

Epigenetic aging clock predicts the biological age of individual cells

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One of the more promising biomarkers to measure biological aging is DNA methylation, an epigenetic modification that alters a specific sequence of DNA nucleotides known as CpG sites. Researchers have traditionally used epigenetic clocks, biochemical tests measuring the levels of DNA methylation, to profile the epigenetic age in bulk tissue samples. Using bulk samples can give an average of the patterns of

methylation in tissue but obscures the differences that exist across individual cells.

To visualize these patterns in single cells, researchers at the Brigham have developed a technique known as scAge, a statistical program capable of capturing epigenetic age at a single-cell resolution. With scAge, researchers elucidated the mechanisms driving the aging process, attenuation of epigenetic aging, and early embryogenesis-related rejuvenation in murine hepatocytes, muscle, and embryonic stem cells, respectively. Using epigenetic clock approaches, researchers found that individual cell lineages within organisms indeed age and that research on biological aging, at the previously elusive level of the individual cell, is now a possibility.

"Our single-cell approach with scAge may have profound clinical applications for mammalian, somatic, germline, and cancer cells within heterogeneous tissues," said senior author Vadim N. Gladyshev, PhD, of the Division of Genetics in the Department of Medicine. "Through this paper we wanted to present a framework to profile epigenetic age in [single cells](#), and in the process, found an exciting application at the interface of aging, rejuvenation, and emerging single-cell technologies."

The study is published in *Nature Aging*.

More information: Alexandre Trapp et al, Profiling epigenetic age in single cells, *Nature Aging* (2021). [DOI: 10.1038/s43587-021-00134-3](https://doi.org/10.1038/s43587-021-00134-3)

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