Title :
Reading and Transcription of a Tetra-Stranded Genetic Polymer : Decoding Channels, Controlled Ambiguities, and the Formal Definition of the Q-Code

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Abstract

Transcription is commonly defined as template-directed RNA synthesis mediated by a polymerase. However, this definition is historically contingent on duplex DNA and is not a logical necessity for heredity. In this work, I develop a **general framework for reading and transcription in Q-DNA**, defined as a **canonical tetra-stranded hereditary polymer**, without assuming the existence of a classical RNA polymerase. I introduce the notion of **decoding channels**, formalize **local and topological readout mechanisms**, and analyze the emergence and resolution of **controlled ambiguities** inherent to multi-strand encoding. This framework leads to a precise definition of the **Q-code** and establishes explicit constraints on any physical or enzymatic system capable of reading tetra-stranded genetic information.

1. Introduction: What Does It Mean to “Read” a Genome?

In modern biology, “reading” a genome is almost synonymous with transcription by an RNA polymerase. Yet this is an **implementation**, not a definition. At a fundamental level, reading is the process by which **stored hereditary information is mapped onto an operational output** (e.g., functional molecules, regulatory states).

For alternative genetic systems, the key question is therefore not:

> **Can Q-DNA be transcribed like DNA?**

but rather:

> **What constitutes a valid decoding operation for a tetra-stranded genome?**

2. Decoupling Reading from RNA Polymerases

2.1 Reading as an information-theoretic mapping

I define reading as a mapping:

R:Q-DNA configurations→output symbols

subject to:

- locality constraints,
- bounded ambiguity,
- reproducibility under noise.

This definition is agnostic to chemistry and focuses on **information flow.**

2.2 Why duplex assumptions fail

Duplex DNA reading assumes:

- linear templates,
- unambiguous base identity,
- strand independence.

In Q-DNA:

- information may be **distributed across strands,**
- local configurations may be **context-dependent**,
- single-strand projection may be ambiguous.

Thus, new decoding paradigms are required.

3. Decoding Channels in Q-DNA

I introduce the concept of **decoding channels**: distinct physical mechanisms by which information can be extracted from Q-DNA.

3.1 Sequence-based channel

Partial projection of Q-DNA onto one strand or strand pair.
✔️ Fast
❌ Loses multi-body information

3.2 Local-window (contextual) channel

Information is read over a **finite window** of length **ℓ ,** incorporating:

- strand identities,
- relative registry,
- local geometry.

This resembles sliding-window decoding in information theory.

3.3 Topological / geometric channel

Information is encoded and read via:

- strand crossings,
- twist states,
- bundle topology.

This channel is **non-linear** and non-sequential.

4. Local Readout Models ("Reading Windows")

4.1 Window-based decoding

I define a decoding window $\mathbf{W}_{\ell}$

that samples a local Q-DNA configuration.

The output symbol depends on:
$\mathbf{s} = \mathbf{f}(\text{geometry}, \text{strand registry}, \text{local topology})$

Increasing $\boldsymbol{\ell}$:

- reduces ambiguity,
- increases energetic and kinetic cost.

4.2 Trade-off: resolution vs accessibility

There exists an optimal window size:

- too small → ambiguous decoding,
- too large → kinetically inaccessible.

This is a **fundamental constraint** on Q-readers.

5. Ambiguities: Inevitable but Controllable

5.1 Sources of ambiguity

Ambiguities arise from:

- projection of multi-body states onto lower dimensions,
- degeneracy of admissible configurations,
- noise and thermal fluctuations.

Importantly, ambiguity is **not a failure**—it is a design parameter.

5.2 Ambiguity resolution strategies

I identify three generic strategies:

1. **Consensus decoding** across multiple channels
2. **Temporal integration** (reading the same region multiple times)
3. **Structural filtering**, excluding inconsistent states

These mirror error-correcting strategies in communication systems.

6. Formal Definition of the Q-Code

I define the **Q-code** as:

> The set of admissible mappings between local tetra-stranded configurations and output symbols, subject to structural, topological, and readout constraints.

Key properties:

- non-linear,
- context-dependent,
- redundancy-rich.

The Q-code is not a simple alphabet—it is a **constraint-satisfying codebook**.

7. Constraints on Q-Readers

Any viable Q-reader must satisfy minimal constraints:

- multi-strand recognition capability,
- sensitivity to geometry/topology,
- tolerance to ambiguity with bounded resolution time,
- coupling between readout and structural stabilization.

These constraints apply whether the reader is:

- enzymatic,
- ribozyme-based,
- or physico-chemical.

8. Predicted Experimental Signatures

- **P1:** Reading outputs depend on window size and geometry, not just sequence
- **P2:** Decoding ambiguity decreases non-linearly with contextual integration

- **P3:** Topological perturbations disrupt reading even when sequence is preserved

- **P4:** Multiple inequivalent readout channels coexist

9. Discussion

9.1 Why Q-DNA transcription is fundamentally different

Q-DNA does not encode linear instructions alone.
It encodes **relations**, **constraints**, and **geometries**.

Thus, “transcription” may produce:

- molecules,
- structural states,
- regulatory configurations.

9.2 Relation to evolution and regulation

Ambiguity allows:

- context-dependent expression,
- robustness to noise,
- regulatory richness.

This parallels modern epigenetic and RNA-structure-based regulation.

9.3 Falsification criteria

Q-DNA fails this axis if:

- no bounded-ambiguity decoding exists,
- reading collapses to simple duplex projection,
- readout is irreproducible under noise.

10. Conclusion

I have developed a general framework for **reading and transcription in a tetra-stranded hereditary polymer**, independent of classical RNA polymerases. By defining decoding channels, controlled ambiguities, and the Q-code, I show that transcription in Q-DNA is a constrained information-mapping problem rather than a simple templating reaction. This work establishes decoding as a decisive and testable criterion for tetra-stranded heredity.

Figures

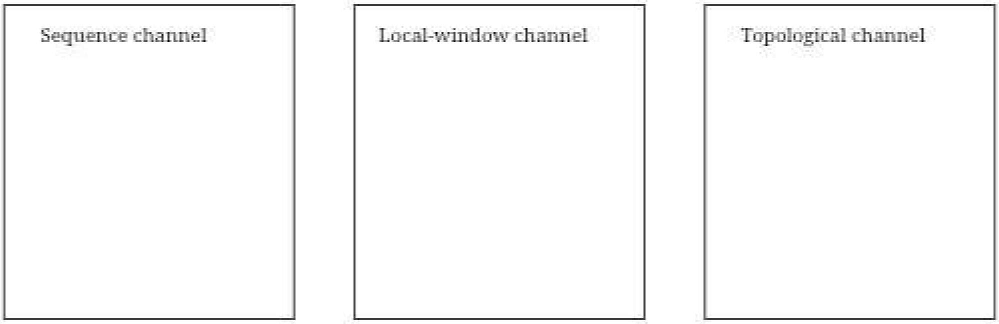

Figure 1 — Decoding channels

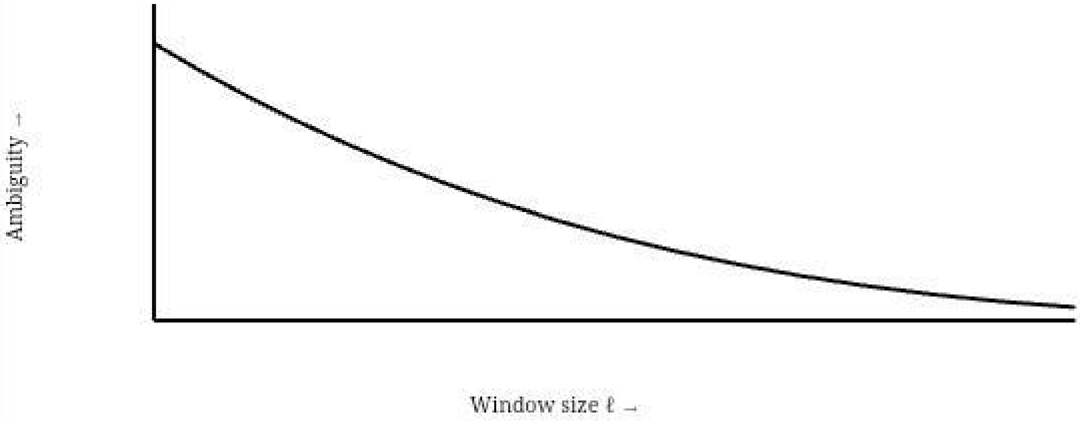

Figure 2 — Reading window and ambiguity

Consensus across channels

Temporal integration

Structural filtering

Figure 3 — Ambiguity resolution strategies

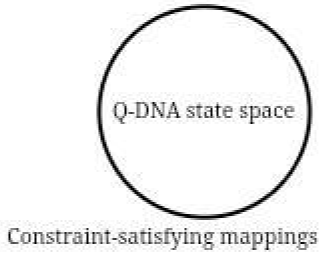

Figure 4 — The Q-code

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