



Computational Advances for Single-Cell Omics Data Analysis

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Message from the Guest Editors

Dear colleagues,

Recent technological advances have enabled high-throughput profiling of genomes, transcriptomes, epigenomes, and proteomes at single cell resolution. These revolutionary single-cell -omics technologies promise to bring unprecedented insights into tissue heterogeneity and unveil subtle regulatory processes that are undetectable by bulk sample analysis.

The goal of this Special Issue is to publish review and research articles on the latest developments in computing infrastructure, mathematical and statistical modeling, algorithms, and visualization methods for single-cell -omics data. Topics of interest mainly include:

- Quality control for single-cell sequencing data
- Single-cell RNA-Seq quantification
- Variant calling and haplotyping
- Modeling of missing data and imputation
- Normalization and batch effect removal
- Clustering and cell type inference
- Single-cell spatial reconstruction
- Lineage inference
- Single-cell phylogenetics
- Visualization
- Single-cell bioinformatics workflows and benchmarking
- Integration of multi-omics single-cell data
- Cell atlases





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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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Rapid publication: Manuscripts are peer-reviewed and a first decision provided to authors approximately 19.7 days after submission; acceptance to publication is undertaken in 5.8 days (median values for papers published in this journal in the second half of 2018).

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