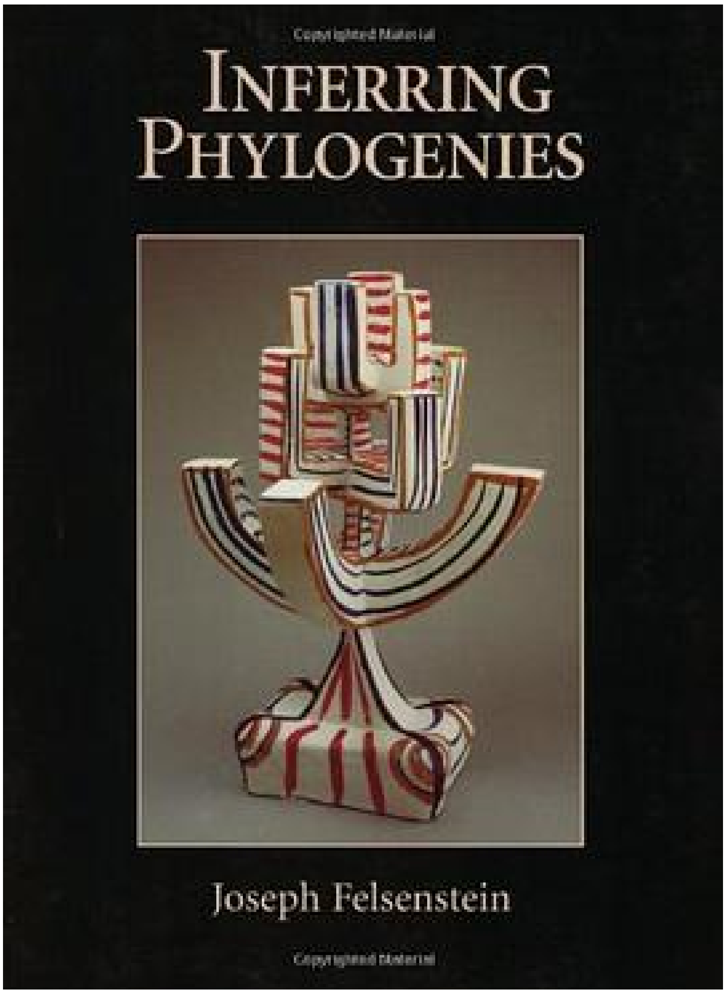
Inferring Phylogenies



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出版者:Sinauer Associates

出版时间:2003-9-4

装帧:Paperback

isbn:9780878931774

Phylogenies (evolutionary trees) are basic to thinking about and analyzing differences between species. Statistical, computational, and algorithmic work on them has been ongoing for four decades, with great advances in understanding. "Inferring Phylogenies" explains clearly the assumptions and logic of making inferences about phylogenies, and using them to make inferences about evolutionary processes. It is an essential text and reference for anyone who wants to understand how phylogenies are reconstructed and how they are used. As phylogenies are inferred with various kinds of data, this book concentrates on some of the central ones: discretely coded characters, molecular sequences, gene frequencies, and quantitative traits. Also covered are restriction sites, RAPDs, and microsatellites. This work is intended for graduate level courses, assuming some knowledge of statistics, mathematics (calculus and fundamental matrix algebra), molecular sequences, and quantitative genetics.

作者介绍:

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