Associated with causal genes and their genetic diseases is an important problem concerning human health. Linkage analysis is such a method that can identify which unknown disease genes are located in chromosomal region out of hundreds of candidate genes according to their functions, interactions, and pathways which is good identification of genes associated with general/hereditary disorders. Here, we used method for prioritization of candidate genes of Dementia by the use of a global network distance measure, Random Walk Analysis, which detects neurological disorder been associated with distribution of sub-network among the genes.

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