What's your body really worth? New AI model reveals your true biological age from 5 drops of blood

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Abstract

This study developed a novel AI-powered model to provide a more precise assessment of biological age, an indicator of an individual's physiological health and aging progression. By focusing on steroid metabolism and integrating information from pathways of steroidogenesis into a deep neural network (DNN), the model evaluates health-related aging patterns from only a few drops of blood. Twenty-two key steroids are simultaneously measured, and their relative ratios are analyzed to reduce the influence of individual variability and measurement noise. Incorporating steroid pathways into the DNN enables the creation of a biologically interpretable AI model, while a refined learning design captures the widening inter-individual differences that emerge with aging. This approach offers a reliable way to assess biological age, supporting personalized health monitoring and early detection of age-related risks.

Background & Results

As life expectancy increases, maintaining good health throughout aging becomes a central concern. Biological age, which reflects functional health rather than chronological years, provides a more meaningful indicator for monitoring well-being and preventing disease. Traditional methods, such as DNA methylation or protein biomarkers, often fail to capture the complex physiological homeostasis, limiting their utility for precise health assessment.

Steroids play key roles in metabolism, immune function, and stress response. In this study, we analyzed 22 major steroids in small blood samples, focusing on their relative balance rather than absolute levels. These data were integrated into a DNN model that incorporates pathways of steroidogenesis, allowing the AI to evaluate aging patterns in a biologically interpretable manner. To reflect the increasing variability among individuals as they age, the learning design was refined to capture diverse aging trajectories rather than simply minimizing error relative to chronological age.

This approach revealed important insights. For example, elevated cortisol, a hormone associated with stress, was linked to accelerated biological aging, with doubling of cortisol levels corresponding to approximately 1.5 times higher biological age. Such findings illustrate how specific steroid profiles can inform precise assessments of an individual's physiological aging, rather than chronological age.

Significance of the research and Future perspective

This AI-driven biological age model offers a new, objective measure for health evaluation, enabling early identification of age-related risks and supporting personalized interventions. Beyond individual health monitoring, it deepens our understanding of how steroid networks influence aging, providing actionable insights for preventive medicine and healthy aging strategies.

Future work will expand the dataset and integrate additional biomarkers to further enhance the model's ability to assess physiological aging accurately and interpretably. By combining AI with biological knowledge, this study establishes a foundation for more precise health assessments, promoting interventions that could extend healthy lifespan and improve well-being across populations.

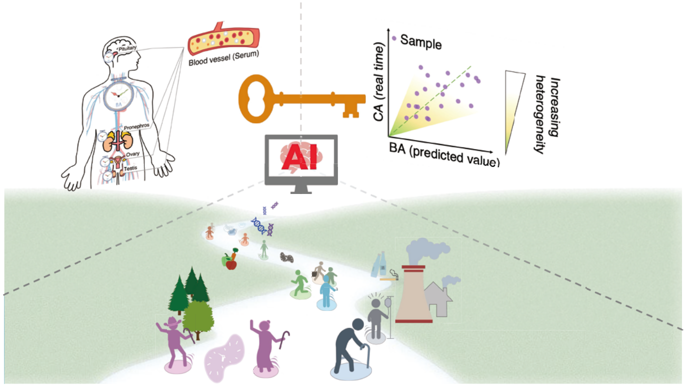

Fig.1. A general diagram of the AI-powered biological age model.
Top Left: A small blood sample is analyzed to measure 22 key steroids, and the data is fed into an AI system to calculate biological age.
Top Right: The AI-predicted biological age (BA) shows a general correlation with chronological age (CA), but individual differences widen over time.
Bottom: Using the metaphor of a "river widening as it flows downstream," the illustration visualizes how biological age evolves with the passage of time.

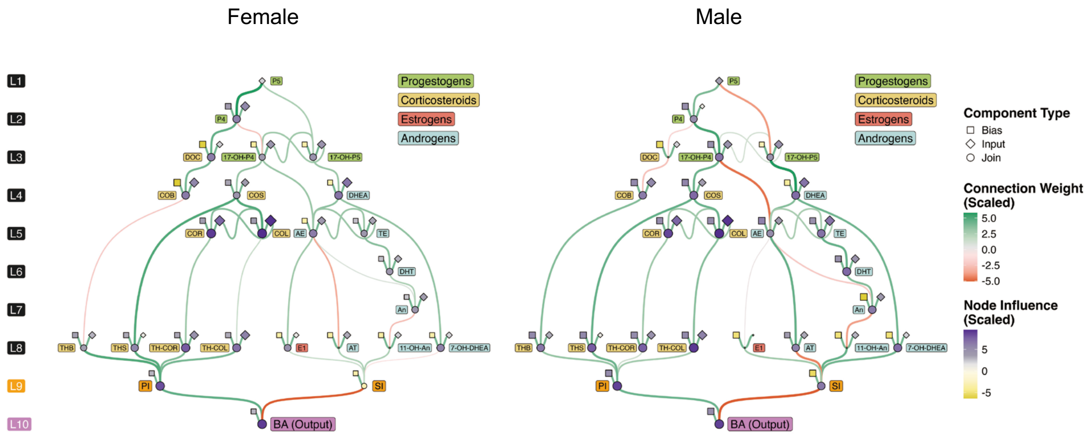

Fig. 2. Visualization of the DNN model constructed on pathways of steroidogenesis.
Sex-specific variations in steroid pathways for female and male models. Distinct colors are used to represent different steroid classes in the steroid labels. Connection weights reflect the influence of hierarchical steroidogenic pathways on BA prediction. Node influence reflects the average contribution of each node as it propagates through the pathway network. Component types illustrate the various sources of endogenous and exogenous influences. Bias, contribution from external pathways; Input, initial concentration; Join, summarized contributions from upstream metabolites.

Patent	
Treatise	Wang, Qiuyi; Wang, Zi; Takao, Toshifumi et al. Biological age prediction using a DNN model based on pathways of steroidogenesis. Science Advances. 2025, 11(11), eadt2624. doi: 10.1126/sciadv.adt2624
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