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Mathematical Models to Understand the Dynamics of Water Borne Disease and its Impact on Public Health

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ABSTRACT

Waterborne diseases, such as cholera, typhoid fever, and malaria, remain major global health concerns, and their transmission rates are largely driven by contaminated water sources, poor sanitation conditions, and human behavioral factors. Mathematical modelling has, therefore, become an important tool for enhancing knowledge of the complex dynamics of transmission of these diseases, as well as for the evaluation of the efficiencies of public health interventions. This review integrates current modelling approaches, emphasizing both model formulation and analytical methods. It highlights some of the gaps in the literature, such as the limited number of models that integrate multiple transmission pathways and the tendency for very few to properly account for delays in the implementation of interventions. Recent developments, including deterministic and stochastic models, sensitivity analyses, and the newer approach of fractional-order systems, are discussed in terms of their potential for closing the gap between theoretical frameworks and real-world epidemiological patterns. Overall, the review emphasizes the utility of mathematical modelling to help develop effective strategies for water purification, vaccination, and community education that will lower the burden of waterborne diseases.

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Received: April 27, 2026; Accepted: July 16, 2026; Published: July 20, 2026

Keywords: Waterborne Disease, Mathematical Modeling, Cholera, Typhoid, Public Health

Introduction

Water is universally recognized as essential for life; it remains a primary vector for debilitating illnesses in many parts of the world. Waterborne diseases are caused by pathogenic microbes that are transmitted through contaminated freshwater [1,2]. The most frequent and significant of these illnesses- including diarrhea, cholera, giardia, dysentery, Escherichia coli, typhoid, malaria, hepatitis A, and hepatitis B- pose a severe public health challenge [3,4].

These pathogens are typically spread when individuals use infected water for drinking, food preparation, or washing [5,6]. This crisis is acutely felt in developing nations, where inadequate infrastructure and economic constraints prevent the widespread use of water purification systems, particularly in rural areas. Consequently, poor hygiene and low immunity make children the primary victims of these often-life-threatening diseases [8,9]. The awareness of these diseases has increased due to globalization, which has directed research attention towards previously neglected pathogenic microorganisms. The scale of this public health burden is staggering worldwide.

According to the World Health Organization (WHO), approximately 844 million people lack basic drinking water services, and roughly 159 million rely on untreated surface water. Alarming, at least 2 billion individuals use drinking water sources contaminated with feces, a situation attributed to approximately 502,000 diarrheal deaths annually.

The global landscape of communication diseases poses a continuous and dynamic threat to individual health, requiring strict and adaptive techniques to forecast, control, and reduce outbreaks. Since the transmission of disease from ancient waterborne pathogens to new viral threats is naturally complex and determined by the interaction of biological, environmental, and socio-behavioral factors, mathematical modeling has emerged as a critical tool. Models provide a logical foundation for effective disease management by explaining the movement of pathogens and estimating intervention effectiveness using parameters such as the basic reproduction number [10].

Mathematical epidemiology has significantly evolved to address these challenges. The field has progressed from rudimentary compartmental models, such as the SIR and SEIR frameworks to a complex interdisciplinary domain incorporating nonlinear dynamics, control theory, and spatial analysis [11-13]. To model pathogens persistence, researchers frequently subdivide the population into susceptible, infected, and recovered groups, with a separate compartment representing the water environment. Advanced models now incorporate spatial and environmental factors using reaction-diffusion equations and patch models, where nodes representing cities or villages are interconnected by water flow and human activities [14,15]. Furthermore, because epidemics are frequently nonlinear, sophisticated analytical methods are required to study them. Transcriptional bifurcation analysis was used to derive the critical thresholds between disease eradication and endemicity, whereas Hopf bifurcation research forecasts oscillating outbreaks, where stable endemic equilibria become unstable under specific scenarios [16]. In the

modern era, epidemiological modeling has increasingly focused on implementing proactive and reactive intervention strategies. Optimal control theory has become a crucial tool for determining how to allocate scarce public health resources efficiently and balance treatment with preventive measures such as vaccination, disinfection, and education. Additionally, the intersection of mathematical modelling and artificial intelligence has opened new frontiers in predictive epidemiology research. The application of machine learning, particularly artificial neural networks, allows for the approximation of nonlinear relationships and high dimensional systems [17]. When applied to waterborne diseases, these computational models capture the complex interplay between environmental variables and dynamics, serving as a potent complement to conventional analytical methods [18,19].

The goal of this review is to summarize the current trends in the field of dynamics analysis and computational tools in the context of infectious disease modelling [20, 21]. It discusses how bifurcation analysis can explain epidemic stability, how optimal control theory can be used to develop intervention strategies, and how machine learning models can improve prediction accuracy. These topics are explored in the following section to demonstrate their significant contributions to the development of epidemiological modeling and the future evolution of this vital field.

Materials and Method

A systematic literature review was conducted to identify studies employing mathematical modelling of waterborne diseases. The selection process was guided by predefined inclusion and exclusion criteria. The search was performed in Google Scholar, Scopus, and Science Direct using the following keywords and their combinations: “waterborne disease,” “mathematical modelling,” “nonlinear differential equation,” “pathogen,” and “environmental transmission,” with at least two terms appearing in the title or abstract. Articles were included if they were published in peer-reviewed journals, utilized nonlinear differential equation models, and examined pathogen dynamics and environmental transmission. Non-journal publications, papers lacking nonlinear modelling frameworks and analyses that unrelated to waterborne pathogens were excluded. Using this approach, approximately 80 publications were initially uncovered, of which 50 were excluded using the above criteria. The remaining 30 articles underwent a detailed evaluation, wherein each study was assessed in detail for model formulation, transmission mechanisms, environmental pathogen dynamics, and stability analysis. This systematic review provides an overall understanding of how nonlinear differential equation models have been used in the study of waterborne disease transmission.

Mathematical Models

Examined how seasonal changes and fear of infection influence the spread of typhoid fever [22]. The authors created a nonlinear mathematical model (1) that accounts for both transmissions between people and indirect transmission through the environment. The model incorporates elements such as rainfall and poor sanitation, which contribute to outbreaks during certain seasons. The authors used mathematical techniques to analyze the steady states and stability of the systems. They also ran simulations to identify which factors most affected the spread of the disease. The findings show that typhoid transmission increases significantly during the wet season due to the presence of more bacteria in contaminated water. Additionally, fear can lead people to change their behavior, such as practicing better hygiene or avoiding social interactions, which can help reduce the spread of the disease. The model suggests that if the basic reproduction number (R_0) is

less than one, the disease will eventually die out. However, they recognized that their model had limitations, such as a lack of real-world data for validation. They recommended the use of actual data to improve accuracy. Overall, the study emphasizes how seasonal changes and human behavior affect typhoid fever transmission, offering a helpful framework for public health planning and disease control in areas with limited resources. The typhoid fever model was formulated as follows:

$$\left. \begin{aligned} \frac{dS}{dt} &= \Lambda - (\lambda_1 + \lambda_2)S - \mu_h S + \rho R, \\ \frac{dI}{dt} &= (\lambda_1 + \lambda_2)S - qI, \\ \frac{dR}{dt} &= \varepsilon I - (\mu_h + \rho)R, \\ \frac{dB}{dt} &= g_b B \left(1 - \frac{B}{k_1}\right) \left(1 + \xi \sin\left(\frac{2\pi t}{365}\right)\right) + \alpha I - \mu_b B, \end{aligned} \right\} \begin{aligned} S(0) &= S_0 > 0 \\ B(0) &= B_0 \geq 0 \\ I(0) &= I_0 \geq 0 \\ R(0) &= R_0 \geq 0 \end{aligned} \quad (1)$$

where $q = \mu_h + \varepsilon$, and $N(t)$, $S(t)$, $I(t)$, $R(t)$ and $B(t)$ are human population, susceptible individuals, typhoid infected individuals, bacteria respectively. Thus $N(t) = S(t) + I(t) + R(t) + B(t)$ provide a valuable mathematical investigation into how vaccination and hygiene standards impact typhoid fever transmission [23]. A compartmental model (2) that includes both vaccination and hygiene components for a more realistic representation of the dynamics of typhoid transmission is presented in this study. Using the Next Generation Matrix Method, the authors calculated the control reproduction number (R_0). Their results showed that typhoid can be eliminated when $R_0 < 1$, while it remains persistent above the threshold value. In the model presented here, parameters are estimated Nigerian data. Numerical simulations were performed to assess the transmission patterns. The results of the analysis under the current conditions indicate that typhoid is endemic. The sensitivity analysis identified four key drivers of transmission: human-to-human transmission rate, environmental bacterial decay rate, vaccine efficacy, and treatment rate. The study further highlights how control efforts focused on school-aged children and food handlers, for instance, would have meaningful reductions in infection rates. Generally, this work stands out because of its high-quality mathematical formulation and relevance to public health. It closely links theoretical epidemiology to practical disease control strategies. The nonlinear model governing typhoid transmission is given by the following system of ordinary differential equations:

$$\left. \begin{aligned} \frac{dS}{dt} &= (1 - \phi)\Lambda + \kappa V + \varepsilon R - \beta S(B_c + \eta I) - (\pi + \mu)S, \\ \frac{dV}{dt} &= \pi S - (1 - m)\beta V(B_c + \eta I) - (\kappa + \mu)V, \\ \frac{dE}{dt} &= \beta(B_c + \eta I)(s + (1 - m)V) - (\alpha + \mu)E, \\ \frac{dI}{dt} &= \alpha E + \xi T - (\gamma + \sigma_1 + \mu + \delta_1)I, \\ \frac{dT}{dt} &= \gamma I - (\xi + \sigma_2 + \mu + \delta_2)T, \\ \frac{dR}{dt} &= \sigma_1 I + (1 - \phi)\sigma_2 T - (\theta + \varepsilon + \mu)R, \\ \frac{dM}{dt} &= \phi\Lambda + \phi\sigma_2 T + \theta R - \mu M, \\ \frac{dB_c}{dt} &= \rho I - \mu_b B_c, \end{aligned} \right\} \begin{aligned} S(0) &= S_0 > 0 \\ V(0) &= V_0 \geq 0 \\ E(0) &= E_0 \geq 0 \\ I(0) &= I_0 \geq 0 \\ T(0) &= T_0 \geq 0 \\ R(0) &= R_0 \geq 0 \\ M(0) &= M_0 \geq 0 \\ B_c(0) &= B_c \geq 0 \end{aligned} \quad (2)$$

Where $N(t)$, $S(t)$, $V(t)$, $E(t)$, $I(t)$, $T(t)$, $R(t)$, $M(t)$ and (t) are the humans population, susceptible humans, vaccinated humans, exposed humans, symptomatic infectious humans, treated humans, recovered individuals, medically hygienic and conscious human, bacterial population, respectively.

provides extensive mathematical modelling to reduce the transmission of typhoid fever based on optimal control methods [24]. This study proposes a new model combining a medically hygienic compartment with treatment and environmental controls for sanitation to make the dynamic transmission of the disease more realistic. The authors applied the maximum principle of Pontryagin and thus determined the required conditions to be optimized, and then used a fourth-order Runge-Kutta solution of the resulting system. Three control mechanisms were studied: environmental sanitation and personal hygiene, treatment of the infected, and a combination of the two. The simulation results showed that all interventions decreased the infection level, and their combination showed the most significant decrease in the number of exposed, infected, and bacteria in the environment. Efficiency analysis showed that the treatment-only strategy was marginally more efficient than the combined strategy, whereas the latter proved to be the most sustainable and viable strategy for implementation in real life. In this study, it was noted that good sanitation practices, personal hygiene, and timely medical treatment are important agents for controlling typhoid fever, especially in endemic countries such as Africa and South Asia. Altogether, the study offers useful information about the optimization of public health with mathematical models, with a focus on interdisciplinary strategies incorporating epidemiology, mathematics, and public health policy to address the challenges of overcoming infectious diseases. The optimal control model for typhoid fever dynamics is obtained as:

$$\left. \begin{aligned} \frac{dS}{dt} &= (1-\phi)\Lambda + \varepsilon R - (1-u_1(t))\beta S(B_c + \eta I) - \mu S, \\ \frac{dE}{dt} &= (1-u_1(t))\beta S(B_c + \eta I) - (\alpha + \mu)E, \\ \frac{dI}{dt} &= \alpha E + \xi T - (u(t) + \sigma_1 + a_2 u_2(t) + \mu + (1-a_2 u_2(t))\delta_1)I, \\ \frac{dT}{dt} &= u_2(t)I - (\xi + \sigma_2 + a_2 u_2(t) + \mu + (1-a_2 u_2(t))\delta_2)T, \\ \frac{dR}{dt} &= (\sigma_1 + a_2 u_2(t))I + (1-\phi)(\sigma_2 + a_2 u_2(t))T - (\theta + \varepsilon + \mu)R, \\ \frac{dM}{dt} &= \phi\Lambda + \phi(\sigma_2 + a_2 u_2(t))T + \theta R - \mu M, \\ \frac{dB_c}{dt} &= (1-a_2 u_2(t))\rho I - (\mu_1 - a_2 u_2(t))B_c, \end{aligned} \right\} \begin{aligned} S(0) &= S_0 \\ E(0) &= E_0 \\ I(0) &= I_0 \\ T(0) &= T_0 \\ R(0) &= R_0 \\ M(0) &= M_0 \\ B_c(0) &= B_{c0} \end{aligned} \quad (3)$$

where the total human population is given by: - $N(t) = S(t) + E(t) + I(t) + T(t) + R(t) + M(t)$ and $S(t)$, $E(t)$, $I(t)$, $T(t)$, $R(t)$, $M(t)$ and $B_c(t)$ are susceptible humans, exposed humans, infected humans with symptoms, individuals undergoing treatment for typhoid fever infection, recovered persons, medically vigilant and hygienic humans, and population of bacteria respectively.

Provides a detailed approach to the mathematics of understanding and controlling the cholera outbreak, especially in the Nigerian context [25]. This study conducts an adapted SIR-B (Susceptible Infected Recovered Bacteria) model, which does not consider natural recovery because most cholera recoveries are due to medical care as opposed to immunity. This study examined the dynamics of the disease through a system of nonlinear ordinary differential equations by adding treatment rates, water hygienic, and environmental sanitation to the equation system. The model estimates the basic reproduction number (R_0) to establish the

basic quantity by dividing the continuation and elimination of disease. Through of stability analysis and numerical simulation using MathCAD14, the authors proved that cholera transmission can be reduced by better treatment and sanitation practices. Even moderate levels of water hygiene and sanitation compliance can reduce R_0 to below one, so that the epidemic is effectively controlled, as the results indicate. The graphical outcome also demonstrates the reduction in the number of infected people and bacterial concentration, and the growing number of recovered people over time. This study found that cholera eradication is dependent on the synergistic effects of control measures, including medical treatment, accessibility of clean water, and cleanliness of the environment. The paper as a whole is a good contribution to epidemiological modelling as it brings useful insights into the means of controlling cholera using mathematical analysis and explanations on how to apply the policy using practical approaches, which forms a good framework to be used by policymakers in developing nations. The model consists of the following system of nonlinear ordinary differential equations:

$$\left. \begin{aligned} \frac{dS}{dt} &= \beta N - \frac{a(1-c_w)B}{K+B}S + \omega R - \mu S \\ \frac{dI}{dt} &= \frac{a(1-c_w)B}{K+B}S - (\tau + \mu + \delta)I \\ \frac{dB}{dt} &= e(1-c_s)I - \rho B \\ \frac{dR}{dt} &= \tau I - (\omega + \mu)R \end{aligned} \right\} \quad (4)$$

Where $N = S + I + R$, and $S(t)$, $I(t)$, $R(t)$, $B(t)$ and N Are Susceptible human population, Infected human population, Recovered human population, Concentration of vibrio cholera population, and total human population respectively.

Proposed an enhanced mathematical model that aims to better understand cholera transmission dynamics and determine possible regions of control [26]. They formulated a time-delayed SIQRB model, which consists of five compartments: Susceptible, Infected, Quarantined, Recovered and Bacterial concentration. This model includes a time delay to show the incubation period between infection and symptoms, making the model more biologically realistic and increasing its ability to fit empirical data, especially regarding the outbreak of cholera in the Artibonite Department in 2010-11. The study also provided a rigorous mathematical analysis in which biological validity was established, the disease-free and endemic equilibria were derived, and the basic reproduction number (R_0), was computed. It is shown that cholera persists when R_0 exceeds unity. The delay component facilitates fundamental insights into the stability of the equilibria and the long-term dynamics of the disease. The study further applies optimal control theory, using Pontryagin's Minimum Principle for the computation of effective quarantine strategies that minimize both infection levels and costs of treatment. Numerical simulations calibrated with real epidemic data showed that timely quarantine and appropriately scaled intervention intensity significantly reduced infection peaks and environmental bacterial load. In general, the study combines mathematical rigor with clear public health relevance, therefore providing practical guidance in the design of cost-effective cholera control measure. formulation of the cholera model as follows: -

$$\left. \begin{aligned} \frac{dS}{dt} &= \Lambda - \frac{\beta B(t)}{\kappa + B(t)} S(t) + \omega R(t) - \mu S(t), \\ \frac{dI}{dt} &= \frac{\beta B(t - \tau)}{\kappa + B(t - \tau)} S(t) - (\delta + \alpha_1 + \mu) I(t), \\ \frac{dQ}{dt} &= \delta I(t) - (\varepsilon + \alpha_2 + \mu) Q(t), \\ \frac{dR}{dt} &= \varepsilon Q(t) - (\omega + \mu) R(t), \\ \frac{dB}{dt} &= \eta I(t) - dB(t) \end{aligned} \right\} \quad (5)$$

Where S, I, Q, R, and B Are Susceptible, Infected, Quarantined, Recovered, and bacteria respectively.

Performed an in-depth mathematical analysis of the antimicrobial resistance (AMR) burden that is increasingly faced in the treatment of cholera [27]. The authors developed a multidrug-resistant (MDR) cholera epidemic model with staged switching between first-line and second-line of antibiotics to investigate how switching between the two classes of antibiotics impacts disease transmission and resistance development. The deterministic compartmental framework captures both human and bacterial dynamics, including direct human-to-human transmission and environment-to-human transmission pathways. The basic reproduction number (R_0) and its components were applied to identify the main parameters that drive the spread of sensitive and resistant *Vibrio cholera* strains, using rigorous stability and sensitivity analyses. Validation of the model is done with equilibrium analysis using center Manifold Theory and Markov Chain Monte Carlo simulations. It shows that carefully designed antibiotic-switching practices can significantly reduce the prevalence of MDR cholera while maintaining effective treatment, underlining the importance of antibiotic stewardship. A key strength of the model is the realistic treatment delays and gradual build-up of resistance to reflect resource-limited settings. Overall, this study contributes to valuable quantitative insights into optimizing antimicrobial strategies for controlling cholera and provides practical implication for both researchers and policymakers. We have the following system of equation to model the transmission dynamics of the cholera in the presence of antibiotic resistance and switching:

$$\left. \begin{aligned} \frac{dX}{dt} &= \Lambda - (\mu + A)X, & X(0) &\geq 0 \\ \frac{dI_s}{dt} &= (f\lambda + \lambda_s)X - (\mu + \delta_s + \theta_s + \sigma_s)I_s, & I_s(0) &\geq 0 \\ \frac{dT_{s1}}{dt} &= \sigma_s I_s - (\mu + \delta_{s1} + \theta_{s1} + \sigma_{s1})T_{s1}, & T_{s1}(0) &\geq 0 \\ \frac{dT_{s2}}{dt} &= \sigma_{s1} T_{s1} - (\mu + \delta_{s2} + \theta_{s2})T_{s2}, & T_{s2}(0) &\geq 0 \\ \frac{dI_r}{dt} &= ((1-f)\lambda + \lambda_r)X - (\mu + \delta_r + \theta_r + \sigma_r)I_r, & I_r(0) &\geq 0 \\ \frac{dT_{r1}}{dt} &= \sigma_r I_r - (\mu + \delta_{r1} + \theta_{r1} + \sigma_{r1})T_{r1}, & T_{r1}(0) &\geq 0 \\ \frac{dT_{r2}}{dt} &= \sigma_{r1} T_{r1} - (\mu + \delta_{r2} + \theta_{r2})T_{r2}, & T_{r2}(0) &\geq 0 \\ \frac{dQ}{dt} &= \theta_s I_s + \theta_{s1} T_{s1} + \theta_{s2} T_{s2} + \theta_r I_r + \theta_{r1} T_{r1} + \theta_{r2} T_{r2} - \mu Q, & Q(0) &\geq 0 \\ \frac{dB}{dt} &= gB + \phi_s I_s + \phi_r I_r - \mu_b B, & B(0) &\geq 0 \end{aligned} \right\} \quad (6)$$

Where X, Q, I_s , I_r , T_{s1} , T_{s2} , T_{r1} , T_{r2} and B Are Susceptible, recovered individuals, untreated infected with strain sensitive to both antibiotics, untreated infected with strain resistant to antibiotic 1, infected with sensitive strain on treatment with antibiotic 1, infected with sensitive strain on treatment with antibiotic 2, infected with resistant strain on treatment with antibiotic 1, infected with resistant strain on treatment with antibiotic 2, and bacteria respectively. And the total human population at any time t is given by
 $N(t) = X(t) + I_s(t) + I_r(t) + T_{s1}(t) + T_{s2}(t) + T_{r1}(t) + T_{r2}(t) + Q(t)$.

Provides the mathematical study of the dynamic of cholera spread with the use of vaccination and environment control [28]. The paper constructs a new type of delay differential model, which is based on the two key delays, including the latent period of infection, and the delay in the application of disinfection to polluted water. The dual-delay mechanism of the model is more realistic in the sense that it represents the biological and environmental processes that get involved in the transmission of cholera. The study incorporates human population compartments of the vulnerable, exposed, infected and recovered population as well as the bacterial concentration and disinfectant concentrations. They obtain the basic reproduction number (R_0) by means of the Next Generation Matrix technique and perform sensitivity to calculate the impact of different parameters on the spread of diseases, including infection rate, recovery, disinfection, and vaccination. The findings indicate that the rate of bacterial growth in water can be controlled successfully, and the vaccination coverage has a strong effect on the reduction. R_0 establishing the effectiveness of these interventions. The paper ascertains that under delay conditions, the endemic equilibrium is stable, and the disease-free-equilibrium is stable when $R_0 < 1$.

The study reveals that by applying numerical simulation through the predictor-corrector technique, it becomes possible to suppress the oscillations in disease dynamics by means of vaccination and ad-hoc disinfection stabilizing the system. Altogether, the study is a successful synthesis of epidemiology, mathematics and public health knowledge that provides solid a good theoretical and practice contribution to policymakers and health agencies that would seek to reduce the outbreak of cholera in prone areas. The mathematical system for the model is

$$\left. \begin{aligned} D_t^\alpha [S(t)] &= \Lambda + \omega R(t) - \mu_h S(t) - \left(\beta_e \frac{C(t)}{K + C(t)} + \beta_h I(t) \right) S(t) - \nu S(t), \\ D_t^\alpha [E(t)] &= \left(\beta_e \frac{C(t)}{K + C(t)} + \beta_h I(t) \right) S(t) - \left(\beta_e' \frac{C(t - \tau_1)}{K + C(t - \tau_1)} + \beta_h' I(t - \tau_1) \right) S(t - \tau_1) - \mu_h E(t), \\ D_t^\alpha [I(t)] &= \left(\beta_e' \frac{C(t - \tau_1)}{K + C(t - \tau_1)} + \beta_h' I(t - \tau_1) \right) S(t - \tau_1) - (\mu_h + \psi + \rho) I(t), \\ D_t^\alpha [R(t)] &= \rho I(t) + \nu S(t) - (\mu_h + \omega) R(t), \\ D_t^\alpha [C(t)] &= \beta_{ce} C(t) - \mu_c C(t) + \beta_{ch} I(t) - \varphi N(t) C(t) - \xi_2 C(t) D(t), \\ D_t^\alpha [D(t)] &= \xi C(t - \tau_2) - \chi D(t) - \xi_1 C(t) D(t), \end{aligned} \right\} \quad (7)$$

Under the initial conditions

$$\begin{aligned} \tau_1 > 0, \tau_2 > 0 \\ \text{and } S(\theta) &= \phi_1(\theta), E(0) = E_0, I(\theta) = \phi_2(\theta), R(0) = R_0, C(\theta) = \phi_3(\theta), \\ D(0) &= D_0, (-\tau_1, \tau_2 \leq \theta \leq 0), \end{aligned}$$

Where N, S, E, I, R, C and D Are Human population, Susceptible, Exposed, Infected, Recovered, Toxigenic Vibrio cholera concentration in the water and concentration of disinfectant in the water respectively.

Provides a sophisticated mathematical modelling method of the relationship between epidemic of cholera and typhoid diseases in a human population [29]. The study presents a mathematical model of co-infection between two bacterial illnesses that is based on the Laplace Adomian Decomposition Method of studying the dynamics of the processes (LADM) that is simulated in MATLAB. The model separates all the population into multiple compartments that encompass susceptible, infected, treated, and recovered individuals per disease as well as the environment of bacterial reservoirs. This structure allows the study to capture the feedback loop between the two diseases which is a symbiotic relationship; that is, the greater the case of cholera, the more the prevalence of typhoid and the opposite. The two authors highlight the need to enhance sanitation, hygiene, and health facilities as a way of mitigating the transmission of the two diseases at the same time. The sensitivity analysis and calculations of the reproduction number that they performed can be used as a good indication of the most influential parameters that propagates disease transmission. The fractional-order approach provided by the model enables a more precise modeling of disease behavior over the time span, therefore considering memory effects and slow transitions between states. The novelty of the study is that the researcher has connected two predominant waterborne diseases mathematically and focused on how they interact to increase the burden of public health in developing areas, and particularly in Africa. Overall, this study has a great impact on epidemiological modeling and disease control strategies, which provides policymakers and public health officials with a framework of evidence-based interventions that ensure the development of an integrated intervention that aims at controlling not a single disease but diseases collectively. It is a relevant and practical contribution to the literature of mathematical epidemiology due to the evident theoretical analysis with the support of computational validation. The model of joint dynamics of cholera and typhoid are as follows:

$$\left. \begin{aligned} S' &= \Lambda - (\lambda_{c1} + \lambda_c + \lambda_{t1} + \lambda_{t2})S - \mu S + \eta_c R_c + \eta_t R_t + \eta_{ct} R_{ct} \\ I'_c &= (\lambda_{c1} + \lambda_{c2})S - (\lambda_{t3} + \lambda_{t4})I_c - (\mu + \delta_c + \xi_c + \tau_c)I_c \\ T'_c &= \tau_c - (\mu - \xi_c)T_c \\ I'_t &= (\lambda_{t1} + \lambda_{t2})S - (\lambda_{c3} + \lambda_{c4})I_t - (\mu + \delta_t + \xi_t + \tau_t)I_t \\ T'_t &= \tau_t - (\mu - \xi_t)T_t \\ I'_{tc} &= (\lambda_{t3} + \lambda_{t4})I_c - (\lambda_{c3} + \lambda_{c4})I_t - (\mu - \theta - \delta_{ct})I_{tc} \\ T'_{ct} &= \theta I_{ct} - (\tau_{ct} - \mu)T_{ct} \\ R'_c &= \delta_c I_c - (\mu + \eta_c)R_c \\ R'_t &= \delta_t I_t - (\mu + \eta_t)R_t \\ R'_{tc} &= \delta_{ct} I_{ct} - (\mu + \eta_{ct})R_{tc} \\ Z'_c &= d_c B_c \left(1 - \frac{B_c}{k_c}\right) + \gamma_c I_c + \phi_c I_{tc} + \rho_c I_c - \mu Z_c \\ Z'_t &= d_t B_t \left(1 - \frac{B_t}{k_t}\right) + \gamma_t I_{tc} + \phi_t I_{tc} + \rho_t I_t - \mu Z_t \end{aligned} \right\} \quad (8)$$

Where N(t), S(t), IC(t), TC(t), It(t), Tt(t), Ic(t), Rc(t), Rt(t), RCt(t) and ZC(t), Zt(t) are Human population, Susceptible class, cholera

infection class, cholera treatment class, typhoid infection class, typhoid treatment class, a co-infection class, cholera recovery class, typhoid recovery class, co-infection recovery class and bacterial concentration of Salmonella Typhi, vibrio cholera respectively.

Provides a mathematical model investigation of malaria transmission patterns depending on the age structure of a population [30]. They formulate a deterministic two-group SEIRS-type model in which humans are classified as children below the age of five and adults with the assumption that human can be infected, recovery and immunity rates of human are different between children and adults. Using the derivation of the differential equations, the paper calculates the basic reproduction number (R0) and determines the local and global stability of the disease-free equilibrium and endemic equilibrium. The findings reveal that the diseases die when R0 is less than one, and a steady transmission occurs when R0 exceeds one. It is important to note that the phenomenon of backward bifurcation is exposed by the model, and even with R0 under 1, malaria can be sustained which has been countered to the traditional control methods. Sensitivity analysis with Latin hyperbole sampling and partial rank correlation coefficient determines that the mosquito biting rate and recovery rate of children below the age of five are the most influential parameters of the disease transmission and therefore the critical role of this population group in perpetuating endemicity. Numbers of simulations support the fact that the contact of mosquitoes with young children is one of the key factors that decrease the cases of infection among the whole population. The merit of the study is that age-dependent immunity has been realistically incorporated, and stability examined in detail that can be of great help to the people in the context of health intervention. They conclude that prevention programs to reach all children under five such as using treated bed nets, vaccination as well as timely cure treatment is best way to reduce overall transmission. All in all, the paper is a rigorous and insightful contribution to the malaria epidemiology with the appropriate balance of mathematical accuracy and high public health relevancy. We establish the following system of non-linear system of ordinary differential equation:

$$\left. \begin{aligned} S'_e &= \Lambda_e + \omega_e I_e - (\lambda_e + \xi + \mu_h)S_e \\ S'_a &= \xi S_e + u \omega_a I_a + \delta_a R_a - (\lambda_a + \mu_h)S_a \\ E'_e &= \lambda_e S_e - (\sigma_e + \mu_h)E_e \\ E'_a &= \lambda_a S_a - (\sigma_a + \mu_h)E_a \\ I'_e &= \sigma_e E_e - (\omega_e + \mu_h + d_1)I_e \\ I'_a &= \sigma_a E_a - (\omega_a + \mu_h + d_2)I_a \\ R'_a &= (1 - u) \omega_a I_a - (\mu_h + \delta_a)R_a \\ S'_v &= \Lambda_v - (\lambda_v + \mu_v)S_v \\ E'_v &= \lambda_v S_v - (\sigma_v + \mu_v)E_v \\ I'_v &= \sigma_v E_v - \mu_v I_v \end{aligned} \right\} \quad (9)$$

Where Se, Sa, Ee, Ea, Ia, Ie, Ra, Sv, Ev, Iv are Susceptible, human population over 5-year-old, infected human under 5-year-old, infected human over 5-year-old, infectious human over 5-year-old, recovered human over 5-year-old, susceptible mosquitoes, population of infected mosquitoes, and population of infectious mosquitoes respectively.

Provide a mathematical model that seeks to analyze malaria transmission due to awareness campaigns' influence [31]. The model incorporates human and mosquitos' population and presents knowledge of their population as dynamics which is modified by media and community intervention. The model can capture behavioral effects on the spread of disease through the division of the human population into the conscious, unconscious, and infected. Theses mathematical properties that the authors investigate are the existence and stability of equilibrium points and the calculation of the basic reproduction number (R_0) where malaria can be eradicated when R_0 is less than 1 and cannot be eliminated when R_0 is larger than 1. The most effective methods of integrating treatment, use of insecticides, and awareness programs are done using optimal control theory (mainly the minimum principle of pontryagin). The use of numerical models indicates that media and local-level awareness campaigns significantly reduce the rate of infection and the general disease control expenses. The article emphasizes the importance of behavioral awareness of community participation in the process of preventing diseases and how education and communication have an important role as medical interventions. The study offers an ideal structure that can be used by policymakers in developing effective malaria control intervention by integration of mathematical modelling, epidemiology insights, and optimal control. This paper overall helps to learn more about how malaria management can be more sustainable, affordable and effective, with the help of awareness-based interventions and the need to minimize the transmission and ensure the promotion of the well-being of the population. the mathematical model is derived as

$$\left. \begin{aligned} \frac{dH_u}{dt} &= \Pi_h - \alpha H_u M - \frac{\lambda_1 H_u V_i}{N} - d_h H_u + \frac{g H_a}{1+M} & H_u(0) &= H_{u0} > 0 \\ \frac{dH_a}{dt} &= \alpha H_u M - d_h H_a + r H_i M - \frac{\lambda_2 H_a V_i}{N} - \frac{g H_a}{1+M} & H_a(0) &= H_{a0} > 0 \\ \frac{dH_i}{dt} &= \frac{\lambda_1 H_u V_i}{N} + \frac{\lambda_2 H_a V_i}{N} - r H_i M - (d_h + \delta) H_i & H_i(0) &= H_{i0} > 0 \\ \frac{dV_s}{dt} &= \Pi_v - \frac{\beta H_i V_s}{N} - \mu V_s - \gamma V_i M & V_s(0) &= V_{s0} > 0 \\ \frac{dV_i}{dt} &= \frac{\beta H_i V_s}{N} - \mu V_i - \gamma V_i M & V_i(0) &= V_{i0} > 0 \\ \frac{dM}{dt} &= \omega + \sigma H_i - \theta M & M(0) &= M_0 > 0 \end{aligned} \right\} \quad (10)$$

The human population is derived into three parts Susceptible Unaware H_u , Susceptible aware H_a , and infected H_i , with total population N given by $N = H_u + H_a + H_i$. Similarly, the vector population is split into susceptible V_s and infected V_i .

Summarize the most important factors that determine the malaria transmission and control [32]. The research incorporates the key elements, including immunity, reinfection, drug resistance, awareness, and aggressive treatment, to learn the dynamics of the disease and educate the interventions. The authors construct and solve in an organized way a deterministic model in which human and mosquito population are separated into multiple compartments by a system of differential equations. The research performs the condition under which the disease can persist and vanish in the future, based on mathematical methods like equilibrium analysis and next-generation matrix to calculate the basic reproduction number R_0 . The analysis of numerical simulation shows that such factor as drug resistance, loss of immunity, and reinfections contribute greatly to the increase of the rates of infections, whereas the awareness program, control of vector and strong immunity decrease the transmission. The sensitivity analysis of the spread of malaria shows the impact on parameter values

which are identified as the enhancement of immunity and increase in public awareness. The findings prove that the most effective reduction in infection and the mosquito population would be achieved in the combined interventions. In general, the given paper is a valuable contribution to the topic of malaria because it involves biological, epidemiological, and mathematical knowledge that provides a comprehensive picture of the malaria dynamics. It gives useful implications to health policymakers to come up with interventions of control and come up with more effective antimalarial interventions. The extensive modeling nature of the study is a useful indicator of making predications and preventing the spread of malaria in endemic areas. The following equation for the mathematical malaria model is:

$$\left. \begin{aligned} \frac{dS_h}{dt} &= \Lambda_h + \tau_h R_h - \frac{b_{vh} A_v S_h}{N} - \mu_h S_h \\ \frac{dL_h}{dt} &= \frac{b_{vh} \gamma A_v S_h}{N} - (1-a) \alpha L_h - a \alpha L_h - \mu_h L_h \\ \frac{dA_h}{dt} &= (1-a) \alpha L_h + \frac{b_{vh} \gamma \xi R_h S_h}{N} - \phi_h A_h - (\omega_h + \mu_h) A_h - \sigma_h A_h \\ \frac{dRe_h}{dt} &= \phi_h A_h - \lambda_h Re_h - (\omega_h + \mu_h) Re_h \\ \frac{dR_h}{dt} &= \sigma_h A_h + \lambda_h Re_h + a \alpha L_h - \frac{b_{vh} \gamma \xi R_h A_v}{N} - \tau_h R_h - \mu_h R_h \\ \frac{dS_v}{dt} &= \Lambda_v - \frac{\gamma b_{hv} S_v A_h}{N} - (\mu_v + \delta_v) S_v \\ \frac{dL_v}{dt} &= \frac{\gamma b_{hv} S_v A_h}{N} - \rho L_v - (\mu_v + \delta_v) L_v \\ \frac{dA_v}{dt} &= \rho L_v - (\mu_v + \delta_v) A_v \end{aligned} \right\} \quad (11)$$

where $S_h, L_h, A_h, R_h, S_v, L_v, A_v$ and ξ are Susceptible host population, Latently infected host population, Actively infected host population, Resistant to antimalarial drug host population, Recovered host population, Susceptible vector population, Latently infected mosquito vector, Actively Infected mosquito vector population and is the rate at which recovered become recrudescence and get active malaria respectively.

Provides mathematical investigation on the malaria transmission dynamics [33]. The paper constructs a deterministic compartmental model that is unique in terms of incorporating the impact of relapse and the contribution of the so called even-know-ignorant-human-or-infected individuals, the individuals who do not know they have been infected. The authors consider the stability of disease with the help of a system of differential equations and the effective reproduction number (R_r) calculated with the method of the next-generation matrix. It has been shown by local and global stability analysis, using the Routh Hurwitz and Lyapunov methods respectively, that the malaria dies out at $Re=1$ and is maintained elsewhere. The model uses human and mosquito population and presents a sanctified human compartment to determine the impact of preventive behavior. Sensitivity analysis indicates the most sensitive parameters that affect the spread of malaria as mosquito and human transmission rates, mosquito recruitment and movement between protection stated as the most sensitive parameters positively affecting Re , and death rates, recovery, and treatment rates as the most sensitive parameters affecting Re negatively. The simulation also demonstrates that growing public awareness, improving treatment, and improving protection measures can help reduce the cases of infection and relapse dramatically. The results present the significance of preventive

measures featuring insecticide-treated bed nets and repellents against treatment-only control on malaria transmission. All in all, this paper has presented meaningful information about the joint effect of behavioral awareness and biological relapse mechanisms on malaria persistence that can be used as a convincing argument of the mathematical need to adopt integrated control methods. The following model equation are:

$$\left. \begin{aligned} \frac{dS_H}{dt} &= (1-\Pi)\Omega_H + \theta P_H + \alpha \eta R_H - \beta_H S_H I_V - (\mu_H + \nu) S_H \\ \frac{dP_H}{dt} &= \Pi\Omega_H + (1-\alpha)\eta R_H + \nu S_H - (\mu_H + \theta) P_H \\ \frac{dI_H}{dt} &= \beta_H S_H I_V + \sigma L_H - (\gamma + \mu_H + \delta) I_H \\ \frac{dL_H}{dt} &= \gamma(1-\tau) I_H - (\mu_H + \sigma) L_H \\ \frac{dR_H}{dt} &= \gamma \tau I_H - (\mu_H + \eta) R_H \\ \frac{dS_V}{dt} &= \Psi - \beta_V S_V I_H - \mu_V S_V \\ \frac{dI_V}{dt} &= \beta_V S_V I_H - \mu_V I_V \end{aligned} \right\} \begin{aligned} S_H(0) &= S_{H0} \\ P_H(0) &= P_{H0} \\ I_H(0) &= I_{H0} \\ L_H(0) &= L_{H0} \\ R_H(0) &= R_{H0} \\ S_V(0) &= S_{V0} \\ I_V(0) &= I_{V0} \end{aligned} \quad (12)$$

Where $S_H(t)$, $P_H(t)$, $I_H(t)$, $L_H(t)$, $R_H(t)$, $S_V(t)$, and $I_V(t)$ are susceptible human, protected human, infected human, infected ignorant human, recovered individuals with temporary immunity, susceptible mosquito's populations and the size of infections mosquito population respectively. The total human population is represented as follows: $N_H(t) = S_H(t) + P_H(t) + I_H(t) + L_H(t) + R_H(t)$.

Discussion and Conclusion

Mathematical models have indeed become indispensable tools to understand the transmission dynamics of several major waterborne diseases, such as cholera and typhoid fever, and to evaluate the efficiency of various public health interventions. First, one observes that the literature is characterized by an evolution from simple compartmental structures, like the classic SIQRB models for cholera, to more complex frameworks aimed at capturing biological, behavioral, and environmental realism. Typical sophistications include the introduction of the delays to represent latent infection stages or the delay in the enforcement of control measures like vaccination or water chlorination. The increasing adoption of fractional-order calculus added flexibility to models, allowing them to incorporate memory effects and non-local interactions commonly present in biological systems.

A common thread through many models, however, is the critical function of the environment in propagating the disease. Many integrate indirect waterborne routes and direct person-to-person routes, requiring the combination of microbial ecology, sanitation quality, climatic variability, and hydrological processes. More recent models also include human behavioral responses to awareness, fear, compliance with water treatment, and hygiene practices, which affect not only disease spread but also intervention success.

Accordingly, optimal control theory has now emerged as the robust analytical framework for determining the efficient allocation of limited resources among interventions like chemotherapy, vaccination, sanitation improvements, and vector control. Further, co-disease dynamics modelling that considers the co-transmission of multiple diseases such as cholera and typhoid could provide specific valuable insights into integrated public health strategies in co-endemic regions. The incorporation frontier is one that offers superior forecasting capabilities when combined with more

classical mechanistic modelling.

Mathematical modelling remains a cornerstone of evidence-based planning for waterborne disease control. It helps predict epidemic trajectories, critical epidemiological thresholds, and the effectiveness of interventions in a long-term perspective. However, there are several gaps that need to be addressed for making these models more reliable and useful in practical applications. First, most contemporary models rely on simplifying assumptions that fail to capture the profound socio-ecological heterogeneity of real-world settings. Spatial variability in environmental features, infrastructure, and climate-driven fluctuations in water quality all constitute key elements missing from future models of disease ecology. Second, parameter estimation remains a significant challenge, especially in low-resource settings with limited or unreliable surveillance data. More thorough empirical validation and better data collection systems are needed to undergird increasingly complex modelling systems.

Third, advanced modelling components include fractional derivatives, multistage delays, and behavior-driven feedback, which need to be systematically validated against real epidemic data to assess their actual performance. Finally, future work should focus more on hybrid modelling frameworks that combine classical compartmental structures with machine-learning algorithms that can perform real-time forecasting and adaptive decision-making. Expanding the models to capture multi-disease interactions and deeply mechanistic behavioral dynamics will further strengthen their relevance to policymaking. In general, long-term multidisciplinary collaboration, quality datasets, and enhanced computational tools will be crucial to guarantee that mathematical models keep guiding effective, timely, and equitable public health interventions against waterborne diseases.

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