Proposal for 2022 IEEE BIBM Workshop

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1. Workshop title

The 13th Integrative Data Analysis in Systems Biology (IDASB 2022)

2. Introduction to workshop

Systems biology as a discipline aims to understand complex biological processes and relatedness to phenotype at the systems level. Systems biology studies biological systems by systematically perturbing them (biologically, genetically, or chemically); monitoring the gene, protein, small molecule, and informational pathway responses; integrating these data; and ultimately, formulating mathematical models that describe the structure of the system and its response to individual perturbations. As we are now in big data era, integrated "omics" approaches have created exciting opportunities for systems biology researchers. This workshop provides a forum for exchange and discussion on integrated data analysis approaches in systems biology research such as network, panomics, pattern recognition, feature learning, data representation and visualization.

3. Research topics included in the workshop

This workshop will feature the theme of "integrated approach" and "complex biological system." The scope of this workshop is to integrate and use genome, transcriptome, single cell omics, epigenome, proteome, metabolome, microbiome, drug, phenotype, and other data to contribute to the understanding of biological system, health and disease. Integration of "omics" data with imaging, functional, structural and lifestyle/environmental data are also welcome. Research areas include, but are not limited to:

- o Large-scale or cross-species data integration for the reconstruction of networks and pathways
- o Genomic data analysis using systems biology approaches
- o Analysis, methods and tools for the data from single cells, tissue specificity, and time series.
- O Quantitative understanding of dynamics of regulatory, signalling, interaction and metabolic networks through modelling and simulation techniques
- o Prediction of protein/RNA structure and biological networks interactions
- o Single cell multi-omics data analysis and visualization
- O Deep learning of complex biological or biomedical data
- Data integration and knowledge driven approach in biomarker identification and drug discovery
- o Enhancement and enablement of knowledge discovery in functional genomics of disease and other phenotypes through integrated omics approach
- o Semantic webs and ontology-driven biological data integration methods
- O Data standardization from multi-domains
- o Development of integrated systems biology visualisation and analysis tools
- o Complex network analysis in systems biology
- o Integration of heterogeneous and omics data in medicine
- o Big data analysis in biological systems
- o Multiscale modelling and computing in systems biology and systems medicine
- Metagenomics in systems biology
- o Integrative analysis of omics data with images or phenotypic data.
- Multi-omics Integrated Database and Web service development in systems biology
- o Integrative analysis of spatial multi-omics data

4. Important dates

October 10, 2022: Due date for full workshop papers submission November 5, 2022: Notification of paper acceptance to authors

November 21, 2022: Camera-ready of accepted papers

December 6-9, 2022: Workshop.

5. Program chairs or co-chairs:

Prof. Huiru (Jane) Zheng, Professor, School of Computing, Ulster University, UK. Email: h.zheng@ulster.ac.uk

Dr. Ming Xiao, College of Computer Science, Sichuan University, Chengdu, China. Email: xiaoming@scu.edu.cn

Prof. Zhongming Zhao, Professor, School of Biomedical Informatics, University of Texas, and Vanderbilt University, USA. Email: zhongming.zhao@uth.tmc.edu

6. Program committee members (approval pending)

Dr. Patrizo Arrigo, National Research Council (ISMAC), Italy

Dr. Jaine Blayney, Centre for Cancer Research & Cell Biology, Queen's University Belfast, UK

Prof. Danail Bonchev, Center for the Study of Biological Complexity, Virginia Commonwealth University, USA

Dr. Fiona Browne, Ulster University, UK

Dr. Minghua Deng, Center for Theoretical Biology, Peking University, China

Prof. Werner Dublizky, Biomedical Research Institute, University of Ulster, UK

Dr. Xiaodan Fan, Department of Statistics, Chinese University of Hong Kong

Dr. Luca Giancardo, University of Texas, USA

Dr. Kun Huang, Department of Biomedical Informatics, Ohio State University, USA

Dr. Peilin Jia, Beijing Institute of Genomics, China

Dr. Vladimir A. Kuznetsov, Bioinformatics Institute/A*STAR, Singapore

Dr. Hyunju Lee, Gwangju Institute of Science and Technology, Korea

Dr. Kang Li, School of Electronics, Electrical Engineering and Computer Sciences, Queen's University Belfast, UK

Dr. Shao Li, MOE Key Laboratory of Bioinformatics and Bioinformatics Division, Tsinghua University, China.

Prof. Xiaohui Liu, School of Information Systems and Computing, Brunel University, UK

Dr. Antonio Sanfilippo, Computational and Statistical Analytics Division, Pacific Northwest National Laboratory, USA

Dr. Lukas Simon, Baylor College of Medicine, USA

Dr. Momiao Xiong, University of Texas Health Science Center at Houston, USA

Dr. Jun Wan, Indiana University, USA

Dr. Haiying Wang, Computer Science Research Institute, University of Ulster, UK

Dr. Ying Wang, Xiamen University, China

Dr. Yong Wang, Academy of Mathematics and Systems Science, Chinese Academy of Sciences, China

Dr. Hong Yue, Department of Electronic and Electrical Engineering, University of Strathclyde, UK

Dr. Xingming Zhao, Fudan University, China

Dr. Shihua Zhang, Chinese Academy of Sciences, China

Dr. Feng Zeng, Xiamen University, China

Prof. Wei Chen, Chengdu University of Traditional Chinese Medicine, China

Prof. Jin Liu, School of Computer Science and Engineering, Central South University, China.

Prof. Liang Yu, School of Computer Science and Technology, Xidian University, China

7. Contact and further information

Further information can be found at the workshop website (running at three sites in USA, China, and UK)

8. Notes to BIBM workshop chair:

- 1. The workshop website will be alive when the proposal is accepted.
- 2. The selected papers will be published in a special issue in IJCBDD, as we did in the past eight years.