

## Preface

In recent years many new data types and settings have become available through new large-scale and high-throughput technologies, but also through initiatives that seek to collect biological and epidemiological data in society at large. These data types provide new perspectives on the organisation, complexity, functionality and dynamics of biological entities and potentially offer a deeper insight into what constitutes a cell or organism, and how cells, organisms and species are related through common origin, evolution and development.

However, the new data types are by themselves exceedingly complex and barely understandable without further processing or analysis. Many of the new data types, such as transcriptomic, metabolomic and protein interaction data, have provided means to define corresponding new ‘omes’ – for example, the transcriptome, metabolome and interactome – that not only reflect the data type and technology, but also structure the functionality and organisation of the organism conceptually. In relation to this, mathematical theory, in particular network theory, has been essential and proven an indispensable tool for understanding and interpreting data.

A link in a network or graph represents an interaction between two entities; the interaction could represent direct physical contact, e.g. the binding of two molecules to each other, that the presence of one molecule stimulates the presence of another molecule, or a path through which a disease can spread. We are becoming accustomed to talking about ‘biological networks’ or ‘biological network data’ and by this we mean the relevant biological data structured by a network interpretation. The biological network data is not the ‘raw’ biological data, but the data imposed onto a network.

Apart from their apparent usability for visualisation of highly interdependent data, networks allow stringent mathematical and statistical analysis. Network or graph theory goes back to Leonard Euler with his famous example of the seven bridges of Königsberg and has since proven its usefulness in numerous connections and a diverse set of different academic disciplines. A large body of graph theory exists and evolutionary, statistical and computational methods have over the last 50 years been developed to facilitate analysis of network data. Some of these developments have already been incorporated into analysis of biological network data, while at the same time new methods have been developed and applied to data.

These methods and their application to biological questions and issues are the

subject of this book. It reviews and explores statistical, mathematical and evolutionary theory and tools for understanding biological networks. It is divided into comprehensive and self-contained chapters that each focuses on an important biological network type, explains concepts and theory and illustrates how concepts and theory can be used to obtain insight into biologically relevant processes and questions. Keywords are complexity, organisation and dynamics of networks – how they come about, can be detected and measured, and how they are influenced by network evolution and functionality. The book has chapters on metabolic, transcriptomic, protein interaction and epidemiological networks, as well as chapters that deal with theoretical and conceptual material.

The authors in this volume have all contributed substantially to the discipline of network biology and we are grateful for their contributions and their patience with the editors. This is now a field which is beginning to reach maturity, and which has shaped the gestation of this volume. We hope that new investigators to this field will find the chapters in this book a useful introduction to the quantitative and evolutionary biological analysis of networks.