

Special Issue

Single-Cell RNA-Seq Technologies and Related Computational Data Analysis

Message from the Guest Editor

Single-cell technologies and computational methods provide opportunities to investigate cellular heterogeneity in a wide range of tissues and cell populations, yielding deep insights into the composition, dynamics, and gene regulation of cell states in biological processes. Despite substantial advances made to date, significant challenges remain, particularly in the analysis of single-cell data because of the sparsity, complexity, and high noise levels of the data. New advances in computational biology have been emerging to provide important biological insights and to fully utilize the advantages of single-cell sequencing data. Therefore, to introduce the latest developments in single-cell data analysis, we bring you this Special Issue of *Genes*. This Special Issue aims to provide a forum for advancement in the development and applications of computational single-cell methods. New developments of algorithms for single-cell data analysis, and their applications in clinical and biological research are welcome in the form of review articles and papers on methodologies and practical application.

Guest Editor

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Deadline for manuscript submissions

closed (20 July 2024)

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About the Journal

Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving 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. Why not consider *Genes* for your next genetics paper?

Editor-in-Chief

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