Title :

Four-Strand Pairing Beyond Watson–Crick: Interaction Hypergraphs, Controlled Degeneracy, and Sequence Constraints

Author :

Ndenga Lumbu Barack (alias BarackEinstein97)
Independent Researcher
Kinshasa, Democratic Republic of the Congo
📧 **ndengabarack@gmail.com**
📞**(+243) 837767430**

Abstract

Canonical DNA heredity relies on **pairwise Watson–Crick base pairing**, a remarkably simple recognition rule that underlies duplex stability and faithful replication. However, a canonical tetra-stranded hereditary polymer such as Q-DNA cannot rely exclusively on pairwise interactions without collapsing into a duplex-dominant description. In this work, I introduce a **multi-body pairing framework** for four-stranded genomes, formalized using **interaction hypergraphs** rather than simple base-pair graphs. I define classes of **four-strand hydrogen-bonding units**, analyze their energetic and informational degeneracy, and derive **sequence–structure compatibility rules** required for genome-scale coherence. The result is a **dictionary of Q-recognition units** and a set of **design constraints** that make tetra-stranded encoding possible, distinct, and testable.

Keywords: Q-DNA, hydrogen bonding, non-Watson–Crick pairing, hypergraphs, multi-body interactions, sequence constraints

1. Introduction

1.1 Why Watson–Crick pairing is insufficient for Q-DNA

Watson–Crick pairing is fundamentally **binary:** one base recognizes exactly one complementary partner. This binary logic is perfectly adapted to duplex heredity but becomes problematic for tetra-stranded systems. If four strands interact only via pairwise Watson–Crick rules, the system naturally decomposes into duplex subunits, undermining the canonical tetra-state.

I therefore argue that **Q-DNA requires a new language of recognition**, one that is:

- intrinsically multi-strand,
- cooperative rather than additive,
- and not reducible to independent base pairs.

1.2 From base pairs to recognition units

Rather than thinking in terms of “base pairs,” I introduce the notion of **recognition units**: minimal sets of nucleotides across multiple strands whose collective interaction stabilizes the structure and encodes information.

This shift mirrors transitions in other fields (e.g., from pairwise to many-body potentials in condensed matter physics).

2. Conceptual Framework: Hypergraphs for Molecular Recognition

2.1 Graphs vs hypergraphs

In duplex DNA, recognition can be represented as a **graph**:

- nodes = bases,
- edges = hydrogen bonds between complementary bases.

In Q-DNA, recognition is inherently **multi-body**. I therefore use **hypergraphs**, where:

- nodes still represent bases,
- **hyperedges** connect three or four nodes simultaneously.

This formalism captures interactions that are:

- cooperative,
- context-dependent,
- and non-decomposable into pairwise terms.

2.2 Definition of a Q-recognition hyperedge

A **Q-hyperedge** is defined as a set:

$$H = \{b_i^{(1)}, b_j^{(2)}, b_k^{(3)}, b_l^{(4)}\}$$

where one base from each strand participates in a joint hydrogen-bonding network.

Such a hyperedge is:

- either stabilizing (allowed),
- weakly stabilizing (conditional),
- or forbidden (geometrically or chemically incompatible).

3. Classes of Four-Strand Pairing Units

3.1 Fully symmetric four-base units

In this class, all four bases participate equally in a closed hydrogen-bonding network.

Properties:

- maximal cooperativity,
- low degeneracy,
- high structural specificity.

These units strongly favor canonical Q-states.

3.2 Asymmetric four-base units

Here, three bases form a primary interaction, while the fourth plays a stabilizing or modulatory role.

Properties:

- increased degeneracy,
- tunable stability,
- useful for controlled flexibility.

3.3 Hybrid units (3+1 and 2+2)

Hybrid units combine:

- one triadic interaction plus a weaker fourth contact,
- or two coupled non-Watson–Crick pairs.

These units naturally mediate **Q↔D transitions** by allowing partial duplex character.

4. Controlled Degeneracy and Information Encoding

4.1 Degeneracy as a design parameter

In duplex DNA, degeneracy is limited: mismatches are usually destabilizing. In Q-DNA, **controlled degeneracy** can be advantageous:

- multiple sequences map to the same recognition unit,
- robustness to mutations increases,
- but excessive degeneracy reduces information capacity.

I treat degeneracy as a tunable parameter rather than a flaw.

4.2 Information encoding with hyperedges

Encoding in Q-DNA is not strictly linear along a single strand. Instead:

- information is distributed across strands,
- recognition units act as **constraints**, not symbols,
- reading requires satisfying hyperedge compatibility rather than matching pairs.

This creates a fundamentally different encoding logic from Watson–Crick DNA.

5. Sequence–Structure Compatibility Rules

5.1 Local compatibility

At the local level, sequence quadruplets must:

- fit the geometry of the hyperedge,
- satisfy hydrogen-bond donor/acceptor balance,
- avoid steric clashes.

5.2 Global consistency

At genome scale, local units must tile without conflict:

- no incompatible hyperedges sharing nodes,
- no propagation of geometric frustration,
- no accumulation of unresolved strain.

This defines a **constraint satisfaction problem** over the genome.

5.3 Forbidden sequences

Certain sequences are forbidden not because of chemistry alone, but because they induce **topological or geometric inconsistency** when tiled repeatedly.

6. Dictionary of Q-Recognition Units

6.1 Structure of the dictionary

I propose a dictionary where each entry specifies:

- participating bases,
- geometry class,
- energetic strength,
- degeneracy level,
- compatibility constraints.

6.2 Minimal viable alphabet

I argue that Q-DNA may require:

- either an expanded base alphabet,
- or chemically modified bases,

to achieve sufficient diversity of stable hyperedges.

7. Discussion

7.1 Why biology converged on pairwise recognition

Pairwise recognition is fast, simple, and sufficient for duplex heredity. Multi-body recognition increases complexity and kinetic barriers, which likely explains why it is rare or absent in extant biology.

7.2 Why Q-recognition is still plausible

Synthetic systems are not constrained by evolutionary legacy. Engineered chemistries can exploit cooperative multi-body interactions deliberately.

7.3 Implications for replication and error correction

Multi-body recognition naturally enables:

- consensus-based error suppression,
- correlated mutation handling,
- structural proofreading.

These features will be central to later papers on replication and evolvability.

8. Conclusion

I have introduced a **formal language for four-strand recognition** based on interaction hypergraphs rather than Watson–Crick pairs. By defining classes of multi-body hydrogen-bonding units, analyzing their degeneracy, and deriving sequence–structure compatibility rules, I establish the conceptual foundation for **information encoding in a canonical tetra-stranded genome**. This framework yields a dictionary of Q-recognition units and concrete design rules, enabling systematic exploration of tetra-stranded heredity beyond duplex DNA.

Figures

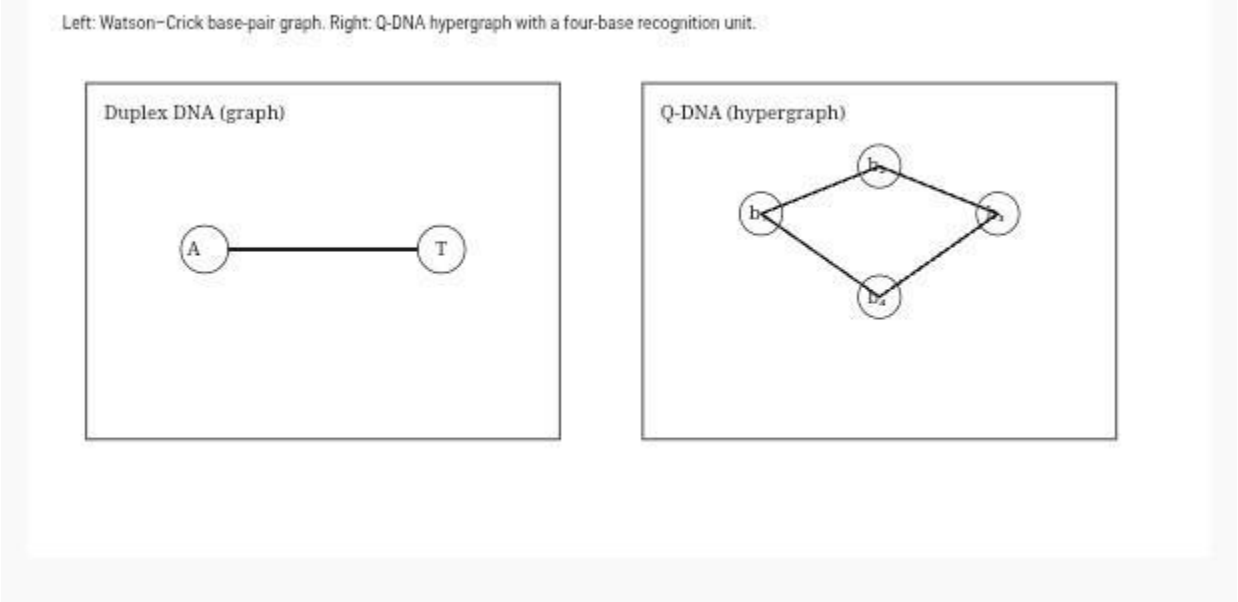

Figure 1 — From Base Pairs to Hypergraph Recognition

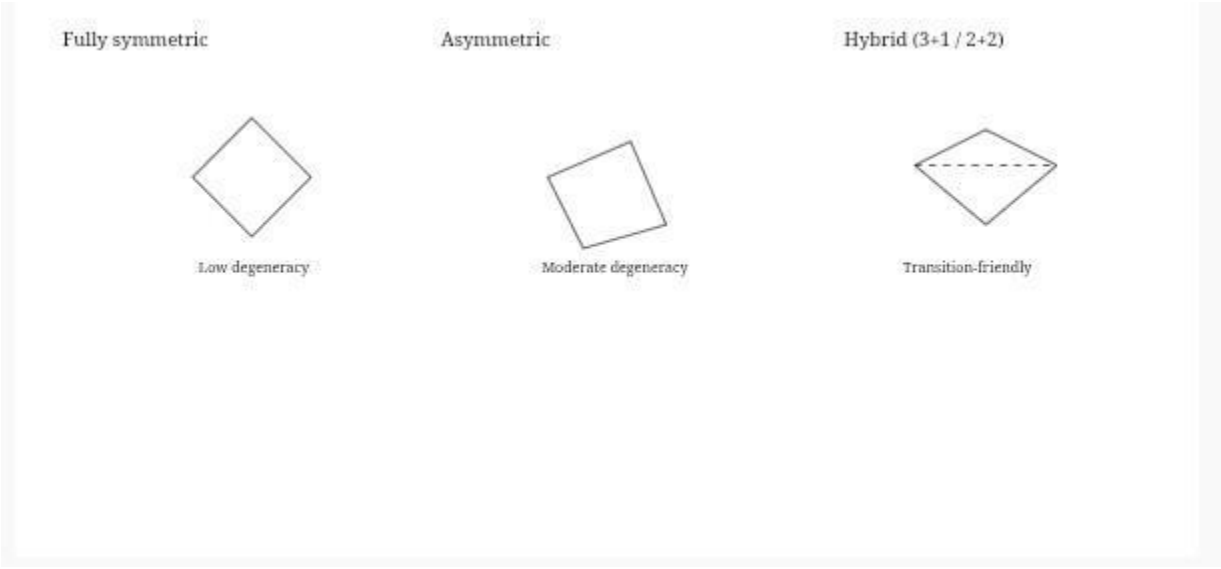

Figure 2 — Classes of Four-Strand Recognition Units

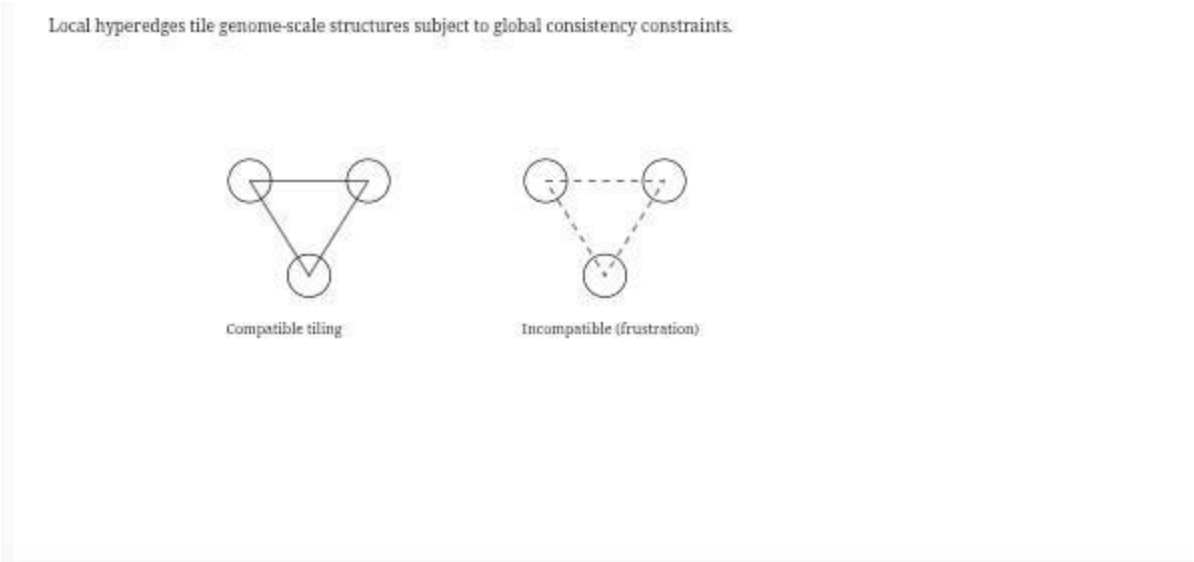

Figure 3 — Sequence–Structure Compatibility as a Constraint Network

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