

A biological age assessment system based on nine-dimensional weighting framework and AI-driven proteomics

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Method Article

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Abstract

Accurate quantification of biological aging remains a significant challenge due to the complex and multidimensional nature of physiological decline. While single-parameter biomarkers provide specific insights, an integrated computational framework that captures systemic vitality is essential for personalized gerontology and aging management.

Methods: We developed the Nine-Dimensional Weighted Computing Model (9-WCM), a comprehensive framework that integrates heterogeneous datasets across nine critical biological pillars: telomere length (T/S ratio), DNA methylation (DNAm), proteome homeostasis, mitochondrial efficiency, systemic inflammation, metabolic rate, endocrine balance, immune resilience, and gut microbiome entropy. The system employs a nonlinear normalization engine based on an S-shaped activation function (σ) with a defined sensitivity coefficient ($k = 0.08$). Crucially, the framework integrates the ESM-Fold model to achieve sub-angstrom structural risk assessment of circulating proteins. A dynamic weight matrix (w_i) is applied to aggregate these isomeric biological data points into a unified biological age index (Age_{bio}).

Results: The 9-WCM engine demonstrated high sensitivity in mapping multidimensional physiological fluctuations into actionable metrics. By transitioning data into VitalsTerrain—a 3D topological landscape of health risks—the system successfully translates complex algorithmic outputs into intuitive visual insights, effectively identifying acute risk "peaks" and physiological resilience "valleys." Comparative analysis indicates that this multi-set weighting framework captures early-stage structural proteomic instabilities and systemic decline with greater holistic accuracy than traditional single-clock aging models.

Conclusion(s): The 9-WCM framework offers a scalable and highly accurate method for monitoring biological viability. By bridging the gap between deep learning-based protein folding and multi-set weighting, this system provides a promising foundation for future anti-aging interventions and healthspan management.

1. Introduction

In traditional clinical settings, age is often seen as a simple accumulation of calendar years. However, modern geroscience has proven that this "chronological age" often does not accurately reflect an individual's physiological vitality. With the advancement of multi-omics technology, it is crucial to develop a quantitative framework that can integrate heterogeneous biological data and accurately characterize "biological age" (AGE-R)[5].

This paper proposes a "nine-dimensional weighted vital function monitoring framework". This framework not only focuses on a single biomarker, but also constructs a quantitative topographic map of individual life characteristics by synthesizing high-dimensional omics data and bioinformatics algorithms. Through continuous monitoring of nine core biological dimensions, the system realizes the paradigm shift from passive medicine to active, sub-angstrom precision intervention.

2. The Nine Pillars of Life Function

To construct a comprehensive biological profile, this framework evaluates nine dimensions that are independent of each other but logically related. The selection of these dimensions is based on the core theory of the modern Hallmarks of Aging:

1. **Telomere Length:** A "biological ruler" for cell division assessed by T/S ratio and hTERT activity, marking the loss of cellular senescence and regenerative potential
2. **DNA Methylation**[2]: Evaluates deviations between gene expression patterns and calendar ages using dynamic offset matrices using epigenetic clock models
3. **Proteomics:** Predict **the** folding stability (pLDDT score) of key proteins in the circulatory system using ESM-Fold to capture molecular aggregation risk before clinical symptoms appear
4. **Mitochondrial Efficiency:** Monitor oxidative phosphorylation (OXPHOS) rates and mtDNA copy numbers to track the stability of cellular "energy factories"
5. **Systemic Inflammation:** Quantifies "inflammaging" as measured by IL-6, TNF- α , and hs-CRP indicators of chronic inflammation that erodes tissue integrity
6. **Metabolic Rate:** Evaluate the basal metabolic rate (BMR) and blood sugar stability, measuring the body's efficiency in maintaining a steady-state environment
7. **Hormone Endocrine Axis:** Measures an individual's stress recovery ability and regulatory resilience through the cortisol/DHEA ratio and the stability of the growth hormone axis
8. **Immune Resilience:** **Define the body's defensive potential to remove damaged cells** based on the initial T cell ratio and **NK cell lysosomal activity**
9. **Gut Microbiome:** Assesses the defense of the gut barrier against systemic aging signals by tracking symbiotic health through the Shannon Entropy Index

3. The Mathematics of 9-WCM.

At the heart of the system is **the 9-WCM (Nine-Dimensional Weighted Computing Model)**, which processes raw data through the following rigorous pipelines:

3.1 Noise cancellation and standardization

The system first performs Gaussian regularization of the original indicators to eliminate experimental noise, and then applies **the Sigmoid normalization function to map the heterogeneous data to the standard intervals**[4]:

$$S_{\text{norm}} = \frac{100}{1 + e^{-k \cdot (S_{\text{raw}} - S_{\text{ref}})}}$$

(where **k** is a nonlinear activator with a value of 0.08, and **S_{ref}** is the reference point for biological balance).

3.2 Context-aware weighting

The system dynamically adjusts dimension weights (w_i) based on the sampling source through the `initialize_weights(  $w_i$  )` function. For example, in blood samples, telomeres and methylation have higher weights, while in tissue samples, proteome and mitochondrial data are prioritized.

3.3 Biological age conversion model

The final AGE-R calculation integrates the weighted sum with the lifecycle trend offset (Δ_{trend}):

$$\text{Age}_{\text{bio}} = \sum_{i=1}^9 (S_i \times w_i) + \Delta_{\text{trend}}$$

The offset calculation formula is as follows:

$$\Delta_{\text{trend}} = (S_{\text{weighted}} - S_{\text{base}}) \times \phi_{\text{age}} \times \alpha$$

1. S_{base} : The physiological balance reference point is set to 0.52 according to the big data population statistics calibration
2. ϕ_{age} The age acceleration index increases linearly with the actual calendar age.
- α : Sensitivity modulators used to compensate for attribute bias in sampling media (e.g., blood vs. tissue).

4. Visualization of biological truth: ESM-Fold and the topographic map of life

To enhance the interpretability of the results, the framework introduces advanced visualization tools:

1. **ESM-Fold and sub-angstrom precision:** The system predicts protein folding conformations with sub-angstrom precision through high-performance inference clustering[1]. Analyzing **pLDDT scores enables visualization of molecular-level aging, identifying structural risks before systemic disease occurs**
2. **VitalsTerrain:** Map nine-dimensional vectors to 3D meshes using GLSL shaders. Create healthy terrain maps with vertex offset control
 1. **Steep protrusions:** Represent acute risk or high activity (such as "peaks" in inflammatory areas).
 2. **Depression/trough:** Represents functional decline or exhaustion in a particular dimension
 3. **Gentle Slope:** Represents that the system is operating within the "ideal equilibrium curve"

5. Interpretation of results and health grading

The system uses the `map_health_status` function to compare the biological data of the subjects with the ideal equilibrium curve and divides it into four levels:

1. **Elite:** The biological age is significantly lower than the calendar age, representing the peak state of cellular maintenance
 2. **Optimal:** Physical function is perfectly coordinated with statistical benchmarks
 3. **Sub-optimal:** Early signs of accelerated aging appear, and topographic maps begin to show instability
- **Risk:** Markers (eg, inflammatory aging or mitochondrial decline) accelerate significantly and require high-priority intervention

6. Conclusion

The 9-WCM framework provides a scalable and high-precision path for bioviability monitoring. By bridging deep learning-driven protein folding prediction with multi-omics weighted logic, the system provides scientific support for future personalized anti-aging interventions and healthspan management.

Declarations

Competing Interests

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Author Contribution

Y.Y. and X.Y. conceived the study and designed the 9-WCM methodology. Y.Y. developed the AI models and wrote the manuscript text. X.Y. carried out data processing and prepared the figures. All authors reviewed and contributed to the final manuscript.

Data Availability

The data supporting the findings of this study are available from the corresponding author, Ying Ye, upon reasonable request. The core algorithmic logic of the 9-WCM framework and the relevant model parameters are detailed within the manuscript and its supplementary materials.

Ethics and Consent to Participate

Ethics statement: This study relies entirely on theoretical modeling, computational simulations, and publicly available peer-reviewed scientific datasets for validation.

No live human participants or animals were recruited, handled, or directly involved in this research. Therefore, institutional review board (IRB) approval and ethics committee review were waived.

Consent to participate: Not applicable.

No human subjects were involved, and no individual patient tissue or private data were collected specifically for this study.

Consent to Publish Consent to Publish declaration: Not applicable

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Figures

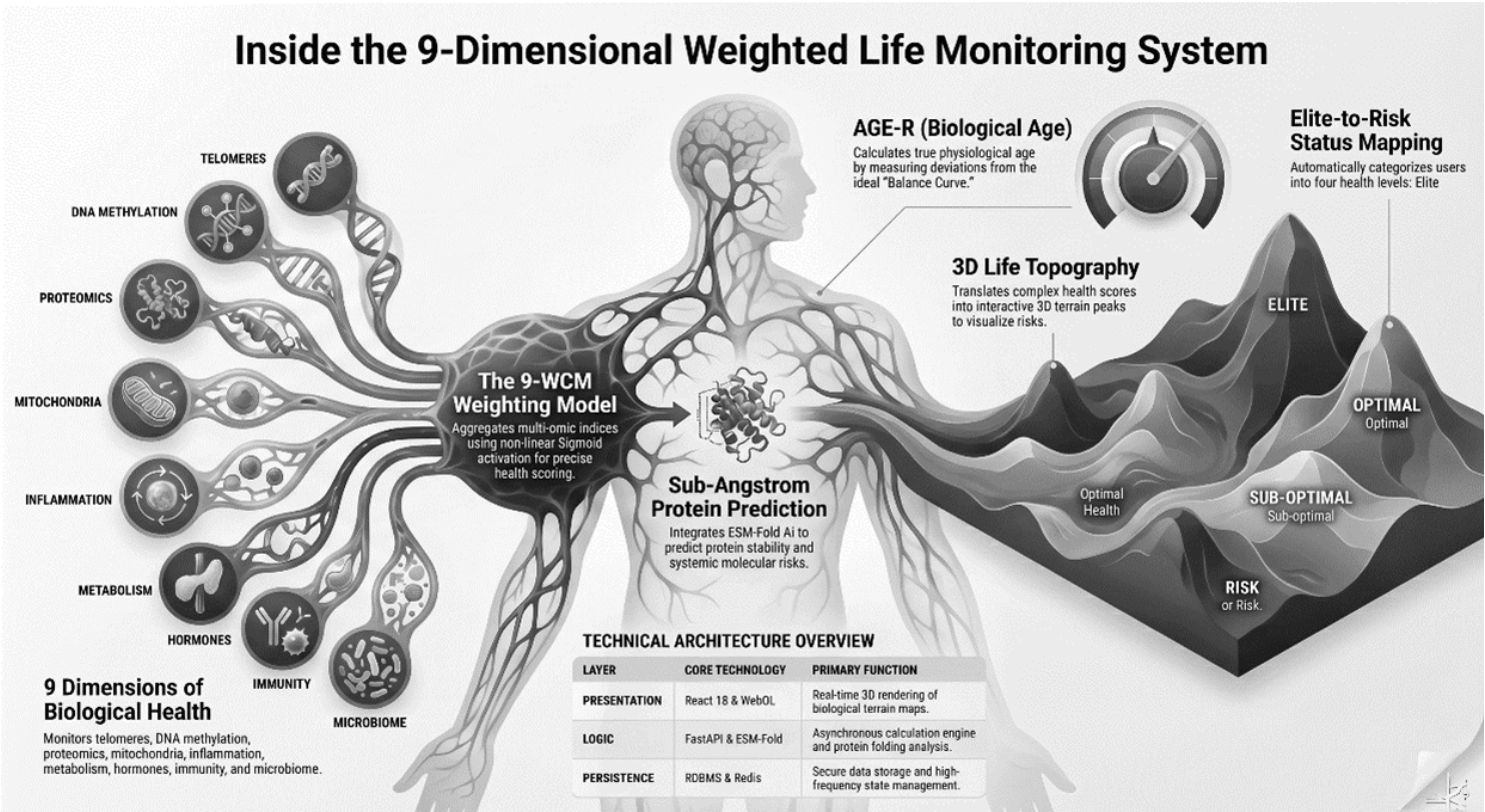


Figure 1

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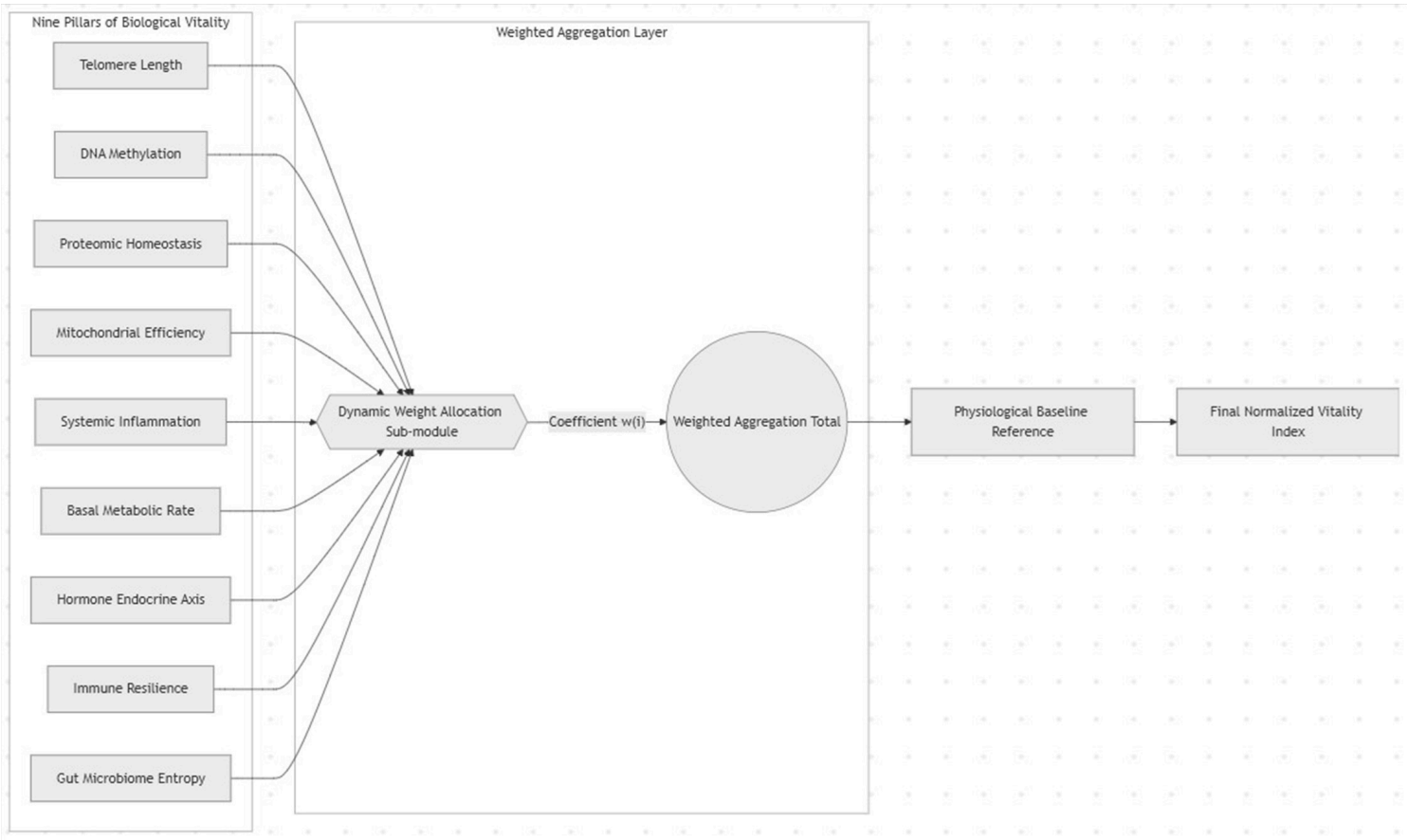


Figure 2

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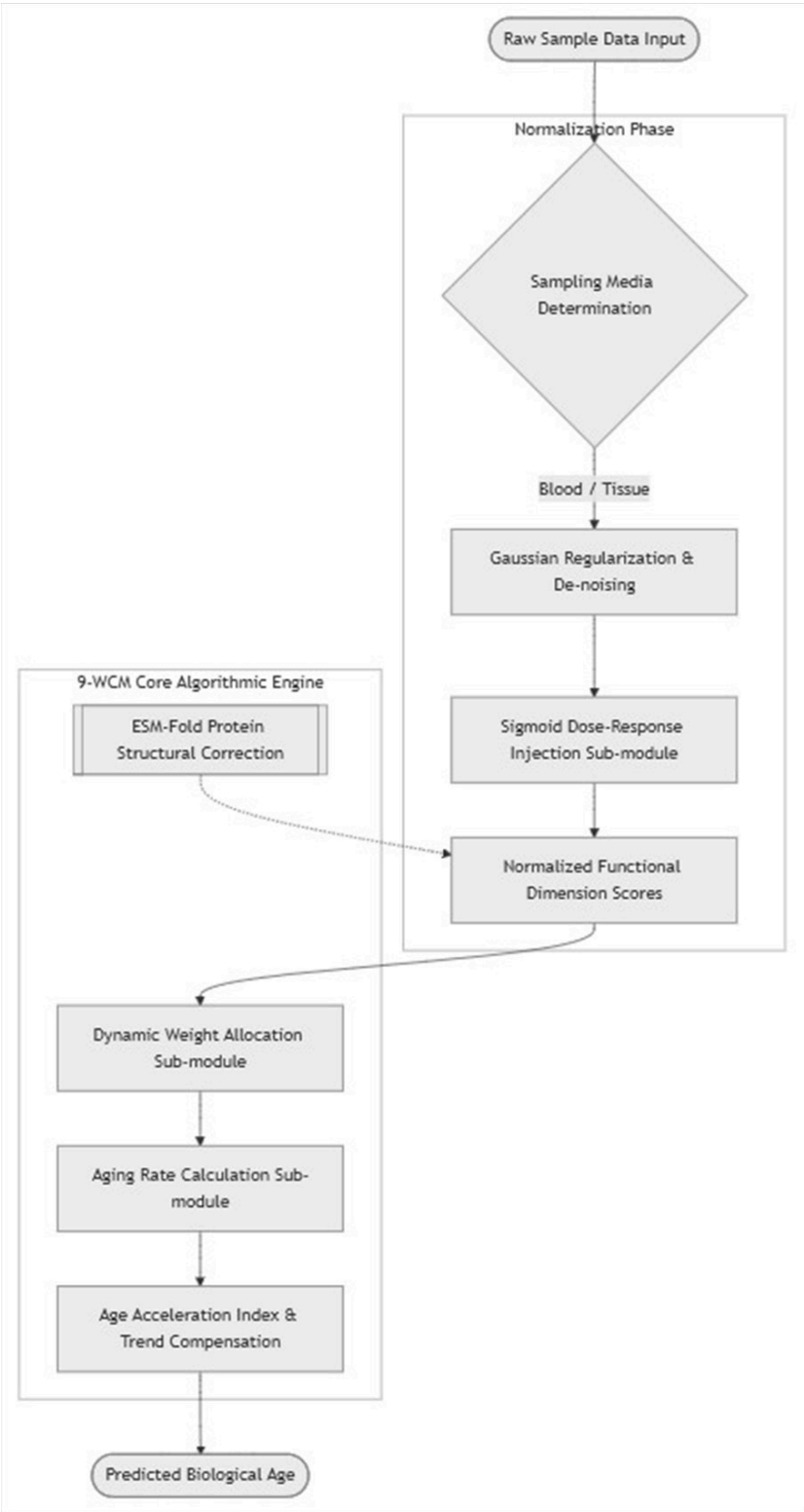


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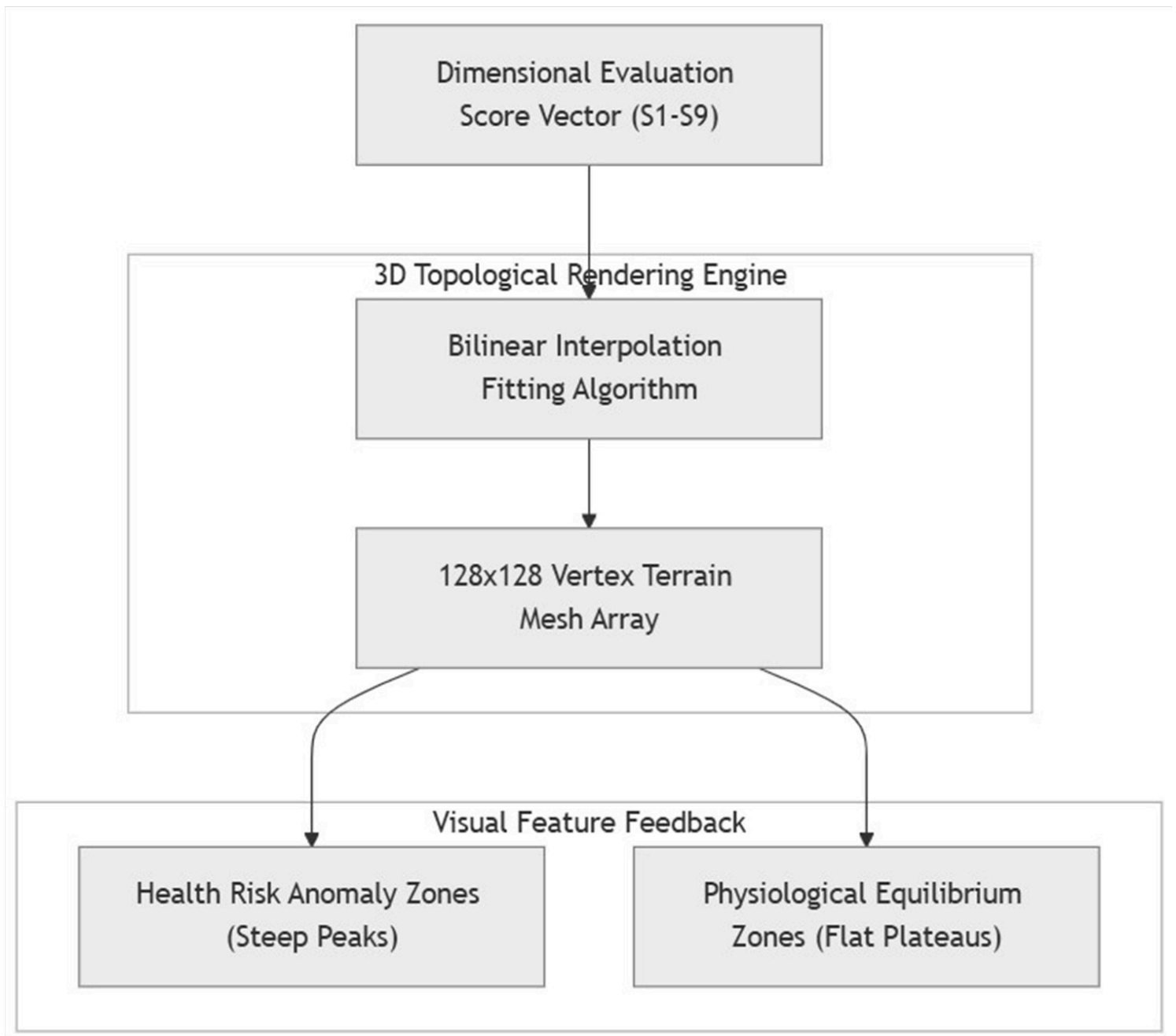


Figure 4

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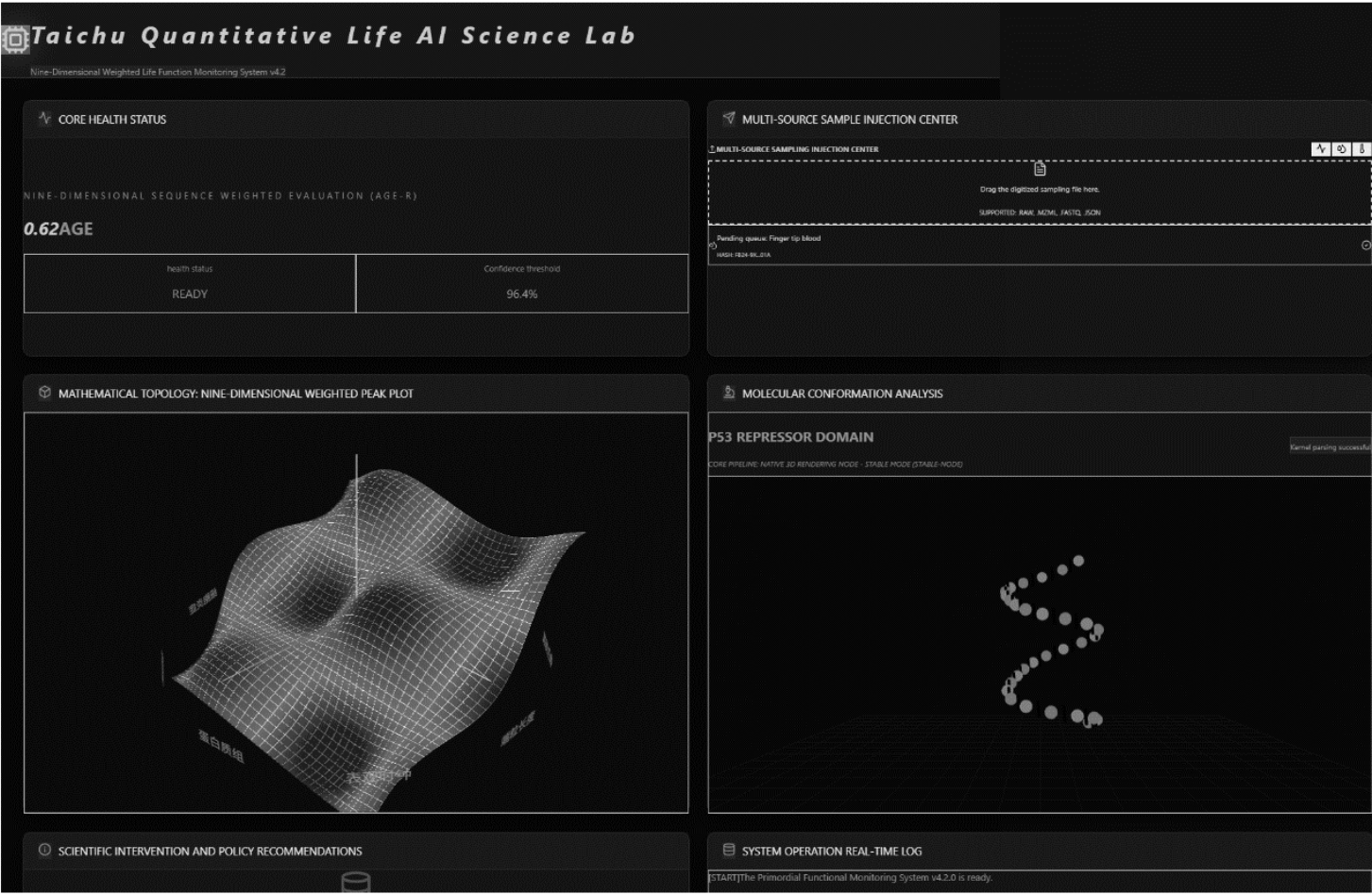


Figure 5

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