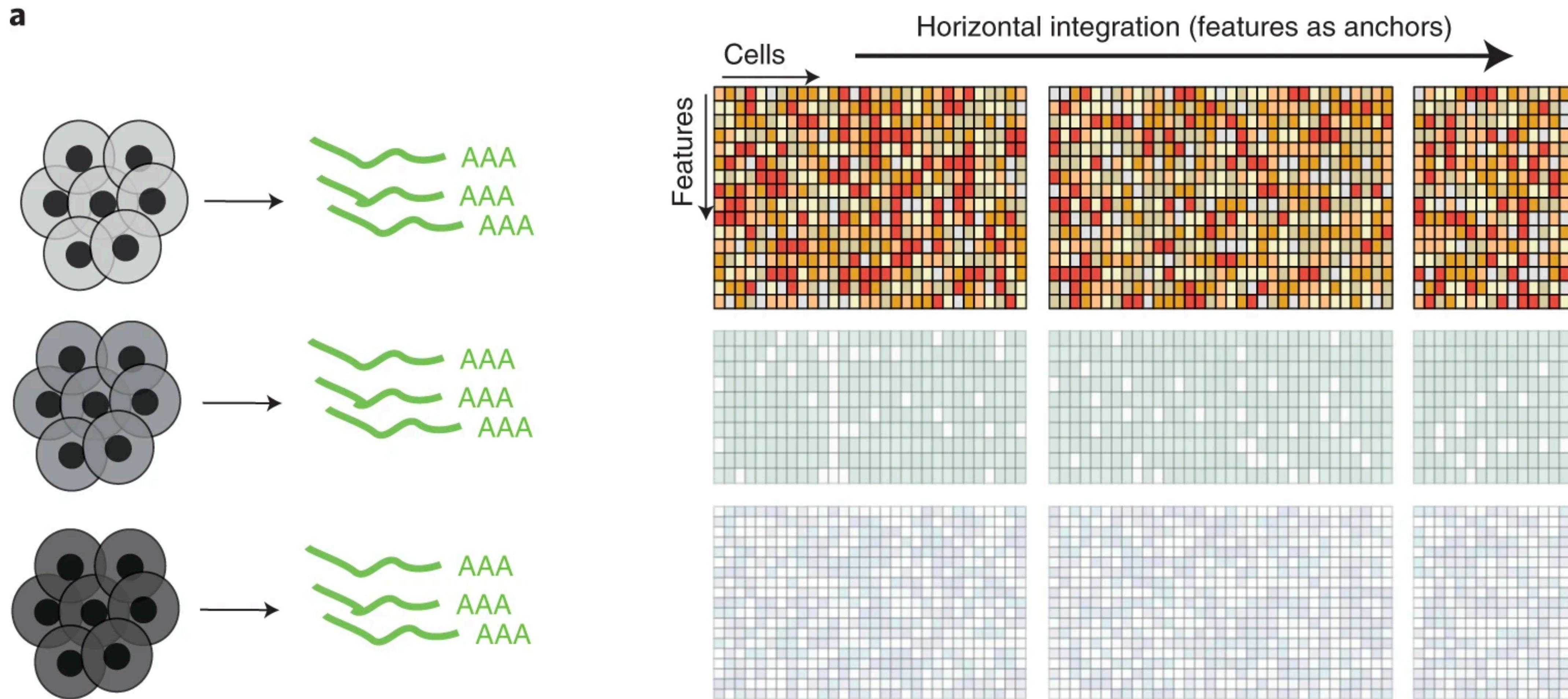
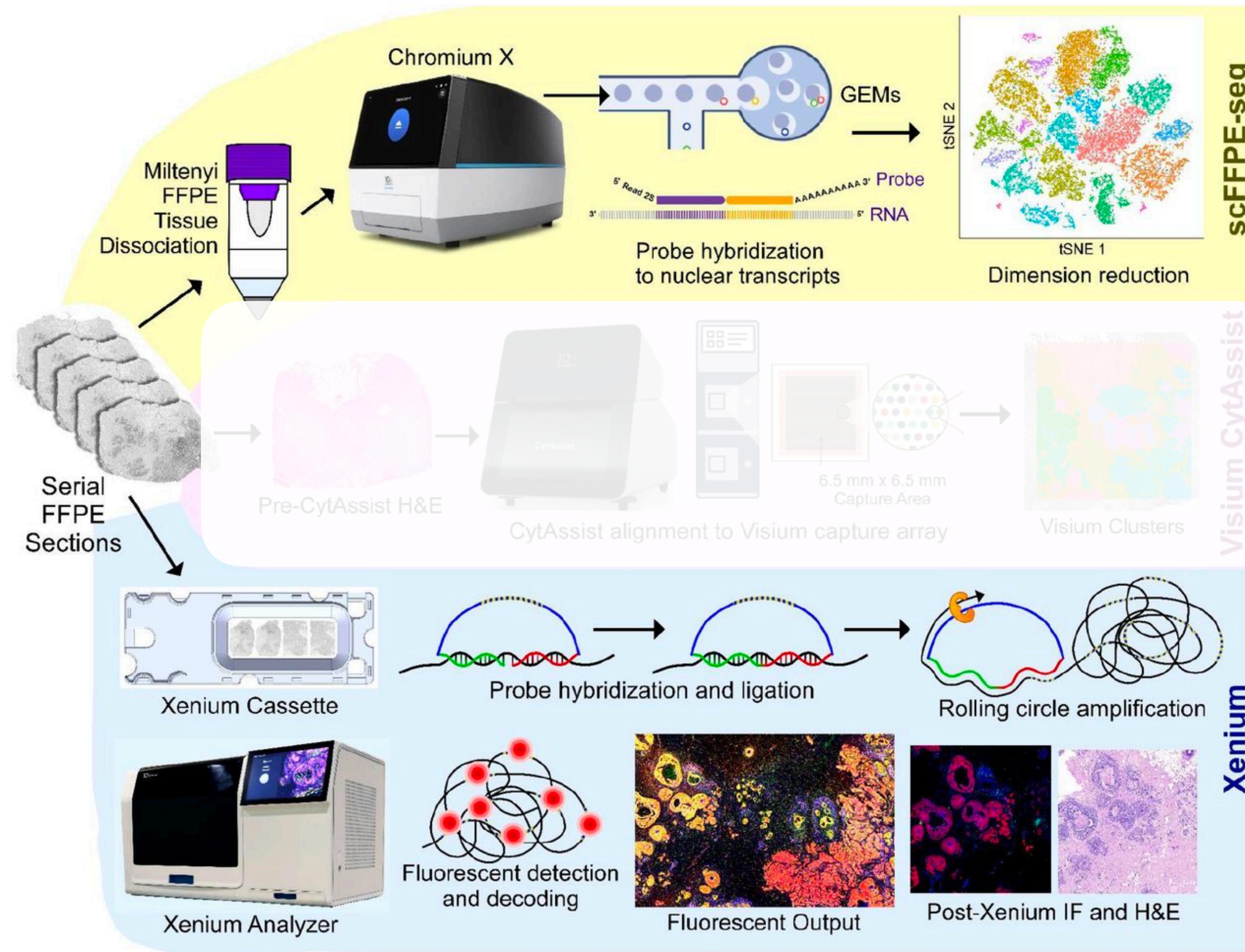


# Part 2: Horizontal data integration

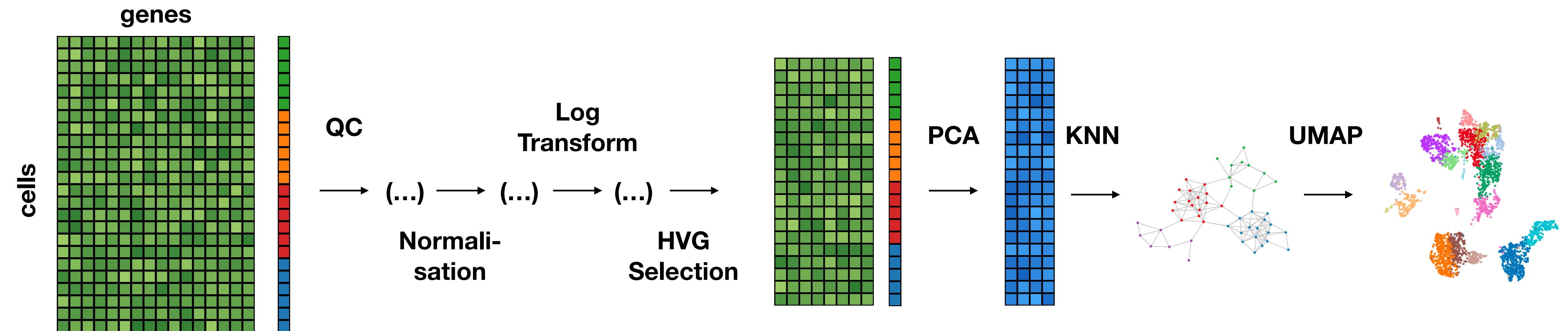


# Part 2: Horizontal data integration

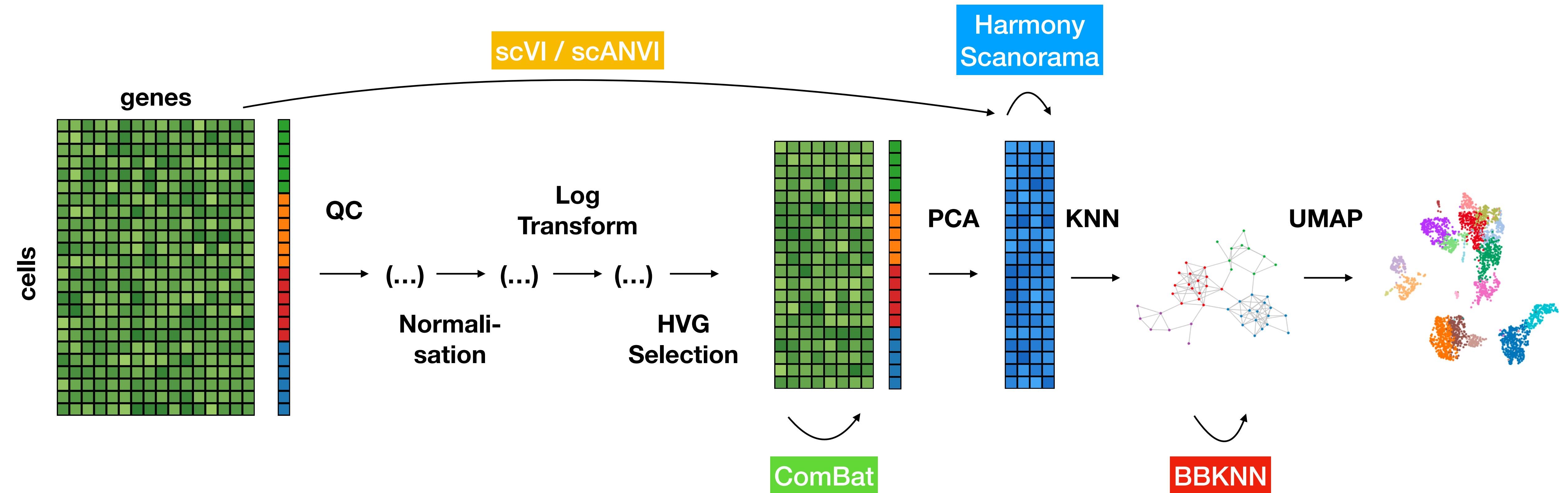


**Integrate single cells  
from scFFPE-seq  
with cells from Xenium**

# The single-cell analysis workflow



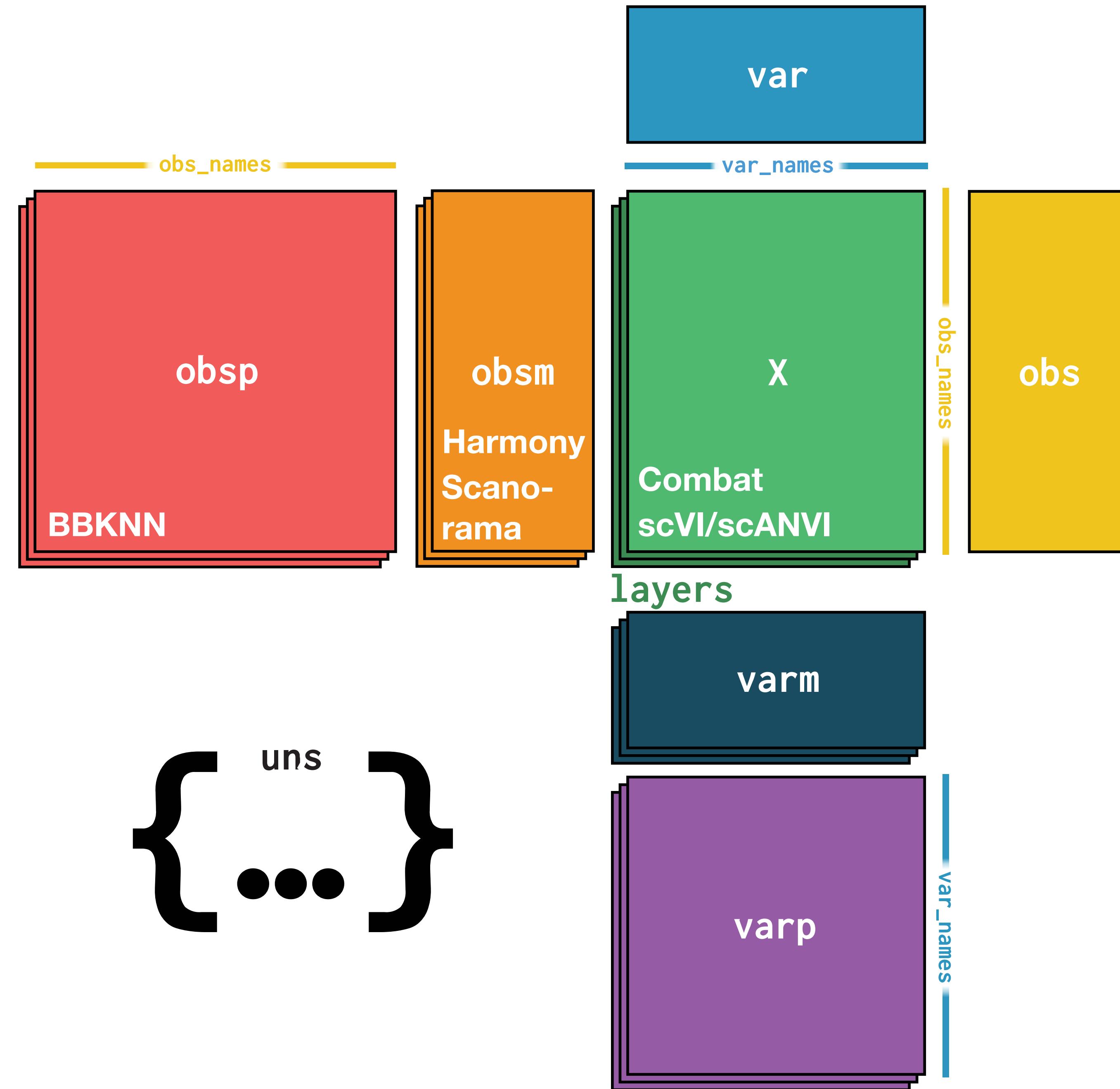
# (Some) batch integration methods



# Overview of (some single-cell) integration tools

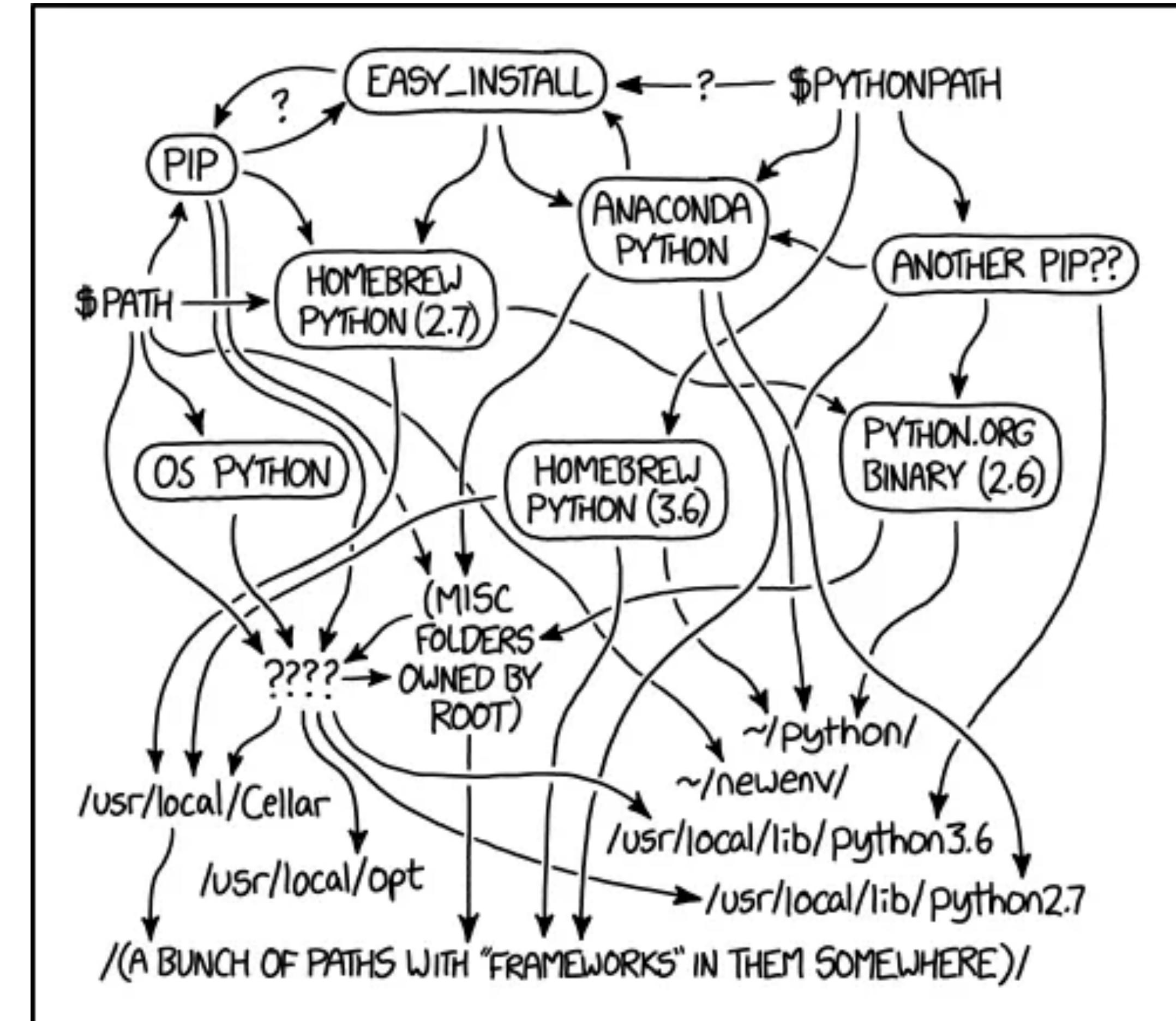
	Combat	BBKNN	Harmony	Scanorama	scVI/scANVI
Input (+ batch covariate)	(Log1p transformed) expression matrix	KNN graph	PCA embeddings	PCA embeddings	Raw counts (+ cell type annotations for scANVI)
Output	Batch corrected expression matrix	Batch corrected KNN graph	Batch corrected PCA embeddings	Batch corrected PCA embeddings	Batch corrected cell embeddings
Methodology	Linear regression (+ Empirical bayes)	“approximate neighbour detection” (annoy package)	Soft clustering (“maximum diversity clustering”)	Mutual nearest neighbour matching	(Variational) autoencoder
Notes	Linear, Loc/scale model	Purely dependent on the graph representation		Does not require shared cell types	Non-linear, Complex

# Anndata



# Dependency hell

- VM
- Clone/Download the latest repo!
- Google Colab



MY PYTHON ENVIRONMENT HAS BECOME SO DEGRADED  
THAT MY LAPTOP HAS BEEN DECLARED A SUPERFUND SITE.

# Don't try this at home!

velten-group / EMBO-multi-omics-course

<> **Code** Issues Pull requests 1 Projects Wiki Security Insights

main ➔ **EMBO-multi-omics-course / day3 / 2-horizontal\_integration.ipynb** Go to file t ...

sagar87 final changes to the horizontal integration tutorial 27f71b2 · 13 hours ago History

6.97 MB

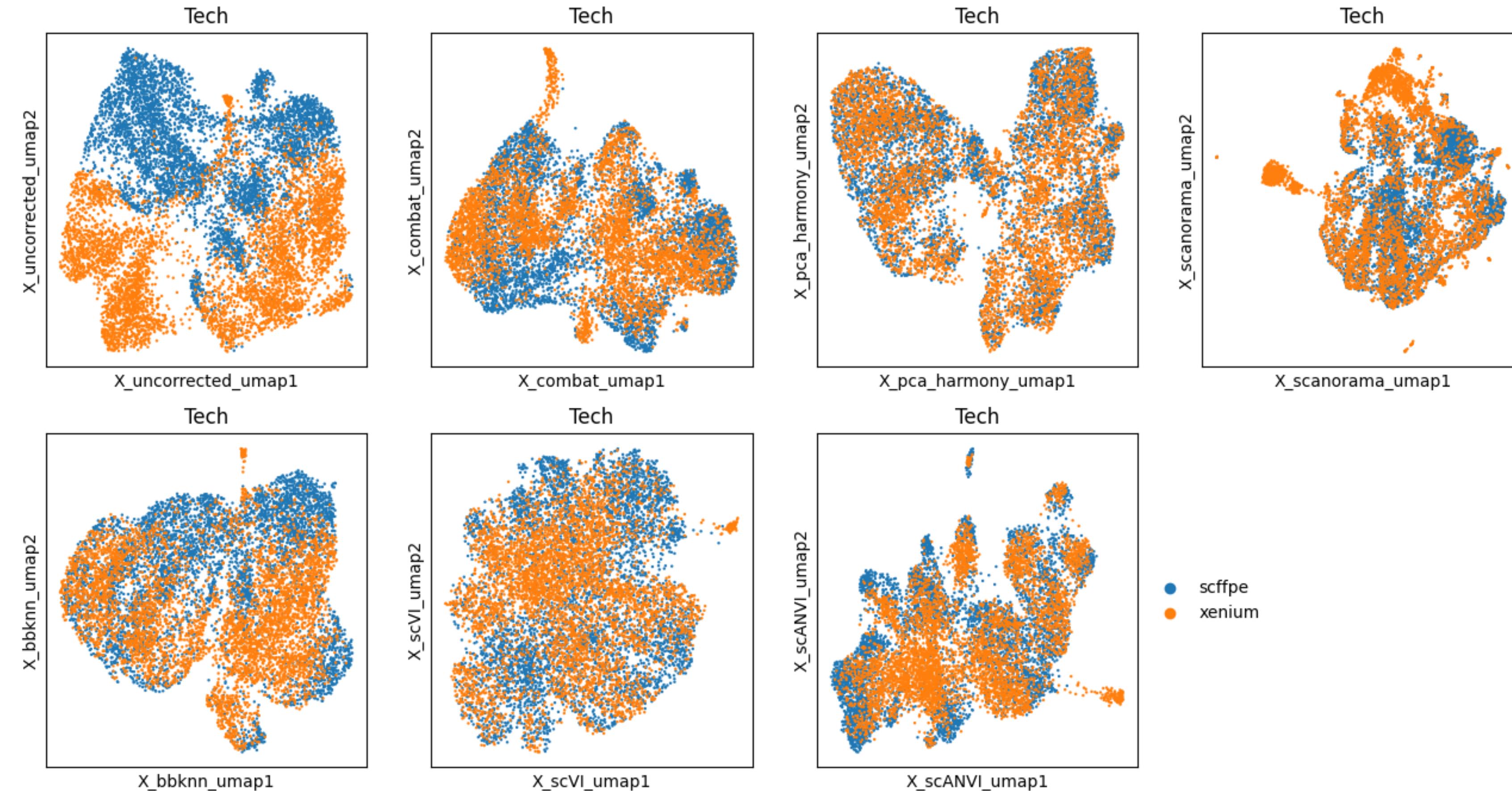
**Uncomment** Click

Note: We noted some memory issues with google colab (eventually subsample the data). For best performance of `scvi-tools` make sure that you run the notebook on a GPU instance, i.e. choose from the menu bar Runtime > Change Runtime > Hardware acceleration > GPU.

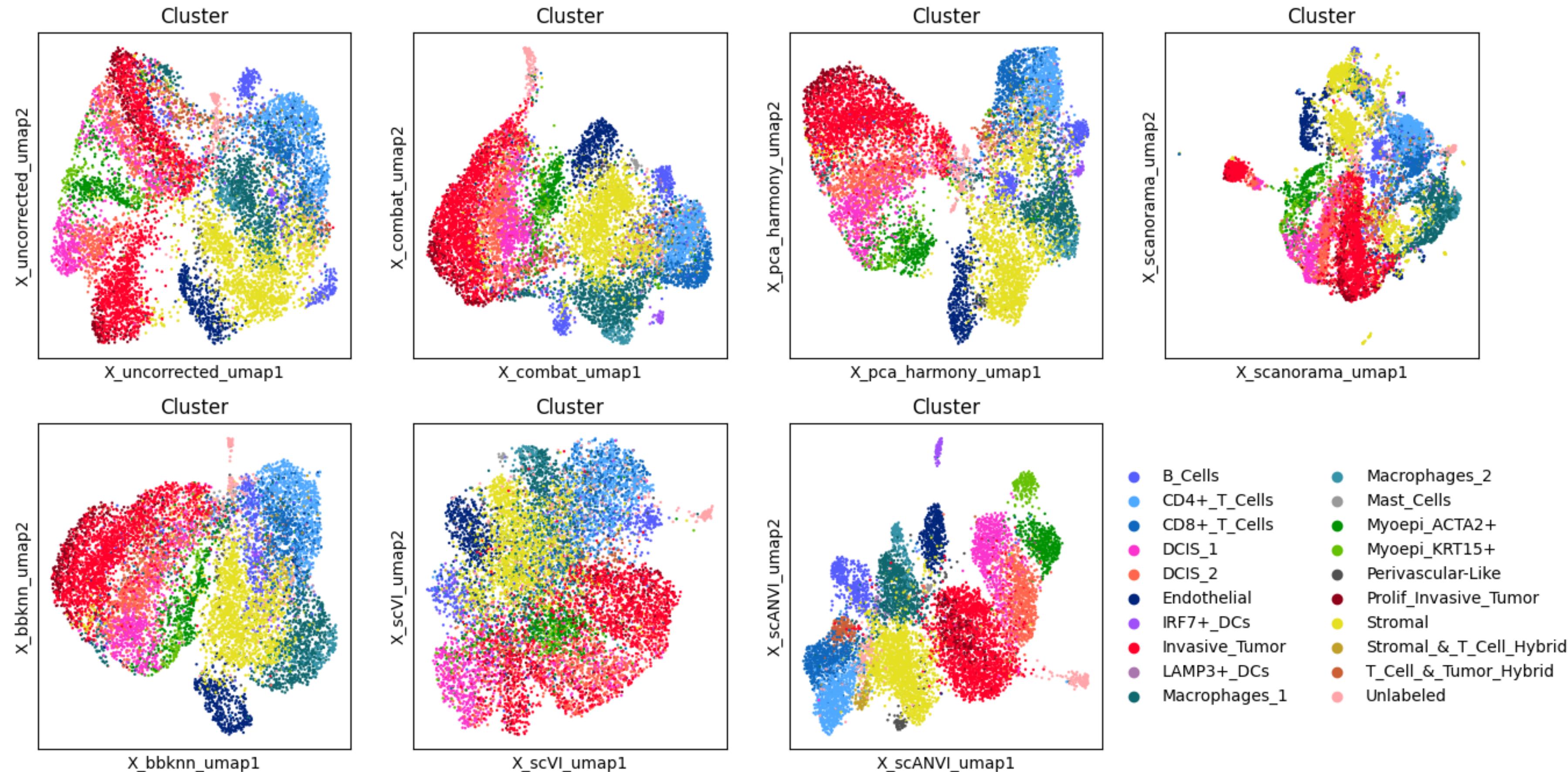
**Open in Colab**

In [ ] # Install scanpy + dependencies  
# !pip install --quiet scanpy scikit-misc scib-metrics scvi-tools scanorama harmonypy bbknn

# Results - Technology



# Results - Cell types



# Results - Integration metrics

