Special Issue

Algorithms and Data Analysis of High Throughput Sequencing in Cancers

Message from the Guest Editors

The acquisition of cancer hallmarks requires molecular alterations at multiple levels, including genome, epigenome, transcriptome, proteome, and metabolome levels. High-throughput DNA sequencing has contributed to the identification of cancer-specific mutations, epigenetic alterations, and molecular subtyping of tumors. Moreover, large-scale tumor molecular profiling programs across different cancer types hold the promise of improving diagnostics, prognostics, and personalized treatment. High-throughput omics data create huge bioinformatic challenges including storage, transmission, manipulation, and analysis, making the downstream processing of data a daunting task. Therefore, new bioinformatic methods are required to biologically extract sequencing data from meaningful information and present them in an easily interpretable format. In this Special Issue, we will discuss bioinformatic methodologies and statistical approaches, with a special emphasis on how the omics data are being analyzed, stored, and manipulated to aspire or create new ways of diagnosing and treating cancers.

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Message from the Editor-in-Chief

Cancers is an international online journal addressing both clinical and basic science issues related to cancer research. The journal is publishing in Open Access format, which will certainly evolve to ensure that the journal takes full advantage of the rapidly changing world of information and knowledge dissemination. It publishes high-quality clinical, translational, and basic science research on cancer prevention, initiation, progression, and treatment, as well as other related topics, particularly to capture the most seminal studies in the rapidly growing area of immunology, immunotherapy, and tumor microenvironment.

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