Special Issue

Statistical Methods for the Analysis of Genomic Data

Message from the Guest Editors

In recent years, technology breakthroughs have greatly enhanced our ability to understand the complex world of molecular biology. Rapid developments in genomic profiling techniques, such as high-throughput sequencing, have brought new opportunities and challenges to the fields of computational biology and bioinformatics. Furthermore, by combining genomic profiling techniques with other experimental techniques, many powerful approaches (e.g., RNA-Seq, ChIP-Seq, single-cell assays, Hi-C) have been developed in order to help explore the complex biological systems. As more genomic datasets become available, both in volume and variety, the analysis of such data has become a critical challenge as well as a topic of interest. Consequently, statistical methods dealing with the problems associated with these newly developed techniques are in high demand. This Special Issue will highlight the state-of-the-art statistical methods for the analysis of genomic data, and explore potential future directions for improvement.
Dr. Zhi He

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Deadline for manuscript submissions

closed (30 November 2019)

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Impact Factor 2.8
CiteScore 5.5
Indexed in PubMed

mdpi.com/si/25722

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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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