**Abstract**

Droplet-based single-cell RNA sequencing (scRNA-seq) is a powerful tool for elucidating developmental, physiological, and pathological processes in biological systems. Unsupervised clustering of scRNA-seq data is a crucial(key/indispensable/necessary/obligatory) step in scRNA-seq analysis workflows that enables the identification of distinct cell types, subtypes, and states. However most clustering algorithms require an estimate of the number of distinct cell types present, as well as the dimensionality of the data. Such *a priori* knowledge is not always available, especially for poorly characterized tissues, which can result in many different interpretations of identical datasets. To address this unmet challenge, we have developed AutoClustR, a tool for automated and unbiased single-cell clustering. We compared 7 methods of dimensionality selection and 14 different ICVIs to empirically ground AutoClustR’s approach to automated clustering. AutoClustR was benchmarked and shown to accurately identify (x percent of cells?), outperforming 6 alternate scRNA-seq analysis platforms. Then, AutoClustR was applied to a real-world dataset derived from human embryonic stem cell-derived inner ear organoids to reveal a previously unappreciated diversity of cell types. AutoClustR’s approach allows researchers to characterize novel datasets, and the empirical support for this approach is a valuable resource for fellow bioinformaticians.