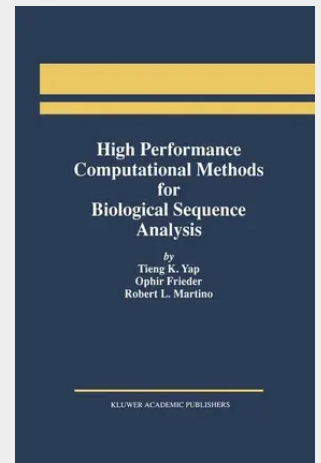


High Performance Computational Methods for Biological Sequence Analysis

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This work focuses on high performance computational approaches that are used to perform computationally intensive biological sequence analysis tasks: pairwise sequence comparison, multiple sequence alignment, and sequence similarity searching in large databases. These computational methods are becoming increasingly important to the molecular biology community allowing researchers to explore the increasingly large amounts of sequence data generated by the Human Genome Project and other related biological projects. The approaches presented by the authors are state-of-the-art and show how to reduce analysis times significantly, sometimes from days to minutes. is tremendously important to biomedical science students and researchers who are interested in applying sequence analyses to their studies, and to computational science students and researchers who are interested in applying new computational approaches to biological sequence analyses.

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