Abstract

Dynamical systems described by deterministic differential equations represent idealized situations where random implications are ignored. In the context of biomathematical modeling, the introduction of random noise must be distinguished between environmental (or extrinsic) noise and demographic (or intrinsic) noise. In this last context it is assumed that the variation over time is due to demographic variation of two or more interacting populations, and not to fluctuations in the environment. The modeling and simulation of demographic noise as a stochastic process affecting single units of the populations involved in the model are well known in the literature and they result in discrete stochastic systems. When the population sizes are large, these discrete stochastic processes converge to continuous stochastic processes, giving rise to stochastic differential equations. If noise is ignored, these stochastic differential equations turn to ordinary differential equations. The inverse process, i.e., inferring the effects of demographic noise on a natural system described by a set of ordinary differential equations, is an issue addressed in a recent paper by Carletti M, Banerjee M, A backward technique for demographic noise in biological ordinary differential equation models, Mathematics 7:1204, 2019. In this paper we show an example of how the technique to model and simulate demographic noise going backward from a deterministic continuous differential system to its underlying discrete stochastic process can provide a discrepancy effect, modifying the dynamics of the deterministic model.

This article is part of the “Special Issue on Advances in Mathematical Ecology and Epidemiology at MPDEE 2022”, edited by Ezio Venturino (Université de Franche-Comté, France) and Sergei Petrovskii (University of Leicester, UK).

Keywords:

Biomathematical ModelingDemographic NoiseChemical Kinetics