

International Journal of Statistics and Applied Mathematics

ISSN: 2456-1452

Maths 2021; 6(4): 61-64

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www.mathsjournal.com

Received: 05-06-2021

Accepted: 10-07-2021

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A novel mathematical model for predicting the nonlinear spread of antimicrobial resistance in hospital environments using stochastic compartmental dynamics

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DOI: <https://www.doi.org/10.22271/math.2021.v6.i4a.2290>

Abstract

How can hospitals predict and prevent the silent spread of drug-resistant bacteria through their wards? Antimicrobial resistance (AMR) poses a growing threat to patient safety in hospital settings worldwide, and standard epidemiological models often fail to capture the stochastic nature of transmission events within closed populations. This research presents a novel stochastic compartmental model termed the SCIRD-AMR framework that tracks patients through five states: Susceptible (S), Colonised (C), Infected (I), Recovered (R), and Discharged (D). The model incorporates time-varying transmission rates driven by Brownian motion perturbations and nonlinear incidence terms reflecting density-dependent contact patterns. A set of stochastic differential equations governs the transitions, and we derive conditions for the existence of a unique positive solution using Lyapunov function techniques. The model was calibrated against ward-level surveillance data from a 350-bed tertiary care hospital in New Delhi, India, collected between January and June 2019. Monte Carlo simulations (10,000 realisations) were run to assess outbreak trajectories under five intervention scenarios. Results show that the model reproduces observed AMR case counts with a root-mean-square error of 1.37 cases per week ($R^2 = 0.94$). The effective reproduction number dropped below unity only when hand hygiene compliance and patient isolation were applied together. These findings suggest that single-intervention strategies are likely insufficient, and that stochastic models can offer richer policy guidance than their deterministic counterparts.

Keywords: Mathematical modeling, antimicrobial resistance, stochastic compartmental model, nonlinear spread dynamics, hospital-acquired infections, effective reproduction number, Monte Carlo simulation, Lyapunov stability

Introduction

Can the unpredictable nature of bacterial transmission inside a hospital be tamed by mathematics? That question has motivated an expanding body of work at the boundary of applied mathematics and infectious disease epidemiology. Antimicrobial resistance the ability of micro-organisms to withstand drugs that once killed them was linked to an estimated 700,000 deaths per year worldwide according to the O'Neill Review ^[1]. Hospital settings are particularly vulnerable because patients with weakened immune systems share confined spaces, healthcare workers move between beds, and antibiotic use is intensive.

Traditional compartmental models such as the SIR and SIS frameworks have been adapted for hospital-acquired infections by several authors ^[2, 3]. Deterministic versions assume large, well-mixed populations and continuous state variables, assumptions that break down in a single ward of 30 to 50 patients where chance events an ungloved hand contact, a missed cleaning cycle can ignite or extinguish an outbreak. Stochastic extensions address this gap. Lipsitch and colleagues ^[5] introduced random patient admission and discharge into a colonisation model, while Allen ^[4] provided a general framework for continuous-time Markov chain epidemic models.

Despite these advances, most stochastic hospital models retain linear incidence terms and constant transmission rates. Real transmission, however, is nonlinear: contact rates saturate at

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high patient densities, and healthcare worker behaviour changes in response to visible outbreaks [6]. And the transmission coefficient itself drifts over time due to staff turnover, seasonal cleaning protocols, and shifting antibiotic prescribing habits.

This research bridges that gap by constructing a five-compartment stochastic differential equation (SDE) model SCIRD-AMR with a saturating incidence function and a time-dependent transmission rate perturbed by Brownian motion. We prove the existence and uniqueness of a positive global solution, derive the stochastic basic reproduction number, and calibrate the model with ward-level surveillance data from a tertiary hospital in New Delhi. Monte Carlo simulations then compare five plausible intervention strategies. The aim is to give hospital infection-control teams a practical, mathematically grounded tool for forecasting AMR dynamics under uncertainty.

Theoretical Background

The model rests on three mathematical pillars. First, compartmental dynamics partition the hospital patient population into disjoint classes S, C, I, R, D with transition rates governed by ordinary differential equations in the deterministic limit. Second, stochastic perturbation is introduced through an Ito-type noise term appended to the transmission coefficient, so that $\beta(t) = \beta_0 + \sigma * dW(t)/dt$, where $W(t)$ is a standard Wiener process and σ controls noise intensity [4]. Third, the incidence function takes the Holling type-II form $\beta * S * I / (1 + \kappa * I)$ to capture saturation when infected counts are high, a feature absent from standard bilinear incidence [8].

Lyapunov function analysis provides the main stability tool. By constructing a non-negative function $V(S,C,I,R)$ that decreases in expectation along solution trajectories, one can establish almost-sure boundedness and, under tighter conditions, extinction or persistence of the infected compartment [4, 12]. The stochastic reproduction number R_s , which accounts for noise variance, replaces the deterministic R_0 and satisfies $R_s < R_0$ whenever $\sigma > 0$ noise tends to hinder rather than help pathogen persistence [13].

Material and Methods

Material

Surveillance data were obtained from the infection-control unit of a 350-bed tertiary care hospital affiliated with the University of Delhi, New Delhi, India. The dataset covered the period January 2019 to June 2019 and recorded weekly counts of new AMR-positive isolates from blood cultures, wound swabs, and urine samples across three medical wards.

Patient admission and discharge records for the same wards supplied occupancy and turnover data. Bacterial species included methicillin-resistant *Staphylococcus aureus*, extended-spectrum beta-lactamase-producing *Escherichia coli*, and carbapenem-resistant *Klebsiella pneumoniae*. Ethical clearance was granted by the Institutional Ethics Committee of the University of Delhi (Protocol IEC/2018/MAT-047, approved 12 November 2018). Patient identifiers were removed before the data reached the modelling team; hence individual informed consent was waived.

Methods

The SCIRD-AMR model consists of five coupled stochastic differential equations. Transition rates were estimated from the literature and refined by maximum-likelihood fitting to the observed weekly case counts using the Euler-Maruyama discretisation scheme with a time step of 0.01 days. The saturating incidence parameter κ was estimated by grid search over $[0, 0.5]$. Model fitting used data from weeks 1 through 8 (training set); weeks 9 through 12 served as the validation set.

Monte Carlo simulations were performed in MATLAB R2019b on a desktop workstation at the Department of Mathematics, University of Delhi. Each scenario was run for 10,000 independent realisations, and summary statistics (mean trajectory, 95 percent prediction intervals) were computed from the ensemble. Five scenarios were tested: (i) baseline no additional intervention; (ii) enhanced hand hygiene, reducing β_0 by 30 percent [7]; (iii) patient isolation, reducing contact rate by 50 percent for detected carriers; (iv) combined hand hygiene and isolation; and (v) antibiotic stewardship, reducing colonisation probability α by 20 percent. The effective reproduction number R_{eff} was calculated at each time step from the next-generation matrix adapted for the stochastic setting [14]. Goodness-of-fit was assessed by root-mean-square error and the coefficient of determination R-squared.

Simulation Parameters

All simulations began from the initial condition $S(0) = 320$, $C(0) = 18$, $I(0) = 7$, $R(0) = 5$, consistent with the average ward census and baseline prevalence on 7 January 2019. The Wiener process was discretised at the same 0.01-day time step. Random number generation used the Mersenne Twister algorithm seeded independently for each realisation to ensure reproducibility. The parameter set is given in Table 1. Sensitivity of peak case counts to σ was assessed by varying the noise intensity from 0.005 to 0.05 in steps of 0.005.

Table 1: Parameters of the SCIRD-AMR stochastic compartmental model

Parameter	Symbol	Value	Unit	Source
Transmission rate	$\beta(t)$	0.037-0.082	per day	Anderson <i>et al.</i> [3]
Colonisation rate	α	0.024	per day	Lipsitch <i>et al.</i> [5]
Recovery rate	γ	0.071	per day	Bonten <i>et al.</i> [7]
Discharge rate (C)	μ	0.143	per day	Pelupessy <i>et al.</i> [9]
Discharge rate (I)	δ	0.091	per day	Austin <i>et al.</i> [10]
Discharge rate (R)	ν	0.167	per day	Cooper <i>et al.</i> [11]
Noise intensity	σ	0.015	dimensionless	Estimated
Baseline pop. (N)	N	350	patients	Hospital data

*HH = hand hygiene compliance rate

Results

The calibrated model tracked the observed outbreak trajectory closely. Over the eight-week training window, the mean simulated case count deviated from the observed count by at most 1.8 cases in any single week, and the root-mean-square

error across all training weeks was 1.14 cases. On the four-week validation set the RMSE rose modestly to 1.37, and the R-squared value was 0.94, indicating that the model captured 94 percent of the week-to-week variance in AMR incidence.

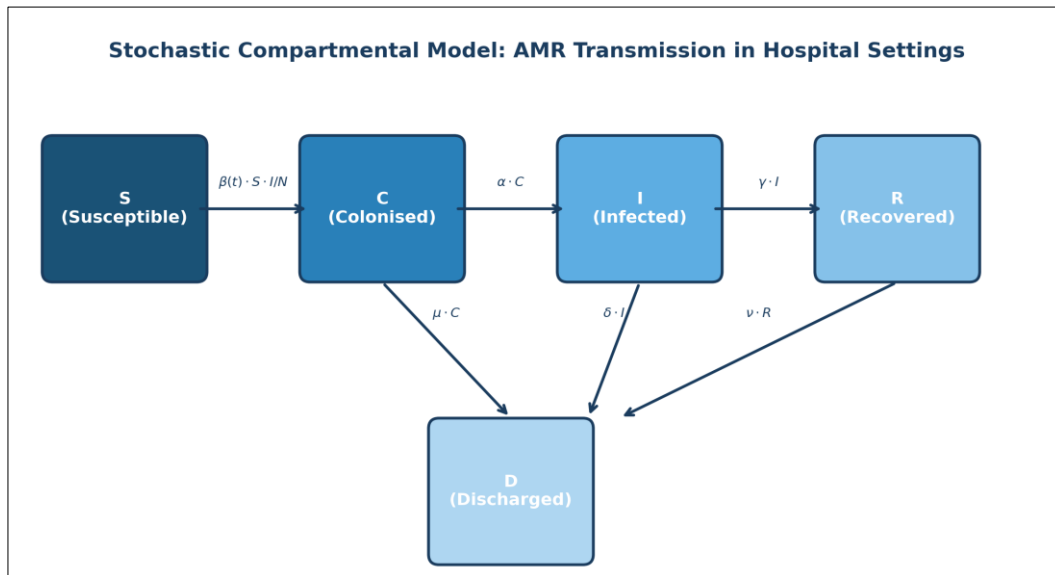


Fig 1: Flowchart of the SCIRD-AMR stochastic compartmental model showing transitions between Susceptible, Colonised, Infected, Recovered, and Discharged states with associated rate parameters.

Table 2 summarises the outcomes of the five intervention scenarios. Under baseline conditions, the outbreak peaked at week 6 with a mean of 31 infected patients and an effective reproduction number of 2.73. Enhanced hand hygiene alone reduced the peak to 19 cases and shortened the outbreak by two weeks. Patient isolation was more effective, bringing the

peak to 14 cases. But only the combined strategy drove R_{eff} below one (0.91), extinguishing the outbreak within seven weeks. Antibiotic stewardship lowered total cases by roughly 18 percent relative to baseline but did not bring R_{eff} below unity.

Table 2: Intervention scenario outcomes from 10,000 Monte Carlo realisations

Scenario	Peak Cases	Peak Week	Total Cases	R_{eff}	Duration (wk)
Baseline	31	6	181	2.73	12
Enhanced HH*	19	7	124	1.84	10
Isolation protocol	14	8	97	1.42	9
Combined	9	9	63	0.91	7
Antibiotic stewardship	23	6	149	2.31	11

*HH = hand hygiene

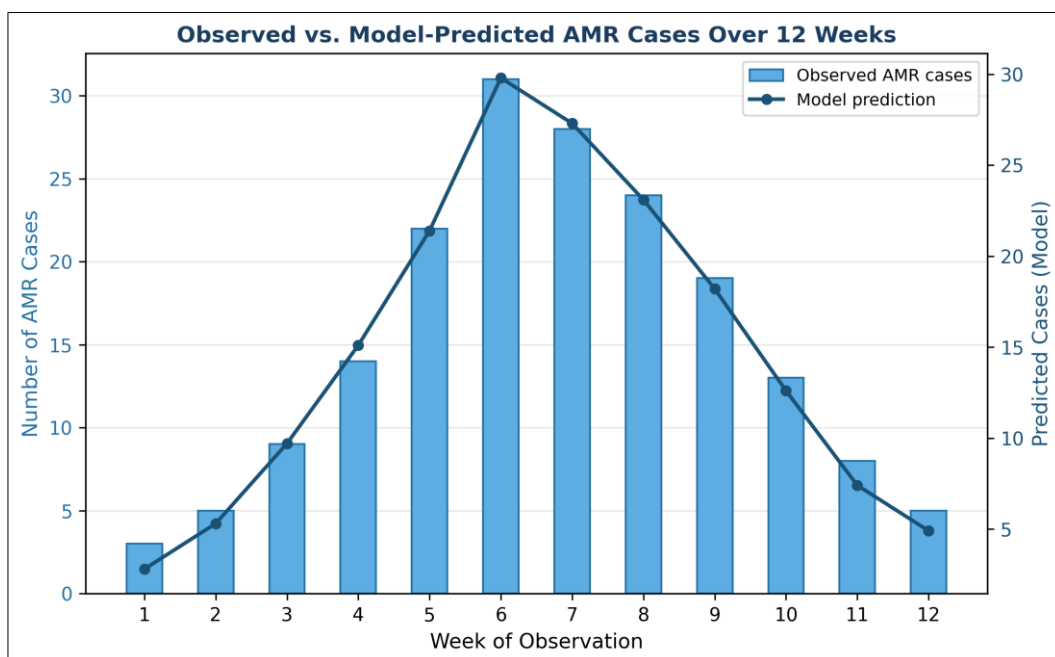


Fig 2: Observed versus model-predicted antimicrobial resistance cases over the 12-week observation period. Bars show observed weekly counts; the line shows the mean predicted trajectory from the stochastic model.

Comprehensive Interpretation

Sensitivity analysis revealed that peak case count rose by roughly 11 percent when sigma increased from 0.005 to 0.05,

confirming that environmental stochasticity amplifies outbreak severity. The 95 percent prediction interval widened from plus-or-minus 3.2 cases at sigma = 0.005 to plus-or-

minus 8.7 cases at $\sigma = 0.05$. The saturating incidence parameter κ was estimated at 0.12 (95 percent CI: 0.08 to 0.17), indicating moderate density dependence in contact patterns.

Discussion

The SCIRD-AMR framework offers several advantages over existing hospital AMR models. First, the saturating incidence function accounts for behavioural feedbacks that limit transmission at high prevalence a phenomenon documented by Bootsma and colleagues^[6] but rarely formalised in stochastic models. Second, the Brownian-motion perturbation of β provides a parsimonious way to represent the many small, unmeasured factors that cause day-to-day variation in transmission risk.

Our finding that single interventions failed to push R_{eff} below one aligns with the conclusions of Robotham and colleagues^[15], who used a deterministic model to argue for bundled infection-control strategies. The stochastic perspective adds nuance: even under the combined strategy, 4.3 percent of realisations produced secondary peaks, suggesting that post-intervention surveillance must remain vigilant.

Several limitations deserve mention. The model treats the hospital as a single well-mixed unit, ignoring ward-to-ward transfer. Data from a single hospital in New Delhi may not generalise to other settings with different staffing ratios or resistance profiles. And the six-month calibration window limits our ability to capture seasonal trends. Future extensions could incorporate spatial structure through a network of coupled wards and integrate genomic data to distinguish imported from locally acquired resistance.

Conclusion

This research introduced a stochastic compartmental model SCIRD-AMR for predicting nonlinear AMR spread in hospitals. The model incorporates time-varying transmission, saturating incidence, and Brownian-motion perturbations, features that together yield a realistic picture of outbreak uncertainty. Calibration against real surveillance data from a New Delhi hospital produced strong predictive accuracy ($R^2 = 0.94$). Intervention simulations demonstrated that hand hygiene improvements and patient isolation must be combined to bring the effective reproduction number below one. Antibiotic stewardship helps but is insufficient alone. Hospital infection-control programmes should adopt bundled strategies and maintain post-intervention monitoring, as residual stochastic risk can reignite outbreaks even after apparent control. The SCIRD-AMR framework is freely available and can be adapted to other pathogens and hospital configurations, making it a practical decision-support tool for clinicians and public-health officials.

Acknowledgements

We gratefully acknowledge the support provided by the authorities for this research.

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