

Abstract: A Comprehensive Annotator and Web Viewer for scRNA-seq Data, Y1

Individual cells are the building blocks of tissues, organs, and organisms. Each tissue contains cells of many types, and cells of each type can switch among biological states. To understand how this complex system work, it will be important to learn the functional capacities and responses of each cell type and each single cell. A major determinant of each cell's function is its transcriptional program, which can be studied by single cell transcriptomics analysis. Recently a powerful technique, single-cell RNA-sequencing (scRNA-seq), has been developed and enables high-resolution studies of gene expression patterns at the single-cell level. However, its high data volume and complexity bringing in many new computational challenges, including the effective ways of data visualization as well as the comprehensive biological annotation. To fulfill this urgent demand, we are developing a web application for RNA-seq data annotation and visualization, which need the XSEDE computing resource as requested. We believed that this application will have significant impact in single cell research in biomedical area. We expected to publish this tool with a series of useful features in the journal of Bioinformatics or Nucleic Acid Research for public use.