## Data Processing Overview

Reads are demultiplexed by **cellranger mkfastq** (which utilizes **bcl2fastq**).

Alignment is performed by **cellranger count** (which utilizes **STAR**). A UMI count matrix is generated.

Secondary analysis is performed by the **cellranger count** pipeline, **Seurat**, and **Monocle**, offering different perspectives on the data. The sample output of each workflow is shown below.

## Sample Secondary Analysis

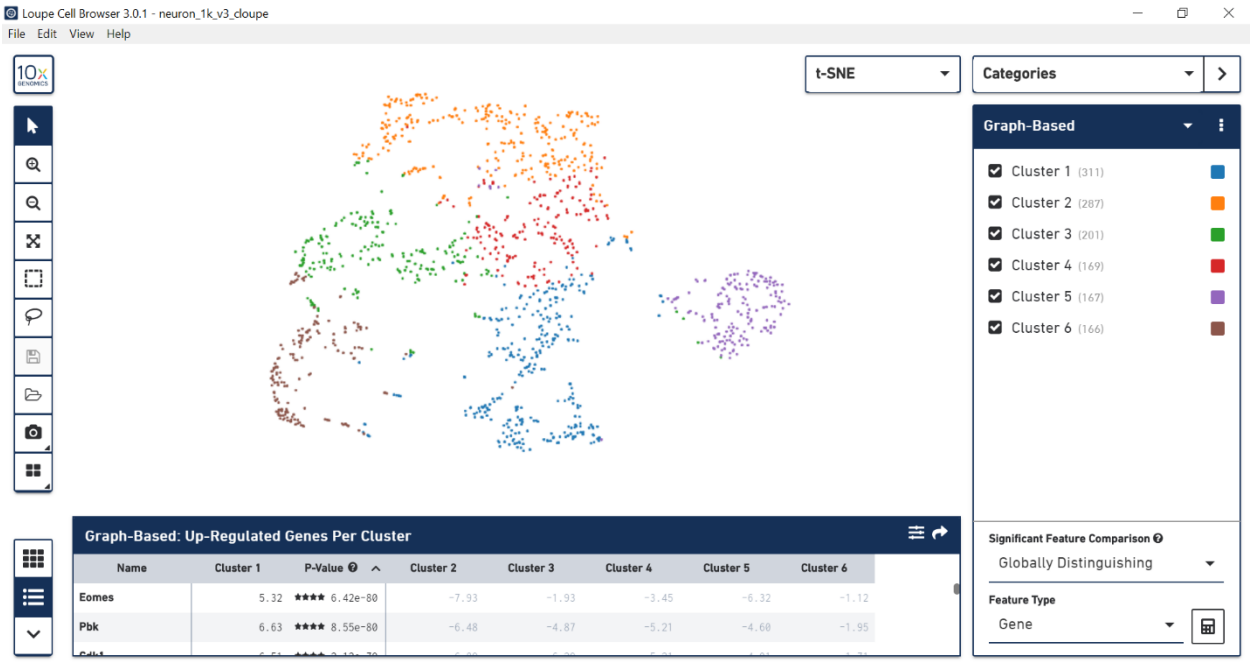
The sample data is the 1k Brain Cells from an E18 Mouse (v3 chemistry) dataset from 10x genomics.

### Cell Ranger

(Sample report)

The **cellranger count** pipeline performs dimensionality reduction, clustering, and differential expression analysis.

Interactive viewing of analysis results in **Loupe Cell Browser**:

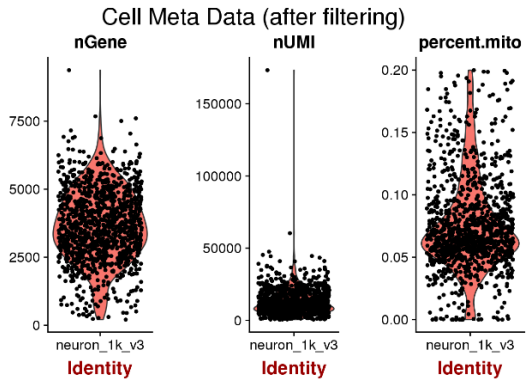



### Seurat

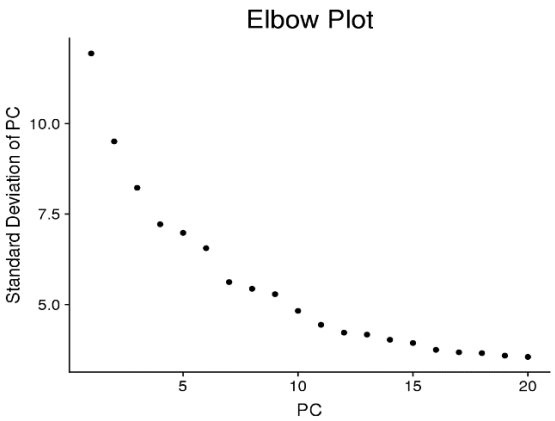
(Sample report)

The **Seurat** workflow includes QC, dimensionality reduction, clustering, and differential expression analysis, with more flexibility in the choice of parameters.

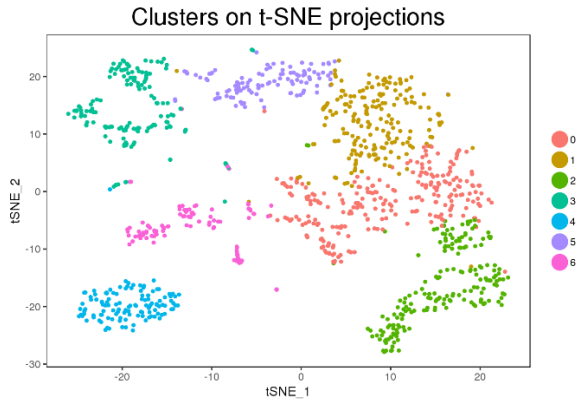
**QC**



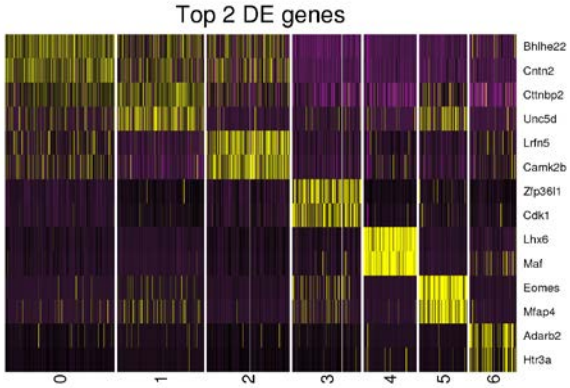

**Dimensionality reduction**




**Clustering**




**Differential expression**

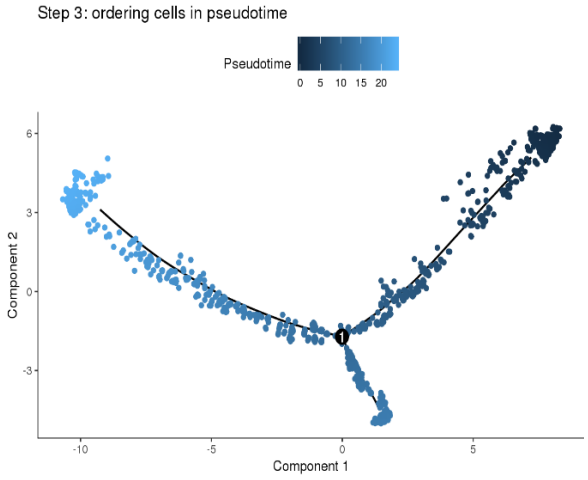



## Monocle

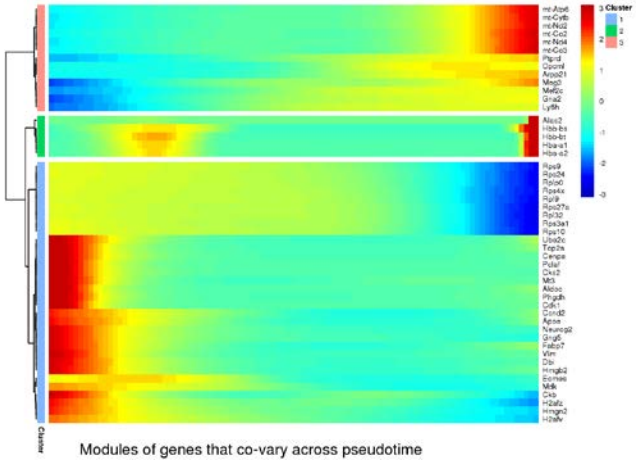
([Sample report])

The **Monocle** workflow includes pseudotime analysis in addition to the analysis steps in **Seurat**.

**Single Cell Trajectories**




**DE genes over pseudotime**



## Tools

Tools used in the pipeline:

- Cell Ranger
- Seurat
- Monocle

Other tools that can be useful:

- VisR: A platform of R Apps allowing users to run R functions/workflows in a GUI (including **Seurat** and **Monocle**).
- BackSPIN: Hierarchical bi-clustering of single cell expression data
- Velocyto: Generating a force field plot that predicts the future states of cells
- WebGestalt: A web based gene ontology analysis tool