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Fan Yang (Eds.)

# Computational Mathematics Modeling in Cancer Analysis

First International Workshop, CMMCA 2022  
Held in Conjunction with MICCAI 2022  
Singapore, September 18, 2022  
Proceedings

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# Preface

The 1st Workshop on Computational Mathematics Modeling in Cancer Analysis (CMMCA 2022) was held in conjunction with the 25th International Conference on Medical Image Computing and Computer Assisted Intervention (MICCAI 2022) on September 18, 2022. Due to the COVID-19 pandemic restrictions, CMMCA 2022 was held virtually.

Cancer is a complex and heterogeneous disease that often leads to misdiagnosis and ineffective treatment strategies. Pilot mathematical and computational approaches have been implemented in basic cancer research over the past few decades, such as the emerging concept of digital twins. These methods 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, in which the multimodal cancer data include, but are not limited to, radiography, pathology, genomics, and proteomics. Motivated by rigorous mathematical theory and biological mechanisms, the advanced computational methods for cancer data analysis are robust and clinically practicable, which will result in strong interpretability in combining clinical data and algorithms in an era of artificial intelligence.

CMMCA provides a platform to bring mathematicians, biomedical engineers, computer scientists, and physicians together to discuss novel mathematical methods of multimodal cancer data analysis. A major focus of CMMCA 2022 was to identify new cutting-edge techniques and their applications in cancer data analysis in response to trends and challenges in theoretical, computational, and applied aspects of mathematics in cancer data analysis.

The workshop attracted worldwide attention, including experts in radiography, pathology, and genomics multi-modality data, as well as learning-based imaging processing and computational modeling for cancer analysis. All submissions underwent rigorous double-blind peer review by at least two members (mostly three members) of the Program Committee, composed of 26 well-known research experts in the field. The paper selection was based on methodological innovation, technical merit(s), relevance, the significance of results, and clarity of presentation. Finally, we received 16 submissions, out of which 15 papers were accepted for presentation at the workshop and inclusion in this Springer LNCS volume.

We are grateful to the Program Committee for dedicating their time to reviewing the submitted papers and giving constructive comments and critiques, to the authors for

submitting high-quality papers, to the presenters for excellent presentations, and to all the CMCCA 2022 attendees from all over the world.

September 2022

Wenjian Qin  
Nazar Zaki  
Fa Zhang  
Jia Wu  
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