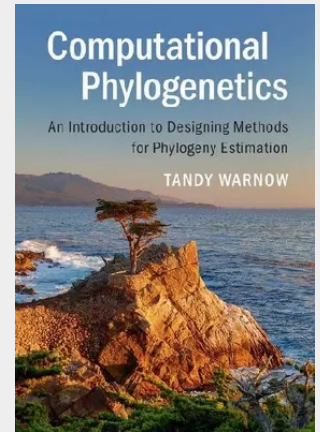


## Computational Phylogenetics

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A comprehensive account of both basic and advanced material in phylogeny estimation, focusing on computational and statistical issues. No background in biology or computer science is assumed, and there is minimal use of mathematical formulas, meaning that students from many disciplines, including biology, computer science, statistics, and applied mathematics, will find the text accessible. The mathematical and statistical foundations of phylogeny estimation are presented rigorously, following which more advanced material is covered. This includes substantial chapters on multi-locus phylogeny estimation, supertree methods, multiple sequence alignment techniques, and designing methods for large-scale phylogeny estimation. The author provides key analytical techniques to prove theoretical properties about methods, as well as addressing performance in practice for methods for estimating trees. Research problems requiring novel computational methods are also presented, so that graduate students and researchers from varying disciplines will be able to enter the broad and exciting field of computational phylogenetics.

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