Guest Editorial—Special Issue on '-Omics' Based Companion Diagnostics for Personalized Medicine

COMPANION diagnostics are essential to the success of personalized medicine. For example, electronic glucose sensing companion diagnostics offer millions of diabetic patients around the world tangible benefits from monitoring their health and helping them make informed decisions about medications and treatment strategies. If used properly, companion diagnostics can help change our dietary habits, lifestyle, and exercise routines to help with disease mitigation and prevention. With the rapid advances made in high throughput molecular biology, such as genomics, proteomics, and metabolomics, in the past two decades, scientists, researchers and engineers are beginning to harvest the power of '-omics' to develop companion diagnostic circuits and systems. These systems can be used to diagnose, monitor or predict not just a single disease, but multiple diseases simultaneously. This allows for the management of disease at a personal level, i.e., accordingly to the biology, needs and lifestyle of individual patients. Foreseeing this emerging trend, we are pleased to present this special issue to: (i) provide a road map of '–omics' networks, circuits and systems; (ii) encourage cross-disciplinary collaboration in this emerging research field; and (iii) report the cutting edge development of these circuits and devices with potential for translation into the clinic.

A number of submissions were received, covering a wide range of circuits and systems related '-omics' topics, such as (i) DNA, RNA, protein, and small molecule sensors for companion diagnostics; (ii) micro/nanofluidics technologies related to '-omics'; and (iii) circuit based modeling and simulation of '-omics' systems including gene regulatory and signaling networks. After rigorous peer review nine papers were finally selected in this special issue. The papers can be broadly divided into three groups and briefly introduced below.

A. Tutorial Overview

S. MacKay, D. Wishart, J. Z. Xing, and J. Chen present an overview of '-omics' based companion diagnostics devices and applications for personalized medicine in "Developing Trends in Aptamer-based Biosensor Devices and Their Applications." This review article, in particular, examines the research and design of RNA and DNA aptamer based biosensor systems and applications as well as their potential for integration into effective biosensor devices.

B. Designs at the Devices and Circuits Level

Y. C. Lim, A. Z. Kouzani, W. Duan, X. J. Dai, A. Kaynak, and D. Mair present the design and development of a microcantilever-based aptasensor in "A Surface-Stress-Based Microcantilever Aptasensor." The authors used SU-8 polymer as the fabrication material and demonstrate label-free detection of thrombin molecules with high specificity using their fabricated aptasensor. Compared to the deflection of a silicon nitride microcantilever biosensor, the measured accuracy of the proposed design is one order of magnitude higher.

X. Liu, L. Li, and A. J. Mason show a CMOS microhotplate array tailored to protein interfaces for thermoregulation in a liquid sample environment within $\pm 1^{\circ}\mathrm{C}$ in "Thermally Controlled Electrochemical CMOS Microsystem for Protein Array Biosensors." The authors demonstrate the microhotplates can provide suitable thermal control for biosensor temperature ranges without the complicated procedures often used in most previously reported microhotplates.

J. Guo, W. Lei, X. Ma, P. Xue, Y. Chen, and YJ Kang present a fluidic circuit-based microcytometer in "Design of A Fluidic Circuit-based Microcytometer for Circulating Tumor Cell Detection and Enumeration." By measuring the bandwidth and amplitude of the bias-voltage pulses induced by the microparticles' physical blockage, the microcytometer can characterize red blood cells and circulating tumor cells.

P. Zhu and J. Han present a circuit and system design of a stochastic multiple-valued gene network to model the noise effect and perturbation in gene regulatory networks in "Stochastic Multiple-valued Gene Networks." The simulation results show that the proposed design can be used to effectively evaluate the network dynamics and steady state distribution of the p53-Mdm2 and the WNT5A networks under random gene perturbation.

C. Algorithm Designs at the System Level

S. Edri, E. Gazit, E. Cohen, and T. Tuller introduce an RNA polymerase flow model (RPFM) in "The RNA Polymerase Flow Model of Gene Transcription." RPFM can be used to model the fundamental cellular processes, such as DNA to RNA transcription and other intracellular biological phenomena such as translation initiation.

T. Narayanan and S. Subramaniam present a Newtonian Community Detection algorithm for protein-protein interaction networks of *E. coli*, *C. elegans*, and *S. cerevisiae* in "A Newtonian Framework for Community Detection in Biological Networks." The results from the E. coli network case study illustrate that the algorithm yields communities possessing structural properties comparable to real biological networks.

M. Masnadi-Shirazi, M. Maurya, and S. Subramanian developed a novel framework for reconstructing signaling networks involved in macrophage activation in "Time-Varying Causal Inference from Phospho-Omics Measurements in Macrophage Cells." By reconstructing the time-dependence of the phosphoprotein network, they were able to estimate connectivity, Granger causality and the dynamics of information flow.

Digital Object Identifier 10.1109/TBCAS.2014.2308993

P. Wang, J. H. Lu, X. H. Yu, and Z. R. Liu developed a new measure to characterize the structurally dominant proteins in protein-protein interaction networks in "Identification and Evolution of Structurally Dominant Nodes in Protein-Protein Interaction Networks." The authors further investigated the evolution of the defined dominant nodes in temporal evolving real and artificial protein-protein interaction networks.

The guest editors would like to thank all the authors and reviewers. Finally, this special issue would not be possible without the help and guidance of Dr. Gert Cauwenberghs, the editor-in-chief of IEEE TRANSACTIONS ON BIOMEDICAL CIRCUITS AND SYSTEMS and the support of the editorial board.

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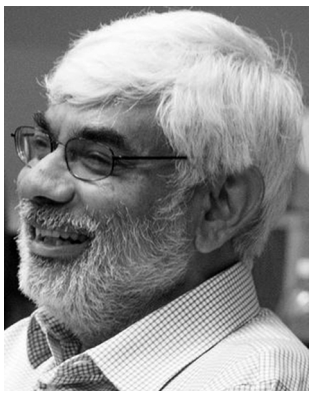
He is a Professor of the ECE Department and an Adjunct Professor of the Biomedical Engineering Department at the University of Alberta, Edmonton, AB, Canada, as well as a Research Officer of the Canadian National Research Council/National Institute for Nanotechnology. His research on designing a miniaturized ultrasound device for intra-oral dental tissue formation was listed by *Reader's Digest* as a major medical breakthrough in Canada in 2006. In partnership with the University of Toronto, the device is in a Phase 2 clinical trial. He also helped establish a Bell-Lab spin-off company (focusing on developing the 4th-generation wireless network) that was acquired by QUALCOMM in San Diego in 2005. His current interdisciplinary research interests are (i) impedance-based portable devices for metabolic sensing, (ii) a low intensity pulsed ultrasound device for cell therapy and increasing renewable biofuel production, and (iii) a nanotechnology-based platform for gene and drug delivery.

Dr. Chen was elected as a Fellow of the Engineering Institute of Canada and has received numerous awards such as the Canada Foundation for Innovation Leaders' Opportunity Award, the IEEE Distinguished Lecturer Award by the Circuits and Systems Society, and Best Student Paper Award at the IEEE/National Institutes for Health (NIH) 2007 Life Science Systems and Applications Workshop.



Shankar Subramaniam received the B.S. and M.S. degrees from Osmania University, Hyderabad, India, and the Ph.D. degree in chemistry from the Indian Institute of Technology Kanpur, Kanpur, India.

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