

IEEE JOURNAL OF BIOMEDICAL AND HEALTH INFORMATICS

J-BHI Special Issue on “Advanced Machine Learning and Artificial Intelligence Tools for Computational Biology: Methodologies and Challenges”

The management and analysis of biological data have experienced exponential growth in recent years by the application of advanced machine learning and artificial intelligence (AI) technologies. This is coupled with the overwhelming increase in biological data volume and acquisition rate. Conventional analysis strategies lack the strong potential to analyze big data and extract valuable knowledge from them. Thus, they fail to provide innovative solutions to medical challenges and consequently patient care. Advanced AI tools, on the other hand, possess high potentials to develop algorithms and analytical models for interpreting biological information. Particularly, advanced deep learning tools provide deep insights into biological data to extract hidden valuable structure/features to assist in making accurate predictions and/or decisions.

This special issue calls for attractive, recent, and innovative work utilizing ML and AI research for emerging problems in the field of computational biology and relevant problems from the life sciences. Full-length papers of original and unpublished research work as well as review manuscripts related to the applications of ML/AI for the **understanding, visualizing, and interpreting biomedical data for biology are welcomed**. Another important aspect of this issue is to investigate the cutting-edge AI techniques in the interdisciplinary field of computational biology. This will be achieved by providing discussions about the best models and their details for biological data analysis

Topics of interest include, but are not limited to, the following:

- Novel learning approaches in computational biology
- Explainable AI for Bioinformatics/Enzymoics/Proteomics/metabolomics etc.
- Intelligent algorithms for analyzing complex systems in biology
- Scalable and heterogeneous learning methods for computational biology
- Graph-based modelling techniques for the interactions of genes and proteins
- Bioinformatics data analysis for therapeutics discovery and development
- Advanced mathematical modelling for biological-image analysis
- Human-level explainable DL in chemical informatics/medical informatics/smart healthcare/nursing informatics
- Detection and discovery of predictive and prognostic biomarkers
- Machine Learning for molecular traits predictions from DNA sequence

Guest Editors

- [1] Fahmi Khalifa, Faculty of Engineering, Mansoura University, Egypt, fahmikhhalifa@mans.edu.eg
- [2] Imran Razzak, University of New South Wales, Australia, imran.razzak@unsw.edu.au
- [3] Mohammad Amjad Kamal^{1,2,3,4}, prof.kamal@diu.edu.bd
 - ¹ Institutes for Systems Genetics, Frontiers Science Center for Disease-related Molecular Network, West China Hospital, Sichuan University, China
 - ² King Fahd Medical Research Center, King Abdulaziz University, Jeddah 21589, Saudi Arabia
 - ³ Department of Pharmacy, Faculty of Allied Health Sciences, Daffodil International University, Dhaka 1207, Bangladesh
 - ⁴ Enzymoics, 7 Peterlee place, Hebersham NSW 2770; Novel Global Community Educational Foundation, Australia
- [4] Ahmed Soliman, Faculty of Engineering, Mansoura University, Egypt, ahmedsoliman@mans.edu.eg

Key Dates

Deadline for Submission: 31 March, 2023
First Reviews Due: 1 June, 2023
Revised Manuscript Due: 1 July, 2023
Final Decision: 1 October, 2023