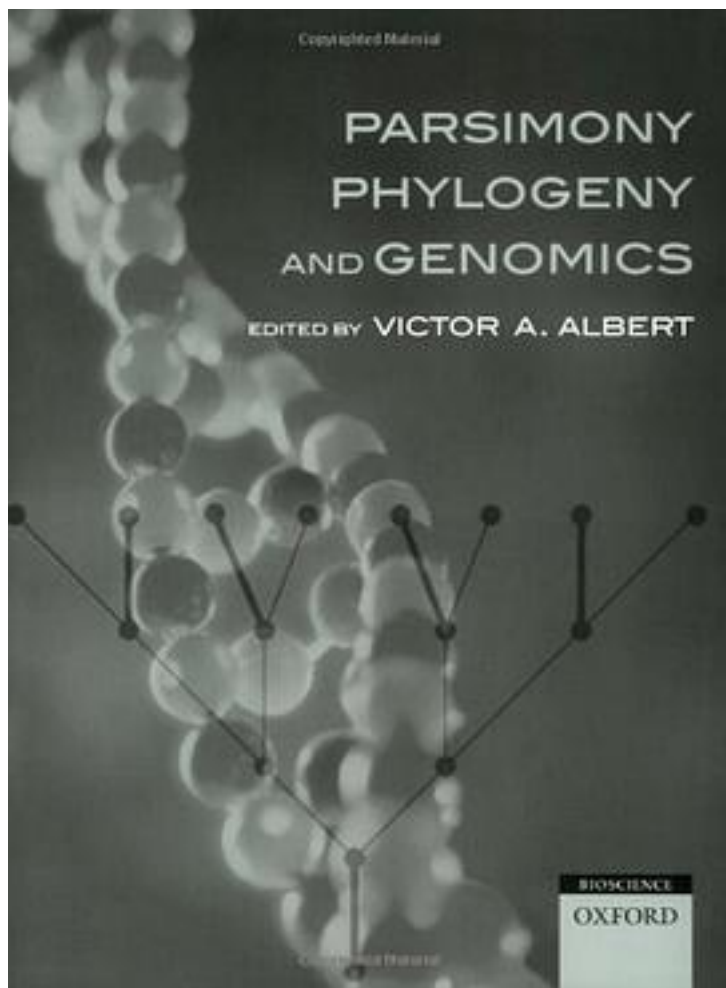


Parsimony, Phylogeny, and Genomics



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著者:Albert, Victor A. 编

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Parsimony analysis (cladistics) has long been one of the most widely used methods of phylogenetic inference, in the fields of systematic and evolutionary biology. Moreover it

has mathematical attributes that lend itself for use with complex, genomic-scale data sets. This book demonstrates the potential that this powerful hierarchical data summarization method, also has for both structural and functional comparative genomic research.

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