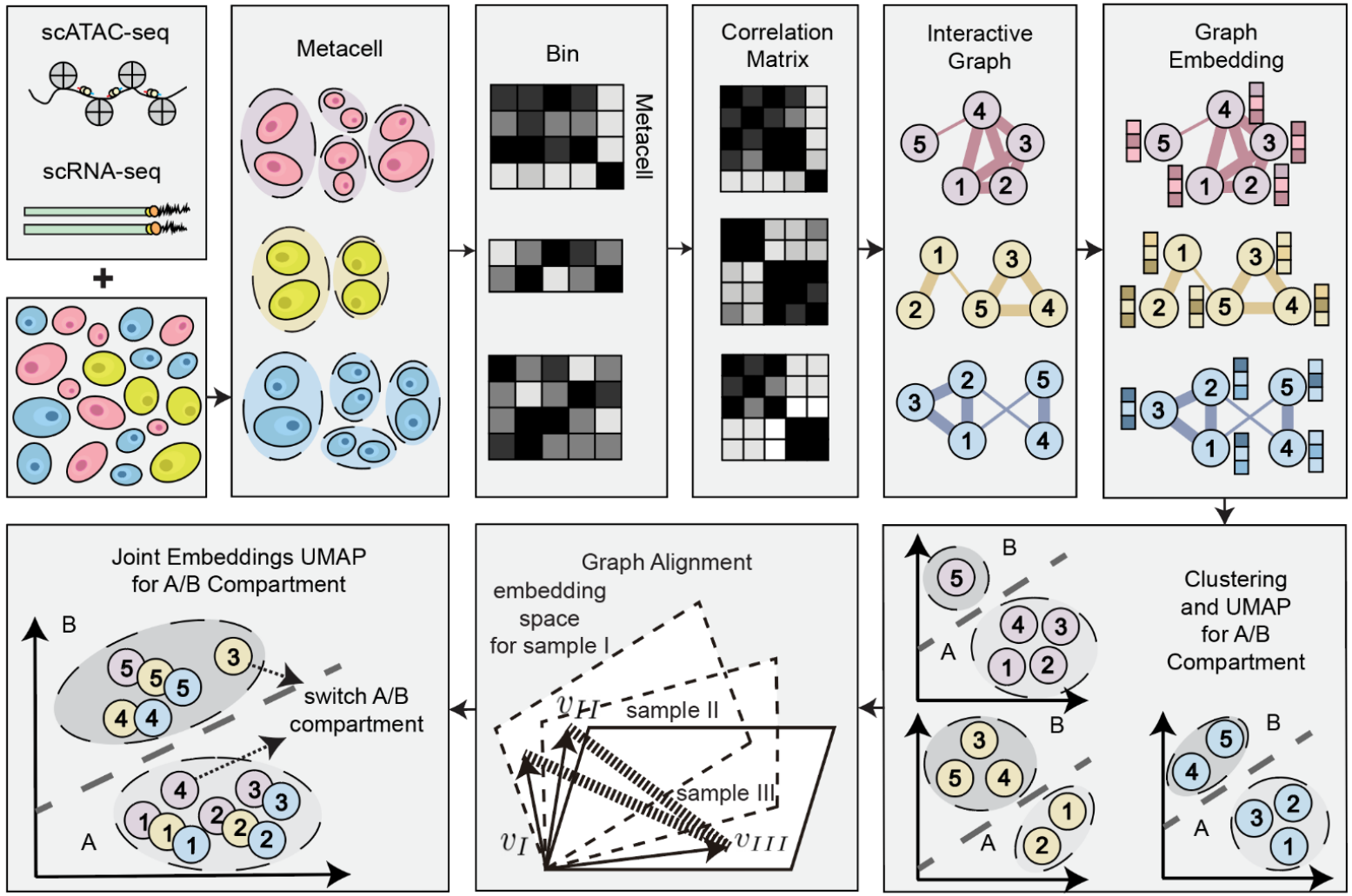
Goal:
Reconstruct chromatin compartments from affordable single-cell epigenetic data.

Key questions:
1. How to overcome the sparsity of epigenetic data?
2. How to model long-range chromatin interactions?
3. How to quantify chromatin conformation switches?

Approach:
1. Metacell construction
2. Correlation graph
3. Embedding alignment



scENCORE: leveraging single-cell epigenetic data to predict chromatin conformation using graph embedding

Briefings in Bioinformatics, 2024

Bin:
fixed-length genome regions (chr1:1-1,000,000).

Metacell:
group of similiar cells constructed to mitigate sparsity.

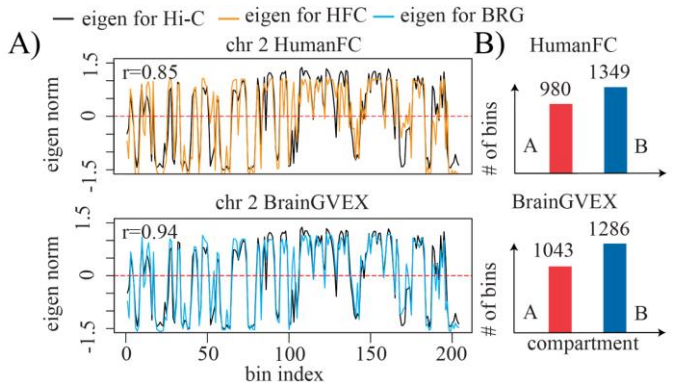
Problem Formulation:
Given a scATAC-seq matrix F (N bins, c metacells), we determine a binary vector H in {0,1}^N to represent the compartment type.

Zhang Lab

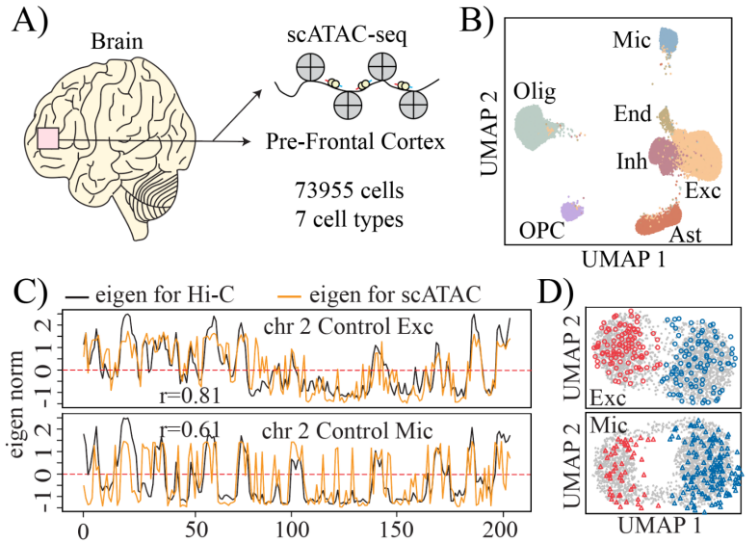
Code

Data

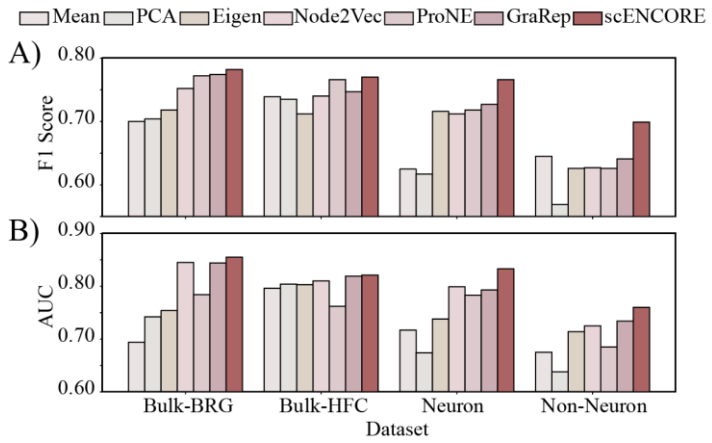
scENCORE recovers Hi-C chromatin map from bulk ATAC-seq



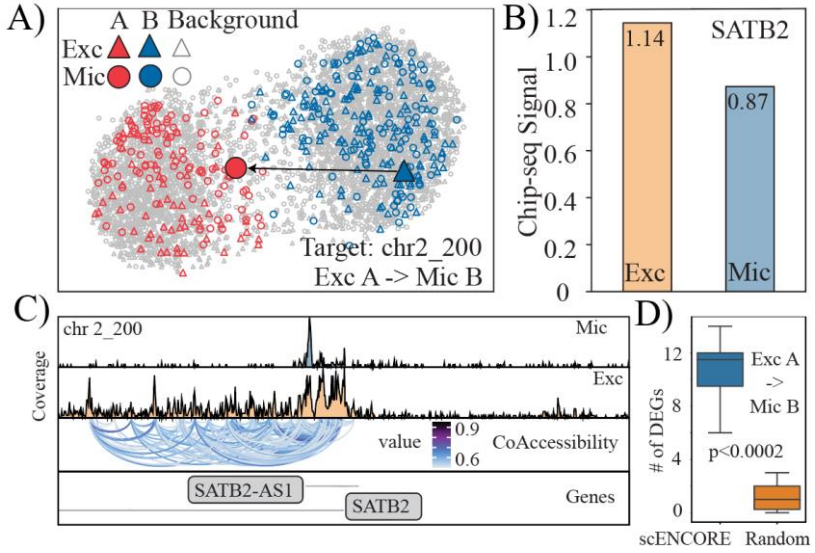
scENCORE reconstructs A/B compartments validated by cell-specific Hi-C data



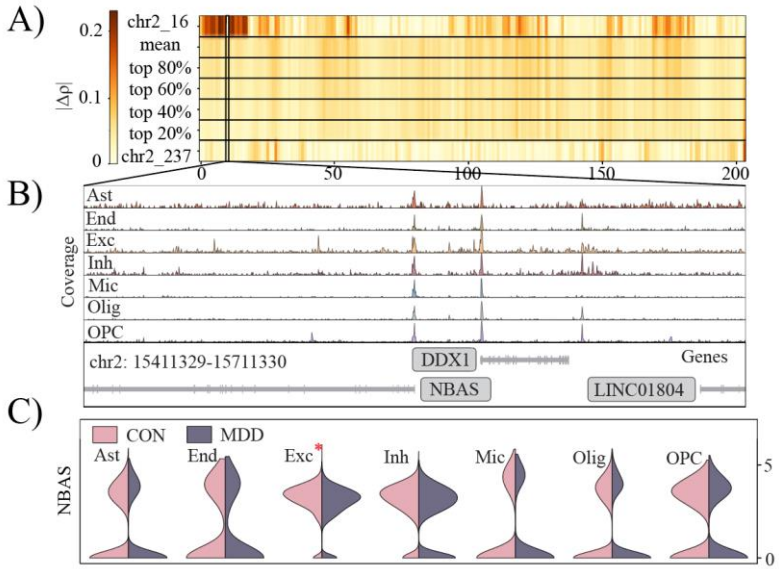
Chromatin Conformation Benchmark



scENCORE identifies key compartment switching events between different cell types



scENCORE highlights extensive cell-type-specific chromatin re-structuring events in brain disorders



scENCORE & scHi-C