

# An Evolutionary Hypothesis on the Persistence of Non-Coding DNA in Complex Genomes: The Passive Selfish DNA Model

Author: Francesco Sancamillo

sancamillofrancesco1@gmail.com

## Abstract

Non-coding DNA constitutes the vast majority of eukaryotic genomes, yet its evolutionary role remains largely unresolved. This manuscript proposes a theoretical model in which non-coding DNA persists not due to functional utility, but as "passive selfish DNA"-elements that replicate by coexisting with coding sequences in vital genomes. Drawing analogies with endogenous retroviruses and vertically transmitted transposons, this perspective reframes the issue of genomic persistence in terms of replicative neutrality and genomic compatibility rather than function. The model suggests new directions for investigating genome architecture and evolutionary neutrality.

Keywords: non-coding DNA, genome evolution, selfish DNA, endogenous retroviruses, passive replication

## 1. Introduction

Only a small fraction of the human genome-about 2%-codes for proteins. The remaining 98%, often labeled "junk DNA," was long considered functionless, although recent studies have uncovered some regulatory and structural roles. However, a substantial portion of this DNA still lacks a clear functional characterization.

This article proposes an alternative evolutionary hypothesis: non-coding DNA is conserved not because it serves a direct physiological role, but because it benefits from being embedded in genomes that express coding genes. These genes produce organisms, which act as "genetic duplication machines." In this way, non-coding DNA is passively replicated as long as it does not negatively affect the host organism's viability.

## 2. The Concept of Selfish DNA and the Proposed Theory

According to Dawkins' (1976) selfish gene theory, genes can be viewed as entities shaped by natural selection to ensure their own replication. Extending this concept, I propose that non-coding sequences can also act as selfish genetic elements-not through active transposition or expression, but by passively persisting within replicating genomes.

The organism, generated by the expression of coding genes, enables replication of the entire genome. As long as non-coding sequences are part of this genome and remain neutral or non-deleterious, they are replicated during cell division, ensuring their evolutionary continuity.

## 3. Analogy with Transposons and Endogenous Retroviruses

This hypothesis finds a natural analogy in transposons, particularly in human endogenous retroviruses (HERVs). These elements, which make up at least 8% of the human genome (with some estimates up to 25%), derive from ancient viral integrations and are inherited vertically.

Transposons are examples of active selfish DNA—they replicate autonomously but must avoid harming the host to persist. Similarly, passive non-coding DNA does not move autonomously, but benefits from replication within genomes that support the organism's survival. Its persistence may depend more on evolutionary neutrality and compatibility than on utility.

#### **4. Implications and Future Directions**

This model suggests that non-coding DNA is not necessarily maintained for physiological reasons, but rather for its replicative compatibility within vital genomes. This framework opens new avenues for research:

- Co-evolution of coding and non-coding genomic regions
- Genome architecture in species with high non-coding DNA content
- Comparative studies of non-mobile selfish elements

Computational simulations could test the long-term stability and evolutionary dynamics of passive selfish sequences under different selective regimes.

#### **5. Conclusions**

The theory presented proposes that non-coding DNA, or at least a significant portion of it, persists not for a physiological role but because it can exploit the genomic replication driven by coding DNA expression. In this sense, it represents a form of passive selfish DNA.

The resemblance to the behavior of transposons—especially non-pathogenic, vertically transmitted ones like HERVs—supports this view and provides a framework for future experimental validation.

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