FOREWORD

In 1949, Norbert Wiener declared, “Many perhaps do not realize that the present age is ready for a significant turn in the development toward far greater heights than we have ever anticipated. The point of departure may well be the recasting and unifying of the theories of control and communication in the machine and in the animal on a statistical basis.” Wiener was doing nothing short of declaring the arrival of the age of systems biology; that is, biology as the study of stochastic dynamical systems. Genomic signal processing (GSP) plays a key role in this endeavor because it involves the modeling, analysis, and control of dynamical systems on a statistical basis. In particular, it addresses the two salient problems of translational genomics: (1) the design of therapeutic intervention and control strategies in biomolecular regulatory systems and (2) the development of biomolecular classifiers for diagnosis and prognosis. In line with its historical successes in other areas of engineering, GSP aims to develop rigorous statistical analysis and control in medical applications.

This Special Issue is comprised of eight papers that present important research problems and recent advances in the broad area of Genomic Signal Processing.

The paper by Fnaiech et al. proposes a sliding model control method as a variable structure control approach for network intervention in biological networks modeled as S-systems. While several control approaches have been proposed for intervention in S-systems, the proposed sliding model control enables robust control even when there is uncertainty in model parameters, which is typical in modeling biological systems. The experimental results based on the glycolytic-glycogenolytic pathway demonstrate the effectiveness of the proposed method.

In Bosio et al.’s paper, a two-step classification framework is implemented to improve the accuracy and reliability of gene expression classification. By combining hierarchical clustering to form “metagenes” as a larger pool of new features and an improved sequential floating forward feature selection algorithm to select final predictive features, the authors show reproducible improvements based on simulated data as well as the microarray gene expression data obtained from the Micro Array Quality Control Study (MAQC).

Meng et al. propose a novel Bayesian sparse non-negative factor regression (BSNFR) model for the inference and analysis of joint-regulation of genes by transcription factors and microRNAs. The proposed BSNFR model enables the integration of multiple data sources, and the developed Gibbs sampling solution can be used to infer TF/microRNA-mediated mRNA regulations and to uncover TF activities based on the model.

The paper by Hua et al. proposes a systems approach to study the dynamic measurements of reporters in individual cells based on a GFP reporter-based technology. The dynamical approach can be applied for identifying cell subpopulations with different drug sensitivities, analyzing the effects of drug concentration on cellular response, and designing combination therapies.
Berlow and Pal investigate the problem of Bayesian robust control in a class of Markov chains with uncertainty. A sequential search algorithm based on efficient steady-state distribution re-computation is developed for the generation of a sub-optimal stationary control policy. Based on classes of Markov chains modeling the dynamics in small synthetic networks, the authors demonstrate that the proposed algorithm can generate effective robust stationary control policies with considerable reduction of computational complexity.

Layek and Datta apply testing techniques from digital design to the problem of detection and intervention in a cancerous biological system. The biological system is modeled as a Boolean Network (BN) based on pathway knowledge and cancer is modeled as signaling faults in the BN.

The paper by Kakumani et al. provides an approach based on matched filtering that can be used for predicting RNA secondary structures with pseudoknots. The proposed approach is evaluated on RNA sequences derived from PseudoBase and compared with existing RNA secondary structure prediction algorithms to illustrate its effectiveness.

Intrinsically disordered proteins are commonly found in nature and they are known to possess diverse biological functions that are complementary to those of traditional ordered proteins. The paper by Howell et al. analyzes the protein length scaling of intrinsic disorder in eukaryotic proteins and investigates the presence of length-dependent functions of proteins with long disordered regions.

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