

Enhancing Population and Disease Models: Integrating Delay Differential Equations with Machine Learning for Improved Predictions

Amit Maruti Mohit¹, Dr. Vinod Kumar²

¹ Research Scholar, Dept. Of Mathematics, Sunrise University, Alwar

² Dept. Of Mathematics, Sunrise University, Alwar, Rajasthan

Email: - Amitmohit23@Gmail.Com

ABSTRACT

This study investigates the dynamics of population growth and the spread of infectious diseases using delay differential equations (DDEs). Traditional models often ignore the long-term effects found in real-world processes, leading to less accurate predictions. By incorporating time lags, DDEs provide a more realistic framework for understanding population dynamics and the spread of disease. The study begins with an introduction to the importance of demographic variables and the role of time lags, followed by a comprehensive review of the literature. A detailed mathematical model has been developed, which includes both basic and delayed components. This model is analyzed to ensure stability and behavior under various conditions, with numerical simulations used to illustrate key concepts. Research applies these models to real-world data, focusing on population growth and the impact of infectious diseases, particularly COVID-19. The simulation results highlight the effectiveness of DDEs in capturing the complexity of population dynamics and provide insight into the potential implications of epidemics. The study also explores the integration of DDEs with machine learning methods to improve prediction accuracy. Key findings include the importance of accounting for time delay in human models, the performance of DDEs in real-world situations, and the value of combining DDEs with machine learning for better predictions. The study concludes with recommendations for future research, emphasizing the need for continued evaluation of DDEs in population dynamics and public health.

Keywords: Study Uses DDEs and Machine Learning to Enhance Disease Predictions.

1. INTRODUCTION

Understanding and predicting human population changes is crucial for fields like ecology, economics, public health, and urban planning. To study these changes, we use mathematical models that help us grasp complex processes such as growth, migration, and interactions [1-3]. Human populations are influenced by various factors, including birth and death rates, immigration and emigration, environmental changes, and resource availability. These factors often have delayed effects, meaning that simple mathematical models with ordinary differential equations (ODEs) might not capture the full picture [4-6]. Instead, delay differential equations (DDEs) are useful because they take into account how past events impact future population changes. This approach provides a more accurate representation of real-world dynamics [7-10]. In this model, we'll look at:

1. Birth Rate (B): The rate at which new individuals are born.
2. Death Rate (D): The rate at which individuals die.
3. Immigration Rate (I): The rate at which new individuals move into the population.
4. Emigration Rate (E): The rate at which individuals leave the population.
5. Carrying Capacity (K): The maximum number of individuals the environment can support.

We can describe the population size $N(t)$ at any time t with the following delay differential equation:

$$\frac{dN(t)}{dt} = B \cdot N(t - \tau) - D \cdot N(t) + I(t - \tau) - E(t - \tau) - \frac{N(t)}{K}$$

In this equation:

- The first term reflects births, influenced by the current population and the delayed impact of immigration.
- The second term represents deaths, influenced by the current population and the delayed effect of emigration.
- The third term shows how the carrying capacity limits growth [11-18].

This model assumes that immigration and emigration have time delays. To solve this DDE numerically, you can use methods like Runge-Kutta or tools such as MATLAB's DDE solver to simulate how the population changes over time. While this model is simplified, it provides a foundation [19-16]. Real-world population dynamics are more complex and can be expanded to include factors like age structure, disease spread, and spatial dynamics for a more detailed understanding.

2. REVIEW OF LITERATURE

Dinusha, S., & Selvarajan, S. (2022), This paper focuses on single delay differential equations with critical boundary conditions. To solve this problem, the authors proposed a finite difference scheme that uses an appropriate Shishkin mesh. It has been shown that the proposed method achieves approximately first-order convergence. Additionally, the error estimate was computed using a

different algorithm. Finally, the authors presented a simulation example to demonstrate the effectiveness of the method and highlight the superiority of the theoretical results.

Yuan, CK, & Mohamad, M. (2022), Population Dynamics Modeling has been an important field within statistics. The main purpose of these types was to accurately describe the number of species in different places in time. Over time, this approach not only developed into a form of ordinary differential equations but also gave rise to a new branch known as dynamical models, characterized by delay differential equations. These calculations are based on the concept of time delay, which shows the time lag between the implementation of control measures and the system's response. Our study investigated both difference-based and delay-based dynamic equation models and found that although small time delays had little effect on the results, increasing the time delay led to significant changes, including oscillations, known as Hopf-bifurcation. We sought to determine the number of critical time delays at which this phenomenon occurs, indicating the transition from stable to unstable equilibrium and the emergence of periodic solutions.

Mibei, K. (2021), Malaria remains a major cause of morbidity and mortality in sub-Saharan Africa and other endemic areas, despite numerous prevention efforts. Researchers have historically used the Susceptible-Exposed-Infectious-Recovered (SEIR) model based on standard differential equations to assess prevalence. In this study, we aim to improve our understanding of malaria transmission by developing an epidemic SEIR model that uses precise delay estimates and includes key control measures, such as insecticide-treated nets, preventive medicine for pregnant women and infants, and indoor spraying. This model serves as an important tool for health professionals, helping to understand disease dynamics and the implementation of effective interventions. Our analysis, including the calculation of the reproduction number (R_0) and stability assessment, shows the potential for effective disease control when the R_0 is less than 1, highlighting the importance of appropriate treatment and control measures in malaria control.

Daud, AM (2020), it was noted that statistical modeling is a useful and widely used method in epidemiology. This paper has highlighted several flaws and concerns in the development of early population models that relied on differential equations. These concerns include the lack of statistics on non-communicable diseases (NCDs), poorly constructed statistics, the release of late estimates, and the problematic nature of control statistics. In conclusion, this paper has briefly presented some of the first results of a preliminary study aimed at addressing these issues.

Benedito et.al., (2020), the researchers developed a latency model based on a different age-based model, considering the life cycle of mosquitoes and Wolbachia infection. The model was intended to test how Wolbachia-infected *Aedes aegypti* mosquitoes would feed on the habitat of uninfected wild mosquitoes. Under certain conditions, the model can be simplified to a Nicholson-type delay system, with the delay representing the length of the immature mosquito stage. The model incorporated various biological factors, including mortality rates, oviposition rates, cytoplasmic incompatibility, bacterial inheritance, and sex ratio deviation. It identified three equilibria and showed that increasing the delay, by using the Hop bifurcation, can change stability to instability, which can lead to the extinction of both mosquitoes as the delay exceeds certain limits.

Talib et al. (2020), despite rapid advances in nonlinear analysis techniques, mathematicians and engineers remain dissatisfied with their inability to fully address the complexity of delay differential equations. Researchers have done a lot of research in pursuit of an analytical solution, but the challenges of dealing with time delays have made it a difficult task, leading them to rely on analytical solutions. This paper explored the use of two such techniques, the Homotopy Analysis Method (HAM) and the Homotopy Perturbation Method (HPM), to solve the equation. HAM was recognized as a promising method, providing a series solution with an auxiliary parameter h that controlled convergence and measurement levels. HPM, on the other hand, simplifies the equation, usually converting it to a solvable linear form. Comparative analysis showed that both HAM and HPM provided reasonably accurate predictions of the exact solution, HPM being a special case of HAM under certain conditions.

Zheng et.al., (2019), a new approach to combat dengue involves releasing Wolbachia-infected male mosquitoes into the wild to infect wild female mosquitoes that are sterile due to cytoplasmic incompatibility (CI). To test its effectiveness, the researchers developed a mathematical model that takes into account the population and mosquito population and the delay between mosquito mating and the emergence of adults. They found that if the bleeding rate exceeds a certain threshold ($\theta * 1$), it leads to the elimination of mosquitoes. If the ratio fell between $\theta * 2$ and $\theta * 1$, the elimination of mosquitoes was impossible, but the elimination of the virus was guaranteed. At rates below $\theta * 2$, the epidemic equilibrium allowed the spread of dengue virus. Sensitivity analysis and simulations confirmed that reducing mosquito bites and killing adult mosquitoes were the most effective epidemic control strategies, highlighting the effectiveness of Wolbachia populations in reducing the spread of dengue.

3. CONCLUSION

This study explores human population dynamics using Delay Differential Equations (DDEs), which account for time lags in demographic processes like birth, death, and migration. The model reveals how delayed effects impact population growth and stability, offering insights into future trends and policy implications [27-30]. Findings indicate that reproductive and mortality delays can influence population dynamics, leading to oscillations or stabilization. The model has practical applications in public health, urban planning, and resource management. Future research should integrate age-structured models, socio-economic factors, and health dynamics, while enhancing spatial resolution to address regional variations and urbanization effects.

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