

Supplementary Tables

Table S1: **Bioconductor software package for single-cell analyses.**

Analysis	Package name	Description
Data Input	<i>scPipe</i> [32]	Uses the <i>Rsubread</i> [33, 34] package to align sequencing reads
	<i>tximport</i> [38]	Wrappers for psuedoalignment algorithms such as Salmon [36] and Kallisto [37]
	<i>DropletUtils</i> [54]	Reading in a matrix of UMI counts from droplet-based protocols, such as 10X Genomics [35]
	<i>beachmat</i> [165]	A C++ interface for accessing single-cell data with sparse, dense and file-backed matrices, such as the HDF5 file format [166]
	<i>rhdf5</i> [167]	Access and store data in HDF5 file formats [166]
Data Infrastructure	<i>HDF5Array</i> [168], <i>DelayedArray</i> [169], <i>DelayedMatrixStats</i> [170]	Efficiently work with data in HDF5 file formats [166] using array-like containers and delayed operations
	<i>SingleCellExperiment</i> [40]	Package for the <i>SingleCellExperiment</i> class that stores and accesses data from single-cell assays or experiments
Quality control, normalization, feature reduction	<i>DropletUtils</i> [54], <i>scater</i> [56], <i>simpleSingleCell</i> [59]	Perform cell and gene quality control for both read and UMI count data
	<i>SCnorm</i> [33], <i>scran</i> [29], <i>BASiCS</i> [54, 55], <i>zinbwave</i> [31], and <i>MAST</i> [28]	Normalizations methods to remove gene and/or cell-specific biases in scRNA-seq data
	<i>scone</i> [86]	Compare normalization strategies and parameterizations
	<i>scran</i> [59], <i>Oscope</i> [71]	Adjust for variation from differences in cell-cycle phases in data from humans and mice
	<i>batchelor</i> [75], <i>scran</i> [59, 74], <i>scMerge</i> [76], <i>scmap</i> [77], <i>scAlign</i> [78]	Methods for integrating two or more scRNA-seq datasets
	<i>scran</i> , [59], <i>BASiCS</i> [54, 55], <i>M3Drop</i> [84]	Methods for feature selection
	<i>scater</i> [56]	Performs and visualizes results from dimensionality reduction methods including PCA, <i>t</i> -SNE components [44], UMAP components [45, 88], and diffusion maps [89]
	<i>BiocSingular</i> [90]	Exact and approximate methods for singular value decomposition that uses the <i>BiocParallel</i> [91] framework to parallelize operations
	<i>zinbwave</i> [31]	Performs model-based dimensionality reduction based on the ZINB-WaVE model [31]
	<i>BiocNeighbors</i> [97-100]	Exact and approximate methods for nearest neighbor detection that uses the <i>BiocParallel</i> [91] framework to parallelize operations
Downstream statistical analyses	<i>SC3</i> [102], <i>clusterExperiment</i> [103], <i>SIMLR</i> [104], <i>mbkmeans</i> [106], <i>BEARscc</i> [107], <i>clustree</i> [108]	Unsupervised clustering frameworks for single-cell data
	<i>edgeR</i> [3, 52], <i>DESeq2</i> [7], <i>limma</i> [115]	Methods developed for bulk RNA-seq differential expression that can be used in combination with methods such as <i>zinbwave</i> [31, 116] to account for the zero-inflation
	<i>MAST</i> [28], <i>scDD</i> [117], <i>BASiCS</i> [54, 55], <i>SCDE</i> [118]	Methods to identify differentially expressed features using statistical models that directly model zero-inflation
	<i>slingshot</i> [126], <i>TSCAN</i> [30], <i>monocle</i> [123, 124, 127], <i>cellTree</i> [128]	Methods for trajectory analysis or pseudotime inference
	<i>MAST</i> [28], <i>AUCell</i> [141], <i>scmap</i> [77], <i>PADOQ</i> [139], <i>fgsea</i> [137], <i>goseq</i> [138], <i>slalom</i> [142], <i>scCoGAPS</i> [143, 144], <i>EnrichmentBrowser</i> [140]	Methods for gene set / signature enrichment analysis
	<i>iSEE</i> [148]	Interactive data exploration and visualization
	<i>countsSimQC</i> [153], <i>batchQC</i> [154], <i>iSEE</i> [148]	Making analyses accessible and reproducible for producing analytical reports
	<i>ExperimentHub</i> [152], <i>DuoClustering2018</i> [109], <i>CellBench</i> [80]	Single-cell published data packages such as <i>TENxPBMCData</i> , <i>TENxBrainData</i> , <i>HCADData</i> , <i>HCABrowser</i> or benchmarking datasets
	<i>splatter</i> [157]	Packages to simulate single-cell data useful for benchmarking statistical methods