Mathematical Biosciences Institute Lecture Series 1.4
Stochastics in Biological Systems

Vincent Bansaye · Sylvie Méléard

Stochastic Models for Structured Populations

Scaling Limits and Long Time Behavior

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Marty Golubitsky, Michael Reed
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Mathematical Biosciences Institute Lecture Series
Volume 1: Stochastics in Biological Systems

Stochasticity is fundamental to biological systems. While in many situations the system can be viewed as a large number of similar agents interacting in a homogeneously mixing environment so the dynamics are captured well by ordinary differential equations or other deterministic models. In many more situations, the system can be driven by a small number of agents or strongly influenced by an environment fluctuating in space or time. Stochastic fluctuations are critical in the initial 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 form a network. Systems 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 smooth and simplify in others.

Volume 1 provides a series of lectures by well-known international researchers 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

Stochastic Population and Epidemic Models
Linda S. Allen

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

Stochastic Models for Structured Populations
Vincent Bansaye; Sylvie Méléard

Branching Process Models of Cancer
Richard Durrett

Stochastic Neuron Modeling
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The Mathematics of Intracellular Transport
Scott McKinley; Peter Kramer

Population Models with Interaction
Etienne Pardoux

Correlations from Coupled Enzymatic Processing
Ruth Williams

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ISSN 2364-2297 ISSN 2364-2300 (electronic)
Mathematical Biosciences Institute Lecture series
ISBN 978-3-319-21710-9 ISBN 978-3-319-21711-6 (eBook)
DOI 10.1007/978-3-319-21711-6

Library of Congress Control Number: 2015945107

Mathematics Subject Classification (2010): 60J80, 60J75, 60G57, 60H10, 92D25, 92D15

Springer Cham Heidelberg New York Dordrecht London

Printed on acid-free paper

Springer International Publishing AG Switzerland is part of Springer Science+Business Media (www.springer.com)

To
Marius, Margot, Martin

Contents

Part II Structured Populations and Measure-valued Stochastic Differential Equations

Chapter 1
Introduction

This course concerns the stochastic modeling of population dynamics. In the first part, we focus on monotype populations described by one-dimensional stochastic differential equations with jumps. We consider their scaling limits for large populations and study the long time behavior of the limiting processes. It is achieved, thanks to martingale properties, Poisson measure representations, and stochastic calculus. These tools and results will be used and extended to measure-valued processes in the second part. The latter is dedicated to structured populations, where individuals are characterized by a trait belonging to a continuum.

In the first section, we define birth and death processes with rates depending on the state of the population and recall some long time properties based on recursion equations. A pathwise representation of the processes using Poisson point measures is introduced, from which we deduce some martingale properties. We represent the carrying capacity of the underlying environment through a scaling parameter $K \in \mathbb{N}$ and state our results in the limit of large K. Depending on the demographic rates, the population size renormalized by K is approximated either by the solution of an ordinary differential equation or by the solution of a stochastic differential equation. The proofs are based on martingale properties and tightness-uniqueness arguments. When the per individual death rate is an affine function of the population size, in the limit we obtain either a so-called logistic equation or a logistic Feller diffusion process. The long time behavior of these limiting dynamics is studied. Assuming a constant per capita death rate leads to a Feller diffusion which satisfies the branching property: two disjoint subpopulations evolve independently. In that case, specific tools using Laplace transforms can be used. We extend this class of processes by adding jumps, which may be due either to demographic stochasticity or to environmental stochasticity. We consider them separately and we characterize their finite dimensional laws and long time behavior using the branching property, the generator and martingale properties. First, we focus on Continuous State Branching Processes, which arise as scaling limits of branching processes when the individuals may have a very large number of offspring. This gives rise to a jump term whose

V. Bansaye, S. Méléard, *Stochastic Models for Structured Populations*, Mathematical Biosciences Institute Lecture Series 1.4, DOI 10.1007/978-3-319-21711-6_1