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Application of Bioinformatics in Plants

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Deadline for manuscript
submissions:

closed (20 June 2023)

Message from the Guest Editor

Dear Colleagues,

The discovery of high-throughput sequencing (HTS) and its employment in genomics, transcriptomics and other omics disciplines paved the way for the production of a staggering amount of big biological data. The inference of meaningful results from ever-increasing biological data regarding structures and functions of genes, their evolutions over time, protein–protein or protein–ligand interactions and to shed light on metabolic processes and pathways all depend on the effective and accurate processing of big biological data. In this context, bioinformatics plays a major role in deciphering behaviors, interactions and networks of biological molecules and structures. Today, the employment of neural network methods under artificial intelligence and machine learning gives further impetus to understand living systems through more efficient and effective data mining and data processing of the accumulated biological big data. With this Special Issue, I wish to invite the submission of high-quality original research manuscripts or review articles on any topic related to: “Application of Bioinformatics in Plants”.



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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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