Special Issue

Bioinformatics Toolkit for Plant Studies

Message from the Guest Editor

Advances in high-throughput technologies, including next-generation sequencing, have revolutionized the field of plant biology. Big Data is becoming increasingly important in plant biology. A significant amount of omics data, including those of genomics, transcriptomics, proteomics, metabolomics, methylomics, interactomics, and phenomics, are now available in various databases across the globe, which has presented opportunities to interrogate these data and gain new insights into plants at the molecular, physiological, and systems levels. A number of bioinformatics tools have already been developed, with many more in the works, to analyze and interpret these data and facilitate a system-level understanding of the processes within plants. Examining plant data at different levels using bioinformatics tools is enabling the development of next-generation technologies to engineer plants for a variety of purposes, including rendering them resilient to climatic changes and breeding crops for a sustainable planet. This Special Issue will highlight current and new bioinformatics tools, both standalone and pipeline based, for plant data analysis and interpretation.

Guest Editor

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Deadline for manuscript submissions

closed (31 August 2023)

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Message from the Editor-in-Chief

Plants is an open access journal which provides an advanced forum for research findings in areas related to plant function, its physiology, biology, taxonomy, stresses, and its interactions with other organisms. It publishes original research articles, reviews, reports, conference proceedings (peer reviewed full articles) and communications. In original research papers, it is important that full experimental details are provided. We also encourage timely reviews and commentaries on topics of interest to the plant research community.

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