


[nature](#) > [nature aging](#) > [resources](#) > article

Resource | Published: 05 November 2024

Phenome-wide associations of human aging uncover sex-specific dynamics

[Lee Reicher](#), [Noam Bar](#), [Anastasia Godneva](#), [Yotam Reisner](#), [Liron Zahavi](#), [Nir Shahaf](#), [Raja Dhir](#), [Adina Weinberger](#) & [Eran Segal](#) 

[Nature Aging](#) **4**, 1643–1655 (2024)

3763 Accesses | **50** Altmetric | [Metrics](#)

Abstract

Aging varies significantly among individuals of the same chronological age, indicating that biological age (BA), estimated from molecular and physiological biomarkers, may better reflect aging. Prior research has often ignored sex-specific differences in aging patterns and mainly focused on aging biomarkers from a single data modality. Here we analyze a deeply phenotyped longitudinal cohort (10K project, Israel) of 10,000 healthy individuals aged 40–70 years that includes clinical, physiological, behavioral, environmental and multiomic parameters. Follow-up visits are scheduled every 2 years for a total of 25 years. We devised machine learning models of chronological age and computed biological aging scores that represented diverse physiological systems, revealing different aging patterns among sexes. Higher BA scores were associated with a higher prevalence of age-related medical conditions, highlighting the clinical relevance of these scores. Our analysis revealed system-specific aging dynamics and the potential of deeply phenotyped cohorts to accelerate improvements in our understanding of chronic diseases. Our findings present a more holistic view of the aging process, and lay the foundation for personalized medical prevention strategies.

This is a preview of subscription content, [access via your institution](#)

Access options

Access Nature and 54 other Nature Portfolio journals

Get Nature+, our best-value online-access subscription

\$29.99 / 30 days
cancel any time

[Learn more](#)

Buy this article

- Purchase on SpringerLink
- Instant access to full article PDF

[Buy now](#)

Subscribe to this journal

Receive 12 digital issues and online access to articles

\$119.00 per year
only \$9.92 per issue

[Learn more](#)

Prices may be subject to local taxes which are calculated during checkout

Additional access options:

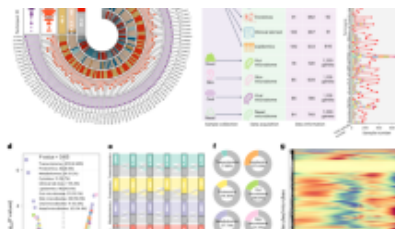
- [Log in](#)
- [Learn about institutional subscriptions](#)
- [Read our FAQs](#)
- [Contact customer support](#)

Similar content being viewed by others



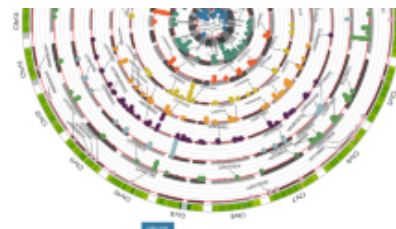
Biomarkers selection and mathematical modeling in biological age estimation

Article | Open access
01 July 2023



Nonlinear dynamics of multi-omics profiles during human aging

Article | Open access
14 August 2024



The genetic architecture of biological age in nine human organ systems

Article | 28 June 2024

Data availability

Data in this paper are part of the Human Phenotype Project and are accessible to researchers from universities and other research institutions at <https://humanphenotypeproject.org/>. Interested bona fide researchers should contact info@pheno.ai to obtain instructions for accessing the data.

Code availability

Analysis source code is available at <https://github.com/noambar/BiologicalAge>.

References

1. Niccoli, T. & Partridge, L. Ageing as a risk factor for disease. *Curr. Biol.* **22**, R741–R752 (2012).

2. Sampathkumar, N. K. et al. Widespread sex dimorphism in aging and age-related diseases. *Hum. Genet.* **139**, 333–356 (2020).

3. Merz, A. A. & Cheng, S. Sex differences in cardiovascular ageing. *Heart* **102**, 825–831 (2016).

4. Austad, S. N. Sex differences in health and aging: a dialog between the brain and gonad? *Geroscience* **41**, 267–273 (2019).

5. Foo, H., Mather, K. A., Thalamuthu, A. & Sachdev, P. S. The many ages of man: diverse approaches to assessing ageing-related biological and psychological measures and their relationship to chronological age. *Curr. Opin. Psychiatry* **32**, 130–137 (2019).

6. Earls, J. C. et al. Multi-omic biological age estimation and its correlation with wellness and disease phenotypes: a longitudinal study of 3,558 individuals. *J. Gerontol. A* **74**, S52–S60 (2019).

7. Klemmera, P. & Doubal, S. A new approach to the concept and computation of biological age. *Mech. Ageing Dev.* **127**, 240–248 (2006).

8. van den Akker, E. B. et al. Metabolic age based on the BBMRI-NL ¹H-NMR metabolomics repository as biomarker of age-related disease. *Circ. Genom. Precis. Med.* **13**, 541–547 (2020).

9. Nie, C. et al. Distinct biological ages of organs and systems identified from a multi-omics study. *Cell Rep.* **38**, 110459 (2022).

10. Liu, Z. et al. Underlying features of epigenetic aging clocks in vivo and in vitro. *Aging Cell* **19**, e13229 (2020).

11. Rossiello, F., Jurk, D., Passos, J. F. & d'Adda di Fagagna, F. Telomere dysfunction in ageing and age-related diseases. *Nat. Cell Biol.* **24**, 135–147 (2022).

12. Chatsirisupachai, K., Palmer, D., Ferreira, S. & de Magalhães, J. P. A human tissue-specific transcriptomic analysis reveals a complex relationship between aging, cancer, and cellular senescence. *Aging Cell* **18**, e13041 (2019).

13. Lehallier, B. et al. Undulating changes in human plasma proteome profiles across the lifespan. *Nat. Med.* **25**, 1843–1850 (2019).

14. Chen, R. et al. Personal omics profiling reveals dynamic molecular and medical phenotypes. *Cell* **148**, 1293–1307 (2012).

15. Hillary, R. F. et al. Epigenetic measures of ageing predict the prevalence and incidence of leading causes of death and disease burden. *Clin. Epigenetics* **12**, 115 (2020).

16. Shilo, S. et al. 10 K: a large-scale prospective longitudinal study in Israel. *Eur. J. Epidemiol.* **36**, 1187–1194 (2021).

17. *The Global Prevalence of Anaemia in 2011* (World Health Organization, 2015); <https://iris.who.int/handle/10665/177094>

18. McKinlay, S. M. The normal menopause transition: an overview. *Maturitas* **23**, 137–145 (1996).

19. Talaulikar, V. Menopause transition: physiology and symptoms. *Best Pract. Res. Clin. Obstet. Gynaecol.* **81**, 3–7 (2022).

20. Farlay, D. et al. Bone remodeling and bone matrix quality before and after menopause in healthy women. *Bone* **128**, 115030 (2019).

21. Bittner, V. Menopause, age, and cardiovascular risk: a complex relationship. *J. Am. Coll. Cardiol.* **54**, 2374–2375 (2009).

22. *Global Health Observatory Visualizations: Causes of Death* (World Health Organization, 2018);
<https://apps.who.int/gho/data/view.wrapper.MGHEMORTCAUSE10?lang=en>

23. Graham, J. W. Missing data analysis: making it work in the real world. *Annu. Rev. Psychol.* **60**, 549–576 (2009).

24. Brooks, R. C. & Garratt, M. G. Life history evolution, reproduction, and the origins of sex-dependent aging and longevity. *Ann. N. Y. Acad. Sci.* **1389**, 92–107 (2017).

25. Holdcroft, A. Gender bias in research: how does it affect evidence based medicine? *J. R. Soc. Med.* **100**, 2–3 (2007).

26. NIH policy on sex as a biological variable. *National Institutes of Health Office of Research on Women's Health* <https://orwh.od.nih.gov/sex-gender/nih-policy-sex-biological-variable> (2016).

27. Matsui, S. et al. Changes of liver enzymes and triglyceride during the menopausal transition in Japanese women. *J. Obstet. Gynaecol.* **36**, 806–811 (2016).

28. Beyene, H. B. et al. High-coverage plasma lipidomics reveals novel sex-specific lipidomic fingerprints of age and BMI: evidence from two large population cohort studies. *PLoS Biol.* **18**, e3000870 (2020).

29. Ameratunga, D., Goldin, J. & Hickey, M. Sleep disturbance in menopause. *Intern. Med. J.* **42**, 742–747 (2012).

30. Seeman, E. During aging, men lose less bone than women because they gain more periosteal bone, not because they resorb less endosteal bone. *Calcif. Tissue Int.* **69**, 205–208 (2001).

31. Osibogun, O., Ogunmoroti, O. & Michos, E. D. Polycystic ovary syndrome and cardiometabolic risk: opportunities for cardiovascular disease prevention. *Trends Cardiovasc. Med.* **30**, 399–404 (2020).

32. Gonzalez-Covarrubias, V. Lipidomics in longevity and healthy aging. *Biogerontology* **14**, 663–672 (2013).

33. Holmes, M. V. et al. Lipids, lipoproteins, and metabolites and risk of myocardial infarction and stroke. *J. Am. Coll. Cardiol.* **71**, 620–632 (2018).

34. Michos, E. D., McEvoy, J. W. & Blumenthal, R. S. Lipid management for the prevention of atherosclerotic cardiovascular disease. *N. Engl. J. Med.* **381**, 1557–1567 (2019).

35. Wang, Q. et al. Metabolic characterization of menopause: cross-sectional and longitudinal evidence. *BMC Med.* **16**, 17 (2018).

36. Aggarwal, N. R. et al. Sex differences in ischemic heart disease: advances, obstacles, and next steps. *Circ. Cardiovasc. Qual. Outcomes* **11**, e004437 (2018).

37. Drewnowski, A. & Shultz, J. M. Impact of aging on eating behaviors, food choices, nutrition, and health status. *J. Nutr. Health Aging* **5**, 75–79 (2001).

38. Mather, K. A., Jorm, A. F., Parslow, R. A. & Christensen, H. Is telomere length a biomarker of aging? A review. *J. Gerontol. A* **66**, 202–213 (2011).

39. Shokhirev, M. N. & Johnson, A. A. Modeling the human aging transcriptome across tissues, health status, and sex. *Aging Cell* **20**, e13280 (2021).

40. Broll, S. et al. Interpreting blood GLUcose data with R package iglu. *PLoS ONE* **16**, e0248560 (2021).

41. Fan, S. et al. Systematic error removal using random forest for normalizing large-scale untargeted lipidomics data. *Anal. Chem.* **91**, 3590–3596 (2019).

42. Rothschild, D. et al. An atlas of robust microbiome associations with phenotypic traits based on large-scale cohorts from two continents. *PLoS ONE* **17**, e0265756 (2022).

43. Leviatan, S., Shoer, S., Rothschild, D., Gorodetski, M. & Segal, E. An expanded reference map of the human gut microbiome reveals hundreds of previously unknown species. *Nat. Commun.* **13**, 3863 (2022).

44. Bycroft, C. et al. The UK Biobank resource with deep phenotyping and genomic data. *Nature* **562**, 203–209 (2018).

45. Popa, A. et al. Quantification of liver fibrosis, steatosis, and viscosity using multiparametric ultrasound in patients with non-alcoholic liver disease: a “real-life” cohort study. *Diagnostics* **11**, 783 (2021).

46. Zhou, Y. et al. AutoMorph: automated retinal vascular morphology quantification via a deep learning pipeline. *Transl. Vis. Sci. Technol* **11**, 12 (2022).

47. Ke, G. et al. *LightGBM: A Highly Efficient Gradient Boosting Decision Tree* (Curran Associates Inc., 2017); <https://papers.nips.cc/paper/6907-lightgbm-a-highly-efficient-gradient-boosting-decision-tree.pdf>

Acknowledgements

We thank past and present members of the Segal group for useful discussions. N.B. received a PhD scholarship for Data Science from the Israeli Council for Higher Education via the Weizmann Data Science Research Center and is supported by a research grant from the Estate of Tully and Michele Plessner. E.S. is supported by the Crown Human Genome Center; by D. L. Schwarz, J. N. Halpern and L. Steinberg; and by grants funded by the European Research Council and the Israel Science Foundation.

Author information

These authors contributed equally: Lee Reicher, Noam Bar.

Authors and Affiliations

Department of Computer Science and Applied Mathematics, Weizmann Institute of Science, Rehovot, Israel

Lee Reicher, Noam Bar, Anastasia Godneva, Yotam Reisner, Liron Zahavi, Nir Shahaf, Adina Weinberger & Eran Segal

Department of Molecular Cell Biology, Weizmann Institute of Science, Rehovot, Israel

Lee Reicher, Noam Bar, Anastasia Godneva, Yotam Reisner, Liron Zahavi, Nir Shahaf, Adina Weinberger & Eran Segal

Lis Maternity and Women's Hospital, Tel Aviv Sourasky Medical Center, Tel Aviv University, Tel Aviv, Israel

Lee Reicher

Swiss Institute of Allergy and Asthma Research (SIAF), University of Zurich, Davos, Switzerland

Raja Dhir

Contributions

L.R. and N.B. conceived the project, designed and conducted all analyses, interpreted the results and wrote the manuscript. Y.R. developed protocols, interpreted the results and wrote the manuscript. A.G. and L.Z. performed data analysis. N.S. developed lipidomics processing, performed lipidomics analyses and wrote the manuscript. A.W. designed the project, developed protocols, and oversaw sample collection and processing. E.S. conceived and directed the project and analyses, designed the analyses, interpreted the results and wrote the manuscript.

Corresponding author

Correspondence to [Eran Segal](#).

Ethics declarations

Competing interests

The authors declare no competing interests.

Peer review

Peer review information

Nature Aging thanks the anonymous reviewers for their contribution to the peer review of this work.

Additional information

Publisher's note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Extended data

[Extended Data Fig. 1 Dispersion of biological aging scores from a model based on bone density parameters.](#)

A Ridgeline plot showing the distribution of the BA scores (x-axis) from a model of CA based on bone density parameters. Distributions are separated into CA groups (40-45, 45-50, 50-55, 55-60, 65-70, 70-75; y-axis) and to males and females.

[Extended Data Fig. 2 Dispersion of biological aging scores from a model based on diet parameters.](#)

A Ridgeline plot showing the distribution of the BA scores (x-axis) from a model of CA based on diet parameters. Distributions are separated into CA groups (40-45, 45-50, 50-55, 55-60, 65-70, 70-75; y-axis) and to males and females.

Extended Data Fig. 3 Distribution of sample sizes grouped by age is similar across profiled systems.

Figure panels show the normalized distribution of sample sizes of each profiled system (y-axes) grouped by CA (x-axes). **a–n**, Blood lipids system (**a**), cardiovascular system (**b**), immune system (**c**), liver health system (**d**), renal function (**e**), bone density (**f**), gut microbiome (**g**), body composition (**h**), frailty (**i**) lifestyle (**j**), diet (**k**), hematopoietic system (**l**), insulin resistance (**m**) and sleep characteristics (**n**).

Supplementary information

Reporting Summary

Supplementary Table 1

Blood lipids system parameters. The full list of parameters within blood lipids category, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 2

Cardiovascular system parameters. The full list of parameters within cardiovascular system, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 3

Immune system parameters. The full list of parameters within Immune system category, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 4

Liver health system parameters. The full list of parameters within liver health category, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 5

Renal function parameters. The full list of parameters within renal function, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 6

Bone density parameters. The full list of parameters within bone density, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 7

Gut microbiome parameters. The full list of parameters within gut microbiome, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 8

Body composition parameters. The full list of parameters within body composition, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 9

Frailty parameters. The full list of parameters within frailty category, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 10

Lifestyle parameters. The full list of parameters within lifestyle category, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 11

Diet parameters. The full list of parameters within diet category, along with the number of participants (males and females) for which each parameter was available.

Supplementary Table 12

Hematopoietic system parameters. The full list of parameters within hematopoietic system, along with the number of participants (males and females) for which each parameter was available.

[Supplementary Table 13](#)

Insulin resistance parameters. The full list of parameters within insulin resistance category, along with the number of participants (males and females) for which each parameter was available.

[Supplementary Table 14](#)

Sleep characteristics parameters. The full list of parameters within sleep characteristics, along with the number of participants (males and females) for which each parameter was available.

[Supplementary Table 15](#)

Number of self-reported medical diagnoses by profiled system and sex.

[Supplementary Table 16](#)

Medical diagnoses associated with biological aging scores. Two-sided odds ratios computed with logistic regression.

[Supplementary Table 17](#)

Medical diagnoses associated with biological aging scores. Two-sided odds ratios computed with logistic regression.

[Supplementary Table 18](#)

Medical conditions of similar physiological characteristics.

Rights and permissions

Springer Nature or its licensor (e.g. a society or other partner) holds exclusive rights to this article under a publishing agreement with the author(s) or other rightsholder(s); author self-archiving of the accepted manuscript version of this article is solely governed by the terms of such publishing agreement and applicable law.

[Reprints and permissions](#)

About this article

Cite this article

Reicher, L., Bar, N., Godneva, A. *et al.* Phenome-wide associations of human aging uncover sex-specific dynamics. *Nat Aging* **4**, 1643–1655 (2024). <https://doi.org/10.1038/s43587-024-00734-9>

Received

19 March 2024

Accepted

19 September 2024

Published

05 November 2024

Issue Date

November 2024

DOI

<https://doi.org/10.1038/s43587-024-00734-9>

Subjects

[Ageing](#)

• [Computational biology and bioinformatics](#)

• [Predictive markers](#)

Nature Aging (*Nat Aging*) | ISSN 2662-8465 (online)