

Single-cell RNA sequencing (scRNA-seq) technology allows massively parallel characterization of thousands of cells at the transcriptome level. scRNA-seq is emerging as an important tool to investigate the cellular components and their interactions in the tumor microenvironment. scRNA-seq is also used to reveal the association between tumor microenvironmental patterns and clinical outcomes and to dissect cell-specific effects of drug treatment in complex tissues. Recent advances in scRNA-seq have driven the discovery of biomarkers in diseases and therapeutic targets. Although methods for prediction of drug response using gene expression of scRNA-seq data have been proposed, an integrated tool from scRNA-seq analysis to drug discovery is required. We present scDrug as a bioinformatics workflow that includes a one-step pipeline to generate cell clustering for scRNA-seq data and two methods to predict drug treatments. The scDrug pipeline consists of three main modules: scRNA-seq analysis for identification of tumor cell subpopulations, functional annotation of cellular subclusters, and prediction of drug responses. scDrug enables the exploration of scRNA-seq data readily and facilitates the drug repurposing process. scDrug is freely available on GitHub at <https://github.com/ailabstw/scDrug>.