



Instructor Guide:

Analyzing Transcriptomic Data to Explore Alzheimer's Disease Pathology

Estimated Lesson Timeline:

90 minutes total

- 20 minutes: Review of transcriptomics
- 40 minutes: Guided Tour of CZ cellxgene database
- 30 minutes: Students perform a differential gene expression analysis using the SEA-AD cellxgene database and the NIH gene database

Learning Objectives:

- Students will be able to articulate how transcriptomic data is collected and processed
- Students will be able to interpret transcriptomic data visualized within Uniform Manifold Approximation and Projections (UMAPs)
- Students will be able to navigate the Seattle Alzheimer's Disease Brain Cell Atlas (SEA-AD) database in order to interpret transcriptomic data
- Students will be able to filter data based on specific biomarker and/or demographic characteristics they are interested in exploring
- Students will be able to independently perform an analysis of transcriptomic data using the cellxgene interface
- Students will be able to compare gene expression between cell types using the cellxgene interface
- Students will be able to navigate the NIH gene database to explore the known functions of genes

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