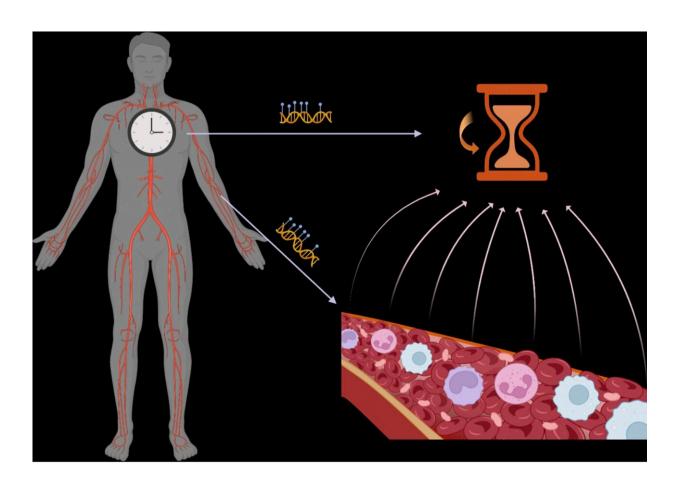


## Recalibrating principles of epigenetic aging clocks in human health

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Epigenetic clocks reflect the average DNA methylation signal across multiple cell types/states in a tissue. Variations in this composition impact the interpretation of such clocks. Credit: 2024 Zhang et al.

As detailed in the opening of this editorial, DNA methylation-based



epigenetic clocks are used as biomarkers of biological age in human health. Multiple epigenetic clocks have rapidly emerged in the past decade by modeling DNA methylation changes with age in large cohorts, primarily using peripheral blood samples.

Despite efforts to understand the functional implications of features used to estimate biological age, the underlying mechanisms of these clocks remain poorly understood, leading to potential misinterpretations of their associations with health outcomes.

The researchers explored the association of 12 immune cell types with epigenetic age acceleration (EAA) in both healthy and diseased populations. Their work sheds light on the complex interplay between immune cell composition and epigenetic aging, utilizing high-resolution methylation cytometry in blood samples.

"In this editorial, we aim to address the key implications of our study on epigenetic aging clocks in <a href="https://human.health">human health</a> from a broader perspective. While epigenetic clocks are widely hyped as aging biomarkers today, it's essential to recalibrate some <a href="fundamental concepts">fundamental concepts</a> in this field," the authors explained.

The paper is <u>published</u> in the journal *Aging*.

**More information:** Ze Zhang et al, Recalibrate concepts of epigenetic aging clocks in human health, *Aging* (2024). DOI: 10.18632/aging.206027

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