ComputAgeBench: Epigenetic Aging Clocks Benchmark

Dmitrii Kriukov*
Skoltech[1], AIRI[2]
dmitrii.kriukov@skoltech.ru

Evgeniy Efimov*
Skoltech[1]
evgeniy.efimov@skoltech.ru

Ekaterina Kuzmina
Skoltech[1], AIRI[2]
Ekaterina.Kuzmina@skoltech.ru

Ekaterina E. Khrameeva†
Skoltech[1]
E.Khrameeva@skoltech.ru

Dmitry V. Dylov†
Skoltech[1], AIRI[2]
D.Dylov@skoltech.ru

Abstract

The success of clinical trials of longevity drugs relies heavily on identifying integrative health and aging biomarkers, such as biological age. Epigenetic aging clocks predict the biological age of an individual using their DNA methylation profiles, commonly retrieved from blood samples. However, there is no standardized methodology to validate and compare epigenetic clock models as yet. We propose ComputAgeBench, a unifying framework that comprises such a methodology and a dataset for comprehensive benchmarking of different clinically relevant aging clocks. Our methodology exploits the core idea that reliable aging clocks must be able to distinguish between healthy individuals and those with aging-accelerating conditions. Specifically, we collected and harmonized 66 public datasets of blood DNA methylation, covering 19 such conditions across different ages and tested 13 published clock models. We believe our work will bring the fields of aging biology and machine learning closer together for the research on reliable biomarkers of health and aging.

Code: https://github.com/ComputationalAgingLab/ComputAge
Dataset: https://huggingface.co/datasets/computage/computage_bench

1 Introduction

Longevity drugs (*a.k.a., geroprotectors*) appear to be on the brink of entering clinical practice to slow down or reverse the features of aging [1, 2]. The research community is yet to identify proper biomarkers of aging and rejuvenation that could be used as clinical trial endpoints instead of or in combination with observations on patient lifespans [3]. Biological age (BA) has been proposed as one of such surrogate biomarkers of aging, defined as a *generalized measure of human health* compared to the average health of individuals at a given age within a population [4, 5]. Thus, if an individual has a

*These authors contributed equally.
†Co-senior authors.
[1]Skolkovo Institute of Science and Technology
[2]Artificial Intelligence Research Institute

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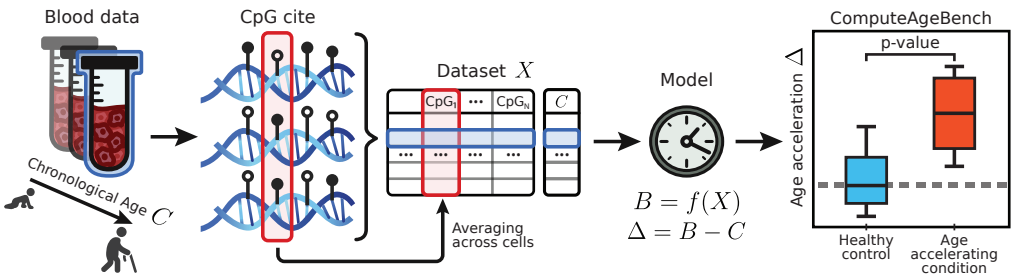


Figure 1: ComputAgeBench: benchmarking various epigenetic aging clock models. For a dataset X, obtained by profiling DNA methylation at CpG sites in bulk blood samples, an aging clock model f is trained to distinguish healthy individuals from those with pre-defined aging-accelerating conditions.

biological age of 40 at the chronological age of 30, it is assumed that their overall health corresponds to that of an average 40-year-old in the population. This relationship can be concisely expressed as

$$B = C + \Delta\,, \tag{1}$$

where B represents biological age, C denotes chronological age (*i.e.*, time since birth), and Δ symbolizes BA *acceleration* (or deceleration, if negative).

In general, BA can be estimated from a set of biomarkers X with a model (algorithm) $f : X \to B$, also called an *aging clock*. However, BA is latent: it has no ground truth value that can be measured directly and then used to train an aging clock model f in a classical supervised fashion, making clock validation a nontrivial task [6]. This obstacle forces researchers to introduce various additional assumptions about the aging clock behavior [7–10], as well as to experiment with different machine learning models (including penalized linear regressions, such as ElasticNet, support vector machines, decision trees, transfomer-based neural networks, *etc*. [10, 11]) and underlying types of data X [12–14]. The vast majority of aging clocks, though, rely primarily on DNA methylation data, also called *epigenetic* aging clocks [15–19]. Summarizing abundant discussions about a "good" mathematical description of BA in the literature [1, 10, 20], we elicited four of its defining properties, formalized as follows.

Let $X \in \mathbb{R}^p$, where p is the number of biomarkers in data, $B \in \mathbb{R}$, and $f : X \to B$. Given the aging acceleration $\Delta = B - C$, the following four properties hold:

1. B is expressed in the same time units as C;
2. Δ allows distinguishing between healthy individuals and individuals with aging-accelerating or decelerating conditions (AACs or ADCs), such as severe chronic diseases;
3. B helps to predict the remaining lifespan better than C does [20];
4. B helps to predict the time to onset of chronic age-related diseases (*e.g.*, the Alzheimer's) better than C does [20].

Garnered together, these properties motivated us to construct a benchmarking methodology for validating the potential biological age predictors. In property #1, the model f should output age values in a biologically meaningful range, comparable with a typical lifespan, *e.g.*, from 0 to 120 years for the humans. To investigate if a model f satisfies the 2nd property, we can define a panel of aging-accelerating (or decelerating) conditions and test if the predicted Δ allows distinguishing the individuals with an AAC/ADC from a control group, according to an appropriate statistical test. To validate the compliance with the 3rd and the 4th properties, one also needs data on mortality and multi-morbidity. That is, the information about the timing of death or the onset of chronic age-related diseases, along with a prior measurement of a set of relevant biomarkers. It is important to note that such data are highly sensitive and are generally not publicly available.

DNA methylation (DNAm) is the most prevalent measurement employed in the construction of aging clocks [21]. From a chemical point of view, DNA methylation refers to a covalent modification of DNA nucleotides by the methyl groups [22]. Specifically, cytosine nucleotides (C) followed by guanine nucleotides (G), also referred to as cytosines in a CpG context or simply CpG sites (CpGs), are methylated most often in the mammalian cells, making it the most well-studied type of DNA

methylation [23] (refer to Fig. 1 for visualization of the DNA and CpGs). This epigenetic modification plays a crucial role in regulating gene expression and is engaged in a variety of cellular events, varying significantly across different species, tissues, and the lifespan. DNA methylation levels per site are usually reported quantitatively as beta values that represent the methylation proportion at a specific CpG site in the range from 0 to 1, where 0 indicates no methylation, and 1 indicates complete methylation across all the cells in the sample (Fig. 1).

Importantly, despite the numerous recent publications of various aging clocks [4, 10, 21], including the ones built on DNA methylation, no systematic open access benchmark, which would include standardized panel of datasets, diseases, interventions, or other conditions, has been proposed to date to validate the aforementioned properties. In this paper, we introduce such a benchmark to validate the 1st and the 2nd properties in epigenetic aging clocks. To do this, we developed a methodology for identifying aging-accelerating conditions, which relies on simple, yet strict and evidence-based principles for defining and selecting a panel of aging-accelerating conditions. We collected an unprecedented number of DNA methylation datasets for the respective conditions from dozens of published studies. We also developed a cumulative benchmarking score that aggregates two error-based tasks and two simple, but informative tasks based on common statistical tests. Ultimately, this cumulative score enables comparing aging clock ability to satisfy the 1st and the 2nd properties.

To demonstrate our methodology in a clinically relevant scenario, we specifically focused on the blood-, saliva-, and buccal-based epigenetic biomarkers obtained via a microarray-based technology. Such biomarkers are widespread in clinical testing and aging clock construction [10, 24]. We then examined 13 published epigenetic clocks and provided their benchmarking results.

2 Related work and Background

2.1 Aging clock construction methodology

Because the BA ground truth values cannot be measured, and, therefore, a direct validation of aging clocks is problematic, previous studies introduced various approaches to construct aging clocks with different underlying assumptions. The most widespread one, belonging to the so-called "first-generation aging clocks", uses an assumption that a model f can be trained to predict chronological age, *i.e.*, $C = \hat{C} + \varepsilon = f(X) + \varepsilon$, and its predictions will correspond to BA: $B = \hat{C}$. The simplicity of this approach has made it attractive for decades, and it is still used today to train new aging clocks on new types of data [25–29]. In fact, BA obtained by this approach can satisfy the 2nd [8] and the 3rd [30] properties from our definition. However, using this assumption in Eq. (1) leads us to the conclusion that $\varepsilon = -\Delta$. It then turns out that the perfect solution of the chronological age prediction problem, *i.e.*, minimizing the prediction error so that $\varepsilon \to 0$, leads to the inability of a clock to identify any aging acceleration or deceleration. Namely, it implies that $\Delta \to -0$, which is also known as *the biomarkers paradox* [7, 31]. Supporting this concept, it has been shown that the clocks featuring strong correlation with the chronological age poorly correlate with the population mortality [32] (hence they fail to satisfy the 3rd property). As a consequence, validating clock performance in terms of accuracy of chronological age prediction becomes meaningless, because high accuracy may not necessarily correspond to a biologically relevant clock. Despite the obvious methodological challenges of this approach, it is worth noting that the vast majority of aging clocks belong to the first generation [6].

Seeking for a better solution, researchers experimented with survival models, which led to the development of "second-generation aging clocks". In this approach, models are trained to predict time to death [16, 17, 33], and the resulting prediction is rescaled to age units to represent BA, therefore addressing the 3rd and the 4th properties of a "good" BA estimator. However, there is no open large-scale DNA methylation data containing time-to-death or multi-morbidity measurements, with existing studies being either available upon an authorized request or being held completely private (see Appendix A.6).

2.2 Attempts to compare epigenetic aging clocks

Despite reported attempts to compare the performance of different aging clocks, a benchmark with a standardized panel of datasets, diseases, interventions, or other conditions has not been proposed yet. As a result, different comparative studies employ widely varying validation data and approaches

[1, 19, 30, 34–40]. As highlighted in a recent review on biomarker validation by Moqri *et al.*, "*for a reliable comparison across studies, <... > biomarker formulations should be established 'a priori' and not be further modified during validation"* [1]. In the same line of thought, we propose to define a standardized and a justified procedure for clock benchmarking *before* constructing any predictive model.

Two approaches we propose as essential tasks in our benchmark entail related prior art. For example, Porter *et al.* [41] and Mei *et al.* [34] used one-sample or two-sample aging acceleration tests for clock validation. Ying *et al.* [19] employed two-sample tests across multiple aging clocks. These authors implicitly tested the 2nd property of "good" aging clocks discussed above. Likewise, there were also attempts to test the 3rd and the 4th properties separately. In works [30, 35, 40], the authors calculated hazard coefficients with statistical significance to test if BA estimates of selected clocks are capable of predicting all-cause mortality or the onset of age-related diseases [36, 37] (*e.g.*, cardiovascular events). However, these studies are either small-scale [19], missing standardized datasets and comparing only a small number of models [34, 41], or limited to predicting the chronological age [38].

3 Methods

An infographic overview of the proposed benchmarking of aging clocks is shown in Fig. 2.

3.1 Criteria for selecting aging-accelerating conditions

In the context of clock benchmarking, we propose to define an aging-accelerating condition (AAC) as a biological condition that satisfies the following three criteria (Fig. 2B). First, having an AAC must lead to decreased life expectancy (LE) compared to the general population, even when treated with existing therapies. Second, an AAC must be chronic (to safely assume that it has sufficient time to drive observable changes in DNAm). And third, an AAC must manifest itself systemically, so that it can be expected to affect DNAm in blood, saliva, and buccal cells (hereafter referred to as BSB).

Importantly, the decrease in LE and the corresponding increase in mortality must result mainly from intrinsic organismal causes rather than from socioeconomic factors and self-destructive behaviors related to a given condition. The second criterion is aimed at excluding short-term conditions such as acute infectious diseases, stressful events, and other confounding DNAm-alternating accidents, whose effects might not induce significant changes in DNAm data obtained from BSB, or, on the contrary, might last too briefly to be reliably detected. The third part of the AAC definition precludes us from considering events with long-lasting and life-threatening consequences that might be difficult to observe in BSB-derived data. For instance, a bone fracture (unless it is a critical bone marrow reserve) or some types of malignancies.

Conversely, an aging-decelerating condition (ADC) is defined as a condition that increases LE, compared to the general population, and features the same second and third criteria as an AAC. With human data, however, the ADCs are difficult to determine, as the human lifespan-increasing interventions are yet to emerge. To avoid ambiguous interpretation, we omitted such conditions in our benchmarking of human aging clocks (see Appendix A.4 and Table A1 for more details).

3.2 Criteria for dataset selection

Aiming to provide a comprehensive, easily accessible, and clinically relevant toolbox for the ongoing research on human epigenetic clocks, we relied on the following five criteria while performing the datasets aggregation (Fig. 2C). *First*, all datasets in the benchmark must feature *open access to pre-processed data*, without any data access requests or raw data processing required. *Second*, we only used data obtained from the BSB samples. *Third*, chronological ages must be annotated with, at most, one year intervals (*e.g.*, without age binning by decades), including only samples from the age range of 18–90 years[3]. The only exception to this requirement are the individuals with certain *progeroid* conditions, such as the Hutchinson-Gilford progeria syndrome, who survive approximately 12 to 13 years on average [42]. These conditions resemble premature aging so strikingly that we included patients aged under 18 years into the benchmark. *Fourth*, we employ data obtained only with the Illumina Infinium BeadChip (27K, 450K, and 850K) methylation microarrays, as they remain

[3]Reporting increased or decreased biological age for people outside of this range is debatable.

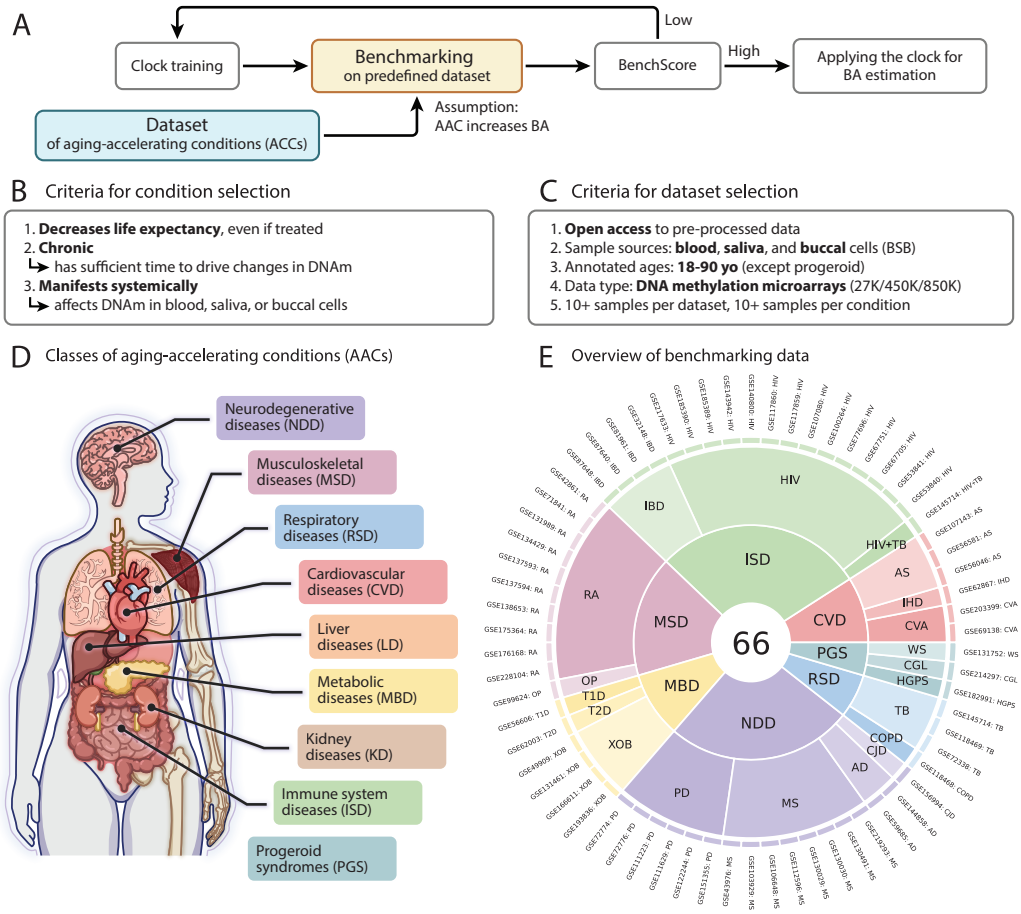


Figure 2: ComputAgeBench methodology. A) The proposed pipeline for constructing aging clocks features an important step of validating the model on pre-defined aging-acceleration conditions that satisfy criteria (B) and are collected into datasets that meet criteria (C) for individual study design. D) Major classes that include putative aging-accelerating conditions. E) Aggregated dataset panel for benchmarking aging clocks, comprising 66 unique data sources (labeled by their Gene Expression Omnibus dataset identification numbers and conditions) from more than 50 studies. See Table A1 for the full names and Table A2 for the population-based evidence for including each condition.

to be the most popular technologies for human DNAm profiling and clock construction. *Fifth*, we applied thresholds of at least 10 samples per dataset, 5 samples with an AAC per dataset, and 10 samples with an AAC across all datasets to attain sufficient statistical power.

3.3 Collecting AAC datasets for benchmarking

To cover as many organismal systems affected by age-related conditions as possible, we split the aggregated data into nine broad categories (Fig. 2D): cardiovascular diseases (CVD), immune system diseases (ISD), kidney diseases (KDD), liver diseases (LVD), metabolic diseases (MBD), musculoskeletal diseases (MSD), neurodegenerative diseases (NDD), respiratory diseases (RSD), and progeroid syndromes (PGS). In each class, we identified several AACs relying on the established lists of age-related diseases and on the leading causes of death [34, 43, 44], including closely associated conditions and other conditions mentioned in a variety of epigenetic clock studies [8, 16, 19, 34, 45]. The corresponding AACs with their abbreviations and population-based evidence for their inclusion are provided in Appendix (Tables A1 and A2, respectively).

Dataset search was performed using the NCBI Gene Expression Omnibus (GEO) database, an *omics* data repository with unrestricted access (`https://www.ncbi.nlm.nih.gov/geo/`). We applied filters to include the *Homo sapiens* species and all methylation-related studies: methylation profiling

by array, methylation profiling by genome tiling array, and methylation profiling by high throughput sequencing (methylation microarray data can be found in any of these studies).

Upon performing the dataset search, only a portion of AACs from seven condition classes were retained (see Appendix and Table A2). All five dataset selection criteria were met by none of the found kidney- and liver-related AAC datasets. The resulting list of 66 datasets [46–95] comprises 65 blood studies and 1 saliva study, and is visualized in Fig. 2E. Age distributions for each condition are shown in Fig. A1. Descriptive statistics for all datasets are provided in Fig. A2.

3.4 Epigenetic age predictors

Any blood-based epigenetic aging clock that predicts BA in age units (or can be re-scaled to them) can be validated in our benchmark. We tested 13 publicly available epigenetic clock models trained on adult human data to evaluate sample age (Table A3), with the model coefficients retrieved from the corresponding studies. Among the collected first-generation clocks, 6 were trained purely on blood samples [15, 19, 96, 97], and 3 models were trained on multiple tissues [8, 32, 45]. Among the second-generation clocks, all were blood-based, and 2 models relied entirely on CpG sites as predictive features [16, 98], while the other 2 required additional information about gender and chronological age as inputs [17, 99]. Because the extracted datasets contained missing values, we imputed them with the "gold standard" beta values averaged for each CpG site retrieving them from the R "SeSAMe" package [100]. We also ensured that no data in the benchmark was used to train any of the selected clocks. The clock models evaluated by us are described in Table A3.

3.5 Benchmarking tasks for evaluating aging clocks

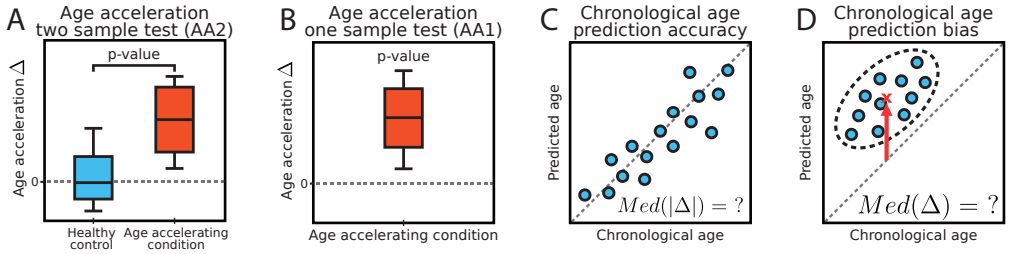
To benchmark aging clock models, we propose four tasks: relative aging acceleration prediction (Fig. 3A), absolute aging acceleration prediction (Fig. 3B), chronological age prediction accuracy (Fig. 3C), and systematic chronological age prediction bias (Fig. 3D). In the first two tasks, the clocks are tested if they can correctly predict aging acceleration in the predefined panel of AAC datasets.

In the relative aging acceleration prediction task (AA2 task), we test aging clock ability to distinguish AAC from healthy control (HC) samples in a dataset containing both sample groups. After predicting ages in each dataset corresponding to this task using various clock models, we apply a two-sample Welch's test per dataset and calculate a one-sided P-value (*i.e.*, $H_A : \Delta_{AAC} > \Delta_{HC}$) to determine if average aging acceleration in the AAC cohort is significantly greater than that in the HC cohort (Fig. 3A). Next, we apply the Benjamini-Hochberg correction procedure for controlling the false discovery rate (FDR) of predictions across all datasets, with an adjusted P-value less than 0.05 considered indicative of statistical significance. We selected a parametric test due to the assumption of normal distribution of Δ, a fundamental trait of the multivariate linear regression models commonly used in aging clock construction.

In the absolute aging acceleration prediction task (AA1 task), we test clock ability to correctly predict positive aging acceleration for an AAC in the absence of the HC cohort. For each dataset in this task, we predict ages using various clock models, apply a one-sample Student's t-test and calculate a one-sided P-value (*i.e.*, $H_A : \Delta_{AAC} > 0$) to determine if median aging acceleration in the AAC cohort is significantly greater than zero (Fig. 3B). As before, we apply the Benjamini-Hochberg correction procedure for controlling FDR with the same adjusted P-value threshold.

Clearly, the first task provides a more rigorous way to test aging clocks, because it helps to control potential covariate shifts, but the second task deserves its place in the list, as it allows including more data into the panel to overcome data scarcity. The third task is aimed at distinguishing good predictors of chronological age from predictors of biological age. Due to the paradox of biomarkers mentioned above, it is highly unlikely that the same model could combine both these properties. Yet, the good predictors of chronological age are believed to be useful in forensics [101] or data labeling, where the chronological age information is lacking. We chose median absolute aging acceleration ($Med(|\Delta|)$), a full equivalent of median absolute error, for testing clock performance. We calculate it across HC samples from the whole dataset panel and report it as a single number expressed in years.

The goal of the fourth task is to control for systemic bias in clock predictions. Because a clock is trained on healthy controls, we expect age deviation of HC samples to be zero on average (*i.e.*, $E(\Delta_{HC}) = 0$). In practice, however, due to the presence of a covariate shift between the training



E Age acceleration two sample test (AA2) results

Model	CVD	ISD	MBD	MSD	NDD	PGS	RSD	Total
PhenoAgeV2	0/3	7/10	0/4	3/6	6/12	1/3	3/4	20/42
GrimAgeV2	0/3	7/10	0/4	1/6	2/12	2/3	2/4	14/42
GrimAgeV1	0/3	7/10	0/4	1/6	2/12	2/3	2/4	14/42
PhenoAgeV1	0/3	5/10	0/4	2/6	0/12	1/3	1/4	9/42
YingCausAge	0/3	4/10	0/4	0/6	1/12	1/3	0/4	6/42
YingAdaptAge	0/3	3/10	0/4	0/6	1/12	1/3	0/4	5/42
Lin	0/3	4/10	0/4	0/6	0/12	0/3	1/4	5/42
HorvathV2	0/3	4/10	0/4	0/6	0/12	1/3	0/4	5/42
HorvathV1	0/3	3/10	0/4	0/6	0/12	0/3	0/4	3/42
Zhang19_EN	0/3	1/10	0/4	0/6	0/12	1/3	0/4	2/42
Hannum	0/3	1/10	0/4	0/6	0/12	0/3	0/4	1/42
VidalBralo	0/3	0/10	0/4	0/6	0/12	0/3	0/4	0/42
YingDamAge	0/3	0/10	0/4	0/6	0/12	0/3	0/4	0/42

F Age acceleration one sample test (AA1) results

Model	CVD	ISD	MBD	MSD	NDD	Total
GrimAgeV2	3/3	9/9	2/2	2/5	4/5	20/24
Zhang19_EN	0/3	9/9	1/2	5/5	4/5	19/24
Hannum	1/3	9/9	2/2	2/5	3/5	17/24
GrimAgeV1	1/3	9/9	2/2	2/5	1/5	15/24
VidalBralo	1/3	9/9	1/2	1/5	1/5	13/24
HorvathV2	0/3	9/9	0/2	0/5	3/5	12/24
HorvathV1	0/3	7/9	1/2	2/5	2/5	12/24
YingAdaptAge	1/3	4/9	1/2	2/5	3/5	11/24
Lin	0/3	8/9	0/2	0/5	1/5	9/24
PhenoAgeV2	0/3	5/9	1/2	2/5	1/5	9/24
PhenoAgeV1	0/3	6/9	0/2	0/5	1/5	7/24
YingDamAge	0/3	5/9	1/2	0/5	0/5	6/24
YingCausAge	0/3	2/9	0/2	0/5	0/5	2/24

Figure 3: ComputAgeBench tasks and performance of aging clock models. A-D) The four benchmarking tasks. E) AA2 task results split into columns by condition class, where scores demonstrate the number of datasets per class, where a given clock model detected significant difference between the HC and AAC cohorts. F) AA1 task results: same as (E), but the statistics are calculated for datasets containing the AAC cohort alone.

and testing data, a clock might produce biased predictions, resulting in a systemic bias and adding or subtracting extra years to a healthy individual coming from an external dataset. As a benchmarking metric for this task, we calculated median aging acceleration ($Med(\Delta)$) across HC samples from the entire dataset panel.

3.6 Cumulative benchmarking score

We define cumulative benchmarking score such that it would account for the main drawback of AA1 task, namely, the sensitivity to positive model bias. Let S_{AA2} denote total score of a model in AA2 task and S_{AA1} from the AA1 task (both S_{AA2} and S_{AA1} represent the number of datasets evaluated correctly by a model in the respective task), then the cumulative benchmarking score is:

$$BenchScore = S_{AA2} + S_{AA1} \cdot \left(1 - \frac{\max(0, Med(\Delta))}{Med(|\Delta|)}\right). \quad (2)$$

Consequently, if a model is positively biased, its performance in the AA1 task will be penalized by the bracketed coefficient by the S_{AA1}, the largest when the model bias $Med(\Delta)$ is zero. Because $Med(\Delta) \leq Med(|\Delta|)$, this coefficient is limited to the $[0, 1]$ interval.

4 Results

The most rigorous of the four, AA2 task demonstrates that second-generation aging clocks (PhenoAgeV2 [98], GrimAgeV1 [17], GrimAgeV2 [99], and PhenoAgeV1 [16]) appear on top, particularly at predicting aging acceleration for the ISD class (Fig. 3E, Supplementary Materials Fig. A5). Nevertheless, all clocks failed to detect aging acceleration in patients with cardiovascular and metabolic diseases, at least at the statistically significant level (see Figs. A3 and A4 for results without FDR correction). Modest scores (<50% datasets in total) on the AA2 task across all models are expected, as no clocks had specifically been calibrated to pass this benchmarking task.

Table 1: Benchmarking results.

Model name	AA2 score	AA1 score	$Med(\|\Delta\|)$, years	$Med(\Delta)$, years	$BenchScore$
PhenoAgeV2	**20**	9	7.6 ±0.1	-2.6 ±0.1	**29.0**
GrimAgeV1	14	15	7.5 ±0.1	5.7 ±0.1	17.4
PhenoAgeV1	9	7	8.0 ±0.1	-4.2 ±0.2	16.0
GrimAgeV2	14	20	9.8 ±0.1	9.3 ±0.1	15.1
HorvathV1	3	12	5.4 ±0.1	-0.1 ±0.1	15.0
HorvathV2	5	12	**4.1 ±0.1**	1.1 ±0.1	13.9
VidalBralo	0	13	9.1 ±0.1	0.1 ±0.2	12.8
Lin	5	9	7.5 ±0.1	2.1 ±0.2	11.4
YingAdaptAge	5	11	20.0 ±0.2	12.5 ±0.5	9.1
YingCausAge	6	2	9.0 ±0.1	1.3 ±0.2	7.7
YingDamAge	0	6	19.5 ±0.3	-14.5 ±0.5	6.0
Zhang19_EN	2	19	10.5 ±0.2	9.6 ±0.2	3.7
Hannum	1	17	7.5 ±0.1	6.3 ±0.1	3.7

In contrast, the first-generation aging clocks by Zhang *et al.* [32] and Hannum *et al.* [15] populated the top of the AA1 leaderboard, in addition to the GrimAge, exhibiting good scores across multiple condition classes (Fig. 3F, Supplementary Materials Fig. A6). Notably, combining the results of this task with the model bias task exposes the potential source of the exceptional "robustness" in predicting accelerated aging in datasets without healthy controls.

The task of chronological age prediction accuracy reveals two undeniable leaders: Horvathv2 [45] and Horvathv1 [8] clocks (Table 1), specifically tuned for this task on large multi-tissue datasets. Notably, clocks predicting chronological age with $Med(|\Delta|) \geq 18$ years would be inferior to a constant model yielding a 50 y.o. prediction (average age across all HC samples in the benchmark). Unless scaled, such clocks can hardly be used for inferring accelerated aging.

Finally, to prove the validity of AA1 performance, a clock should also pass the task for being unbiased. We show that the AA1 leader, GrimAgeV2 clock [99], is also characterized by a large prediction bias for the HC samples (Table 1), warning us against considering its AA1 task score reliable. On the other hand, the top-2 unbiased Horvathv1 clock [8] and VidalBralo clock [97] have low prediction bias, rendering their AA1 performance as more trustworthy.

To account for the discrepancies of AA1 task interpretation regarding the prediction bias, we devised *cumulative benchmarking score* (Table 1) which penalizes AA1 score by the magnitude of prediction bias (see Eq. 2). With such a metric, a second-generation aging clock PhenoAgeV2 [98] becomes the most robust model in terms of distinguishing individuals with aging-accelerating conditions from the healthy cohort. This model is a leader according to the cumulative benchmarking score and the AA2 task score. Closely behind it, are the other second-generation clocks: GrimAgeV1 [17], PhenoAgeV1 [16], and GrimAgeV2 [99]. On the other hand, our results indicate that even classic first-generation aging clocks, such as HorvathV1 [8] and HorvathV2 [45], can perform quite reliably in predicting biological age, at least for some condition classes. It is noteworthy that in both AA1 and AA2 tasks, many aging clocks perform well in detecting accelerated aging caused by immune system diseases, which are mostly represented by human immunodeficiency virus (HIV) infection in our dataset, while the other disease classes are only captured by *some* clocks, allegedly indicating that they were implicitly and unintentionally trained for certain subset of diseases. These results generalize previous findings [34] and show that comprehensive benchmarking of aging clocks can resolve the controversy regarding their robustness and utility.

5 Discussion

Biological age is an elusive concept that cannot be measured and validated directly, which necessitates careful choice of model assumptions to avoid methodological errors and false discoveries while estimating it. While maintaining some degree of correlation between predicted and chronological age is desirable, the biomarkers paradox [7] precludes one from automatically accepting a BA estimation

as acceptable (via the classic performance metrics of chronological age prediction accuracy). From a methodological perspective, training BA predictors to estimate time to death or a disease onset remains the most rigorous approach to aging clock validation, as these events can be measured directly. However, obtaining such data is challenging due to various ethical and financial constraints. At present, no open access data of DNA methylation with mortality labels are available for public clock benchmarking (see Appendix A.6).

While mortality data remain unavailable, we propose to validate clocks by their ability to demonstrate BA acceleration *in a fixed pre-determined panel of datasets* for established aging-accelerating diseases or predict decelerated aging in the datasets of lifespan-prolonging interventions. For that, we developed our benchmark, where each aging clock could be tested across 4 distinct tasks. We gathered an unprecedented number of DNA methylation datasets from more than 50 studies, covering 19 putative aging-accelerating conditions. Notably, no aging-decelerating conditions have been confirmed for the benchmark study (see Appendix A.4). It should be taken into account that *in vitro* cell reprogramming cannot serve as validation data for the deceleration effect, because, as we have previously shown [102], such data are essentially out-of-domain with regard to blood DNA methylation across aging.

To showcase our benchmark, we tested 13 different published models and revealed that the second-generation aging clocks, namely, PhenoAge [16], GrimAge [17], and their upgraded variants [98, 99], were the most successful, according to the cumulative benchmarking score. As these clocks had initially been designed to predict all-cause mortality, they were expected to be robust in distinguishing aging-accelerating conditions. Yet, our findings reinforce the growing trends in training BA predictors based on mortality rather than chronological age [1, 4].

As blood DNA methylation generally comes from the immune cells, which would be directly affected by the HIV, it is not surprising that the majority of clocks managed to discern accelerated aging in the immune system-related conditions (featured predominantly by the HIV infection in our dataset). This result supports the notion that the blood-based clocks might be implicitly attuned to such conditions, while only a few clocks are capable of successfully capturing accelerated aging in the other disease classes.

Remarkably, some datasets were evaluated incorrectly *by all models*, which may have several possible explanations apart from the poor clock performance. First, a strong covariate shift between these data and the training data might impede model performance on some datasets. Second, some selected conditions might not induce accelerated aging in blood, either by itself or by the design of the original study (see Limitations in Appendix A.1). Third, the multidimensionality of aging as a biological phenomenon might not allow for correct prediction of all aging-accelerating conditions by such univariate measures as the blood-based epigenetic clocks. In favor of this notion, it has recently been shown that different organ systems have different aging trajectories [103, 104], suggesting several directions for the future research, outlined in Appendix A.2.

6 Conclusion

In this work, we developed the first systematic benchmark for evaluating blood-based epigenetic aging clocks. We believe it will help longevity researchers and data scientists to better gauge the power of existing biomarkers of aging, quantitatively assessing their role, limitations, and reliability. We anticipate that, as a result of such computational paradigm, rapid and reliable clinical trials of lifespan-extending therapies will become an attainable reality in a not-so-distant future.

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A Appendix

A.1 Limitations

The current version of our benchmark harbors several important limitations. First, some selected conditions might not actually fulfill the suggested criteria, especially regarding their effect on blood DNA methylation, although we did our best to identify the most unambiguous ones. From the other hand, some conditions that fit our criteria might have escaped our attention. Second, the conditions are not represented uniformly, with some being featured in 10+ datasets (HIV, rheumatoid arthritis), and some present in a single dataset with few samples (ischemic heart disease, chronic obstructive pulmonary disease, congenital generalized lipodystrophy). The third limitation arises from the known issue of hidden subgroups of patients and mislabeled instances [1]. For the AAC cohorts, having hidden co-morbidities is acceptable, as they would supposedly exaggerate aging acceleration even stronger. Conversely, having severe, but unlabeled diseases in the HC cohort would likely substantially alter the findings of our benchmark. Unfortunately, we can neither expand our dataset to cover all conditions equally, nor explicitly confirm if all studies at hand comply with our requirements.

A.2 Future work

We plan to further extend our benchmarking dataset by incorporating open access data of additional modalities, such as clinical biochemistry, transcriptomics, proteomics, metabolomics, etc. To overcome the aforementioned limitations, we strongly urge an open discussion on developing a panel of conditions and datasets that would serve as the gold standard for reliable and comprehensive validation of emerging biomarkers of aging. We also believe that it is important to expand the benchmark to animal models, since collecting the required data and developing preclinical biomarkers of aging in some animals is associated with fewer ethical and financial challenges. Hopefully, all these issues and developments will be addressed by the efforts of a recently established Biomarkers of Aging Consortium (`https://www.agingconsortium.org/`). Ultimately, the "correct" BA estimator should satisfy all four properties we defined in the Introduction. Regardless of the clock generation or data modality, reliable aging clock models must also be able to assess the uncertainty of their own predictions before being integrated in clinical trials [2, 3]. And indeed, an example of uncertainty-aware aging clocks has recently been proposed [4].

A.3 Societal impact

The obvious positive societal impact of our work is the prospect of increased active lifespan and that of healthy longevity. Our benchmarking methodology assists in determining the most accurate predictors of the biological age, which, in turn, assists in delineating the crucial biomarkers and factors that might prolong the healthy life. The potential negative impact entails the common issues emphasized when a fundamental biological problem is tackled with the AI tools. Specific to the subject of longevity are the issues of pre-mature excitement in the mass media when a certain factor is hypothesized to prolong life. A relevant fraud in the pharmaceutical industry is also plausible, if not regulated. One could also envision the depletion of resources caused by an overpopulation of the Earth, which might happen if the longevity drug is found. These negative possibilities are not expected to be sudden and could be mitigated gradually – similarly to a plethora of other benchmarking works established for solving important biological problems.

A.4 Motivation behind including or excluding particular conditions

Our first criterion for selecting aging-accelerating conditions (AACs) was that having an AAC must lead to decreased life expectancy (LE) compared to the general population, even when treated with existing therapies. As we have mentioned earlier, this decrease in LE and the corresponding increase in mortality must result mainly from intrinsic organismal causes rather than from socioeconomic factors and self-destructive behaviors related to a given condition. Thus, while Down syndrome (DS) is associated with elevated prevalence of multiple chronic diseases [5–7], LE of DS individuals has grown dramatically by over 450% from 1960 to 2007 [8], even though no cure for DS has been developed, suggesting strong non-biological confounding factors at play. Additionally, while some authors expect DS to display accelerated epigenetic aging [9], others anticipate deceleration

when applying epigenetic clocks to DS blood samples, as DS individuals are hypothesized to feature juvenile blood [10]. Schizophrenia (SZ) is another example of a controversial condition: while we can find increased incidence of age-related comorbidities such as cardiovascular diseases, cancers, or chronic obstructive pulmonary disease [11–13], the rates of suicide and substance-induced death are also increased in people with SZ [11]. We therefore suggest excluding such ambiguous conditions from robust clock benchmarking, as it is currently difficult to disentangle functional organismal deterioration from external and behavioral condition-related confounders and evaluate the degree to which the latter influence LE.

Regarding cancers in general, it is difficult to formulate a pre-hoc hypothesis about the directionality of epigenetic age changes. Even though we know that DNAm can be used to create signatures of various cancers, and that changes in some DNAm sites are shared between aging and cancers [14], we cannot be certain that an aging clock would indicate accelerated aging in cancerous samples, as some cancer-specific and stem cell-like features such as telomere maintenance might prompt a clock model to treat it as a marker of partial rejuvenation. In support of these considerations, epigenetic age predictions were found to exhibit no correlation with multiple TCGA cancer types [15]. To avoid possible speculation as far as possible, we recommend excluding cancer from clock benchmarking, as it is difficult to hypothesize about clock performance in such complex phenomena.

Aging-decelerating condition (ADC) is defined as a condition that increases LE compared to the general population and features the same second and third criteria as an AAC. With respect to human data, however, the ADCs are difficult to determine, as human lifespan-increasing interventions are yet to emerge. There are genetic mutations, such as Laron syndrome (growth hormone insensitivity) or isolated growth hormone deficiency (growth hormone releasing hormone insensitivity), that appear to protect against some age-related pathologies, but they do not feature a prolonged lifespan [16]. To avoid dubious interpretation, we recommend omitting the inclusion of any condition into the ADC category when benchmarking human aging clocks.

The resulting list of condition classes and conditions selected to represent accelerated aging is listed in Table A1. Population-based evidence for condition inclusion and the number of datasets found and selected per condition are displayed in Table A2

A.5 On data types used for aging clocks construction

Multiple data modalities were previously used for aging clocks construction. Some examples beyond DNA methylation data include also clinical blood samples [119], psycho-social questionnaires [120], facial images [121], urine metabolites [122], and different omics data, gene expression [123], DNA accessibility [124], plasma proteins [125], etc. Interestingly, DNA methylation data allow one the most accurate prediction of chronological age compared to other data modalities, second only to facial imaging data [126], and it continues to be used most widely in aging clock construction [127]. It is also important to note that from a practical point of view, in order to construct a clinically relevant aging clock, the method of obtaining the data should not be too invasive and heavy-handed. For this reason, many clock developers prefer using blood, saliva, or buccal epithelial samples as data sources.

A.6 On accessibility of existing epigenetic mortality data

Although there are some existing biobanks that aggregate sensitive human data and provide them in an open-access manner, (e.g., NHANES: `https://wwwn.cdc.gov/nchs/nhanes/`), most biobanks rely on authorized access to their data (e.g., UK Biobank: `https://www.ukbiobank.ac.uk/`). The similar semi-open situation occurs with DNA methylation data. Here, we provide information about 12 cohort studies containing DNA methylation data and mortality/morbidity information simultaneously, but all of which allow downloading their data upon a reasonable request by contacting with the principal investigators of each cohort or by requesting data on a special platform. These studies include the Framingham Heart Study (FHS), the Women's Health Initiative (WHI), the Lothian Birth Cohorts (LBC), the Atherosclerosis Risk in Communities (ARIC), the Cardiovascular Health Study (CHS), the Normative Aging Study (NAS), the Invecchiare in Chianti (InCHIANTi), the Cooperative Health Research in the Region of Augsburg (KORA), the Epidemiologische Studie zu Chancen der Verhütung, Früherkennung und optimierten Therapie chronischer Erkrankungen in der älteren Bevölkerung (ESTHER), the Danish Twin Register sample (DTR), the Rotterdam Study (RS), and the Coronary Artery Risk Development in Young Adults (CARDIA) [128, 129]. While we

Table A1: Aging-accelerating conditions. ICD-10: class or condition code(s) from the International Classification of Diseases Version 10; a dash indicates lack of specific code; abbrev.: abbreviation.

Condition class	Class ICD-10	Class abbrev.	Aging-accelerating condition (AAC)	Condition ICD-10	Condition abbrev.
Cardio-vascular diseases	I00-I99	CVD	Atherosclerosis	I70	AS
			Ischemic heart disease	I20-I25	IHD
			Cerebrovascular accident	I60-I63	CVA
			Heart failure	I50	HF
			Myocardial infarction	I21-I22	MCI
Immune system diseases	—	ISD	Inflammatory bowel disease	K50-K51	IBD
			Human immunodeficiency virus infection	B20-B24	HIV
Kidney diseases	N00-N99	KDD	Chronic kidney disease	N18	CKD
Liver diseases	K70-K77	LVD	Nonalcoholic steatohepatitis	K75.81	NASH
			Primary biliary cholangitis	K74.3	PBC
			Primary sclerosing cholangitis	K83.01	PSC
			Cirrhosis	K70.3, K74.3-K74.6	CIR
Metabolic diseases	E00-E90	MBD	Extreme obesity	E66.01, E66.2	XOB
			Type 1 diabetes	E10	T1D
			Type 2 diabetes	E11	T2D
			Metabolic syndrome	E88.810	MBS
Musculo-skeletal diseases	M00-M99	MSD	Sarcopenia	M62.84	SP
			Osteoporosis	M80-M81	OP
			Osteoarthritis	M15-M19	OA
			Rheumatoid arthritis	M05-M06	RA
Neuro-degenerative diseases	G00-G99	NDD	Alzheimer's disease	G30	AD
			Parkinson's disease	G20	PD
			Multiple sclerosis	G35	MS
			Dementia with Lewy bodies	G31.83	DLB
			Creutzfeldt-Jakob disease	A81.0	CJD
Respiratory diseases	J00-J99	RSD	Chronic obstructive pulmonary disease	J44	COPD
			Idiopathic pulmonary fibrosis	J84.112	IPF
			Tuberculosis	A15	TB
Progeroid syndromes	—	PGS	Werner syndrome	E34.8	WS
			Hutchinson-Gilford progeria syndrome	E34.8	HGPS
			Congenital generalized lipodystrophy	E88.1	CGL
			Dyskeratosis congenita	Q82.8	DKC

Table A2: Population-based evidence for condition inclusion, and the number of datasets found and selected for each condition. GEO: Gene Expression Omnibus database.

Class abbreviation	Condition abbreviation	Evidence of decreased life expectancy	Number of items in the GEO query	Number of datasets after filtering
CVD	AS	[17–21]	22	3
	IHD	[22–25]	21	1
	CVA	[22, 26–28]	10	2
	HF	[22, 29, 30]	14	0
	MCI	[22, 31, 32]	19	0
ISD	IBD	[33–39]	30	4
	HIV	[22, 40–43]	44	15
KDD	CKD	[44–46]	6	0
LVD	NASH	[47, 48]	8	0
	PBC	[49, 50]	1	0
	PSC	[51, 52]	2	0
	CIR	[22, 53, 54]	68	0
MBD	XOB	[22, 55–58]	96	4
	T1D	[59–64]	14	1
	T2D	[22, 65–69]	45	1
	MBS	[22, 70–72]	17	0
MSD	SP	[73–75]	2	0
	OP	[76–79]	5	1
	OA	[22, 80–82]	26	0
	RA	[83–86]	37	10
NDD	AD	[22, 87–90]	43	2
	PD	[91–93]	37	6
	MS	[94–96]	29	8
	DLB	[97–99]	5	0
	CJD	[100–102]	1	1
RSD	COPD	[22, 103–105]	14	1
	IPF	[106–109]	14	0
	TB	[22, 110, 111]	13	3
PGS	WS	[112–114]	7	1
	HGPS	[112, 115]	14	1
	CGL	[116, 117]	1	1
	DKC	[118]	2	0
Total number of datasets			**667**	**66**

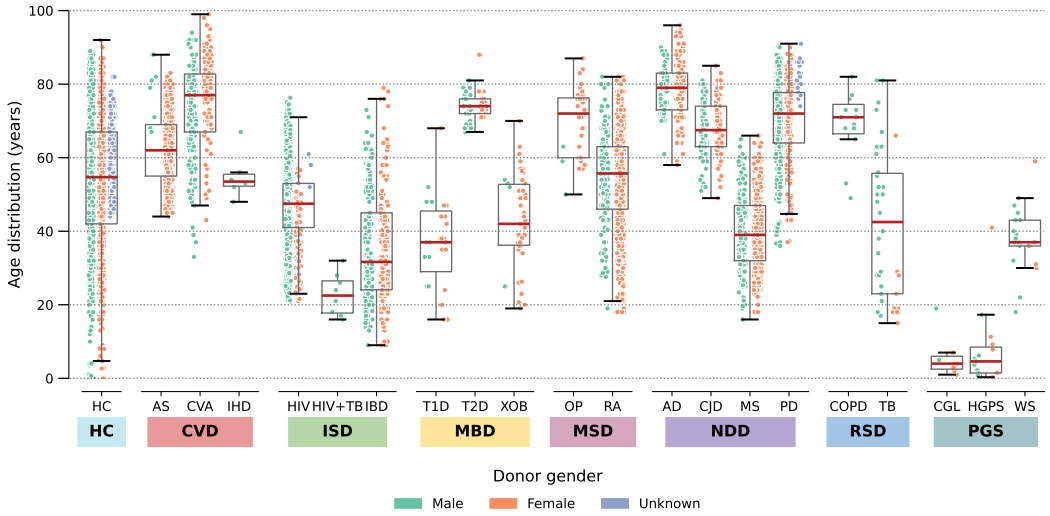


Figure A1: Distribution of dataset samples per condition across ages.

recognize the risks associated with releasing sensitive patient data into the public domain, we also want to emphasize that comprehensive independent validation of the aging clock is difficult without this important datasets. The confidentiality of this data also does not allow us to use it as part of this open-access benchmark. Instead, we focused on epigenetic data from patients with AACs distributed across human lifespan, which did not contain information on mortality, but was publicly accessible.

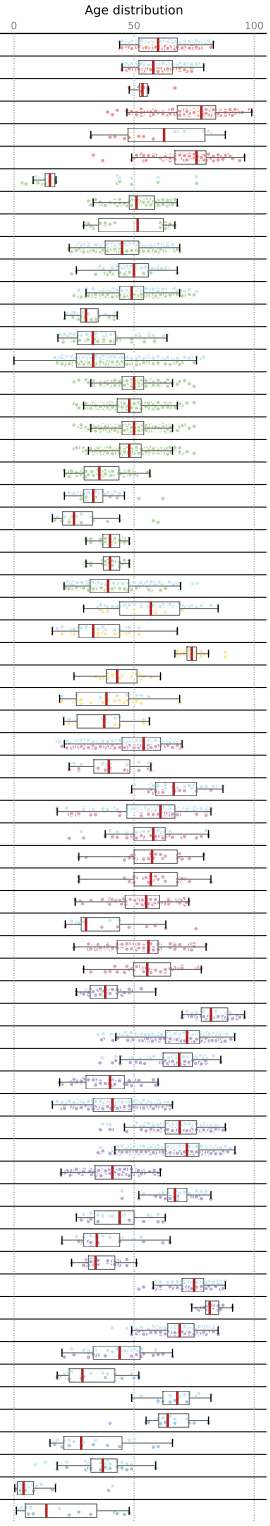
A.7 DNA methylation data collection

As we have mentioned in the Methodology section, dataset search was performed using the NCBI Gene Expression Omnibus (GEO) database, an unrestricted-access omics data repository (`https://www.ncbi.nlm.nih.gov/geo/`) which shares data using the Open Database License (ODbL). The resulting list of 66 AAC datasets [130–179] indicated in Table A2 is visualized in Fig. 2E and includes: atherosclerosis (AS), ischemic heart disease (IHD, also known as coronary heart disease), cerebrovascular accident (CVA, also known as stroke), inflammatory bowel disease (IBD, including Crohn's disease and ulcerative colitis), human immunodeficiency virus infection (HIV), extreme obesity (XOB, defined by having BMI $\geq$ 40 kg/m2 [180, 181]; also known as class III obesity, severe obesity, or morbid obesity), type 1 diabetes mellitus (T1D), type 2 diabetes mellitus (T2D), rheumatoid arthritis (RA), osteoporosis (OP), Alzheimer's disease (AD), Parkinson's disease (PD), multiple sclerosis (MS), Creutzfeldt-Jakob disease (CJD), chronic obstructive pulmonary disease (COPD), tuberculosis (TB), Werner syndrome (WS, including atypical Werner syndrome), Hutchinson-Gilford progeria syndrome (HGPS, including non-classical progeroid laminopathies), and congenital generalized lipodystrophy (CGL, also known as Berardinelli-Seip lipodystrophy). Age distribution across conditions is demonstrated in Fig. A1. An overview of all datasets and their age distributions is provided in Fig. A2. The information on how patient consent was obtained and which ethics procedures were implemented can be accessed in the respective publications. As per NCBI GEO guidelines, all submitters must "ensure that the submitted information does not compromise participant privacy" (`https://www.ncbi.nlm.nih.gov/geo/info/faq.html`).

A.8 DNA methylation data processing

After pre-processing raw output from microarrays or sequencing machines, DNA methylation levels per site are reported quantitatively either as beta values, or as M values. Briefly, beta values represent the ratio of methylated signal (probe intensity or sequencing read counts) to total signal per site (sum of methylated and unmethylated probe intensities or sequencing read counts), while M value is the log2 ratio of the methylated signal versus an unmethylated signal. A more thorough comparison of the two measures can be found in Du et al., 2010 [182]. In the original datasets deposited on GEO, DNA methylation values were represented either as a beta fraction (ranging from 0 to 1),

Name	Dataset ID	Platform	Tissue	Class	Condition	N samples
Reynolds, 2014	GSE56046	450K	B	CVD	AS	339 / 789
Reynolds, 2014	GSE56581	450K	B	CVD	AS	66 / 133
Nazarenko, 2014	GSE62867	27K	B	CVD	IHD	6
Soriano-Tárraga, 2016	GSE69138	450K	B	CVD	CVA	185
Istas, 2017	GSE107143	450K	B	CVD	AS	8 / 8
Cullell, 2022	GSE203399	450K, 850K	B	CVD	CVA	121
Harris, 2012	GSE32148	450K	B	ISD	IBD	19 / 27
Horvath, 2015a	GSE53840	450K	B	ISD	HIV	111
Horvath, 2015a	GSE53841	450K	B	ISD	HIV	24
Gross, 2016	GSE67705	450K	B	ISD	HIV	91 / 189
Horvath, 2015a	GSE67751	450K	B	ISD	HIV	69 / 23
Zhang, 2016	GSE77696	450K	B	ISD	HIV	117 / 261
Li Yim, 2016	GSE81961	450K	B	ISD	IBD	26 / 15
Ventham, 2016	GSE87640	450K	B	ISD	IBD	84 / 156
Ventham, 2016	GSE87648	450K	B	ISD	IBD	178 / 204
Zhang, 2017	GSE100264	450K	B	ISD	HIV	386
Zhang, 2017	GSE107080	850K	B	ISD	HIV	405
Zhang, 2018	GSE117859	450K	B	ISD	HIV	608
Zhang, 2018	GSE117860	850K	B	ISD	HIV	529
Oriol-Tordera, 2020	GSE140800	450K	B	ISD	HIV	70
	GSE143942	450K	B	ISD	HIV	12 / 42
DiNardo, 2020	GSE145714	850K	B	ISD	HIV+TB	10 / 8
Oriol-Tordera, 2022	GSE185389	450K	B	ISD	HIV	56
Oriol-Tordera, 2022	GSE185390	850K	B	ISD	HIV	30
Esteban-Cantos, 2023	GSE217633	850K	B	ISD	HIV	43 / 368
Day, 2013	GSE49909	27K	B	MBD	XOB	40 / 9
Rakyan, 2011	GSE56606	27K	B	MBD	T1D	63 / 27
Lunnon, 2015	GSE62003	450K	B	MBD	T2D	58
Ramos-Molina, 2019	GSE131461	850K	B	MBD	XOB	20
	GSE166611	450K	B	MBD	XOB	17 / 11
Noronha, 2022	GSE193836	450K	B	MBD	XOB	11 / 10
Liu, 2013	GSE42861	450K	B	MSD	RA	335 / 354
	GSE71841	450K	B	MSD	RA	12 / 12
Fernandez-Rebollo, 2018	GSE99624	450K	B	MSD	OP	16 / 32
Rhead, 2017	GSE131989	450K	B	MSD	RA	123 / 230
Unpublished	GSE134429	850K	B	MSD	RA	17 / 47
Clark, 2020	GSE137593	850K	B	MSD	RA	32
Clark, 2020	GSE137594	850K	B	MSD	RA	31
Tao, 2021	GSE138653	850K	B	MSD	RA	80
de la Calle-Fabregat, 2021	GSE175364	450K, 850K	B	MSD	RA	13 / 8
Julià, 2022	GSE176168	850K	B	MSD	RA	113
Chen, 2023	GSE228104	850K	B	MSD	RA	40
Marabita, 2013	GSE43976	450K	B	NDD	MS	52
Lunnon, 2014	GSE59685	450K	B	NDD	AD	9 / 48
Horvath, 2015b	GSE72774	450K	B	NDD	PD	219 / 289
Horvath, 2015b	GSE72776	450K	B	NDD	PD	38 / 46
Castro, 2019	GSE103929	450K	B	NDD	MS	49
Kular, 2019	GSE106648	450K	B	NDD	MS	139 / 140
Chuang, 2017	GSE111223	450K	S	NDD	PD	134 / 128
Chuang, 2017	GSE111629	450K	B	NDD	PD	237 / 335
Ntranos, 2019	GSE112596	850K	B	NDD	MS	112
	GSE122244	850K	B	NDD	PD	34 / 35
Ewing, 2019	GSE130029	450K	B	NDD	MS	11 / 20
Ewing, 2019	GSE130030	450K	B	NDD	MS	14 / 14
Carlström, 2019	GSE130491	850K	B	NDD	MS	82
Roubroeks, 2020	GSE144858	450K	B	NDD	AD	96 / 93
Go, 2020	GSE151355	450K	B	NDD	PD	20
Dabin, 2020	GSE156994	450K	B	NDD	CJD	105 / 114
Bingen, 2023	GSE219293	850K	B	NDD	MS	18 / 29
Esterhuyse, 2015	GSE72338	450K	B	RSD	TB	20 / 16
Chen, 2021	GSE118468	450K	B	RSD	COPD	6 / 15
Chen, 2020	GSE118469	450K	B	RSD	TB	6 / 12
DiNardo, 2020	GSE145714	850K	B	RSD	TB	10 / 14
Maierhofer, 2019	GSE131752	850K	B	PGS	WS	24 / 21
Bejaoui, 2022	GSE182991	850K	B	PGS	HGPS	12 / 15
Qannan, 2022	GSE214297	850K	B	PGS	CGL	9 / 7



Condition classes included in the benchmarking dataset

HC CVD ISD MBD MSD NDD RSD PGS

Figure A2: Descriptive statistics of datasets included in the benchmark. B: blood, S: saliva. Ages are indicated in years.

Table A3: Aging clock models tested in our benchmark.

Model name	Year	Number of CpGs	Generation	Extra parameters	Tissues used for training	Ref.
Hannum	2013	71	1	—	Blood	[183]
HorvathV1	2013	353	1	—	Multi-tissue	[9]
Lin	2016	99	1	—	Blood	[184]
VidalBralo	2016	8	1	—	Blood	[185]
HorvathV2	2018	391	1	—	Blood, Skin	[186]
PhenoAgeV1	2018	513	2	—	Blood	[187]
Zhang19_EN	2019	514	1	—	Blood, Saliva	[188]
GrimAgeV1	2019	1030	2	Age, Sex	Blood	[189]
GrimAgeV2	2022	1030	2	Age, Sex	Blood	[190]
PhenoAgeV2	2022	959	2	—	Blood	[191]
YingAdaptAge	2024	999	1	—	Blood	[192]
YingCausAge	2024	585	1	—	Blood	[192]
YingDamAge	2024	1089	1	—	Blood	[192]

beta percentages (ranging from 0 to 100), or M-values (can be both negative and positive, equals 0 when beta equals 0.5). We converted all data to the beta-value fractions ranging from 0 to 1. The values outside this range were treated as missing values (NaNs), as they are not biological. In each dataset, only samples that were relevant for benchmarking (that is, were annotated by age, tissue, and condition) were retained.

The resulting datasets meta-data contains the following fields: DatasetID (datasets GEO ID), PlatformID (GEO ID of a DNA methylation profiling platform), Tissue (sample source tissue: "Blood" stands for peripheral blood samples, "Saliva"—for saliva samples, and "Buccal"—for buccal swab samples), CellType (sample cell type: either a specific cell population, e.g., immune cell subtypes with cell type-specific molecular markers, or broader categories such as whole blood, buffy coat, peripheral blood mononuclear cells (PBMC), or peripheral blood leukocytes (PBL); some samples lack this annotation), Gender (abbreviated sample donor gender: M = Male, F = Female, U = Unknown), Age (sample donor chronological age in years; in the original datasets deposited on GEO, it can be either rounded by the researchers to full years, or converted from months, weeks, or days; where available, we calculated years from the smaller units), Condition (one of AACs or HC), and Class.

We did not perform any post-processing, inter-dataset normalization, or batch effect correction, because different clock models are trained on data obtained using various processing approaches, as there is no gold standard approach to DNA methylation microarray processing. Therefore, so as to test all models under common conditions, we employed only processed DNA methylation data.

A.9 Aging clocks included in the benchmarking

The full list of published aging clocks used in this analysis is provided in Table A3.

A.10 Benchmarking results without FDR correction

Figures A3 and A4 demonstrate benchmarking results before applying FDR correction.

A.11 Data and code availability

The entire dataset assembled for this work can be accessed from Hugging Face at `https://huggingface.co/datasets/computage/computage_bench`. The GitHub repository containing code required to reproduce paper results and to benchmark other clock models is published at

Model	CVD	ISD	MBD	MSD	NDD	PGS	RSD	Total
PhenoAgeV2	0/3	7/10	0/4	4/6	6/12	1/3	3/4	21/42
GrimAgeV2	0/3	7/10	0/4	3/6	2/12	2/3	3/4	17/42
GrimAgeV1	0/3	7/10	0/4	3/6	2/12	2/3	2/4	16/42
PhenoAgeV1	0/3	6/10	0/4	2/6	1/12	1/3	1/4	11/42
YingAdaptAge	0/3	6/10	0/4	1/6	1/12	2/3	0/4	10/42
Lin	0/3	7/10	0/4	0/6	1/12	0/3	1/4	9/42
YingCausAge	0/3	4/10	0/4	1/6	1/12	2/3	0/4	8/42
HorvathV2	0/3	4/10	0/4	0/6	2/12	2/3	0/4	8/42
VidalBralo	0/3	5/10	0/4	1/6	0/12	1/3	0/4	7/42
HorvathV1	0/3	5/10	0/4	0/6	0/12	1/3	0/4	6/42
Hannum	0/3	3/10	0/4	1/6	1/12	1/3	0/4	6/42
YingDamAge	0/3	3/10	0/4	0/6	1/12	1/3	0/4	5/42
Zhang19_EN	0/3	2/10	0/4	0/6	0/12	1/3	0/4	3/42

Figure A3: AA2 task results split into columns by condition class **without FDR correction of P-values**. Scores demonstrate the number of datasets per class, in which a given clock model detected significant (at the 0.05 level of significance) difference between the HC and AAC cohorts.

Model	CVD	ISD	MBD	MSD	NDD	Total
GrimAgeV2	3/3	9/9	2/2	2/5	4/5	20/24
Zhang19_EN	0/3	9/9	1/2	5/5	4/5	19/24
Hannum	1/3	9/9	2/2	2/5	4/5	18/24
GrimAgeV1	1/3	9/9	2/2	2/5	2/5	16/24
VidalBralo	1/3	9/9	1/2	1/5	1/5	13/24
HorvathV2	0/3	9/9	0/2	0/5	3/5	12/24
HorvathV1	0/3	7/9	1/2	2/5	2/5	12/24
YingAdaptAge	1/3	4/9	1/2	2/5	3/5	11/24
PhenoAgeV2	0/3	6/9	1/2	2/5	1/5	10/24
Lin	0/3	8/9	0/2	0/5	1/5	9/24
PhenoAgeV1	0/3	6/9	0/2	0/5	1/5	7/24
YingDamAge	0/3	5/9	1/2	0/5	0/5	6/24
YingCausAge	0/3	2/9	0/2	1/5	0/5	3/24

Figure A4: AA1 task results **without FDR correction of P-values**: same as Fig. A3, but the statistics are calculated for datasets containing the AAC cohort only.

https://github.com/ComputationalAgingLab/ComputAge. Benchmark calculations can be reproduced in Google Colab using its free plan computational resources. The corresponding notebook for reproducing the results of the paper is accessible in our GitHub repository.

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