

# Network Modeling and Analysis in Health Informatics and Bioinformatics Journal

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Welcome to the first issue of the first volume of the *Network Modeling and Analysis in Health Informatics and Bioinformatics (NetMAHIB) journal*. The *NetMAHIB* journal project started 2 years ago to fill a gap and to satisfy a need. The last decade witnessed great interest and huge growth in the research efforts targeting the interrelated areas of health informatics and bioinformatics. This is highly attributed to the development in technology which has affected almost all aspects of the daily life and even the way of thinking. Automated systems have been developed to keep track of clinical activities and records, and to monitor the workflow between the treatment in the clinic, the tests in the laboratory and the admission to the hospital. On the other hand, the development of sequencing technologies has led to the production of huge amounts of data. The personnel involved in health informatics, including nurses and medical doctors communicate on regular and ad hoc basis forming networks. Clinics, hospitals, laboratories, pharmacies, etc. are also connected by networks. Other types of networks also exist within the human body connecting various molecules, including proteins, genes, etc. A forth category of networks connects molecules inside the cell to external entities like drugs, diseases, etc. All these networks could be analyzed for better knowledge discovery to the benefit of the patients.

In addition to the fact that health informatics and bioinformatics complement each other towards more robust and comprehensive analysis and achievements, as mentioned above, both areas involve a kind of network as it is the case with most of the other areas investigated by the

research community, e.g., criminal networks, terror networks, friendship networks, etc.

To realize a network for a given domain, it is enough to identify at least one class of entities related to the area under investigation. Of course entities are interrelated and the relationships between entities whether within the same class or across classes will lead to links connecting the entities to reflect certain semantics. The entities and the links form a network. In the area of health informatics possible entities are patients, diseases, general practitioners, specialists, nurses, hospitals, clinics, pharmacies, etc. Some examples of relationships could be between general practitioners who consult with each other or between patients and specialists they visit. On the other hand, genes, proteins, RNA, miRNA, etc. are possible entities related to bioinformatics. Example relationships may exist between genes and proteins.

Analysis of the networks from the two domains may lead to novel and interesting discoveries that complement each other. Network-based analysis allows researchers and practitioners to reveal some information which otherwise may remain hidden within the given data produced from the domain under investigation.

*NetMAHIB* is the journal which targets at combining the two interrelated areas, health informatics and bioinformatics under one umbrella. Thus *NetMAHIB* is unique in its scope, coverage and mission. This will allow the two communities of researchers to interact and communicate in a smooth way. This is well reflected in the first issue which includes six papers from the two domains. The research outcome described in the papers justifies further the need for *NetMAHIB* as a unified platform. I would like to thank all the contributing authors for the wonderful articles that will turn this issue into a valuable source for researchers and practitioners. Special thanks go to the associate editors

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and reviewers who dedicated their time and effort to produce timely constructive reviews.

The first article, “Data simulation and regulatory network reconstruction from time-series microarray data using stepwise multiple linear regression” by Yiqian Zhou, Rehman Qureshi and Ahmet Sacan, builds on how time-series microarray data can capture dynamic genomic behavior not available in steady-state expression data. By considering time series data analysis, the authors address three computational problems, namely, the prediction of gene expression levels from previous time steps, the simulation of an entire time-series microarray dataset, and the reconstruction of gene regulatory networks. They conducted extensive testing on several yeast cell-cycle datasets.

The second article, “An exon/intron disparity framework based on the nucleotide profile of single sequence” by Sing-Wu Liou and Yin-Fu Huang, proposes an exon/intron discrimination framework (EIDF) to profile the intrinsic differences between exons and their immediate introns based on information of single sequence. They built a classifier and reported the results of their experiments.

The third article, “Link prediction and classification in social networks and its application in healthcare and systems biology” by Wadhah Almansoori, Shang Gao, Tamer N. Jarada, Abdallah M. Elsheikh and Ayman N. Murshed, et al., tackles the interesting problem of link prediction and extensively studies its applications in health informatics and bioinformatics. Two case studies are described in the paper. The first case study concentrates on predicting links in the network of general practitioners and specialists. The second case study handles link prediction in gene expression networks.

The fourth article, “Image metadata reasoning for improved clinical decision support” by Sonja Zillner and Daniel Sonntag, describes the usage of reasoning technologies to post-process medical image annotations in the

context of the automated staging process of lymphoma patients.

The fifth article, “Threshold-based feature selection techniques for high-dimensional bioinformatics data” by Jason Van Hulse, Taghi M. Khoshgoftaar, Amri Napolitano, and Randall Wald, proposes 11 new threshold-based feature selection techniques and compares the performance of these new techniques to that of six standard filter-based feature selection procedures. The authors conducted experiments using 17 different bioinformatics datasets.

The sixth article, “Detecting ALS and Parkinson’s disease in rats through locomotion analysis” by Wenlong Tang, Paul Yarowsky and Uri Tasch, describes a methodology for detecting locomotion deficiencies due to amyotrophic lateral sclerosis (ALS) and Parkinson’s disease (PD) in laboratory rats. The authors performed three different comparisons to recognize locomotion deficiencies.

Last but not least, I would like to acknowledge contributions of the hard workers behind the scene who have significant share to the achieved success. Various people from Springer deserve large credit for their help and support in all the issues related to the *NetMAHIB* journal in general and in producing this issue of the first volume in particular. I would like to thank Stephen Soehnlen for his continuing generous support in terms of time and effort required to keep the momentum. Stephen has always been positive. Also, I would like to thank Judy Pieren for doing an amazing job taking care of the submissions system, handling all inquiries from the authors and alerting me whenever necessary. I heartedly thank Petra Meyer vom Hagen who has been very patient in handling the requests and in following-up with the timely production of the accepted articles.

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Editor-in-Chief