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### AI IN IDENTIFYING AGING MARKERS

**Resume.** As the global population ages, there is a growing need to understand the complex processes associated with aging and to identify reliable markers that can aid in early diagnosis, intervention, and personalized healthcare. This article provides a comprehensive review of the applications of Artificial Intelligence (AI) in identifying aging markers. The integration of AI techniques, such as machine learning and data analytics, has significantly advanced our ability to analyze vast and diverse datasets related to genomics, proteomics, metabolomics, imaging, and clinical records. The review discusses the integration of clinical data, lifestyle factors, and environmental information using AI, providing a holistic understanding of aging markers. The investigation explores the use of AI in predicting an individual's risk of accelerated aging by considering diverse factors.

The integration of AI into the identification of aging markers represents a paradigm shift in aging research. This review underscores the potential of AI in revolutionizing our understanding of aging and paving the way for innovative strategies in age-related disease prevention and management.

**Key words:** Artificial Intelligence, aging biomarkers, machine learning, deep learning.

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### ҚАРТАЮ МАРКЕРЛЕРІН АНЫҚТАУДАҒЫ ЖАСАНДЫ ИНТЕЛЛЕКТ

**Түйін.** Бүкіл әлем халқы қартайған сайын қартаюмен байланысты күрделі процестерді түсіну және ерте диагностикаға, араласуға және жекелендірілген медициналық көмекке көмектесетін сенімді маркерлерді анықтау қажеттілігі артып келеді. Бұл мақалада қартаю маркерлерін анықтауда Жасанды Интеллекттің (AI) қолданылуына жан-жақты шолу берілген. Машиналық оқыту және деректерді талдау сияқты ЖИ әдістерін біріктіру геномика, протеомика, метаболомика, бейнелеу және клиникалық жазбаларға қатысты кең және әртүрлі деректер жиынын талдау қабілетімізді айтарлықтай арттырды. Шолу қартаю маркерлері туралы тұтас түсінік бере отырып, ЖИ пайдалана отырып, клиникалық деректерді, өмір салты факторларын және қоршаған орта туралы ақпаратты біріктіруді талқылайды. Зерттеу әртүрлі факторларды ескере отырып, адамның тез қартаю қаупін болжау үшін ЖИ қолдануды зерттейді.

ЖИ қартаю маркерлерін анықтауға біріктіру қартаюды зерттеудегі парадигманың өзгеруін білдіреді. Бұл шолу ЖИ қартаю туралы түсінігімізді өзгертудегі және жасқа байланысты аурулардың алдын алу мен басқарудың инновациялық стратегияларына жол ашудағы әлеуетін көрсетеді.

**Түйінді сөздер:** Жасанды Интеллект, қартаю биомаркерлері, машиналық оқыту, тереңдетіп оқыту

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### ИСКУССТВЕННЫЙ ИНТЕЛЛЕКТ В ВЫЯВЛЕНИИ МАРКЕРОВ СТАРЕНИЯ

**Резюме.** По мере старения населения во всем мире растет потребность в понимании сложных процессов, связанных со старением, и в выявлении надежных маркеров, которые могут помочь в ранней диагностике, вмешательстве и персонализированном медицинском обслуживании. В этой статье представлен всесторонний обзор применения искусственного интеллекта (ИИ) для выявления маркеров старения. Интеграция методов искусственного интеллекта, таких как машинное обучение и анализ данных, значительно расширила наши возможности по анализу обширных и разнообразных наборов данных, связанных с геномикой, протеомикой, метаболомикой, визуализацией и клиническими записями. В обзоре обсуждается интеграция клинических данных, факторов образа жизни и информации об окружающей среде с использованием ИИ, позволяющая получить целостное представление о маркерах старения. В исследовании рассматривается использование ИИ для прогнозирования риска ускоренного старения человека с учетом различных факторов.

Интеграция ИИ в идентификацию маркеров старения представляет собой смену парадигмы в исследованиях старения. В этом обзоре подчеркивается потенциал ИИ в революционизировании нашего понимания старения и прокладывании пути для инновационных стратегий профилактики и лечения возрастных заболеваний.

**Ключевые слова:** Искусственный интеллект, биомаркеры старения, машинное обучение, глубокое обучение

**Introduction.** Research on biomarkers of aging is an urgent and important area of scientific research in the modern world. Due to the increase in life expectancy and the aging of populations around the world, understanding the aging processes and identifying biomarkers associated with this process are becoming key aspects for developing strategies for healthy aging, preventing age-related diseases, and improving the quality of life. A recent study by Sara Green [1] examines the relevance of preventing age-related disorders within the framework of health policy, with an emphasis on early intervention in degradation processes to promote a healthy and long life. The author discusses new possibilities for slowing down the aging process, in particular, in the field of personalized nutrition. It is indicated that data-based studies have the potential to improve the accuracy of existing risk factors by replacing crude markers such as blood cholesterol levels with more detailed multidimensional biomarkers. The authors present an attempt to develop a new biomarker of aging focused on predicting various age-related conditions that are preventable through personalized nutrition. The article combines philosophical analysis and ethnographic research to explore the possibilities and challenges of managing aging through physical signs that are not directly related to the symptoms of diseases. The authors document how improved measurement methods create new conceptual difficulties in the demarcation of healthy and unhealthy conditions. In addition, it is emphasized that rethinking aging as a risk has social and ethical consequences, forming normative ideas about what is considered successful aging and good citizenship. Furthermore, in this paper written about the COUNTERSTRIKE project is a joint research initiative between the University of Copenhagen, the University of Amsterdam and industrial partners Arla Amba group, Bruker and Unilever. It aims to create biomarkers for the distribution of lipoproteins to combat sarcopenia in the elderly. The project includes metabolomics, health statistics, physiology, and medicine. The study focuses on the analysis of lipoproteins in relation to diet, physiological parameters, and microbiome. Using 3,000 biological samples from people over the age of 65, the project aims to develop a method for determining lipoproteins in the blood and link the results to predictive indicators of aging. COUNTER STRIKE is a continuation of the CALM project, using its samples and adding new participants to form a diverse cohort. The project is described as highly experimental, with an emphasis on an experimental approach to the problem of muscle loss during aging [1]. Clinical studies on premature vascular aging include remodeling of the wall of large arteries in

the form of thickening of the "intima-media" complex, increase in diameter, presence, and progression of atherosclerotic plaques (ASB), endothelial dysfunction and reduction of elastic properties of the arterial wall. The main method of detecting these changes is ultrasound duplex scanning. Today it is the main method of large vessel assessment in epidemiological and clinical studies [2]. Changes in elastic properties of the vascular wall, namely, decreased pliability, increased stiffness are independent predictors of the development of atherosclerosis, which underlies age-associated diseases of the cardiovascular system and, as a consequence, the risk of cardiac complications, which is especially important in asymptomatic individuals. Many studies have proved the high significance of another instrumental method as an early marker of vascular wall damage by atherosclerosis and, consequently, the risk of CVD and complications, including in patients with asymptomatic course of atherosclerosis: pulse wave velocity (PWV) measurement [3]. Another index of arterial stiffness, independent of blood pressure, is the cardio-ankle vascular index (CAVI). CAVI reflects the stiffness of the arterial wall in the aorta, femoral, and brachial arteries. It has been shown that this parameter is associated with the presence and severity of coronary atherosclerosis, thus it is proposed as a predictor for it [4,5]. In the next review of biomarker conducted by Alexander Burkle [6] studies of aging highlights that none of the proposed candidates provides a stable measurement of biological age in cross-sectional studies. The MARK-AGE study, supported by the European Commission, was conducted with the participation of more than 3,200 subjects in order to identify a set of biomarkers of aging. The main idea was to create a combination of parameters with weights that would more accurately measure biological age than individual markers. The work highlights the multi-causal and multi-systemic nature of the aging process and the promise of an integrated approach to measuring biological age. Biomarkers of human aging are extremely necessary to identify a high risk of age-related diseases. They will allow for targeted examinations, make preventive changes and start treatment at an early stage. Given the increase in life expectancy, effective strategies are needed to prevent age-related diseases. Biomarkers can be "neutral" markers of age, not directly related to the risk of disease, and markers of the overall risk of age-related diseases. Both types can provide important information about the state of health and the risk of age-related changes [6]. For example, recent research [7] suggests to use machine learning methods. The study was conducted in order to search for clinical and biomarkers most associated with sarcopenia in old age using machine

learning methods. Data from two populations from the north (Pavia) and the south (Apulia) were analyzed Italy, including clinical records and biological markers. The applied machine learning method, random forest (RF), revealed the most predictive parameters of sarcopenia. Common variables such as the index of muscle mass, arm strength, free weight of legs and arms, as well as gender are determined. Biomarkers such as albumin, C-reactive protein (CRP), folate, and age are also considered important. The results highlight the importance of these biomarkers in the screening of sarcopenia in an aging population and the need to improve medical prevention to mitigate the impact of sarcopenia on overall health, quality of life and the provision of medical care to an aging population. The article highlights the importance of including albumin, C-reactive protein (CRP), vitamin D and serum folate in the screening process for sarcopenia, especially in the male population of the elderly. Improving the health and quality of life of an aging population is an urgent task. The authors propose using a multidimensional methodology to model risk management pathways, which can help stratify the risk of sarcopenia in preventive medical settings and facilitate the identification of deteriorating health conditions in the

elderly population. [Roberta Zupo, 2023]. More specific research questions will be introduced and investigated in the work of Alex Zhavoronkov [8]. The article highlights the prospects of using modern artificial intelligence algorithms in aging research. Deep learning methods allow you to create age predictors, opening up new possibilities for analyzing dynamic and static data. AI-based biomarkers of aging provide a holistic view of biological processes and allow the creation of new methods for constructing causal models. The development of generative confrontations and reinforcement learning makes it possible to generate a variety of synthetic data, identify new biological targets and create new molecular compounds and geroprotectors. These techniques can be combined into a single pipeline of biomarker development, target identification, drug discovery and real-world data analysis, which helps accelerate and improve pharmaceutical research and development. It is assumed that modern artificial intelligence will contribute to the authority and importance of longevity biotechnology in the healthcare and pharmaceutical industries, as well as to the convergence of many areas of research.

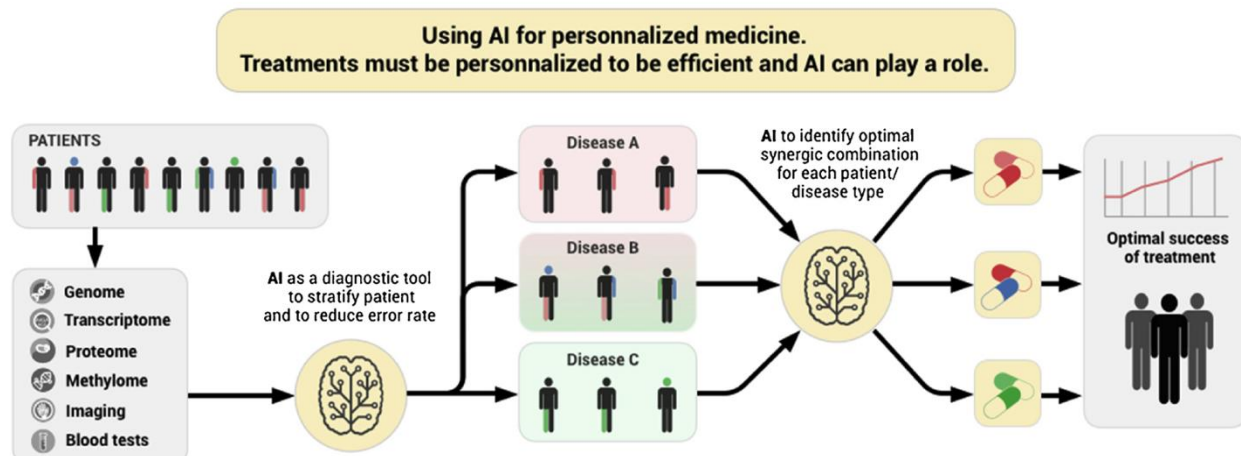


Figure 1 - The using of AI for personalized medicine.

AI has diverse applications in tailoring treatments, serving as a diagnostic tool to minimize errors and enabling patient stratification based on their unique health conditions. Integrating precise diagnostics and enhanced patient understanding, AI platforms can be leveraged to formulate more efficient treatment approaches. AI technology's ability to analyze vast amounts of data enables the identification of patterns for predicting patient prognosis and advising medical practitioners on personalized medicine options and experimental therapies, including participation in clinical trials. For instance, convolutional neural networks (CNNs) [9] have been trained to classify cancer patients based on tumor tissue immunohistochemistry [Vandenberghe et al., 2017]. Additionally, machine learning-based tumor classifiers [10], such as those developed for breast cancer pattern classification and forecasting, further demonstrate the potential of AI in healthcare [Capper et al., 2020]. Moreover, in his research discussed about the revolution in deep learning and its application in aging research. Deep neural networks and machine learning techniques have been successfully used to develop biomarkers of aging, such as the "aging clock", which estimates are based on various data. Artificial intelligence applications in the field of aging and longevity

provide promising results, and it is expected that combined approaches using modern artificial intelligence methods will lead to new applications in medicine. Regulators are beginning to develop a framework for the use of artificial intelligence technologies in healthcare, but it is important to balance data protection and support for technological development. International cooperation and data exchange are becoming key for further research and application of biomarkers of aging. The systems based on aging clocks such as Young.AI (<http://young.ai>) estimating a person's estimated biological age using several types of data, can provide valuable insights into a person's health status and evolve into applications for certain diseases. Unfortunately, in modern world these systems do not work [8]. According to other author [11], the Kivach clinic has developed a special medical program in the sanatorium to prevent aging in metabolic, cardiovascular, and neurological conditions. They investigated the effect of this program on biomarkers of the biological age of patients during their stay in order to objectify the potential of sanatorium treatment to influence the risk of age-related events. Using Artificial deep learning model Aging.ai 3.0 was based on blood parameters. Test available by following the link [test by following the link](#)

<https://www.unhooked.co.uk/diversity-ai/aging/aging->

<v1/index.html>.



## Deep Biomarkers Of Human Aging

How old by basic blood test

### Aging.AI<sup>1.0</sup>

- 41 input parameters
- $r = 0.91$
- $Rsq = 0.82$
- $MAE = 5.5$  years

Test your samples

### Aging.AI<sup>2.0</sup>

- 33 input parameters
- $r = 0.79$
- $Rsq = 0.63$
- $MAE = 6.2$  years

Test your samples

### Aging.AI<sup>3.0</sup>

- 19 input parameters
- $r = 0.80$
- $Rsq = 0.65$
- $MAE = 5.90$  years

Test your samples

Please try our [Young.AI](#) - a tool for tracking your predicted age over time using the multiple

**Figure 2 - Aging AI versions**

In figure 2 illustrates the design of the web site. Exists three versions of this system, which upgraded year by year. In fig.3 and fig.4 demonstrates the markers the patient need to fill in order to know the aging. In fig.5 shown that at least 7 parameters patients need to fill in order to predict aging.

Enter your weight:  kg    Enter your height:  cm    Do you smoke?  Yes  No

[Load an example](#)

Blood Marker*	Your Value	Units and Sample Metric**
Albumin**	<input type="text"/>	35 - 52 g/l
Glucose**	<input type="text"/>	3.9 - 5.8 mmole/l
Urea**(BUN)	<input type="text"/>	2.5 - 6.4 mmole/l
Cholesterol**	<input type="text"/>	3.37 - 5.96 mmole/l
Protein total**	<input type="text"/>	64 - 83 g/l
Sodium**	<input type="text"/>	136 - 146 mmole/l
Creatinine**	<input type="text"/>	53 - 97 mmole/l
Hemoglobin**	<input type="text"/>	11.7 - 15.5 g/dl
Bilirubin total	<input type="text"/>	1.7 - 21 mcmmole/l
Triglycerides	<input type="text"/>	0.68 - 6 mmole/l
HDL Cholesterol	<input type="text"/>	< 3.3 mmole/l
LDL cholesterol (by Friedewald)	<input type="text"/>	1.81 - 4.04 mmole/l

**Figure 3 - Markers of aging**

Calcium	<input type="text"/>	2.15 - 2.65 mmole/l
Potassium	<input type="text"/>	3.4 - 5.1 mmole/l
Hematocrit	<input type="text"/>	37 - 50 %
MCHC	<input type="text"/>	31.5 - 35.7 g/dL
MCV	<input type="text"/>	82 - 95 fl
Platelets	<input type="text"/>	150 - 450 10 <sup>9</sup> /mcl
Erythrocytes (RBC)	<input type="text"/>	3.5 - 5.5 10 <sup>6</sup> /mcl

Submit

**Figure 4 - Markers of aging[2]**

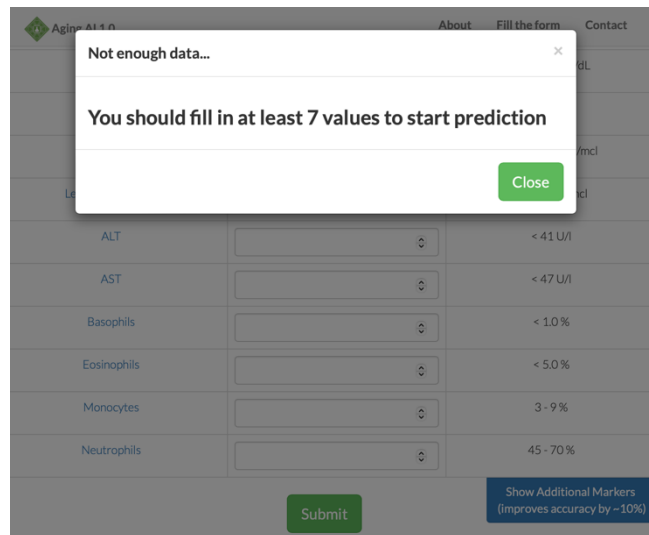


Figure 5 - Alert about filling parameters

Main part of the study confirms that two-week comprehensive medical programs in the sanatorium, including a calorie-restricted diet, a medical spa (physiotherapy for cleansing the gallbladder and enterosorption, stimulation of excretory organs), phytotherapy, hydrotherapy and thermal procedures, can reduce the biological age of a person (Aging.AI 3.0). Medical spa programs show the potential to improve the quality of aging. A more comprehensive description can be found in the investigation of Evgeny Putin [12]. The research addresses a significant challenge in the study of human aging – the absence of a comprehensive set of actionable biomarkers for assessing the effectiveness of therapeutic interventions. The study introduces a modular ensemble of 21 deep neural networks, designed with varying depth, structure, and optimization, to predict human chronological age based on a standard blood test. Trained on a dataset of over 60,000 samples from routine health exams, the best-performing model within the ensemble demonstrated an 83.5% accuracy, identifying albumin, glucose, alkaline phosphatase, urea, and erythrocytes as the most crucial markers. An online testing system (<http://www.aging.ai>) was developed for public use, potentially offering a cost-effective and minimally invasive approach to monitoring aging biomarkers in humans. Additionally, the ensemble approach may aid in cross-species feature importance

analysis [12]. However, for nowadays the link is not working. A large number of existing studies in the broader literature have examined machine learning. So, the literature review of David Bernard [13] shows that investigators created an innovative explainable machine learning framework called Personalized Physiological Age (PPA) using data from NHANES study. PPA predicts chronic diseases and mortality independently of chronological age by analyzing 26 variables. Using SHapley Additive exPlanations (SHAP), it quantifies deviations from normative data for personalized health monitoring. Glycated hemoglobin (HbA1c) is a significant predictor. Clustering profiles based on explanations offer tailored clinical follow-up. PPA offers robust, quantitative, and explainable monitoring of personalized health. In this investigation three classes of models were compared: tree-based (Decision Tree, Random Forests, XGBoost), neural networks (Multi-Layer Perceptron), and penalized linear models (Elastic Net). Hyperparameter tuning was conducted using grid-search exploration with cross-validation. Model training aimed to minimize mean absolute error (MAE) and included a custom objective function for XGBoost to address performance discrepancies across age groups. Evaluation metrics included R2 and MAE on both train and test sets, with standard deviations provided for the train set using fivefold cross-validation.

$$grad_i = (\hat{y}_i - y_i) \times \left| \frac{\sum_{j \in age(i)} (\hat{y}_j - y_j)}{|age(i)|} \right| \left| \frac{\sum_{k=1}^N (\hat{y}_k - y_k)}{N} \right|$$

The gradient ( $grad_i$ ) to be calculated for the  $i$ th individual depends on the model's prediction ( $\hat{y}$ ) for that iteration. Here,  $y$  represents the chronological age of the individual, and  $age(i)$  refers to all individuals who share the same age as the  $i$ th individual.  $N$  represents the total number of individuals in the dataset. Overall, the work offers a practical tool for medical care and a comprehensive explainable machine learning framework for understanding complex physiological phenotypes, with potential applications in precision medicine and various other fields [13]. Studies of Polina Mamoshina [14] are well documented, it is also well acknowledged that a deep

learning-based hematological aging clock trained on a diverse dataset including Canadian, South Korean, and Eastern European populations. The combined clock shows improved predictive accuracy within individual populations compared to population-specific clocks. Evaluation on American population samples suggests population-specific aging patterns and hematologic clocks predict all-cause mortality. These models have been integrated into the Aging.AI system, enhancing tools for analyzing human aging. In this investigation the following formulas used to find the accuracy of the age prediction.

$$1) \text{ Pierson correlation coefficient } r = \frac{\sum_{i=1}^N (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^N (x_i - \bar{x})^2} \sqrt{\sum_{i=1}^N (y_i - \bar{y})^2}}$$

Where  $x_i$  is chronological age value,  $\bar{x}$  is the mean of  $x$ ,  $y_i$  is predicted age value and  $\bar{y}$  is the mean of  $y$ .  $N$  is the number of examples and  $r$  is the strength of a linear between predicted and actual age.

2) *Coefficient of detemination*  $R^2 = 1 - \frac{\sum_{i=1}^N (\hat{y}_i - y_i)^2}{\sum_{i=1}^N (y_i - \bar{y})^2}$

Where  $y_i$  the real value,  $\hat{y}_i$  is the predicted value  $\bar{y}$  is the mean of  $y$ .  $R^2$  describes the percentage of variance between predicted and actual age.

3) *Mean Absolute Error MAE*  $= \frac{1}{N} \sum_{i=1}^n |\hat{y}_i - y_i|$

Where  $\hat{y}_i$  is the predicted age,  $y_i$  is the age value and  $N$  is the number of examples.

Glucose, albumin, sex, urea, hemoglobin, HDL cholesterol, and triglycerides emerged as the top seven significant markers for the Canadian population. In contrast, hemoglobin, albumin, erythrocytes, sex, cholesterol, glucose, and sodium were identified as the seven key markers for the South Korean population. For the Eastern European population, albumin, glucose, LDL cholesterol, gender, urea, and erythrocytes were highlighted as the most important markers. Notably, across all three population-specific predictors, albumin, hemoglobin, urea, and glucose were consistently identified as the most influential markers for predictive accuracy. In conclusion of this research, deep learning-based hematological aging clocks, even with limited feature space, show high accuracy in predicting chronological age. They capture nonlinear relationships between blood parameters and age, allowing for robust characterization. Population-adjusted clocks generalize well across diverse patient populations, improving performance in age prediction and biological age quantification. Incorporating more population-specific datasets aims to enhance predictive power further. The continually updated Aging.AI system is accessible for free on the aging.ai website. As well, in the work of Minh Chung [15] was written about skin aging, influenced by both internal and external factors, reflects an individual's overall well-being. Recent advancements in computerized systems, particularly artificial intelligence (AI), offer solutions for identifying early signs of aging and improving treatments. AI plays a crucial role in enhancing patient care within the realm of skin aging. Despite this, there is a knowledge gap regarding the present and future directions of AI in this domain. The review aims to outline current and potential applications of AI in addressing skin aging, providing

insights into upcoming developments. AI models have the potential to boost patient involvement in skin-care decisions, ultimately enhancing the patient-provider experience. The author bring some information about the background of artificial intelligence (AI) tools, like artificial neural networks (ANN), machine learning, and deep learning. ANN, simulating brain signaling, processes vast amounts of data rapidly. Machine learning techniques, such as supervised and unsupervised learning, train AI models for pattern recognition and classification, aiding in diagnostics and risk assessment. Unsupervised learning identifies patterns within a dataset, offering novel ways to classify patients and optimize treatments. Reinforcement learning, akin to operant conditioning, adapts therapy based on outcomes. Deep learning enables AI to learn without human intervention, improving accuracy over time. In dermatology, AI is applied to classify skin lesions, assess disease progression, and optimize therapeutic interventions, holding significant potential for advancing dermatological care. The study addresses to the PROVEN Beauty quiz (<https://www.provenskincare.com/>) collects information from users about their skin, including age, concerns, prescription use, lifestyle, and more. This data is connected to the Beauty Genome Project database, containing millions of reviews, skincare products, ingredients, and articles. An algorithm uses this information to create a personalized skincare regimen for users, offering 527 unique routine combinations tailored to individual needs, including cleansers, SPF moisturizers, and night creams [15]. In fig.6 shown how the website looks like. In order to know your skin age, you need to press "Get my formula" and answer the many questions.

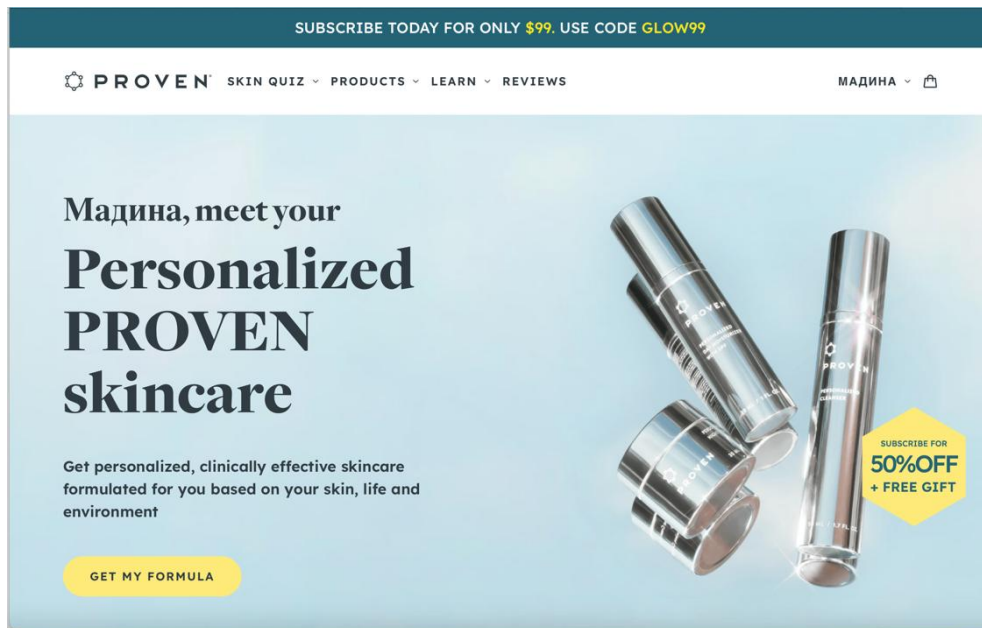


Figure 6 - Proven skincare

The goal of this review is to provide a technical overview of the advances and opportunities offered by AI for aging biomarkers. With the advent of artificial intelligence (AI), new perspectives are opening for the identification and analysis of markers of aging, which may lead to more accurate methods for determining the biological age of a person. This article examines current strategies in aging research in order to identify biologically more significant features and simplify the interpretation of models based on artificial intelligence. The most significant and popular advances in artificial intelligence are:

- Machine learning

Machine learning (ML) [16] involves the use of algorithms capable of learning from data and making predictions by constructing a model based on sample inputs. ML is often utilized in computing tasks where creating effective algorithms through explicit programming is challenging or impractical. Currently, prevalent traditional ML techniques encompass k-nearest neighbors (kNN) [Kramer, 2013].

- Deep learning

Deep structured learning, also known as deep learning (DL) or hierarchical learning, pertains to a category of machine learning techniques that leverage multiple layers of non-linear computational units to capture intricate relationships within data [8]. These structures, comprising numerous layers, are commonly referred to as deep neural networks (DNNs) or stacked neural networks. The key distinction between the initial single-hidden-layer artificial neural networks (ANNs) and DNNs

lies in their depth, indicating the number of layers through which data undergoes processing. Typically, having more than three layers (including input and output) qualifies a system as "deep" learning. Therefore, "deep" serves as a technical term denoting the presence of more than one hidden layer. Similar to other standard neural network architectures, DNNs function as efficient universal approximators. [Alex Zhavoronkov, 2019].

As written above, for nowadays exists only several applications which identifies aging of the person: Aging clocks, Aging AI etc. Examples of such aging clocks include Horvath's Clock and Hannum's Clock, which are based on DNA methylation analysis. These aging clocks, although providing interesting research results, are still under development, and their widespread use in clinical practice requires additional research and validation. The second one is needed a plenty of your biomarkers to identify your aging.

Based on the above-mentioned approaches, for the first one is needed DNA, which is takes a lot of time and for the second requires too many analyses, therefore an experimental study is proposed with a several biomarkers, encompassing 800 patients divided into age groups: 65–75, 75–90, and 90 and above. In table 1 shown the major indicators which was selected to analyze the premature aging and calculate the correlation. These patients need to take blood tests and the results will be processed in database and python-based software will be created.

**Table1** - Main biomarkers

	BP baseline (sitting)	Upper	Lower	Pulse	Haemoglobin	Leucocytes	Thrombocytes	Erythrocytes	Lymphocytes	Lymphocytes without %	COE (mm/hour)	Glucose (mmol/l)	Weight(kg)	Smoking
1														
2	120/80	120	80	74	122	5,6	270	4,1	0,125	12,5	20	5,94	70	0
3	120/80	120	80	75	141	5,6	324	4,59	0,424	42,4	22	13,81	90	0
4	120/80	120	80	76	125	6,5	304	4,5	0,3	30	23	4,23	65	0
5	170/100	170	100	78	133	7,8	230	4,63	0,268	26,8	12	4,81	60	0
6	170/80	170	80	70	89	3,7	265	3,5	0,323	32,3	43	3,78	53	0
7	135/90	135	90	72	161	8,6	167	4,7	0,35	35	13	5,23	72	0
8	160/90	160	90	73	132	6,5	348	4,1	0,252	25,2	26	5,25	75	0
9	150/90	150	90	65	134	8,7	156	4,5	0,173	17,3	22	5,16	75	0
10	125/75	125	75	95	151	8,7	209	5,83	0,116	11,6	10	6,15	90	0
11	120/80	120	80	65	160	9,2	226	5,3	0,303	30,3	3	5,31	85	0
12	120/80	120	80	84	160	3,7	237	4,8	0,468	46,8	12	3,7	53	0
13	155/90	155	90	75	125	5,8	287	4,1	0,336	33,6	6	4,97	74	0
14	145/80	145	80	68	132	5,3	244	4,6	0,512	51,2	26	4,95	68	0
15	165/80	165	80	72	133	6	192	4,76	0,301	30,1	23	8,6	87	0
16	140/80	140	80	64	128	7,1	261	4,2	0,434	43,4	6	6,22	74	0
17	175/90	175	90	78	115	7,5	274	3,9	0,223	22,3	30	4,96	69	0
18	150/80	150	80	70	122	3,7	237	4,8	0,468	46,8	12	3,7	82	0
19	180/90	180	90	88	132	5,7	215	4,84	0,348	34,8	22	10,1	60	0
20	175/90	175	90	90	98	8,7	252	4,2	0,201	20,1	10	4,45	60	1
21	120/80	120	80	93	133	10,3	347	4,73	0,364	36,4	26	7,49	96	0
22	180/90	180	90	85	111	5,7	217	3,61	0,417	41,7	14	4,51	67	0
23	130/80	130	80	76	130	7,5	229	4,35	0,478	47,8	25	6,33	70	0
24	140/80	140	80	60	112	8,1	362	4,02	0,271	27,1	34	4,94	51	0
25	120/80	120	80	97	99	10,7	235	3,56	0,125	12,5	32	9,68	75	0
26	130/90	130	90	98	158	8	175	5,4	0,324	32,4	20	5,18	90	0
27	155/100	155	100	72	132	6,8	279	4,58	0,294	29,4	24	22,27	60	0
28	150/90	150	90	75	155	8,2	221	5,1	14,6	14,6	10	8,67	91	0
29	140/80	140	80	94	82	5,4	326	4,3	0,321	32,1	30	4,87	91	0
30	130/90	130	90	64	165	6,5	177	5,47	0,341	34,1	14	4,75	63	0
31	150/80	150	80	76	135	10,3	343	3,9	0,142	14,2	54	5,98	60	0
32	150/90	150	90	90	159	9	210	5	0,23	23	10	5,36	77	0
33	140/80	140	80	100	129	5,7	217	4,48	42,7	42,7	11	7,62	80	0
34	120/80	120	80	106	95	7,3	385	4,17	0,237	23,7	25	6,48	60	1
35	160/90	160	90	76	109	4,8	202	3,8	0,477	47,7	12	4,96	50	0
36	165/90	165	90	84	137	7	244	4,67	0,279	27,9	10	8,96	78	0
37	155/80	155	80	62	164	6	257	7,03	0,302	30,2	13	6,27	84	0

To sum up, in this review different approaches of identifying aging biomarkers and existing applications which determines premature aging. A large number of existing studies in the broader literature have written about Aging.Ai system. A new approach is therefore needed for investigation premature aging with artificial intelligence. An increase in life expectancy does not mean an increase in active longevity. One of the main problems of the modern world, in addition to population ageing, can be considered the increase in age-associated diseases and, above all, cardiovascular diseases (CVD). Cardiovascular diseases are the main cause of mortality and the burden of disability both worldwide and in Kazakhstan. According to WHO data, Kazakhstan belongs to regions with a high risk of developing CVDs. [17]. At the same time, mortality rates in Kazakhstan are among the highest in Central Asia. In this regard, the main modern task of cardiologists is to reduce cardiovascular mortality from these diseases. The task of AI is timely detection and prevention of CVD, and on the basis of immunological and biochemical markers to give a prognosis, risks and possible causes of reduced life expectancy of the population. Being age-associated diseases, CVDs are considered as one of the obvious manifestations of pathological ageing of the organism, and the state of the cardiovascular system reflects the so-called "biological" age of a person. It is also relevant for AI to search for aging markers, to determine the role of endocrine, metabolic, immunological, structural and functional disorders in the development of vascular aging in their interrelation. Thus, age-associated markers represent a general qualitative and quantitative indicator of the functional state of a person. One indicator cannot reflect the picture of the state of the organism, its age, and the assessment of the aging rate should be comprehensive, change with age, allow to anticipate the early stages of age-related diseases, be accessible and minimally invasive. Effective early prevention therefore involves identifying targets for markers that will reflect the rate of cardiovascular ageing and accordingly help to assess the effectiveness of interventions. To address the prevention of early

cardiovascular aging, a comprehensive study of a number of clinical, biochemical, immunological, and instrumental studies is planned. On the basis of new data with the help of AI it is possible to create the most effective programmes of primary and secondary prevention of the main geriatric syndromes. The study will result in the development of methodological recommendations and relevant regulatory documents on geriatrics. To conclude, Artificial intelligence plays a key role in modern research aimed at identifying and understanding markers of aging. This opens new prospects for the prevention of age-related diseases and improving the quality of public health. However, careful handling of data and consideration of ethical issues are necessary to maximize benefits and minimize risks.

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