

First steps

Katarzyna Sikora

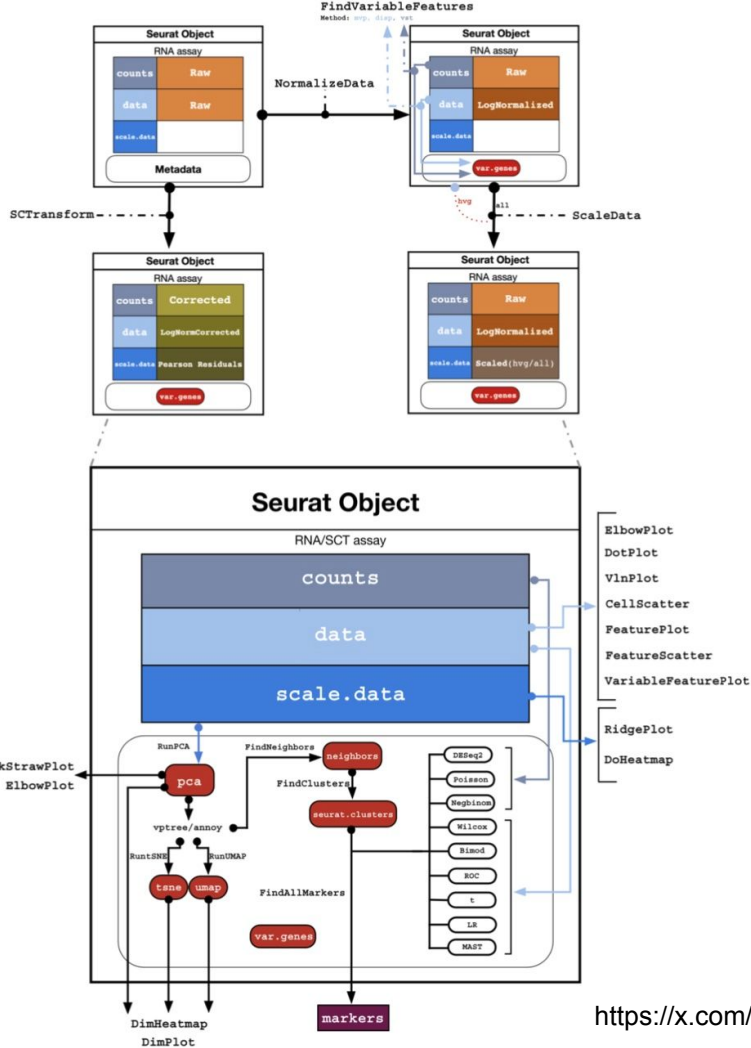
Overview

- 10x scRNAseq output data
- Seurat Object

Standard 10x scRNAseq output

- matrix.mtx -> feature(gene) x cell counts
- genes.tsv -> gene annotation (ensembl ID - > gene symbol)
- barcodes.tsv -> barcode list

Seurat Object

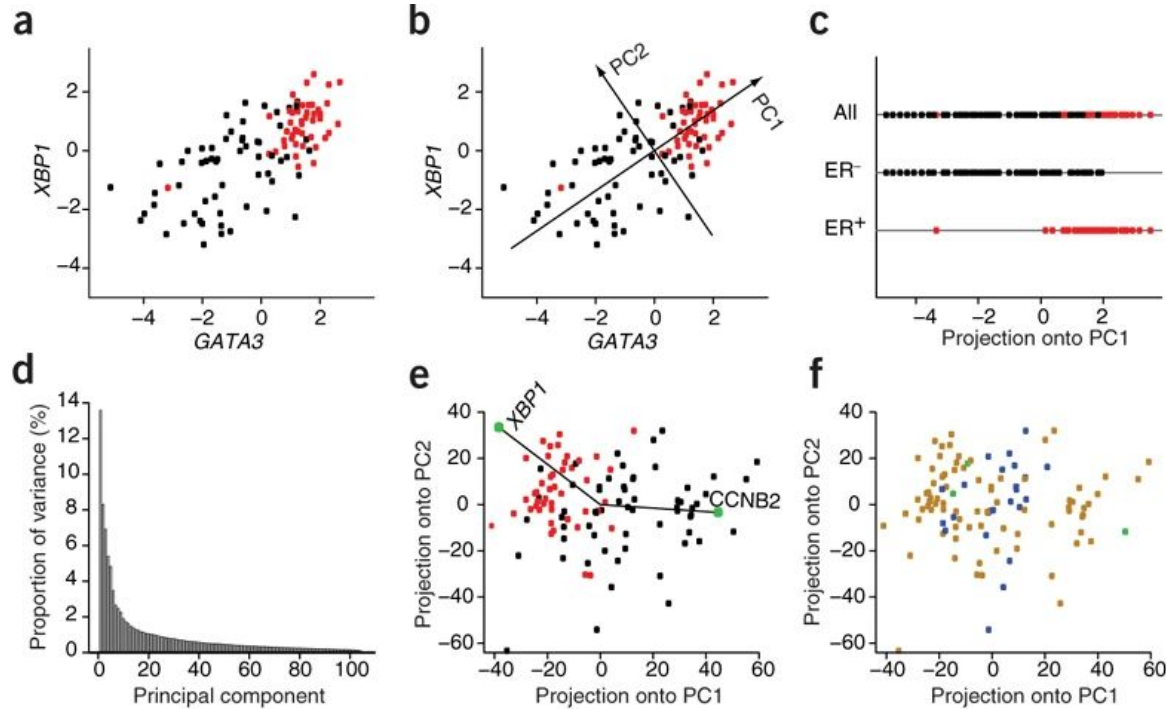


Accessors & accessor functions:

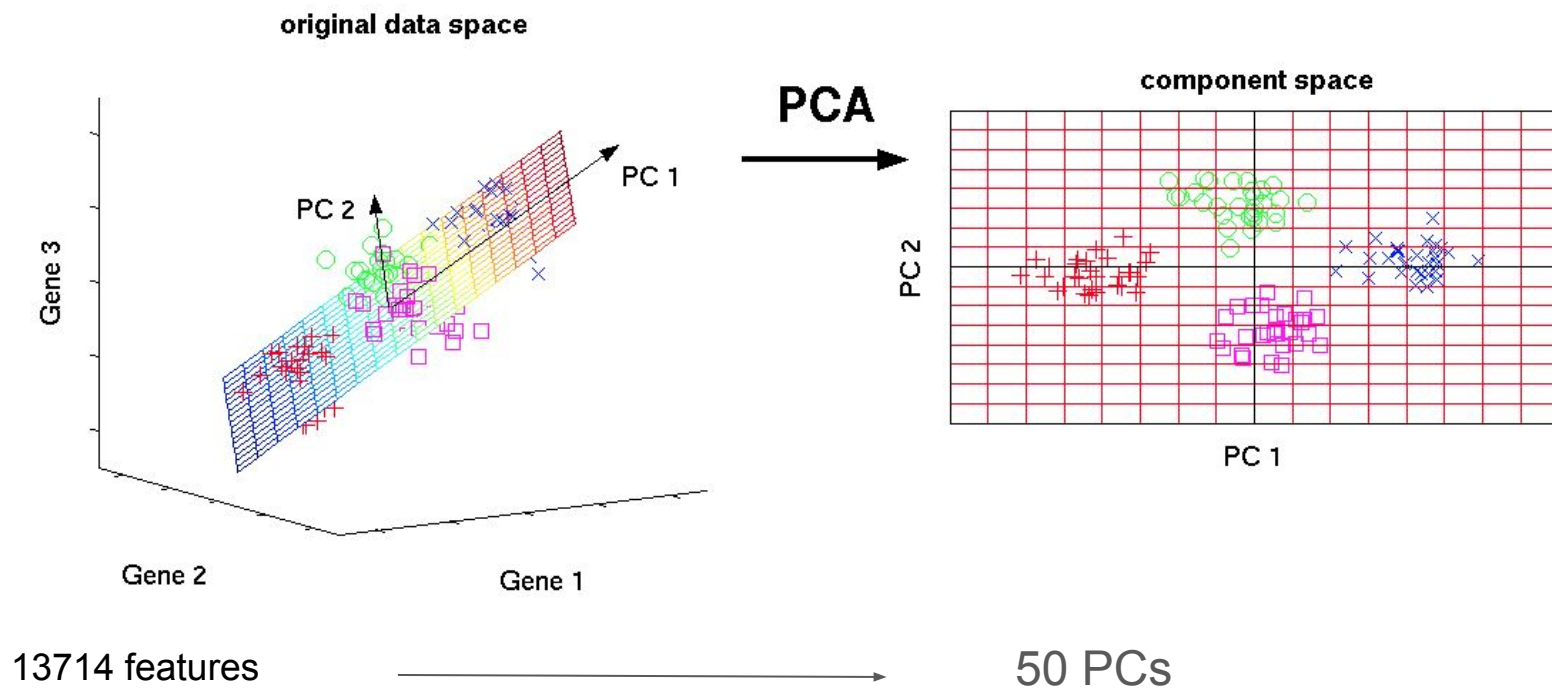
- [obj@meta.data](#)
- `obj[[assay]]@layers$slot`
- `LayerData()`
- `FetchData()`
- `Layers()`
- `Assays()`
- `Features()`
- `Cells()`
- `Embeddings()`

https://satijalab.org/seurat/articles/essential_commands#seurat-object-data-access

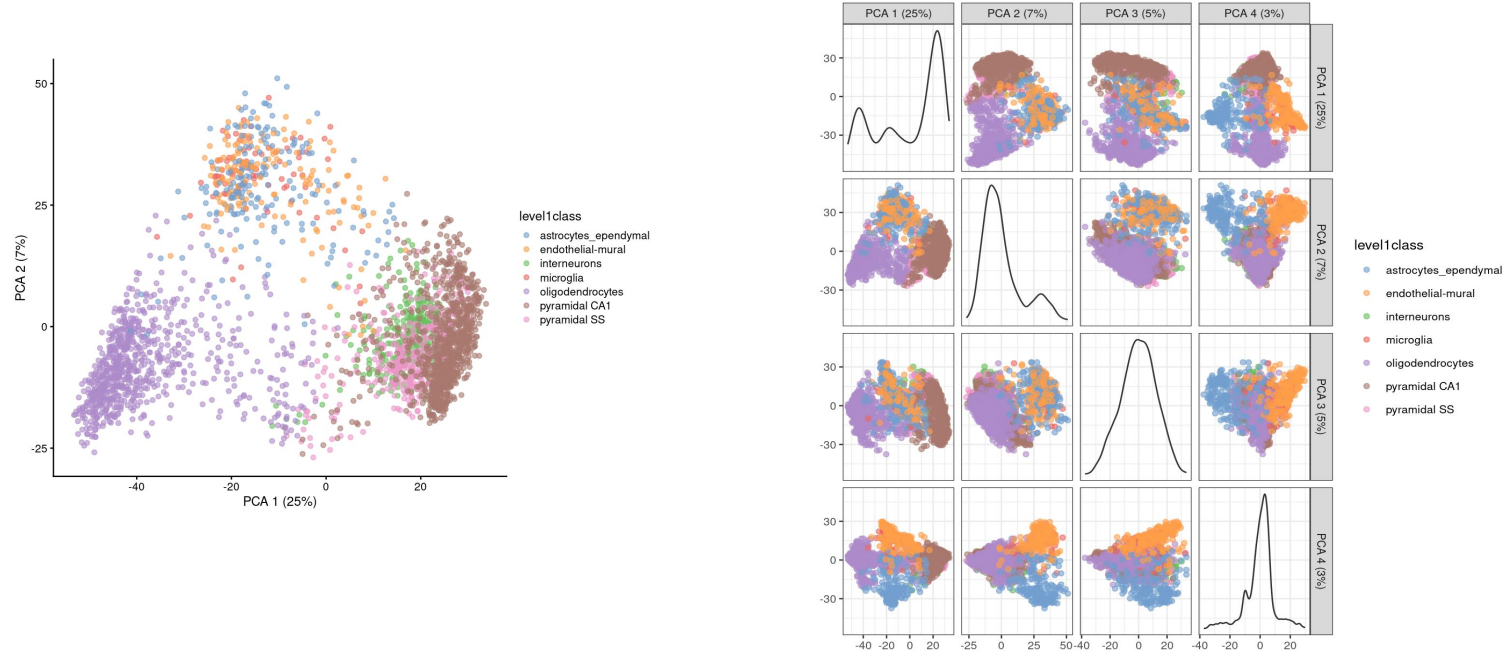
PCA: a simple example



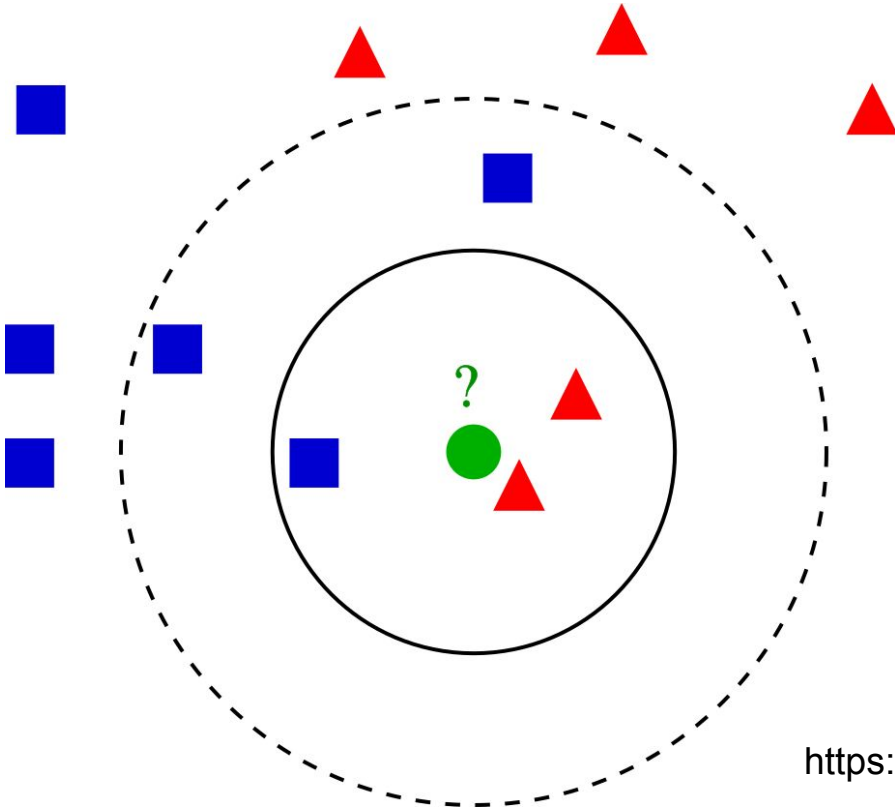
PCA: multiple dimensions



PCA on a scRNAseq dataset

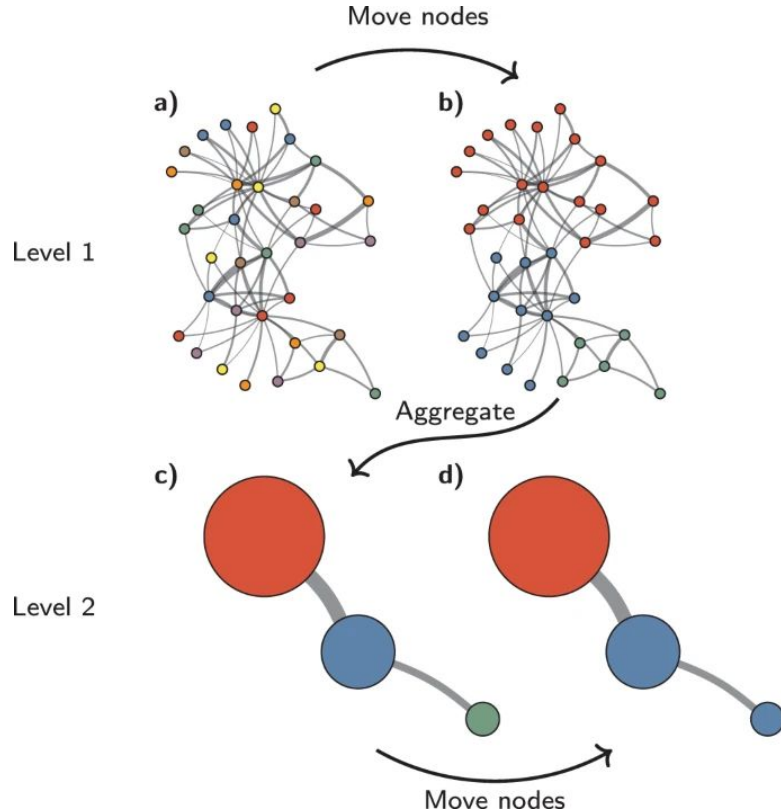


Shared nearest neighbour graph construction



1. find k nearest neighbours for each cell
2. calculate neighbourhood overlap (Jaccard index)
3. construct SNN graph

Louvain/Leiden clustering on the SNN graph



Resolution parameter:
Higher resolutions lead to more
communities, while lower
resolutions lead to fewer
communities.

<https://www.nature.com/articles/s41598-019-41695-z>