

## Special Issue on Advances in Computational Genomics

### Call for Papers

Computational Genomics refers to the use of computational analysis to decipher biology from genome sequences and related data, including both DNA and RNA sequences and other “postgenomic” data. Next generation sequencing (NGS) technologies have been rapidly applied in biomedical and biological research since their advent only a few years ago and have produced an avalanche of genome sequences. Transforming genomic information into biological knowledge requires creative and innovative new computational methods for all aspects of genomics. With the current abundance of massive biological datasets, computational studies have become one of the most important avenues for biological discovery.

We invite investigators to contribute original research articles, as well as review articles, that will stimulate the continuing efforts in Computational Genomics for more efficient analysis of big genomics data. Emphasis of implementations on high performance computing systems, parallel algorithms, and knowledge extraction from genome-wide genomics data will be seen favorably. Advances in computational methods are welcome, though all submissions should include genome-scale analyses. Potential topics include, but are not limited to:

- Functional genomics
- Evolutionary genomics
- Comparative genomics
- Metagenomics
- Epigenomics, noncoding RNA analysis, and DNA methylation analysis
- Applications in NGS analysis

Before submission authors should carefully read over the journal's Author Guidelines, which are located at <http://www.hindawi.com/journals/bmri/guidelines/>. Prospective authors should submit an electronic copy of their complete manuscript through the journal Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/bmri/genomics/acg/> according to the following timetable:

Manuscript Due	Friday, 6 June 2014
First Round of Reviews	Friday, 29 August 2014
Publication Date	Friday, 24 October 2014

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