Special Issue

Algorithms for Exploring the Molecular Mechanisms of Tumorigenesis and Evolution

Message from the Guest Editors

The molecular mechanisms of tumorigenesis and evolution play an important role in the diagnosis and treatment of tumors. Such mechanisms have been described in multi-omics data (e.g., genomics, epigenetics, gene expression, metabolomics and proteomics). Currently, through large tumor sequencing databases such as The Cancer Genome Atlas (TCGA) and The International Cancer Genome Consortium (ICGC), many algorithms have been applied for corresponding data analysis, and extensive studies have been performed in tumorigenesis and evolution, including the use of various models to determine the dependencies between relevant factors from multiple perspectives of temporal and spatial dynamics. Various algorithms have been used to compute and identify potential biomarkers and drug targets in tumorigenesis and evolution for novel tumor diagnosis and treatment. The aim of this Special Issue is to provide new algorithms to explore the molecular mechanisms of tumorigenesis and evolution in order to gain a more comprehensive understanding of the conventional mechanisms of cancer, and to provide several potentially useful targets for further tumor diagnosis and treatment.

Guest Editors

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Deadline for manuscript submissions

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Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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