Novel Algorithms for Computational Analysis of Bioinformatics Data

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Message from the Guest Editors

In the past decade, the notion of biological data, which encompass genomics, proteomics, metabolomics, other - omics and related phenotypic data, has shifted in magnitude. To extract useful information from these datasets rapidly, the field of bioinformatics is increasingly relying on machine learning (ML) algorithms to conduct predictive analytics and gain greater insights into the complex biological processes. Machine learning involves programming computers to classify or predict events using example data or past experience. Machine learning includes deep learning, natural language processing, and biocuration tools that are becoming increasingly important to transform huge volumes of genomic data both from research and clinical contexts into actionable knowledge. Now is the time for coordinated community efforts that address the challenges and opportunities in bioinformatics for the next decade. In this Special Issue, we invite you to present your leading work in novel algorithms and tools for computational analysis of Bioinformatics data, thus contributing to this collection of some of the most recent advances in our field in one place.

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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