Population dynamics through hierarchically embedded Markov chains

Pacheco, J.[1]

[1] CBMA, Universidade do Minho, ATP-Group, Portugal

jorgem.pacheco@gmail.com

The study of dynamical phenomena in finite populations often requires the consideration of population Markov processes of significant mathematical and/or computational complexity, which rapidly becomes prohibitive with increasing population size or increasing number of individual configuration states. Ubiquitous examples are found in Darwinian evolution and social dynamics, whose state space is often sizeable. Here, I will discuss a framework that allows one to define a hierarchy of approximations to the stationary distribution of general systems amenable to be described as discrete Markov processes with time invariant transition probabilities and (possibly) a large number of states. The framework allows the efficient study of the dynamics of social and biological communities in the presence of stochastic effects — such as mutations in evolutionary dynamics and random exploration of choices in social systems — including situations when the dynamics encompasses the existence of stable polymorphic configurations, thus overcoming limitations of existing methods. The general scope of the formalism makes it relevant and widely applicable to a variety of interdisciplinary problems.