A140 · POLARIS: concordance-aware joint analysis of cells and features in single-cell multiomic data

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Single-cell multiomic assays jointly profile gene expression and chromatin accessibility in the same cell, enabling direct study of cross-layer coordination. Yet how strongly these layers agree varies across cells, and most integration methods prioritize shared structure, integrating this partial decoupling away even though it may carry biological signal. Here we present POLARIS, a concordance-aware spectral framework that quantifies cross-modality agreement and carries it into downstream analysis. From one paired low-rank cell representation, POLARIS computes per-cell concordance, a joint cell embedding, and an induced cross-modal feature embedding. In the cell embedding, separations strong in either modality are retained rather than averaged away, sharpening cell-type and state resolution. The feature embedding scores regulatory element-gene (RE-G) candidates without repeated pairwise model fitting, each with a closed-form jackknife standard error. Across immune, neural and developmental datasets, concordance is reproducible and cell-resolved, and cells with low concordance are enriched for modality-specific structure. The RE-G map includes distal links supported by Hi-C contacts and fine-mapped eQTL. Because it is linear and low-rank, POLARIS is computationally efficient, and extends directly to other paired assays such as CITE-seq, linking surface proteins to genes. POLARIS is available as open-source software for unified cell- and feature-level analysis of paired data.