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## Statistical Methods for the Analysis of Genomic Data

Guest Editors:

### Dr. Hui Jiang

Department of Biostatistics,  
University of Michigan, Ann  
Arbor, MI 48109-2029, USA

### Dr. Zhi He

Department of Biostatistics,  
University of Michigan, Ann  
Arbor, MI 48109-2029, USA

Deadline for manuscript  
submissions:

**closed (30 November 2019)**

### Message from the Guest Editors

Dear Colleagues,

In recent years, technology breakthroughs have greatly enhanced our ability to understand the complex world of molecular biology. Rapid developments in genomic profiling techniques, such as high-throughput sequencing, have brought new opportunities and challenges to the fields of computational biology and bioinformatics. Furthermore, by combining genomic profiling techniques with other experimental techniques, many powerful approaches (e.g., RNA-Seq, ChIP-Seq, single-cell assays, Hi-C) have been developed in order to help explore the complex biological systems. As more genomic datasets become available, both in volume and variety, the analysis of such data has become a critical challenge as well as a topic of interest. Consequently, statistical methods dealing with the problems associated with these newly developed techniques are in high demand. This Special Issue will highlight the state-of-the-art statistical methods for the analysis of genomic data, and explore potential future directions for improvement.

Dr. Hui Jiang

Dr. Zhi He

*Guest Editors*



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# Special Issue



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### **Prof. Dr. Selvarangan Ponnazhagan**

Department of Pathology, The  
University of Alabama at  
Birmingham, 1825 University  
Blvd, SHEL 814, Birmingham, AL  
35294-2182, USA

## Message from the Editor-in-Chief

Genes are central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fastmoving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised.

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*Genes* Editorial Office  
MDPI, St. Alban-Anlage 66  
4052 Basel, Switzerland

Tel: +41 61 683 77 34  
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