Statistical methods for biological age estimation: past, present, and future perspectives

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Thursday 22 Feb 2024 | 2.30 p.m.
Room Benvenuti
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Among individuals of the same chronological age, there is high variability in the rate of aging. The concept of biological age is postulated to capture this variability better and hence to be a superior indicator of an individual's true aging status compared to chronological age. Identifying biomarkers of biological age is a central focus in current aging research. However, the concept of biological age lacks a clear operationalization, leading to the development of various biological age prediction approaches without a solid statistical foundation. In this presentation, I will first address the popular cross-sectional aging clocks, revealing that they are all based on the same strong and untestable assumption. Next, I will introduce a new methodological framework for the conceptualization and analysis of biological age data, integrating advanced survival analysis techniques into the omics-based prediction modeling framework. Our hypothesis posits that biological age, being of latent and holistic nature, can be operationalized in terms of observable time-to-event outcomes such as age-at-onset profiles of age-related diseases and/or mortality. Finally, I will conclude with future perspectives on how the simultaneous analysis of detailed age-at-disease-onset profiles from electronic health records represents a new opportunity for methodological research in aging, along with the challenges it poses.

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