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Modelling HIV Superinfection with Two Unique Viral Strains

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HIV superinfection, the acquisition of a second distinct viral strain in an individual already infected, presents challenges to HIV management and vaccine development. Understanding the dynamics and implications of superinfection is crucial for advancing HIV research and developing more effective prevention and treatment strategies. While HIV superinfection is recognized, the mechanisms, factors influencing its occurrence, and its impact on disease progression remain inadequately understood. This study addresses the gaps in knowledge regarding HIV superinfection by employing mathematical modelling to analyze the dynamics of coexistence and competition between two unique viral strains within the same host. A HIV superinfection model with two unique viral strains was developed. The viral strains-free and viral strains equilibria states were obtained and found to be stable. Numerical simulations showed that in order to prevent HIV superinfection, treatment at 95% level of efficacy should begin at any time, $t < 50$ days, before the second strain is fully integrated in the population of primarily infected cells. We conclude that the HIV superinfection model developed in this study minimizes the rate of infection and the rate at which new viruses are produced by the second strain. The models also show that the second strain of HIV contributes to the persistence of HIV in the system, increases viral load, orchestrates the multiplication of infected cells and results in the decline of the population of healthy cells.

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