



BioMed Research International

Special Issue on
**Functional Genomics, Genetics, and Bioinformatics
2016**

CALL FOR PAPERS

Biology has become the land of the “-omics,” including genomics, transcriptomics, proteomics, lipidomics, and metabolomics. Each of these “-omics” generates a huge amount of high-throughput data, and it is a challenge both to analyze these data and to further investigate the function of specific molecules. Though more genomes have been completed due to the rapid development of sequencing technology, we cannot understand the information contained within a genome until we mine out its implicated functions. Therefore, the major challenges we meet today are not those of the traditional approach but instead fall under the task of functional annotation of genomes, which includes dynamic aspects such as gene identification, gene transcription, translation, modification, and protein-protein interactions using bioinformatic tools and high-throughput methods. In addition, the genetic information implicated in a genome sequence is critical for understanding the relationship between the genome and its expressed traits. Some diseases are reported as being caused by genetic disorders, such as changes or mutations of DNA, which can be inherited from parents; for example, Edward syndrome is caused by the anomalous presence of three copies of chromosome 18 in each cell. In contrast to such genetic causes, epigenetic ones are thought of as changes of gene expression without changes of DNA sequence, and epigenetic alternation may be caused by environment or other postnatal factors. Most diseases such as colorectal cancer are caused by both accumulated alternations of genetic and epigenetic factors, so faster and more accurate methods are urgently needed for next-generation sequence data analysis. In this special issue, we would focus on functional “-omics” and bioinformatics.

The special issue will provide a platform to integrate the most recent development and ideas in the field.

Potential topics include, but are not limited to:

- ▶ Translational bioinformatics, focusing more on using bioinformatics methods to analyze “-omics” data
- ▶ Functional study of specific molecular and pathway analysis
- ▶ Computational systems biology
- ▶ Bioinformatics algorithm and tool development: any new tools, methods, and their evaluation for “-omics” data analysis
- ▶ Medical and health informatics by using “-omics” data
- ▶ Integrative data analysis
- ▶ Genome annotation and comparative genomics
- ▶ Traditional bioinformatics

Authors can submit their manuscripts via the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/bmri/bioinformatics/ggb16/>.

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First Round of Reviews

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