

Mathematical Models for Infectious Disease Dynamics and Control Strategies

*Mr. Vinayak Kishan Nirmale¹, Dr. G. Kuppuswami², Dr. P. Satish³, Dr. N. Konda Reddy⁴, Dr. Arvind R. Bhagat Patil⁵, Dr. Rajat Pandit⁶, Mrs. Ruchira Tare⁷

¹Lecturer in Mathematics, Department of Polytechnic, MIT World Peace University, Pune, Maharashtra, India, Pincode: 411038. Email : vinayak.nirmale@mitwpu.edu.in

²Assistant Professor, Department of Mathematics, Panimalar Engineering College, Chennai, Tamilnadu, India, Pincode: 600123. Email id: gkuppuswamiji@gmail.com

³Associate Professor, Department of Mathematics, Aditya University, Surampalem, Andhra Pradesh, India, Pincode: 533437. Email Id- satishmaths.7@gmail.com

⁴Associate Professor, Department of Mathematics, Koneru Lakshmaiah Education Foundation, Greenfields, Vaddeswaram, Guntur, Andhra Pradesh, India, Pincode: 522302. E Mail: kondareddymamatha@gmail.com

⁵Dean, Department of Computer Technology, Yeshwantrao Chavan College of Engineering, Nagpur, India, Pincode: 441110. Email: arbhagatpatil@gmail.com

⁶Assistant Professor, Department of Computer Science, West Bengal State University Barasat, West Bengal, India, Pincode: 700126. Email: rajatpandit123@gmail.com

⁷Assistant Professor, Department of Computer Engineering, Bharati Vidyapeeth (Deemed to be University) College of Engineering, Pune, Maharashtra, India, Pincode: 411043. Email id- rktare@bvucoep.edu.in

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Abstract:

The study explores mathematical models related to the dynamics of infectious diseases and approaches to manage them. These models are essential resources for comprehending how illnesses spread throughout people and assessing how well control strategies work. The study of infectious disease epidemiology heavily relies on mathematical modeling and analysis. Here, we give a clear overview of the spread of disease, explain how to mathematically model this stochastic process, and show how to utilize this mathematical representation to analyze the emergent dynamics of real-world epidemics. The advancement of mathematical analysis and modeling is crucial to our expanding comprehension of the evolution and ecology of pathogens. This study emphasizes how important mathematical modeling is to improving our knowledge of the dynamics of infectious diseases and how crucial it is to creating efficient management plans to lessen the burden of infectious diseases on public health.

Keywords: Mathematical, Models, Infectious, Disease, Dynamics, epidemics

1. INTRODUCTION

Containing several threats to both global health security and societal well-being, infectious illnesses have long been a major public health concern. Research in epidemiology and public health has revolved around the study of the dynamics of infectious diseases and the creation of efficient control methods. Clarifying the complex dynamics of infectious diseases in populations and evaluating the effects of different treatments for disease control and prevention are made possible by mathematical modeling. The significance of mathematical models in comprehending the dynamics of infectious diseases is summarized in this introduction, along with how they help shape evidence-based management measures. To develop prompt and efficient control strategies, it is imperative to

comprehend the dynamics of infectious disease spread and transmission. An effective way to represent the intricate interactions between variables affecting the spread of disease, such as pathogen traits, environmental factors, and population demography, is through mathematical models. Researchers can experiment with various scenarios, model disease outbreaks, and evaluate the potential efficacy of control techniques prior to deployment by integrating these data into mathematical frameworks. By using modeling, public health professionals and policymakers can lessen the strain on healthcare systems, prevent the spread of disease, and anticipate disease patterns. They can also allocate resources more effectively and implement focused treatments. Mathematical models also give light on important variables including pathogen development, herd immunity, and the influence of human behavior on disease spread. These insights into the fundamental mechanisms driving infectious disease dynamics are very valuable. The creation of more effective control techniques and a greater comprehension of disease epidemiology are both aided by these models' ability to clarify the intricate relationships between host, pathogen, and environment. Mathematical modeling offers a range of techniques for investigating various aspects of infectious disease dynamics and control, from basic compartmental models, such as the susceptible-infectious-recovered (SIR) framework, to more complex agent-based and network models.

New infectious disease outbreaks, like the COVID-19 pandemic, have highlighted the value of mathematical modeling in epidemic preparedness and response in recent years. The forecasting of disease spread, evaluation of the effects of measures like social distance and immunization, and provision of guidance for policy decisions aimed at halting transmission and saving lives were all greatly aided by mathematical models. Researchers, policymakers, and public health practitioners are working together to improve data quality, refine models, and strengthen collaboration as a result of the COVID-19 pandemic, which has brought to light both the advantages and disadvantages of current modeling methodologies.

1.1 Role of Mathematical Modeling

Mathematical modeling plays a crucial role in the dynamics of infectious diseases, providing researchers with an invaluable tool to examine complex patterns of transmission, assess the efficacy of intervention efforts, and formulate public health policy. Researchers may replicate the intricate interactions between hosts, infections, and their environment using mathematical models, which provides important insights into the epidemiology of diseases. These models help build evidence-based strategies for disease prevention and control by offering a platform to investigate different scenarios, predict illness trends, and evaluate the possible effects of control measures. Mathematical modeling is crucial to improving our understanding of infectious illnesses and directing efforts to lessen their impact on public health because it bridges the gap between theory and real-world data.

1.2 Diverse Modeling Approaches

A wide range of approaches are included in mathematical modeling, from more intricate agent-based and network models to more conventional compartmental models such as the susceptible-infectious-recovered (SIR) framework. Researchers can address different elements of disease transmission and control by utilizing the distinct strengths and capabilities that each modeling approach provides to the study of infectious disease dynamics. Compartmental models, like SIR models, are helpful for analyzing population-level interventions and comprehending general patterns of transmission because they offer a condensed picture of disease dynamics. Agent-based models, on the other hand, replicate individual interactions within populations and capture heterogeneity and spatial dynamics, providing information about the spread of disease locally and the best ways to intervene. Conversely, network

models investigate how illness transmission and control strategies are influenced by the topology of social or contact networks.

2. REVIEW OF LITREATURE

Anirudh et al. (2020) gives a thorough analysis of the function that mathematical modeling plays in anticipating and reducing the spread of Covid-19. The significance of transmission dynamics in guiding public health measures is emphasized by their study. Anirudh et al. used mathematical models to provide light on possible pandemic trajectories, providing insightful information for both policymakers and medical experts.

Asamoah et al. (2018) concentrate on the dynamics of bacterial meningitis transmission, use mathematical modeling to investigate the effects of different control strategies. Their research emphasizes how important it is to use proactive intervention techniques to stop the spread of illness. Asamoah et al. show the potential efficacy of focused control measures through their models, offering important direction for public health activities.

Lastly, Bekiros and Kouloumpou (2020) present SBDiEM, a novel mathematical model designed to comprehend the dynamics of infectious diseases. Their research incorporates aspects of the complexity and unpredictability present in real-world disease processes, providing a novel viewpoint on modeling methodologies. Bekiros and Kouloumpou's model, which incorporates stochasticity and network structures, enhances our comprehension of the transmission of infectious diseases and opens the door to more complex control tactics.

Berge et al. (2018) provide a thorough analysis of contact tracing as an Ebola virus disease (EVD) control method. The authors investigate the efficacy of contact tracing in limiting epidemics of EVD by mathematical modeling. Their research emphasizes how crucial prompt and comprehensive contact tracking is to reducing the spread of illness. For public health professionals and politicians charged with EVD control efforts, Berge et al. offer invaluable insights by quantifying the influence of numerous parameters, such as contact tracking efficiency and intervention timing.

(Brauer et al., 2019), The writers provide a thorough rundown of the mathematical modeling methods used in epidemiological studies. This landmark study is an invaluable tool for beginning and experienced scholars alike in the subject. A wide range of subjects are covered by Brauer et al., such as evolutionary dynamics, spatial epidemiology, and compartmental models. The authors clarify the use of mathematical models in comprehending illness transmission dynamics and assessing intervention options through case studies and instructive examples. Because of its multidisciplinary approach, which connects mathematical theory with epidemiological applications, the book is a vital resource for both practitioners and researchers.

3. MATHEMATICAL MODELING METHODOLOGIES IN EPIDEMIOLOGY

Quick evaluation is possible with mathematical modeling and simulation. When there are a lot of experimental settings to test or when data collection is unaffordable, simulation is frequently utilized. Various techniques have been invested over effort, each resolving the issue from an alternate point. These fall into three general classes (see Fig. 1): (1) measurable procedures for following episodes and recognizing spatial examples in genuine pandemics; (2) numerical models implanted in dynamical frameworks (otherwise called state-space models) that anticipate the course of a "speculative" or continuous scourge; and (3) AI/master strategies for anticipating the course of a continuous pestilence. There are different ways used to wind around an immense and shifted collection of writing for every one of these three gatherings. Here, we endeavor to delineate these procedures and make sense of the key thoughts that help them.

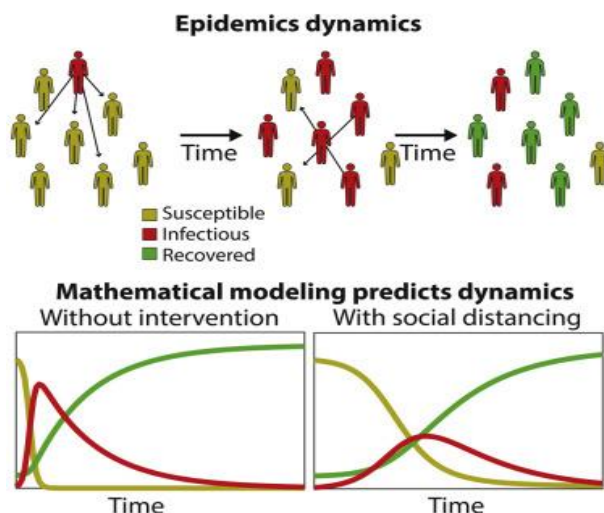


Figure 1: Infectious disease mathematical models.

3.1 Statistical-Based Methods for Epidemic Surveillance

The checking of expected flare-ups and designs that could support halting a spread is one of the most vital pieces of pandemic administration. A prominent early accomplishment in the field is the replication of the London cholera pandemic in 1854. Doctor John Snow assembled spatiotemporal information around then and, after planning them, found a particular example encompassing the Wide Road water siphon, which filled in as the transmission zero point. His examination made the ailment wiped out. The principal Teacher of The study of disease transmission and Insights at the London School of Cleanliness and Tropical Sicknesses at the turn of the twentieth century was Greenwood, a disease transmission specialist and analyst who laid out a thorough numerical connection between fields.

Worldwide status and productive homegrown reaction instruments are presently essential for worldwide drives to control pandemics. The World Wellbeing Association and the Habitats for Infectious prevention are initiating an enormous worldwide work to facilitate the making of a worldwide reconnaissance organization. Pandemics that have as of late surfaced, such Guides, SARS in 2002-2003, and the H1N1 pig influenza in 2009, act as a wake up call of the worth of early episode recognition and reconnaissance. Factual methods have worked on our capacity to battle pandemics by empowering fast evaluations of new conditions. It's implied that precise information and the right strategy determination are fundamental for building measurable models that successfully and heartily catch the highlights of irresistible sicknesses.

3.2 Regression methods

Relapse models track a measurement of detailed tainted cases, say $y(t)$, trying to recognize an episode from time-series of scourge free spans. At the point when an edge, suppose k , is surpassed — characterized by an outer record containing a picture, delineation, and so forth — a pandemic caution is raised.

The item name is viru-4-295-e1.jpg, with μ addressing the time-series circulation mean worth inside a 95 percent certainty stretch.

Serfling's relapse model, which was first worked to follow flu related passings in light of the yearly example of pneumonia and flu passings, is an essential relapse model. The sickness shows occasional way of behaving; thus the accompanying cyclic relapse model has been inspected:

$$y(t) = a + bt + \sum_{i=1}^m c_i \cos \theta + \sum_{i=1}^m d_i \sin \theta + e(t)$$

While the coefficients should be tracked down utilizing a boundary recognizable proof procedure, θ is a straight capability of time t . Repetitive occasional examples are approximated utilizing the cosine and sine terms; the commotion, $e(t)$, is gathered from the time-series and is thought to be Gaussian conveyed with mean zero and fluctuation σ^2 . The normal mean worth of all passings from flu and pneumonia, communicated in units of four-week spans, was signified by the image $y(t)$ in the first Serfling study. Information from 108 US urban communities during a three-year time frame starting in September 1955 were utilized to fit the model.

After utilizing least squares estimation, Serfling arrived at the subsequent model:

$$y(t) = 300.5 + 2.1t + 97.6 \cos \left(\frac{2\pi t}{13} - 2.67 \right)$$

There have also been proposals for other models that use square terms and t^2 to account for long-term changes welcomed on by factors like populace increment or ailment evaluation.²⁷ The Habitats for Infectious prevention in the US, Australia, France, and Italy at present utilize the previously mentioned strategy to distinguish flu plagues.

Despite the fact that disease transmission specialists exceptionally favor this strategy for reconnaissance and expectation, one should utilize alert while applying it on the grounds that the type of the situations ordinarily relies upon impromptu suppositions about the connection between the elements of a sickness and the free factors (factors) that control its spread. Moreover, there ought to be a "note of mindfulness" while utilizing the model (straight or nonlinear) and the presumptions made about the measurable qualities (like freedom, typical circulation, and fixed change) of the unmodeled elements (addressed by $e(t)$), especially while involving them for reconnaissance and flare-up expectation of recently arising pandemics.

Autoregressive models, including the autoregressive integrated moving average model (ARIMA) and seasonal ARIMA (SARIMA), as well as neural networks, are utilized in times series analysis.

These methods ease the assumptions around the autocorrelation of regression models and the assumptions surrounding basic autoregressive models, such as ARMA (autoregressive moving) and AR (autoregressive), which do not account for historical disturbances. ARIMA models are the most widely employed in this category. In general, they look like this:

$$A(z^{-1})[\Delta^d y(t) - \mu] = B(z^{-1})e(t)$$

where Δ^d is the differencing operator of order d defined by $\Delta^d \geq (1 - z^{-1})^d$; $A(z^{-1})$ is the autoregressive operator defined as A_n an external file that holds an image, illustration, etc.; and $y(t)$ denotes a stationary stochastic process at time t with mean value $E(y(t)) = \mu$.

The moving-average operator $B(z^{-1})$ is defined by an external file containing an image, illustration, etc. The object name is `viru-4-295-e5.jpg`.

The object is named `viru-4-295-e6.jpg`, and the part of the measurement that cannot be anticipated from earlier measurements is represented by the residual, or noise, at time t , or $e(t)$. The moving average model is obtained for $d = 0$ and $n_a = 0$, and the random walk with drift is obtained for $d = 1$ and $n_a = n_b = 0$. By taking into account the seasonal differencing operator, seasonal differencing naturally joins the framework mentioned above. an external file containing an image, diagram, etc.

The picture is called viru-4-295-e7.jpg, where S is the level of occasional differencing that creates a progression of changes starting with one season then onto the next and k is the length of the occasional cycle.

After then, at that point, the time series is separated into two sets: a preparation set comprised of the times series and a test (approval) set comprised of the leftover information. Regularly, the Akaike Data Criterion³⁵ is utilized to decide the best model request by finding some kind of harmony between the amount of boundaries and decency of-fit. Then, the fitted model is utilized to the disease advancement anticipating. The primary elements restricting the unwavering quality of these strategies are (1) factual vulnerability in assessing the upsides of obscure boundaries and (2) guesses concerning the measurable attributes of the related time series.

Statistical process control techniques include exponentially weighted moving average (EWMA)^{42,43}-based approaches and cumulative sum (CUSUM) charts.

Likely the most broadly used strategy for recognizing sickness episodes is CUSUM. By following a combined execution metric over the long haul, this is achieved. Presently, how about we take a gander at the quantity of tainted cases ($y(t_i)$) that were seen at different moments ($t_i, I = 1, 2, \dots n$). For a cycle with a solitary boundary, CUSUM can be just communicated as

$$CUSUM(i) = \sum_{t=1}^i (y(t_i) - k)$$

or on the other hand as a recursive

$$CUSUM(0) = 0$$

$$CUSUM(i) = \max(0, CUSUM(i-1) + y(t_i) - k), i \geq 1.$$

where the distinction between the in-charge and crazy means is addressed by the reference esteem k . If $CUSUM(i) < h$, where h is a limit (frequently multiple times the standard deviation from the pattern/mean worth of in-control perceptions), then the cycle is considered to be taken care of. Assuming $CUSUM(i)$ is more than h , an interaction caution is set off at time t_i ; this demonstrates that the cycle is wild. The methodologies in view of probability proportions are utilized to decide the reference esteem k .⁴⁴⁻⁴⁹ Accordingly, the reference esteem is as per the following, meaning by $f(\mu_0)$ and $f(\mu_1)$ the likelihood capability of the in-charge and crazy cycles with boundaries μ_0 and μ_1 , separately:

$$k = -\log \frac{f(\theta_1 | y(t_i))}{f(\theta_0 | y(t_i))}$$

Information from past periods can be utilized to gauge the likelihood capabilities $f(\theta_0)$ and $f(\theta_1)$ as well as their boundaries. The relationship above for Poisson circulations is as per the following:

$$k = \frac{\mu_1 - \mu_0}{\log(\mu_1) - \log(\mu_0)}$$

where the in-charge and wild Poisson appropriations' mean qualities are signified by μ_0 and μ_1 , separately.

4. STATE-SPACE MODELS IN MATHEMATICS AND MECHANICS

Mathematical models fall into one of the following types based on how closely they approximate reality and how complicated they get.

4.1 Differential and/or (integro)-partial differential equations are "continuum" models.

The population's coarse-grained dynamics of the epidemics are described by continuum models.^{87–90} For instance, one may research a model for how the illness has changed over time in relation to age and immunization history.^{91,92} or look into the effects of isolating or quarantining the afflicted portion of the community.^{93,94} Robust analysis techniques for ordinary or partial differential equations can be applied to investigate such models. However, the majority of continuum models that are currently available are frequently simply qualitative caricatures that cannot capture all of the features, which compromises epidemiological realism due to the complexity and stochasticity of the phenomenon.

According to their current health, the population is separated into compartments within this framework, such as susceptible (S), infected (I), and recovered (R). Other population statuses like vaccinated (V) and quarantined (Q), which are associated with control programs, are also employed.

These models are based on the compartmental SIR mass-action model of Kermack and McKendrick (1922). It is assumed in this form that an infected person has a probability of $p_{S \rightarrow I}$ to infect a susceptible, and that a probability of $p_{I \rightarrow R}$ indicates that an infected person recovers. The following three ordinary differential equations can be used to approximate the dynamics of the system under the mass-balance framework.

$$\frac{dP_t(S)}{dt} = -p_{S \rightarrow I} \sum_{N(S)} P_t(S, I), \quad \frac{dP_t(I)}{dt} = -p_{I \rightarrow R} P_t(I), \quad \frac{dP_t(R)}{dt} = p_{I \rightarrow R} P_t(I)$$

where $P_t(A,B)$ is the pair joint likelihood to have states A_n and B conveying at time t ; $N(S)$ demonstrates the arrangement of connections of a powerless individual; and $P_t(\{S, I, R\})$ shows the opportunity that an individual is on one of the states $\{S, I, R\}$ at time t . There is definitely not a shut structure for the situations above. $P_t(S,I) = P_t(S)P_t(I)$, accepting Markovian way of behaving of the basic cycle. The probabilities are identical to the normal (mean) upsides of the related factors in the populace under the mean field guess, which expects that the populace is impeccably blended and that everybody helpless has a similar probability of getting the disease. The accompanying arrangement of conditions results from these assumptions:

$$\frac{dS}{dt} = -\alpha SI, \quad \frac{dI}{dt} = \alpha SI - \beta I, \quad \frac{dR}{dt} = \beta I$$

where α and $1/\beta$ represent the mean values of the disease transmission probability and the amount of time that a person can spread the illness before getting better, respectively. S , I , and R stand for expected (mean) values. The well-known Kermack and McKendrick model is represented by the set of equations above. After a duration of time $1/\gamma$, the recuperated person regains susceptibility, at which point the SIRS mean field model takes on the following form:

4.2 Random models, such as discrete and continuous-time Markov-chain models based on individual observations

These are often individual-level models that introduce the uniqueness of the individual behavior including numerous heterogeneous attributes, relaxing the assumption of the mean field approximations of infinite population and perfect mixing. Discrete Markov chains are the primary

representative of the category (DMC). Time and states are both specified on a discrete set of values in DMC. Every discrete time step, the states of the individuals vary in a probabilistic way based on straightforward rules involving their own states and the states of their links that satisfy the Markov property, which states that the values of the states at time $t + \Delta t$ in the future only depend on the values of the states at time t in the past, i.e.

These transition rules, for a stochastic SIRS-type model, would look like this:

- Rule #1: If there is active physical communication between an infected individual (I) and a susceptible (S) connection, then there is a probability $p_{S \rightarrow I} = \lambda$ for the infection.
- Rule #2: The likelihood that an infected person (I) would recover is $p_{I \rightarrow R} = \delta$.
- Rule #3: There is a probability $p_{R \rightarrow S} = \gamma$ that a recovered individual (R) will become susceptible (S). The situation of temporal immunity is expressed by this condition.

The Markov process is referred to as a time homogeneous Markov process when these transition probabilities do not change over time. The disease spreads through a contact network made up of the connections between people. This network is taken to be a completely connected graph in basic DMC models, which leads to homogenous mixing of people. The stochastic model can be thought of as a mean field deterministic model in this situation and in the limit of an infinite number of individuals. The governing equations are as follows for a uniform distribution with z links per individual and in the limit of an infinite size population:

$$\frac{dS}{dt} = -\lambda z S I + \gamma R, \quad \frac{dI}{dt} = \lambda z S I - \delta I, \quad \frac{dR}{dt} = \delta I - \gamma R$$

However, when the presumptions regarding an unlimited size population, homogenous people, homogenous or random regular networks fail to hold, the deterministic mean field approximations mentioned above may impose significant bias. Therefore, at the coarse-grained/emergent (continuum) level, they can overlook crucial numeric and/or qualitative information. As the heterogeneity increases (e.g., interactions on more complicated networks with finite size populations), the problem gets worse.

4.3 Completing the previous stochastic models' conjecture that individual interactions are immediate and homogeneous are complex network models 118–120.

Among the most important issues in epidemics are the dynamic impacts of heterogeneity in the contact network. Individual contacts occur in a variety of complex and highly heterogeneous modes that are driven by a wide range of factors, from the intrinsic variability of the pathogen and the stochasticity of the host-pathogen interaction that characterize the mechanisms of a given disease's transmission to population-level factors that are complicated by seasonal, environmental, economic, and demographic factors. Moreover, the contact social network's architecture frequently influences how an epidemic spread, and the emergent dynamics of the epidemic influence how the transmission network dynamically evolves. For instance, during a major epidemic outbreak, a shift in the endemicity of a specific population subset might lead to a substantial alteration in the transmission network's properties (due to, e.g., link-cutting due hospitalization). Controlling disease outbreaks through public health interventions and regulations requires a thorough understanding of this complicated behavior. A well-planned vaccination, isolation, and/or antiviral medication program targeting certain population segments is necessary to effectively confront an emerging pandemic. Inadequate comprehension of the dynamics of infectious diseases, which arise from varied contact interactions, can lead to grave adverse

outcomes. A great deal of work has been done in recent years to understand how the underlying architecture of the transmission network interacts with the emergent dynamics of infectious illnesses.

5. CONCLUSION

The use of mathematical modeling techniques is essential for comprehending and managing infectious diseases. Researchers can monitor outbreaks, establish spatial trends, and spot epidemics early on through statistically based tools like regression models and statistical process control techniques. This allows for timely intervention and mitigation measures. Moreover, a continuous approach to researching disease dynamics is provided by state-space models, such as differential and partial differential equations, which enable the investigation of population-level interactions and the results of treatments. Furthermore, random models that reflect individual-level behaviors and heterogeneity, including discrete and continuous-time Markov-chain models, shed light on the complex dynamics of disease transmission. Ultimately, the dynamic effects of contact network heterogeneity are clarified by complex network models, which provide important information for developing focused public health initiatives and successfully managing disease outbreaks. All things considered, the wide range of mathematical modeling approaches covered in this study highlights their significance in expanding our knowledge of infectious illnesses and directing evidence-based tactics for illness prevention and control.

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