

COMPUTATIONAL METHODS WITH APPLICATIONS IN BIOINFORMATICS ANALYSIS

This compendium contains 10 chapters written by world renowned researchers with expertise in semantic computing, genome sequence analysis, bimolecular interactions, time-series microarray data analysis, and machine learning algorithms.

The salient feature of this compendium is that it highlights eight types of computational techniques to tackle different biomedical applications. These techniques include unsupervised learning algorithms, principal component analysis, fuzzy integral, graph-based ensemble clustering method, semantic analysis, interolog approach, molecular simulations and enzyme kinetics.

The unique volume will be a useful read for advanced undergraduate scientists, computational biologists and professionals.

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