Review article

Single-cell classification, analysis, and its application using deep learning techniques

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ABSTRACT

Single-cell analysis (SCA) improves the detection of cancer, the immune system, and chronic diseases from complicated biological processes. SCA techniques generate high-dimensional, innovative, and complex data, making traditional analysis difficult and impractical. In the different cell types, conventional cell sequencing methods have signal transformation and disease detection limitations. To overcome these challenges, various deep learning techniques (DL) have outperformed standard state-of-the-art computer algorithms in SCA techniques. This review discusses DL application in SCA and presents a detailed study on improving SCA data processing and analysis. Firstly, we introduced fundamental concepts and critical points of cell analysis techniques, which illustrate the application of SCA. Secondly, various effective DL strategies apply to SCA to analyze data and provide significant results from complex data sources. Finally, we explored DL as a future direction in SCA and highlighted new challenges and opportunities for the rapidly evolving field of single-cell omics.

1. Introduction

Single-cell analysis (SCA) technique has become popular for studying cell-to-cell heterogeneity and single-cell sequencing at single-cell resolution (Guyer et al., 2022). SCA has enhanced our understanding of heterogeneity and functional diversity within different single cells (DNA, RNA Protein cells). SCA's biology and precision medicine opportunities in cell, morphology, tumor cell growth, and COVID-19 detection form distinct subpopulations for disease prevention. In artificial technologies, SCA and Deep Learning (DL) have redefined the ability to analyze vast amounts of data using complex artificial neural network techniques. Moreover, protein interaction with different cells showing the effectiveness and suggests that it could be employed for single-cell analytics (Sarker, 2021). The combination of SCA and DL has revolutionized the field of single-cell analysis, allowing for more accurate and precise predictions of cell behavior and function. DL models extract meaningful information from large and complex datasets generated by SCA and identify hidden patterns that traditional statistical methods help to detect disease. DL models have been applied to various SCA datasets, such as single-cell RNA sequencing (Jovic et al., 2022), single-cell proteomics (REDIT et al., 2023), and single-cell epigenomics (Schwartzman and Tanay, 2015), and showed great promise in identifying novel cell subpopulations (Liu et al., 2023), predicting cell differentiation pathways (Zhu et al., 2021), and predicting drug response in different cells (Kuenzi et al., 2020). Moreover, integrating SCA and DL has also shown great potential in advancing precision medicine. By analyzing single cells at an impossible resolution, researchers can better understand the cellular and molecular mechanisms that drive diseases, such as cancer and COVID-19, and develop more personalized treatments based on the individual patient's cellular profile. The application of SCA and DL in precision medicine can transform, diagnose, and treat diseases, leading to better patient outcomes (El Hoss et al., 2022). One of

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