



Inferring Phylogenies

Joseph Felsenstein

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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. Yet no book has summarized this work until now. *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.

Inferring Phylogenies is intended for graduate-level courses, assuming some knowledge of statistics, mathematics (calculus and fundamental matrix algebra), molecular sequences, and quantitative genetics.

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