

# Bifurcation analysis of a two-infection transmission model with explicit vector dynamics

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The investigation of epidemiological scenarios characterized by chaotic dynamics is crucial for understanding disease spread and improving disease control strategies. Motivated by dengue fever epidemiology, in this study we introduce the SIRSIR-UV model, which accounts for differences between primary and secondary infections and explicit disease vector dynamics. Our analysis, employing nonlinear dynamics and bifurcation theory, provides key insights into how vectors contribute to the overall system dynamics. In this paper, the formalization of backward bifurcation using center manifold theory, computation of Hopf and global homoclinic bifurcation curves, and derivation of analytical expressions for transcritical and tangent bifurcations deepen the understanding. The observation of chaotic behavior with the inclusion of seasonal forcing in the vector population underscores the importance of considering external factors like climate in disease spread. Our findings align with those from previous models, emphasizing the significance of simplifying assumptions, such as implicit vector dynamics, when constructing models without vector control. This study brings significant insights to the mathematical modeling of vector-borne diseases, providing a manageable framework for exploring complex epidemiological scenarios and identifying key factors influencing disease spread. While the absence of strain structure may limit predictive power in certain scenarios, the SIRSIR-UV model serves as a starting point for understanding vector-borne infectious disease dynamics.

## References

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