Statistical Approaches for the Analysis of Genomic Data

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Deadline for manuscript submissions:
closed (10 September 2022)

Message from the Guest Editors

Newly developed techniques have produced a wealth of multiple layers of omics data, including genomics, transcriptomics, proteomics, and phenomics, which help us in understanding the underlying biological processes of traits of interest. Therefore, the research community requires new computational approaches in order to efficiently handle big omics data.

This Special Issue is calling for submissions of original studies about computational approaches for the analysis of omics data. The topics that are welcome include but are not limited to:

- Computational approaches and reviews for GWAS, genomic selection, selective sweep, and imputation;
- Approaches for efficient handling of big omics data;
- Computational approaches for integrating multi-omics data and new gene-phenotype associations identified by multi-omics integration approach;
- Advanced phenotyping approaches and new discoveries of gene-phenotype associations.

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Special Issue

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Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving 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.

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