

Preface to the Special Issue on Bioinformatics

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Bioinformatics aims to solve biological problems by using techniques from mathematics, statistics, computer science, and machine learning. Recent years have observed the essential use of these techniques in bioinformatics. Examples of such applications include those to gene expression data analysis, gene-protein interactions, protein folding and structure prediction, genetic and molecular networks, sequence and structural motifs, genomics and proteomics, and so on. Bioinformatics provides opportunities for developing novel techniques in the fields of mathematics, statistics, computer science, and machine learning; and these fields play a key role in advancing bioinformatics.

This special issue consists of six papers, chosen from twenty submissions. These papers address the following problems in bioinformatics: data integration in bioscience, informative gene selection via bootstrapping, microarray data analysis using wavelet techniques, genetic algorithms, and artificial neural networks, peptide identification via tandem mass spectrometry, and mass spectrometry proteomic data classification using kernel methods. We believe this special issue will be interesting to readers and useful for their research in bioinformatics.