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Dynamics of prey-predator network model with application to virus and immune response evolution

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Recent work has sought to understand assembly and coexistence of interacting species in ecosystem models. However, the overwhelming number of species combinations and connecting the models to evolution have challenged researchers, especially in higher dimensional systems. Here, we aim to address this gap by looking through an evolutionary genetics lens in a prey-predator model of virus-immune dynamics, where viral variants can be represented by binary sequences which encode their resistance to immune responses. First, persistence and stability of equilibria are studied using Lyapunov functions and invasion analysis. Then, bifurcations between distinct ecological network structures are linked to epistasis (non-additivity) in the viral fitness landscape. Results are discussed in the context of HIV escape of host immune responses and, more generally, finding simplifying rules for prey-predator network evolution.

References

[1] C. J. Browne, F. Yahia, Virus-immune dynamics determined by prey-predator interaction network and epistasis in viral fitness landscape, *Journal of Mathematical Biology*, 86:9, 2023.

[2] B. R. Magalis, P. Autissier, K. C. Williams, X.Chen, C. Browne, M. Salemi, Predator-Prey Dynamics of Intra-Host Simian Immunodeficiency Virus Evolution Within the Untreated Host, *Frontiers in Immunology*, 12:709962, 2021.

[3] C. J. Browne, H. L. Smith, Dynamics of virus and immune response in multi-epitope network, *Journal of Mathematical Biology*, 77:1833–1870, 2018.