

Qualitative behavior analysis and identification issues of generalized Lotka-Volterra models of microbial communities

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Abstract:

Generalized Lotka-Volterra (gLV) models are mathematical Ordinary Differential Equation systems widely used to describe the dynamics of interacting populations, including microbial communities. By capturing species' growth rates and their interactions, it serves as a versatile tool for studying species coexistence and the stability of microbial ecosystems. Parameter estimation in gLV models typically involves fitting the model to temporal data using methods such as least squares, maximum likelihood, or Bayesian inference to determine the parameters that best describe the observed dynamics. Given the complexity of microbial systems, this study investigates the gLV stationary solutions compatible with the available experimental data and assesses the stability of the coexistence equilibrium, offering a faster alternative to computationally intensive numerical techniques. The scalability of this framework makes it particularly well-suited for larger and more complex systems, enabling rapid stability assessments that are critical for high-dimensional ecological models.

The proposed approach leverages stationary data from *in vitro* reconstructed probiotic consortia to perform parameter estimation via least-squares method, utilizing the Moore-Penrose pseudoinverse. The analysis at equilibrium considers constraints arising from subsystems and demonstrates that, as the system grows larger, their number increases faster than the number of model parameters, with additional species and measurements introducing new constraints. This characteristic provides guidelines for determining the necessary number of subsystem measurements to ensure the system identifiability. The estimated parameters are subsequently used to evaluate the stability properties of equilibrium points based on well-established stability conditions. The insights gained from this method pave the way for analyzing larger and more complex ecological systems, where rapid and reliable stability evaluations are critical, as well as for faster assessments of bacterial abundances and the stability of delicate ecosystems' equilibria under perturbations.