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Computational Intelligence Technologies Meet Medical Informatics -From Prediction to Prognosis

J.UCS Special Issue

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Computational Intelligence technologies such as evolutionary computation, neural networks, decision tree, etc., have made great progress in recent decades and attracted the growing interest of researchers and scientists in a number of various applications. Medical informatics is an emerging multidisciplinary scientific field that aims to effectively utilize biomedical data and clinical information and knowledge through development and applications of principles of computer science and computational intelligence to improve healthcare via diagnosis, prediction, prognosis, and prevention of diseases, injury, physical and mental impairments.

This special issue of the Journal of Universal Computer Science intends to select innovative and high-quality research with a goal to provide a comprehensive overview of contemporary studies in computational intelligence technologies with medical informatics applications from prediction to prognosis. In this special issue, we received 31 submissions, including papers submitted to the International Conference on Medical and Health Informatics 2017 (ICMHI 2017). Each contribution went through second rounds of peer-review, each with peer review in the fields of medicine and computational intelligence. Eight contributions were then selected

based on the quality of their work, reviewers' comments, and editorial judgement. We summarized each contribution as follows.

The first paper, entitled "A Hybrid Machine Learning Scheme to Analyze the Risk Factors of Breast Cancer Outcome in Patients with Diabetes Mellitus" by Linglong Ye, Tian-Shyug Lee and Robert Chi, presents a hybrid machine learning scheme to cope with imbalanced data in the analysis of risk factors of breast cancer in patients with diabetes mellitus. Their scheme integrates the undersampling based on the clustering algorithm, the k-means algorithm, and the extreme gradient boosting algorithm. Experimental results identify that that occlusion stroke, diabetes with peripheral circulatory disorders, peripheral angiopathy in diseases classified elsewhere, and other forms of chronic ischemic heart disease are four important risk factors, which can be used to assist health care providers to appropriately counsel patients on the risk of breast cancer and improve screening strategies.

The second paper, entitled "Cancer Classification by Gene Subset Selection from Microarray Dataset" by Asit Kumar Das, Soumen Kumar Pati, Hsien-Hung Huang and Chi-Ken Chen, proposes a Pareto-optimality-based multi-objective genetic algorithm to select non-dominated solution set providing minimum number of relevant genes for cancer classification. The method uses two fitness functions separately based on the concepts of both rough set theory and information theory to select the informative genes. Experiments from publicly available microarray cancer datasets demonstrate the effectiveness of the algorithm.

The third paper, entitled "Identifying Cleavage Sites of Gelatinases A and B by Integrating Feature Computing Models" by Quan Zou, Chi-Wei Chen, Hao-Chen Chang and Yen-Wei Chu, develops a prediction model by integrating feature computing models and machine learning models for the prediction of substrates and the cleavage sites of gelatinases to enable screening and exploring the physiological and pathological mechanisms of these enzymes. The model can be used to aid the discovery of regulatory paths and provide references for drug design.

The fourth paper, entitled "Unsupervised Feature Selection for Microarray Gene Expression Data Based on Discriminative Structure Learning" by Xiucai Ye and Tetsuya Sakurai, proposes a novel unsupervised feature selection method by incorporating local regression, discriminant analysis, and l2;1-norm regularization for structure learning on microarray gene expression data. Experiments on six real microarray gene expression datasets demonstrate that the proposed method optimizes for selecting the most discriminative genes that have less redundancy and a higher accuracy in predictive results.

The fifth paper, entitled "Adapting an Evidence-based Diagnostic Model for Predicting Recurrence Risk Factors of Oral Cancer" by Chien-Sheng Cheng, Pei-Wei Shueng, Chi-Chang Chang and Chi-Wen Kuo combines rules and four machine learning classification techniques to present an evidence-based diagnostic model for the prediction of risk factors of recurrent oral cancer. Their results reveals that KSTAR technique can generate the best prediction accuracy. Moreover, surgical margins, behavior code and lifestyle factors (smoking and betel nut chewing) are the important risk factors for predicting recurrence of oral cancer in Taiwan.

The sixth paper, entitled "Research on Computational Intelligence in Medical Resource Allocation Based on Mass Customization" by Yang Xu, Shuwen Liu and

Binglu Wang, proposes a medical resource allocation model to optimize and balance the uneven distribution of medical resources by considering patient needs and medical costs. The model is based on mass customization parameters and applies genetic algorithm to improve the computational efficiency.

The seventh paper, entitled "Medical Diagnosis of Chronic Diseases Based on a Novel Computational Intelligence Algorithm" by Yenny Villuendas-Rey, Mariana-D. Alanis-Tamez, Carmen-F. Rey Benguría, Cornelio Yáñez-Márquez and Oscar Camacho-Nieto, introduces a novel classification model, Assisted Classification for Imbalance Data model (ACID), to the diagnosis of chronic diseases. The model is able to handle imbalanced data with mixed categorical and numerical attributes and missing values. Experimental results demonstrate that ACID outperforms several state-of- the-art classifiers, in nine of the 15 medical datasets.

The last paper, entitled "Integrating Feature Ranking with Ensemble Learning and Logistic Model Trees for the Prediction of Postprandial Blood Glucose Elevation" by Jason Chou-Hong Chen, Hsiao-Yen Kang and Mei-Chin Wang, proposes a hybrid model that integrates feature ranking methods with ensemble learning and logistic model trees for the classification of Postprandial blood glucose (PBG) in a cohort study. Empirical study reveals that the hybrid model can provide promising results for predicting the PBG levels, and 27 risk factors are identified as important risk factors for PBG elevation.

This special issue has successfully addressed the critical research needs for medical informatics and computational intelligence. The guest editors would like to express their sincere appreciations to the anonymous reviewers for their invaluable contributions in reviewing the manuscripts and providing constructive feedback. The guest editors also sincerely thank the Journal of Universal Computer Science for offering this great opportunity to organize this special issue. The guest editors would like to acknowledge the managing editor, Christian Gütl, and the assistant editor, Dana Kaiser, for their patience and support. Finally, the editors thank to all the authors for contributing their excellent research to this special issue.