Special Issue

Discoveries in Sequencing Data Analysis

Message from the Guest Editors

High-throughput sequencing has been widely used in functional genomics studies and has revolutionized biological sciences. It enables researchers to perform a wide range of investigations and to study biological systems at an unprecedented level. Analysis of sequencing data converts sequence information into meaningful knowledge and insights, which involves algorithm development, annotation or cataloguing information, multi-omics data integration, biomarker and drug target discovery, and disease diagnosis and drug response prediction. Novel discoveries in sequencing data analysis are critical to pinpoint the key players in pathological conditions, especially for cancer and other age-related diseases.

The aim of this Special Issue is to provide a broad and up-to-date overview of "Discoveries in Sequencing Data Analysis" to elucidate new approaches analyzing sequencing data, integrating multi-omics data, discovering biological mechanisms, and developing novel treatments or therapies for diseases. Contributions in the form of research papers and reviews from experts in the field are needed to improve our understanding of relevant biological issues.

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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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