Project Hypothesis and Aim: Exploring Immune Response and Neuroinflammation in Alzheimer's Disease (AD)

Hypothesis: This research hypothesizes that the progression of Alzheimer's Disease (AD) is significantly influenced by an age-dependent and cell-type-specific immune response, primarily mediated by microglial and astrocytic activation. It proposes that persistent neuroinflammation and dysregulated immune signaling pathways exacerbate neurodegeneration, with distinct patterns of immune activation emerging in different disease stages. By studying the differential expression of immune-related genes across cell types and ages, the project aims to identify critical regulatory pathways and genes contributing to the chronic inflammation observed in AD.

Specifically, genes such as **TOLLIP** (Toll-Interacting Protein), **SIRPA** (Signal Regulatory Protein Alpha), **C1QA** (Complement C1q A Chain) and **NLRP3** (NLR Family Pyrin Domain Containing 3) are hypothesized to exhibit altered expression in AD compared to normal samples, potentially indicating pathways responsible for prolonged immune activation. The research will focus on how these genes impact microglial and astrocyte functions.

Aim: The project aims to:

1. **Map Immune Gene Expression in AD**: Analyze the expression of immune-related genes such as *TOLLIP*, *SIRPA*, *C1QA*, and *NLRP3* across different cell types (e.g., microglia, astrocytes) in AD versus control groups. This will reveal cell-specific roles in AD pathology.
2. **Characterize Age-Related Differences in Immune Activation**: Examine age-related gene expression changes in immune response pathways within AD samples. By clustering samples by age groups, this analysis aims to determine if immune responses intensify or shift in later stages of the disease.
3. **Identify Potential Therapeutic Targets**: Through pathway enrichment and co-expression analysis, identify genes and pathways that could serve as potential therapeutic targets for modulating immune response in AD, focusing on genes that mediate neuroinflammation and oxidative stress.

Code Approach (Outline):

1. **Data Preprocessing**: Filter single-cell transcriptomics data to select immune-related genes (e.g., *TOLLIP*, *SIRPA*, *C1QA, NLRP3*) across different cell types.
2. **Differential Expression Analysis**: Compare gene expression levels between AD and control groups for selected immune-related genes, using age and cell type as variables.

***Link**: https://colab.research.google.com/drive/15cDSYp8mp7Zkt7qLIO7Zlw-tB_UD_YMw#scrollTo=OrUqJqE5RLTr*