

First steps

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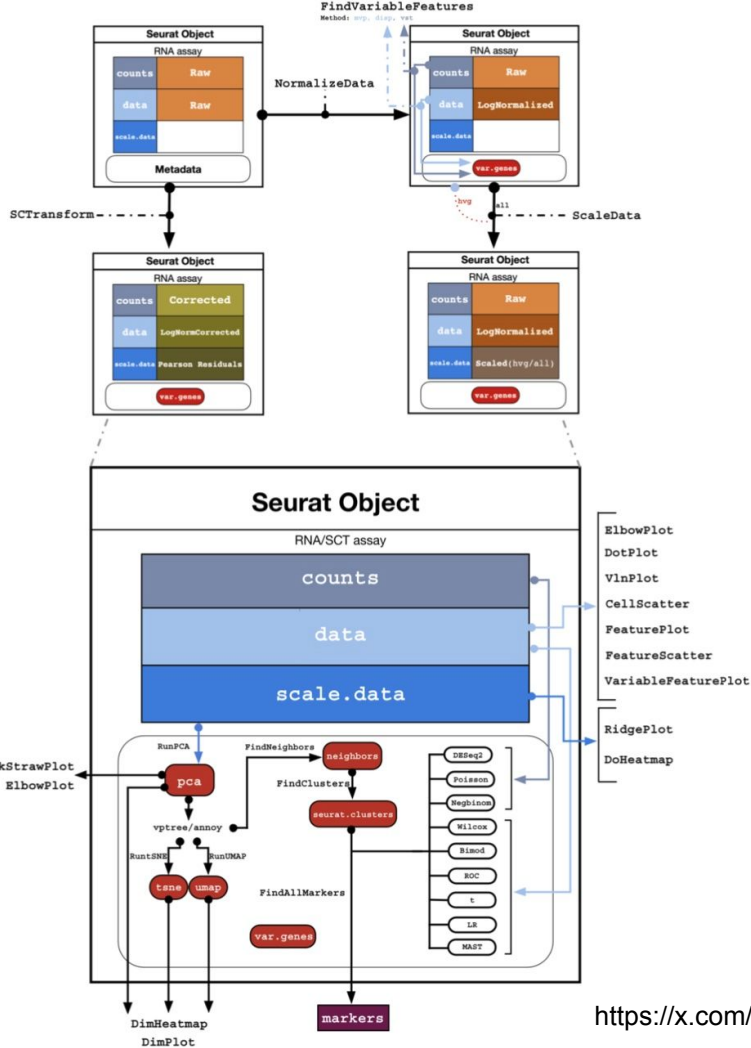
Overview

- 10x scRNAseq output data
- Seurat Object
- PCA

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



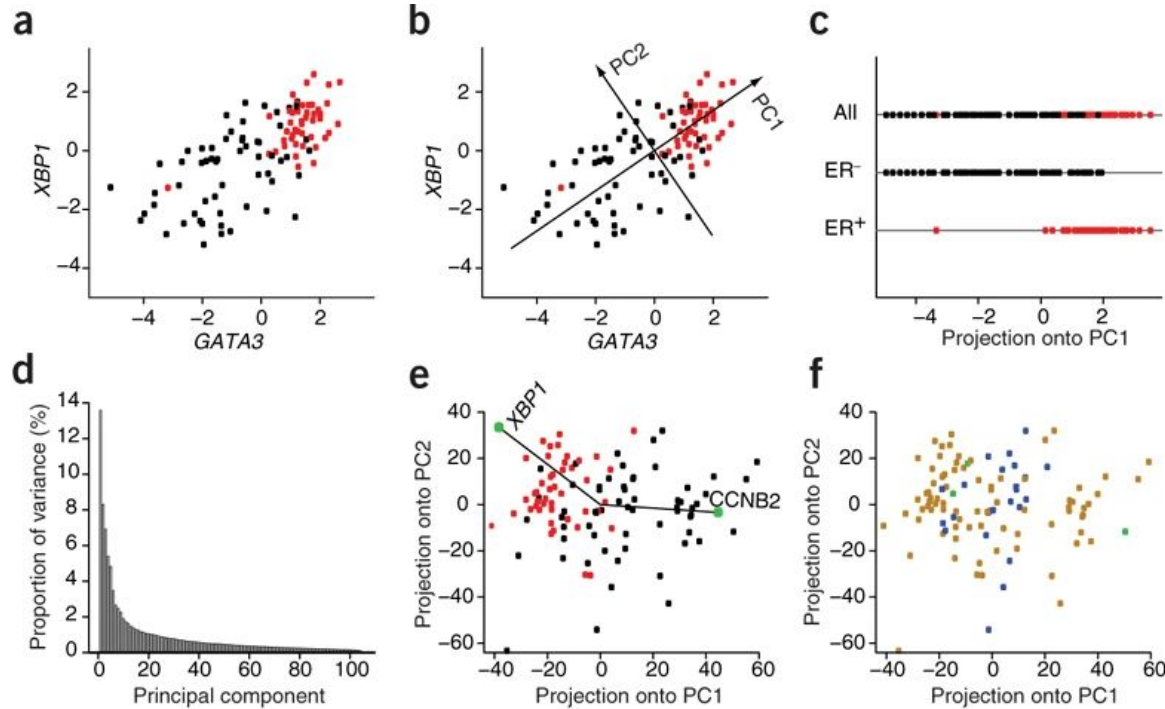
Accessors & accessor functions:

- [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

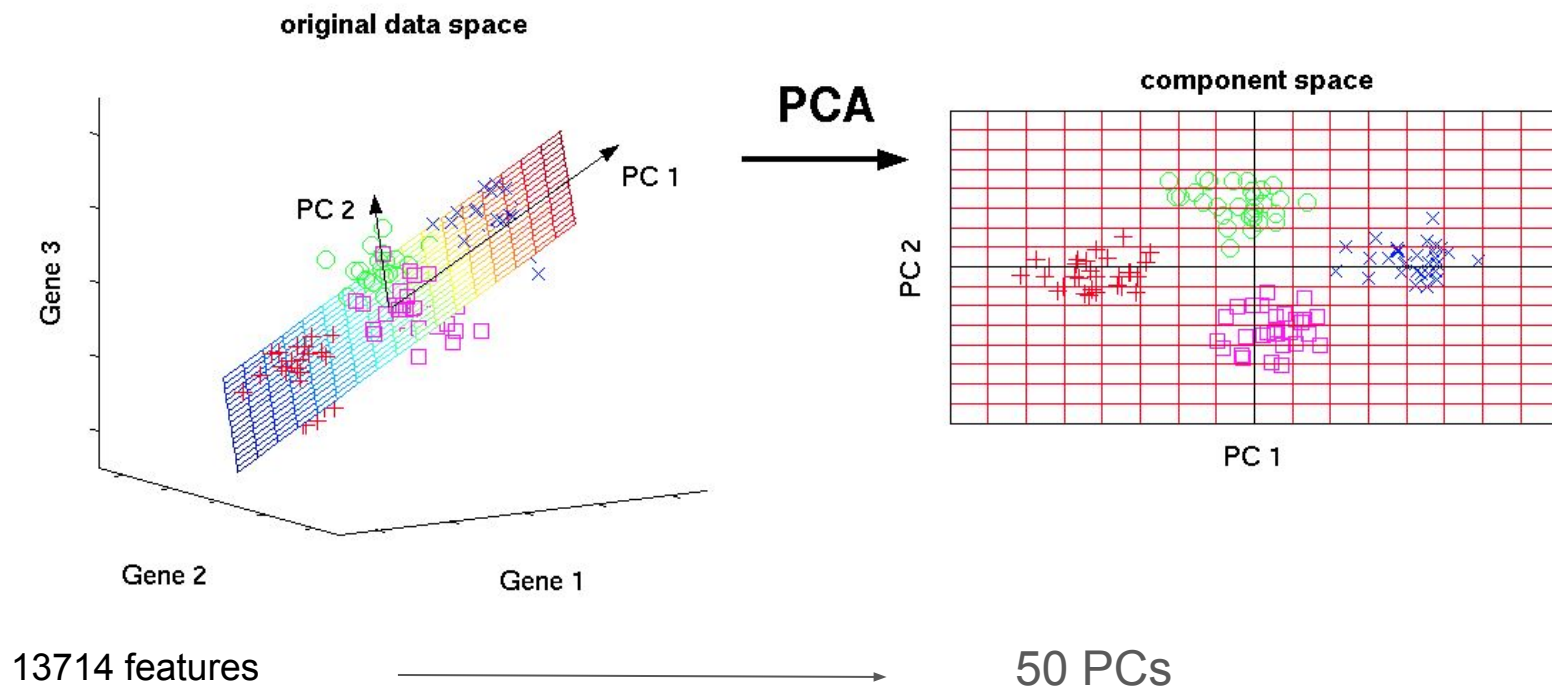
PCA: a simple example



2 genes

all genes

PCA: multiple dimensions



PCA on a scRNAseq dataset

