Bioinformatics analysis study on neurodegeneration (Alzheimer's)

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Introduction and objective:

This project aims to investigate the genetic link between SARS-CoV-2 infection and Alzheimer's Disease (AD). We want to understand how the virus might trigger or worsen neurodegeneration.

Introduction and objective:

Alzheimer's Disease (AD): A neurodegenerative disorder involving amyloid-beta, tau protein, and mitochondrial dysfunction.

COVID-19 (SARS-CoV-2): Primarily respiratory, but linked to neurological complications and cognitive decline.

Objective: To identify shared biological signatures and molecular connections between the two conditions through transcriptional changes.

Methodology:

- Visual: Figure 1 & Figure 2 (Histograms of Gene Expression).

- Datasets were obtained from public database repositories (e.g. Gene Expression Omnibus (GEO database)) and standardized.
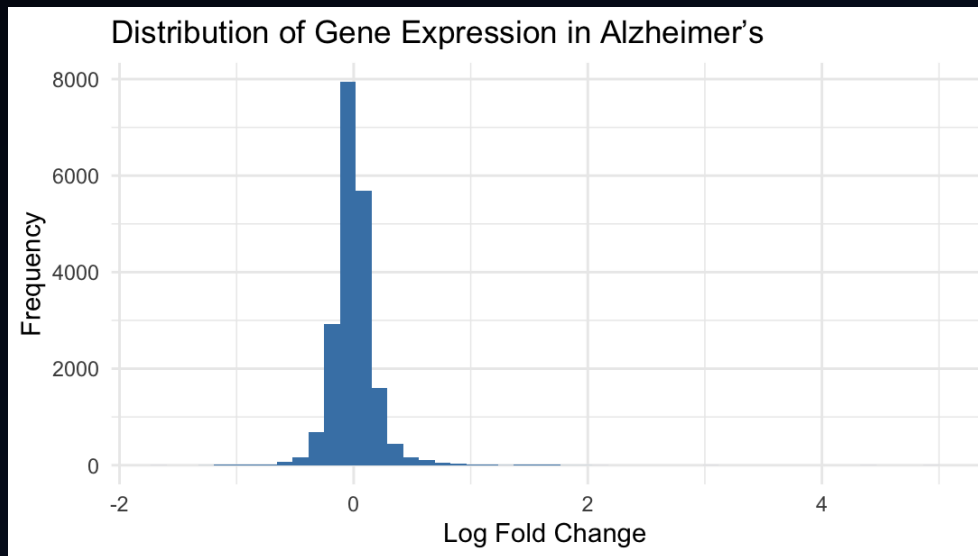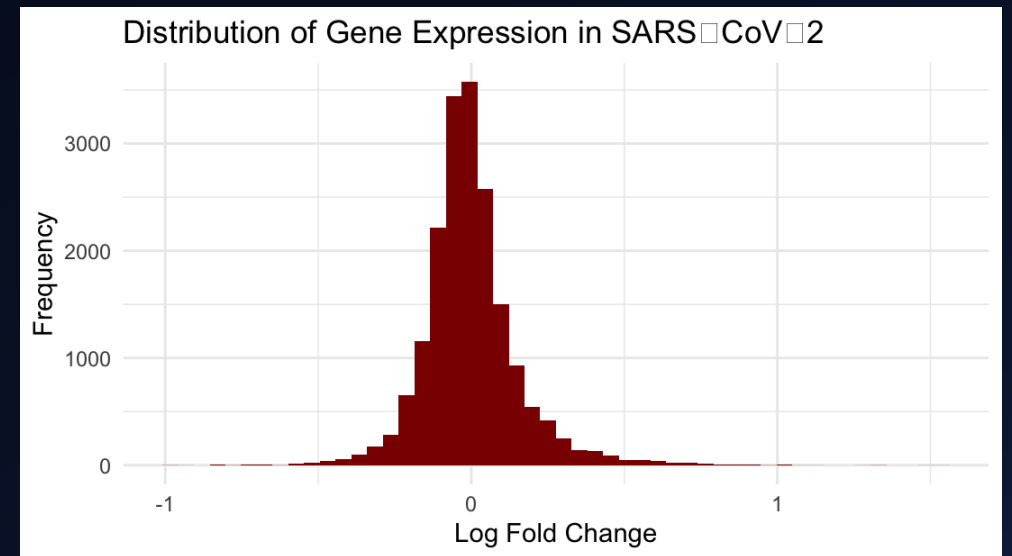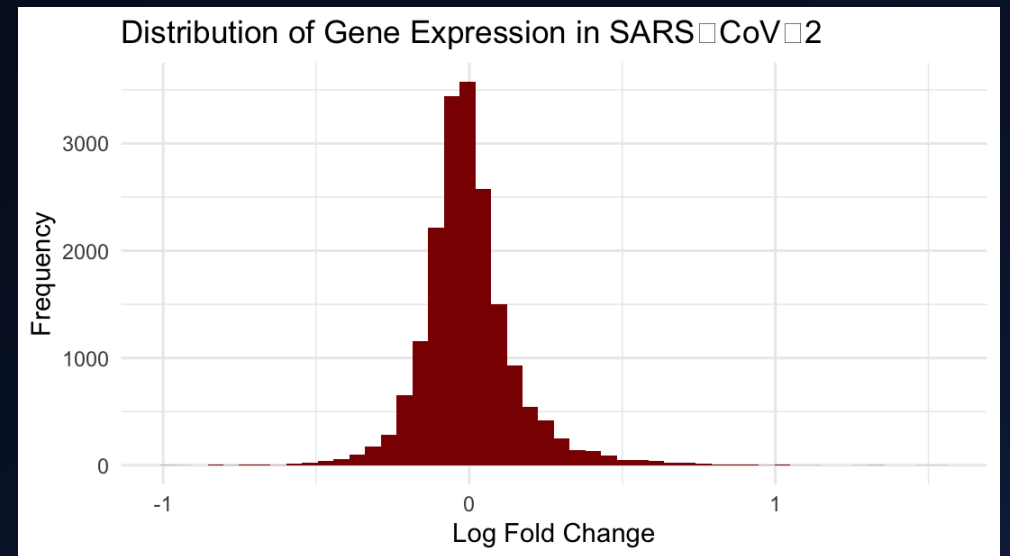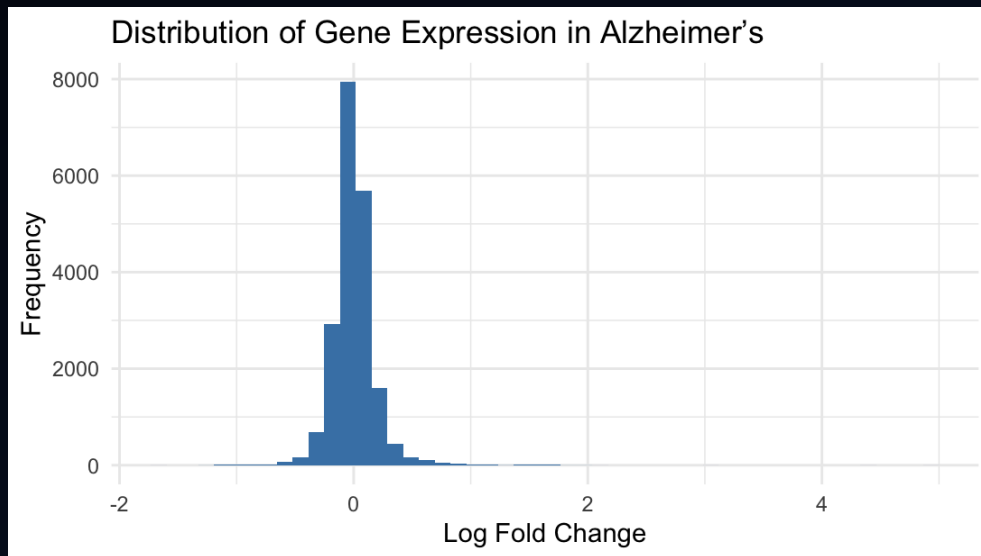

Figure 1

Figure 2

Methodology:

- These histograms show the distribution of log fold change values. We used these to ensure our data was cleaned and filtered consistently before comparing the two diseases.

Distribution of Gene Expression in Alzheimer's

Distribution of Gene Expression in SARS☐CoV☐2

Differential Expression Analysis (DEA):

- Thresholds used: Adjusted p-value < 0.05.

- |Log2 Fold Change| > 0.5.

- The Volcano Plot helps us see the 'big picture' The dots high up and far to the sides represent genes that are statistically significant and have a strong change in expression—highlighting clear patterns of upregulation and downregulation.
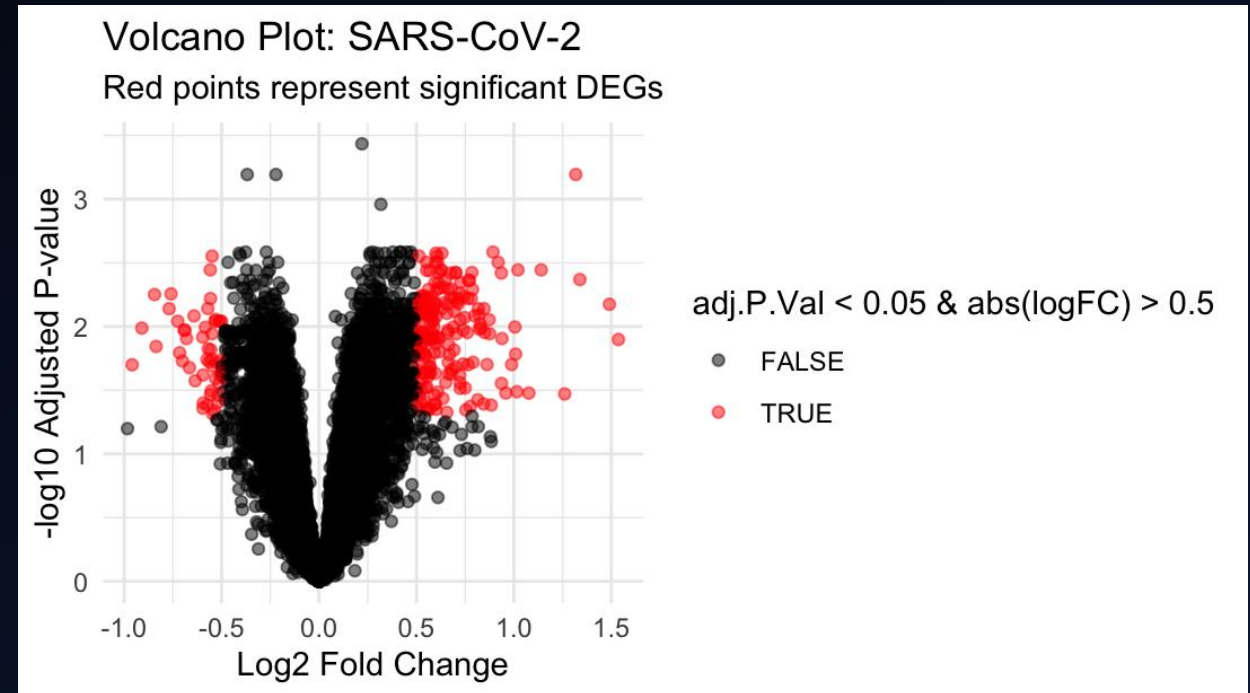
Figure 3: (Volcano Plot of SARS-CoV-2).

Venn diagram:

- This figure shows a Venn diagram comparing differentially expressed genes in COVID-19 and Alzheimer's disease. While most genes are unique to each condition, 11 genes are shared between both diseases. These shared genes suggest overlapping molecular mechanisms, possibly related to inflammation or immune response.
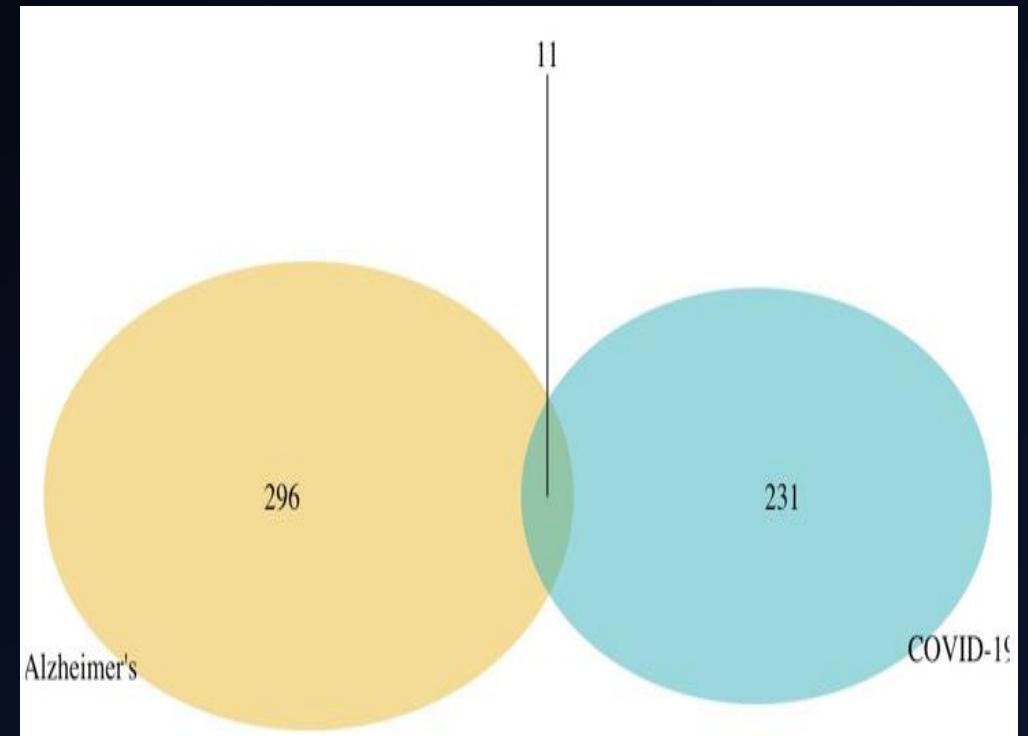
Co-Expression & Correlation

Heatmap of Shared Differentially Expressed Genes
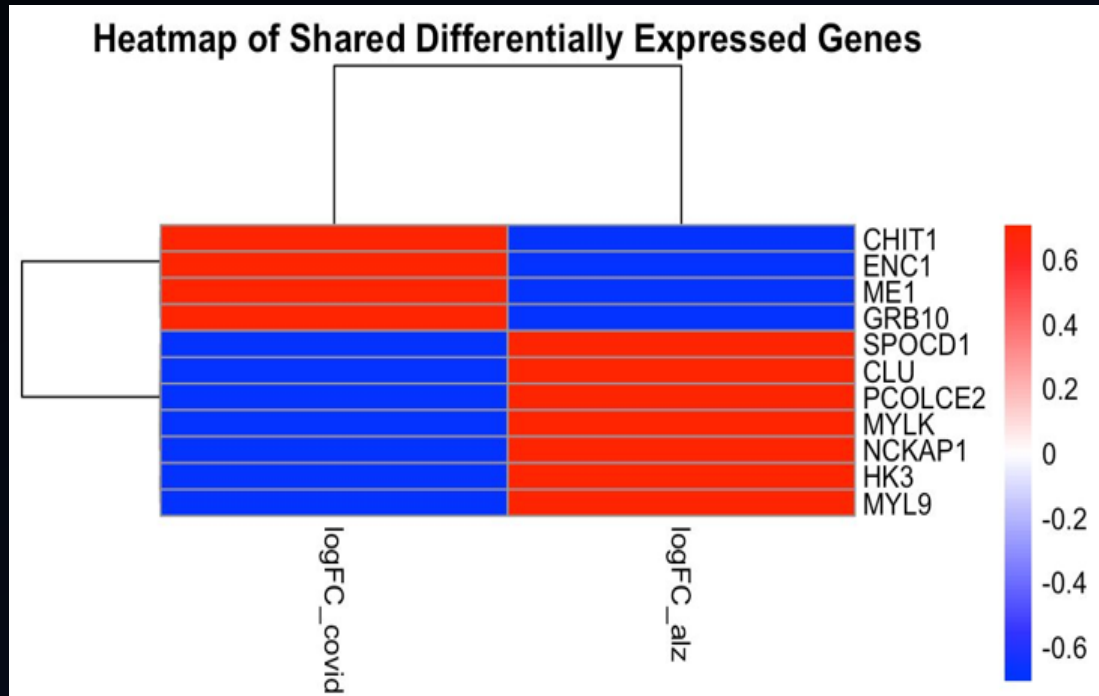
Heatmap:
The heatmap shows clustering of shared differentially expressed genes with consistent expression patterns across both diseases, indicating strong co-expression and correlation. This suggests that these genes may be involved in common biological pathways

Co-Expression & Correlation

The correlation plot shows a strong relationship between log fold-change values of common genes across both diseases, indicating coordinated gene regulation and shared molecular responses.
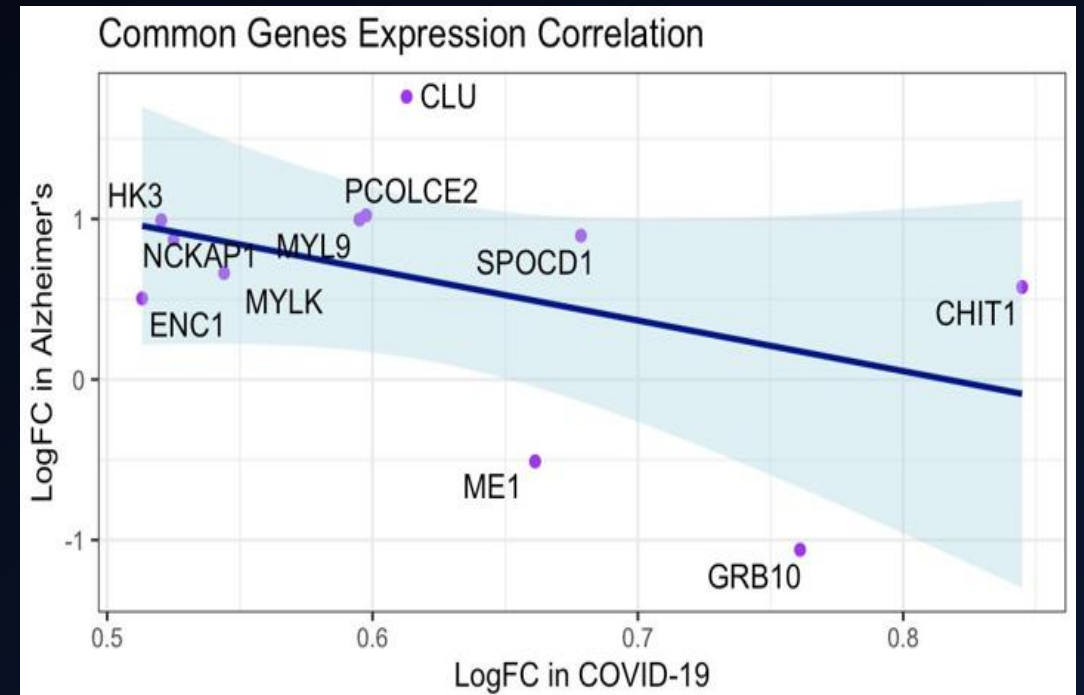
Top Dysregulated Genes

Visual: Figure 8 (Bar Plot).

How to explain Figure 8: "This bar plot highlights the 'Top 10' shared genes. These are the most strongly dysregulated genes common to both diseases, making them the most likely candidates for further biological study or potential biomarkers."

Figure 8 : Top 10 Shared Differentially Expressed Genes
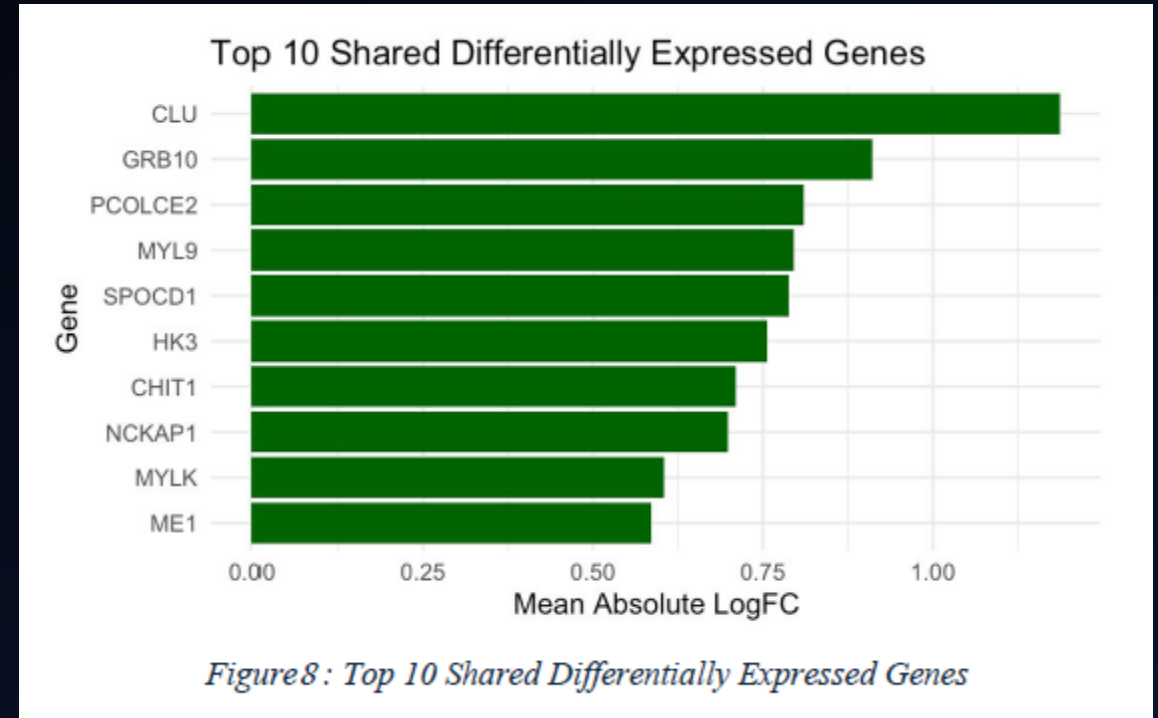
Pathway Enrichment Analysis

Tool: Gene Set Enrichment Analysis (GSEA) using the KEGG database.

Shared Pathways Identified:
- Oxidative phosphorylation,
- Mitochondrial dysfunction,
- Immune and inflammatory signalling,
- Neurodegenerative disease pathways.

Significance: Energy metabolism and cellular stress are key drivers in both conditions.

Discussion & Conclusion

Hypothesis Support: Results confirm that COVID-19 and AD share important molecular features.

Mechanism: Viral infection may worsen neurodegeneration through systemic stress and immune activation.

Final Thought: Identifying these shared genes supports future biomarker discovery and therapeutic research for both diseases.