Editorial

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Biographical notes: Ying (Ada) Chen is an Assistant Professor in the Department of Electrical and Computer Engineering and Biomedical Engineering Graduate Program at Southern Illinois University, Carbondale, Illinois. She received her PhD from Duke University. Her research interests include biomedical imaging, image reconstruction, digital tomosynthesis and image quality analysis.

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The main objective of this special issue is to promote importance, success, challenges and perspectives of emerging medical imaging and biocomputing technologies as well as to present the new innovations in related fields. This special issue contains full-length articles of research focusing on modern imaging modalities and computation technologies with biomedical applications varying from genetic aspects to neural activity detection and therapy. All papers were subjected to a rigorous review process before publication. A total of six papers have been selected to be included to represent important original scientific contributions to medical imaging and biocomputing fields.

Modern medical imaging and biocomputing have led to advance in our understanding of structural and functional information of human beings and biological samples. Various imaging and computation technologies have been widely used to achieve innovations and accomplishments in developing new devices, procedures, drugs, instruments, etc., to improve diagnosis and detection. Utilising the medical imaging and biocomputing technologies for interdisciplinary research in biomedical fields has stated to lead many advances.

Medical imaging modalities are used widely as efficient tools for diagnosis purposes. It is also used frequently for a variety of detections. In this special issue, Chen et al. presented a novel laser imaging technology for rapid microbial source tracking. Microbial source tracking is an important method to identify the source of microbial contamination

of water, with emphasis on DNA typing approaches. A non-invasive method using laser scattering imaging on bacterial colonies and optical scattering image analysis was developed. The proposed laser imaging method is promising to provide high-resolution information for rapid microbial source tracking.

In functional medical imaging fields, functional Magnetic Resonance Imaging (fMRI) enables non-invasive study of brain functionalities. Li et al. described a graphical model inference method to investigate neural activity with fMRI images, based on statistical data analysis and probabilistic graphical models. The proposed approach demonstrated advantages in terms of computational cost and robustness in neural activity detection.

Biocomputing involves the application of engineering, mathematics, statistics and computational methods for the improvement of biological design and human health. Researchers have been working on various developments of computational algorithms and simulation models for diagnosis, treatment and other related applications. Saripalli and Botros described a novel computing simulation and modelling of colorectal cancer using a hardware descriptive language package. Results suggested that this computing simulation method is an effective way to conduct the research on cancer modelling and simulation to improve the understanding of cancer mechanism and cancer detection.

As an emerging new modality in non-invasive thermal ablation for cancer and tumour treatment, high intensity focused ultrasound has been invstigated as a potential alternative method for cancer therapy. Zhou proposed a fast algortihm to improve the time-comsuming on-site treatment planning procedure. This may serve as a solid foundation to boost the future potential clinical applications.

A research paper in this special issue presented a parallel computing approach to multiple sequences alignment and phylogenetic tree node labelling. A phylogenetic tree describes an evolutionary relationship among species. Results showed that this biocomputing technique significantly reduced the computation time and memory cost. This emerging biocomputing method is capable to effectively fulfil the phylogenetic tree node labelling tasks.

The last paper of this special issue proposed a novel method for determining differentially expressed genes. This new method used the probe-level intensity data to filter differentially expressed genes from non-differentially expressed genes and compared with methods based on expression values by using two spikein data sets. The authors provided theoretical analysis and experimental results from application to real microarray data, and demonstrated advantageous features of their novel method.

This special issue of *International Journal of Computational Biology and Drug Design* was the products of much effort by many people. We are especially grateful to the anonymous reviewers for devoting their expertises and to the Editors for their great support, very valuable help and discussion.