

LOTKA-VOLTERRA PREDATOR-PREY SYSTEMS MODELING VIRUS DYNAMICS IN MARINE ECOSYSTEMS AND HIV INFECTION

H.L. Smith^{*1},
D. Korytowski² and C. Browne³

¹School of Mathematical and Statistical Sciences,
Arizona State University, Tempe, AZ, USA

²Department of Mathematics and Statistics,
Idaho State University, Pocatello, Idaho 83209

³Department of Mathematics,
University of Louisiana-Lafayette, Lafayette, Louisiana, 70504

halsmith@asu.edu (*corresponding author),

Marine ecosystems may contain diverse populations of bacteria which are supported by relatively few limiting nutrients and which are predated upon by an equally diverse set of bacteriophages (viruses). The network defined by which virus kill which bacteria strongly influences the overall persistence of the marine community [1, 2, 3].

The dynamics of virus and immune response within a host can also be viewed as a complex ecological system. The immune response predates on the pathogen, and distinct viral strains compete for a target cell population, while immune response populations compete for the virus since their proliferation occurs upon pathogen recognition. For example, during HIV infection an extensive family of CTL immune cells recognize specific viral proteins presented on the surface of infected cells to effectively mediate their killing. However HIV can rapidly evolve resistance to CTL attack at different epitopes. The ensuing battle creates a dynamic network of interacting viral strains and immune response variants with variable levels of (strain) reactivity [4].

It is unsurprising that similar mathematical models can be used to better understand the role of the predation network structure on the ultimate bio-diversity of the community in each of these cases. The models we consider consist of systems of Lotka-Volterra-like ordinary differential equations. The talk will describe recent joint work with colleagues Dan Korytowski and Cameron Browne on the dynamics of such models.

References

- [1] Korytowski, D. & Smith, H.L. (2015). *How Nested and Monogamous Infection Networks in Host-Phage Communities Come to be*, *Theoretical Ecology*, 8 (1), 111–120. <https://doi.org/10.1007/s12080-014-0236-6>

*11th Conference on Dynamical Systems Applied
to Biology and Natural Sciences DSABNS 2020
Trento, Italy, February 4-7, 2020*

- [2] Korytowski, D. & Smith, H.L. (2017). *Permanence and Stability of a Kill the Winner Model in Marine Ecology*, Bulletin of Math. Biology, 79 (5),995-1004. <https://doi:10.1007/s11538-017-0265-6>
- [3] Korytowski, D. & Smith, H.L. (2017). *Persistence in Phage-Bacteria Communities with Nested and One-to-One Infection Networks*, with Dan Korytowski, Discrete and Continuous Dynamical Systems-B. 22(3), 859–875. <https://doi:10.3934/dcdsb.2017043>
- [4] Browne, C. & Smith H.L. (2018). *Dynamics of Virus and Immune Response in Multi-Epitope Network*, J. Math. Biol. 77(6-7), 1833–1870. <https://doi.org/10.1007/s00285-018-1224-z>