

The text introduces the significance of Single-cell RNA sequencing (scRNA-seq) technology, which allows for the parallel characterization of thousands of cells at the transcriptome level. This technology is becoming a crucial tool for investigating cellular components and their interactions within the tumor microenvironment. Additionally, scRNA-seq is employed to unveil associations between tumor microenvironmental patterns and clinical outcomes, as well as to dissect cell-specific effects of drug treatments in complex tissues. Despite the proposal of methods for predicting drug response using gene expression data from scRNA-seq, there is a need for an integrated tool that spans from scRNA-seq analysis to drug discovery. In response to this, the authors present scDrug, a bioinformatics workflow encompassing a one-step pipeline for cell clustering in scRNA-seq data and two methods for predicting drug treatments. The scDrug pipeline consists of three primary modules: scRNA-seq analysis for identifying tumor cell subpopulations, functional annotation of cellular subclusters, and prediction of drug responses. This integrated tool, scDrug, allows for the exploration of scRNA-seq data and streamlines the drug repurposing process. Importantly, scDrug is made freely available on GitHub at <https://github.com/ailabstw/scDrug>, providing accessibility for researchers and practitioners in the field.