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Systems-Level Insights into Alzheimer's Disease through Gene Interaction Network Analysis

Keywords: Alzheimer's disease, Multi-omics integration, Genome-wide association studies (GWAS), Transcriptomics, Epigenomics

Extended Abstract

Alzheimer's disease (AD) is a progressive neurodegenerative disorder characterised by cognitive decline, memory impairment, and synaptic dysfunction, with complex genetic factors. Recent advances in high-throughput genomics and network biology have opened a door to a world of possibilities, enabling the identification of key molecular players that contribute to AD onset and progression. Building a gene interaction network that captures the genetic architecture of AD provides a systems-level perspective to elucidate disease mechanisms. This integrates multi-omics data, including genome-wide association studies (GWAS), transcriptomics, and epigenomics, to detect disease-associated variants, expression changes, and regulatory interactions. By constructing and analysing these networks, researchers can uncover novel biomarkers, identify convergent molecular pathways, and highlight potential therapeutic targets. Such approaches not only deepen our understanding of the genetic determinants of AD but also offer a scalable framework to extend to related neurodegenerative disorders with shared pathophysiology. Ultimately, gene network modelling bridges the gap between isolated genetic variants and systemic disease phenotypes, enabling precision medicine strategies for diagnosis, prognosis, and treatment of Alzheimer's disease and beyond.