Distinguished Lectures

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DEPARTMENT OF MATHEMATICS

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A Wearable-Based Aging Clock Associates with Disease and Behavior

by

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Time: 4:00pm – 5:00pm

Venue: B5-311, Yeung Kin Man Academic Building

ABSTRACT

Biomarkers of aging play a vital role in understanding human longevity and have the potential to inform clinical decisions and assess interventions. Existing aging clocks are typically based on blood, saliva, vital signs, or imaging collected in a clinical setting. Wearables, however, can make convenient, frequent, and inexpensive measurements throughout daily life, scaled to an entire population. Based on a foundational model of time series signals we developed, we propose PpgAge, a biomarker that is non-invasively, passively, and longitudinally measurable by photoplethysmography (PPG) at the wrist from a consumer wearable. With data from the Apple Heart & Movement Study (n=213,593 participants and over 149 million participant-days), we develop a model of healthy aging and study its association with disease and behavior. PpgAge predicts chronological age with mean absolute error (MAE) of 2.43 years (95% CI 2.33–2.53) in a healthy cohort and 3.18 years (95% CI 3.16–3.19) in a general cohort. Among participants with a PpgAge gap (i.e., the deviation between predicted age and chronological age) larger than 6 years, diagnosis rates of heart disease, heart failure, and diabetes are 1.5–5 times the age- and sex-adjusted average. PpgAge gap also predicts incident disease — a PpgAge gap of 6 years is associated with a significantly increased risk of adverse cardiac events (hazard ratio 1.40 [95% CI 1.26–1.54]) when controlling for other risk factors. PpgAge is also associated with behavior, including smoking, exercise, and sleep. In longitudinal analyses, PpgAge exhibits a sharp increase during pregnancy and around the time of certain types of cardiac events. With additional evidence, PpgAge may be a useful surrogate for healthy aging in the study of human longevity and the treatment of age-related conditions. Finally, we discuss how this work illustrates the value of errors in machine learning. Joint work with A. Miller, J. Futoma, S. Abbaspouazad, C. Heniz-Deml, S. Emrani, and I. Shapiro. (ClinicalTrials.gov Identifier NCT04198194.)

~ALL ARE WELCOME~