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Bioinformatics Analysis for Diseases

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Message from the Guest Editor

This Special Issue will be devoted to bioinformatics analysis methods for diseases. This Special Issue provides the opportunity to provide more details on bioinformatics analysis methods for disease identification, classification, diagnosis, and prognosis. Article topics may include but are not limited to the following:

- Alignment-free methods for disease gene identification;
- Pan-genomic approaches to better distinguish between non-disease and disease variants;
- Methodology and tools for variant calling, evaluation, filtering, and visualization;
- New approaches to gene expression analysis, in particular probabilistic methods, for both single-cell and bulk expression analysis;
- Methods for identifying regulatory regions involved in diseases;
- Identification of disease-related non-coding RNA molecules;
- Re-analysis of published datasets with new or significantly improved bioinformatics methods that lead to new insights;
- Best-practice workflows for any workflow management system.



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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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