

Special Issue on
Statistical Methods and Software Tools for Biological Big Data

CALL FOR PAPERS

With the advent of high-throughput technology, such as high-throughput sequencing, we are able to generate massive biological Big Data (e.g., massive genomic, epigenomic, and transcriptomic datasets) within a short period of time. This gives us unique opportunities for better understanding of human health and disease. However, biological Big Data is high dimensional, highly variable, and highly heterogeneous. Life scientists are encountering challenges with processing, interpreting, and exploring insights to further lead to biological discoveries.

We invite investigators to contribute original research articles as well as review articles that seek to develop statistical methods and/or software tools to analyze biological Big Data. A particular interest will be given to papers developing or applying machine learning approaches for integrative analysis of biological Big Data.

Potential topics include but are not limited to the following:

- ▶ Developing statistical methods and/or tools for analysis of high-throughput biological data (e.g., RNA-seq, CLIP-Seq, SELEX-Seq, and ChIP-seq)
- ▶ Developing or applying machine learning approaches for integrative analysis of biological Big Data (e.g., integrating transcriptomic, methylomic, and metabolomic data to build statistical models to predict gene regulatory networks in development and disease)
- ▶ Applying machine learning approaches for solving bioinformatics problems in high-throughput data (e.g., predict microRNAs from small RNA sequencing dataset and predict circRNAs from transcriptome sequencing data)
- ▶ Developing software tools for analysis or visualize biological Big Data

Authors can submit their manuscripts through the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/cmmm/smst/>.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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