

Special Issue

Single-Cell Bioinformatics and Machine Learning

Message from the Guest Editor

The single-cell technology revolution refers to the recent technological advent that makes it possible and economically feasible to obtain robust quantitative measurements (such as mRNA abundance levels) from thousands of individual cells per assay. The development of machine learning as part of the more general field of artificial intelligence has a relatively long history, with its groundwork laid down in the middle of the last century. However, increasingly powerful computers, harnessed to algorithms refined over the past decade, are driving an explosion of applications in every field, from business to healthcare. The marriage of the two technologies—single-cell technology and machine learning—is inevitable. With the development of high-throughput single-cell RNA sequencing (scRNA-seq) platforms, it is becoming almost a routine matter to obtain complete transcriptome information from hundreds of thousands and even millions of individual cells. Therefore, scRNA-seq data currently represent a truly Big Data opportunity with superior statistical power and open new horizons for applying machine learning for data analysis.

Guest Editor

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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?

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