BIOINFORMATICS and biomedicine research is fundamental to our understanding of complex biological systems, impacting the science and technology of fields ranging from agricultural and environmental sciences to pharmaceutical and medical sciences. This type of research requires close collaboration among multidisciplinary teams of researchers in computer science, statistics, physics, engineering, life sciences and medical sciences, and their interfaces. The IEEE International Conference on Bioinformatics and Biomedicine aims to provide an open and interactive forum to catalyze the cross-fertilization of ideas from these disciplines and to bridge our knowledge gaps.

The IEEE BIBM 2016 was held in Shenzhen, China from December 15-18, 2016. The scientific program highlights five themes to provide breadth, depth, and synergy for research collaboration: (1) genomics and molecular structure, function, and evolution; (2) computational systems biology; (3) medical informatics and translational bioinformatics; (4) cross-cutting computational methods and bioinformatics infrastructures, and (5) healthcare informatics. IEEE BIBM 2016 received 366 research paper submissions from 1457 authors and co-authors at 40 countries. The 233 Program Committee members from 25 countries accepted 144 papers this year, of which 70 (19.1%) are regular research papers and 74 (20%) are short papers. Based on the PC review recommendation, 8 papers are selected from the IEEE BIBM 2014 conference for this special issue, each paper has been extended significantly based on the conference papers.

The first paper by Chen Zhang et al. presents a field-programmable gate array (FPGA)-based implementations of both methods for further acceleration. The capability of FPGAs on handling different image processing components in these methods is discussed. A fast and memory-saving image warping approach is proposed. The algorithms are reformulated to build a highly efficient pipeline on FPGA.

The paper by Wu et al. investigates the MSSs of biomolecular networks by considering the drug binding information. The biomolecules in the MSSs with binding preference are enriched with known drug targets and are likely to have more chemical-binding opportunities with existing drugs compared with randomly chosen MSSs, suggesting novel applications for drug target identification and drug repositioning.

Gao et al. propose BalanceAli, a novel approach for global alignment of multiple PPI networks that achieves high k-coverage and k-consistency simultaneously. With six data sets consisting of various numbers of PPI networks from five species, we evaluate the experimental results using different k values. The performance evaluations of our approach against other three state-of-the-art methods demonstrate the preferable comprehensive strength of our approach.

High dimensionality has become a typical feature of biomolecular data. The paper by Kong et al. presents a novel dimension reduction method named p-norm singular value decomposition (PSVD) to seek the low-rank approximation matrix to the biomolecular data. To enhance the robustness to outliers, the Lp-norm is taken as the error function and the Schatten p-norm is used as the regularization function in the optimization model. To evaluate the performance of PSVD, the Kmeans clustering method is then employed for tumor clustering based on the low-rank approximation matrix.

It has been reported that chronic heroin intake induces both structural and functional changes in human brain; however, few studies have investigated the carry over adverse effects on brain after heroin withdrawal. Zhao et al. examined the neurophysiological differences between the abstinent heroin addicts (AHAs) and healthy controls (HCs) using nonlinear dynamic analysis and source localization analysis in resting-state electroencephalogram (EEG) data; 5 min resting EEG data from 20 AHAs and twenty age-, education-, and gender-matched HCs were recorded using 64 electrodes. The results of nonlinear characteristics (e.g., the correlation dimension, Kolmogorov entropy, and Lempel-Ziv complexity) showed that the EEG signals in alpha band from AHAs were significantly more irregular.

The paper by Zhan et al. aims to infer social influence of these campaigns, and the problem is formally referred to as the Social Influence inference of anti-Tobacco mass media campaigns (Site) problem. To address the Site problem, a novel influence inference framework, TV advertising social influence estimation (Asie), is proposed based on our analysis of two real anti-tobacco campaigns.

The 7th paper presents a fast post-processing pipeline including cropping, background subtraction, center of rotation (COR) correction and 3D reconstruction. Regarding to the COR correction, a novel algorithm based on interest point detection of sinogram is proposed by considering the principle of OPT imaging.

Tan et al. proposes an algorithm to identify STR markers with high discriminative abilities from the next-generation sequencing (NGS) data. Our algorithm could select a customized set of loci for a given population with pre-specified discriminative thresholds.
Xiaohua Tony Hu received the Ph.D. degree in 1995. He joined Drexel University in 2002. Earlier, he was a Research Scientist with the world-leading research and development centers, such as the Nortel Research Center and the Verizon Lab. In 2001, he founded DMW Software in Silicon Valley, CA, USA. He founded the *International Journal of Data Mining and Bioinformatics* (SCI indexed) in 2006 and the *International Journal of Granular Computing, Rough Sets and Intelligent Systems* in 2008. He is currently a Full Professor and the Founding Director of the Data Mining and Bioinformatics Lab, College of Computing and Informatics. He is also serving as the Founding Co-Director of the NSF Center (I/U CRC) on Visual and Decision Informatics (NSF CVDI), the IEEE Computer Society Bioinformatics and Biomedicine Steering Committee Chair, and the IEEE Computer Society Big Data Steering Committee Chair. He is also a Scientist, a Teacher, and an Entrepreneur. He has a lot of experience and expertise in converting original ideas into research prototypes, and eventually into commercial products; many of his research ideas have been integrated into commercial products and applications in data mining fraud detection and database marketing.

He has graduated 20 Ph.D. students from 2006 to 2017 and is currently supervising ten Ph.D. students. His research projects are funded by the National Science Foundation, U.S. Department of Education, the PA Department of Health, and the Natural Science Foundation of China. He has obtained more than U.S. $9 million research grants in the past ten years as PI or Co-PI (PIs of nine NSF grants, PI of one IMLS grant in the last eight years). His current research interests are in data/text/web mining, big data, bioinformatics, information retrieval and information extraction, social network analysis, healthcare informatics, and rough set theory and application. He has authored over 270 peer-reviewed research papers in various journals, conferences, and books, such as various IEEE/ACM Transactions (the IEEE/ACM TCBB, the IEEE TFS, the IEEE TDKE, the IEEE TITB, the IEEE SMC, IEEE COMPUTER, IEEE NanoBioScience, and IEEE Intelligent Systems), JIS, KAIS, CI, DKE, IJBRA, SIG KDD, the IEEE ICDM, the IEEE ICDE, SIGIR, the ACM CIKM, the IEEE BIBE, and the IEEE CICBC, and co-edited 20 books/proceedings.