

Editorial

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The advent of new methods to obtain large-scale surveys of gene expression in which transcript levels can be determined for thousands of genes simultaneously has facilitated the expansion of biological understanding from the analysis of individual genes to the analysis of systems of genes (and proteins). This change characterizes the movement into the era of functional genomics. Central to this movement is an appreciation of the gene's role in cellular activity as it functions in the context of larger molecular networks.

Two salient goals of functional genomics are to screen for key genes and gene combinations that explain specific cellular phenotypes (e.g. disease) on a mechanistic level, and to use genomic signals to classify disease on a molecular level. Signals generated by the genome must be processed to characterize their regulatory effects and their relationship to changes at both the genotypic and phenotypic levels. Since transcriptional (and posttranscriptional) control involves the processing of numerous and different kinds of signals, mathematical and computational methods are required to model the multivariate influences on decision-making in complex genetic networks.

Historically, it has been within the domain of signal processing where such methodologies have been extensively studied and developed—in particular, estimation, classification, pattern recognition, automatic control, information theory, networks, computation, imaging, and coding. Moreover, signal processing is based on a holistic view of regulation and communication. As a discipline, signal processing involves the construction of model systems composed of

various mathematical structures, such as systems of differential equations, graphical networks, stochastic functional relations, and simulation models. Therefore it is not surprising that the advent of high-throughput genomic and proteomic technologies is drawing a growing interest from the signal processing community in relation to attacking the fundamental issues of expression-based functional genomics.

The twin aims of tissue classification and pathway modeling require a broad range of signal processing approaches, including signal representation relevant to transcription and system modeling using nonlinear dynamical systems. To capture the complex network of nonlinear information processing based upon multivariate inputs from inside and outside the genome, regulatory models require the kind of nonlinear dynamics studied in signal processing and control. Genomics requires its own model systems, not simply straightforward adaptations of currently formulated models. New systems must capture the specific biological mechanisms of operation and distributed regulation at work within the genome. It is necessary to develop nonlinear dynamical models that adequately represent genomic regulation for diagnosis and therapy.

Genomic signal processing (GSP) is the discipline that studies the processing of genomic signals. The aim of GSP is to integrate the theory and methods of signal processing with the global understanding of functional genomics, with special emphasis on genomic regulation. Hence, GSP encompasses various methodologies concerning expression profiles: detection, prediction, classification, control, and

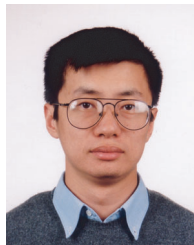
dynamical modelling of gene networks. Moreover, since RNA coding is controlled by DNA sequencing, the analysis of DNA sequences, treated as signals in their own right, can be considered within the domain of GSP. Overall, GSP is a fundamental discipline that brings to genomics the structural model-based analysis and synthesis that form the basis of mathematically rigorous engineering.

This special issue of EURASIP JASP contains some examples of GSP applications. The issue starts with three papers (Song et al., Chakravarthy et al., and Sussillo et al.) on spectral analysis of DNA sequences. The next paper by Hero et al. treats statistical signal-processing-based gene selection. The following two papers (Wu et al. and Giurcãneanu et al.) develop signal processing techniques for gene clustering. The next two papers treat DNA sequence segmentation using statistical signal processing (Nicorici and Astola) and image processing (Hua et al.), respectively. Signal processing methods for gene prediction and regulatory network inference are developed in the papers by Fox and Carreira, Zhou et al., and Ivanov et al., respectively. The paper by Cristea deals with revealing large-scale chromosome features by analysis of genomic signals. In addition, the paper by Lennartsson and Nordin treats peptides identification using genetic programming. Finally, an invited tutorial by Dougherty et al. discusses key issues in GSP.

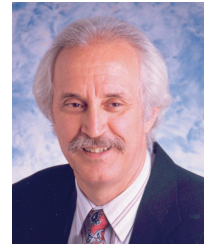
The guest editors would like to thank all the authors for contributing their work to this special issue. We would also like to express our deep gratitude to all reviewers for their diligent efforts in evaluating all submitted manuscripts.

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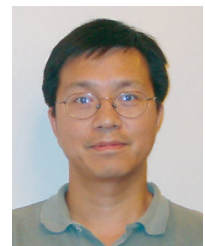
Xiaodong Wang received the B.S. degree in electrical engineering and applied mathematics (with the highest honor) from Shanghai Jiao Tong University, Shanghai, China, in 1992; the M.S. degree in electrical and computer engineering from Purdue University in 1995; and the Ph.D. degree in electrical engineering from Princeton University in 1998. From July 1998 to December 2001, he was an Assistant Professor in the Department of Electrical Engineering, Texas A&M University. In January 2002, he joined the Department of Electrical Engineering, Columbia University, as an Assistant Professor. Dr. Wang's research interests fall in the general areas of computing, signal processing, and communications. He has worked in the areas of digital communications, digital signal processing, parallel and distributed computing, nanoelectronics, and bioinformatics, and has published extensively in these areas. His current research interests include wireless communications, Monte Carlo based statistical signal processing, and genomic signal processing. Dr. Wang received the 1999 NSF CAREER Award and the 2001 IEEE Communications Society and Information Theory Society Joint Paper Award. He currently serves as an Associate Editor for the IEEE Transactions on Communications, the IEEE Transactions on Wireless Communications, the IEEE Transactions on Signal Processing, and the IEEE Transactions on Information Theory.



Edward R. Dougherty is a Professor in the Department of Electrical Engineering at Texas A&M University in College Station. He holds an M.S. degree in computer science from Stevens Institute of Technology in 1986 and a Ph.D. degree in mathematics from Rutgers University in 1974. He is the author of eleven books and the editor of other four books. He has published more than one hundred journal papers, is an SPIE Fellow, and has served as an Editor of the Journal of Electronic Imaging for six years. He is currently Chair of the SIAM Activity Group on Imaging Science. Prof. Dougherty has contributed extensively to the statistical design of nonlinear operators for image processing and the consequent application of pattern recognition theory to nonlinear image processing. His current research focuses on genomic signal processing, with the central goal being to model genomic regulatory mechanisms. He is Head of the Genomic Signal Processing Laboratory at Texas A&M University.



Yidong Chen received his B.S. and M.S. degrees in electrical engineering from Fudan University, Shanghai, China, in 1983 and 1986, respectively, and his Ph.D. degree in imaging science from Rochester Institute of Technology, Rochester, NY, in 1995. From 1986 to 1988, he joined the Department of Electronic Engineering of Fudan University as an Assistant Professor. From 1988 to 1989, he was a Visiting Scholar in the Department of Computer Engineering, Rochester Institute of Technology. From 1995 to 1996, he joined Hewlett Packard Company as a Research Engineer, specialized in digital halftoning and color image processing. Currently, he is a Staff Scientist in the Cancer Genetics Branch of National Human Genome Research Institute, National Institutes of Health, Bethesda, Md, specialized in cDNA microarray bioinformatics and gene expression data analysis. His research interests include statistical data visualization, analysis and management, microarray bioinformatics, genomic signal processing, genetic network modeling, and biomedical image processing.



Carsten O. Peterson is a Professor at the Department of Theoretical Physics and Head of the Complex Systems Division at Lund University, Sweden. His current research area is computational biology with the focus on microarray analysis, genetic networks, systems biology, and alignment algorithms. Dr. Peterson's research interests were initially in theoretical particle physics, multiparticle production, quantum chromodynamics, and also statistical mechanics. His research areas have subsequently evolved into spin systems, data mining, and time series analysis with some emphasis on biomedical applications, resource allocation problems, Monte Carlo sampling methods and mean field approximations, thermodynamics of macromolecules, protein folding/design, and computational biology in general. Dr. Peterson joined the Department of Theoretical Physics at Lund University in 1982, had an industrial intermission with Microelectronics and Computer Corporation (Austin, Tex) during 1986–1988, and held postdoctoral positions at Stanford (1980–1982) and Copenhagen (1978–1979). Dr. Peterson received his Ph.D. degree in theoretical physics and M.S. degree in physics from Lund University in 1977 and 1972, respectively.

