**Additional resources regarding single-cell analysis**

*Experimental Design*

Using hashtags to demultiplex/ pool samples

* <https://genomebiology.biomedcentral.com/articles/10.1186/s13059-018-1603-1>

Using natural genetics to demultiplex individuals

* <https://www.nature.com/articles/nbt.4042>

*Clean up*

Removing ambient RNA

* <https://bioconductor.org/packages/3.16/bioc/html/DropletUtils.html>

Doublet finder

* <https://bioconductor.org/packages/3.16/bioc/html/scDblFinder.html>

*Normalisation*

Downsampling instead of scaling

* Lun, A. 2018. “Overcoming Systematic Errors Caused by Log-Transformation of Normalized Single-Cell Rna Sequencing Data.” bioRxiv.

ScTransform

* <https://genomebiology.biomedcentral.com/articles/10.1186/s13059-021-02584-9>

*Dimension Reduction*

OpenTSNE: extending tSNE (including adding new points to pre-existing embeddings)

* <https://opentsne.readthedocs.io/en/stable/> (Python, but Snifter is an R-wrapper for it - <https://bioconductor.org/packages/3.16/bioc/html/snifter.html>)

Densviz: Incorporating density into tSNE & UMAP

* <https://www.nature.com/articles/s41587-020-00801-7>

*Clustering*

Silhouette width: to evaluate cluster sepration

Cluster purity: to determine if cells from different clusters intermingle

* approxSilhouette() function in bluster package <https://bioconductor.org/packages/3.16/bioc/html/bluster.html>

Cluster stability: ideally clusters are stable to input data perturbations (ie. bootstrapping to evaluate clustering algorithm stability using the package scran)

* Von Luxburg, U. 2010. “Clustering Stability: An Overview.” Foundations and Trends in Machine Learning 2 (3): 235–74.

*Differentiation gene expression*

edgeR: one of the most powerful DEG tests

* <https://bioconductor.org/packages/3.16/bioc/html/edgeR.html>