

Mathematical Methods and Models in Biosciences

June 15–20, 2025, Sofia, Bulgaria

<https://biomath.math.bas.bg/biomath/index.php/bmcs>

Exploring the stability of a generalised Lotka-Volterra ecological model

Richard Pretorius, Andriamihaja Ramanantoanina, Jacek Banasiak

Department of Mathematics and Applied Mathematics,
University of Pretoria, South Africa
u20516020@tuks.co.za
a.ramanantoanina@up.ac.za
jacek.banasiak@up.ac.za

Lotka-Volterra models have long been used as a mathematical tool to model relatively simple biotic interactions, especially where interspecific competition occurs. As such, Lotka-Volterra models have been utilised extensively in the study of microbial environments, where the assumptions of the model are more easily shown to be met [1]. However, recent evidence points to the viability of Lotka-Volterra models as qualitative predictors of certain ecosystem patterns in more varied, larger scale ecosystems [2]. Even so, traditional Lotka-Volterra models remain unable to model more complex interactions [3].

In this talk, a generalized Lotka-Volterra model with many species is considered. In contrast with the standard model (as formulated in the 30's) this model does not restrict population growth in the absence of other species to exponential or logistic forms. Various functional responses are also admitted by this model. As such, this model succeeds in capturing the dynamics of systems that would otherwise not be of a Lotka-Volterra type.

This talk develops Lyapunov functions for this generalised Lotka-Volterra model. These Lyapunov functions are used to determine stability criteria in terms of the inter-specific interactions within the community. Finally, explorations of results for various community structures are conducted through numerical simulations.

Keywords: Lotka-Volterra models, Lyapunov functions, stability

MSC2020: 92-10, 92D25, 92D40

References

- [1] S. Dedrick, V. Warrior, K. P. Lemon, B. Momeni, When does a Lotka-Volterra model represent microbial interactions? Insights from *in vitro* nasal bacterial communities, *mSystems*, 8:e00757-22, 2023.

- [2] B. Shorrocks, Competition, Interspecific, In: *Encyclopedia of Biodiversity*, Third Edition, 5:22–40, 2024.
- [3] B. Momeni, L. Xie, W. Shou, Lotka-Volterra pairwise modeling fails to capture diverse pairwise microbial interactions, *eLife*, 6:e25051, 2017.