

MONTE CARLO STUDIES IN ECOLOGY AND EPIDEMIOLOGY

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1. Introduction

“Monte Carlo” investigations, that is (at least in the present context), the simulation of real phenomena, or idealized models of them, involving a random or probabilistic element in their structure, by the deliberate use of “random” (or pseudorandom) numbers, have already played an important role in many applications of stochastic models and processes, both by way of background material in understanding qualitatively some of the properties of such models, and more quantitatively, in the study of particular problems that are not amenable to complete mathematical solution. The advent of electronic computers has especially facilitated the extension of such investigations to include more realistic conditions not easily incorporated into tractable mathematical models; and in physics, for example, a growing use of Monte Carlo studies is evident. However, it is in biology that some of the most important developments are being realized, partly because of the often complex situations to be studied, but also because no genuine progress can be made until biologists themselves accept some of the consequences and predictions to be deduced from theoretical models. Such acceptance is often more convincing to them if the properties of the models are demonstrated numerically in typical cases than if presented in abstract mathematical terms; often, as already noted, the latter results are unavailable anyway.

In the study of biological populations changing over time, two types of process, one involving discrete units of time (or generations), and the other continuous time, are conveniently separated. In the first type, the probability $f(\mathbf{n}_r)$ of the vector number \mathbf{n} (a scalar if only one type of individual is involved) at time r is given in the model in terms of the number \mathbf{n}_{r-1} at time $r - 1$; the model is for simplicity assumed Markovian in \mathbf{n}_r , though not necessarily homogeneous as regards the time, and the Monte Carlo study consists of generating one or more random series of the vector \mathbf{n} as the time r increases. In the second type, the process (again assumed Markovian) is usually specified by infinitesimal transition probabilities $g(\mathbf{n}_t, \mathbf{m}) dt$ for \mathbf{n}_t changing to $\mathbf{m} (\neq \mathbf{n}_t)$. While this process is sometimes conveniently approximated by an appropriate process in discrete time steps δt , a precise realization (first suggested, I believe, by D. G. Kendall [14])