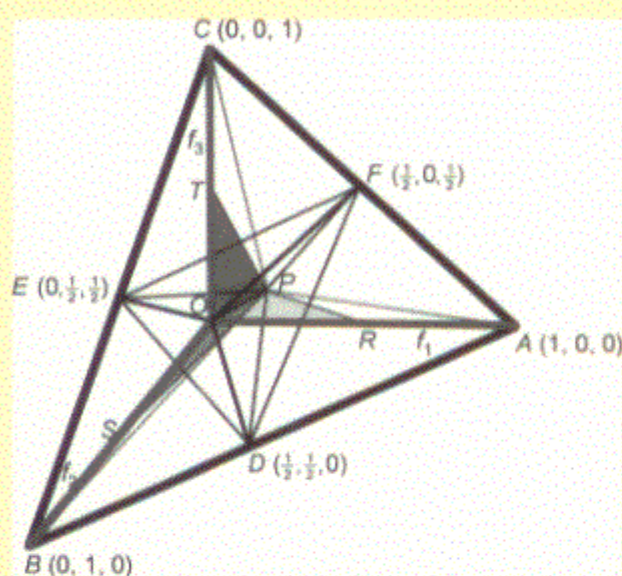


Oxford Series in Ecology and Evolution
Edited by Paul H. Harvey and Robert M. May



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The field of molecular evolution has experienced explosive growth in recent years due to the rapid accumulation of genetic sequence data, continuous improvements to computer hardware and software, and the development of sophisticated analytical methods. The increasing availability of large genomic data sets requires powerful statistical methods to analyse and interpret them, generating both computational and conceptual challenges for the field.

Computational Molecular Evolution provides an up-to-date and comprehensive coverage of modern statistical and computational methods used in molecular evolutionary analysis, such as maximum likelihood and Bayesian statistics. Yang describes the models, methods and algorithms that are most useful for analysing the ever-increasing supply of molecular sequence data, with a view to furthering our understanding of the evolution of genes and genomes. The book emphasizes essential concepts rather than mathematical proofs. It includes detailed derivations and implementation details, as well as numerous illustrations, worked examples, and exercises. It will be of relevance and use to students and professional researchers (both empiricists and theoreticians) in the fields of molecular phylogenetics, evolutionary biology, population genetics, mathematics, statistics and computer science. Biologists who have used phylogenetic software programs to analyse their own data will find the book particularly rewarding, although it should appeal to anyone seeking an authoritative overview of this exciting area of computational biology.

Front cover illustration: computer model of a protein molecule of matrix porin found in *E. Coli*. © Corbis.

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