

Special Issue

Bioinformatics Methods for Single Cell Sequencing Data Analysis

Message from the Guest Editors

As an emerging biotechnology, single cell sequencing has become widely used. However, single cell data analysis is still challenging. Compared with traditional bulk sequencing, single cell sequencing data is sparse. There are many genes in cells that cannot be measured. Another difference is that the sample size of single cell data is usually much larger than that of bulk sequencing data, enabling the applications of lasted deep learning methods, which require large sample size. Furthermore, the QC (quality control) of single cell sequencing data is different from that of bulk sequencing. There are many new issues. For example, a cell with a unique barcode may be doublet, which leads to different data processing methods. To address these challenges in single cell sequencing data analysis, new bioinformatics methods are needed. Therefore, we would like to organize a Special Issue of *Life* to introduce the latest methods in single cell data analysis.

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Deadline for manuscript submissions

closed (15 June 2022)



Life

an Open Access Journal
by MDPI

Impact Factor 3.2
CiteScore 4.3
Indexed in PubMed



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