



Compact Handbook of Computational Biology

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The assimilation of computational methods into the life sciences has played an important role in advancing biological research. From sequencing genomes to discovering motifs in large collections of functionally equivalent sequences of nucleic acids and proteins, the value of powerful computational tools has become abundantly clear. The Compact Handbook of Computational Biology describes the foundational concepts, techniques, and challenges of biomolecular sequence analysis, biopolymer structure analysis and prediction, genomics, and molecular evolution.

Comprising contributions from renowned scientists, many of whom pioneered current methodologies, the Compact Handbook of Computational Biology offers interdisciplinary and authoritative coverage of methods for analysis of nucleic acid and protein sequences and structures, definition and detection of motifs in nucleic acid and protein sequences, protein structure prediction, and discrete modeling of biopolymers. Specific computational topics include computer-assisted research on protein folding, computer-assisted studies of DNA-protein interactions, computer-assisted genomics, proteomics, and comparative genomics, and computer-assisted studies of genome evolution at the molecular (DNA) level.

Offering a survey of specific algorithms that have proven successful in molecular biology, genomics, structural biology, and bioinformatics, this invaluable handbook is an authoritative source covering terminology, software, and applications of computational biology.

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