Categorical Longevity and The Mathematical Systems Biology of Aging

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Abstract

Categorical longevity (category-theoretic approaches to the mathematical systems biology of aging) is within the co-evolution of human and machine intelligence, which sees higher-structure mathematics as a shared conceptual frontier where biological and artificial systems meet. As machine learning systems grow more capable in the modeling of complex multi-scalar processes, they begin to operate in the same mathematical regimes (hierarchical state spaces, symmetry-breaking transitions, and compositional dynamics) underlying systems theory of aging approaches. Human inquiry is being pushed toward more abstract, categorical, and structural representations precisely because AI systems can now handle various modeling and data analysis tasks. The result is a kind of reciprocal shaping: biological aging motivates richer mathematical formalisms that AI systems are uniquely suited to explore, while AI's representational capacities encourage humans to reconceptualize biological processes in terms of higher-order theories. In this sense, modeling the systems biology of aging through higher-structure mathematics becomes part of a broader co-evolutionary process in which human and machine intelligence jointly expand the possibility space of scientific explanation and intervention.

Longevity: Global Health and Well-Being

Aging is a costly global challenge, reflected both in rising economic burdens and in human suffering associated with late life disease, decline, and frailty. The proportion of the world's population over age 60 is projected to nearly double from 12% in 2015 to 22% by 2050 (WHO, 2025). Yet aging has remained resistant to contemporary biomedical approaches, prompting growing interest in a new era of human–AI collaboration to accelerate progress. Longevity science aims to address the diseases driven by aging itself, including cardiovascular disease, type 2 diabetes, and neurodegenerative disorders, all of which increase as organisms undergo age related entropy (Cipriano et al., 2024).

A major advance in the field is the development of **biomarkers of aging**: highly reproducible molecular signatures spanning epigenetic clocks, proteomic profiles, and metabolomic patterns (Moqri et al., 2023). Epigenetic clocks quantify predictable shifts in DNA-methylation associated with morbidity and mortality risk; proteomic signatures capture systemic physiological changes such as inflammation, immune remodeling, and tissue-maintenance decline; and metabolomic profiles reflect alterations in mitochondrial function, metabolic flexibility, and cellular stress responses. Together, these biomarkers provide a multidimensional framework for estimating biological age and evaluating interventions. Clinically, practitioners now employ tools such as DNAmAge, GrimAge, and PhenoAge (based on nine routine blood biomarkers such as albumin, creatinine, glucose, lymphocytes, and C-reactive protein).

Preventive strategies may be approaching feasibility. Mount Sinai (2025) is conducting a clinical trial evaluating widely used longevity interventions (spermidine, rapamycin, metformin, and GLP-1 agonists) to assess their effects on cognitive, muscular, and immune function. The effort is one of forty entries in the XPRIZE Healthspan competition, a global push to extend healthy human lifespan.

Categorical Longevity

The complexities of the systems biology of aging call for higher-structures mathematics because aging arises from interacting, multi-scale, and non-linear processes that cannot be captured by conventional models, making categorical longevity a natural approach for representing these processes through compositional, hierarchical, and structurally coherent mathematical frameworks. **Category theory** is a branch of mathematics that studies relationships and processes between structures rather than the structures themselves, making it well-suited to modern fields like the systems biology of aging where complex, multi-scale processes must be understood as interconnected systems. The formalization method is based on the relations and processes between objects rather than on their contents (Eilenberg &

MacLane, 1945), and has been widely developed in computational physics, chemistry, and biology (Spivak, 2014).

Systems biology is a unified picture of molecular, cellular, and tissue-level processes. Traditionally, the mathematics of systems biology are based on (1) dynamical systems and differential equations, (2) probability and stochastic processes, and (3) information theory and optimization.

Application #1: Gene Regulatory Networks

Aging at the molecular scale can be understood as a sequence of **irreversible, symmetry-breaking transitions** across gene-regulatory, epigenetic, and redox networks, suggesting that classical dynamical-systems models are too limited to capture their compositional and hierarchical organization. Gene regulatory networks (GRNs) illustrate this most clearly: their attractor landscapes, noise-driven transitions, and regulatory irreversibilities resemble higher-categorical state spaces in which configurations behave like infinity-groupoids and transitions act as structured morphisms (Wu, 2023; Tuyeras, 2023; Baez & Pollard, 2017).

Aging in GRNs thus reflects the **collapse of regulatory symmetries**, the fusion of previously distinct attractors, and the emergence of unstable basins (dynamics aligned with anima-style higher categories (Clausen, 2026) and non-invertible symmetry (Schäfer-Nameki, 2023)), where morphisms cannot be reversed and fusion rules encode the loss of youthful regulatory states. Parallel molecular processes exhibit similar structure: epigenetic drift involves non-invertible chromatin-state transitions with partially broken symmetries; chromatin remodeling functions as defect-like operators that reshape local regulatory environments; and oxidative or redox dynamics display directional, irreversible flows that may be captured by categorical thermodynamics or factorization-algebraic formalisms.

The irreversible nature of many aging transitions (such as the disappearance of youthful attractors or the commitment to senescent transcriptional programs) fits naturally within non-invertible symmetry frameworks, where state changes cannot be undone and fusion rules describe how configurations merge or collapse. GRNs may therefore serve as a biological exemplar of the kinds of systems for which these higher-mathematical formalisms were originally developed.

Application #2: Cellular and Tissue Scales

At the cellular and tissue levels, the alignment with higher-structure mathematics becomes more selective but remains conceptually suggestive. Proteostasis and cellular repair pathways involve complex networks of chaperones, degradation systems, and quality-control mechanisms that can be modeled compositionally using Petri nets or monoidal categories (Hipp et al., 2019). These frameworks capture the flow of molecular species and the irreversible nature of misfolding and aggregation events.

Conclusion

Categorical longevity frames aging as a problem in **higher-structure systems biology**, arguing that these mathematical formalisms provide a unified language for processes shaped by directional transitions, broken symmetries, and complex state-spaces. In this view, aging reflects progressive deformations in the morphism structure of biological organization (seen in the collapse of regulatory attractors, erosion of epigenetic symmetries, exhaustion of stem-cell lineages, and rewiring of immune networks) rather than simple parameter drift in a fixed dynamical landscape. Interventions could be designed in concert with these structural principles. As one of several top-down metamathematical programs in the vein of Galois Smartnetwork Field Theory (Swan et al., 2026), categorical longevity likewise contributes to the broader attempt to integrate mathematics, computation, and physics through higher-structure and symmetry-based reasoning. The aim is a future of well-being in which human and machine intelligence co-evolve through abstract, compositional frameworks towards the shared well-being of standalone and hybrid biological–AI systems.

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