

Categorical Longevity: Higher Tokens, Petri Net Computads, and Well-being

Melanie Swan¹, Takashi Kido², Renato P. dos Santos³

¹University College London

²Teikyo University

³academicum.ai

melanie@DIYgenomics.org, kido.takashi@gmail.com, info@academicum.ai

Abstract

Categorical Longevity is introduced as a computational systems biology approach which applies category theory to unify and formalize the activity, metrics, and interventions of biological systems in addressing the accelerated multisystem decline characteristic of human aging. By providing a comprehensive and computation-ready structure, this method integrates diverse mathematical models and data representations, enabling a deeper understanding of biological dynamics across scales. While advancements such as hallmarks of aging, biomarkers, epigenetic clocks, and organ-specific aging metrics have proliferated, the absence of a standardized framework limits their joint analysis and practical application. Categorical Longevity addresses this gap, offering tools for multiscale analysis, robust dynamical modeling, and the integration of computational technologies such as blockchain to facilitate scalable, secure population-level deployment.

Categorical Longevity

Longevity entails potentially curing the diseases of aging. Aging is the primary driver of many leading causes of death, including cardiovascular disease, type 2 diabetes, and neurodegenerative disease, as organisms experience accelerated decline (entropy) with aging (Cipriano et al. 2024). A recent advance is the quantization of aging through biomarkers (Lyu et al. 2024), hallmarks (Lopez-Otin et al. 2024), and remedies (Guarente et al. 2024). The implication is metrics for targeted intervention, however, these measures have yet to be assembled into an overarching formal structure.

The main tools employed by practitioners are twenty validated biomarkers of aging and twelve hallmarks of aging. Top-tier biomarkers include epigenetic clocks (DNAmAge and GrimAge) and the PhenoAge test (nine routine blood biomarkers: albumin, creatinine, glucose, C-reactive protein, ALK, lymph, MCV, RDW, WBC). The twelve hallmarks of aging are genomic instability, telomere attrition, epigenetic alterations, loss of proteostasis, loss of macro-autophagy, deregulated nutrient-sensing, mitochondrial dysfunction,

cellular senescence, stem cell exhaustion, altered intercellular communication, chronic inflammation, and dysbiosis.

The main biomarker is the rate of epigenetic mutation (observed through epigenetic clocks and blood biomarkers) and the predominant hallmark is genomic instability (the rate of decline in DNA damage repair). Dynamical modeling with a focus on rate-based analysis is implicated.

This work introduces Categorical Longevity as a research program to consolidate the quantitative systems biology of aging into a standardized approach. Category theory is chosen as a formalization method based on the relations and processes between objects rather than their contents (Eilenberg and MacLane 1945), as widely developed in computational physics, chemistry, and biology (Spivak 2014).

Categorical Deep Learning

Categorical deep learning is the application of category theory to machine learning particularly as a formal approach to neural network architecture design (Gavranovic et al. 2024). Specific to digital biology (e.g. drug discovery and longevity intervention) is a proposal for probabilistic molecular programming networks (Lessard 2022). The research program works with large networks of chemical reactions, treats chemistry as a probabilistic process, and models molecular conformations as fields of interactions. The solution is a computation-amenable (practical type theory for symmetric monoidal categories) interpretation of Petri nets, that is probabilistic (via Markov categories), with molecular conformations modeled in space-valued computads (categories in which objects and morphisms (relations) are spaces).

Categorical Network Science

Categorical network science or higher-order networks is the categorical formulation of networks to capture relationships beyond the linear interaction of two nodes (Bick et al. 2023).

Geometric and topological primitives (building blocks) are used such as persistent homology (multiscalar features in topological data analysis), simplicial complexes (basic shapes glued together), and hypergraphs (general graphs).

Petri Nets. Petri nets are a categorical network modeling tool for distributed systems. In the basic setup, Petri nets consist of three elements: places (vertices), transitions (vertices), arcs (edges between places and transitions). However, Petri nets have the additional innovation of token balances stored at nodes which can accumulate and trigger an event, for example firing a chemical reaction. The token system has three aspects: tokens (resource balances at nodes), markings (overall network configurations of token balances), and firing events (processes for updating network token balances). The token system creates a second system level (L2) at which dynamics can be studied directly.

Higher Petri Nets. Various forms of higher Petri nets (Petri nets with additional categorical structure) have been developed. Whole-grain nets are a geometric-algebraic dual interpretation of Petri nets amenable to both non-fungible token (NFT) and fungible token modeling (Kock 2023). The geometric interpretation treats NFTs by explicitly mapping sets of tokens (with individual bookkeeping). The algebraic interpretation treats fungible tokens using multisets (as collective state transitions). Sigma-nets offer further refinement selectivity as to which non-fungible (individual) and fungible (collective) tokens are fired (Baez et al. 2021).

Categorical Longevity

The categorical longevity formalism proposal has two parts: Petri net computads (inspired by categorical deep learning) and higher tokens (extended from categorical networks).

Petri Net Computads. The notion of Petri net computads encapsulates the space-valued computad formulation of probabilistic molecular programming for longevity. Computational probabilistic categories are needed to model probabilistic outcomes in longevity such as genetic mutation impact, intervention efficacy, and population-scale programs.

Higher Tokens. Higher tokens are the concept of a 2-category (maps between maps) extension of Petri net token systems with blockchain primitives such as UTXO (unspent transaction output) and ZKP (zero-knowledge proofs). The higher-dimensional 2-category of tokens may help to reduce the complexity in whole-grain sigma-net formulations, and to enhance functionality, offering gradient-based control and smart routing in Petri net digital twin systems. Higher-token Petri nets could provide a Level 2 system (like the Lightning Network) for smart contract longevity DAOs (decentralized autonomous organizations) and other DeSci (decentralized science) applications. Higher tokens are a 2-category for longevity but connote the additional structure of an infinity category concretized in a homotopy theory.

HoTT Longevity. Higher-token Petri net computads are just one element towards a broader homotopy type theory of longevity and biosystems more broadly. A homotopy type theory continues into higher-dimensional formulations: space-valued and time-valued paths lift to paths between paths and higher homotopies, creating an overall abstraction apparatus, one of whose proximate consequences could be a cognitive interface to digital twin systems.

Categorical Longevity Research Agenda

Higher-token Petri net computad projects could include:

- Categorical Alzheimer's dynamics (Norton et al. 2024)
- Enzyme kinetics (Michaelis-Menten) for epigenetic mutation and damage repair rates (Bardini et al. 2016)
- 2-Segal space immune pathway analysis (Lin et al. 2024)
- AQFT-FQFT field theory of senescent cell clearance
- Feynman category fibration analysis of inflammaging
- Open Petri net model of longevity SIR (Baez et al. 2022)

References

- Bardini, R.; Benso, A.; Di Carlo, S.; et al. 2016. Using Nets-Within-Nets for Modeling Differentiating Cells in the Epigenetic Landscape. *IWBBIO*. Granada ES April 20-22, 2016. Pp. 315-321.
- Baez, J.; Cho, S.; Cicala, D.; et al. 2022. Applied category theory in chemistry, computing, & social networks. *AMS* 69(2):292-297.
- Baez, J.; Genovese, F.; Master, J. and Shulman, M. 2021. Categories of Nets. arXiv:2101.04238v2.
- Bick, C.; Gross, E.; Harrington, H.; et al. 2023. What Are Higher-Order Networks? *SIAM Review* 65(3):686-731.
- Cipriano, A.; Moqri, M.; Maybury-Lewis, S. Y.; et al. 2024. Mechanisms, pathways and strategies for rejuvenation through epigenetic reprogramming. *Nat Aging* 4(1):14-26.
- Eilenberg, S. and MacLane, S. 1945. General Theory of Natural Equivalences. *Trans AMS* 58(2):231-94.
- Gavranovic, B.; Lessard, P.; Dudzik, A.; et al. 2024. Position: Categorical deep learning is algebraic theory. arXiv:2402.15332v2.
- Guarente, L.; Sinclair, D. A. and Kroemer, G. 2024. Human trials exploring anti-aging medicines. *Cell Metabolism* 36(2):P354-376.
- Lessard, P. 2022. A Computadic Intro to Shulman's PTT and Variations for Semi-cartesian/Markov Categories. Topos Institute.
- Lopez-Otin, C.; Blasco, M. A.; Partridge, L.; et al. 2023. Hallmarks of aging: An expanding universe. *Cell* 186(2):243-278.
- Lyu, Y. X.; Fu, Q.; Wilczok, D.; et al. 2024. Longevity biotechnology: bridging AI, biomarkers, geroscience and clinical applications for healthy longevity. *Aging* 16(20):12955-12976.
- Kock, J. 2023. Whole-grain Petri nets. arXiv:2005.05108v4.
- Lin, X.; Chang, X.; Zhang, Y.; et al. 2024. Automatic construction of Petri net models for computational simulations of molecular interaction network. *npj Syst Biol Appl* 10(131).
- Norton, J.; Seah, N.; Santiago, F.; et al. 2024. Multiple aspects of amyloid dynamics in vivo integrate to establish prion variant dominance in yeast. *Front. Mol. Neurosci* 17:1439442.
- Spivak, D. I. 2014. *Category Theory for the Sciences*. Cambridge MA: The MIT Press.