
Editorial

Tianming Liu

Department of Computer Science
and Bioimaging Research Center,
University of Georgia,
Athens, GA, 30602, USA
E-mail: tliu@cs.uga.edu

Fuhui Long

Janelia Farm Research Campus,
Howard Hughes Medical Institute,
Ashburn, VA, 20147, USA
E-mail: longf@janelia.hhmi.org

Biographical notes: Tianming Liu is an Assistant Professor of Computer Science at UGA. Liu is also an affiliated faculty with the UGA Bioimaging Research Center (BIRC), the UGA Institute of Bioinformatics (IOB), the UGA Biomedical and Health Sciences Institute (BHSI), the UGA Neuroscience Program, and the UGA Faculty of Engineering. Before he moved to UGA, he was a faculty member of Weill Medical College of Cornell University (Assistant Professor, 2007–2008) and Harvard Medical School (Instructor, 2005–2007). He has a post-doctorate in neuro-imaging from the University of Pennsylvania (2002–2004) and Harvard Medical School (2004–2005). He received his PhD in Computer Science from Shanghai Jiaotong University in 2002. Liu is the recipient of the Microsoft Fellowship Award (2000–2002) and the NIH NIBIB K01 Career Award (2007–2011).

Fuhui Long is currently a Senior Research Scientist at Janelia Farm Research Campus, Howard Hughes Medical Institute. Her research interest has been focusing on bio-image informatics and computational biology. In particular, she has been developing novel bio-imaging, bio-image informatics, machine learning, and data mining techniques to address challenging questions in systems biology, neuroscience, developmental biology and cell biology. Before joining Janelia Farm Research Campus, she did her postdoctoral training at Lawrence Berkeley National Lab Life Sciences Division and Duke University Medical Center. She has co-chaired and organised several bio-image informatics workshops over the past several years.

In recent years, microscopic bioimaging has played an increasingly vital role in many biological research studies such as pathway analysis, target identification, drug discovery, and systems biology. Driven by these applications, computerised analysis of bioimages has been actively studied. Despite the tremendous progresses in the development of computational algorithms and software tools from the bioimage informatics community, there are still many issues that need to be addressed urgently and adequately.

For instances, bioimage informatics software systems that are capable of adding new data analysis and management capabilities quickly and easily are much needed, and software tools with user-friendly interfaces that are accessible to average biologists without limiting the full power of these tools to more experienced users are also in urgent needs. This special issue aims to take a snapshot of recent efforts in the development of computational algorithms and software tools from the bioimage informatics community, in order to address the major challenges in the fast-growing field of bioimaging.

This special issue includes four papers entitled ‘Research on segmentation of dorsal diencephalon and ventral midbrain of zebrafish embryo based on active contour model’, ‘Entropy based unsupervised feature selection in digital mammogram image using rough set theory’, ‘Axonal transport analysis using multitemporal association tracking’, and ‘Fast leukocyte image segmentation using shadowed sets’. The first paper introduced an algorithmic pipeline for segmenting dorsal diencephalon and ventral midbrain of zebrafish embryo from microscopic images. This paper proposed an active contour model that integrates region-based active contour model and geodesic active contour for automatic segmentation of zebrafish images. The authors reported that the agreement between the algorithm and manual segmentation is more than 90%. This paper contributes to the important zebrafish bioimage informatics field. The second paper contributed an entropy based unsupervised feature selection method for digital mammogram image analysis. The authors compared this method with existing supervised methods and reported that it can effectively remove redundant features. This paper contributes to the general field of mammogram image analysis. The third paper applied the multi-temporal association tracking method on image sequences to quantify deficiencies in axonal transport. The authors reported that the proposed method achieved a reduction in error rate of around 8 times, in comparison with an application specific bipartite matching tracker, and around 45 times compared to a generic single frame tracker. This paper contributes to the topic of axonal transport analysis. The fourth paper proposes a fast leukocyte image segmentation method via shadowed sets. The authors performed comparative analysis which revealed that the proposed algorithm is fast and robust in segmenting stained blood microscopic images in the presence of outliers. This paper contributes to the field of leukocyte image segmentation and analysis. The fifth paper presents a novel flow field tracking method on surface for touching cell segmentation, and contributes to the general field of biological object segmentation. The sixth paper presents a novel study of morphological shape analysis of zebrafish tails and demonstrated reasonably good performance of the computational pipeline. This paper contributes to the general field of biological shape analysis. In short, these six papers have demonstrated that bioimage informatics is an enabling field that can significantly advance biology and scientific discovery in general.

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