

Big data-based studies on neurodegenerative-related interactome, aging and longevity

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Abstract: Latest trends in bioinformatics and computational biology play a crucial role in analyzing large and complex biological datasets, understanding molecular mechanisms of life and disease, and accelerating the development of novel therapies. This talk focuses on the neurodegenerative-related interactome, machine learning-based biological age prediction, and human aging and longevity knowledge graph.

We conducted a comprehensive analysis of neurodegenerative disease-related proteins and their interactions, generating a high-resolution network with structural information. The Neurodegenerative Disease Atlas (NDAtlas) was developed, allowing for 3D molecular graphics beyond traditional 2D network information. We proposed a composite machine learning-based biological age (ML-BA) model based on biomarkers obtained from medical examination data. The composite ML-BA is strongly associated with healthy risk indicators and various diseases, providing improved aging measurement capabilities and supporting the potential application of machine learning in aging research. We introduced HALD, a text mining-based human aging and longevity knowledge graph containing essential entities in the field of aging and longevity and related literature curated from PubMed. HALD enables a comprehensive understanding of aging and longevity mechanisms, providing a foundation for developing anti-aging therapies for aging-related diseases.

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