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Abstract

This book is intended for undergraduate and graduate students studying Bioinformatics and Computational Biology. It can be used as a textbook in almost all Bioinformatics courses taught at Greek universities, and will also serve as a good basis for teaching certain courses at postgraduate level. The book is also aimed at scientists in the biological sciences or computer science who wish to deepen their knowledge of bioinformatics. The only requirement for the reader is a basic familiarity with the terminology of molecular biology (DNA, proteins, cell functions, organelles, etc.). The book covers most of the areas traditionally

found in a modern Bioinformatics textbook, such as: - Protein and nucleic acid databases - Algorithms for pair-wise sequence alignment and database searches (Smith-Waterman, Needleman-Wunch, BLAST, FASTA, etc.) -Multiple sequence alignment -Phylogenetic analysis -Sequence pattern searching (patterns and profiles) -Prediction methods based on protein, RNA, and DNA sequences -Markov models in sequence analysis (Markov chain models, Hidden Markov Models) - Neural networks - Stochastic grammars - Genomics and comparative genomics - Analysis of data from DNA microarrays - Analysis of complex biological networks.









