SEMINAR 5

About the Speaker:

Feng Gao, PhD

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Topic: “An epigenetic view of aging dynamics”

Abstract: Aging is one of the most important risk factors for many diseases, and is a complex process that involves multiple factors from genetics to environmental and lifestyle factors. In the meanwhile, aging related epigenetic changes such as DNA methylation can participate in the regulation of the aging process. Therefore, understanding the epigenetic mechanisms including the dynamics in aging will provide new insights into developing new approaches for disease prevention. Indeed, the rapid development of DNA methylation analysis has provided rich information about epigenetic regulations. For example, DNA methylation analysis can measure more than 450K and 850K CpG sites through microarray technology. These data provide great opportunities to study aging, however, also pose great challenges in learning useful information from high dimensional data. In this talk, he shared their recent research on aging. Specifically, talked about how they leverage novel computational models to reveal biological patterns and decipher the complex information embedded in high dimensional epigenetics data to study aging. He also discussed their findings about the dynamics of aging process. Finally, talked about their future directions in leveraging multi-omics data for aging studies.

Dr. Freng Gao’s recent seminar offered a comprehensive look into the connection between aging and neurodegenerative diseases like Alzheimer’s and Parkinson’s, underscoring aging as a primary risk factor. He highlighted the need to pinpoint and target therapeutic opportunities that could help mitigate these age-related conditions. A key topic was the use of biological aging clocks, specifically Horvath’s clock, to track aging at the molecular level. Dr. Gao discussed how these clocks measure aging through biological changes, particularly in DNA methylation, which influences gene expression as organisms age.

One central element of his talk was a recent study involving genome-wide methylation profiling of colon tissues from 82 male mice, aimed at identifying age-related methylation patterns. His team used this data to find Differential Methylation Regions (DMRs), specific areas where DNA methylation patterns shift with age. Through mapping these DMRs, they constructed complex networks to analyze methylation variations across age groups and developed a “methylation velocity” model, which tracks the pace of these changes to provide a dynamic view of aging.

To further enhance prediction accuracy, Dr. Gao employed graph neural networks to predict links within these DMR networks, ultimately building a DMR-based aging clock. This model estimates biological age based on methylation patterns, presenting a cutting-edge, data-driven approach to understanding and measuring aging in biological tissues.