Integrating and analysing -omics data from different sources in Alzheimer research

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Abstract: Large-scale genomics studies have plaid a key role in unravelling the causes and consequences of Alzheimer's disease (AD). Historically, genetic research has been a major driver of our understanding the aetiology of AD. The past decade has seen rapid changes in the availability of publicly accessible data sets involving -omics data beyond the genome: transcriptomics, proteomics, metabolomics and metagenome (microbiome). These data are not only generated in patient and controls but increasingly in cellular models. The integration of these data with genetic data have fuelled Alzheimer research. However, the wealth of data raises new questions on how to optimize the analysis of high-dimensional correlated data and how to deal with possible confounders. Examples of cross-omics studies integrating (epi)genetic, transcriptomic, proteomic, metabolomic and microbiome data in Alzheimer research will be discussed.