

IEEE JOURNAL OF BIOMEDICAL AND HEALTH INFORMATICS

J-BHI Special Issue on “Computational Mathematics Modeling in Cancer Analysis”

Cancer is a complex and heterogeneous disease which often leads to misdiagnosis and ineffective treatment strategies. Many mathematical and computational approaches have been implemented in basic cancer research over the past few decades. These approaches allowed a better understanding of this complex group of diseases, generated new hypotheses and predictions, and guided scientists towards the next series of more informative and successful experimental works. In the field of clinic application, numerous mathematical methods dealing with multimodal cancer data analysis have been widely applied, such as cancer subtype identification, stage classification and prognostic prediction, and many other applications. Motivated by rigorous mathematical theory and biological mechanisms, the advanced computational methods for cancer data analysis are robust and clinically practicable, which will be strong interpretability combining clinical data and algorithms in an era of artificial intelligence. Moreover, these methods also allow a deeper exploration of cancer from the perspective of computational science, such as the mapping of biological and computational correlations among multiple omics data at various scales and views. The multimodal cancer data include but are not limited to radiographic, pathology, genomics, and proteomics.

This Special Issue will focus on major trends and challenges in theoretical, computational, and applied aspects of computational mathematics in cancer data analysis for cancer research and clinical diagnosis/therapy. This Special Issue will follow the organization the 1st WORKSHOP on Computational Mathematics Modeling in Cancer Analysis (CMMCA2022) to be held in conjunction with the 25th International Conference on Medical Image Computing and Computer-Assisted Intervention, MICCAI 2022. The special issue will be comprised of extensions of some of the best works announced in the workshop, along with papers submitted within the open call, taking also into account the target audience of the JBHI journal. If the submission is extended from an early conference publication, we request it to consist of at least 70% new material compared to the published conference paper, and all papers will go through a peer review process.

Topics of this Special Issue include (but are not limited to) computational mathematics modeling (e.g., Deep learning, Differential equation, Multi-scale modeling, Cellular automaton, Spatial graph network, Nonlinear dynamical systems, and Probability methods) with applications to:

- Interpretability-based learning mathematics theory for cancer imaging analysis;
- Medical image analysis of anatomical structures/functions and tumors;
- Computer-aided tumor detection/diagnosis;
- Multi-modality fusion for cancer analysis, diagnosis, and surgery/treatment plans;
- Molecular/pathologic/cellular image analysis in the microenvironment, immunity, invasion, treatment, and resistance;
- Computational modeling characterizes tumor growth, metabolism, evolution;
- Topological tumor graphs for prognosis analysis;
- Biologically-based mathematical modeling in tumor vasculature and angiogenesis.
- Spatiotemporal modeling for heterogeneity and evolution of the tumor microenvironment

Guest Editors

Wenjian Qin, Shenzhen Institute of Advanced Technology, Chinese Academy of Sciences (wj.qin@siat.ac.cn)

Tianming Liu, University of Georgia (tliu@cs.uga.edu)

Fa Zhang, Institute of Computing Technology, Chinese Academy of Sciences (zhangfa@ict.ac.cn)

Key Dates

Deadline for Submission: September 30, 2022

First Reviews Due: November 30, 2022

Revised Manuscript Due: December 30, 2022

Final Decision: January 30, 2023