



**Note on: Exploring Alzheimer's Disease Molecular Variability via
Calculation of Personalized Transcriptional Signatures.**

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Fragment

Despite huge investments and major efforts to develop remedies for Alzheimer's disease (AD) in the past decades, AD remains incurable. While evidence for molecular and phenotypic variability in AD have been accumulating, AD research still heavily relies on the search for AD-specific genetic/protein biomarkers that are expected to exhibit repetitive patterns throughout all patients. Thus, the classification of AD patients to different categories is expected to set the basis for the development of therapies that will be beneficial for subpopulations of patients. Here we explore the molecular heterogeneity among a large cohort of AD and non-demented brain samples, aiming to address the question whether AD-specific molecular biomarkers can progress our understanding of the disease and advance the development of anti-AD therapeutics. We studied 951 brain samples, obtained from up to 17 brain regions of 85 AD patients and 22 non-demented subjects. Utilizing an information-theoretic approach, we deciphered the brain sample-specific structures of altered transcriptional networks. Our in-depth analysis revealed that 7 subnetworks were repetitive in the 737 diseased and 214 non-demented brain samples. Our results emphasize the need to expand the biomarker-based stratification to patient-specific transcriptional signature identification for improved AD diagnosis and for the development of subclass-specific future treatment.

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References

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