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Bioinformatics and Computational Biology for Cancer Prediction and Prognosis

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Deadline for manuscript submissions:
closed (1 May 2024)

Message from the Guest Editors

Dear Colleagues,

Bioinformatics tools play a vital role in understanding the biological complexity of cancer through the extraction of meaningful information from a large volume of diverse datasets. Of utmost importance are tools for data analysis, visualization, and interpretation that would aid in the realization of personalized medicine based on omics (genomic, transcriptomic, or proteomic) data, as well as on images and text.

This Special Issue aims to provide an overview of new and current bioinformatics tools for cancer prediction and prognosis. Contributions may describe novel approaches, or the application of new and existing ones, that aid in the identification of diagnostic, prognostic, or predictive cancer biomarkers; that identify potential therapeutic targets and important cancer-related pathways; or that otherwise provide valuable insight into cancer biology and treatment. To make progress in the field of cancer bioinformatics, contributions by experts in the field in the form of research papers and critical reviews are welcomed.

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Special Issue

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Message from the Editor-in-Chief

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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