

Quantum-Inspired DNA Computing: A Four-Dimensional Nucleotide State Space Framework with Superposition, Entanglement, and Error Correction

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Abstract - We present a comprehensive quantum-inspired DNA computing framework implemented in IcsDNA using the InChroSil Virtual Machine [11], a production-ready DNA computing platform. Our approach extends the classical four-letter nucleotide alphabet $\{A, G, C, T\}$ into a four-dimensional complex Hilbert space \mathcal{H}_4 , enabling superposition states, entanglement between nucleotide pairs, and quantum gate operations adapted to the biological domain. The framework introduces novel adaptations of fundamental quantum computing primitives, including Pauli gates, Hadamard transforms, rotation operators, and Bell-state generation, to a quaternary (base-4) nucleotide encoding. We further implement quantum-inspired algorithms for DNA sequence alignment, pattern matching via Grover-like amplitude amplification, Fourier analysis of genomic sequences, and quantum error correction for DNA storage integrity. The system provides both a high-level C++ object-oriented stack and a C API for integration into bioinformatics pipelines. Experimental evaluation demonstrates the applicability of quantum-inspired techniques to probabilistic genomic analysis, DNA-based cryptographic key generation, and fault-tolerant DNA data storage with decoherence simulation.

Keywords - DNA computing, quantum-inspired algorithms, nucleotide superposition, quantum error correction, Grover search, DNA cryptography, electronic DNA, bioinformatics

I. INTRODUCTION

A. Motivation

DNA computing, first demonstrated by Adleman [1], for solving instances of the Hamiltonian path problem, exploits massive parallelism inherent in biochemical reactions. Simultaneously, quantum computing leverages superposition and entanglement to achieve computational advantages for specific problem classes. The intersection of these paradigms (quantum-inspired DNA computing) offers a rich framework for modelling uncertainty, parallelism, and error correction in genomic computation.

Classical DNA computation encodes information using the four nucleotide bases: Adenine (A), Guanine (G), Cytosine (C), and Thymine (T). Each nucleotide carries $\log_2(4) = 2$ bits of information. However, biological reality introduces ambiguity: sequencing errors, polymorphisms, and variant calling

uncertainties mean that a given position in a genome may not be deterministically assigned a single nucleotide.

We propose a model for each nucleotide position as a quantum-like state vector \mathbb{C}^4 that enables the representation of uncertainty, superposition of possible bases, and correlations (entanglement) between positions. This paper describes the theoretical foundations, implementation architecture, and algorithmic applications of this framework within the IcsDNA platform [10] [11].

B. Related Work

Quantum computing models for DNA have been explored in several directions. Reif and LaBean [6] investigated DNA-based quantum logic gates. Mao et al. [4] demonstrated molecular implementations of Boolean computation using DNA tiles. Brun [2] proposed quantum-walk-based DNA search algorithms. More recently, Sarkar et al. [7] explored quantum machine learning for genomic classification.

Our approach differs in that we do not require physical quantum hardware. Instead, we implement a *classical simulation* of quantum-inspired operations on DNA data structures, providing the mathematical framework of quantum mechanics as a computational abstraction for probabilistic genomic analysis.

C. Contributions

The principal contributions of this work are:

- A four-dimensional Hilbert space model for nucleotide states, with complex probability amplitudes enabling superposition over $\{A, G, C, T\}$.
- Quantum gate operations (Pauli-X, Pauli-Y, Pauli-Z, Hadamard, rotation) adapted for the base-4 nucleotide domain.
- Bell-state generation and entanglement between nucleotide pairs for correlated position modelling.
- Quantum-inspired algorithms, including Grover-like search, quantum Fourier transform, and probabilistic sequence alignment.
- Quantum error correction with decoherence simulation for fault-tolerant DNA data storage.

- A dual-layer API (C++ stack and C interface) enabling integration into high-performance bioinformatics workflows.

II. THEORETICAL FOUNDATIONS

A. Nucleotide State Space

In standard quantum computing, a qubit exists in a two-dimensional Hilbert space $\mathcal{H}_2 = \text{span}\{|0\rangle, |1\rangle\}$. For DNA computing, we extend this to a four-dimensional space:

$$\mathcal{H}_4 = \text{span}\{|A\rangle, |G\rangle, |C\rangle, |T\rangle\}$$

A quantum nucleotide state $|\psi\rangle$ is a normalized vector in \mathcal{H}_4 :

$$|\psi\rangle = \alpha_A|A\rangle + \alpha_G|G\rangle + \alpha_C|C\rangle + \alpha_T|T\rangle$$

where $\alpha_i \in \mathbb{C}$ and the normalization constraint holds:

$$\sum_{i \in \{A, G, C, T\}} |\alpha_i|^2 = 1$$

The probability of measuring a nucleotide i upon observation is given by the Born rule:

$$P(i) = |\alpha_i|^2$$

B. Classical Basis Encoding

We define the computational basis states with the following binary encoding:

| Nucleotide | Ket Notation | Binary | Integer |
|------------|--------------|--------|---------|
| Adenine | $ A\rangle$ | 00 | 0 |
| Guanine | $ G\rangle$ | 01 | 1 |
| Cytosine | $ C\rangle$ | 10 | 2 |
| Thymine | $ T\rangle$ | 11 | 3 |

Table 1: Binary Encoding.

A classical nucleotide is represented as a pure basis state, e.g., $|A\rangle = (1, 0, 0, 0)^T$

C. Superposition and Equal Probability States

The equal superposition state represents maximum uncertainty:

$$|\psi_{\text{equal}}\rangle = \frac{1}{2}(|A\rangle + |G\rangle + |C\rangle + |T\rangle)$$

Each nucleotide has measurement probability $P(i) = 1/4$. The normalization factor is $1/\sqrt{4} = 1/2$ for a four-state system.

A two-state superposition between states $|s_1\rangle$ and $|s_2\rangle$ takes the form:

$$|\psi\rangle = \alpha|s_1\rangle + \beta|s_2\rangle, \quad |\alpha|^2 + |\beta|^2 = 1$$

D. Quantum Entropy

The von Neumann-like entropy of a nucleotide state quantifies uncertainty:

$$S(\psi) = - \sum_{i \in \{A, G, C, T\}} |\alpha_i|^2 \log_2 |\alpha_i|^2$$

This ranges from $S = 0$ (pure classical state) to $S = 2$ bits (equal superposition). Our implementation computes this as:

$$S = - \sum_i P(i) \log_2 P(i) \quad \text{where } P(i) = |\alpha_i|^2$$

E. Fidelity

The quantum fidelity between two nucleotide states $|\psi\rangle$ and $|\phi\rangle$ measures their overlap:

$$F(\psi, \phi) = |\langle \psi | \phi \rangle|^2 = \left| \sum_i \alpha_i^* \beta_i \right|^2$$

Fidelity ranges from 0 (orthogonal states) to 1 (identical states).

III. QUANTUM GATE OPERATIONS FOR DNA

A. Pauli-X Gate (Nucleotide Bit Flip)

The Pauli-X gate, adapted for the nucleotide domain, performs Watson-Crick-inspired pairwise swaps:

$$X_{\text{DNA}}: A \leftrightarrow G, \quad C \leftrightarrow T$$

In matrix form over \mathcal{H}_4 :

$$X_{\text{DNA}} = \begin{pmatrix} 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \end{pmatrix}$$

This maps $\alpha_A \leftrightarrow \alpha_G$ and $\alpha_C \leftrightarrow \alpha_T$.

B. Pauli-Y Gate (Complex Bit Flip)

The Pauli-Y gate introduces phase factors during the swap:

$$Y_{\text{DNA}}|A\rangle = i|G\rangle, \quad Y_{\text{DNA}}|G\rangle = -i|A\rangle$$

$$Y_{\text{DNA}}|C\rangle = i|T\rangle, \quad Y_{\text{DNA}}|T\rangle = -i|C\rangle$$

In matrix representation:

$$Y_{\text{DNA}} = \begin{pmatrix} 0 & -i & 0 & 0 \\ i & 0 & 0 & 0 \\ 0 & 0 & 0 & -i \\ 0 & 0 & i & 0 \end{pmatrix}$$

C. Pauli-Z Gate (Phase Flip)

The Pauli-Z gate applies a phase inversion to the G and T amplitudes:

$$Z_{\text{DNA}} = \begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & -1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & -1 \end{pmatrix}$$

This operation is undetectable through measurement alone (only relative phases change) but affects interference patterns in subsequent operations.

D. Hadamard Gate (Four-State)

The generalized Hadamard transform for \mathcal{H}_4 creates equal superposition from any basis state:

$$H_4 = \frac{1}{2} \begin{pmatrix} 1 & 1 & 1 & 1 \\ 1 & -1 & 1 & -1 \\ 1 & 1 & -1 & -1 \\ 1 & -1 & -1 & 1 \end{pmatrix}$$

Applied to the basis state $|A\rangle = (1,0,0,0)^T$:

$$H_4|A\rangle = \frac{1}{2}(|A\rangle + |G\rangle + |C\rangle + |T\rangle)$$

This is the 4×4 Hadamard matrix (order-2 Walsh-Hadamard matrix), normalized by $1/2$ to preserve unitarity.

E. Rotation Gate

A parametric rotation in nucleotide space, parameterized by angles θ and ϕ :

$$R(\theta, \phi) = \begin{pmatrix} \cos \frac{\theta}{2} & 0 & e^{i\phi} \sin \frac{\theta}{2} & 0 \\ 0 & \cos \frac{\theta}{2} & 0 & e^{i\phi} \sin \frac{\theta}{2} \\ -e^{-i\phi} \sin \frac{\theta}{2} & 0 & \cos \frac{\theta}{2} & 0 \\ 0 & -e^{-i\phi} \sin \frac{\theta}{2} & 0 & \cos \frac{\theta}{2} \end{pmatrix}$$

This rotates between purine-pyrimidine subspaces: $\{A, C\}$ and $\{G, T\}$ are coupled through the angle parameters.

IV. ENTANGLEMENT AND BELL STATES

A. Bell-State Pairs for DNA

We define a DNA Bell state as a maximally entangled pair of nucleotides:

$$|\Psi_{\text{Bell}}\rangle = \frac{1}{\sqrt{2}}(|AG\rangle + |CT\rangle)$$

This is decomposed into two correlated single-nucleotide states:

$$\text{Nucleotide 1: } |\psi_1\rangle = \frac{1}{\sqrt{2}}(|A\rangle + |C\rangle)$$

$$\text{Nucleotide 2: } |\psi_2\rangle = \frac{1}{\sqrt{2}}(|G\rangle + |T\rangle)$$

Upon measurement of nucleotide 1, the outcome constrains nucleotide 2: - If nucleotide 1 collapses to $|A\rangle$, nucleotide 2 collapses to $|G\rangle$ - If nucleotide 1 collapses to $|C\rangle$, nucleotide 2 collapses to $|T\rangle$

This mirrors the Watson-Crick base-pairing rule ($A \leftrightarrow G$ purine pairing, $C \leftrightarrow T$ pyrimidine pairing in this encoding scheme), providing a biologically motivated entanglement structure.

B. Entanglement in Strand Context

Within a QuantumDNAstrand, two positions i and j can be entangled:

$$|\psi_{i,j}\rangle = \frac{1}{\sqrt{2}}(|A_i G_j\rangle + |C_i T_j\rangle)$$

This is useful for modelling correlated mutations, co-evolving positions, and linked polymorphisms in genomic sequences.

V. QUANTUM DNA STRAND ARCHITECTURE

A. Strand Representation

A Quantum DNA Strand of length n is a tensor product of n nucleotide states:

$$|\Phi\rangle = |\psi_1\rangle \otimes |\psi_2\rangle \otimes \cdots \otimes |\psi_n\rangle$$

where each $|\psi_k\rangle \in \mathcal{H}_4$. The full state space is $\mathcal{H}_4^{\otimes n}$ with dimension 4^n .

In practice, we store individual nucleotide states independently (product-state approximation) and explicitly track entanglement connections, avoiding the exponential memory requirements of the full tensor-product representation.

B. Measurement and Collapse

Measuring the entire strand yields a classical DNA sequence $s = s_1 s_2 \cdots s_n$ where each $s_k \in \{A, G, C, T\}$ is sampled according to:

$$P(s_k = i) = |\alpha_i^{(k)}|^2$$

After measurement, the strand's coherence is destroyed (isCoherent \leftarrow false) and all superposition states collapse to definite basis states.

C. Coherence Measure

The coherence of a strand quantifies the fraction of positions remaining in superposition:

$$\mathcal{C}(\Phi) = \frac{1}{n} \sum_{k=1}^n \mathbb{1}[\text{isSuperposition}(\psi_k)]$$

where $\mathbb{1}[\cdot]$ is the indicator function. $\mathcal{C} = 1$ indicates full quantum coherence; $\mathcal{C} = 0$ indicates a fully classical strand.

VI. QUANTUM-INSPIRED ALGORITHMS

A. Grover-Like Sequence Search

We adapt Grover's quantum search algorithm for DNA pattern matching. Given a quantum strand of length n and a target pattern of length m , the algorithm:

Initialization: Apply Hadamard gates to all positions, creating equal superposition.

Oracle evaluation: For each candidate position $i \in [0, n - m]$, compute the match probability:

$$P_{\text{match}}(i) = \prod_{j=0}^{m-1} P(\psi_{i+j} = \text{pattern}[j])$$

Amplitude amplification: Positions with $P_{\text{match}} > 0.5$ are returned as matches.

In the classical simulation, this provides a probabilistic pattern-matching framework where partial matches (positions in superposition) contribute fractional probabilities.

B. Quantum Fourier Transform on DNA

The Quantum Fourier Transform (QFT) applied to a DNA strand performs frequency domain analysis of the nucleotide probability distribution. For a strand of n positions:

Apply Hadamard gate H_4 to each position k .

For each pair (k, j) with $j > k$, apply controlled phase rotation:

$$\theta_{k,j} = \frac{2\pi}{2^{j-k+1}}$$

This enables spectral analysis of periodic patterns in genomic sequences (e.g., codon periodicity, repeat elements).

C. Quantum Sequence Alignment

Quantum-inspired alignment between two strands $|\Phi_1\rangle$ and $|\Phi_2\rangle$ of lengths n_1 and n_2 computes probability overlap:

$$\text{Score}(\Phi_1, \Phi_2) = \frac{1}{\min(n_1, n_2)} \sum_{k=1}^{\min(n_1, n_2)} \sum_{i \in \{A, G, C, T\}} P_1^{(k)}(i) \cdot P_2^{(k)}(i)$$

This generalizes classical sequence comparison: when both strands are in pure classical states, the score reduces to the fractional identity. When strands contain superpositions, the score captures probabilistic similarity across all possible classical realizations.

D. Quantum DNA Cryptographic Key Generation

The key generation algorithm leverages quantum measurement randomness:

Create nucleotide in equal superposition:

$$|\psi\rangle = \frac{1}{2}(|A\rangle + |G\rangle + |C\rangle + |T\rangle)$$

Apply Hadamard gate for additional mixing.

Measure to obtain a random nucleotide (2 bits of entropy per measurement).

Repeat for desired key length.

For a key of length L nucleotides, this produces $2L$ bits of entropy. The randomness quality depends on the underlying random number generator seeding the measurement process.

VII. QUANTUM ERROR CORRECTION AND DECOHERENCE

A. Error Detection

Quantum error correction in our framework detects normalization violations as an indicator of bit-flip errors:

$$\epsilon = \left| \sum_i |\alpha_i|^2 - 1 \right|$$

If $\epsilon > 10^{-6}$ a bit-flip error is signalled. This simple criterion is effective because all valid quantum states must satisfy the normalization constraint.

B. Error Correction

Upon error detection, a two-step correction is applied:

$$\text{Renormalization: } \alpha_i \leftarrow \alpha_i / \sqrt{\sum_j |\alpha_j|^2}$$

Anti-concentration: If $\max_i |\alpha_i|^2 > 0.9$ (state too concentrated, suggesting collapse), apply Hadamard to restore superposition, then renormalize.

C. Decoherence Model

Decoherence—the gradual loss of quantum properties—is modeled as exponential decay toward the maximally mixed state:

$$\alpha_i(t) = e^{-t/\tau} \cdot \alpha_i(0) + (1 - e^{-t/\tau}) \cdot \frac{1}{2}$$

where τ is the coherence time (default: 1000-time units). As $t \rightarrow \infty$, all amplitudes converge to $1/2$, yielding the equal superposition state—the quantum analog of complete information loss.

The decoherence rate can be parameterized by temperature:

$$\tau(T) \propto T^{-1}$$

Higher temperatures accelerate decoherence, modeling thermal noise in DNA storage systems.

VIII. QUANTUM DNA MEMORY ARCHITECTURE

A. Memory Organization

The *QuantumDNAMemory* class organizes quantum strands in an $R \times C$ matrix (default $16 \times 16 = 256$ cells), where each cell stores a complete *QuantumDNA Strand*. This architecture enables:

- **Addressable quantum storage:** Store and retrieve strands by (row, col) coordinates.
- **Non-destructive inspection:** Access quantum state without measurement collapse.
- **Destructive readout:** Measure strand, obtaining classical sequence but destroying superposition.
- **Global error correction:** Apply quantum error correction across all stored strands.
- **Decoherence simulation:** Model time-dependent coherence loss across the entire memory.

B. Memory Statistics

The system tracks quantum properties at the memory level:

| Metric | Description |
|----------------------|---|
| Total qubits | Sum of all nucleotide positions across all stored strands |
| Average coherence | Mean fraction of positions in superposition |
| Entangled pairs | Number of active entanglement connections |
| Error rate | Estimated bit-flip error rate |
| Superposition states | Count of positions in non-classical states |

Table 2: Memory Level

IX. REVERSIBLE CIRCUIT INTEGRATION

A. Reversible Gate Framework

The IcsDNA quantum module integrates with a reversible circuit layer implementing classical reversible gates on nucleotide data:

- **CNOT (Controlled-NOT):** $|c, t\rangle \rightarrow |c, t \oplus f(c)\rangle$, where the target is conditionally flipped based on the control nucleotide.
- **Toffoli (CCNOT):** Three-nucleotide gate; target flips only when both controls satisfy a condition.
- **Fredkin (CSWAP):** Controlled swap of two target nucleotides.
- **Complement Gate:** Watson-Crick complementation ($A \leftrightarrow T, C \leftrightarrow G$).
- **Rotation Gate:** Cyclic permutation $A \rightarrow G \rightarrow C \rightarrow T \rightarrow A$ with configurable step count.

These gates operate on nucleotide encodings ($A = 00, C = 01, G = 10, T = 11$) and preserve reversibility, ensuring no information loss during computation.

B. Circuit Simulation

A *ReversibleDNASimulator* (part of IcsDNA electronic DNA framework) manages collections of quantum circuits, tracking: - Circuit fidelity metrics - Entanglement statistics - Reversibility verification - Simulation step counts

X. IMPLEMENTATION ARCHITECTURE

A. Software Stack

The implementation follows a two-layer architecture:

C++ Stack Layer:

- **Quantum Nucleotide State** — Core quantum state with gates and measurement
- **Quantum DNA Strand** — Quantum strand with entanglement and algorithms
- **Quantum DNA Memory** — Matrix-organised quantum storage with error correction
- **Quantum DNA Algorithms** — Static algorithm suite (alignment, search, compression, crypto)

C API Layer:

- Opaque handle types (Quantum nucleotide, strand and memory)
- **Create/destroy lifecycle management** - Gate application functions - Measurement and probability query functions
- Algorithm invocations (Grover search, QFT, Shor factorization)

B. Design Decisions

Product-state approximation: Individual nucleotide states are stored independently rather than as an exponentially large tensor product, making memory $O(4n)$ instead of $O(4^n)$.

Explicit entanglement tracking: Entangled pairs are recorded using string identifiers, and correlated measurements are enforced programmatically.

Hardware-agnostic random measurements

Thread-safe random number generation: Each memory instance maintains its own RNG state, seeded from steady_clock.

C. Dependencies

The quantum module builds upon the IcsDNA electronic DNA layer.

XI. DISCUSSION

A. Computational Complexity

| Operation | Time Complexity | Space Complexity |
|--|----------------------|------------------|
| Gate application (single nucleotide) | $O(1)$ | $O(1)$ |
| Strand measurement (n nucleotides) | $O(n)$ | $O(n)$ |
| Grover-like search (pattern length m) | $O((n - m) \cdot m)$ | $O(n)$ |
| QFT (n positions) | $O(n^2)$ | $O(n)$ |
| Sequence alignment | $O(n)$ | $O(n)$ |
| Error correction (full strand) | $O(n)$ | $O(1)$ |
| Memory error correction ($R \times C$ matrix, avg strand length \bar{n}) | $O(RC\bar{n})$ | $O(1)$ |

Table 3: Computational Complexity

B. Advantages of Quantum-Inspired Approach

Uncertainty representation: Superposition naturally models sequencing uncertainty, variant allele frequencies, and ambiguous base calls.

- **Probabilistic analysis:** Probability distributions enable soft matching and fuzzy alignment without ad-hoc similarity thresholds.
- **Correlated positions:** Entanglement captures co-evolutionary constraints and linkage disequilibrium.
- **Error resilience:** Quantum error correction provides a principled framework for maintaining data integrity in DNA storage applications.
- **Cryptographic applications:** Measurement-based randomness provides a natural source of entropy for DNA-encoded keys.

C. Applications

The framework is applicable to:

- **Variant calling:** Represent uncertain base calls as superposition states with quality-score-derived amplitudes.
- **Haplotype phasing:** Model phase uncertainty using entangled nucleotide pairs.
- **DNA data storage:** Apply quantum error correction to protect stored information against degradation.
- **Forensic genetics:** Quantify mixture proportions in degraded DNA samples as superposition weights.

- **Synthetic biology:** Design DNA sequences with specified probability distributions for directed evolution experiments.

XII. EXPERIMENTAL RESULTS

A. Experimental Setup

All validation reported in this section was produced on the current main branch build of IcsDNA using the in-repo CMake/CTest workflow.

B. Validation Summary

| Metric | Result |
|-------------------------------|--|
| CTest target | QuantumDNATest |
| Test status | Passed |
| Runtime | 0.03 s (0.04 s wall-clock total in CTest report) |
| GTest suites (listed) | 15 |
| GTest test cases (listed) | 121 |
| CTest project tests available | 20 total targets |

Table 4: Validation Table

The suite spans low-level state algebra and high-level DNA workflows, including: superposition state construction, Bell/entanglement primitives, Fourier transforms, Grover-like search, density-matrix channels, tomography reconstruction, reversible DNA gates/circuits, and C API integration tests.

C. Coverage Results (Quantum Subsystem)

From LCOV HTML reports:

| File | Line Coverage | Function Coverage | Lines Hit/Total | Functions Hit/Total |
|--------|---------------|-------------------|-----------------|---------------------|
| Source | 87.8% | 94.6% | 706/804 | 70/74 |
| Header | 99.6% | 100.0% | 758/761 | 490/490 |

Table 5: Coverage Results

D. Interpretation:

The implementation file shows high function-level exercise (94.6%), indicating broad path activation across quantum primitives.

The test harness itself is almost fully covered (99.6%), reducing risk of dead or unexecuted test logic.

Remaining uncovered implementation lines concentrate in edge/error paths and non-dominant control branches (as expected for defensive logic).

E. Algorithmic Behavior Observed in Tests

The quantum test target includes explicit checks for the following behavioral contracts:

- **Probability conservation:** gate application and noise channels preserve normalization to numerical tolerance.
- **Entropy bounds:** pure states remain near $S = 0$, while mixed/superposed states respect $0 \leq S \leq 2$ for base-4 encoding.

- **Fidelity consistency:** identical states/circuits produce near-unit fidelity; orthogonal states produce near-zero overlap.
- **Search correctness:** Grover-like routines return expected target loci on synthetic DNA databases.

Fault tolerance primitives: decoherence and error-correction routines retain valid normalized states under perturbation.

F. Reproducible Command-Line Validation

To complement the automated test suite, we added a standalone executable, “*example_quantum_long_sequence*,” that demonstrates long-strand quantum workflows: 512-base-strand construction, position-level superposition, Fourier transform, quantum memory store/retrieve/search, and Grover-like candidate selection.

In this environment, “*ctest -R QuantumDNATest --output-on-failure*” reported a pass with 0 failures. The full executable output and stage-by-stage interpretation are provided once in **Section G** to avoid duplication.

G. Practical Implication of Results

These results support the claim that the framework is not only mathematically defined but also executable as a stable software substrate. In particular, high coverage in “*ics_stack_quantum_dna.cpp*,” along with a passing 121-case quantum-focused suite, indicates readiness for integration into probabilistic genomics pipelines that require uncertainty-aware computation.

H. Full End-to-End Example (Long Sequence)

This section presents a complete, reproducible workflow as demonstrated in “*example_quantum_long_sequence.cpp*”.

Objective

Demonstrate, in a single executable run, a long-sequence quantum-inspired C API flow:

- Build a 512-base strand from a deterministic motif.
- Introduce explicit superposition at selected long-strand positions.
- Apply quantum Fourier transform and verify structural consistency.
- Store, retrieve, and search the long strand in quantum memory.
- Run Grover-like search across long candidate strands.

Representative Program Output

```
IcsDNA quantum long-sequence example
== Input configuration ==
target_length=512 bases
source_fasta=./examples/rCRS.fasta
search_pattern=AAGTGTGT
long_sequence_preview=GATCACAGGT...TACAACCCCC
GCCATCCTACCCA
```

```
== Create long quantum strand ==  
loaded_classical_bases=512  
  
== Inject superposition at selected positions ==  
superposition_position_100=(A,G)  
with amplitudes (1/sqrt(2),1/sqrt(2))  
superposition_position_500=(C,T)  
with amplitudes (1/sqrt(2),1/sqrt(2))  
long_strand_length=512  
  
== Apply quantum Fourier transform ==  
transformed_length=512  
length_preserved=PASS  
  
== Store and retrieve from quantum memory ==  
stored_address=long:0  
measured_length=512, memory_search_results=1,  
addresses=long:0  
measured_sequence_preview=GATCACAGGTCTATCACCC  
CTATTA...TACAACCCCCGCCCATCCTACCCA  
  
== Grover-like search across long candidates ==  
candidate_lengths = (512,512,512)  
pattern_injected_into=candidate_1 at offset=200  
grover_found_index=1 (expected 1)  
grover_result=PASS  
example_status=success
```

Interpretation

The run validates the expected behavior of each stage:

- **Long-strand handling:** the example explicitly reports 512-base input creation and loading into the quantum strand.
- **Quantum-state injection:** two selected positions are converted to equal superposition states with documented amplitudes.
- **Transform consistency:** Fourier transform preserves sequence length and reports length_preserved=PASS.
- **Memory semantics:** long-strand storage/retrieval and pattern search succeed, returning the expected address (long:0).
- **Grover-like selection:** candidate setup and injected offset are shown, and the expected candidate is selected (grover_result=PASS).
- **End-to-end stability:** the workflow completes with explicit success status.

This single example serves as the canonical executable reference for the paper.

XIII. CONCLUSION

We have presented a comprehensive quantum-inspired DNA computing framework within the IcsDNA platform that bridges quantum mechanical formalism and practical bioinformatics computation. By embedding the four-nucleotide alphabet into a four-dimensional complex Hilbert space, we enable a rich set of operations (superposition, entanglement, quantum gates, error correction, and quantum-inspired algorithms) that extend the capabilities of classical DNA computing.

The framework provides a principled mathematical foundation for handling uncertainty in genomic data, with applications ranging from probabilistic sequence analysis to DNA-based cryptography. While operating as a classical simulation, the quantum-inspired abstractions offer conceptual and practical advantages in modelling the inherent probabilistic nature of biological systems.

Future work will explore full tensor-product state representation for small subsystems, integration with actual quantum computing backends, and application to large-scale genomic datasets for variant calling and population genetics.

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