Call for Papers

IEEE Journal of Selected Topics in Signal Processing

IEEE Signal Processing Society

Special Issue on Genomic and Proteomic Signal Processing

Genomic and proteomic signal processing is a rapidly growing field within the signal processing community. Over the past decade, signal processing methods have become increasingly important in the analysis of genomic and proteomic data. The potential impact of signal processing tools to extract critical information from molecular biological data is enormous.

The field of genomic and proteomic signal processing aims to gain insight and reveal the structure and function of molecular biological systems such as DNA, RNA, and proteins. The challenge posed in this area is to harness the tools of signal processing for genomic and proteomic analysis, which will shed light on the evolution and operation of biological systems. The ultimate goal is to rely on this knowledge to aid drug design and therapeutic treatment in order to combat diseases such as cancer.

A great deal of interest has been devoted to the use of information technology to gain knowledge in biology and medicine. The rise in popularity of the field of bioinformatics provides ample evidence to the importance of information technology in forging new frontiers in medicine and biology. From a signal processing perspective, molecular structure can be viewed as discrete-time sequences represented by a finite alphabet. Nucleic and amino acid sequences can be represented as signals that are used to model molecular systems. Moreover, many biological data acquisition methods provide quantifiable measures that naturally lend themselves to representation using signal and image processing techniques, e.g. gene expression levels gathered from microarrays. The realization that many biological processes can be represented in terms of fundamental signal and system methods has served as the impetus for a tremendous effort to address problems in bioinformatics using signal processing techniques.

Genomic and proteomic data pose enormous challenges to the signal processing community due to the high variability of the data acquisition process and high dimensionality of the data space. This special issue focuses on the application of signal processing methods to genomics and proteomics and the development of new signal processing tools for specific problems related to biological systems.

The motivation for this special issue is to bring to light the increasing role of genomic and proteomic signal processing in bioinformatics and to disseminate important issues in medicine and biology to the signal processing community. Our goal is to feature recent advances in the area of genomic and proteomic signal processing and highlight emerging challenges and applications. The advances can include theoretical, experimental, and

computational methods and results that aim to solve important problems in medicine and biology. We invite original research contributions in all areas relevant to the field. In particular, original paper submissions are encouraged in areas of genomic and proteomic signal processing including, but not limited to, the following topics:

- Signal processing and statistical methods in genomic and proteomic sequence analysis
- Signal processing and statistical approaches for functional genomics and proteomics
- Signal processing analysis of genomic and proteomic structure and evolution
- Reverse engineering of molecular systems
- Data mining and pattern recognition methods for genomics and proteomics
- Signals and systems theory techniques for systems biology
- Models for cellular metabolism and inter-cellular signaling
- Models and analysis of genomic regulatory networks
- Models of genomic and proteomic structures and functions
- Architecture and implementation methods for large-scale functional genomics
- High-throughput systems for genome-scale network modeling
- Genetics-based signal processing approaches and architectures
- Integration of heterogeneous molecular data
- Microarray image and data analysis

Submission procedure

Prospective authors can find submission information at http://www.ece.byu.edu/jstsp. Submitted manuscripts should not have been previously published nor be currently under consideration for publication elsewhere. Authors are advised to follow the Author's Guide for the formats of manuscripts submitted to the IEEE Transactions on Signal Processing as detailed at http://ewh.ieee.org/soc/sps/tsp/. The manuscripts will undergo a standard peer review process.

Manuscript submissions due:	September 1, 2007
First review completed:	November 15, 2007
Revised manuscripts due:	January 5, 2008
Second review completed:	March 5, 2008
Final manuscript due:	April 1, 2008

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