Bioinformatics Visualization:

Introduction to this Special Issue of Information Visualization

Welcome to this special issue on Bioinformatics Visualization of the journal of Information Visualization. *Bioinformatics* involves the application of data-rich computational and informatics methods to support the scientific study of complex biological problems. Recent technological and intellectual advances in bioinformatics are transforming the way biological research is conducted, placing bioinformatics at the forefront of the information-intensive approach to scientific investigation. As a result, biological research is currently experiencing explosive growth in academic, industry, and government sectors.

This trend creates a critical need for information visualization as a central member of the bioinformatics toolbox, along with data mining, digital libraries, modeling and simulation, and other information-related capabilities. It also provides tremendous new opportunities for advanced research in information visualization to overcome the unique and difficult problems in bioinformatics. The emerging field of *bioinformatics visualization* addresses the design of visual metaphors and the implementation of effective software tools that provide insight into complex biological data.

Several key characteristics of bioinformatics offer broad challenges to information visualization researchers:

- Very large quantities of data: High-throughput profiling technologies, such as functional genomics, proteomics, and metabolomics, combined with an emphasis on online

repositories of information ranging from sequence data to taxonomic classification, enable rapid collection and world-wide dissemination of vast data.

- Heterogeneous data: Modern biological discovery often requires the integration of diverse data types, including multidimensional gene expression data, sequence data, 3-dimensional molecular models, tree-structured ontologies and taxonomies, network-structured metabolic pathways, and textual literature documents.

- Complex exploratory tasks: While much current biological research focuses on statistical testing of specific hypotheses, many areas such as systems biology are increasingly emphasizing an open-ended exploratory approach to hypothesis generation and large scale data analysis for gaining insight into exceedingly complex biological phenomena.

- Interdisciplinary teams: Due to the complexity of the biological problems, successful bioinformatics solutions require close collaboration between teams of scientists with different backgrounds, including biologists, physical scientists, computer scientists, engineers, mathematicians, and visualization experts. Visualization tools may be used by any subset of these user classes.

The goal of this special issue is two-fold. First, we attempt to showcase the variety of research underway at various industrial centers and universities examining bioinformatics visualization issues today. Second, we hope to call more visualization researchers to action on the challenges of bioinformatics visualization and, more generally, to the dream of enabling the future of the new biology.

The six selected papers in this special issue highlight implementations of information visualization techniques to bioinformatics problems. Craig, Kennedy, and Cumming begin the special issue by discussing the use of plot animation to explore microarray time series intervals, a core data type in bioinformatics. Gehlenborg, Dietzsch, and Nieselt delve further into visualizing microarray data by augmenting heatmaps with mathematical ranking functions. Kincaid, Ben-Dor, and Yakhini apply multi-level dense views to DNA sequences and comparative genomic hybridization. Saraiya, North, and Duca lay out an analysis and evaluation of tools for visualizing bioinformatics pathway networks and associated data. Graham and Kennedy use structural markers and multiple trees to extend genomic taxonomy visualization methods. Smoot, Bass, Guerlain and Pearson complete the special issue with a discussion of pair plots and animated graph paths to address the visual display of protein sequence alignments.

When we released the Call for Participation for this special issue a year before publication, we had not expected that we would receive so many quality and varied paper submissions. An initial examination of appropriateness to the special issue yielded twelve papers requiring further peer review. Thus, we built an interdisciplinary review process that attempted to match two visualization expert reviewers and one biology expert reviewer to each paper. The review process attempted to evaluate each paper's interdisciplinary contribution to both visualization and biology, in terms of: (1) the technical competency and uniqueness of the visualization techniques being applied; and (2) the impact of the visual display methods on biology research. As a result of this reviewing approach, we accepted these six papers for publication.

As guest editors of this special issue, we have learned that bioinformatics is a scientific domain tasked with the complex challenge of evaluating existing metaphors while simultaneously incorporating new visual representations. Many of the reviewers noted the need for evaluation studies that address the effectiveness of these information visualization techniques to actual biological research. With this special issue, we have attempted to firmly establish the newly emerging territory of bioinformatics visualization. We believe the contents of the special issue represent the significant growth and richness of bioinformatics visualization, and hope that it will encourage further future flourishing of this fledgling field.

We are most appreciative of the authors and reviewers for helping to create a quality special issue that reflects the state of the art in bioinformatics visualization. We also thank Chaomei Chen, Editor-in-Chief of Information Visualization, for supporting our interdisciplinary reviewing approach.

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