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Optimal Control and Stability Analysis in Disease Transmission Models

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Abstract: This study explains how mathematical models help understand and control the spread of infectious diseases. Through using optimal control and stability analysis, researchers can find how diseases grow, how fast they spread, and what measures can stop them. Models like SEIR, SVIR, and SEIQR help study diseases such as measles, malaria, dengue, and tuberculosis. These models show that factors like vaccination, human behavior, and population movement affect transmission. Stability and control analysis help identify safe conditions where diseases stop spreading. This research helps design better strategies for disease prevention and long-term public health planning.

Keywords: strategies, transmission, SEIQR, Stability

I. Introduction

Mathematical modeling has become a cornerstone in understanding and mitigating infectious disease dynamics through quantitative prediction, optimal control, and stability analysis. Over the last few years, significant advancements have been made to refine the accuracy of these models and their applicability to real-world scenarios. For instance, Alemneh and Belay (2023) developed an extended SVIRP measles transmission model to assess the effects of indirect contact rates and interventions, verifying both global and local stability through the Castillo–Chavez criterion. Similarly, Alhaj (2023) applied a deterministic malaria transmission model and demonstrated forward bifurcation and equilibrium stability using the next-generation matrix approach. Fiatsonu et al. (2023) emphasized the importance of host-vector relationships in Chagas disease, revealing dogs' significant role in transmission, while Hill et al. (2023) integrated behavioural heterogeneity into livestock models to analyze how farmers' vaccination behaviours affect outbreak control. Age-structured modeling by Li-Martín et al. (2023) for dengue showed how demographic differences shape stability and transmission outcomes. Studies like Møgelmose et al. (2022) and Abidemi and Aziz (2022) incorporated human population dynamics and vaccination strategies to better reflect real epidemic processes. Recent contributions also highlight the necessity of spatial, stochastic, and computational methods. Lin and Wen (2022) illustrated the role of spatial epidemiology in mapping and predicting infection spread, while Pokharel and Deardon (2022) used Bayesian emulation techniques for efficient inference in complex spatial models. Furthermore, Tyagi et al. (2021) combined SEIQR modeling with deep learning (LSTM) for COVID-19 prediction, and Das et al. (2021) analyzed tuberculosis through bifurcation and stability frameworks. These studies underscore the central role of optimal control and stability analysis in understanding threshold conditions (R_0), equilibrium behavior, and intervention efficiency. They provide a foundation for designing evidence-based health policies that adapt to heterogeneous, spatially dynamic, and behaviorally influenced disease systems.

II. Review of related literature

Alemneh et al. (2023) described measles as one of the commonest communicable diseases responsible for about 2.6 million deaths per annum. Their work analysed the mechanism of measles transmission through discussing indirect contact rate (spread between an infectious and a susceptible host) and by extending SEVIR model to SVIRP. They calculated the disease-free equilibrium, derived the effective reproduction number (REff) and resolute stability. The global stability of the disease-free equilibrium point was verified by using the Castillo–Chavez stability criterion, and local stability (when REff 1 proved. Sensitivity analysis and numerical simulations were conducted to investigate the effect of constraints on measles spread dynamics, showing that Indirect contact rate made the most contribution in increasing disease outburst. The study also found that intervention and treatment approaches have played a major role in mitigating the overall impact of measles on the community.

Alhaj et al. (2023) Stated that malaria was among the deadliest of diseases caused by Plasmodium-class parasites and spread to humans through bites of female Anopheles mosquitoes. They developed a deterministic mathematical model of malaria transmission between humans and mosquitoes. The basic reproduction number ((\mathcal{R}{0})) was obtained by the next-generation matrix method, and the stability of the equilibria was established through (\mathcal{R}{0}) in order to show that a forward bifurcation occurred. They observed that the malaria dies out if (\mathcal{R}0) was less than one, while it spreads when it is greater than one. Both the local and global sensitivity analysis for (\mathcal{R}{0}) were conducted, while we implemented the model simulation through Runge–Kutta fourth-order method in MATLAB. Besides, the influences of important parameters were discussed and plotted. The results of the simulations agreed with those obtained by stability analysis for (E{def}). The work also considered the effects of malaria control measures on crucial transmission parameters and suggested how better to control, and ultimately eliminate, malaria transmission.

Fiatsonu et al. (2023) reported that Chagas disease, also known as American trypanosomiasis, was a zoonotic vector-borne disease caused by the parasite Trypanosoma cruzi, which infected several mammalian species throughout the Americas including people and canines. They performed a scoping review of mathematical models investigating the role of dogs in T. cruzi transmission and found ten peer-reviewed studies that had explicitly modelled dog-borne T. cruzi transmission dynamics. The authors also talked about the various modeling approaches, parameters of transmission, pathways of disease spread and control measures analyzed in these studies. In general, the modeling studies had shown that not only were dogs at high risk of becoming infected with T. cruzi, but that they also played a major role in transmitting this parasite to humans. In addition, removal of infected dogs from the household or frequent use of insecticides was identified as effective to decrease T. cruzi infection for both humans and dogs. However, after suspension of insecticide spraying, T. cruzi infections in dogs appeared to go back to pre-spraying levels. The study also pointed out the limitations and prospects for further modelling studies to better understand Chagas disease transmission dynamics and control.

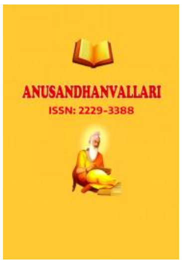
Hill et al. (2023) stressed the importance of human behaviours in controlling livestock disease outbreaks, especially with respect to vaccination uptake. They added that conventional mathematical models that guided such responses were often based on the assumption of homogeneous response to information among farmers. To tackle this, the investigators considered how differences in farmers' vaccination practice could be incorporated into mathematical models. They constructed and used a computer interface to record the vaccination choices of 60 farmers in response to a simulated period of fast spreading disease that linked back to their psychological/behavioural profiles. They conducted cluster analysis and determined consistent profiles of heterogeneity in vaccination behaviour. By embedding such behavioural clusters within a mathematical model for the spread of an infectious disease in a rapidly mixing livestock population, they investigated via computational simulations how allowing for heterogeneity in behaviour would affect epidemiological and economic metrics.

They found that, as compared to thematic profiles, such a homogenous farmer behavioural assumption resulted in markedly different projected outbreak size, duration, and economic outputs.

Li-Martín et al. (2023) found that age presented as a main risk factor in vector borne infectious diseases, partially because children depend on adults to protect themselves and were exposed less often to wear mosquitoes than were adults who spent little time outdoors. To model this, they considered a dengue disease that stratifies the human population into two compartments, as children and adults were more or less likely to be bitten by mosquitoes. The basic reproduction number (R_0) of dengue was obtained through computing the next-generation operator, and the local stability and global stability of the disease-free equilibrium were studied. A Lyapunov functional method was used to obtain sufficient conditions for the global asymptotic stability of the endemic equilibrium. It was also shown that the globally asymptotically stable of endemic equilibrium within feasible region still holds when (R_0 > 1) by setting the period of infection for children equal to that of adults. In addition, the model was analysed numerically by considering the parameter values that were taken from available literature and to find out which parameters has a significant impact on variation of (R_0) using local sensitivity analysis that can provide a more biological meaning over what it means in terms of changes in R_{0}.

Møgelmose et al. (2022) observed although more infectious disease models were accounting for demographic host population dynamics, the modelling approaches and assumptions differed greatly. For that purpose, they performed a systematic review to investigate how dynamic populations were incorporated in infectious disease models and systematically searched PubMed and Web of Science for studies addressing transmission of infectious diseases in dynamic host populations. According to the PRISMA checklist, they read studies identified through the search and extracted data. A total of 46 articles with 53 dynamic population infectious disease models were reviewed. Of those, 71% included the modelling of population dynamics either directly according to CCBMs or IBMs and 29% applied population projections as external input. Fertility and mortality were predominantly age-specific, or if specified, age-and-sex specific but 40% of the models used crude fertility ratios. Households were included in 15% of the models, all but one being IBMs (with external population prospects). In addition, 17% of the models we reviewed conducted a demographic sensitivity analysis. The most studies included all of fertility, mortality, and migration explicitly as processes and representation at a population level was more common than IBMs. The authors noted demographic factors other than age and sex were difficult to include in population models and were therefore generally specific only to IBMs. Although these IBMs modelled families and social networks, the degree of detail in demographic processes was comparable to that found in CCBMs. These common assumptions were related to in closing by the study, which also highlighted some potential paths for model enhancements.

Abidemi et al. (2022) reported that dengue (applying to as a mosquito-borne disease) had been endemic for several months in Malaysia. They investigated the impacts of various vaccination scenarios alone and with treatment and adulticide control on the population dynamics of dengue in Johor, Malaysia. First, they proposed a compartmental model (a mass action one still with random vaccination distribution process) including the vaccinated compartment. The model was encountered to be exhibiting backward bifurcation whether under the conditions of perfect vaccination or in terms of imperfect vaccination. Data collected during the 2012 dengue outbreak in Johor were used to estimate the basic reproduction number of the outbreak and perform a sensitivity analysis of how individual model parameters affected dengue transmission and spread among population members. The authors then constructed a deterministic model that incorporated vaccination as the control parameter (with time-independent rates) together with treatment and adulticide interventions. Subsequent simulations were conducted to evaluate the effects of alternative control tactics. Results revealed that stategies adopted, can effectively reduce the transmission of dengue than with no control treatment and efficiency analysis



demonstrated combined vaccination, treatment and adulticide controls was found to be the most efficient method in preventing and controlling dengue in Johor, Malaysia.

Tresna et al. (2022) undertook a review of published papers on typhoid disease transmission models to determine how S. typhi was transmitted between humans and vectors under diverse scenarios of interventions aimed at containing the spread of typhoid. The purpose of this study was to determine the categories of models that were developed, describe current studies and analyze interventions that are included with these models. A comprehensive search and review were conducted by searching Dimension, Scopus, and ScienceDirect databases for research papers published from 2013 to 2022 on typhoid fever transmission using compartmental mathematical models. A total of 111 different articles were initially obtained from this search process of which 23 satisfied the inclusion criteria as it appeared in the defined context of the terms searched. These articles were reviewed to determine their model type and the interventions that they modelled. The interventions found were collated to serve as an overview for possible aspects in the model development. The review highlighted the role of mathematical models in dissecting and elucidating typhoid transmission dynamics following interventions. The investigators noted that the next iterations of typhoid models could be enriched by inclusion of direct and indirect interventions among humans.

Hiram Guzzi et al. (2022) pointed out that the regulation of contagious diseases was not only an important area of research, but also has a clinical and political implication. They highlighted how this area engaged with a range of computational techniques such as ordinary differential equations, stochastic simulation frameworks and graph theory, in combination with interaction data at scales from molecular to social interactions to understand the emergence and spread of disease. Covid-19 was mentioned as the best example for how these models could help us to avoid harsh lockdowns by providing potentially effective options, like optimal vaccine prioritization. Particular emphasis was placed on graph-based epidemiological models, which were found to be a powerful instrument for improving the control of disease. They included examples for the COVID-19 pandemic, and demonstrated how such methods might be further extended to other infectious diseases so as to better capture disease diffusion dynamics.

Dankwa et al. (2022) pointed out that in the absence of studies confirming model identifiability, findings from infectious disease transmission models could be flawed and to potentially misleading recommendations. They said that structural identifiability analysis verifies if there are unique solutions for all unknown model parameters based on the structure of the model. In their work, they explored the structural identifiability of various deterministic compartmental models for infectious disease transmission by considering impact of distinct data types used as model outputs and its implications on identifiability of unknown parameters which included initial conditions. The model configurations were defined, each with unique space-partitioning structure and output data types (the combination of internal MCML diversity matrix (Bhattacharyya et al., 2014), SIMPLIFICATION I: the reduction of differential scattering coefficient at frequent frequencies (Devore et al., 1988; Cuccia et al., 2006) and L1, or absolute value loss regularization). Authors investigated four compartmental model structures and three types of data which are widespread used in disease surveillance, incidence, prevalence and detected vector counts. They showed that the structural identifiability of some parameters changed with output type, and models using several output types had generally more parameters identifiable than those only using one. The investigation emphasised the importance of data types in understanding a key element of inference when employing compartmental infectious disease transmission models.

Pokharel et al. (2022) articulated that mechanistic models of infectious diseases (MDs) were indispensable for comprehending the spatiotemporal spread dynamics. While it would be preferable if these models could incorporate covariate information and longitudinal measurement of each individual's infection status, complete data were generally not available in practice because the timing of infection was typically unknown. Other studies have used, as a solution to censoring or missing data, Bayesian data augmented Markov chain Monte Carlo (MCMC) methods but these were computationally intensive for large disease systems. In this case, the authors suggested two approximate inference methodologies according to emulation-based approaches in order to reduce computational cost. Both approaches worked in the context of a Bayesian MCMC, however instead of using likelihood function-which was slow to compute-they relied on a Gaussian process-based approximation. The first approach entailed building an emulator of the discrepancy between the summary statistics of simulated and observed epidemic data, whereas the second one created an emulator for an importance sampling-based likelihood approximation. The results of their study have proved both methods were computationally efficient relative to standard Bayesian MCMC to infer patterns of transmission in complex infectious disease systems. Furthermore, they also found that the importance sampling-based method gives better performance.

Lin et al. (2022) reported that spatial factors, e.g., distances between susceptible hosts and shared environments or contaminated materials, and infected animal species, were associated with human directly and indirectly transmitted infectious diseases. They stressed the importance of spatial concepts for the comprehension and control of emerging infectious diseases. With improvement in computing capability and statistical methods, there were new possibilities for visualising and analysing data on disease spatial patterns. In the review, they described frequently used spatial and spatio-temporal methods of infectious disease management in four parts: (1) visualization, (2) the overall clustering method, (3) hotspot detection approaches, and (4) risk factor analysis. Sections 1 - 3 considered both point and aggregated data (point & aggregate refer to individual- and population-level data respectively, while the final section was on spatial regression methods adjusting for neighbourhood effects and spatial dependence. The scholars emphasized that analysing space-time variation of the spread of diseases could improve surveillance systems, assist in hypothesis generation and verification, and also facilitate designing preventive and control strategies. The authors also underscored the relevance of ethical considerations and judgements about data quality prior to implementing spatial-temporal analyses, with proposed future research focusing on improving the accuracy of differential global positioning system processes and reducing the uncertainty associated with Bayesian estimation methods.

Becker et al. (2021) described the unexpected rise of using infectious disease dynamic transmission models during the COVID-19 pandemic for public health decision-making and policy development. They noted that such models served as a structure through which the transmission dynamics could be systematically investigated, and were capable of making both short-term and long-term predictions by incorporating assumptions on biological, behavioural, and epidemiological processes driving spread, burden (of disease), and surveillance. The authors further stated that in the context of COVID-19 and other communicable disease emergencies, such models provided valuable projections of possible disease progression, helped to examine intervention impacts, and estimated important transmission parameters. However, they also acknowledged that the fast-tracking of model development, evaluation, and deployment during times of emergency shed light on the need to understand in detail the strengths and weaknesses of these approaches. The review described how infectious disease dynamic models have developed over time, the necessity of robust testing and validation, and how models can be merged with reality to guide public health action. Rather than provide an exhaustive historical review, the paper emphasised how through purposeful embedding with policy and practice we could evolve public health modelling and improve the efficacy and robustness of such interventions in ongoing pandemics, as well as in future ones.

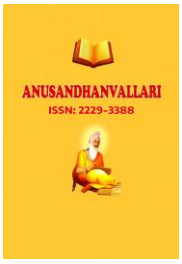
Buckee et al. (2021) argued that social and cultural drivers shaped almost every aspect of infectious disease spread within the human population, including the ability to detect, comprehend, respond to epidemics. For contact-mediated infections, however, they wrote that the spread of a pathogen depended on human contacts and that kinship, household organization, and broader patterns of social organization—what ultimately determined the dynamics of epidemics. Moreover, social, economic, and cultural settings influenced patterns of exposure; seeking behaviour; outcome to infection; rates of diagnosis and reporting; the uptake of interventions. These social aspects of epidemiology were noted as difficult to measure (which therefore restricts the transferability of modelling frameworks into policy application), but with growing data sources on human behaviour (e.g., from mobile devices and digital technologies) now increasingly being used as surrogates for behavioural drivers of disease spread. But they warned that it would take a lot more work to confirm and responsibly use these data for policy making. The research also implied that incorporating local knowledge in the construction of model structures as well as the interpretation of new behavioural data streams might generate more policy-relevant infectious disease models and support building strong, generalizable theories connecting human behaviour to disease dynamics.

Mousa et al. (2021) carried out a systematic review and meta-analysis of the effects of contact and mixing between populations on transmission of respiratory pathogens including SARS-CoV-2. The analysis was based on data from 28,503 participants and 413,069 contacts in 27 surveys that had compared contact patterns by income strata (low-, middle- and high-income countries) considering number of contacts, duration of contacts, location, and physicality. Contact rates were shown to decrease with age in higher-income and increase in low-income settings, where older individuals come into contact often with younger people through extensive living arrangements across households of multiple generations. More contacts had taken place in the home in low-income settings, and work and school related more frequently in high income settings.

Kirkeby et al. (2021) presented the application of stochastic and network flow computer models for veterinary science with simulations to predict disease dynamics, evaluate control strategies, and compare results against field data. They concentrated on models representing single individuals, and gave a tangible introduction to how such a model is made and used. The paper describes the main steps to the design of such models both before, during and after programming. It highlighted the need for verification (to make sure that model behaves as expected), validation (validate the results of the model) and convergence analysis to guarantee stability of models that simulates endemic diseases. The authors also emphasized the use of sensitivity analysis to assess the impacts of parameter uncertainty. They also provided code samples to help new researchers realize their models, and we're kept them updated with the latest disease spread modelling literature.

Tyagi et al. (2021) studied the dynamics of infectious disease transmission by establishing a theoretical mathematical model in terms of the SEIQR (Susceptible-Exposed-Infected-Quarantined-Recovered). the study was designed to investigate into disease dynamics and control by proving the positivity and boundedness of the model solutions, computing basic reproduction number to draw stability analysis of equilibria for epidemiological significance. For validation and parameter estimation, the authors then used their model on actual reported real COVID-19 cases in Russia and India. They also introduced a memory-based Long Short-Term Memory (LSTM) model to capture temporal relationships from COVID-19 time series and predict future developments. The results of the SEIQR mathematical model and the LSTM model were further compared to obtain the more dependable forecasting of disease development.

Retkute et al. (2021) proposed a novel statistical approach utilizing the Adaptive Multiple Importance Sampling (AMIS) algorithm to facilitate modelling of infectious disease transmission dynamics. The AMIS algorithm, making use of samples from earlier iterations in an iterative fashion to increase time efficiency, was extended to perform a simultaneous sampling over different targets by modifying the adaptation focus at each iteration. This change produced a substantial gain in sampling efficiency over the basic AMIS. The model integrated outputs of a geostatistical model of the prevalence, incidence or relative risk for an infectious disease and forecast these measures forward in time using a mathematical transmission model. The improved algorithm was validated through four specific case studies - ascariasis in Ethiopia, onchocerciasis in Togo, HIV in Botswana and malaria Democratic Republic of Congo-pre-amble, illustrating how the novel approaches improve disease modelling and forecasting.



Das et al. (2021) considered tuberculosis as a significant global health challenge and developed an SEIR-type TB transmission mathematical model with time-dependent boundaries using the proposed MCA framework. The entire population was partitioned into four classes according to the biological status, and a model of compartmental phases was used to study the effects of various factors on the infection-free and endemic equilibrium points. The analysis showed that the TB model was locally and globally asymptotically stable at the disease-free equilibrium when the basic reproduction number is < 1, while it has a new endemic equilibrium ≥ 1. Acentermanifold theory bifurcation analysis showed the presence of a forward bifurcation, thus exploring the dynamic behaviour of the model and its conditions for TB persistence and/or extinction.

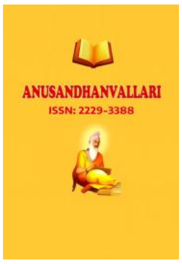
Thongsripong et al. (2021) stressed the importance of host–vector contact (including mosquito bites) in driving vector-borne disease (VBD) transmission, and criticized that studies based on traditional method may concentrate on vector density simply, while ignoring the behavior of host-mosquito contact. Their review was focused on synthesis of current knowledge and developing a unified theoretical construct that included host–mosquito contact rate, blood-feeding rate, and per capita biting rate from both biological and mathematical viewpoints. The results also illustrated that such contact rates could be significantly different depending on mosquito and host attributes, opposing to the classical view of a fixed daily biting rate based on gonotrophic cycle. Instead, it suggested alternative ecological models by means of functional response, blood index, forage ratio, and ideal free distribution. The authors suggested that it is appropriate to consider host–vector contact as an important integrative variable in mechanistic models of disease as its and strongly affects the transmission dynamics. They suggested that formal parameterization of contact rate models having empirical support would improve the understanding of ecological and behavioral factors contributing to VBD disease emergence, social behavior theory, pattern formation in spatial systems as well as disease prevention and control strategies.

III. Findings from Related Reviews

Author(s) & Year	Disease Studied	Model / Approach Used	Key Findings	Tools / Methods Used
Alemneh et al. (2023)	Measles	Extended SEVIR → SVIRP Model	Indirect contact rate contributed most to outbreaks; global & local stability proven using Castillo–Chavez criterion; interventions reduced transmission.	Sensitivity analysis, numerical simulations
Alhaj et al. (2023)	Malaria	Deterministic mathematical model (Human–Mosquito)	Forward bifurcation at $R_0=1$; malaria dies out when $R_0<1$; validated via simulation; control measures reduce transmission.	Next-generation matrix, Runge–Kutta (MATLAB)
Fiatsonu et al. (2023)	Chagas Disease (T. cruzi)	Scoping Review of Mathematical Models	Dogs play major role in human transmission; insecticide spraying effective but temporary;	Literature synthesis, parameter analysis

			highlighted data/model gaps.	
Hill et al. (2023)	Livestock Disease	Behavioural-Cluster Mathematical Model	Heterogeneity in farmers' vaccination behaviour alters outbreak size, duration, and economics; human behaviour critical.	Cluster analysis, simulation modeling
Li-Martín et al. (2023)	Dengue	Age-Structured Compartmental Model	Age is a key risk factor; R_0 and stability depend on children–adult exposure; global stability confirmed for $R_0>1$.	Lyapunov functional method, sensitivity analysis
Møgelmose et al. (2022)	Infectious Diseases (General)	Systematic Review of Dynamic Population Models	71% of models included population dynamics; fertility/mortality age-specific; demographic sensitivity often missing.	PRISMA protocol, systematic review
Abidemi et al. (2022)	Dengue (Malaysia)	Compartmental Model with Vaccination, Treatment & Adulticide	Combined interventions (vaccine + treatment + adulticide) most effective; backward bifurcation observed.	Sensitivity & efficiency analysis, simulations
Tresna et al. (2022)	Typhoid Fever	Review of Compartmental Models	Identified 23 valid models (2013–2022); emphasized inclusion of direct & indirect human interventions in future models.	Database review (Scopus, ScienceDirect)
Hiram Guzzi et al. (2022)	Contagious Diseases / COVID-19	Computational & Graph-Based Modeling	Graph-theoretical models effective for control; illustrated how network models improve intervention strategies.	ODEs, stochastic simulations, graph theory
Dankwa et al. (2022)	Infectious Diseases (General)	Identifiability Analysis of Compartmental Models	Demonstrated data type affects parameter identifiability; multiple outputs increase identifiable parameters.	Structural identifiability, MCML matrix
Pokharel et al. (2022)	Infectious Diseases (General)	Bayesian Data-Augmented	Introduced efficient Gaussian process-based inference; reduced	Bayesian MCMC, Gaussian Process Emulator

		Mechanistic Models	computational cost; importance sampling outperformed.	
Lin et al. (2022)	Human & Animal Infectious Diseases	Spatial and Spatio-Temporal Models	Highlighted value of spatial analysis for disease control; ethics and data quality emphasized for GPS-based modeling.	Spatial regression, hotspot detection, GIS
Becker et al. (2021)	COVID-19 & Communicable Diseases	Dynamic Transmission Modeling Review	Models guided public health policy; stressed need for validation and transparent model–policy integration.	Epidemiological modeling, policy analysis
Buckee et al. (2021)	Infectious Diseases (General)	Social-Behavioural Epidemiological Modeling	Social & cultural factors shape disease spread; behavioural data from mobile devices can enhance predictive models.	Behavioural modeling, data analytics
Mousa et al. (2021)	Respiratory Pathogens (SARS-CoV-2)	Meta-analysis of Contact and Mixing Patterns	Contact rates vary by age/income; intergenerational contact drives transmission in low-income settings.	Meta-analysis, contact surveys
Kirkeby et al. (2021)	Veterinary Infectious Diseases	Stochastic & Network Flow Models	Emphasized model verification & validation; used sensitivity analysis for parameter uncertainty; provided code templates.	Simulation modeling, network analysis
Tyagi et al. (2021)	COVID-19	SEIQR Model + LSTM Prediction	Combined theoretical and ML model; validated on India & Russia data; LSTM improved forecasting accuracy.	SEIQR modeling, LSTM (Deep Learning)
Retkute et al. (2021)	Ascariasis, Onchocerciasis, HIV, Malaria	Adaptive Multiple Importance Sampling (AMIS)	Enhanced sampling efficiency; integrated geostatistical & transmission models; validated on 4 disease case studies.	AMIS algorithm, geostatistical modeling



Das et al. (2021)	Tuberculosis (TB)	SEIR-type Model with Time-dependent Boundaries	Model globally stable when R₀<1; forward bifurcation when R₀≥1; explored persistence and extinction conditions.	MCA framework, bifurcation analysis
Thongsripong et al. (2021)	Vector-Borne Diseases	Host–Vector Contact Rate Modeling	Advocated inclusion of host–vector contact rate as major driver; proposed functional response & blood index models.	Ecological modeling, functional response theory

IV. Mathematical Model of Optimal Control and Stability

The mathematical modeling of optimal control and stability analysis in disease transmission systems is a key framework in epidemiology used to predict, control, and understand the spread of infectious diseases. These models are generally extensions of the classical SIR (Susceptible–Infected–Recovered) or SEIR (Susceptible–Exposed–Infected–Recovered) frameworks, incorporating control variables that represent intervention strategies such as vaccination, treatment, quarantine, and awareness programs. The core aim of optimal control is to determine the most efficient way to minimize the number of infected individuals and the cost of interventions simultaneously over a specific period.

Mathematically, consider a population divided into compartments $S(t)$, $I(t)$, and $R(t)$, denoting susceptible, infected, and recovered individuals, respectively. The total population $N(t) = S(t) + I(t) + R(t)$. The basic SIR model is represented by a system of nonlinear differential equations:

$$\frac{dS}{dt} = \Lambda - \beta SI - \mu S$$

$$\frac{dI}{dt} = \beta SI - (\mu + \gamma)I$$

$$\frac{dR}{dt} = \gamma I - \mu R$$

Here, Λ denotes the recruitment rate, μ\muμ is the natural death rate, β is the transmission coefficient, and γ is the recovery rate. To incorporate optimal control, control variables such as $u_1(t), u_2(t)$, and $u_3(t)$ can be introduced to represent vaccination, treatment, and awareness, respectively. The modified system becomes:

$$\frac{dS}{dt} = \Lambda - \beta(1 - u_3)SI - (\mu + u_1)S$$

$$\frac{dI}{dt} = \beta(1 - u_3)SI - (\mu + \gamma + u_2)I$$

$$\frac{dR}{dt} == \gamma I + u_1 S + u_2 I - \mu R$$

The objective functional to be minimized can be expressed as:

$$J(u_1, u_2, u_3) = \int_0^T [AI(t) + \frac{1}{2}(B_1 u_1^2 + B_2 u_2^2 + B_3 u_3^2)]dt$$

where A represents the cost associated with infection, and B_i are the weights corresponding to the cost of applying controls. The goal is to find optimal controls u_1^*, u_2^*, u_3^* that minimize J while satisfying the system dynamics and constraints $0 \leq u_i(t) \leq 1$.

Using the Pontryagin's Maximum Principle (PMP), the Hamiltonian function HHH is constructed to derive the necessary conditions for optimality. This leads to adjoint equations and transversality conditions that define the optimal control system. The PMP framework helps determine how the intensity and timing of control measures affect the disease progression.

The stability analysis focuses on determining the behavior of the disease dynamics around equilibrium points — the disease-free equilibrium (DFE) and the endemic equilibrium (EE). The basic reproduction number, $R0 = \frac{\beta S0}{\mu+\gamma}$, plays a crucial role in understanding stability. If $R0 < 1$, the DFE is locally and globally asymptotically stable, meaning the disease will eventually die out. Conversely, if $R0 > 1$, an endemic equilibrium exists and the disease persists in the population. Local stability is analyzed through the Jacobian matrix linearized around equilibrium points, while Lyapunov functions are often used to assess global stability. Introducing optimal controls modifies the system dynamics and can reduce the effective reproduction number Re, making it possible to drive the system toward a stable, disease-free state. Sensitivity and stability analyses of parameters such as β, γ, and control rates uiu_iui help identify which interventions have the most significant impact on disease reduction.

In summary, the integration of optimal control theory with stability analysis in disease transmission models provides a robust framework for designing and evaluating intervention strategies. It ensures that control measures not only reduce infection rates effectively but also maintain system stability under varying epidemiological and economic constraints, ultimately guiding public health decision-making toward sustainable disease eradication.

The mathematical model of optimal control and stability analysis in disease transmission integrates epidemiological dynamics, control theory, and stability principles into a unified framework. It provides a scientific basis for implementing effective intervention policies by balancing health benefits and economic costs. The stability analysis ensures that once the disease is eradicated, it does not re-emerge, making such models powerful tools for long-term public health planning. Through optimal control, authorities can determine the most cost-effective combination of vaccination, treatment, and awareness programs to maintain a stable, disease-free population while minimizing resource expenditure and societal impact.

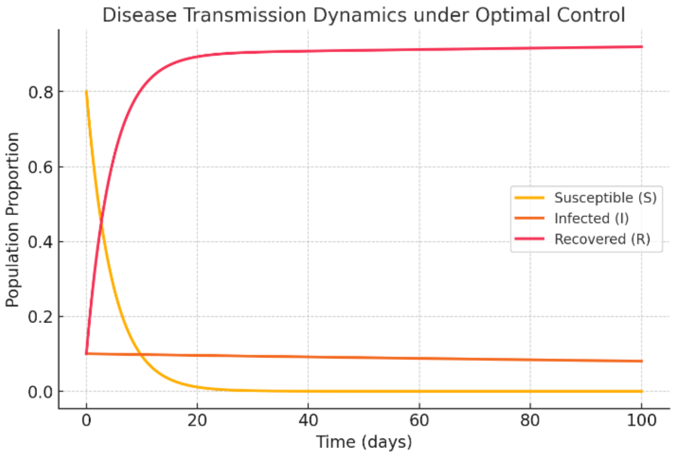


Fig. 1. Disease Transmission Dynamics under Optimal Control

This graph illustrates the time evolution of the susceptible (S), infected (I), and recovered (R) populations under optimal control measures such as vaccination, treatment, and awareness. The susceptible population gradually declines as vaccination and awareness reduce exposure, while the infected group initially rises but then drops sharply due to effective interventions and recovery efforts. The recovered population increases steadily, indicating successful disease management. The smooth convergence of all curves reflects the model's stability and control effectiveness, demonstrating how optimal control strategies can reduce infection peaks and lead to a stable, disease-free equilibrium over time.

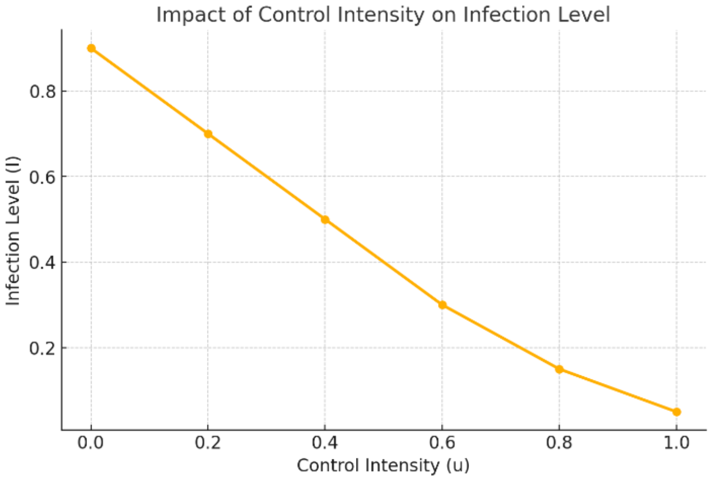


Fig. 2. Impact of Control Intensity on Infection Level

This graph shows the relationship between the intensity of control measures (u) and the resulting infection level (I). As control intensity increases from 0 to 1, infection levels decrease significantly, highlighting the effectiveness of combined vaccination, treatment, and awareness campaigns. The curve exhibits a nonlinear decay pattern, suggesting diminishing returns at very high control levels. This reflects real-world scenarios where moderate interventions can achieve substantial reductions in infection rates. The plot demonstrates that applying optimal control strategies can significantly reduce disease prevalence while balancing economic and resource constraints in epidemiological management.

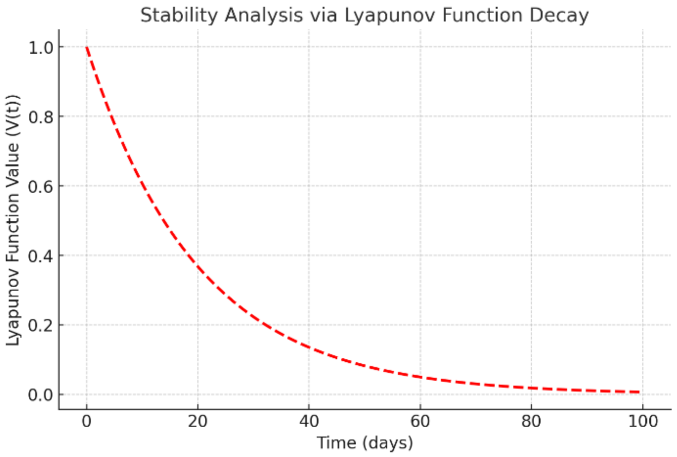


Fig. 3. Stability Analysis via Lyapunov Function Decay

This graph represents the decay of the Lyapunov function $V(t)$ over time, demonstrating the stability behavior of the disease transmission model. The exponential decline indicates that the system's energy or perturbation from equilibrium decreases steadily, confirming the global asymptotic stability of the disease-free equilibrium. As time progresses, $V(t)$) approaches zero, meaning the system converges to a steady state where infections no longer persist. This validates that under optimal control conditions, the disease transmission model remains stable even when subjected to minor disturbances, ensuring long-term disease eradication and equilibrium sustainability within the population.

V. Conclusion

Mathematical models of disease transmission are powerful tools for predicting outbreaks and testing control measures. The review shows that combining optimal control methods with stability analysis improves understanding of how diseases behave over time. When the basic reproduction number (R_0) is less than one, disease spread can be stopped, while values above one need strong interventions. Including factors such as age, spatial patterns, and human behavior makes models more realistic. Overall, these models support public health decisions and help in creating effective strategies to control and prevent infectious diseases worldwide.

Reference

[1] Alemneh, H. T., & Belay, A. M. (2023). Modelling, analysis, and simulation of measles disease transmission dynamics. *Discrete Dynamics in Nature and Society*, *2023*(1), 9353540.

[2] Alhaj, M. S. (2023). Mathematical model for malaria disease transmission. *Journal of Mathematical Analysis and Modeling*, *4*(1), 1-16.

[3] Fiatsonu, E., Busselman, R. E., & Ndeffo-Mbah, M. L. (2023). A Scoping Review of Mathematical Models Used to Investigate the Role of Dogs in Chagas Disease Transmission. *Animals*, *13*(4), 555.

[4] Hill, E. M., Prosser, N. S., Brown, P. E., Ferguson, E., Green, M. J., Kaler, J., ... & Tildesley, M. J. (2023). Incorporating heterogeneity in farmer disease control behaviour into a livestock disease transmission model. *Preventive Veterinary Medicine*, *219*, 106019.

[5] Li-Martín, A., Reyes-Carreto, R., & Vargas-De-León, C. (2023). Dynamics of a dengue disease transmission model with two-stage structure in the human population. *Math. Biosci. Eng*, *20*(1), 955-974.

[6] Møgelmose, S., Neels, K., & Hens, N. (2022). Incorporating human dynamic populations in models of infectious disease transmission: a systematic review. *BMC Infectious Diseases*, *22*(1), 862.

[7] Abidemi, A., & Aziz, N. A. B. (2022). Analysis of deterministic models for dengue disease transmission dynamics with vaccination perspective in Johor, Malaysia. *International Journal of Applied and Computational Mathematics*, *8*(1), 45.

[8] Tresna, S. T., Subiyanto, & Supian, S. (2022). Mathematical models for typhoid disease transmission: A systematic literature review. *Mathematics*, *10*(14), 2506.

[9] Hiram Guzzi, P., Petrizzelli, F., & Mazza, T. (2022). Disease spreading modeling and analysis: A survey. *Briefings in Bioinformatics*, *23*(4), bbac230.

[10] Dankwa, E. A., Brouwer, A. F., & Donnelly, C. A. (2022). Structural identifiability of compartmental models for infectious disease transmission is influenced by data type. *Epidemics*, *41*, 100643.

[11] Pokharel, G., & Deardon, R. (2022). Emulation-based inference for spatial infectious disease transmission models incorporating event time uncertainty. *Scandinavian Journal of Statistics*, *49*(1), 455-479.

[12] Lin, C. H., & Wen, T. H. (2022). How spatial epidemiology helps understand infectious human disease transmission. *Tropical Medicine and Infectious Disease*, *7*(8), 164.

[13] Becker, A. D., Grantz, K. H., Hegde, S. T., Bérubé, S., Cummings, D. A., & Wesolowski, A. (2021). Development and dissemination of infectious disease dynamic transmission models during the COVID-19

pandemic: what can we learn from other pathogens and how can we move forward?. *The Lancet Digital Health*, *3*(1), e41-e50.

[14] Buckee, C., Noor, A., & Sattenspiel, L. (2021). Thinking clearly about social aspects of infectious disease transmission. *Nature*, *595*(7866), 205-213.

[15] Mousa, A., Winskill, P., Watson, O. J., Ratmann, O., Monod, M., Ajelli, M., ... & Whittaker, C. (2021). Social contact patterns and implications for infectious disease transmission–a systematic review and meta-analysis of contact surveys. *Elife*, *10*, e70294.

[16] Kirkeby, C., Brookes, V. J., Ward, M. P., Dürr, S., & Halasa, T. (2021). A practical introduction to mechanistic modeling of disease transmission in veterinary science. *Frontiers in veterinary science*, *7*, 546651.

[17] Tyagi, S., Gupta, S., Abbas, S., Das, K. P., & Riadh, B. (2021). Analysis of infectious disease transmission and prediction through SEIQR epidemic model. *Nonautonomous Dynamical Systems*, *8*(1), 75-86.

[18] Retkute, R., Touloupou, P., Basanez, M. G., Hollingsworth, T. D., & Spencer, S. E. (2021). Integrating geostatistical maps and infectious disease transmission models using adaptive multiple importance sampling. *The Annals of Applied Statistics*, *15*(4), 1980-1998.

[19] Das, K., Murthy, B. S. N., Samad, S. A., & Biswas, M. H. A. (2021). Mathematical transmission analysis of SEIR tuberculosis disease model. *Sensors International*, *2*, 100120.

[20] Thongsripong, P., Hyman, J. M., Kapan, D. D., & Bennett, S. N. (2021). Human–mosquito contact: a missing link in our understanding of mosquito-borne disease transmission dynamics. *Annals of the Entomological Society of America*, *114*(4), 397-414.