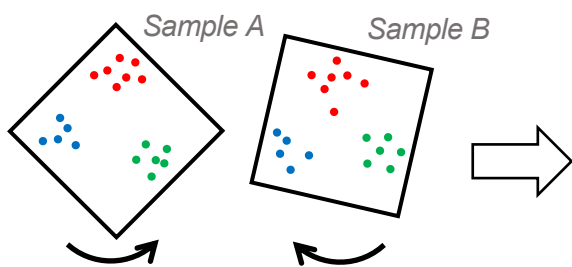


a. Error-prone alignment



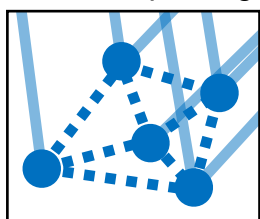
Reduced spaces:

- CPCA
- CCA
- GSVD
- PCA
- JNMF
- genes

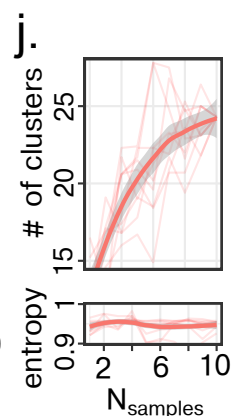
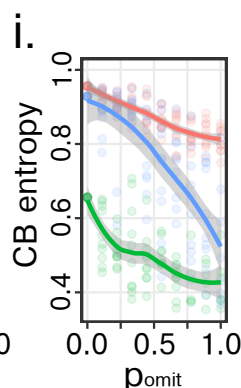
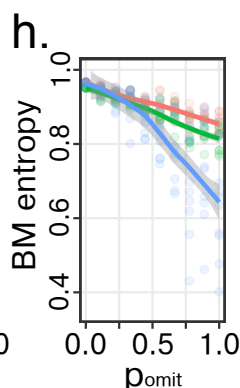
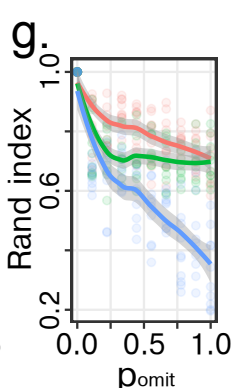
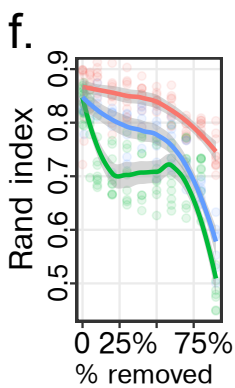
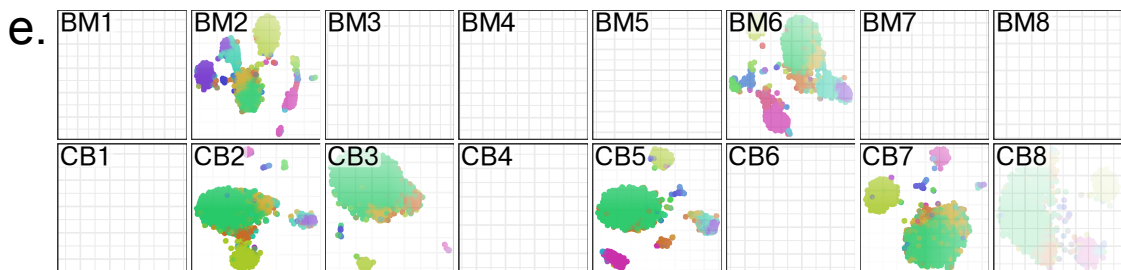
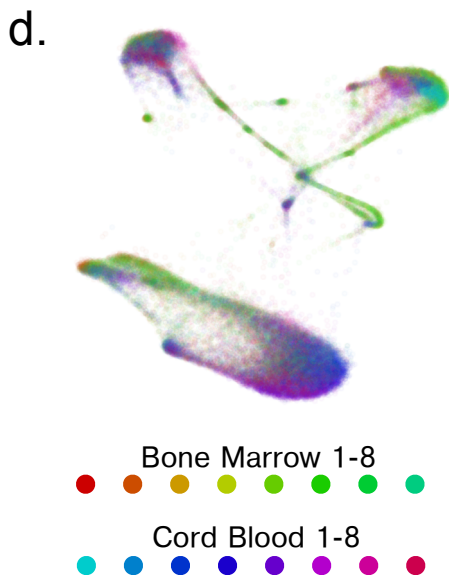
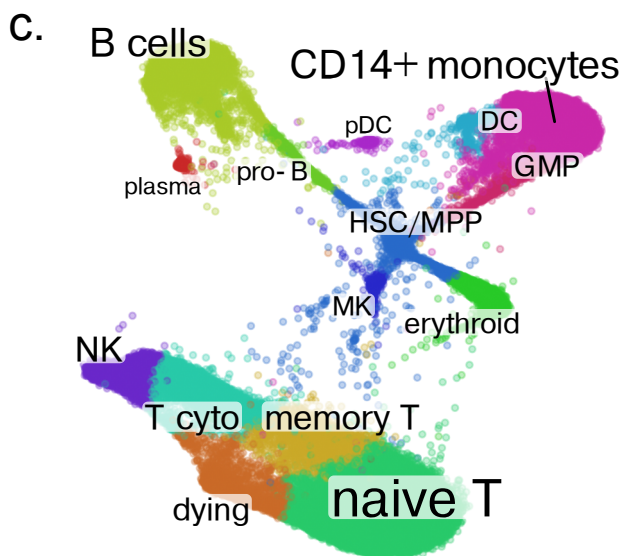
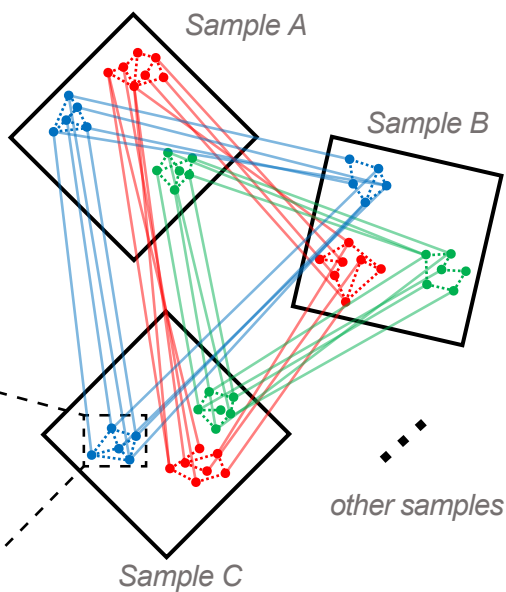
Cell mapping:

- nearest neighbor
- mutual nearest neighbor

within-sample edges



b. All-to-all (joint) graph



method: — conos — scran — seurat