Machine Learning and Graph Analytics in Computational Biomedicine

5 authors, including:

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259 PUBLICATIONS **3,413** CITATIONS

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32 PUBLICATIONS **389** CITATIONS

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38 PUBLICATIONS **270** CITATIONS

Some of the authors of this publication are also working on these related projects:

Nonsense-mediated mRNA decay and gene regulation View project

Splicing links histone modifications to cell fate decision View project

Contents lists available at ScienceDirect

Artificial Intelligence in Medicine

Editorial

Machine learning and graph analytics in computational biomedicine

In recent years, computational methods have been broadly and extensively employed in the biomedicine researches, including medical image analysis, healthcare informatics, and cancer genomics. In particular, many computational problems can be formulated as the prediction task on the biomedical data, such as tumor images, electronic medical records, micro-array, and GWAS data. Therefore, a growing number of machine learning and graph analytics algorithms were employed in the prediction tasks of computational biomedicine.

Machine learning and graph analytics techniques have advanced quickly over the past few years. Several high-impact novel methods were reported in the top journals and conferences. For example, affinity propagation was published in **Science** as a novel clustering algorithm, and deep learning has become a hot topic in the predictions and classifications which is capable of processing big data. Parallel mechanisms, such as Spark and Mahout, are also developed by the scholar and industry researchers to speed up the algorithm. Computer scientists have been devoting themselves to the advanced large scale machine learning and graph analytics techniques. However, the applications on biomedicine are limited and fall far behind the techniques.

This special issue targeted the recent large-scale machine learning and graph analytics techniques in biomedical applications. Submissions came from an open call for paper and with the assistance of professional referees, 7 papers are finally selected out from in total 20 submissions after rigorous reviews. These papers focused on the machine learning methods, and applied these methods to computational biomedicine.

Khajehali et al. proposed a model to demonstrate the way various scenarios of data processing impact on the scale efficiency model. In so doing, the Bayesian boosting ensemble method led to better results in anticipation of LOS (length of stay in hospital). Erdogdu et al. proposed a method for the construction of POMDP (Partially Observable Markov Decision Processes) model of GRN (Gene regulatory Networks) from only raw gene expression data. And they also introduce a novel approach to decompose the POMDP model into sub-POMDP's in order to solve it efficiently. Li et al. built a prediction model for Synergistic Drug combination using Random forest algorithm (SyDRa) by analyzing the effect of drug chemical structure features, drug target network features and pharmacogenomics features. Zhang et al. proposed a multi-scale non-negative sparse coding based medical image classification algorithm to reduce the semantic gap. Wei et al. proposed a selective ensemble learning algorithm based on parallel optimization and hierarchical

selection (PTHS). It suitable for the multi-class problem. And they also proposed a feature selection method called MSRD to successfully solve high-dimensional problems. Qiu et al. proposed a new encoding scheme named position weight amino acid composition to extract sequence information of histone around crotonylation sites. Then they developed a method to identify lysine crotonylation sites on histone. Liu et al. presented a new computational method to identify core transcription factors that contribute to the initiation/reversion of tumorigenesis with a greedy strategy applied.

To conclude, papers in this special issue cover several emerging topics of advanced learning techniques and applications for computational biomedicine and bioinformatics. We highly hope this special issue can attract concentrated attentions in the related fields. We would like to thank Prof. Carlo Combi and Klaus-Peter Adlassnig for providing the chance to organize this special issue. We also thank the reviewers for their efforts to guarantee the high quality of this special issue. Finally, we thank all the authors who have contributed to this special issue.

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