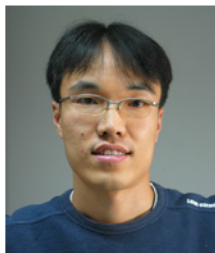


Special Issue on Biomedical Image Informatics



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Biomedical image informatics is a rapidly growing research area that focuses on the processing and analysis of images in biomedical research. The scale of these images is from the cellular and molecular level to organs and the whole body level. With the rapid growth of biomedical imaging technology, biomedical image data with anatomical, physiological, and metabolic information have been explosively created for the past decades, and it provides huge opportunities for novel research and scientific discovery. However, the processing and analysis of biomedical images is challenging as the number of images and modalities continues to expand. Biomedical image informatics helps to overcome these challenges through computational methods, which will eventually enable researchers to process and analyze the rapidly increasing amount of biomedical images. In order to introduce such research trends, we select biomedical image informatics as a theme of this Special Issue of *Biomedical Engineering Letters*. This special issue includes two review articles and

five original research papers covering various state-of-the-art-technologies.

The first paper entitled “The demand for quantitative techniques in biomedical image informatics” by Jang *et al.* introduces computational techniques to process and analyze biomedical images from data acquisition to data analysis [1]. As the number of biomedical images increases, the demand for quantitative techniques rises. In order to increase awareness of the needs and importance of quantitative techniques for biomedical image informatics, this paper reviews several aspects including biomedical imaging, image repositories, and image processing.

The second paper entitled “Automatic cell identification in the unique system of invariant embryogenesis in *Caenorhabditis elegans*” by Azuma and Onami reviews a series of development of the methods for automatically identifying spatio-temporal dynamics of embryonic cells in *Caenorhabditis elegans* (*C. elegans*) and their applications [2]. Those methods allow quantitative and high-throughput analysis for molecular dynamics during embryogenesis. Together with advances in imaging technologies to measure molecular dynamics, and computational methods to identify such dynamics with high accuracy, the unique system of invariant embryogenesis in *C. elegans* will be invaluable to study developmental mechanisms.

The third paper entitled “Constructing 5D developing gene expression patterns without live animal imaging” by Peng and Myers proposes a method reconstructing the

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developing pattern of gene expression with five spatio-temporal intrinsic dimensions computationally without live imaging [3]. The authors developed a computational method to reconstruct a developmental time series of the expression of a gene using 3D in situ images of a large number of *Drosophila* embryos sampled randomly from the desired time interval. The authors further applied this computational approach to reconstruct the developmental time series of the expression of several genes in late blastoderm fly embryos.

The fourth paper entitled “Fusion imaging in neurosonology: clinician’s questions, technical potentials and applicability” by Sakas *et al.* presents how the newly emerging fusion imaging techniques may help to solve a number of ultrasound related problems, including the following three issues [4]: 1. While being an ideal bed-side technique, imaging has some limitations compared to the non-bedside techniques like CT or MRI. 2. With conventional ultrasound, comparison of specific structural findings with other diagnostic modalities such as CT, MRI or PET is not possible. 3. Ultrasound is a “free hand” technique: considering the countless options in choosing an individual insonation plane, imaging of exactly the same region or point of interest during a re-examination can be difficult.

The fifth paper entitled “Automatic left and right heart segmentation using power watershed and active contour model without edge” by Kang *et al.* presents an automatic method to segment a whole heart and separate left and right heart regions in cardiac computed tomography angiography (CTA) efficiently [5]. In experimental results using twenty clinical datasets, the authors showed that the proposed method extracts the left and right heart accurately, demonstrating that this approach can assist the cardiologist.

The sixth paper entitled “A strategy to reduce blocky pattern and contrast loss in emission tomography reconstruction with reduced angular sampling and total variation minimization” by Son *et al.* presents a reconstruction method to suppress deterioration of image quality even with only a small sampling number of projection data in SPECT [6]. The authors showed that EM-TV with the combination of PM and geometric nonlinear diffusion filters was found to improve uniformity while maintaining contrast-to-noise ratio when angular sampling is low.

The seventh paper entitled “Functional connectivity change of the rat brain in response to sensory stimuli using functional near-infrared brain imaging” by Kim *et al.* introduces the functional connectivity of the rat brain could be analyzed using diffuse optical tomography (DOT) system [7]. In the experiments, the authors measured the coactivation in brain regions in response to sensory stimulation using CW-DOT. Concentration changes in oxyhemoglobin and deoxyhemoglobin was calculated using reconstructed absorption coefficients at each nodes in finite-element mesh. Then these time-series node data were mapped on the rat brain MR image. The mapped data were further analyzed to extract coactivation by calculating correlation coefficients between time-series node data and standard response pattern of the two parameters.

As co-organizers of this special issue, we gest editors would like to express our gratitude to the contributing authors for their efforts on reviewing the cutting-edge technologies and providing novel and original research in the field of biomedical image informatics.

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