Quantum-Enhanced Genomic Data Analysis for Evolutionary Biology and Species Adaptation Modeling

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Abstract—**The exponential growth of genomic data has transformed evolutionary biology, enabling large-scale analysis of genetic variation, phylogenetic relationships, and adaptive mechanisms across species. However, classical computational approaches increasingly struggle with the combinatorial complexity, high dimensionality, and nonlinear interactions inherent in genomic datasets. This study explores how quantum-enhanced data analysis can augment evolutionary biology by enabling more efficient modeling of genomic variation and species adaptation. By leveraging quantum computing principles such as superposition, entanglement, and quantum parallelism, quantum algorithms offer the potential to accelerate sequence alignment, genotype–phenotype mapping, evolutionary optimization, and adaptive landscape exploration. Through qualitative synthesis of research in quantum computing, computational genomics, and evolutionary theory, this paper examines how quantum-enhanced frameworks can improve the detection of adaptive patterns, epistatic interactions, and evolutionary constraints. The analysis highlights potential applications in phylogenomic reconstruction, population genetics, and predictive modeling of species responses to environmental pressures. While acknowledging current technological limitations, the study argues that quantum-enhanced genomic analysis represents a promising pathway toward more scalable, precise, and predictive evolutionary models. Ultimately, this work positions quantum computing as a transformative tool for advancing our understanding of biological evolution and species resilience in rapidly changing ecosystems.**

Advances in high-throughput sequencing technologies have revolutionized evolutionary biology by generating unprecedented volumes of genomic data across species, populations, and ecosystems [8]. These datasets enable researchers to study genetic diversity, evolutionary history, and adaptive processes at resolutions previously unattainable. From identifying selective sweeps to reconstructing phylogenetic trees and modeling population dynamics, genomics has become central to understanding how organisms evolve and adapt [4]. However, as genomic datasets grow in scale and complexity, traditional computational methods face increasing limitations in efficiency, scalability, and predictive accuracy.