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Sequence Alignment Algorithms and the Application to Genome Research

Kie-Jung Park*
Genome Center, Korea Research Institute of Bioscience and Biotechnology

Sequence alignment is the most frequently used in sequence analysis to find out homology between sequences and so a core module in analysis packages. Some algorithms for sequence alignment, including dynamic programming approach for optimal alignment and heuristic approaches are introduced. Major concepts and problems in sequence alignment are introduced with emphasis on parameters such as gap, scoring matrix, and evaluation of the significancy of alignments. Multiple sequence alignment algorithms are introduced as an application of sequence alignment and more complex problem than pairwise alignment problem, with some typical multialignment algorithms. Some algorithms of our own, are also introduced. Prospects and impact of alignment theories for genome projects and post-genome projects are mentioned with the trends of bioinformatics.

SIII-2-4

New Approach to Structure and Functoin Study by Molecular Bioinformatics

Seung-Moak Kim
Bioinformatics Team, Genome Center, KRIBB

Molecular Bioinformatics is a newly emerging interdisciplinary research filed. Bioinformatics comprise all areas of bioscience and biotechnology related to information technology such as databases, information retrieval systems, computational analyses, user interfaces and statistics, but the definition of molecular bioinformatics is narrower than that of bioinformatics. It includes the development and application of computational algorithms for the purpose of analysis, interpretation and prediction of data and for the design of experiments in biosciences. New paradigms, artificial intelligence, artificial neural networks, genetic algorithms, evolutionary computing are originated from computer science, and new application areas for molecular biology cover discover of structure/function relationship, design of metabolic pathways and identification of genes.