Mathematical Biosciences Institute Lecture Series 1.1
Stochastics in Biological Systems

Richard Durrett

Branching Process Models of Cancer

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Mathematical Biosciences Institute Lecture Series
Volume 1: Stochastics in Biological Systems

Stochasticity is fundamental to biological systems. In some situations the system can be treated as a large number of similar agents interacting in a homogeneously mixing environment, and so the dynamics are well-captured by deterministic ordinary differential equations. However, in many situations, the system can be driven by a small number of agents or strongly influenced by an environment fluctuating in space and time. For example, fluctuations are critical in the early stages of an epidemic; a small number of molecules may determine the direction of cellular processes; changing climate may alter the balance among competing populations. Spatial models may be required when agents are distributed in space and interactions between agents are local. Systems can evolve to become more robust or co-evolve in response to competitive or host-pathogen interactions. Consequently, models must allow agents to change and interact in complex ways. Stochasticity increases the complexity of models in some ways, but may also simplify and smooth results in other ways.

Volume 1 provides a series of lectures by internationally well-known authors based on the year on Stochastics in biological systems which took place at the MBI in 2011–2012.

Michael Reed, Richard Durrett
Editors

Mathematical Biosciences Institute Lecture Series
Volume 1: Stochastics in Biological Systems

Model Formulation and Simulation of Stochastic Population and Epidemic Models
Linda S. Allen

Stochastic Analysis of Biochemical Systems
David Anderson; Thomas G. Kurtz

Branching Process Models of Cancer
Richard Durrett

Stochastic Neuron Modeling
Pricilla Greenwood; Lawrence Ward

The Mathematics of Intracellular Transport
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Some Stochastic Population Models
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Preface

In this chapter, we will use multitype branching processes with mutation to model cancer. With cancer progression, resistance to therapy, and metastastis in mind, we will investigate τ_k, the time of the first type k mutation, and σ_k, the time of the first type k mutation that founds a family line that does not die out, as well as the growth of the number of type k cells. The last three sections apply these results to metastasis, ovarian cancer, and tumor heterogeneity. Even though martingales and stable laws are mentioned, these notes should be accessible to a student who is familiar with Poisson processes and continuous time Markov chains.

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