scTranslate: Learning to Translate Between Epigenetic and Transcriptomic Single-Cell Assays

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Guiding Questions
Is there a latent space which summarizes both epigenetic and transcriptomic cell state?
Can we use this to translate between single cell RNA-seq data and single cell ATAC-seq data?

Motivation
1. Impute missing assay from single assay data
   Majority of single cell data is scRNA-seq or scATAC-seq. Ability to infer the other assay would provide understanding without needing to perform expensive dual assays.
2. Cell type-specific gene regulatory mechanisms
   Interpretable translator could link changes in open chromatin events to gene expression events.
3. Learn a highly accurate latent space to define cell state from multiple views.

Data
ScRNA-seq: Dual scRNA-seq and scATAC-seq on the same adult mouse cerebral cortex cells (Chen et al. 2019)