BOOK REVIEWS


Evolutionary relationships among organisms are illustrated by means of a phylogenetic tree. Although several evolutionary processes such as horizontal gene transfer and recombination do not fit in complete agreement with the phylogenetic tree hypothesis, they can be treated in a biologically meaningful way by using phylogenetic or evolutionary networks.

The book under review is the most comprehensive one on the subject of computational phylogenetic networks. Each chapter describes the related aspects of phylogenetic networks in a connected manner. The text deals with phylogenetic networks through independent but connected sub-topics such as models of evolution concerned with molecular evolution, and splits and clusters concerned with statistical techniques. This is the main strength of the book and would help a novice easily understand the subject.

Another important aspect of this book is the treatment of mathematical and computational models and methods for phylogenetic networks. One of the chapters (chapter 4) describes myriad phylogenetic networks and throws light on the current state of affairs in these networks. Also focused in some chapters are the various mathematical and statistical techniques and their computable relevance to phylogenetic networks. Several graph-theoretic algorithms are also described.

An interesting feature is the inclusion of some old techniques in phylogenetic...
networks with recent updates and upgraded treatments. Elaboration of various theories such as T-theory and simulation as neighbour networks, T-rex and split networks is one of the prominent aspects of the book and will certainly be enjoyed by the readers. Insertion of many illustrations and numerical examples is a key facet of this book and will help the scientific community understand the contents.

The meticulous inclusion of gold standard evolutionary and phylogenetic methods ranging from neighbour-joining, minimum evolution through UPGMA, maximum parsimony, Bayesian analysis to maximum likelihood is to be commended. This serves as a revision for the readers and also helps to compare these methods with the recent and upcoming methods of phylogenetic network reconstruction.

Another useful point about the book is its content variability, which indirectly helps readers from various backgrounds; it will help biologists, bioinformaticians, computer scientists and evolutionary researchers to deal with this emerging but established area of molecular evolution. It will be of explicit interest to the biologists and bioinformaticians who need new and advanced methods for the development and analysis of phylogenetic networks. On the other hand, it will also give an insight into the area of molecular evolution to computer scientists, mathematicians and statisticians.

In summary, the book under review is enjoyable and will benefit a majority of the scientific community in the concerned area. This book, with three distinct but related segments and fourteen comprehensive chapters, is an asset to the area of computational evolutionary biology.

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