



BioMed Research International

Special Issue on
**Novel Computational Approaches and Applications
in Cancer Research**

CALL FOR PAPERS

Cancer is one of the leading causes of death worldwide and is expected to rise sharply in the next decade. It is a disease caused by a series of genome alterations including DNA sequence changes, copy number aberrations, chromosomal rearrangements, and many other modifications. With the ongoing developments of high throughput biotechnologies for genomes, proteomes, and transcriptomes, it is essential to develop innovative computational methods and to perform comprehensive multiomics data analysis to improve our understanding of cancer initiation and progression.

Currently, The Cancer Genome Atlas (TCGA) project provides the research community with increased amount of data from large-scale multidimensional analysis of different molecular characteristics in human cancer. The data types include DNA sequence, DNA copy number aberration, DNA methylation, mRNA expression, microRNA expression, protein expression, and clinical diagnosis. Therefore, novel computational methods for analyzing these data and integrative analysis for multiplatform data are needed to discover potential cancer-related biomarkers or cancer therapy targets.

In this special issue, we take a great interest in novel computational methods and tools for analyzing multiplatform cancer data, such as somatic mutation analysis, expression analysis, analysis of imaging data, and proteomic analysis. We also welcome those studies focusing on integrative analysis of genomic and epigenomic data as well as the cancer-related pathways or network analysis. We invite authors to contribute relevant original findings as well as review articles.

Potential topics include, but are not limited to:

- ▶ Any novel computational approaches and tools to analyze high-throughput multiplatform data, such as mRNA-seq, miRNA-seq, DNA methylation, DNA-seq, and methods for imaging data analysis
- ▶ Data analysis for genomics, transcriptomics, and metabolomics in cancer research
- ▶ Integrative analysis of cancer genomic and epigenomic data
- ▶ Clinical utility of cancer genomics data in precision cancer targets
- ▶ Cancer-related network analysis or pathway analysis
- ▶ Cancer subtype analysis based on integrated molecular features
- ▶ Big data to advance personalized cancer treatment

Authors can submit their manuscripts via the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/bmri/computational.biology/ncaac/>.

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