Co-expression Toggling of MicroRNAs in Alzheimer's Brain

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Outcome of the Study

A set of 74 microRNAs reported to have association with Alzheimer's disease are found out through extensive literature survey

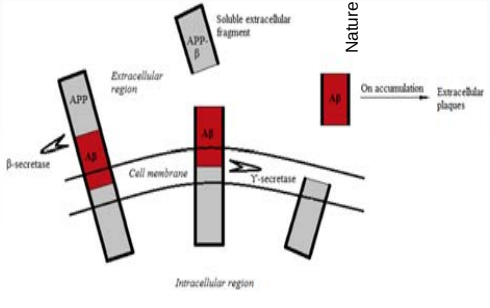
The hsa-miR-423-5p appears to be the hub microRNA in Alzheimer's disease

MicroRNAs having positive co-expression in white matter have higher differential co-expression values than those having positive co-expression in gray matter

The differentially co-expressed microRNAs are predominently enriched in white matter of brain

What is Alzheimer's disease?

A neurodegereative disorder



Literature Survey

Gray matter alterations are predominently found in Alzheimer's disease study

Alterations in gray matter also cause change in the white matter

In 2002, Roher *et al.* first claimed that Alzheimer's disease may also originate in the white matter of brain and the alteration in the white matter was confirmed later in 2010 by nuroimaging

No significant study is there to comparatively analyze the gray and white matter alterations

The Data We Work on

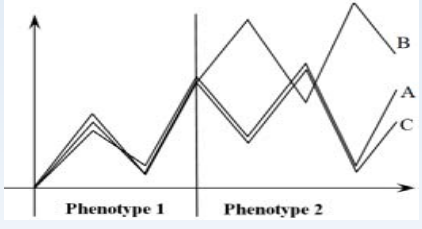
W. X. Wang *et al.*[1] studied the expressions of microRNAs in GM and WM in the temporal cortex of normal and early Alzheimer's-affected nine elderly females

MicroRNA profiling is performed in GM and WM separately using Exiqon Locked Nucleic Acid (LNA) microarrays

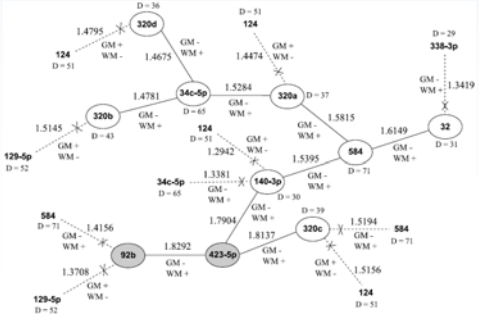
They also studied the enrichment of microRNAs in both gray matter and white matter of brain and counted Alzheimer's lesions

Methodology

Differential co-expression can identify varying patterns in different phenotypes



Given a differentially co-expressed graph $G = (V, E, W, S)$, we target to find out the largest subgraph G' of G without any cycle (i.e., a tree), containing high degree nodes and having a similar *switching pattern* over all the edges in G'



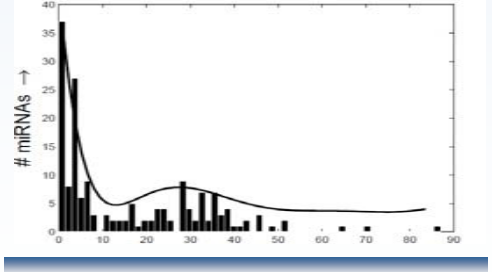
Experimental Results

Student's paired t-test & SAM: Unable to find out microRNAs associated with Alzheimers' disease

Correlation-based analysis: MicroRNAs enriched significantly and associated with Alzheimers' (p-value < 0.001) are idetified

miR-423-5p come out as a high degree node whose removal breaks a significant substructure

Graph clustering: MicroRNA modules are insignificant to explore Alzheimers's-association but degree analysis has some merit



References

1. W. X. Wang *et al.*, Acta Neuropathology, 121(2):193-205, 2010.