Introduction to the *IEEE/ACM Transactions on Computational Biology and Bioinformatics*

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1　INTRODUCTION TO COMPUTATIONAL BIOLOGY AND BIOINFORMATICS

I would like to welcome you to the *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. This inaugural issue introduces the editorial board of *IEEE/ACM TCBB* and begins fulfilling the scientific mission of the journal, with the publication of three regular papers and one survey.

Bioinformatics and computational biology are concerned with the use of computation to understand biological phenomena and to acquire and exploit biological data, increasingly large-scale data. Methods from bioinformatics and computational biology are increasingly used to augment or leverage traditional laboratory and observation-based biology. These methods have become critical in biology due to recent changes in our ability and determination to acquire massive biological data sets, and due to the ubiquitous, successful biological insights that have come from the exploitation of those data. This transformation from a data-poor to a data-rich field began with DNA sequence data, but is now occurring in many other areas of biology. At the same time, we are seeing the beginnings of systems biology, which attempts to integrate diverse types of biological data and knowledge, to obtain insights into the high-level workings of biological systems.

The shift to data-driven biology and the accumulation and exploitation of large-scale data has lead to the need for new computational technology (machines, software, algorithms, theory) and for research into these issues. As this transformation extends into more biological domains, so too will bioinformatics and computational biology expand in scope, importance, and the number of participants. Hence, computational biology and bioinformatics, and research into the underlying computational techniques, have a huge future, requiring a large expansion in publication opportunities. The *IEEE/ACM Transactions on Computational Biology and Bioinformatics* is being launched to provide such publication opportunities for high-quality research papers.

The establishment of *IEEE/ACM TCBB* is supported by several societies of the IEEE and by The Association for Computing Machinery (ACM). The supporting societies in the IEEE are the IEEE Computer Society, the IEEE Engineering in Medicine and Biology Society, and the IEEE Neural Networks Society. *IEEE/ACM TCBB* is also cosponsored by the IEEE Control Systems Society. The cooperation of several IEEE societies, along with the ACM, reflects the wide range of interests in computational biology and

bioinformatics that will be reflected in the journal, and also demonstrates a commitment by those organizations to further the development of the fields of computational biology and bioinformatics.

2　THE SCOPE AND DIRECTION OF *IEEE/ACM TCBB*

The *IEEE/ACM Transactions on Computational Biology and Bioinformatics* will emphasize the algorithmic, mathematical, statistical, and computational methods that are central in bioinformatics and computational biology, the development and testing of effective computer programs in bioinformatics, the development and optimization of biological databases, important biological results that are obtained from the use of these methods, programs, and databases; and the emerging field of systems biology, where many forms of data and biological knowledge are used to create a computer-based model of a complex biological system.

We anticipate the publications will represent a mixture of three research modalities: 1) fundamental methodological, algorithmic, mathematical, and statistical research directly related to biological issues, 2) papers focusing on experimental and implementation issues involved in complex computations, and 3) papers on serious application of methods and programs that lead to discoveries of biological significance. Increasingly, we expect papers will contain elements of all three modalities.

Specific topics of interest include, but are not limited to, sequence analysis, comparison and alignment methods; motif, gene and signal recognition; molecular evolution; phylogenetics and phylogenomics; determination or prediction of the structure of RNA and protein in two and three dimensions; DNA twisting and folding; gene expression and gene regulatory networks; deduction of metabolic pathways; microarray design and analysis; proteomics; functional genomics; molecular docking and drug design; computational problems in genetics such as linkage and QTL analysis, linkage disequilibrium analysis in populations, and haplotype determination; and systems biology.

In addition to original research articles, *IEEE/ACM TCBB* welcomes research and literature reviews and surveys, appropriate tutorials, "vision statements," and letters to the editor. *IEEE/ACM TCBB* will also publish special issues on specific themes and issues that publish expanded journal versions of selected papers from recent conferences. We

invite suggestions for special issues and for one-time and ongoing conference coverage. We invite all researchers in computational biology and bioinformatics to submit your papers for publication in *IEEE/ACM TCBB*, and we welcome suggestions and ideas from everyone on any aspect of *IEEE/ACM TCBB*.

The fields of computational biology and bioinformatics have bright futures, with major growth in range of applications and range of participants. The *IEEE/ACM Transactions on Computational Biology and Bioinformatics* also has a bright future and will grow to be one of the central venues for high quality research in computational biology and bioinformatics.

3 THE *IEEE/ACM TCBB* EDITORIAL BOARD AND STEERING COMMITTEE

I am pleased to introduce the distinguished inaugural members of the Editorial Board. You will find their detailed biographies on the succeeding pages. For links to most of the homepages of the board, see: www.csif.cs.ucdavis.edu/~gusfield/urllinks.html.

The board members represent the broad range of interests of *IEEE/ACM TCBB* and the broad range of support for *IEEE/ACM TCBB*. Members of the board come from several different areas in biology, from computer science and engineering, from statistics, and from mathematics. Many of the board members are simultaneously involved in several of these areas, and are best described as interdisciplinary pioneers. I would like to thank all of the members of the board for their willingness to help establish this journal.

The Transactions are also guided by a Steering Committee who advise and aid the editors, and who represent the concerns of the organizations that support *IEEE/ACM TCBB*. I want to thank all the members of the Steering Committee for their help and for their support. The chair of this committee is Metin Akay. The members of the Steering Committee are Frank Ferrante, Pavel Pevzner, Russ Altman, Richard Karp, Robert Kearney, Evangelia Micheli-Tzanakou, Jacques Cohen, and John Baillieul.

4 INTRODUCING THE INAUGURAL ISSUE

This inaugural issue presents three regular papers and one survey. The papers in this issue are:

1. "Phylogenetic Networks: Modeling, Reconstructibility, and Accuracy," by Luay Nakhleh, Craig R. Linder, Bernard M.E. Moret, Jerry Sun, Anneke Padolina, Anna Tholse, Ruth Timme, and Tandy Warnow. This paper develops a formal model of phylogenetic networks, motivated by hybrid speciation and lateral gene transfer. It provides efficient algorithms for problems defined on the model, and perhaps most important, it establishes that an efficient method for comparing the topologies of phylogenetic networks produces a metric score. That result will facilitate the careful comparison of phylogenetic networks and the methods that construct and estimate them.

2. "Biclustering Algorithms for Biological Data Analysis: A Survey," by Sara Madeira and Arlindo L. Oliveira. This paper surveys algorithms and applications for biclustering of biological data. Biclustering algorithms are increasingly used in bioinformatics and computational biology to reveal important correlations and possible causal relations. The most notable example is in analyzing gene expression data from microarray experiments. This impressive, comprehensive survey partitions the methods according to the type of biclusters they seek, and by the algorithmic ideas that underly them. It will be very helpful to users and researchers in understanding the issues and the recent progress in the area of biclustering algorithms.

3. "Sequencing-by-Hybridization Revisited: The Analog-Spectrum Proposal," by Franco Preparata. This paper revisits the question of the practicality of DNA sequencing by hybridization. It argues that the digital-spectrum model, which has been the basis for for past work on SBH, should be replaced by an analog-spectrum model that more closely reflects biochemical reality. That change leads to the conclusion that SBH could be a practical way to sequence DNA. As stated in the abstract, "the theoretical proposal presented in this paper should be a convincing stimulus for the needed biotechnological work."

4. "Pure Multiple RNA Secondary Structure Alignments: A Progressive Profile Approach," by Matthias Höchsmann, Björn Voss, and Robert Giegerich. This paper presents a method to align multiple RNA secondary structures without the need for sequence similarity. This not only provides a useful way to compare many RNA molecules, but also develops a robust data structure for holding multiple RNA structure information.

This inaugural issue illustrates important and diverse contributions of algorithmic computer science to computational biology and bioinformatics. Future issues of *IEEE/ACM TCBB* will illustrate other areas supported by *IEEE/ACM TCBB*, as detailed in Section 2. We hope you will enjoy this issue and invite you to help support the establishment and growth of *IEEE/ACM TCBB*.

Dan Gusfield
Editor-in-Chief