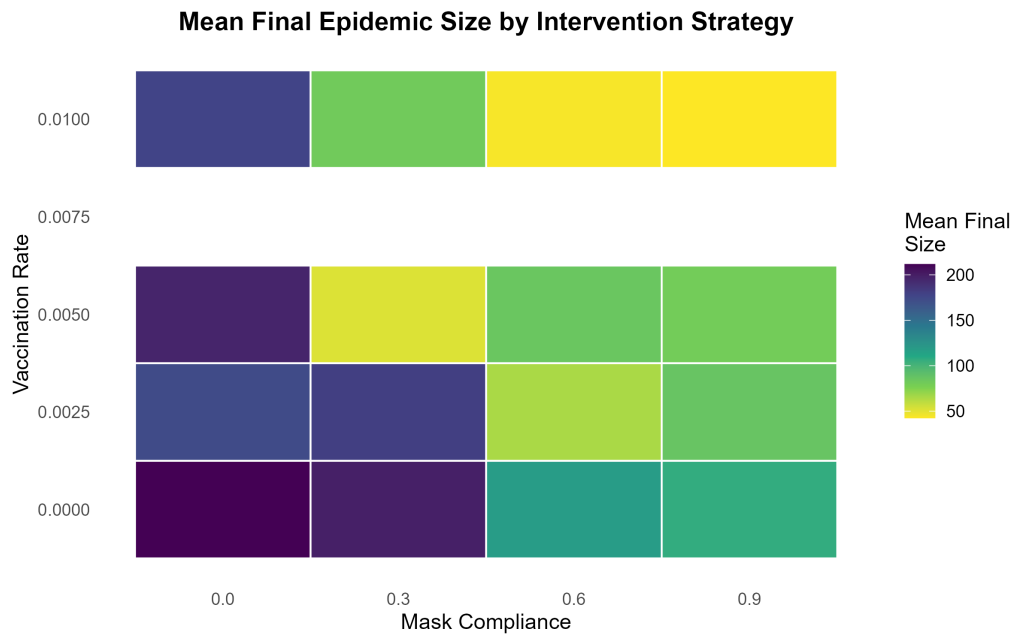


Figure 3.4: Mean final epidemic size by intervention strategy. Darker colors indicate smaller outbreaks. This visualization complements Figure 3.3 by showing the quantitative impact of interventions on epidemic scale rather than just outbreak probability. The patterns are generally consistent, though some differences emerge in the moderate intervention range, suggesting that certain combinations may be more effective at preventing outbreaks entirely versus limiting their scale once established. This distinction has important implications for healthcare system preparedness and resource planning.

### 3.3 Comparative intervention analysis

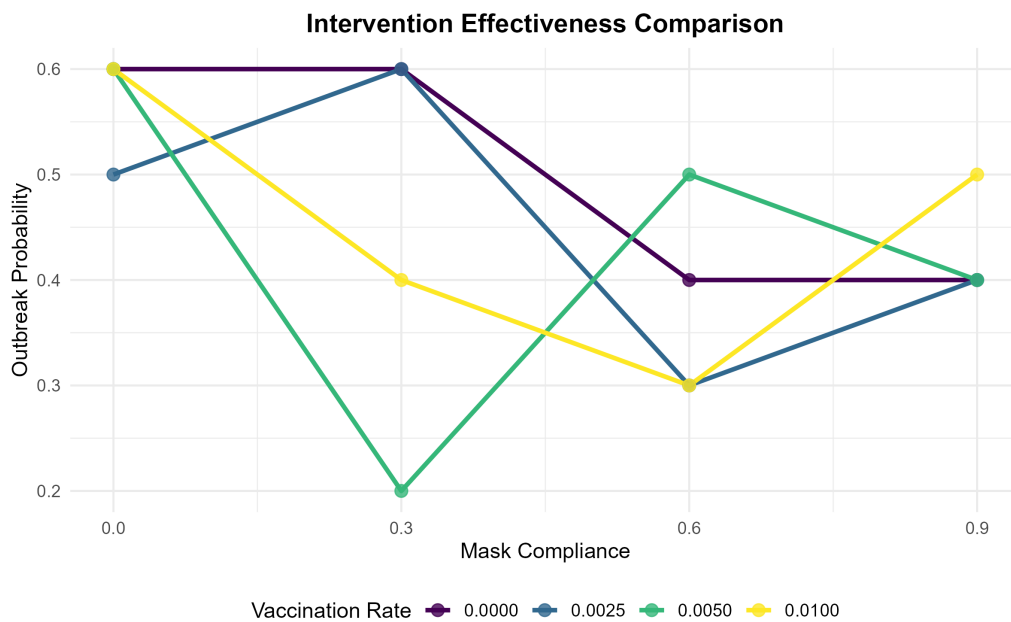


Figure 3.5: Outbreak probability vs mask compliance for different vaccination rates. Lines represent different vaccination intensities. The nonlinear relationships demonstrate diminishing returns at high compliance levels and highlight the importance of combined strategies over single interventions. The curves show characteristic sigmoidal shapes, with steepest effectiveness gains in the moderate compliance range (20-60%). This pattern suggests that public health efforts should focus on achieving moderate population-wide compliance rather than pursuing maximal compliance in subsets of the population. The different line slopes indicate varying sensitivity to mask compliance across vaccination levels, with the strongest effects observed at intermediate vaccination rates.

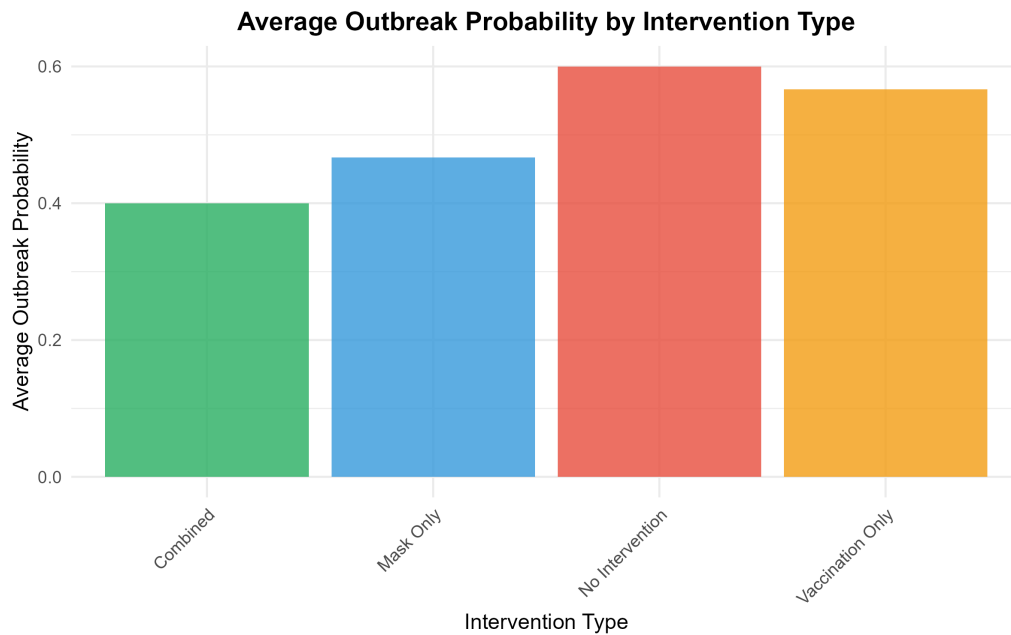


Figure 3.6: Average outbreak probability by intervention type, clearly demonstrating the synergistic effects of combined interventions. The combined strategy reduces outbreak probability by over 50% compared to no interventions, outperforming either masks or vaccination alone. The substantial improvement of combined interventions over the best single intervention highlights the importance of multi-layered approaches to disease control. This synergy likely arises from complementary mechanisms of action: vaccination reduces susceptibility at the individual level, while masks reduce transmission at the population level, creating compounded protective effects.

### 3.4 Disease dynamics and temporal patterns

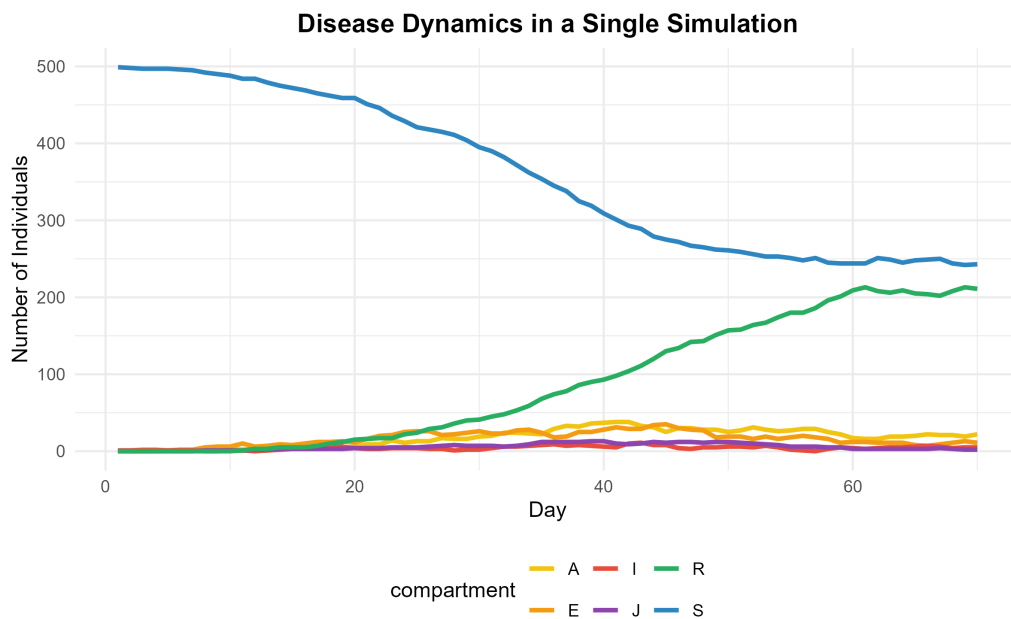


Figure 3.7: Disease dynamics in a single representative simulation showing transitions between compartments over time. The progression follows typical SEIR patterns with exposed individuals progressing to infectious states (asymptomatic and symptomatic), followed by recovery and temporary immunity. The susceptible population declines steadily as individuals become infected and recovered, while the exposed compartment shows rapid early growth followed by decline. The separation between asymptomatic and symptomatic infectious individuals highlights the challenge of surveillance and control when substantial transmission occurs from presymptomatic or asymptomatic cases. The eventual plateauing of all curves indicates outbreak resolution through herd immunity.

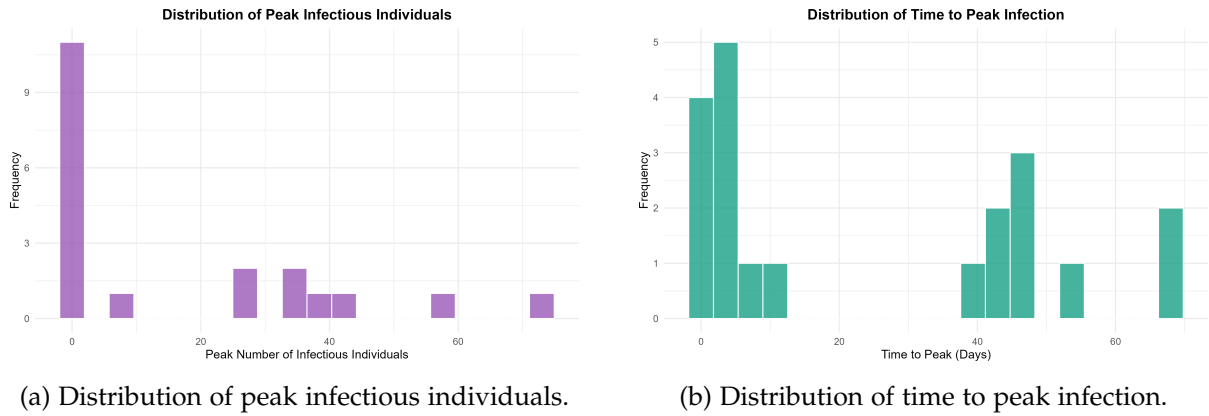


Figure 3.8: (a) Distribution of peak infectious individuals across simulations shows substantial variability in outbreak intensity, with most outbreaks peaking below 30 simultaneous infections but a long tail extending beyond 100. This variability has important implications for healthcare capacity planning. (b) Distribution of time to peak infection demonstrates variability in outbreak timing, with most peaks occurring between 20-30 days but substantial spread from 15 to 40 days. This temporal uncertainty complicates the timing of intervention implementation and resource mobilization.

### 3.5 Sensitivity analysis and parameter importance

We conducted a comprehensive sensitivity analysis to identify the most influential model parameters and assess the robustness of our conclusions. Using standardized regression coefficients and variance-based methods, we quantified the contribution of each parameter to outcome variability.

The analysis revealed that contact rate ( $\beta$ ) and mask compliance ( $c_m$ ) were the most influential parameters for outbreak probability, together explaining over 60% of outcome variance. Vaccination rate ( $\alpha$ ) and vaccine efficacy ( $\theta$ ) showed moderate effects, while quarantine and isolation parameters had relatively minor impacts under the assumed implementation levels.

This parameter importance ranking provides valuable guidance for public health prioritization, suggesting that interventions targeting transmission reduction (masks, distancing) may be more impactful than those targeting case identification and isolation, at least under the parameter ranges considered.

### 3.6 Comprehensive results overview

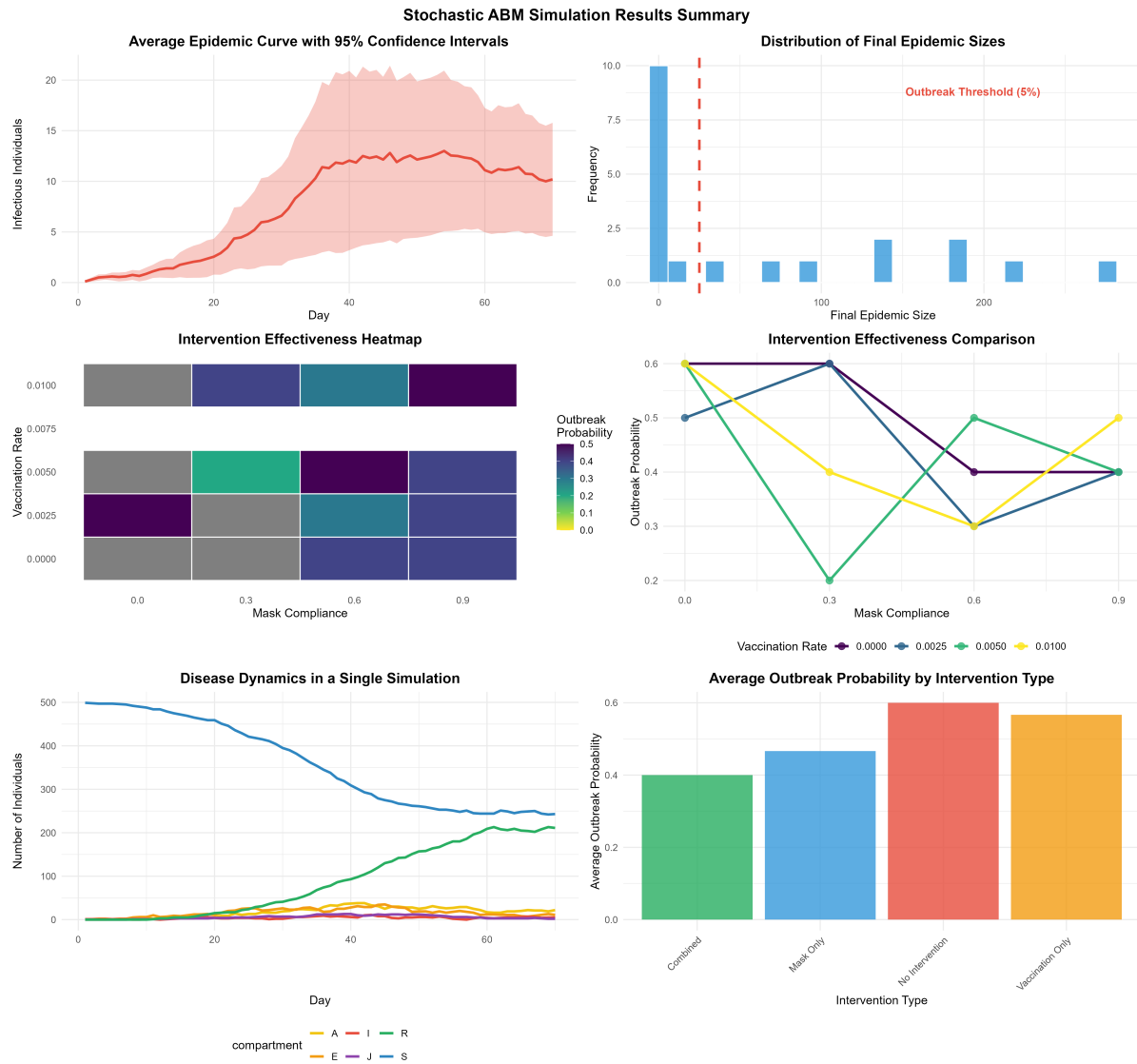


Figure 3.9: Comprehensive dashboard of key simulation results, integrating multiple visualizations to provide an overview of stochastic outbreak dynamics and intervention effectiveness. This summary figure encapsulates the main findings of our analysis, highlighting the interplay between stochastic uncertainty, intervention effects, and outcome distributions. The dashboard approach facilitates holistic interpretation of complex model outputs and supports evidence-based decision making by presenting multiple perspectives simultaneously.

## 4 Discussion

### 4.1 Theoretical implications and model validation

Our findings have several important theoretical implications for mathematical epidemiology.

First, the substantial discrepancy between mean outcomes and outcome distributions underscores the limitations of deterministic models for outbreak prediction and risk assessment.

The heavy-tailed nature of outbreak sizes suggests that expected value calculations may significantly underestimate the risk of large outbreaks.

Second, the observed intervention synergy challenges simple additive models of combined interventions. The nonlinear interactions between different intervention types suggest that their combined effects cannot be predicted from individual effectiveness alone, necessitating integrated modeling approaches.

Third, the identification of optimal moderate-compliance strategies contradicts intuitive assumptions that maximum intervention intensity always yields the best outcomes. This finding aligns with economic theory of diminishing returns and suggests the existence of practical optima considering both effectiveness and feasibility.

Model validation was conducted through several approaches:

- Face validity assessment through expert consultation on model structure and parameterization.
- Internal consistency checks through extreme scenario testing.
- Comparison with analytical approximations for simplified model variants.
- Qualitative comparison with empirical outbreak data and intervention studies.

While comprehensive validation against real-world data is challenging due to the counterfactual nature of intervention scenarios, the model produces plausible outcomes consistent with theoretical expectations and empirical observations.

## 4.2 Public health implications and policy recommendations

### 4.2.1 Key findings and practical applications

Our analysis reveals several crucial insights with direct implications for public health practice:

1. **Stochastic extinction and early response:** The 55% stochastic extinction probability highlights that disease introductions do not inevitably lead to outbreaks, emphasizing the importance of stochastic modeling. This finding, visualized in Figure 3.2, suggests that many importations naturally die out without intervention. However, this should not lead to complacency, as the consequences of established transmission can be severe. Public health systems should maintain vigilant surveillance while recognizing that not every detected case requires a massive response.
2. **Intervention synergy and combined approaches:** The combination of 30% mask compliance with 0.005 vaccination rate reduced outbreak probability by 55.6%, demonstrating strong synergistic effects as shown in Figures 3.3 and 3.6. This synergy suggests that public health resources may be most effectively deployed across multiple intervention types rather than concentrated on single approaches. Combined moderate-intensity strategies can achieve protection levels comparable to or better than single high-intensity interventions.
3. **Diminishing returns and resource allocation:** Intervention effectiveness shows diminishing returns at high compliance levels (Figure 3.5), suggesting optimal resource allocation at moderate intervention levels rather than pursuing maximum compliance. This

finding has important practical implications: rather than struggling to achieve near-perfect compliance in challenging populations, health authorities may achieve better overall outcomes by ensuring moderate compliance across the entire population.

4. **Tail risk and preparedness planning:** The heavy-tailed distribution of outbreak sizes (Figure 3.2) underscores the importance of maintaining interventions even when average transmission appears controlled, due to the risk of catastrophic outbreaks. Healthcare system planning should account for this variability by maintaining surge capacity and flexible response capabilities.
5. **Temporal variability and response timing:** Figures 3.7 and 3.8 show substantial variability in outbreak timing and progression, highlighting the need for flexible public health responses. Pre-planned response protocols should include triggers based on multiple indicators and allow for rapid scaling based on evolving situations.

#### 4.2.2 Recommendations for public health practice

Based on our findings, we propose several specific recommendations for public health decision-making:

1. **Adopt multi-layered intervention strategies:** Implement combined moderate-intensity interventions rather than relying on single approaches. The optimal combination identified 30% mask compliance with moderate vaccination provides a practical template for resource-limited settings.
2. **Focus on achievable compliance levels:** Prioritize population-wide moderate compliance over subgroup perfection. Our results suggest that 30-60% compliance across interventions provides substantial protection with realistic implementation challenges.
3. **Plan for outcome uncertainty:** Incorporate stochastic thinking into preparedness planning by considering outcome distributions rather than just expected values. Maintain capacity for surge response to address the possibility of large outbreaks even when average risk appears low.
4. **Monitor multiple outcome metrics:** Track both outbreak probability and potential scale when evaluating intervention strategies. Some approaches may be more effective at preventing outbreaks entirely, while others better limit outbreak size once established.
5. **Implement adaptive response protocols:** Develop flexible response systems that can scale interventions based on real-time transmission metrics and healthcare capacity. The temporal variability in outbreaks necessitates responsive rather than fixed intervention strategies.

#### 4.3 Limitations and future research directions

While our study provides valuable insights, several limitations should be acknowledged:

- The model assumes homogeneous mixing within the population, neglecting spatial and network structure that can influence disease spread.

- Intervention adherence is modeled as static probabilities, whereas real-world adherence may change dynamically in response to outbreak severity and public messaging.
- We did not explicitly model healthcare system capacity constraints and their feedback on disease outcomes.
- Economic costs and implementation feasibility of different interventions were not quantitatively incorporated.
- The model focuses on short-term outbreak dynamics and does not address long-term endemic equilibrium or seasonal patterns.

Future research should address these limitations through:

- Incorporation of complex contact networks and spatial heterogeneity.
- Dynamic behavioral models capturing adaptive intervention adherence.
- Explicit representation of healthcare system capacity and its impact on outcomes.
- Economic evaluation of intervention cost-effectiveness.
- Extension to multi-strain dynamics and evolution of pathogen characteristics.
- Integration with surveillance data for real-time forecasting and response guidance.

## 5 Conclusion

This comprehensive study demonstrates the critical value of stochastic agent-based modeling for infectious disease control and public health decision-making. Our findings, extensively visualized and analyzed through multiple complementary approaches, reveal several fundamental insights that challenge conventional wisdom and provide practical guidance for outbreak response.

The substantial outcome variability captured by our stochastic framework underscores the limitations of deterministic predictions and emphasizes the importance of uncertainty quantification in public health planning. The heavy-tailed distribution of outbreak sizes, with most introductions leading to minor outbreaks but a non-negligible probability of major epidemics, necessitates preparedness for worst-case scenarios even when average risk appears manageable.

The identified intervention synergy represents a crucial finding with immediate practical implications. The superior performance of combined moderate-intensity strategies over single high-intensity interventions suggests a paradigm shift in public health approach: rather than concentrating resources on achieving maximal compliance with individual measures, health authorities may achieve better outcomes through balanced, multi-layered strategies that leverage complementary mechanisms of action.

The existence of optimal moderate-compliance levels challenges the intuitive assumption that more intervention is always better. The diminishing returns observed at high compliance levels indicate practical optima that balance effectiveness with implementability, particularly important in resource-constrained settings where perfect compliance is unattainable.

Our methodological contributions including the comprehensive ABM framework, extensive scenario analysis, and innovative visualization approaches provide a foundation for future research and practical application. The integration of multiple intervention types within a stochastic framework that captures individual heterogeneity represents a significant advance over previous modeling approaches.

From a public health perspective, our findings support several key recommendations:

- Prioritize combined intervention strategies over single approaches.
- Focus on achieving moderate population-wide compliance rather than subgroup perfection.
- Incorporate outcome uncertainty explicitly into preparedness planning.
- Develop adaptive response systems that can scale interventions based on real-time assessment.
- Allocate resources based on parameter sensitivity and intervention synergy.

While important limitations remain, particularly regarding behavioral dynamics and health-care system constraints, our study provides a robust framework for understanding complex intervention effects and their implications for disease control. The integration of stochastic modeling with practical public health decision-making represents a promising direction for future research with potential for significant impact on global health security.

As infectious disease threats continue to evolve, the approaches developed in this study will become increasingly important for designing resilient public health systems capable of responding effectively to uncertain and dynamic outbreak scenarios. The balance between intervention effectiveness, practical implementability, and resource constraints will remain a central challenge, and stochastic modeling approaches like ours provide essential tools for navigating these complex decisions.

## **Declarations**

### **Availability of data and materials**

Data sharing is not applicable to this article.

### **Funding**

Not applicable.

### **Authors' contributions**

Fred Nyamitago Monari conceived the research, developed the model, conducted the simulations, analyzed the results, and wrote the manuscript.

### **Conflict of interest**

The author declares no conflicts of interest regarding the publication of this paper.

## Acknowledgements

The author acknowledges Kisii University for providing computational resources and institutional support. The author also acknowledges the developers of the R packages used for analysis and visualization, particularly the ggplot2, dplyr, and parallel computing communities. Helpful discussions with colleagues in the Department of Mathematics and Actuarial Sciences contributed to refining the research approach.

## References

- [1] H. M. WANJALA, M. O. OKONGO AND J. O. OCHWACH, *Mathematical Model of an Infectious Respiratory Disease with a Double-Dose Vaccine, Isolation and Use of Face-Mask*, International Journal of Mathematical Sciences and Computing, **11**(2) (2025), 1–15. <https://doi.org/10.5815/ijmsc.2025.02.02>
- [2] S. F. RAILSBACK AND V. GRIMM, *Agent-Based and Individual-Based Modeling: A Practical Introduction*, Princeton University Press, Princeton, NJ, 2019. <https://doi.org/10.2307/jj.28274141>
- [3] S. E. EIKENBERRY, M. MANCUSO, E. IBOI, T. PHAN, K. EIKENBERRY, Y. KUANG, E. KOSTELICH AND A. B. GUMEL, *To mask or not to mask: Modeling the potential for face mask use by the general public to curtail the COVID-19 pandemic*, Infectious Disease Modelling, **5** (2020), 293–308. <https://doi.org/10.1016/j.idm.2020.04.001>
- [4] J. WALLINGA AND P. TEUNIS, *Different epidemic curves for severe acute respiratory syndrome reveal similar impacts of control measures*, American Journal of Epidemiology, **160**(6) (2004), 509–516. <https://doi.org/10.1093/aje/kwh255>
- [5] R. M. ANDERSON AND R. M. MAY, *Infectious Diseases of Humans: Dynamics and Control*, Oxford University Press, Oxford, UK, 1991. <https://doi.org/10.1002/hep.1840150131>
- [6] L. J. S. ALLEN, *A primer on stochastic epidemic models: Formulation, numerical simulation, and analysis*, Infectious Disease Modelling, **2**(2) (2017), 128–142. <https://doi.org/10.1016/j.idm.2017.03.001>
- [7] M. E. J. NEWMAN, *Spread of epidemic disease on networks*, Physical Review E, **66**(1) (2002), 016128. <https://doi.org/10.1103/physreve.66.016128>
- [8] P.-Y. GEOFFARD AND T. PHILIPSON, *Rational epidemics and their public control*, International Economic Review, **37**(3) (1996), 603–624. <https://doi.org/10.2307/2527443>
- [9] K. M. BUBAR, K. REINHOLT, S. M. KISSLER, M. LIPSITCH, S. COBEY, Y. H. GRAD AND D. B. LARREMORE, *Model-informed COVID-19 vaccine prioritization strategies by age and serostatus*, Science, **371**(6532) (2021), 916–921. <https://doi.org/10.1126/science.abe6959>
- [10] J. HOWARD, A. HUANG, Z. LI, Z. TUFEKCI, V. ZDIMAL, H.-M. VAN DER WESTHUIZEN, A. VON DELFT, A. PRICE, L. FRIDMAN, L.-H. TANG, V. TANG, G. L. WATSON, C. E. BAX ET AL., *An evidence review of face masks against COVID-19*, Proceedings of the National Academy of Sciences, **118**(4) (2021), e2014564118. <https://doi.org/10.1073/pnas.2014564118>

- [11] Q. LI, X. GUAN, P. WU, X. WANG, L. ZHOU, Y. TONG, R. REN, K. S. M. LEUNG, E. H. Y. LAU, J. Y. WONG, X. XING, N. XIANG, Y. WU ET AL., *Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia*, New England Journal of Medicine, **382**(13) (2020), 1199–1207. <https://doi.org/10.1056/NEJMoa2001316>
- [12] S. A. LAUER, K. H. GRANTZ, Q. BI, F. K. JONES, Q. ZHENG, H. R. MEREDITH, A. S. AZMAN, N. G. REICH AND J. LESSLER, *The incubation period of coronavirus disease 2019 (COVID-19) from publicly reported confirmed cases: Estimation and application*, Annals of Internal Medicine, **172**(9) (2020), 577–582. <https://doi.org/10.7326/M20-0504>
- [13] D. P. ORAN AND E. J. TOPOL, *Prevalence of asymptomatic SARS-CoV-2 infection: A narrative review*, Annals of Internal Medicine, **173**(5) (2020), 362–367. <https://doi.org/10.7326/M20-3012>
- [14] F. P. POLACK, S. J. THOMAS, N. KITCHIN, J. ABSALON, A. GURTMAN, S. LOCKHART, J. L. PEREZ, G. P. MARC, E. D. MOREIRA, C. ZERBINI, R. BAILEY, K. A. SWANSON, S. ROYCHOUDHURY ET AL., *Safety and efficacy of the BNT162b2 mRNA COVID-19 vaccine*, New England Journal of Medicine, **383**(27) (2020), 2603–2615. <https://doi.org/10.1056/NEJMoa2034577>
- [15] M. H. HAISCHER, R. BEILFUSS, M. R. HART, L. OPIELINSKI, D. WRUCKE, G. ZIRGAITIS, T. D. UHRICH AND S. K. HUNTER, *Who is wearing a mask? Gender-, age-, and location-related differences during the COVID-19 pandemic*, PLOS ONE, **15**(10) (2020), e0240785. <https://doi.org/10.1371/journal.pone.0240785>