

Biological Evolution and Statistical Physics

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Preface

People have always asked what distinguishes the living from the inanimate world and what unifies the two. The fields of biology and physics have a long history of exchange. Milestones at the molecular level were the discoveries of the structure of DNA, RNA, and proteins.

It is not by coincidence that this exchange has intensified in recent years. Laboratory experiments reach down to the level of single molecules. Moreover, there is now a vast amount of genomic information, which is still growing exponentially due to the various sequencing projects. Biologists increasingly feel the need for theoretical models to interpret these data in a quantitative way. At the same time, theoretical physics has made significant progress in areas likely to be relevant for the understanding of biological systems. Some important examples are cooperative phenomena, statistics far from thermodynamic equilibrium, systems with quenched disorder, and soft matter.

Some forms of biological matter have indeed become established areas of research within physics, such as biomembranes, heteropolymers, molecular motors, microtubules, neural systems etc. This volume is focused on a different aspect of the living world that can be called *biological information*, its coding, reproduction, and evolution. Biological information is translated into structures and patterns over an enormous range of scales, from single biomolecules to species networks coupled over entire continents.

The *statistical theory* of biological information lives not only in three-dimensional space. It involves various abstract spaces in which this information is encoded and evolves, such as nucleotide sequences, gene networks, or topologies of the ‘tree of life’. The articles collected highlight a few directions of research that may become important parts of this emerging field.

The first part of the book, *Molecular Information and Evolution*, starts with two articles on sequence similarity analysis, a central theme in bioinformatics which has surprisingly deep connections to statistical physics. The genetic code, RNA, and proteins are three examples of the intricate interplay of sequence, structure, and function in evolution.

Phylogeny is the inference of evolutionary relationships from genomic or phenotypic data. The articles in the second part of the book move beyond the traditional goal of reconstructing the unique historical tree of life and emphasize statistical aspects of a tree ensemble. Examples are biological properties of an

ancestor inferred from phylogeny, the correlation between trees in host–parasite systems, the evolution of traits along trees, and the statistics of tree topologies.

The *Evolution of Populations and Species* results from an interplay of randomness and Darwinian selection. The topics covered in part III include quasispecies and fitness landscapes, evolutionary optimization and the age structure in a population. Fitness values and populations may have spatial structure as well, as shown by the articles on pattern formation and morphogenesis and on spatio-temporal modes of species formation. These examples have an interesting connection to field theories of nonequilibrium systems.

Large-Scale Evolution, the final part of the book, is governed by the ecological interactions between many species organized in a food web or species network. This dynamics, whose temporal scales are measured in millions of years, is described by ‘effective models’ that neglect many details of the lower levels of molecules, individuals, and populations. Which are the important evolutionary forces at the largest scales remains a matter of active debate. In different systems and at different scales of space and time, various articles ask very similar questions on evolution, although there is no common language or agenda of research yet. It is the goal of theory to develop unifying concepts that relate different pictures of evolution in a quantitative way and bridge the gaps between scales. In some of the research areas mentioned, concepts and methods from statistical physics have already led to significant contributions, in others they are likely to do so in the future. The offspring of this new encounter between the two disciplines may not be physics or biology in the traditional sense. What matters, however, is if it is interesting science.

Most of the contributions in this book are based on invited talks given at the workshop *Biological Evolution and Statistical Physics* last year in Dresden. We are grateful to the Max Planck Institute for the Physics of Complex Systems for making this workshop possible and creating a unique environment of scientific exchange. Particular thanks are due to Peter Fulde, Sergej Flach, and Katrin Lantsch. We are also indebted to Reinhard Lipowsky and the Max Planck Institute for Colloids and Interfaces for encouragement and support to produce this volume. Martin Brinkmann is gratefully acknowledged for his help in the editorial process, and Susann Valleriani for designing the conference poster.

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