Molecular evolution — statistical approach

Author: Perktaş, Utku

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Book Review

Yang Z. 2014: Molecular evolution – statistical approach. *Oxford University Press, xv + 492 pp. ISBN: 978-0-19-960261-2 (pbk.).*

In "Molecular evolution – a statistical approach", Ziheng Yang makes a very good and thorough review of the statistical methods and computational algorithms within the context of molecular evolution, phylogenetics, and phylogeography. Phylogenetic and phylogeographic research has been a sharp increase due to the recent methodological advances in molecular biology and bioinformatics (see Scott Edwards et al. in this issue). However, it is imperative that statistical inferences on phylogenies are done carefully in any phylogenetic and/or phylogeographic research (Anisimova et al. 2013). Hence, the author presents a good and up-to-date example of the contributions to understand the logical basis of robust phylogenetic and phylogeographic analyses.

The book has 12 chapters; the first two deal with models of nucleotide, amino acid, and codon substitution models, which are important for maximum likelihood and Bayesian methods of reconstruction. Basic definitions of substitution models are made clear in these two chapters. Chapter 3 is a good start to understand the tree-thinking logic in evolutionary biology, from the general terminology of phylogeny and phylogenetic trees, to the clear and concise discussions on the difference between gene and species trees. In this chapter I also find the first part of a discussion on phylogenetic reconstruction methods; this is a very pertinent discussion as different phylogenetic software use different tree reconstruction methods (e.g. Maximum Parsimony, Maximum Likelihood, Bayesian methods, distance based methods), which are usually perceived as complex methodologies. The discussion is continued in subsequent chapters, which makes this book very useful for most of evolutionary biologists.

Chapter 4 deals with Maximum Likelihood Methods, and focuses on how to calculate the probability of a set of states observed of the leaves of a tree. In chapter 5, Yang gives information on statistical performance evaluation of classical phylogenetic methods, such as consistency, efficiency, and robustness.

Bayesian phylogenetic inference has become widely used lately. In this book, Bayesian theory is discussed from chapter 6 to chapter 9. Methods of computation and Bayesian methods for phylogenetic reconstruction are discussed in chapters 7 and 8 respectively. These chapters have up-to-date information and very strong and comprehensive mathematical background especially for researchers in the field of phylogenetics. After the introduction of gene and species trees in chapter 3, Yang concentrates on coalescent theory and species trees in chapter 9. This is a solid and again a very good and concise chapter about coalescent theory. Chapter 10 and 11 deal with neutral theory and molecular clocks, whereas the last chapter, chapter 12, is about recent advancements of molecular evolution and phylogenetics. Computational simulations are widely used in phylogenetics and in my opinion, Yang should have concentrated more densely on this matter in this last chapter of the book.

When I read this book, I found it to be a very solid contribution in the field of phylogenetics. Each chapter has a concise overview, and has very strong mathematical background, which makes this book very interesting for the experts in molecular evolution, phylogenetics, and phylogeography. Like Felsenstein's "Inferring phylogenies" and Baum and Smith's "Tree thinking – an introduction to phylogenetic biology", Ziheng Yang's text is a valuable work of reference for the evolutionary biologist. For me, it is a very informative read and I really look forward to making use of it.

Literature

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Utku Perktaş