# Multiomics

Multiomics refers to a biological analysis approach in which the data sets are multiple “omes”, such as the genome, proteome, transcriptome, epigenome, and microbiome; in other words, the use of multiple omics technologies to study life in a concerted way.

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No single-omic approach completely elucidates the multitude of alterations taking place in Alzheimer's disease (AD).

Marttinen et al., from Kuopio, coupled transcriptomics and phosphoproteomics approach to determine the temporal sequence of changes in mRNA, protein, and phosphopeptides expression level from human temporal cortical samples, with varying degree of AD-related pathology. This approach highlighted fluctuation in synaptic and mitochondrial function as the earliest pathological events in brain samples with AD-related pathology. Subsequently, increased expression of inflammation and extracellular matrix-associated gene products was observed. Interaction network assembly for the associated gene products, emphasized the complex interplay between these processes and the role of addressing post-translational modifications in the identification of key regulators. Additionally, they evaluated the use of decision trees and random forests in identifying potential biomarkers differentiating individuals with different degree of AD-related pathology. This multiomic and temporal sequence-based approach provides a better understanding of the sequence of events leading to AD [1].

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Marttinen M, Paananen J, Neme A, Mitra V, Takalo M, Natunen T, Paldanius KMA, Mäkinen P, Bremang M, Kurki MI, Rauramaa T, Leinonen V, Soininen H, Haapasalo A, Pike I, Hiltunen M. A multiomic approach to characterize the temporal sequence in Alzheimer's disease-related pathology. Neurobiol Dis. 2018 Dec 14. pii: S0969-9961(18)30479-0. doi: 10.1016/j.nbd.2018.12.009. [Epub ahead of print] PubMed PMID: 30557660.