Title :

Catalogue of Tetra-Stranded Helical Architectures: Classes, Topological Invariants, and Structural Transitions

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Abstract

The structural space of nucleic acids is commonly explored through local conformational variants of duplex DNA. However, if a tetra-stranded hereditary polymer such as Q-DNA is considered as a canonical genome-scale state, topology becomes a primary organizing principle rather than a secondary constraint. In this work, I develop a topological classification framework for tetra-stranded helices, introducing a catalogue of admissiblearchitectures defined by strand number, chirality, winding modes, and inter-strand entanglement. I define generalized topological invariants—including multi-strand linking numbers and generalized supercoiling—and analyze their conservation and transformation across structural transitions. I then formalize Q↔D transitions, describing how a tetra-stranded canonical state may interconvert with duplex-dominant states under controlled topological operations. The result is an atlas of tetra-strandedarchitectures and a conceptual phase diagram of topological regimes, providing a foundation for subsequent energetic, kinetic, and evolutionary analyses of Q-DNA.

Keywords: tetra-stranded helices, DNA topology, linking number, supercoiling, genome architecture, Q-DNA, non-canonical nucleic acids.

1. Introduction

1.1 Why topology is central for tetra-stranded heredity

In duplex DNA, topology is already critical: supercoiling, linking number, and knotting strongly influence replication, transcription, and chromosome segregation. However, these effects are often treated as modifiers of a structurally simple two-strand system.

In contrast, for a canonical tetra-stranded genome, topology is no longer secondary. The number of strands, their mutual winding, and their entanglement define:

- whether a genome-scale structure is physically realizable,
- whether it can be replicated and segregated,
- and whether transitions between structural states are possible without irreversible damage.

I therefore treat topology as a first-class organizing principle of Q-DNA.

1.2 Scope and objectives

The goal of this paper is not to propose a single “correct” tetra-stranded helix. Instead, I aim to:

- Enumerate the space of topologically distinct tetra-stranded helical architectures.
- Define invariants that characterize and distinguish these architectures.
- Describe transitions between tetra-stranded and duplex-dominant states (Q↔D).
- Produce an atlas and phase diagram usable by later energetic and biochemical studies.

2. Conceptual Framework

2.1 Strands as topological objects

I model each strand as a continuous oriented curve embedded in three-dimensional space. A tetra-stranded genome is thus a four-component curve system with:

- mutual winding,
- possible entanglement,
- and global constraints imposed by closure, length, and periodicity.

Unlike duplex DNA—where topology is largely described by a single linking number—tetra-stranded systems require a vector or matrix of invariants.

2.2 Canonical vs non-canonical topological states

I distinguish:

1. Canonical Q-states: genome-scale tetra-stranded conformations that are stable and reproducible.
2. Non-canonical or transitional states: metastable or local configurations encountered during folding or conversion.

This distinction parallels, but goes beyond, the duplex/motif separation discussed in the first Q-DNA paper.

3. Classes of Tetra-Stranded Helical Architectures

3.1 Strand arrangement classes

I identify three primary classes based on strand organization:

Class I — Parallel bundled helices

All four strands wind in the same axial direction, forming a tightly coupled bundle.

- High symmetry
- Potentially high rigidity
- Strong coupling between strands

Class II — Paired duplex helices

Two duplex-like subunits associate into a higher-order tetra-stranded helix.

- Modular
- Naturally compatible with Q↔D transitions
- Likely lower topological barriers

Class III — Interwoven braid helices

All four strands are mutually braided, with no clear duplex substructure.

- Maximum entanglement
- High topological protection
- Potentially slow kinetics

3.2 Chirality and handedness

For each class, I distinguish:

- left-handed vs right-handed global chirality,
- mixed chirality states (e.g., duplex subunits of opposite handedness),
- and chiral frustration regimes where local and global handedness compete.
- Chirality becomes a discrete topological label rather than a minor geometric preference.

4. Topological Invariants for Tetra-Stranded Genomes

4.1 Generalized linking numbers

In duplex DNA, the linking number Lk describes the total winding between two strands.
For tetra-stranded systems, I define a linking matrix:

$$\mathbf{L} = \begin{pmatrix} 0 & L_{12} & L_{13} & L_{14} \\ L_{21} & 0 & L_{23} & L_{24} \\ L_{31} & L_{32} & 0 & L_{34} \\ L_{41} & L_{42} & L_{43} & 0 \end{pmatrix}$$

where each L_{ij} measures the mutual winding between strands i and j.

This matrix:

- captures redundancy,
- reveals symmetry classes,
- and constrains admissible transitions.

4.2 Generalized supercoiling

I extend the classical decomposition:

$$Lk = Tw + Wr$$

to a multi-strand context, where twist and writhe become distributed quantities across the strand network.

This leads to:

- collective torsional modes,
- strand-specific twist reservoirs,
- and new forms of topological stress unique to tetra-stranded genomes.

4.3 Topological protection and fragility

Certain architectures exhibit topological protection, meaning that large-scale rearrangements require strand passage or cutting. Others are topologically fragile, allowing smooth deformation.

This distinction has direct implications for:

- evolvability,
- repair mechanisms,
- and enzymatic accessibility.

5. Structural Transitions: Q ↔ D

5.1 Definition of Q↔D transitions

A Q↔D transition is a structural transformation between:

- a tetra-stranded canonical state (Q),
- and a duplex-dominant state (D),
- without loss of sequence information.

5.2 Transition pathways

I identify three generic pathways:

Pathway A — Duplex pair dissociation

A Class II tetra-helix separates into two duplexes while conserving linking numbers within subunits.

Pathway B — Progressive strand unbundling

A Class I or III structure relaxes through sequential reduction of inter-strand coupling.

Pathway C — Topological rupture

Transitions requiring strand passage (analogous to topoisomerase-mediated events).

Each pathway corresponds to a distinct topological cost and kinetic barrier.

5.3 Conservation laws and forbidden transitions

Certain Q↔D transitions are topologically forbidden without strand cutting. This allows one to predict:

- which architectures can interconvert reversibly,
- which are effectively locked once formed.

6. Atlas of Tetra-Stranded Architectures

6.1 Construction of the atlas

I assemble an architecture atlas indexed by:

- strand arrangement class,
- chirality,
- linking matrix symmetry,
- degree of entanglement.

Each entry corresponds to a distinct topological species.

6.2 Topological phase diagram

I introduce a conceptual topological phase diagram, where axes represent:

- degree of strand coupling,
- entanglement density,
- and topological protection.

Regions correspond to:

- duplex-like regimes,
- Q-DNA canonical regimes,
- kinetically trapped states.

7. Discussion

7.1 Why topology constrains biochemistry

Any attempt to realize Q-DNA experimentally must confront topology first. A chemically stable tetra-strand that is topologically non-replicable is biologically inert. This paper therefore precedes energetic and enzymatic analyses intentionally.

7.2 Implications for replication and evolution

Topologically protected architectures may:

- reduce error rates,
- slow evolutionary dynamics,
- increase robustness.

Conversely, topologically fragile architectures may:

- enable rapid adaptation,
- but at the cost of stability.

This trade-off will be central in later papers on evolvability.

7.3 Relation to known DNA topology

While inspired by duplex DNA topology, the tetra-stranded case introduces fundamentally new invariants. Duplex intuition cannot be naïvely extrapolated; Q-DNA requires its own topological language.

7.4 Figures proposed

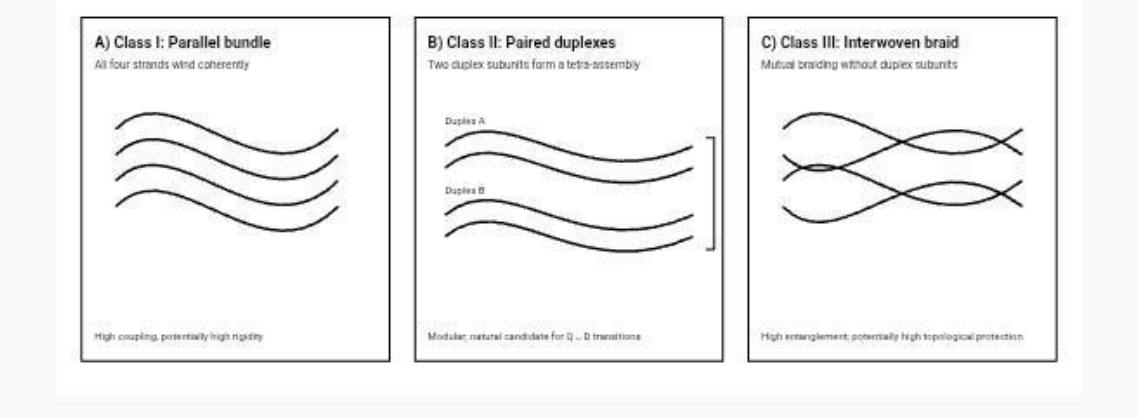

Figure 1. Classes of Tetra-Stranded Helical Architectures
Schematic representations of Class I (parallel bundle), Class II (paired duplex), and Class III (interwoven braid).

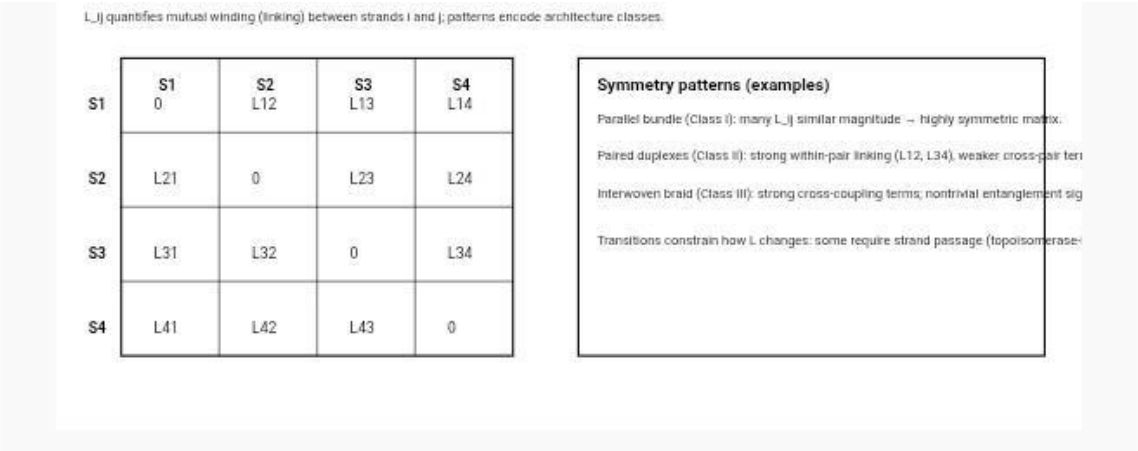

Figure 2. Generalized Linking Matrix for Tetra-Stranded Genomes
Graphical illustration of pairwise linking numbers and symmetry patterns.

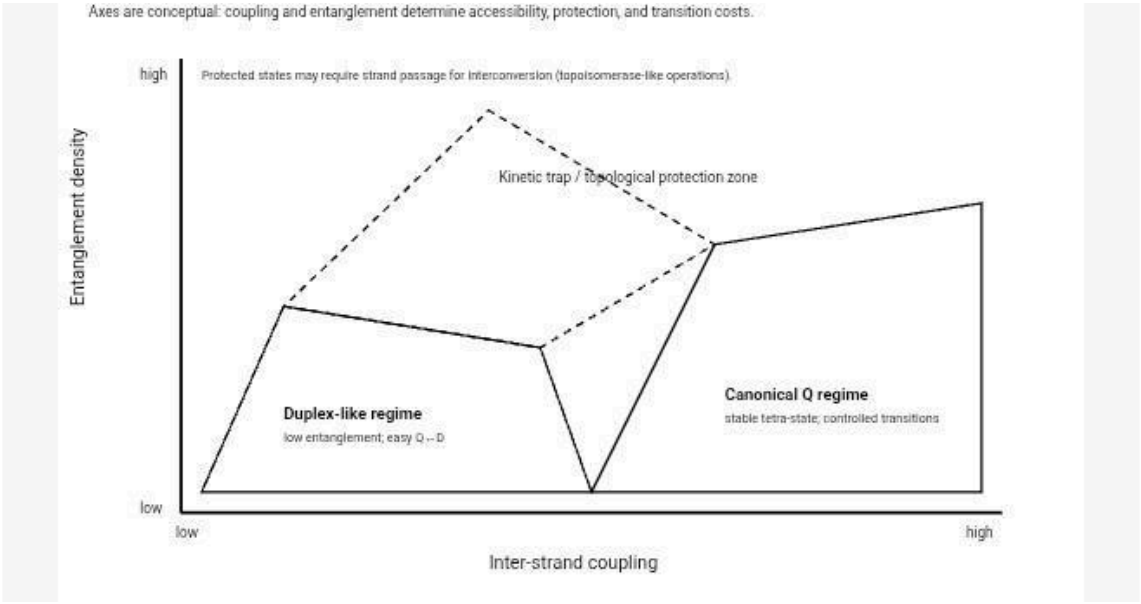

Figure 3. Generalized Supercoiling in Tetra-Stranded Systems
Extension of twist/writhe decomposition to multi-strand structures.

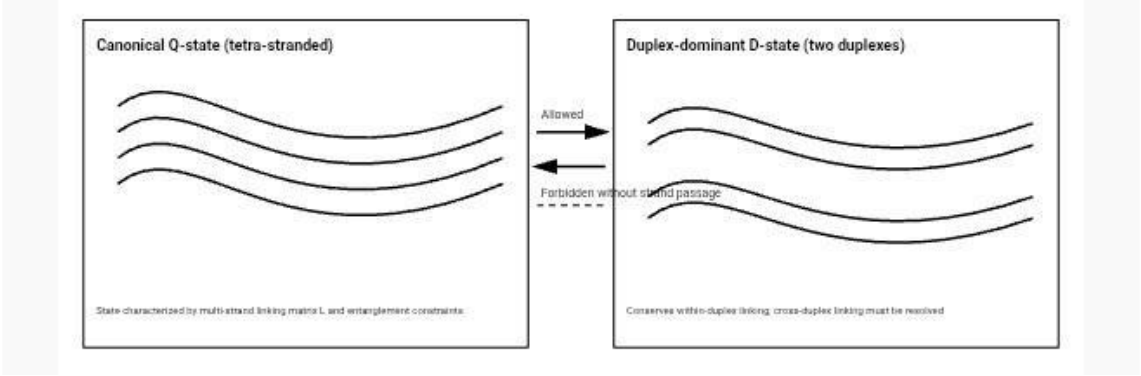

Figure 4. Q↔D Structural Transition Pathways
Cartoons of allowed and forbidden transitions between tetra-stranded and duplex states.

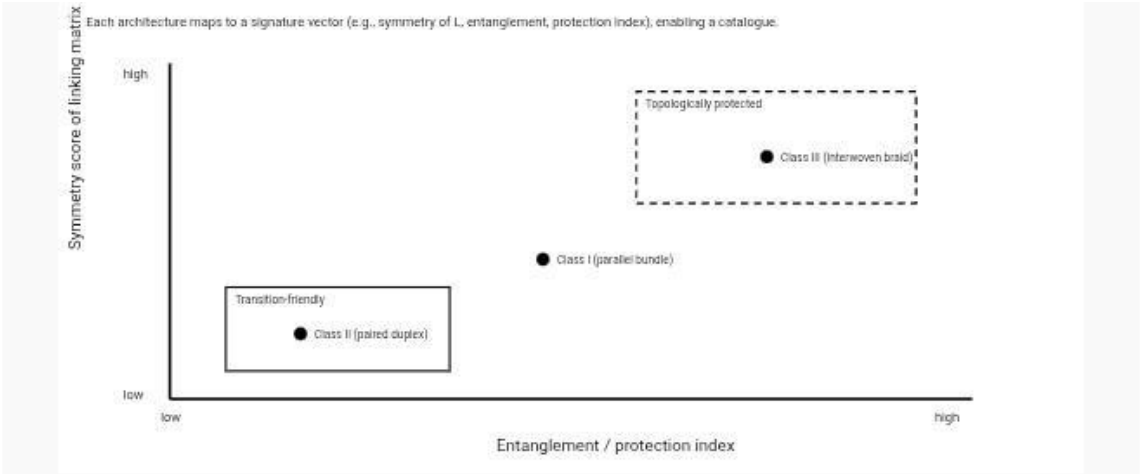

Figure 5. Topological Phase Diagram of Genome Architectures
Conceptual map showing regions of duplex dominance, Q-DNA canonicality, and kinetic trapping.

8. Conclusion

In this paper, I present the first systematic topological classification of tetra-stranded helical architectures relevant to a canonical Q-DNA genome. By defining classes, invariants, and admissible transitions, I establish topology as a foundational constraint on tetra-stranded heredity. The resulting atlas and phase diagram provide a map of what is structurally possible—and what is forbidden—before chemistry or enzymology are considered. This framework sets the stage for subsequent analyses of stability, dynamics, and biological plausibility.

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