

Dynamically-Consistent Finite-difference Discretization for Population Biology Models

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The use of standard numerical integrators, such as the forward Euler and Runge-Kutta family of explicit finite-difference methods, to solve continuous-time models arising from the mathematical modeling of phenomena in the natural and engineering sciences often leads to scheme-dependent instabilities, convergence to spurious solutions and/or contrived chaos. The first half of this talk will address the problem of designing finite-difference methods that preserve the essential qualitative features (such as positivity and boundedness of solutions, as well as capturing the correct bifurcation types) of a wide variety of population biology models. The second half of the talk will focus on modeling and assessing the impact of climate change on the distribution of malaria vector and disease.