
Introduction

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Biographical notes: Dong Xu is James C. Dowell Professor and Chair of Computer Science Department, with appointments in the Christopher S. Bond Life Sciences Center and the Informatics Institute at the University of Missouri. He obtained his PhD from the University of Illinois, Urbana-Champaign, in 1995 and did two-year postdoctoral work at the US National Cancer Institute. He was a Staff Scientist at Oak Ridge National Laboratory until 2003 before joining the University of Missouri. His research includes protein structure prediction, high-throughput biological data analyses, in silico studies of plants, microbes and cancers. He has published more than 160 papers.

Yanqing Zhang is currently an Associated Professor of the Computer Science Department at Georgia State University, Atlanta, USA. He received the PhD Degree in Computer Science and Engineering at the University of South Florida, Tampa, in 1997. His research interests include computational intelligence, data mining, bioinformatics, computational Web intelligence, and intelligent parallel/distributed computing. He has co-authored two books, co-edited two books and four conference proceedings. He published 15 book chapters, 65 journal papers and over 130 conference/workshop papers. He is a Member of Data Mining Technical Committee and Bioinformatics and Bioengineering Technical Committee of the Computational Intelligence Society of IEEE.

Functional informatics and personalised medicine in the new era of biomedical sciences and computational sciences are interactive disciplines that hold great promise for the advancement of cutting-edge research and development in biomedical informatics and pharmaceutical sciences. *IJFIPM* provides an interactive and attractive forum for the advancement of innovative medicine, biotechnology, environmental, biomedical and pharmaceutical sciences driven by functional informatics and personalised medicine.

IJFIPM covers biomedical informatics, health informatics, translational bioinformatics, systems biology, chemical informatics, biomedical imaging, biomedical database, biomedical data mining, customised medicine, traditional medicine, and alternative medicine.

This special issue includes six papers selected from the 2009 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2009), held in Washington DC, USA on 1–4 November, 2009. They present recent advanced biomedical techniques in different areas.

Analysing DNA Copy Number Changes using Fused Margin Regression by Yuanjian Feng, Guoqiang Yu, Tian-Li Wang, Ie-Ming Shih and Yue Wang presents a new fused margin regression method for detecting copy number changes using DNA array data. Experimental results on both CGH and SNP array datasets indicate that the new method is more effective than other commonly used methods.

Biomedical Relationship Extraction from Literature based on Bio-semantic Token Subsequences by Jayasimha Katukuri, Ying Xie and Vijay Raghavan proposes two new biomedical literature mining methods. The first method computes the bio-semantic token subsequence kernel and the second method identifies semantic features from bio-semantic token subsequences. The two novel methods perform better than current biomedical extraction methods for multi-class protein-protein interaction classification.

Hybrid Support Vector Machine for Imbalanced Data in Multiclass Arrhythmia Classification by Aniruddha J. Joshi, Sharat Chandran, Valadi K. Jayaraman and Bhaskar D. Kulkarni makes a new compensatory system with both binary and multiclass SVMs to deal with imbalanced biomedical data. The new hybrid system can use the updated features to achieve higher accuracy than a traditional SVM.

Non-Rigid Registration for Brain MRI: Faster and Cheaper by Yixun Liu, Andriy Fedorov, Ron Kikinis and Nikos Chrisochoides uses both block matching and finite element solver to solve the problem of Non-Rigid Registration (NRR) for intra-operative recovery of brain shift. The high performance computing approach is used to greatly speed up the complex process.

MOACO Biclustering of Gene Expression Data by Junwan Liu, Zhoujun Li, Xiaohua Hu and Yiming Chen develops a biclustering algorithm based on the crowding multiple objective ant colony optimisation for analysing DNA microarray data. Good simulation results on two gene expression data sets are reported.

Analysis of Microarray Data to Infer Transcription Regulation in the Yeast Cell Cycle by Akther Shermin and Mehmet A. Orgun designs a new system based on dynamic Bayesian network using two biological features of gene regulation. Two real microarray datasets of the yeast cell cycle have been applied to evaluate the system in terms of consistency and scalability. The system is computationally efficient and topologically accurate in inferring gene regulation networks.

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