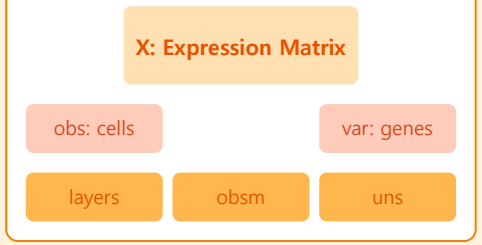
Hands-on: Scanpy Analysis

Scanpy: Python-based Single Cell Analysis

AnnData Structure



Standard Workflow

```
# Import libraries
import scanpy as sc
import pandas as pd
adata = sc.read_10x_h5('file.h5')
```

```
# QC and filter
sc.pp.calculate_qc_metrics(adata)
sc.pp.filter_cells(adata, min_genes=200)
sc.pp.filter_genes(adata, min_cells=3)
```

```
# Normalize and find HVGs
sc.pp.normalize_total(adata)
sc.pp.log1p(adata)
sc.pp.highly_variable_genes(adata)
```

```
# Dimension reduction
sc.tl.pca(adata)
sc.pp.neighbors(adata)
sc.tl.umap(adata)
```

Advanced Scanpy Features

Trajectory Analysis

```
sc.tl.paga(adata)
sc.tl.dpt(adata)
```

RNA Velocity

```
import scvelo as scv
scv.tl.velocity(adata)
```

GPU Acceleration

```
import rapids_singlecell
# 100x speedup!
```

Large datasets

Data Integration

```
sc.external.pp.harmony_
integrate(adata, 'batch')
```

💡 Python ecosystem with extensive documentation