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Dynamical analysis of an HIV infection model including quiescent cells and immune response

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This talk presents a comprehensive analysis of an HIV infection model that incorporates quiescent cells and immune response dynamics within the host. The model, represented by a system of ordinary differential equations, captures the intricate interplay between the host's immune response and the viral infection. The study investigates the fundamental properties of the model, including equilibrium analysis, the computation of the basic reproduction number $\mathcal{R}_0$, stability analysis, bifurcation phenomena, numerical simulations, and sensitivity analysis. An endemic equilibrium, which reflects the persistence of the infection, and a disease-free equilibrium, which represents the possibility of disease control, are both revealed by the analysis. By applying matrix-theoretical methods, stability analysis confirmed that the disease-free equilibrium is both locally and globally stable for $\mathcal{R}_0 < 1$. The research also reveals a transcritical forward-type bifurcation at $\mathcal{R}_0 = 1$, which denotes a critical threshold that affects the behavior of the system. The temporal dynamics of the model are investigated through numerical simulations, and sensitivity analysis determines the most important variables by examining the effects of parameter changes on the system's behavior.