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Preface

This is the fourth volume in the series “Tutorials in Mathematical Biosciences.” These lectures are based on material which was presented in tutorials or developed by visitors and postdoctoral fellows of the Mathematical Biosciences Institute (MBI), at The Ohio State University. The aim of this series is to introduce graduate students and researchers with just a little background in either mathematics or biology to mathematical modeling of biological processes. The first volume was devoted to mathematical neuroscience, which was the focus of the MBI program 2002–2003. The second volume dealt with mathematical modeling of calcium dynamics in signal transduction, the focus of the MBI program in the winter of 2004. The third volume dealt with topics of cell cycle, tumor growth, and cancer therapy; these topics featured in several workshops held at the MBI in the fall of 2003. The present volume deals with a variety of topics of evolution and ecology, which were considered in the MBI during the year 2005–2006. These topics include phylogenetics; evolution of genes through migration–selection; ecological modeling; and evolution of dispersal and population dynamics. Documentation of the 2005–2006 activities, including streaming videos of the workshops, can be found on the Web site: <http://mbi.osu.edu>.

Phylogenetics is the study of the evolutionary relations of genes and organisms. Phylogenetic trees are represented by graphs in which the leaves represent observed biological entities. In constructing such graphs, one tries to trace the evolution of species, traits, or diseases. The first two chapters of this volume deal with phylogenetics. Chapter 1 is a general survey on estimation of phylogenetic trees with emphasis on likelihood methods. Chapter 2 is concerned with computational methods of very large trees, exploring other optimality methods, with application to the study of the evolution of SARS and influenza.

The next three chapters deal with population genetics and population dynamics. Chapter 3 introduces reaction–diffusion equations as a mathematical framework to study ecological models. It then addresses the following ecological questions: what is the minimal patch size necessary to support a

population?; when do biological invasions occur?; and what spatial patterns can form?

Chapter 4 focuses on evolution and genes. The genetic composition of a population is described by genotypic or allelic frequencies, using either deterministic models or stochastic models. The models presented here are both discrete and continuous. The questions discussed include the loss, or the maintenance, of a specified allele, and the stability of completely polymorphic equilibria.

The final chapter is concerned with the effects of dispersal and spatial heterogeneity on population dynamics, via reaction–advection–diffusion models. Issues regarding how advection along resource gradients affect the extinction of species or how invasion of rare species may take place are considered.

It is not uncommon to see the same biological processes benefit by using different mathematical and statistical approaches. This volume is a good example: Although the mathematical and statistical tools developed or reviewed here are quite varied, the biological themes have a common thread as they all deal with the evolution of species in an evolving ecological system.

I express my appreciation and thanks to Daniel Janies, Diego Pol, Laura Salter-Kubatko, Thomas Nagylaki, Yuan Lou, and Chris Cosner for their marvelous contributions. I hope this volume will serve as a useful introduction to those who want to learn about important and exciting problems that arise in evolution and ecology.

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