
Editorial

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Biographical notes: Tuan D. Pham received his PhD in Civil Engineering from the University of New South Wales in 1995. He is an Associate Professor in the ADFA School of Information Technology and Electrical Engineering at the University of New South Wales. He has published two research books and more than 150 papers in edited books, peer-reviewed journals, and peer-reviewed international conference proceedings. His current research interests include image processing, pattern recognition, fuzzy-set algorithms, geostatistics, bioinformatics, and biomedical informatics.

Xiaobo Zhou received his PhD in Mathematics from Peking University, Beijing, China, in 1998. From 2003 to 2006, he was a Research Scientist and Instructor with the Harvard Center for Neurodegeneration and Repair in Harvard Medical School and Radiology Department in Brigham and Women's Hospital, Boston, MA. In 2007, he was an Assistant Professor at Harvard University. Since 2007, he has been an Associate Professor at Cornell

University and Methodist Hospital, Houston, TX. His current research interests include high-content molecular and cellular imaging analysis, biomedical imaging analysis, molecular imaging informatics, neuroinformatics and bioinformatics for genomics and proteomics.

Hong Yan received his PhD from Yale University. He has been Professor of Imaging Science at the University of Sydney and is currently Professor of Computer Engineering at City University of Hong Kong. His research interests include image processing, pattern recognition and bioinformatics. He is elected a Fellow of the IEEE for contributions to image recognition techniques and applications and a Fellow of the IAPR for contributions to document image analysis.

Denis I. Crane obtained his PhD from Griffith University where he was appointed to a lectureship in 1989, and to Professor in 2008. His research fields include molecular cell biology, biochemistry, and human genetics. Current research focuses on the characterisation of mouse models of Zellweger syndrome, as well as the molecular basis of neurodegeneration of this and other neurodegenerative disorders. Other research focuses on mechanisms involved in the import of proteins into peroxisomes.

To be novel in research, a renowned earth scientist has said that a good way is to attend seminars from other departments such as economics and finance. Based on our own experience in our long-standing interdisciplinary collaboration, we believe it is true. Interdisciplinary research involves complementary expertise of researchers from different fields.

In industry, automated methods have been utilised to study honeybee behaviour and in the meantime, honeybee behaviour has been adopted to control unmanned helicopters. This is a good example of the interaction between biology and machine learning. Systems biology is one of the most attractive research areas in modern biology and is an emergent field that aims at system-level understanding of biological systems. System-level understanding has been a long-pursuit goal of biological sciences and has its root in control and communication theories. On the other hand, advanced methods in cybernetics are inspired from the learning of complex biological networks to manipulate machines and accomplish daunting tasks that conventional control theory gives in.

In terms of the entropy measure, the information content or the surprise factor of this special issue is high for the usual community of engineering technology. One may wonder what finite element methods in computational mechanics have something to do with bioinformatics or computational biology or vice versa. In fact, its numerical analysis tools have provided solutions to chemistry and biology. Based on this observation, our objective is to communicate current problems and results in the field of computational life science to the community of engineering science and technology. We hope that researchers from different disciplines can learn from each other to evolve science and technology from unconventional perspectives.

This issue consists of eight papers addressing various computational algorithms for biology, ecology and medicine. Imanishi and Oyama-Higa applied chaos theory to study finger plethysmograms in ergonomics. Pacheco et al. used hidden Markov models, a well-known pattern classification approach to speech recognition, for the recognition of flagellar patterns and identification of actin-associated elements. Wu et al. investigated cross sequence similarities for compressing large amount of DNA sequences.

In medical imaging, Peter et al. developed a parameter estimation method for robust image registration; while Qian et al. applied a knowledge-based system to brain tissue segmentation.

In the context of probabilistic modelling Tsoularis applied Bayesian-based models to simulate the utility of reinforcement learning in predation.

In bioimaging, Mele et al. attempted to develop a fully automated methodology for identifying vesicle-membrane fusion events in TIRF microscopy. This automation procedure helps speed up the screening process and has potential for discovering important biological information of cells to facilitate research in diabetes and obesity. Finally, Zhou et al. presented an interesting method for 3-D neuron image detection and reconstruction, which helps reveal the hypothesised relationship between neurological functions of neuron and its morphology.

We thank all the authors for their timely effort in contributing to this special issue. We are grateful to all the reviewers – their generous offer of assistance greatly helped improve the paper quality. We wish to express our gratitude to Yan Luo, the Editor-in-Chief of the journal, for his encouragement and kind support in making this special issue a valuable contribution to the endeavour of exploring engineering and computational technologies for solving problems in life sciences.