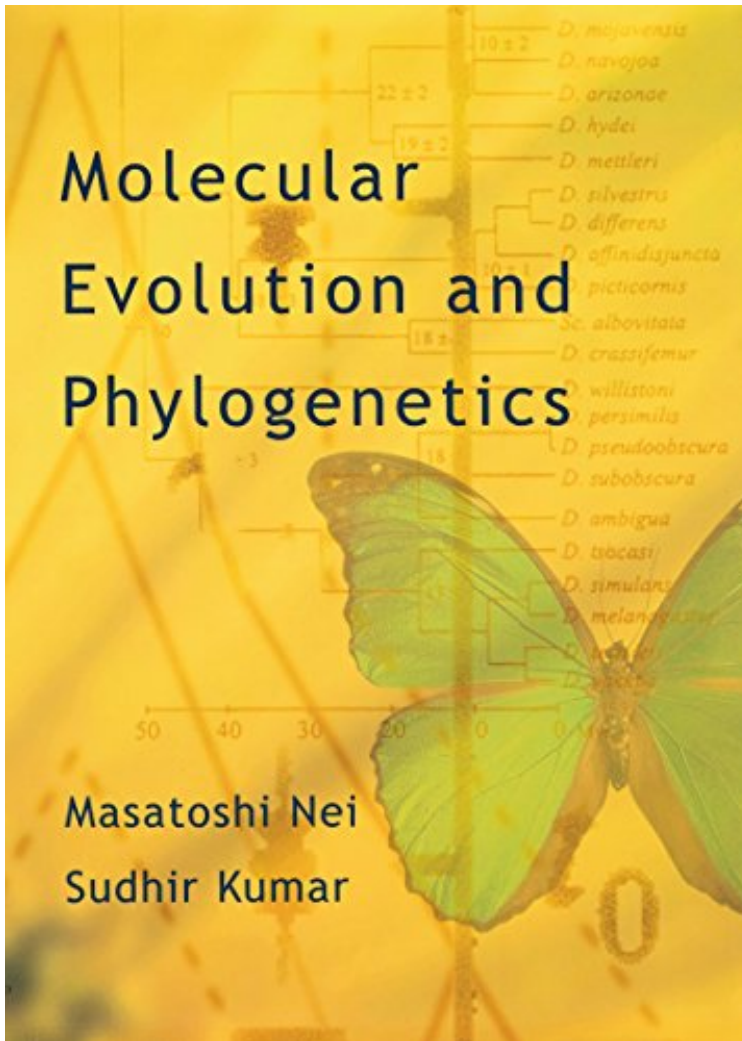


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Description :

Prsentation de l'diteurDuring the last ten years, remarkable progress has occurred in the study of molecular evolution. Among the most important factors that are responsible for this progress are the development of new statistical methods and advances in computational technology. In particular, phylogenetic analysis of DNA or protein sequences has become a powerful tool for studying molecular evolution. Along with this developing technology, the application of the new statistical and computational methods has become more complicated and there is no comprehensive volume that treats these methods in depth. Molecular Evolution and Phylogenetics fills this gap and present various statistical methods that are easily accessible to general biologists as well as biochemists, bioinformatists and graduate students. The text covers measurement of sequence divergence, construction of phylogenetic trees, statistical tests for detection of positive Darwinian selection, inference of ancestral amino acid sequences, construction of linearized trees, and analysis of allele frequency data. Emphasis is given to practical methods of data analysis, and methods can be learned by

working through numerical examples using the computer program MEGA2 that is provided. *Revue de presse* It is worth its price (*Plant Systematics and Evolution*) *Présentation de l'éditeur* During the last ten years, remarkable progress has occurred in the study of molecular evolution. Among the most important factors that are responsible for this progress are the development of new statistical methods and advances in computational technology. In particular, phylogenetic analysis of DNA or protein sequences has become a powerful tool for studying molecular evolution. Along with this developing technology, the application of the new statistical and computational methods has become more complicated and there is no comprehensive volume that treats these methods in depth. *Molecular Evolution and Phylogenetics* fills this gap and presents various statistical methods that are easily accessible to general biologists as well as biochemists, bioinformaticists and graduate students. The text covers measurement of sequence divergence, construction of phylogenetic trees, statistical tests for detection of positive Darwinian selection, inference of ancestral amino acid sequences, construction of linearized trees, and analysis of allele frequency data. Emphasis is given to practical methods of data analysis, and methods can be learned by working through numerical examples using the computer program MEGA2 that is provided.