

Preface

Recently an intensive development of mathematical methods in biological sciences and in particular in genetics is observed. From one point of view, one needs new statistical methods and algorithms to classify and interpret a huge collection of data. On the other hand, there is a need for analytical mathematical methods helping to understand physical and biochemical processes on the molecular level [1].

Modern genetics uses a wide spectrum of mathematical models which describe gene distributions in evolving populations, changes in a single genome or biochemical processes regulated by genes, *cf.* [2, 3] and references therein. Although genetics is concerned with small biological objects, in some cases methods of population dynamics can be successfully applied to study genetic problems [4]. Most models are formulated on the macroscopic level and the possibility of modeling on the level of basic objects involved in processes is still open [5].

This volume contains review papers based on two short courses given by a genetist Stanisław Cebrat and a mathematician Ryszard Rudnicki and two lectures given by physicists, Mirosław Dudek and Adam Lipowski. The courses and lectures were presented during the school “*From Genetics to Mathematics*” held in Zbąszyń, Poland, 18–20 October 2007 (see [6]), organized in the framework of the Marie Curie Research Training Network Research MRTN-CT-2004-503661 “*Modeling, Mathematical Methods and Computer Simulations of Tumor Growth and Therapy*”. The goal of the school was to gather genetists, mathematicians, and physicists to discuss recent advances in mathematical modeling of biological problems in genetics and discuss possibilities of future collaborations. In particular, the school was dealing with issues and problems in genetics which could be addressed by mathematics and theoretical physics. All talks were of expository nature and had a strong pedagogical character and such are papers included in this volume.

The first three chapters are provided by Stanisław Cebrat and his

coworkers. They present an extensive introduction to genetics and discussed their own ideas and models of evolutionary genetics. In particular, evolution of coding sequences, evolution of whole genomes, the noisy Penna model, sympatric speciation and recombination effects are discussed. These dynamical models, like the Penna model, were investigated so far only by numerical simulations. Mathematical analysis of such models may provide some further intuitions and new results.

The aim of Chap. 4, written by Ryszard Rudnicki, is to give a survey of mathematical models and methods of population dynamics in application to genetics. Both discrete and continuous in time and structure models are considered. The author provides the historical background of mathematical modeling of population dynamics, including the classical Lotka–Volterra model and the Kermack–McKendrick model of epidemics. He discusses the Penna model, the model of the evolution of paralog families in a genome, cell-cycle models, and a model of stochastic gene expression. This chapter shows that fundamental models in genetics lead to deep mathematical problems in dynamical systems, partial differential equations, and the theory of Markov operators.

Lotka–Volterra–type models are discussed from different points of view in Chaps. 5 and 6.

Mirosław Dudek and Tadeusz Nadzieja analyze the growth of age-structured population with genetics. They discuss time–delay growth equations with age structure, Lotka–Volterra models with genetics and present computer simulations of the Penna model.

Adam Lipowski and Danuta Lipowska introduce spatial Lotka–Volterra models. To investigate long–run behavior of finite systems of many interacting objects, one has to take into account stochastic fluctuations. They discuss two–species and multi–species models of ecosystems with a particular emphasis on the problem of extinctions. They introduce also a new model of the naming game of bio–linguistics.

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