Methods to compare with

1. **Quality Control**

1)Scater

Davis J McCarthy, Kieran R Campbell, Aaron T L Lun, Quin F Wills, Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R, Bioinformatics, Volume 33, Issue 8, 15 April 2017, Pages 1179–1186, [https://doi.org/10.1093/bioinformatics/btw777]( https:/doi.org/10.1093/bioinformatics/btw777)

2)scPipe

Tian L , Su S , Dong X , et al. scPipe: a flexible R/Bioconductor preprocessing pipeline for single-cell RNA-sequencing data[J]. Plos One, 2018, 13(7):e0200193. <https://doi.org/10.1371/journal.pcbi.1006361>

1. Scran

Lun, Aaron TL, Karsten Bach, and John C Marioni. 2016. “Pooling Across Cells to Normalize Single-Cell Rna Sequencing Data with Many Zero Counts.” Genome Biology 17 (1). BioMed Central: 75.<https://doi.org/10.1186/s13059-016-0947-7>

1. **Differential Expression**

1)MAST

Finak G, Mcdavid A, Yajima M, et al. MAST: a flexible statistical framework for assessing transcriptional changes and characterizing heterogeneity in single-cell RNA sequencing data[J]. Genome Biology, 2015, 16(1):278.<https://doi.org/10.1186/s13059-015-0844-5>

1. DEseq2

Love M I, Huber, Wolfgang, Anders, Simon. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2[J]. Genome Biology, 2014, 15(12):550. <https://doi.org/10.1186/s13059-014-0550-8>

1. SCDE

Kharchenko P V , Silberstein L , Scadden D T . Bayesian approach to single-cell differential expression analysis[J]. Nature Methods, 2014, [11(7):740-742.https://doi.org/10.1038/nmeth.2967](https://doi.org/10.1038/nmeth.2967)

1. **Dimensionality Reduction**

1)ZIFA:

Pierson, E. & Yau, C. Dimensionality reduction for zero-inflated single cell gene expression analysis. Genome Biol. 16, 241 (2015). <https://doi.org/10.1186/s13059-015-0805-z>

1. PCA
2. tSNE

4)ZINB-Wave

Risso D, Perraudeau, Fanny, Gribkova, Svetlana, et al. A general and flexible method for signal extraction from single-cell RNA-seq data[J]. Nature Communications, 2018, 9(1):284.<https://doi.org/10.1038/s41467-017-02554-5>

**4. Batch Effect Correction**

1)ZINB-WaVE

Risso D, Perraudeau, Fanny, Gribkova, Svetlana, et al. A general and flexible method for signal extraction from single-cell RNA-seq data[J]. Nature Communications, 2018, 9(1):284.<https://doi.org/10.1038/s41467-017-02554-5>

2) Seurat

Andrew Butler, Paul Hoffman, Peter Smibert, Efthymia Papalexi, and Rahul Satija.

Integrating single-cell transcriptomic data across different conditions, technologies, and

species. Nature Biotechnology, 36(5):411, 2018. <https://doi.org/10.1038/nbt.4096>

3)MNN

Laleh Haghverdi, Aaron TL Lun, Michael D Morgan, and John C Marioni. Batch effects in single-cell rna-sequencing data are corrected by matching mutual nearest neighbors.

Nature Biotechnology, 36(5):421, 2018. <https://doi.org/10.1038/nbt.4091>

Datasets to use