Replication Analysis of Nonlinear Differential Equations for Epidemic Spread Modelling in Rwanda: Asymptotic Properties and Identifiability Validation

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Abstract

This study builds upon previous work in epidemic spread modelling by exploring the dynamics of nonlinear differential equations to understand and predict the progression of diseases in Rwanda. A replication study was conducted by re-analysing existing data with the same mathematical framework used in the original research. This involved applying a system of nonlinear differential equations to model disease transmission dynamics, ensuring consistency across both studies. The analysis revealed that under certain initial conditions, the solutions to these equations converge towards stable equilibrium points, indicating long-term predictability in epidemic spread patterns within Rwanda's population. This study confirms the original model's ability to capture essential features of disease transmission dynamics, validating its use for epidemiological forecasting and public health planning. The findings suggest that further research should focus on incorporating additional factors such as vaccination rates and varying infection risks across different regions in Rwanda. The analytical core is $\hat{\{y\}}t = mathcal\{F\}(xt;\theta)$ with $\hat{\{\theta\}} = argmin_\theta L(\theta)$, and convergence is established under standard smoothness conditions.

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