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Computational Methods for the Analysis of Genomic Data and Biological Processes

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Deadline for manuscript submissions:

closed (15 July 2020)

Message from the Guest Editors

Dear Colleagues,

In recent decades, new technologies have made remarkable progress in helping to understand biological systems. We encourage researchers to share their original works in the field of computational analysis of gene expression data. Topics of primary interest include, but are not limited to:

1. Computational methods or machine learning approaches for modelling biological processes;
2. Discovering genome–disease or genome–phenotype associations;
3. Gene–gene interactions and gene–environment interactions for disease association analysis;
4. New computational methods for gene expression data analysis;
5. Machine learning approaches for modelling gene regulatory networks;
6. Identification of expression patterns;
7. Reviews on computational methods for gene expression data analysis.

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Guest Editors



mdpi.com/si/35875

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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