Anthology of Eye Single Cell Atlases

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PURPOSE: To curate an accessible and reliable ocular cell-type specific transcriptome database of healthy vertebrate ocular cell types and a matching high performance reactive web application to query gene expression across cell type, species, study, and other factors. METHODS: We queried several public repositories to find all healthy, non-perturbed, ocular tissue single cell RNA-seq samples. As a non-ocular reference, we also downloaded the pan-mouse Tabula Muris raw data. XXX thousand cell labels were curated and projected onto the non-labelled cells. The XX ocular and XX Tabula Muris cells were sent into a Snakemake-based reproducible pipeline we wrote to quantify all known transcripts and genes, removes cells with poor quality, normalizes expression values across each tissue, creates a batch-corrected low dimensional space, performs XX differential expression tests, and outputs all as a single SQLite database file: the Single Cell Eye in a Disk (scEiaD) dataset. Furthermore, we wrote the web application PLAE (<https://plae.nei.nih.gov>) to display scEiaD. RESULTS: The new portal provides quick visualization of vertebrate eye-related transcriptomes published to date by gene/transcript, XX cell types, XX ocular tissues, XX body tissues. As a test of the value of this unified pan-eye dataset, we showed XX. CONCLUSION: The PLAE v1.0 web app serves the pan-ocular and body dataset, scEiaD. This offers the eye community a powerful and quick means to test hypotheses on human gene and transcript expression across 54 body and 19 eye tissues. Futhermore the XXX labelled cells across XX studies, X techologies, and 3 species provides a highly challenging benchmarking resource for single cell algorithm development.

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