Special Issue

Computational Methods for the Analysis of Genomic Data and Biological Processes

Message from the Guest Editors

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:

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

Prof. Dr. Francisco A. Gómez Vela

Prof. Dr. Miguel García Torres

Guest Editors

Prof. Dr. Francisco A. Gómez Vela

Dr. Federico Divina

Dr. Miguel García-Torres

Deadline for manuscript submissions

closed (15 July 2020)

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Genes
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
genes@mdpi.com

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About the Journal

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

Prof. Dr. Selvarangan Ponnazhagan
Department of Pathology, The University of Alabama at Birmingham,
1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

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