

# scATAcat: Cell-type annotation for scATAC-seq data

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Cells whose accessibility landscape has been profiled with scATAC-seq cannot readily be annotated to a particular cell type. In fact, annotating cell-types in scATAC-seq data is a challenging task since, unlike in scRNA-seq data, we lack knowledge of “marker regions” which could be used for cell-type annotation. Current annotation methods typically translate accessibility to expression space and rely on gene expression patterns. We propose a novel approach, scATAcat, that leverages characterized bulk ATAC-seq data as prototypes to annotate scATAC-seq data. To mitigate the inherent sparsity of single-cell data, we aggregate cells that belong to the same cluster and create pseudobulk. To demonstrate the feasibility of our approach we collected a number of datasets with respective annotations to quantify the results and evaluate performance for scATAcat. scATAcat is available as a python package at <https://github.com/aybugealtay/scATAcat>

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