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

Dr. Shouguo Gao
Hematology Branch, National Heart, Lung, and Blood Institute (NHLBI), Bethesda, MD, USA

Deadline for manuscript submissions

closed (20 July 2024)

G C A T
T A C G
G C A T

Genes

an Open Access Journal by MDPI

Impact Factor 2.8
CiteScore 5.5
Indexed in PubMed

mdpi.com/si/194156

Genes
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
genes@mdpi.com

mdpi.com/journal/genes

MDPI