Grenze International Journal of Engineering and Technology, June Issue

AgeAlign: A Biomarker-based System to Support Preventive Healthcare and Analyze Biological Aging

Nutan Patil[1], Akash Mhetre[2], Nilesh Kamble[3], Pankaj Dahiwalkar[4], Abhishek Sakhare[5] and Pranav Gurav[6]
[1-6]Department of Computer Engineering, NMIET, Savitribai Phule Pune University, Pune, India
Email: nutan.patil@nmiet.edu.in, akash.mhetre@nmiet.edu.in, Nilesh.kamble@nmiet.edu.in, abhi11921192@gmail.com, pankajdahiwalkar@gmail.com, pranavgurav133@gmail.com

***Abstract*— Age Align is a project which tries to estimate the true biological age of human beings because chronological age alone cannot actually reflect a person's true health condition. Biological age depends on different types of biomarkers. These biomarkers are obtained from different types of medical checkups. Based on biomarker values, the software calculates biological age using the phenotype age formula, and then takes chronological age as input from the user and calculates the gap between biological age and chronological age.**

Based on the gap, it gives recommendations such as diet, medicines, and other health related recommendations, and also keeps track of the user's previous records. These recommendations help users to reduce the age gap. By reducing the age gap, the user can live a healthier life and can improve his or her life expectancy. In simple words, this software can be used for biological age estimation and preventive healthcare.

***Index Terms*— Biological Age, Biomarkers, Preventive Healthcare, Aging Analysis, Phenotypic Age, Chronological Age.**

I. INTRODUCTION

Most healthcare systems nowadays give recommendations or advice based on chronological age, which does not reflect a person's true physical condition or an individual's health. Individuals within the same age group can have different fitness levels, immunity, genetics, and different lifestyles. This means that the same age does not reflect an individual's physical condition, and that is why it is important to consider biological age, which shows a human's true physical condition rather than the chronologically calculated age. To solve this problem, we have developed a software named AgeAlign.

AgeAlign mainly focuses on biological age and acts as a preventive healthcare tool that encourages users to adopt healthier lifestyles. It uses a data driven approach to analyze an individual's health status and monitor it. It detects early age acceleration, which helps a person to improve and maintain their health and slow down the age acceleration.

The software provides a user-friendly interactive interface which tracks the health condition of an individual. This software uses a modern approach which integrates biomarker analysis and a recommendation system to support healthier and longer lives.

Grenze ID: 01.GIJET.12.2.273_26

II. METHODOLOGY

A. Dataset and Experimental Setup

Figure 1 depicts the Age Align system's general procedure. The system's methodical procedure starts with gathering biomarker data and concludes with producing health recommendations. The user enters both chronological age and biomarker values. After processing this data, the system uses the Phenotype Age model to determine biological age. To find any differences, the calculated figure and the real age are compared. Appropriate health recommendations are produced based on outcome.

After processing this data, the system uses the Phenotype Age model to determine biological age. To find any differences, the calculated figure and the real age are compared. Appropriate health recommendations are produced based on outcome.

B. Layered architecture design

There are three primary layers in the system:

- Frontend Layer: Uses React.js to manage user interaction and show results.
- Backend Layer: Uses Django to handle and compute data
- Data Layer: Uses MySQL to store input and output data

Through APIs, all parts interact locally, guaranteeing that the system doesn't rely on the internet to function.

- Frontend: React.js, HTML, CSS, Chart.js
- Backend: Python, Django
- Database: MySQL
- Libraries: NumPy, Math
- Environment: Windows / Linux

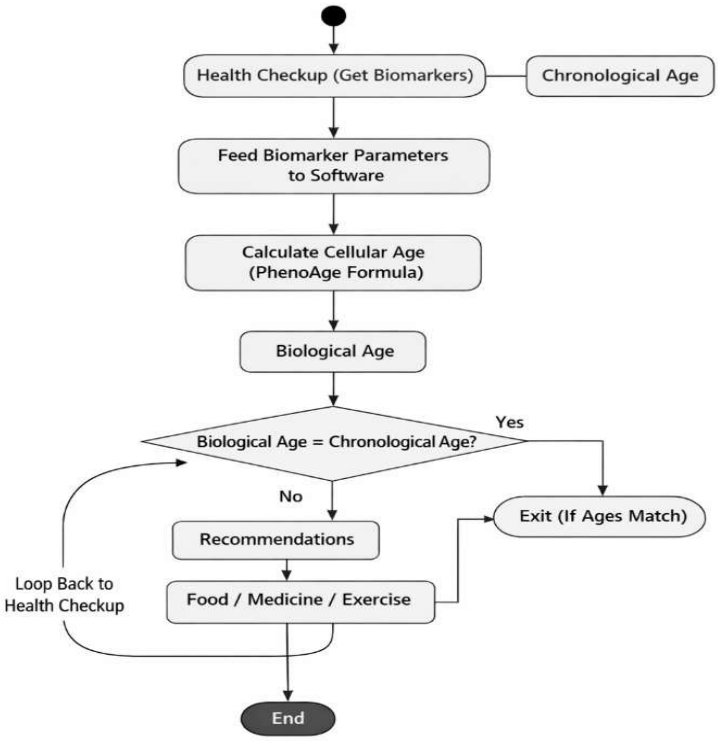

Figure 1. AgeAlign system methodology flowchart

C. Biomarker analysis

Biomarkers like glucose, albumin, CRP, creatinine, alkaline phosphatase, and BMI are processed by the system. Before being employed in computing, the input values are verified and standardized. The computation module receives the processed data and uses it to estimate biological age.

TABLE I. DATASET STATISTICS

Biomarker	Unit	Normal Range	Role in Phenotypic Age	Levine Weight (w_i)
Albumin	g/dL	3.5 – 5.0	Nutritional & liver marker	-0.0336
Creatinine	mg/dL	0.6 – 1.2	Kidney function	0.0095
Glucose	mg/dL	70 – 99	Metabolic health	0.1953
C-Reactive Protein (CRP)	mg/L	< 1.0	Inflammatory marker	0.0954
Lymphocyte %	%	20 – 40	Immune function	-0.0120
Mean Cell Volume (MCV)	fL	80 – 100	Red blood cell health	0.0268
Red Cell Dist. Width (RDW)	%	11.5 – 14.5	Blood cell variability	0.3306
Alkaline Phosphatase	U/L	44 – 147	Liver/bone health	0.00188
White Blood Cell (WBC)	$10^3/\mu L$	4.5 – 11.0	Immune response	0.0554

III. PROPOSED SYSTEM

The Age Align system uses a Django backend to construct a deterministic, data-driven calculation pipeline that is organized into four consecutive algorithmic modules.

A. Data Input and Validation

The first module verifies the completeness, unit consistency, and physiological plausibility of user-submitted biomarker values through syntactic and semantic validation. Before downstream processing, validated inputs are normalized to standardized units (e.g., mg/dL → mmol/L) and out-of-range or missing data are noted for repair.

B. Phenotypic Age Computation (Core Algorithm)

The Levine Phenotypic Age equation is implemented by the central module, which calculates a weighted mortality score as $\text{Mortality\_Score} = \Sigma(w_i \times x_i)$, where x_i is the standardized biomarker value and w_i is the clinically derived biomarker coefficient.

The Phenotypic Age (PA) estimate is then obtained by transforming this score using exponential and natural logarithm methods. The main measure of aging that doesn't require cloud inference or external models is the Age Gap ($\Delta\text{Age} = \text{PA} - \text{Chronological Age}$).

C. Result Interpretation and Feedback:

The computed ΔAge is contextualized in the final module, where a negative value denotes advantageous aging and a positive value denotes accelerated biological aging in relation to chronological age. To produce specific health recommendations, such as glycemic control, food modification, or inflammatory marker monitoring, individual biomarker aberrations are further examined.

IV. RESULTS AND DISCUSSION

The performance of the AgeAlign system was evaluated using a set of sample biomarker inputs collected under controlled conditions. These inputs included key clinical parameters such as glucose level, albumin concentration, creatinine, C-reactive protein (CRP), alkaline phosphatase, and body mass index (BMI). The system processed these values using the Phenotypic Age model to estimate the biological age of individuals. The obtained results indicate that the system is capable of generating consistent and meaningful biological age estimates based on the provided biomarker data. In several test cases, noticeable differences were observed between biological age and chronological age, highlighting variations in individual health conditions. These variations reflect the influence of lifestyle, metabolic health, and physiological factors on the aging process. The ability of the system to identify such differences demonstrates its usefulness in detecting early signs of accelerated or decelerated aging.

The comparison between biological age and chronological age serves as a key indicator of overall health status. When the biological age exceeds the chronological age, it suggests potential health risks and the possibility of faster aging. Conversely, a lower biological age indicates better health and a slower aging process. This comparative analysis provides users with a clear understanding of their current health position. To enhance user interpretation, the results are presented through visual elements such as charts and structured tables. These graphical representations simplify complex data and make it easier for users to understand their health metrics. The inclusion of a recommendation module further strengthens the system by providing actionable suggestions. Based on the observed age difference, the system offers general guidance related to diet, physical activity, and daily habits, helping users take corrective steps toward improving their health.

TABLE II. BIOLOGICAL AGE ESTIMATION RESULTS ACROSS SAMPLE TEST CASES

Case	Chronological Age	Phenotypic Age (PA)	ΔAge	Interpretation
Case 1	28	24.3	−3.7	Favorable aging
Case 2	35	40.1	+5.1	Accelerated aging
Case 3	45	43.6	−1.4	Favorable aging
Case 4	52	58.2	+6.2	Accelerated aging
Case 5	60	61.4	+1.4	Marginal aging

V. FUTURE SCOPE

The AgeAlign system provides a strong foundation for biological age estimation; however, there are several opportunities for further enhancement to improve its accuracy, usability, and real-world applicability. One major area of future development is the integration of advanced biomarkers such as genetic indicators, DNA methylation data, and hormonal profiles. Including these additional parameters can significantly improve the precision of biological age estimation by capturing deeper physiological and molecular changes associated with aging. Another important direction is the incorporation of machine learning and artificial intelligence techniques. By training models on large and diverse health datasets, the system can learn complex relationships between biomarkers and aging patterns. This would enable more personalized predictions and adaptive recommendations tailored to individual health profiles. Over time, such models could continuously improve as more data becomes available.

VI. CONCLUSION

The AgeAlign system offers a useful method for integrating user-friendly digital health monitoring with biological research. By using clinically relevant biomarker computations, it provides a trustworthy and privacy-conscious way to estimate biological age. In contrast to many current applications that rely on cloud infrastructure or sophisticated machine learning models, this system runs purely on a local platform, providing greater control over personal data and preserving user anonymity.

To facilitate seamless data handling and effective computation, the system's architecture combines a MySQL database, a Django-powered backend, and a React.js-based interface. It is simple for users to enter their health indicators, determine their biological age, and compare it with their actual age. The results are presented through an intuitive and interactive dashboard, which assists users in understanding their health status and encourages them to adopt healthier living behaviors for better long-term well-being.

ACKNOWLEDGMENT

This work was completed with the assistance of individuals whose advice was very helpful. Prof. Nutan Patil provided guidance and helpful suggestions throughout the development of this work. Prof. Pritam Ahire offered valuable recommendations that improved the overall quality of the work. The resources and academic environment necessary for this research were supplied by the Department of Computer Engineering.

REFERENCES

[1] M. E. Levine et al., “An epigenetic biomarker of aging for lifespan and health span,” Aging (Albany NY), vol. 10, no. 4, pp. 573–591, 2018.
[2] D. W. Belsky et al., “Quantification of biological aging in young adults,” Proceedings of the National Academy of Sciences (PNAS), vol. 112, no. 30, pp. E4104–E4110, 2015.
[3] M. E. Levine, “Modeling the rate of aging using phenotypic and physiological biomarkers,” Journal of Gerontology: Biological Sciences, vol. 68, no. 7, pp. 667–674, 2013.
[4] S. Jylhävä, N. L. Pedersen, and S. Hägg, “Biological age predictors and their applications,” EBioMedicine, vol. 21, pp. 29–36, 2017.
[5] National Institute on Aging, “Biomarkers of Aging: Research Roadmap,” U.S. Department of Health & Human Services, 2021
[6] S. Horvath, “DNA methylation age of human tissues and cell types,” Genome Biology, vol. 14, no. 10, p. R115, 2013.
[7] J. Belsky et al., “Eleven telomere, epigenetic clock, and biomarker-composite quantifications of biological aging,” eLife, vol. 7, e39828, 2018.
[8] T. B. L. Kirkwood, “Understanding the odd science of aging,” Cell, vol. 120, no. 4, pp. 437–447, 2005.