Inequalities in Statistics and Probability
IMS Lecture Notes–Monograph Series Vol. 5 (1984), 41–53

EIGENVALUE INEQUALITIES FOR RANDOM EVOLUTIONS: ORIGINS AND OPEN PROBLEMS

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This paper has three parts. The first give an expository review of a model from stochastic population biology. This model leads to eigenvalue inequalities for random evolutions. The second gives a proof by Charles M. Newman of one of these inequalities. The third gives conjectures and questions. Some of these have been previously stated; most are new.

1. Introduction. The growth of a population in a random environment can be modeled in a simple way by a stochastic process called a random evolution. Bounds on the growth rate of a population in a random environment can be expressed in terms of certain eigenvalues. The first purpose of this paper is to describe informally how a population can be modelled by a random evolution and why eigenvalue inequalities arise naturally (section 2). The main inequalities to be discussed have been proved by Cohen, Friedland, Kato and Kelly (1982). I shall henceforth refer to this paper as CFKK. The second purpose of this paper is to give a proof (section 3) of one of these inequalities that was discovered by Charles M. Newman of the University of Arizona during my talk at the symposium on Inequalities in Statistics and Probability. The third purpose of this paper is to state conjectures, open problems and questions concerning further inequalities (section 4).

2. Populations in Random Environments and Eigenvalue Inequalities. Suppose one has a vat of bacteria sitting in a laboratory. Suppose the number of bacteria is large enough so that there is no discomfort in taking $N(t)$, the number of bacteria at (real scalar) time t, to be a real variable rather than strictly integer valued. Suppose also that the number of bacteria is small compared to the number of bacteria that the nutrient medium in the vat can support, or that the medium is continuously refreshed. If the division cycles of the bacteria are unsynchronized, then the simplest model of the population is to suppose that the number of fissions that occur per unit time is directly proportional to the number of bacteria in the vat. Thus, for some real constant b,

$$dN(t)/dt = bN(t) \text{ for } t \geqslant 0, N(0) = N_0.$$

It is well known, even among biologists, that the solution of this equation is

$$N(t) = N_0 e^{bt}.$$

In this deterministic model, the long-run growth rate b may be computed from an observed trajectory $N(t)$ of the size of the population from the formula

$$\lim_{t\to\infty} t^{-1} \log N(t) = b.$$

The left side of this equation is referred to as a Liapunov characteristic number of the process.

AMS 1980 subject classifications: Primary 60H25, 15A42; Secondary 60J57, 92A15.

Key words and phrases. Random environment. Liapunov characteristic number. Multiplicative Markov functional. Feynman-Kac formula. Stochastic population biology. Discrete skeleton. Reversible Markov chain. Additive Markov functional.