

Current Bioinformatics

Special Issue on

Plant Bioinformatics: from genome to phenome

Call for Papers

With the exploration of big omics data in plants, we are faced with the problem of how to interpret and exploit the rapidly accumulating sets of publicly available omics data. The development and application of computational algorithms, databases and tools are desirable for the efficient processing, management and visualization of large-scale omics data. However, analyzing such big data and deriving biological knowledge and applying it back for predictions and further experimentation is becoming a challenging task. Bioinformatics analyses are important approaches to comprehensively understand how a plant system works by exploiting computational methods to integrate multiple levels of omics datasets. The main objective of this special issue is to provide a forum for researchers to present latest advances and state-of-the-art techniques, tools and applications in analyzing plant omics data. Both original research papers and review articles related to plant bioinformatics will be considered for publication. Potential topics include, but are not limited to:

- Comparative genomics
- Gene regulatory networks
- Genome-phenome-environment network analysis
- Genome-wide association studies
- High-throughput sequencing analysis and applications
- Proteomics
- Metabolomics
- Big data analytics and discovery
- Complex-data visualization
- Virtual cell modeling

Before submission authors should carefully check the “INSTRUCTIONS FOR AUTHORS” section of the journal *Current Bioinformatics*, which can be found at <http://benthamscience.com/journals/current-bioinformatics/>. Prospective authors should send an electronic copy of their complete manuscript in *Current Bioinformatics* [template](#) to Dr. Youhuang Bai (biobai@zju.edu.cn).

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