Special Issue

Bioinformatics and Computational Biology in Human Diseases

Message from the Guest Editor

Multi-omics, single-cell sequencing technologies, integrative biology, and precision medicine have all been promising approaches for the study of a wide range of human diseases. Understanding the data from genomics, epigenetics, metabolisms, and proteomics, as well as the complex mechanisms in human diseases are the major challenges in current bioinformatics and computational biological studies.

In this Special Issue, we welcome contributions that integrate multi-omics, leverage single-cell sequencing technologies (e.g., scRNA-seq, scATAC-seq, and spatial transcriptomics), develop bioinformatics and computational models, and use machine learning/AI models, aiming at achieving a better understanding of human diseases. It is the aim of this Special Issue to provide a deeper comprehension of multi-omics, single-cell sequencing data, and the association between genetics and phenotypes, as well as biomarker discovery and patient stratification/clinical outcome prediction, that may ultimately lead to early diagnosis and precise and effective treatment.

Guest Editor

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Deadline for manuscript submissions

closed (15 August 2023)

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Genes

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Impact Factor 2.8
CiteScore 5.5
Indexed in PubMed

mdpi.com/si/153447

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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?

Editor-in-Chief

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