

# Introduction to Minitrack: Computational Issues in Bioinformatics

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With a strong foundation in Computational Biology and Computational Chemistry, Bioinformatics is fast emerging as one of the most exciting scientific disciplines in the twenty-first century. A true multidisciplinary field of study, Bioinformatics deals with the development and use of mathematical and computational methods to assist in modeling and solving problems in biosciences. Employing algorithmic approaches are expected to be essential to the development and advancement of many fields in biosciences. This, in part, is due to the recent explosion of biological data, which requires an associated increase in the scale and sophistication of the automated systems and tools that enable researchers to take advantage of its availability. Additionally, there are a large number of research projects and applications that demands automated computational support.

The need for Bioinformatics reflects the radical changes that the biological sciences have undergone recently. As more important biological elements are studied and their roles in complex biological systems are discovered, it is apparent that integrating computational research and experimental work will be crucial in exploring and understanding these discoveries.

Although the Bioinformatics Minitrack focuses on the computational issues in Bioinformatics, its main goal is to provide a venue for researchers from all related fields to present new integrated approaches to address real Bioinformatics problems. This is apparent in all five papers that comprise the minitrack. Each paper presents a new concept, tool or technique that is motivated by an important problem related to Bioinformatics.

The first two papers in the minitrack deal with issues related to whole genomes. In the first paper, "Comparative Genome Annotation for Mapping, Prediction and discovery of Genes," by Kappen and Salbaum, the analysis of specific chromosomes in two genomes, the human genome and the muse genome, leads to fully assemble a large contiguous sequence that contains fourteen genes. While the paper leaning toward the bioscience aspect of Bioinformatics, the second paper employs computational techniques to deal with alignment problems at the genome level. In the paper, titled, "A Prototype for Multiple Whole Genome Alignment," by

Deogun *et al*, graph theoretic approaches as well as advanced algorithmic techniques are used address the problem of whole genome alignment for more than two genomes.

The third paper employs a data mining approach based on multiple criteria linear programming to classify biological datasets related to HIV-1 associated dementia. The paper is titled, "Classification of Neural Dendritic and Synaptic Damage Resulting from HIV-1 Associate Dementia: A Multiple Criteria Linear Programming Approach," by Zheng *et al*. The classification of neural damage resulting from HIV-1 associated dementia is believed to be essential in creating new treatments. The paper provides another clear example that while having valuable biological data is essential to the discovery process, the lack of automated tools would limit the ability to use the available data effectively.

Visual environments in Bioinformatics are important in making various computational techniques accessible by wide range of researchers. This issue is the focus of the fourth paper in the minitrack, "Integrating Biomolecular Analysis and Visual Programming: Flexibility and Interactivity in the Design of Bioinformatics Tool," by Stoffer *et al*. The paper describes the process of integrating a visual programming environment and a command driven molecular visualization and manipulation program. The presented environment is aiming at providing researchers with user-friendly tools to analyze and study complex interactions of molecular systems. The fifth paper, "Grid-Layout Visualization Method in the Microarray Data Analysis Interactive Graphics Toolkit," by Xiao, Shats and Sherman presents another visualization tool that provides an efficient visual presentation of hierarchical clustering of large microarray data. The proposed approach is also integrated with an interactive graphics toolkit for microarrays.

In summary, the papers of the Bioinformatics Minitrack are providing excellent attempts to cross the bridge that connects Biosciences and Computational Sciences. We hope that they will encourage productive dialogues among researchers in all fields related to Bioinformatics and motivate new innovative research in this exciting scientific discipline.