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 Seurat Object RNA assay NormalizeData SCTransform - . - . ----- ScaleData Seurat Object Seurat Object RNA assav **Seurat Object** RNA/SCT assay DotPlot counts VlnPlot CellScatter FeaturePlot FeatureScatter VariableFeaturePlot scale.data RidgePlot RunPCA DoHeatmap JackStrawPlot ElbowPlot FindClusters FindAllMarkers

markers

DimPlot

FindVariableFeatures

Seurat Object

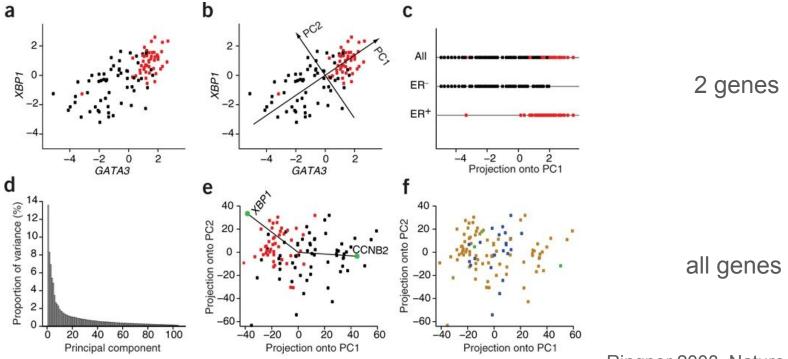
Accessors & accessor functions:

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

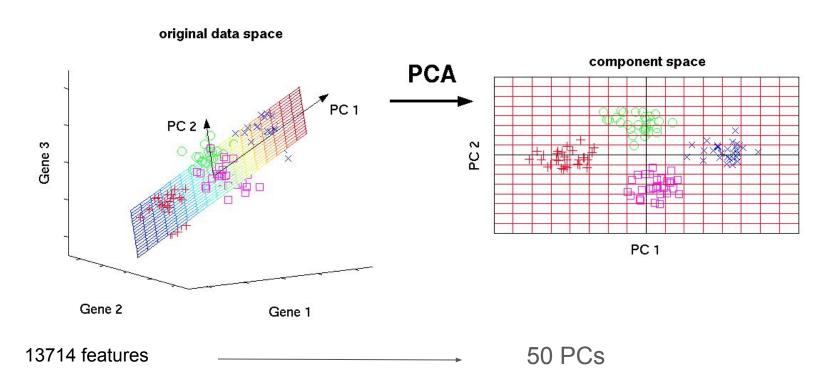
https://satijalab.org/seurat/articles/essential_commands#seurat-object-data-access

PCA

PCA: a simple example



PCA: multiple dimensions



PCA on a scRNAseq dataset

