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Gene Latency: A Systems-Level Framework for Understanding Preserved Genomic Potential in Biotechnology and Drug Discovery

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Abstract

Modern genomics has significantly advanced our understanding of how genes are regulated, expressed, and modified in response to biological and environmental signals. However, a fundamental question remains insufficiently explored: why do genomes preserve large amounts of structurally intact genetic information that remain inactive or non-executing across extended biological timescales?

This presentation introduces Gene Latency Genomic Theory (GLT), a conceptual framework proposing that genomes maintain a substantial portion of their information in a latent state characterized by preserved structure, suspended execution, and conditional recallability. Within this framework, inactive genes are not necessarily evolutionary residues but may represent stored biological potential that can be activated under specific contextual conditions such as environmental stress, developmental transitions, or system-level regulatory shifts.

The theory reframes genome function as a decision architecture in which biological systems manage potential before execution. Concepts such as latency depth, contextual recall thresholds, and latent genomic portfolios are introduced to describe how preserved genetic information contributes to biological memory, adaptability, and evolutionary resilience.

Understanding gene latency has important implications for biotechnology and drug discovery. Latent genomic elements may represent previously overlooked regulatory resources, influence cellular responses to therapeutic interventions, and contribute to unexplained variability in drug metabolism and disease susceptibility.

By integrating theoretical biology with systems genomics and emerging computational approaches, this framework aims to open new directions for interpreting genomic inactivity, modeling biological decision systems, and exploring hidden layers of functional potential within the genome.