

## **Mathematical Biosciences Institute Lecture Series**

The Mathematical Biosciences Institute (MBI) fosters innovation in the application of mathematical, statistical and computational methods in the resolution of significant problems in the biosciences, and encourages the development of new areas in the mathematical sciences motivated by important questions in the biosciences. To accomplish this mission, MBI holds many week-long research workshops each year, trains postdoctoral fellows, and sponsors a variety of educational programs.

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Marty Golubitsky, Michael Reed  
Mathematical Biosciences institute

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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

*Scott McKinley; Peter Kramer*

Some Stochastic Population Models

*Sylvie Méléard; Vincent Bansaye*

Population Models with Interaction

*Etienne Pardoux*

Correlations from Coupled Enzymatic Processing

*Ruth Williams*



Richard Durrett

# Branching Process Models of Cancer

 Springer

**mbi**   
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ISSN 2364-2297                      ISSN 2364-2300 (electronic)  
Mathematical Biosciences Institute Lecture series  
ISBN 978-3-319-16064-1              ISBN 978-3-319-16065-8 (eBook)  
DOI 10.1007/978-3-319-16065-8

Library of Congress Control Number: 2015933144

Mathematics Subject Classification (2010): 60F05, 60G44, 60G52, 60J80, 92C50, 92D25

Springer Cham Heidelberg New York Dordrecht London  
© Springer International Publishing Switzerland 2015

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Printed on acid-free paper

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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 metastasis in mind, we will investigate  $\tau_k$ , the time of the first type  $k$  mutation, and  $\sigma_k$ , 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.

I would like to thank Jasmine Foo, Kevin Leder, and Marc Ryser who have collaborated with me on this work. My work and that of Marc Ryser has been partially supported by NIH grant R01-GM096190.

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