

Generating a mechanism-based taxonomy of Alzheimer's and Parkinson's disease and validating in the course of a prospective clinical trial

TRANSFER TO BIOINFORMATICS

New strategies for disease modelling and data mining, hypothesis generation and validation – applying innovative techniques to identify and validate new disease mechanisms

SCAI VIEW

Knowledge Mining

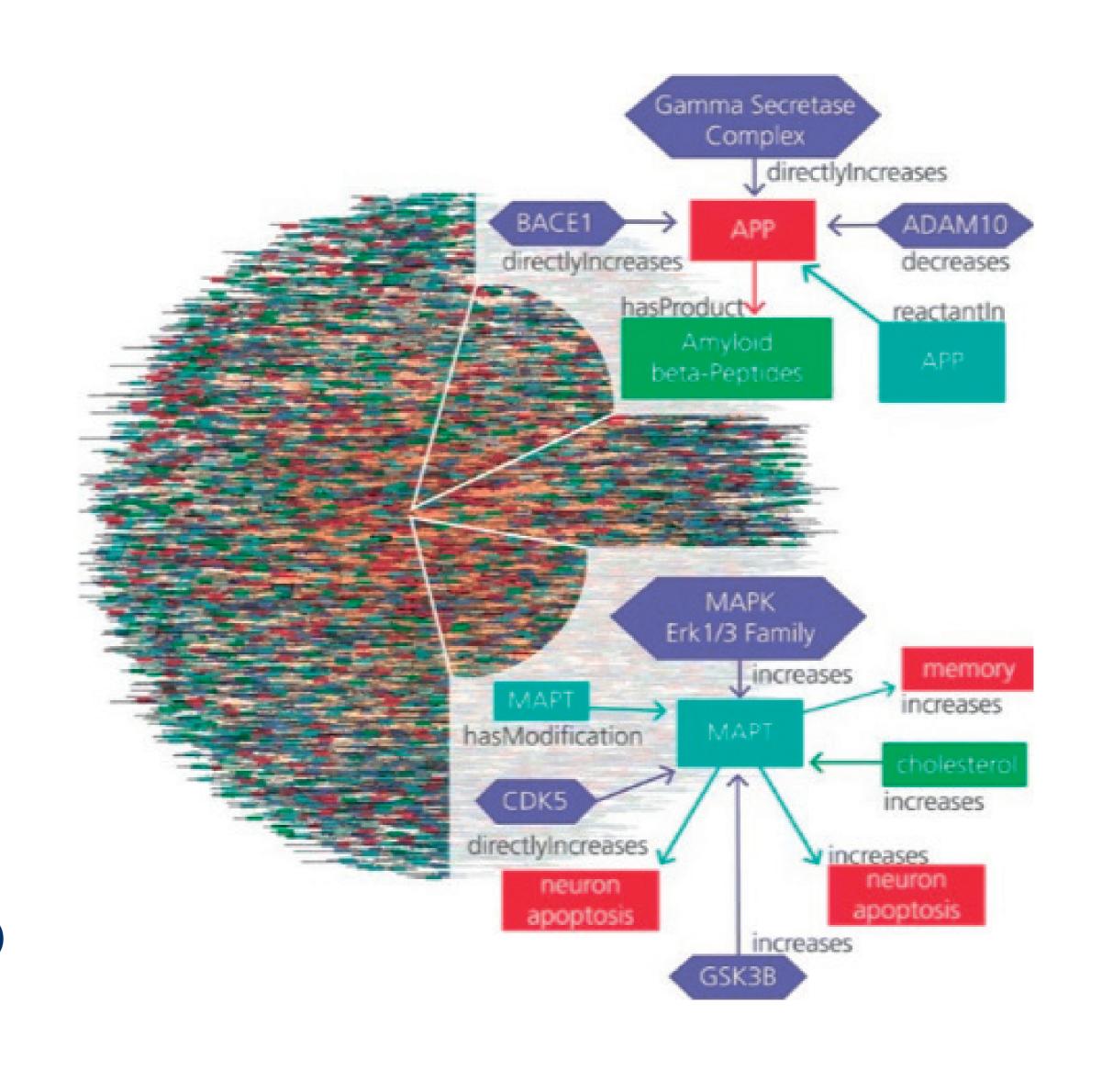
 AETIONOMY generates hypotheses about multi-scale mechanisms of neurodegenerative pathophysiology.

Conceptually, disease specific features are identified and organized at different scales to perform data-driven analysis. This analysis identifies robust combinations of features that correspond to disease sub-types. Selected mechanisms of neurodegeneration, that may distinguish disease subtypes, are tested and validated using

Disease Modelling

patient-level data.

 Disease knowledge assembly models have been generated to capture the vast knowledge around Alzheimer's and Parkinson's disease. The underlying models are based on the Biological Expression Language (BEL), encoding literature-derived "cause and effect" relationships into networks, which can be subjected to causal reasoning using quantitative data such as gene expression.



www.aetionomy.eu









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