Using linkage analysis to identify novel gene-gene interactions in Alzheimer’s disease

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Linkage analysis was a workhorse of disease gene mapping until the advent of more refined genomic scans through genome wide association studies. We developed an approach to identify interacting genes involved in disease, using whole genome sequencing of multiplex Alzheimer’s Disease families. This approach utilizes biological interactions to identify potential disease loci despite genomic distance, thus identifying possible epistatic effects not easily observable in case-control datasets.