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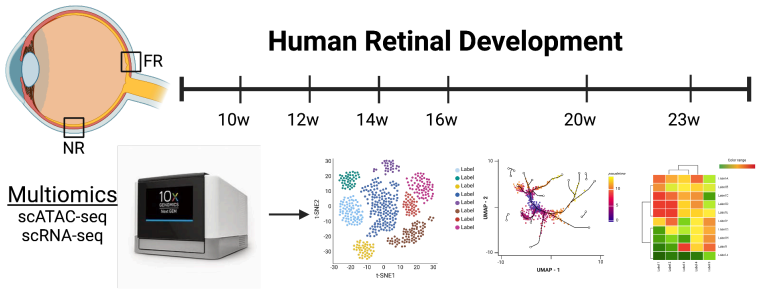
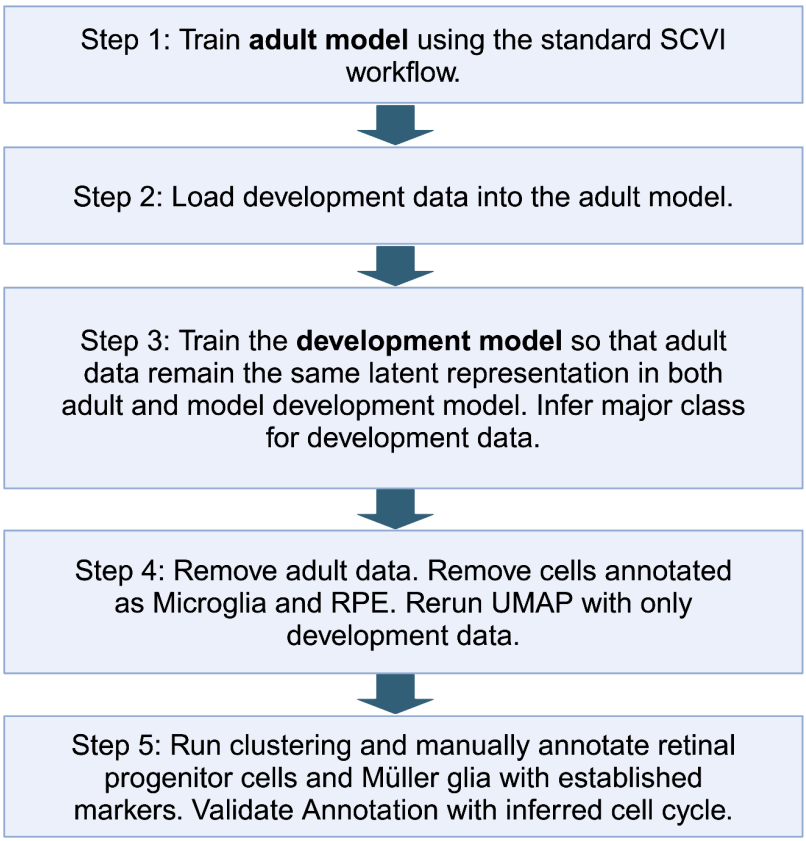
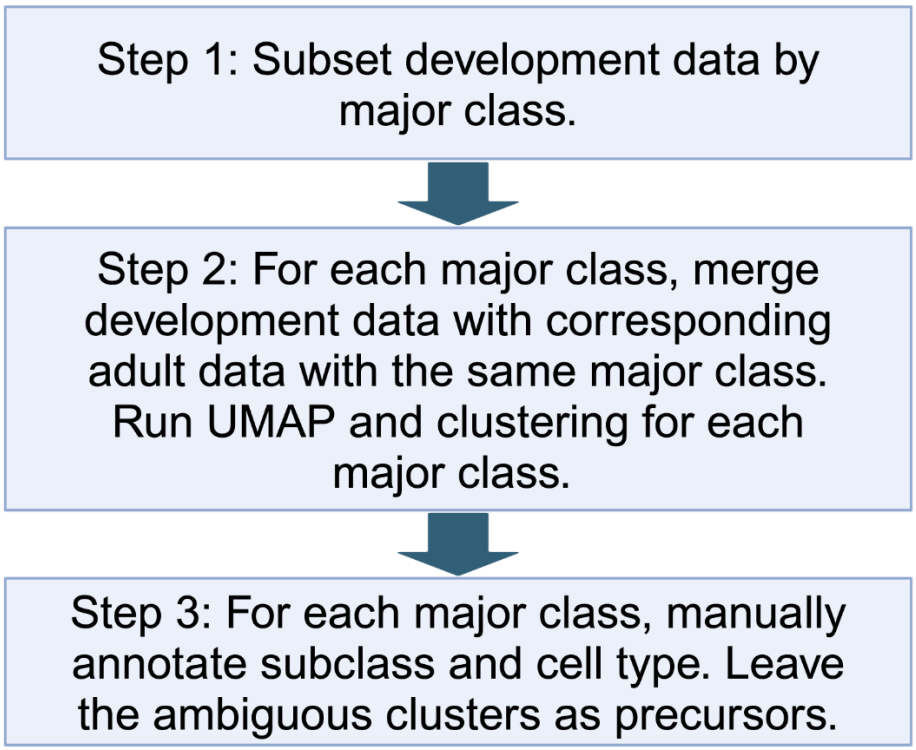


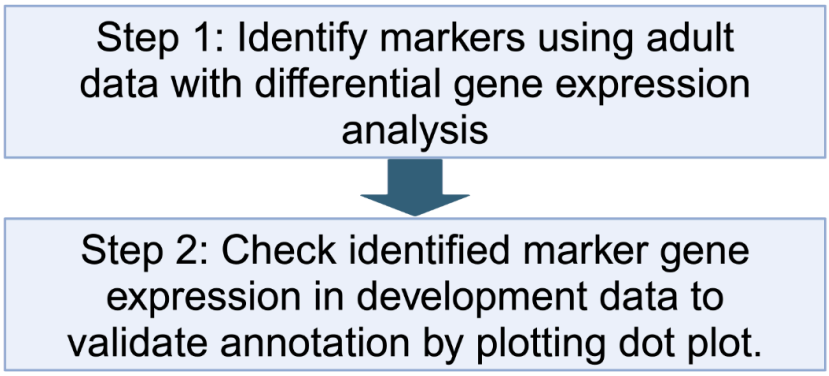
Figure 1A: The study design of this work. Samples were collected from either (1) whole retina at PCW 8, or (2) macula and periphery of the same donor's retina from PCW 10 to PCW 23. Subsequently, with a total of 28 samples from 14 donors, gene expression and open chromatin profiling from the same nuclei was performed using the 10X Chromium sn-dual-omic ATAC + Gene Expression technology (Supplementary Data 1). The bottom panel shows analysis workflow diagrams.



Supplementary Figure 1A: Major class annotation workflow diagram. Step 1-3 are reference mapping with scvi-tools. In step 4 and 5, adult data was removed, and development data was clustered to annotate PRPC, NRPC, and MG based on established markers.



Supplementary Figure 2A: Subclass and cell type annotation workflow diagram. First, adult cells and development cells from the same corresponding major class were integrated together. Second, developmental cells were annotated manually based on gene expression similarities on UMAPs.



Supplementary Figure 3A: Cell type annotation validation workflow diagram: First, marker genes were identified using adult data through a differential gene expression analysis for each major class. Subsequently, for each major class, developmental precursors and annotated data were visualized with those markers to illustrate gene expression patterns. Ideally, annotated development data should have similar gene expression patterns of those markers as adult data. The analysis was then tested using the method="t-test_overestim_var", which stands for overestimating the two-side variance in each group t-test. P-values were corrected using the 6Benjamini-Hochberg method, specifying corr_method="benjamini-hochberg".

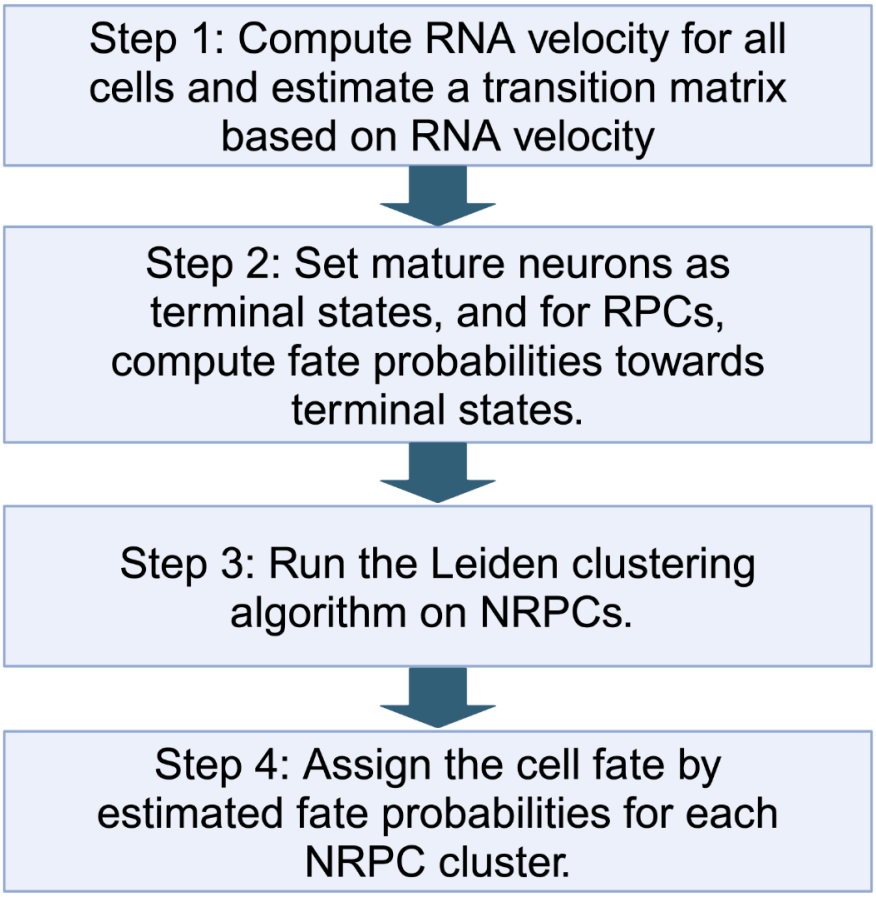
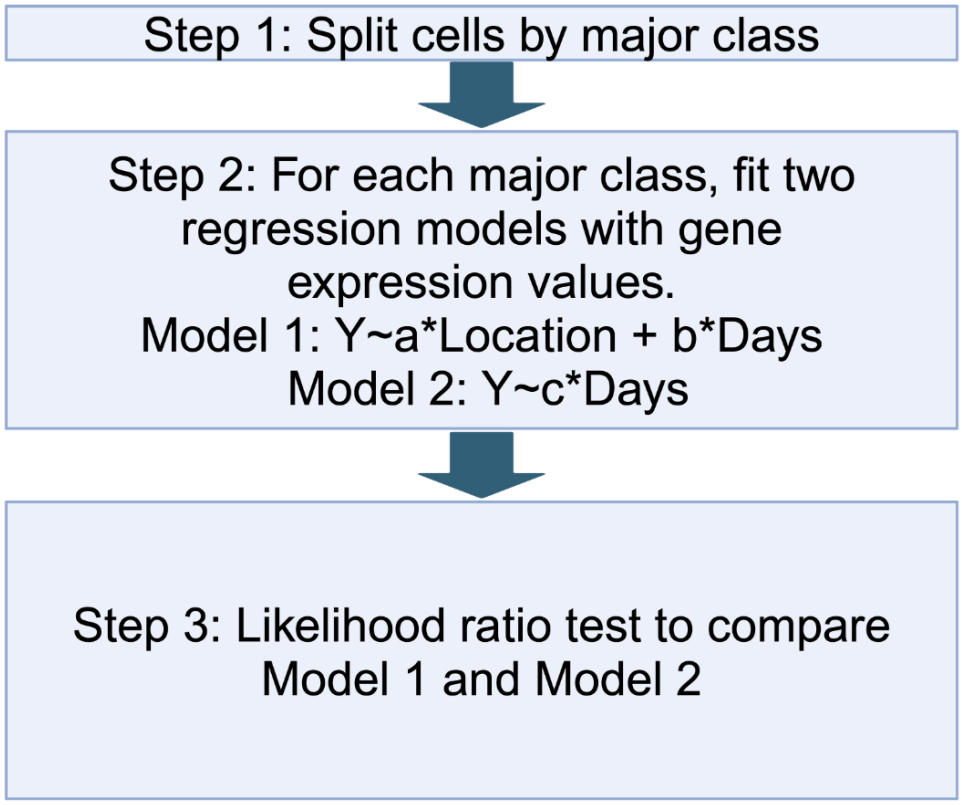
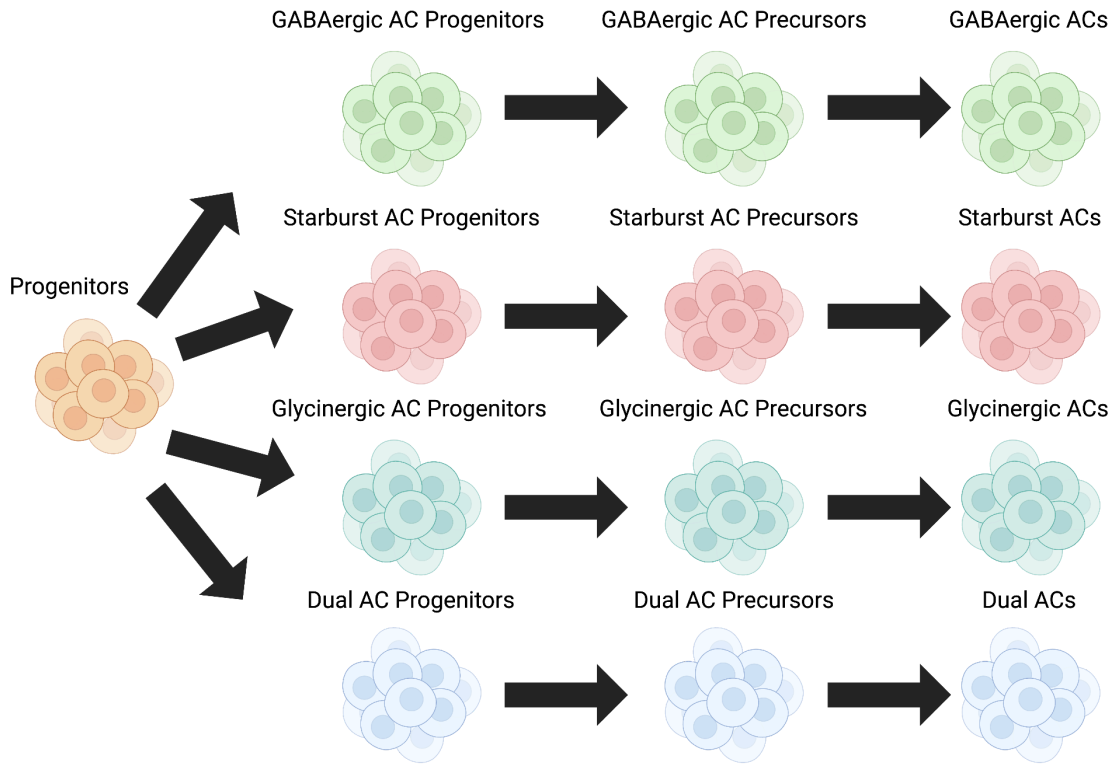


Figure 3A: Diagram of the NRPCs' fate probability inference workflow. Cell fate probabilities for each type of neuron were estimated based on velocity, and cell fate was assigned after performing cell clustering. (B) UMAP of NRPCs colored by inferred fate. Cells for which cell fate cannot be determined are labeled in gray. The UMAP is specifically for NRPCs, distinguishing it from the global UMAP designed for all cells.



Supplementary Figure 9A: Differently expressed gene identification workflow diagram. For each major class, regression models were used for regression out the effects of “Days” during DEGs test between macula and peripheral. Then, a likelihood ratio test was performed for each group of cells by comparing the effects of “Region” and regressing out the effects of “Days”, which is a vector of integer representing sample age (days post conception).



Supplementary Figure 7K: Hierarchical model for AC fate commitment during development of the human retina.

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