Docket #: S22-381

Methods for monitoring molecular biomarkers for aging and disease

Stanford inventors develop a bioinformatic pipeline to measure protein biomarkers from aqueous humor to diagnose patients with eye disease, determine their biological age, understand age-related pathologies and morbidity, monitor molecular pathophysiology and human health, and evaluate therapeutic options and patient eligibility for different treatments.

Molecular biomarkers found in liquid tissues like blood and cerebrospinal fluid are crucial to disease diagnosis and health monitoring. However, the molecular composition of certain body fluids, like the eye's aqueous humor (AH), is poorly understood due to low volumes. Therefore, their full potential to inform us about body state cannot be harnessed. Using a proteomic approach, this gap can be filled as exemplified with AH below.

Stanford researchers collected a small volume of AH and applied it to a proteomic array to measure its biomarkers. Then, a custom bioinformatics analytical pipeline was used to define the molecular basis of known AH functions, including immune response, hemostasis, and proteolysis. Functional grouped network analysis revealed AH physiological roles including regulating angiogenesis, neuroinflammation, and metabolism. The inventors also identified potential biomarkers for aging, age-related pathologies, vitreoretinal diseases, and morbidity. This platform, therefore, significantly adds to a wealth of small-volume liquid biopsy technologies used to monitor health and disease.

Stage of Development
Proof of Concept

Applications

- Diagnosis of patients with eye disease.

- Determining patients' biological age.
- Determining the best therapeutic options for patients.
- Determining patient eligibility for human clinical trials.
- Studying drug efficacy and effectiveness in patients.

Advantages

- There are no products like it out there.

Patents

- Published Application: WO2024073355

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