

SONATA: Disambiguated manifold alignment of single-cell data

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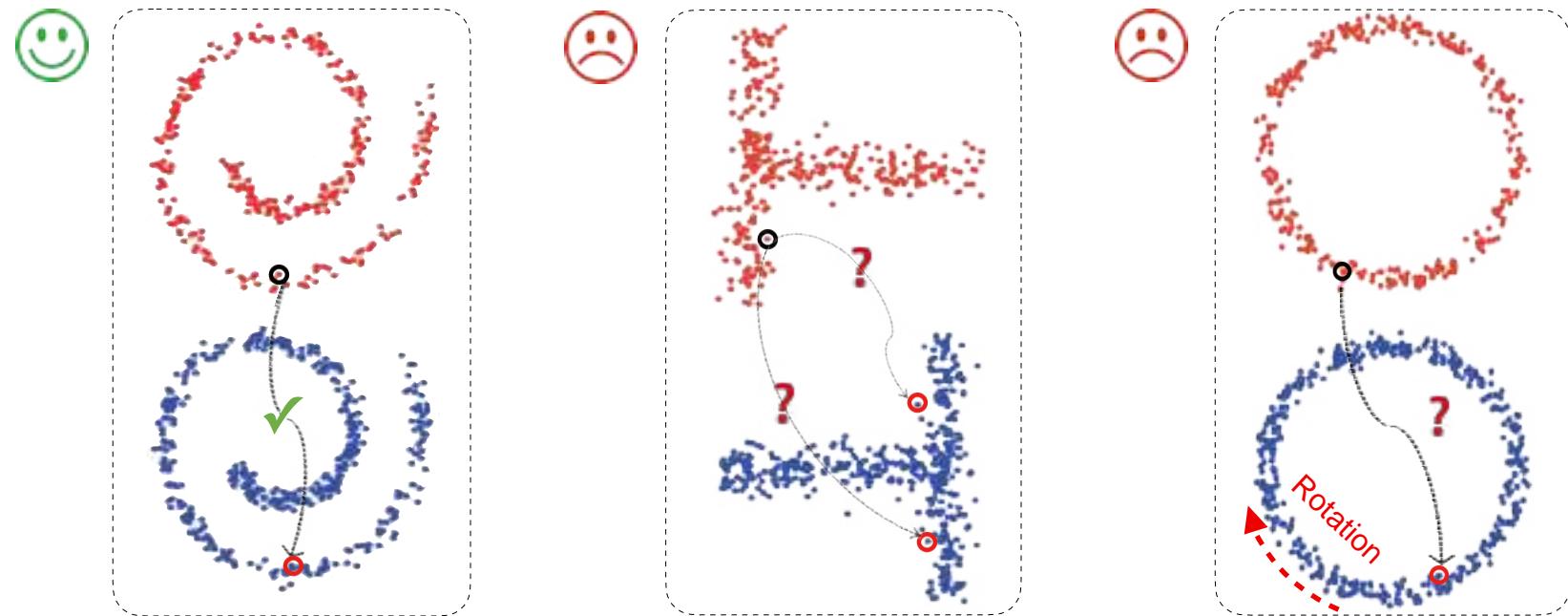


Paper

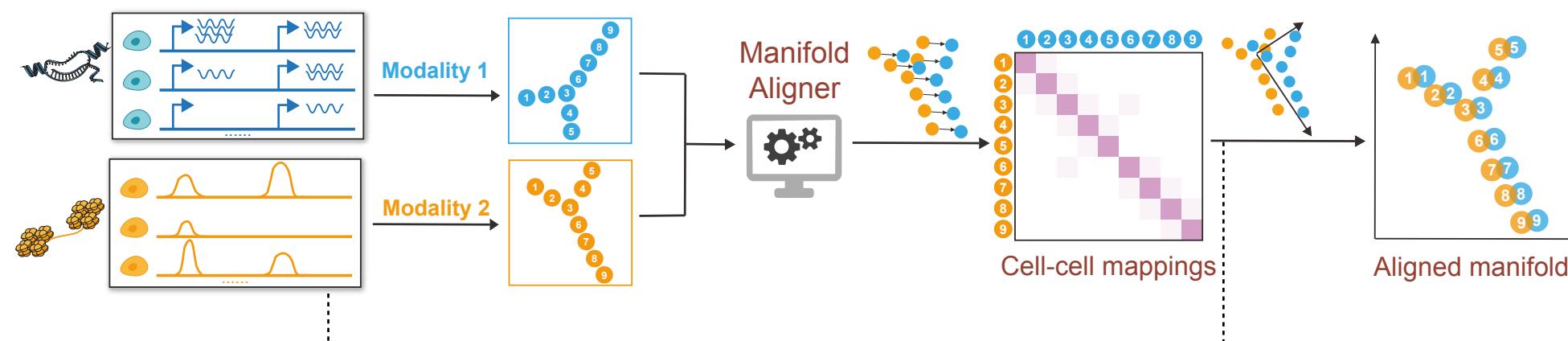
Code

Introduction

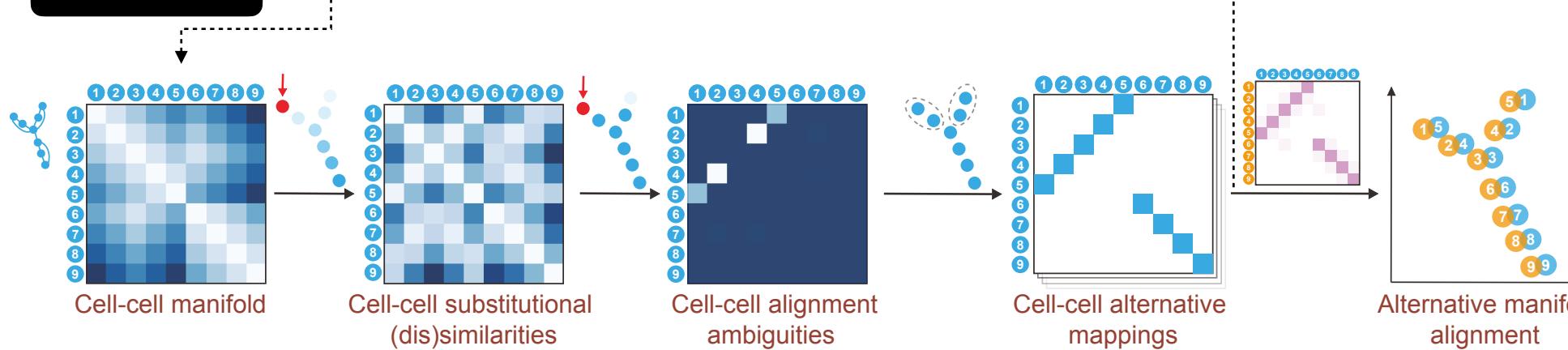
Common manifold alignment methods [1,2] report an arbitrary alignment solution, whether exist or not.



A common manifold alignment workflow.



Methods

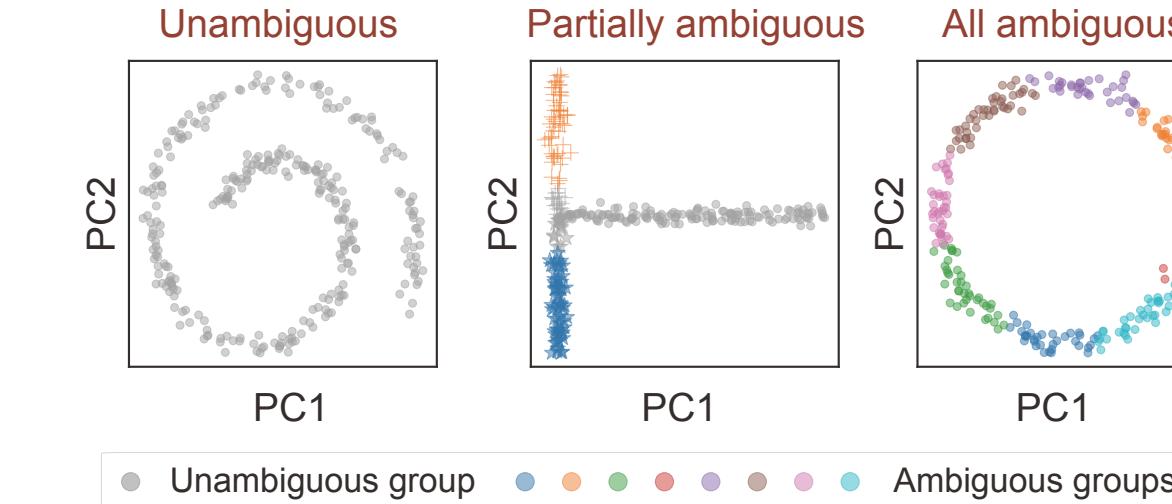


SONATA mitigates the ambiguity of manifold alignment

- ✓ Goal: Distinguish one unique solution or multiple alternative solutions.
- ✓ Key idea: A novel cell-cell ambiguity measurement to gauge the ambiguity.
- ✓ Applicability: Generalizable to any off-the shelf manifold alignment.

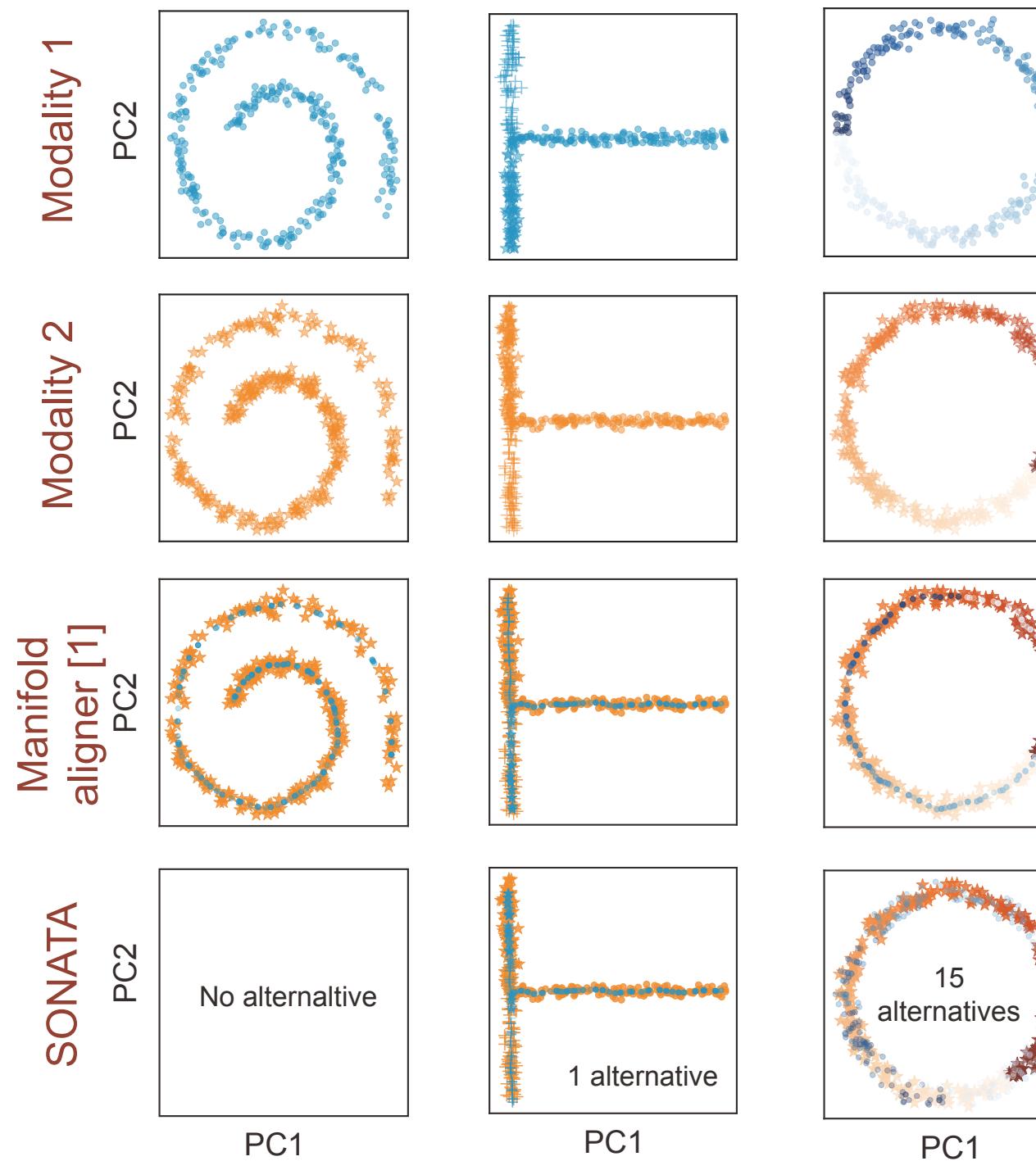
Performance on simulated data

SONATA identifies mutually ambiguous groups



SONATA supports extensive settings

- ✓ Unambiguous
- ✓ Partially ambiguous
- ✓ All ambiguous

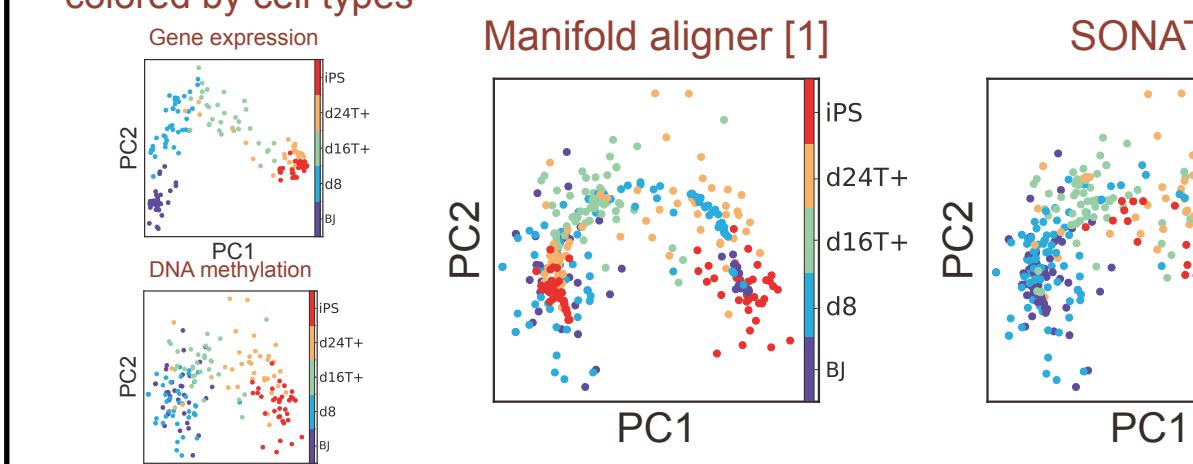
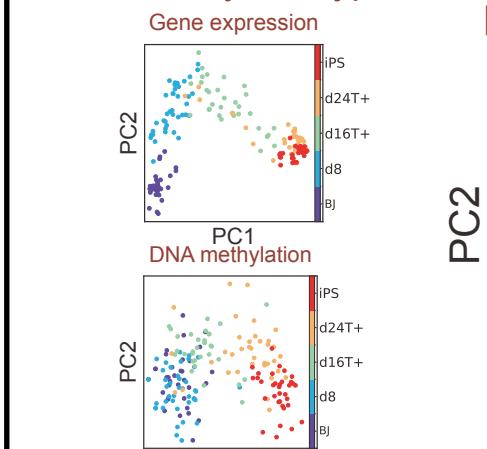


Performance on real data

SONATA correctly aligns real biology modalities.

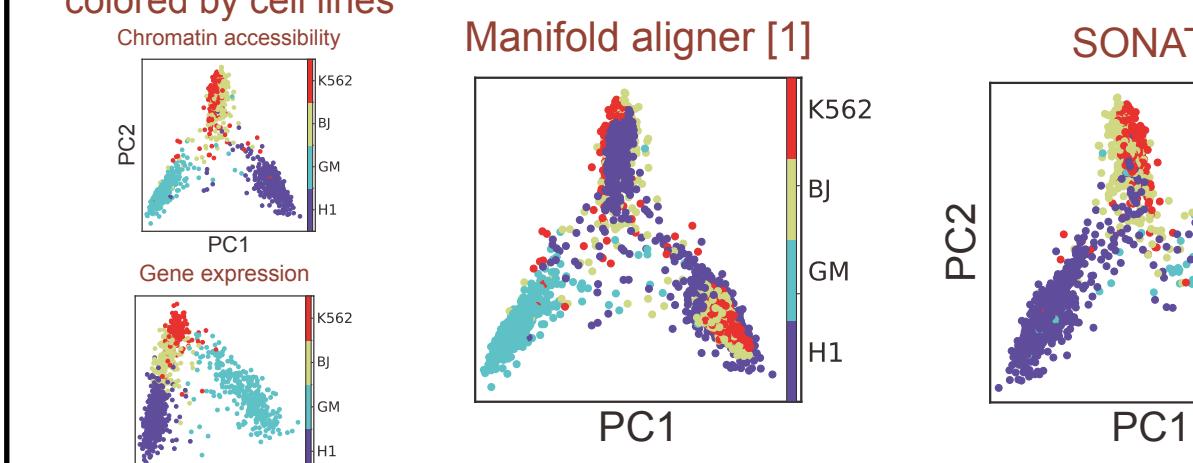
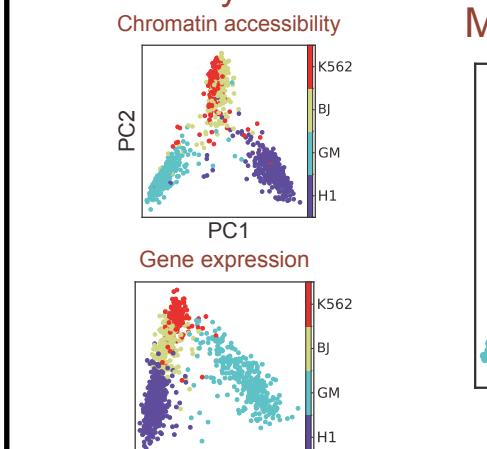
sc-GEM [3]: Gene expression + DNA methylation

Modalities colored by cell types

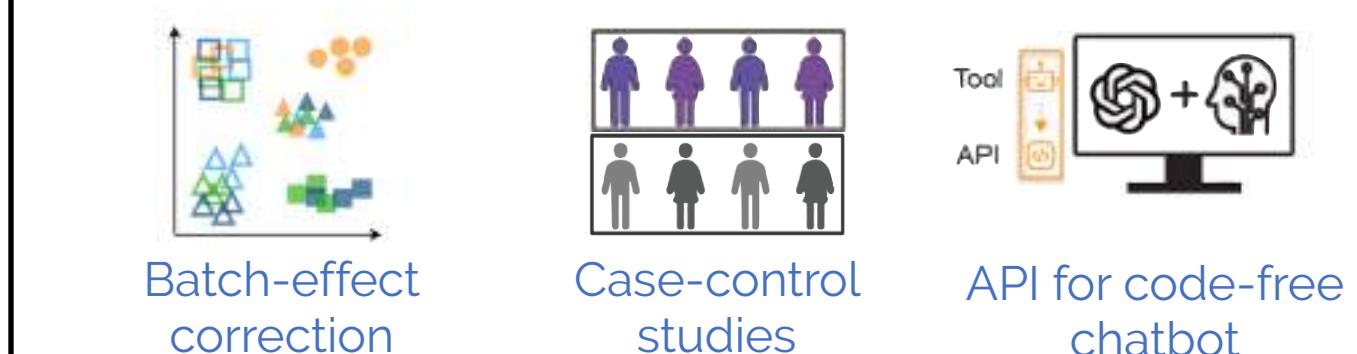


SNARE-seq [4]: Chromatin accessibility + Gene expression

Modalities colored by cell lines



Future work



Reference

- [1] Demetci, P., et al. SCOT: Single-cell multi-omics alignment with optimal transport. *Journal of Computational Biology* 29 (2022).
- [2] Cao, K., et al. Unsupervised topological alignment for single-cell multi-omics integration. *Bioinformatics* 36, i48–i56 (2020).
- [3] Cheow, L. et al. Single-cell multimodal profiling reveals cellular epigenetic heterogeneity. *Nature Methods* 13, 833–836 (2016).
- [4] Chen, S., et al. High-throughput sequencing of the transcriptome and chromatin accessibility in the same cell. *Nature Biotechnology* 37, 1452–1457 (2019).