A Blood-Based Transcriptomic Algorithm and Scoring System for Alzheimer's Disease Detection

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Alzheimer's disease is a neurodegenerative disorder that affects more than 50 million people worldwide. Current diagnostic methods include cerebrospinal fluid testing, which is invasive and expensive, and CT/MRI scans, which are non-specific. The focus of this study was to find alternative diagnostic approaches for early detection by creating a transparent algorithm using blood-based transcriptomic biomarkers associated with Alzheimer's. A microarray dataset from NCBI GEO was obtained, which contained the expression levels of 9956 genes in 180 subjects: 90 Alzheimer's cases and 90 non-Alzheimer's controls. The Mann-Whitney U Test and the Holm-Bonferroni p-value correction were applied for feature selection, yielding 11 statistically significant genes. Symbolic regression using the Quantum Lattice technique was then applied, generating a 3-gene mathematical function that could be utilized for Alzheimer's prediction. The three genes identified in the regression model were FBRSL1, TRIB2, and LY6G6D, the first two being novel discoveries. The results were converted to a 100-point scoring system intended for clinical use, and the diagnostic scores were validated using the testing dataset. The model gave scores lower than 25 to non-Alzheimer's controls with 94% accuracy and scores greater than 75 to Alzheimer's patients with 83% accuracy. The scoring system is a successful proof of concept that can serve as a starting point for more accurate risk systems in the future, and the identified biomarkers can be further validated in other cohorts of Alzheimer's patients.

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