



Developing cholera outbreak forecasting through qualitative dynamics: Insights into Malawi case study

Adrita Ghosh ^a, Parthasakha Das ^b, Tanujit Chakraborty ^{c,d}, Pritha Das ^a,
Dibakar Ghosh ^{e,*}

^a Department of Mathematics, Indian Institute of Engineering Science and Technology, Shibpur, West Bengal, 711103, India

^b Department of Mathematics, Rajiv Gandhi National Institute of Youth Development, Sriperumbudur, Tamil Nadu, 602105, India

^c SAFIR, Sorbonne University Abu Dhabi, Abu Dhabi, United Arab Emirates

^d Sorbonne Centre for Artificial Intelligence, Sorbonne University, Paris, 75006, France

^e Physics and Applied Mathematics Unit, Indian Statistical Institute, 203 B. T. Road, Kolkata, 700108, India

ARTICLE INFO

Keywords:

Cholera model
Parametric calibration
Sensitivity analysis
Bifurcation
Machine learning
Forecasting

ABSTRACT

Cholera, an acute diarrheal disease, is a serious concern in developing and underdeveloped areas. A qualitative understanding of cholera epidemics aims to foresee transmission patterns based on reported data and mechanistic models. The mechanistic model is a crucial tool for capturing the dynamics of disease transmission and population spread. However, using real-time cholera cases is essential for forecasting the transmission trend. This prospective study seeks to furnish insights into transmission trends through qualitative dynamics followed by machine learning-based forecasting. The Monte Carlo Markov Chain approach is employed to calibrate the proposed mechanistic model. We identify critical parameters that illustrate the disease's dynamics using partial rank correlation coefficient-based sensitivity analysis. The basic reproduction number as a crucial threshold measures asymptotic dynamics. Furthermore, forward bifurcation directs the stability of the infection state, and Hopf bifurcation suggests that trends in transmission may become unpredictable as societal disinfection rates rise. Further, we develop epidemic-informed machine learning models by incorporating mechanistic cholera dynamics into autoregressive integrated moving averages and autoregressive neural networks. We forecast short-term future cholera cases in Malawi by implementing the proposed epidemic-informed machine learning models to support this. We assert that integrating temporal dynamics into the machine learning models can enhance the capabilities of cholera forecasting models. The execution of this mechanism can significantly influence future trends in cholera transmission. This evolving approach can also be beneficial for policymakers to interpret and respond to potential disease systems. Moreover, our methodology is replicable and adaptable, encouraging future research on disease dynamics.

1. Introduction

Cholera persists as a formidable global health challenge, necessitating comprehensive strategies to elucidate, model, and effectively control its transmission dynamics. Cholera is an acute gastrointestinal disease characterized by gram-negative based *Vibrio cholerae*. Cholera causes extreme watery diarrhea, resulting in fatal dehydration and, consequently, kidney failure, abdominal cramps, vomiting, hypovolemic shock, and death. Transmission of bacterial infection is materialized through the fecal-oral route from contaminated water or food (Nelson et al., 2009; Faruque et al., 2005; Montero et al., 2023b; Luby et al., 2020; Hartley et al., 2006). *Vibrio cholerae* has emerged as seven important global pandemics during 1817–1824 in India, Asia, and south-

eastern Africa (Muzembo et al., 2022; Camacho et al., 2018; Lopez et al., 2020). In developing and under-developed countries, poor water supply, lack of sanitation, and bad hygiene practices contribute to its transmission (Mukandavire and Morris, 2015). Rapid outbreaks occurred and highlighted how bacterial pathogen and lytic bacteriophage propelled and quenched the cholera epidemic in Zimbabwe during 2008–2009 (Mukandavire et al., 2011). Recently, Malawi, a landlocked country in southeastern Africa, has experienced the worst cholera outbreak (Miggo et al., 2023). Nowadays, emerging as well as re-emerging infections like cholera are an open challenge (Morens et al., 2004) while environmental reservoir has a significant impact on transmission (Kong et al., 2014). In-apparent infections also apprehend a key to expounding the trend of cholera outbreak (King et al., 2008). In order to mitigate deadly

* Corresponding author.

E-mail address: dibakar@isical.ac.in (D. Ghosh).

<https://doi.org/10.1016/j.jtbi.2025.112097>

Received 16 January 2025; Received in revised form 11 March 2025; Accepted 17 March 2025

Available online 20 March 2025

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