Editorial

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Biographical notes: Huiru Zheng received the BEng in Biomedical Engineering from Zhejiang University, China, in 1989, the MSc in Communication and Electronic System from Fuzhou University, China, in 1992, and the PhD in Data Mining and Bioinformatics from the University of Ulster, UK, in 2003. She is Lecturer of Computer Science with the School of Computing and Mathematics, University of Ulster. Before she joined the University of Ulster, she was working in Fuzhou University as an Assistant Lecturer (1992), Lecturer (1995) and Associate Professor (2000). Her research interests include biomedical engineering, medical informatics, bioinformatics, data mining and artificial intelligence. She has over 90 scientific publications in these areas.

Haiying Wang received the BEng and MSc in Optical Electronics Engineering from Zhejiang University, Hangzhou, China, in 1987 and 1989, respectively. He was a Senior Engineer in Applied Electronics at the Fujian Electronic Technology Institute, Fuzhou, China, and received the PhD on Artificial Intelligence in Biomedicine from the University of Ulster, Jordanstown, UK, in 2004. He is currently a Lecturer in the School of Computing and Mathematics at the University of Ulster. His research focuses on artificial intelligence, machine learning, pattern discovery and visualisation, XML, and their applications in medical informatics and bioinformatics.

The main objective of this special issue is to bring together researchers from different research background including computer science, mathematics, statistics and systems biology to present newly developed techniques and innovation applications in the field of microarray data analysis and beyond. After the rigorous two-round review process and stringent evaluation, a total of five papers have been selected to be included in this special issue with topics ranging from the analysis of microarray image data to the selection of microRNA targets.

Image analysis has become a standard approach in analysis of microarray scan images. A number of image analysis systems currently in use differ with the algorithms implemented and the quality of the analysis remains a challenge. Zineddin et al. tackled this challenge with focusing on an image's feature space. Instead of analysing raw microarray image data, they adopted a multi-view approach such that emphasis is placed on certain frequencies or regions of interest and concluded that the Complex Diffusion filter is the best one to work with image transformation engine.

In systems biology, simulation and modelling provide a useful tool for the understanding of biological process. The biological complexity and the computational complexity provide a huge opportunity for systems biology community to explore new algorithms. Li et al. proposed an improved extreme learning machine to improve model sparsity without increasing the overall computational complexity. The effectiveness of the model was tested on the identification of MAPK signal transduction pathway and the transcriptional network of SOS response to DNA damage in *Escherichia coli.*

Development of new classification techniques for solving genomics and proteomic problem is one of the most popular research topics in bioinformatics and systems biology. On the basis of label ranking and delicate decision boundary, Chen et al. presented an improved probabilistic Support Vector Machine (SVM) algorithm for multi-label classification problems and applied it to functional genomics applications.

The fourth paper in this special issue is focused on the prediction of protein structures, in which Blayney and her colleagues presented their recent work on predicting three-dimensional structure of protein fragments from Dihedral angle propensities and molecular dynamics using a threading algorithm and *in vacuo* molecular dynamics simulations. The results presented demonstrate that a data set comprising smaller protein fragments is more effective in the prediction of smaller peptide structure than its full counterpart and the use of molecular dynamics as an evaluation and selection tool to identify the most stable model structure via the most stable trajectory was promising.

This special issue concludes by a research on the identification of disease biomarkers. On the basis of the combination of miRNA and proteomic data, Arrigo et al. proposed a 'reverse' approach for the selection of miRNA targets, which take into account data about miRNA conformational properties to estimate the miRNA–target complex stability. The integrative bioinformatics workflow that combines miRNA and proteomic data mining may be useful to other researchers.

The special issue is a result of the dedication of many contributors. We are especially grateful to the anonymous reviewers for devoting their time and expertise, which guaranteed the quality level achieved in this special issue. We thank the Editors of *International Journal of Computational Biology and Drug Design,* for their support and encouragement.