

Abstract

POPULATION DYNAMICS IN THE LOTKA-VOLTERRA MODEL BY DIRECT SIMULATION

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The Lotka-Volterra (L-V) equations [1] are a pair of coupled non-linear equations, which purport to represent perhaps the simplest model of predator-prey interactions. In this work we apply Monte Carlo (MC) techniques to generate sample populations of each species and model their interaction by MC solutions of the L-V equations. The direct simulation mimics the unpredictable nature of the interaction between individuals in contrast to the differential equations which describe averages over the entire population.

To further quantify aspects of individual interactions, we introduce a genetic algorithm, by means of a two-component vector representing a simple chromosome with two genes for each species. Positive mutational effects in the chromosome of any predator lead to a better hunter whilst such mutational effects in the prey chromosome lead to better survivors. From this model system we are able to recover the characteristic behaviour of the L-V equations as well as observe the onset of self-organised criticality (SOC) [2]. The angle between the genetic vectors for any two animals (prey and predator) is considered to be a measure of the relative fitness of these two animals.