A121 · An Agentic Workflow for Adaptive and Auditable Single-Cell RNA-seq Analysis

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Single-cell RNA sequencing (scRNA-seq) pipelines typically rely on fixed scripts and predefined parameters, while real datasets often require analyst judgment. This work presents an open-source agentic workflow in which a large language model (Claude, via the Anthropic API) drives scRNA-seq analysis through predefined tool functions. Tools return structured summaries to the model, which selects subsequent analysis steps and parameters, while code-level guardrails enforce workflow constraints and all decisions are recorded in a JSONL audit trail.

On PBMC datasets, the model made data-dependent analysis choices rather than following a fixed script. For a single-batch PBMC3k dataset, it selected PCA for dimensionality reduction. For a two-batch dataset, it detected batch structure and selected scVI for batch correction, and relaxed the mitochondrial QC threshold after determining that the standard cutoff would remove most cells. Doublet thresholds were selected from the observed score distribution. The model also identified a small cluster dominated by mitochondrial rather than canonical lineage markers, flagging it as likely stressed or degraded despite CellTypist annotating it as T cells.

The workflow produced biologically plausible cell-type annotations supported by canonical markers. This demonstrates a lightweight framework for adaptive first-pass scRNA-seq analysis in which analyst-like decisions are constrained, reproducible, and auditable.

Code and decision logs are available under the MIT license at github.com/lucrafrancis/agentic-scrna-workflow.