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Single-Cell Bioinformatics and Machine Learning

Guest Editor:

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Deadline for manuscript submissions:
closed (31 December 2021)

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.

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Message from the Editor-in-Chief

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