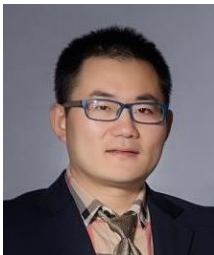




Biomolecular identification of computational and statistical methods for Cancer and related diseases

Guest Editor



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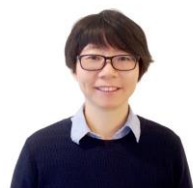
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Message from the Guest Editor

Dear Colleagues,

Cancer is the biggest threat to human life and health. Although the human and financial resources invested in cancer research are increasing, the pathogenesis and clinical treatment of cancer are still unclear. Exploring the molecular characteristics of cancer is the basis and core of cancer treatment. However, the money and time required by the traditional clinical cohort study can not meet the urgent



needs of human treatment.

With the cost reduction of sequencing and various kinds of biomolecular detection, the data of cancer-related genome, transcriptome, proteome and metabolomics increase exponentially. Massive data provide researchers with a treasure house for mining key information of cancer, but also pose a major challenge to the existing computing methods. In the information age, the in-depth study of statistical and computational methods is the key to accurately mining the biological knowledge contained in multi omics data.

The computational and statistical methods of identifying cancer related mechanisms and biomarkers are emerging. These methods have brought forward original opinions on cancer from the basic research and clinical perspective respectively. In view of the above development of computational methods in the research of cancer, we propose a Research Topic, aiming to provide a great opportunity for researchers to share their latest research findings, present novel methods, and discuss the challenges and opportunities in the related fields.

Papers are solicited on, but not limited to, the following topics:

- Machine learning and statistical approaches for identifying cancer-related molecular.
- Analyze the relationship between cancer-related diseases and cancer
- Identification and validation of molecular biomarker for cancers.
- Tools and databases for researching Cancer and related diseases.
- Novel discovery of complex diseases-related genes, RNAs, proteins and metabolites.

Prof. Dr. Liang Cheng, Prof. Dr. Tianyi Zhao and Prof. Dr. Chuan-Xing Li

Guest Editors

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