Title :
Information-Theoretic Capacity of a Tetra-Stranded Hereditary Polymer :
Effective Alphabets, Encoding Density, and Readout Constraints in Q-DNA

Author :

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

Abstract

The informational capacity of a hereditary polymer is constrained not only by its chemical alphabet but also by its structural organization and readout mechanisms. Canonical duplex DNA encodes information primarily through pairwise base complementarity, yielding well-characterized limits on information density and error tolerance. In this work, I develop an **information-theoretic framework for Q-DNA**, a **canonical tetra-stranded hereditary polymer**, and show that tetra-strand coupling enables **non-pairwise, multi-body encoding schemes**. I derive upper bounds on information per unit length under structural and readout constraints, compare Q-DNA to DNA, RNA, and XNA systems, and identify regimes in which tetra-stranded heredity may trade encoding density for robustness—or vice versa. This analysis renders Q-DNA information capacity quantitatively testable and places tetra-stranded heredity within a rigorous communication-theoretic framework.

1. Introduction: Information Is Not Just Alphabet Size

Heredity is fundamentally an **information transmission problem**. A genetic polymer must:

1. encode information,
2. transmit it through noisy replication,
3. allow reliable decoding.

Shannon's information theory provides the minimal language to formalize these requirements, independent of molecular details. Duplex DNA, with its four-letter alphabet and pairwise base pairing, is a specific solution within a much larger design space.

The central question I address here is:

> Does a tetra-stranded canonical polymer allow fundamentally different information encoding regimes than duplex DNA?

2. Baseline: Information Capacity of Duplex DNA

2.1 Alphabet and pairwise encoding

Canonical DNA uses:

- alphabet size $|\Sigma|=4$,
- pairwise Watson–Crick complementarity,
- one effective symbol per base position.

The **maximum raw information per position** is therefore:

$$I_{\max}^{\mathrm{DNA}} = \log_2(4) = 2 \text{ bits/base}$$

In practice, structural constraints, sequence correlations, and error-correction overhead reduce usable capacity.

2.2 Noise, errors, and redundancy

Replication introduces noise. To remain evolvable, the effective information rate must lie **below** the channel capacity determined by:

- error rate,
- repair mechanisms,
- redundancy.

This is the classical **error-threshold problem** in molecular evolution.

3. Defining Information Units in Q-DNA

3.1 Why pairwise thinking breaks down

In Q-DNA, the canonical state is **tetra-stranded**. Information need not be encoded as independent symbols on a single strand or as pairwise complements.

I therefore define the **elementary information unit** not as a base, but as a **multi-strand configuration**.

3.2 Multi-body encoding units

Let a local Q-DNA encoding unit involve (k) strands simultaneously ((k = 3) or (4)).

The number of admissible configurations is not simply $|\Sigma|^k$, but is reduced by:

- structural compatibility constraints,
- energetic filters,
- readout constraints.

Let:

N_{eff} = number of structurally admissible multi-strand states

The **raw information capacity per unit** is:

$$I_Q = \log_2(N_{\text{eff}})$$

4. Upper Bounds on Information Density

4.1 Structural constraint bound

Multi-strand coupling introduces **correlations** between positions. These correlations reduce entropy.

I define an upper bound:

$$I_Q \leq \log_2(N_{\text{eff}}) - \Delta S_{\text{struct}}$$

where ΔS_{struct} accounts for:

- geometric constraints,
- topological admissibility,
- mechanical coupling.

4.2 Readout constraint bound

Information is useless if it cannot be decoded. Any readout mechanism (enzymatic or synthetic) imposes:

- locality constraints,
- ambiguity limits.

Let (**R**) denote the maximum resolvable states by a realistic reader. Then:

$$I_Q^{\text{usable}} \leq \log_2(\min(N_{\text{eff}}, R))$$

This explicitly links **information capacity to biophysical readout**.

5. Comparison: Q-DNA vs DNA / RNA / XNA

5.1 Duplex DNA

- Encoding: pairwise
- Capacity: ~2 bits/base
- Strength: simplicity, speed
- Weakness: limited redundancy per position

5.2 RNA

- Additional folding-based correlations
- Slightly reduced raw capacity
- Increased functional density

5.3 XNA systems

Synthetic alphabets (expanded bases) increase $|\Sigma|$, but often:

- increase error rates,
- increase enzymatic complexity.

Capacity gains may be offset by noise.

5.4 Q-DNA (this work)

Q-DNA introduces a **new axis**:

- **not larger alphabet,**
- but **multi-body encoding**.

This yields:

- potential **higher effective alphabet per unit**, or
- **lower effective error rates via redundancy**, or
- both, depending on regime.

6. Trade-offs: Density vs Robustness

I identify three generic regimes:

Regime A — Density-dominated

- high N_{eff},
- high information per unit,
- low redundancy,
- sensitive to noise.

Regime B — Robustness-dominated

- constrained N_{eff} ,
- information distributed across strands,
- strong error tolerance,
- lower raw density.

Regime C — Duplex-like

- Q-DNA degenerates to effective pairwise encoding,
- little advantage over DNA.

Only Regimes A and B represent **genuinely new information regimes.**

7. Predictions (Falsifiable)

Prediction P1 — Non-integer bits per base

Q-DNA information density will not scale linearly with base count and may show **fractional bits per base** due to multi-strand correlations.

Prediction P2 — Correlated error patterns

Errors will be **correlated across strands**, unlike largely independent base errors in duplex DNA.

Prediction P3 — Density–robustness trade-off curves

Mapping information density vs error tolerance will reveal regimes inaccessible to duplex DNA.

Prediction P4 — Reader-limited capacity

Experimental or synthetic readers will impose sharp capacity ceilings independent of raw structural possibilities.

8. Discussion

8.1 Why Q-DNA is not “just more bits”

The power of Q-DNA is not maximal entropy, but **structured redundancy**. This parallels:

- error-correcting codes,
- distributed representations,
- consensus-based encoding.

8.2 Implications for evolution

A Q-DNA system may:

- evolve more slowly,
- but be more robust to noise,
- or support longer genomes at similar error rates.

This offers a new resolution of the **Eigen error-threshold problem.**

8.3 What would falsify Q-DNA informationally

Q-DNA would fail if:

- multi-body encoding collapses to pairwise equivalence,
- readout ambiguity dominates,
- no regime outperforms duplex DNA on any axis.

9. Conclusion

I have shown that a canonical tetra-stranded hereditary polymer enables **information encoding regimes not accessible to duplex DNA,** arising from multi-body strand correlations rather than expanded chemical alphabets. By deriving explicit upper bounds, trade-offs, and falsifiable predictions, I place Q-DNA information capacity within a rigorous information-theoretic framework. This work establishes encoding capacity as a decisive criterion for evaluating tetra-stranded heredity.

Figures

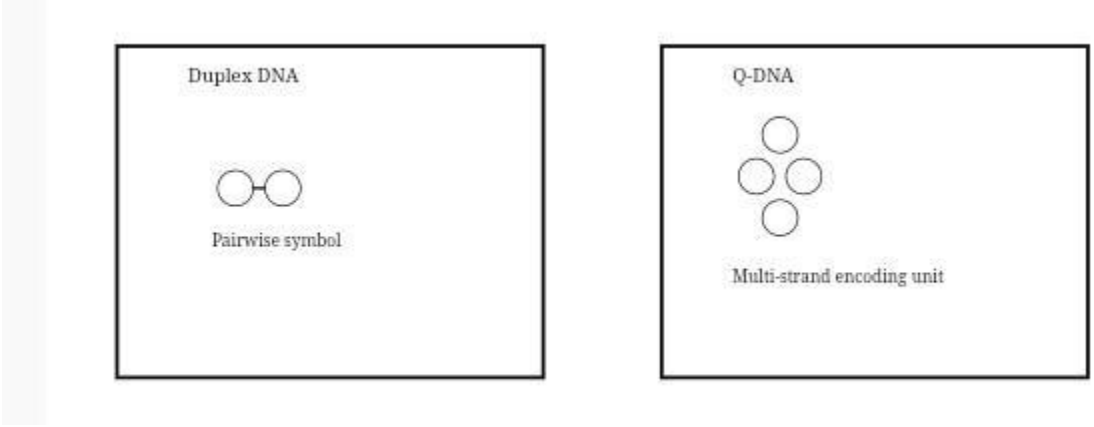

Figure 1. Encoding units in duplex DNA vs Q-DNA

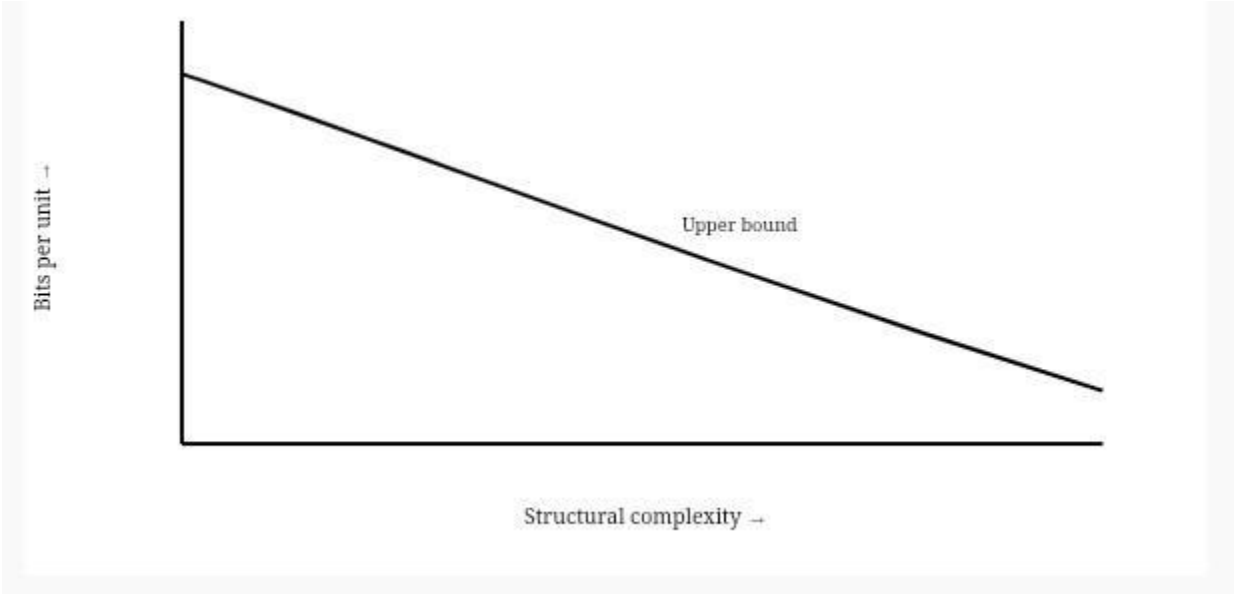

Figure 2. Information density vs structural constraints

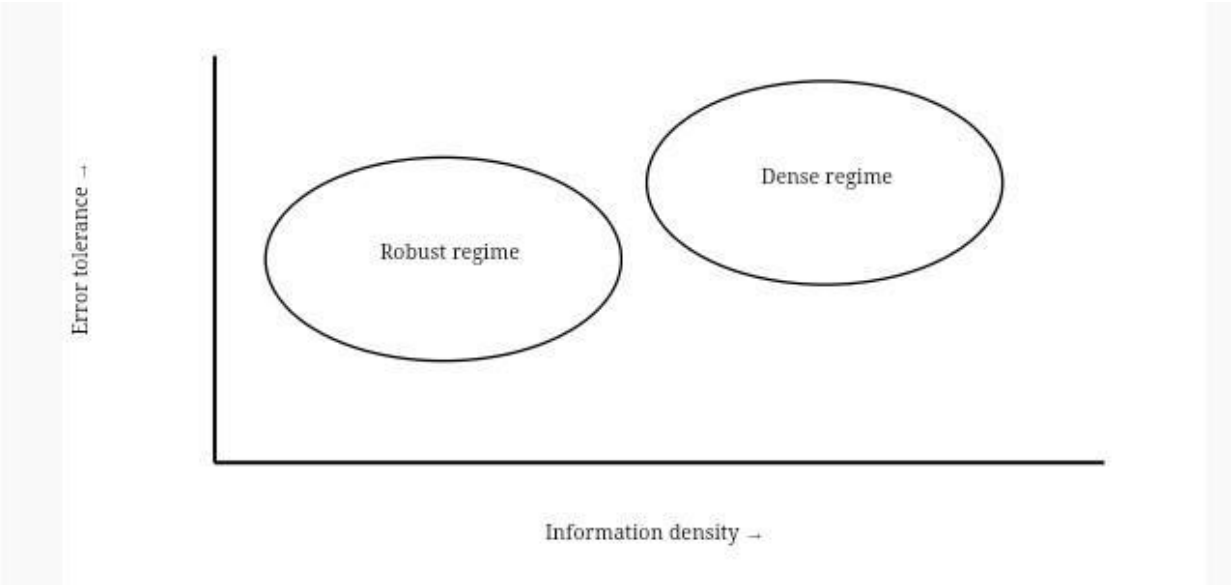

Figure 3. Density–robustness trade-off

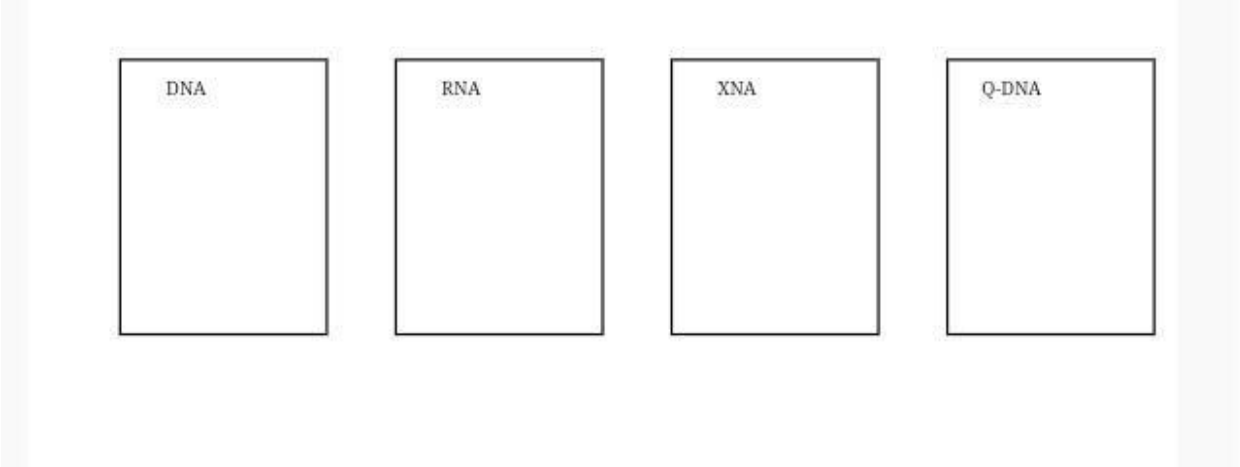

Figure 4. Comparative capacity of hereditary polymers

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