Multi-Task Semantic Communication System for DNA transmission

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***Abstract*—This paper presents DNA-Mamba-DeepSC, a novel multi-task semantic communication system specifically designed for efficient DNA sequence transmission. The proposed system addresses the critical challenges of preserving biological semantics while achieving high compression ratios and transmission reliability by leveraging Mamba-2 architecture with linear computational complexity. Our system simultaneously performs DNA sequence reconstruction and classification tasks through joint optimization, enabling superior performance compared to traditional communication methods. Experimental results demonstrate significant improvements across multiple metrics: up to 98.3% edit distance reduction compared to conventional UTF-8+Turbo methods, consistently high classification accuracy of 95-96% across various SNR conditions (from -6 dB to 18 dB), 62.1% latency reduction for processing long sequences, and 85.3% parameter reduction compared to baseline DeepSC while maintaining superior performance. The multi-task learning framework successfully preserves both sequence-level fidelity and semantic information during transmission, making the system particularly suitable for genomics research, personalized medicine, and biotechnology applications requiring reliable DNA data exchange.**

***Index Terms*—DNA transmission, semantic communication, multi task learning**

I. Introduction

The exponential growth of biological data, particularly DNA sequences, has created an unprecedented demand for efficient and reliable transmission systems in genomics research, personalized medicine, and biotechnology applications. Traditional semantic communication approaches face significant challenges when handling DNA data transmission, including the inability to preserve critical biological semantics during compression, susceptibility to errors that can alter genetic meaning, inefficient bandwidth utilization due to the unique structural properties of genomic sequences, and the extremely long nature of DNA sequences which can contain millions or billions of base pairs, making conventional transmission methods impractical [1]. Semantic communication emerges as a particularly suitable solution for DNA transmission tasks because it can intelligently extract and preserve the essential biological information while discarding redundant data, maintain the semantic integrity of genetic sequences through context-aware encoding, efficiently handle the massive scale of genomic data by focusing on biologically relevant patterns rather than raw sequence length, and adapt to the specific characteristics of DNA data such as base pair complementarity and codon structures, thereby enabling more robust and efficient transmission of genomically meaningful information [2]–[5].

A. Related Work

Semantic communication has evolved from traditional bit-level transmission to meaning-focused paradigms, with recent advances extending into specialized biological domains. Early developments established foundational approaches for conventional data types, while emerging research has begun exploring applications to biological sequences.

Multi-modal and Multi-task Systems: Recent advances have addressed diverse data transmission requirements simultaneously. Zhang et al. [6] proposed unified frameworks serving multiple tasks through domain adaptation techniques. Do et al. [7] introduced Mamba-based architectures for multiuser multimodal communication targeting large language model applications. Cross-modal alignment approaches, such as CA_DeepSC [8], focus on leveraging correlations between different modalities to enhance transmission robustness.

Advanced Visual Communication: Image transmission has seen architectural innovations addressing specific application needs. TranGDeepSC [9] demonstrated knowledge transfer from ViT to CNN-based systems through co-training algorithms. Specialized applications include super-resolution techniques for satellite imagery [10], showing the adaptability of semantic communication to domain-specific requirements.

Knowledge-Enhanced Representations: Sophisticated semantic understanding has been achieved through structural approaches. Xing et al. [11] utilized knowledge graph integration for multi-modal semantic fusion, demonstrating how structural advantages can enhance semantic representation and transmission efficiency.

Biological Data Communication: The application of semantic communication to biological domains represents an emerging frontier. Wu et al. [12] introduced semantic AI-enhanced DNA storage for IoT applications, shifting focus from complete data preservation to semantic extraction. This approach addresses the unique constraints of DNA sequences, including GC content limitations, homopolymer restrictions,

and insertion/deletion errors inherent in synthesis and sequencing processes.

The proposed DNA-Mamba-DeepSC extends this biological semantic communication paradigm by leveraging Mamba-2's linear computational complexity to handle extremely long DNA sequences while simultaneously performing semantic reconstruction and classification tasks, addressing the gap between semantic communication principles and genomic data requirements.

B. Motivations

The development of DNA-Mamba-DeepSC is driven by several critical challenges and opportunities in genomic data transmission that existing communication systems fail to adequately address.

Computational Scalability for Long Sequences: Traditional semantic communication systems, particularly those based on transformer architectures, face significant computational bottlenecks when processing extremely long DNA sequences. With genomic sequences often spanning millions or billions of base pairs, the quadratic complexity of attention mechanisms becomes prohibitively expensive, limiting the practical applicability of existing semantic communication approaches to real-world genomic data transmission scenarios.

Multi-task Learning Requirements: Genomic applications typically require simultaneous preservation of both sequence-level accuracy and high-level semantic information. Current semantic communication systems are primarily designed for single-task optimization, either focusing on reconstruction fidelity or classification accuracy, but not both simultaneously. This limitation prevents effective utilization of shared semantic representations that could benefit both tasks through joint optimization.

Biological Semantic Preservation: DNA sequences contain complex hierarchical semantic structures, from individual nucleotide patterns to functional genomic elements such as genes, regulatory regions, and structural motifs. Conventional communication methods treat DNA as generic text data, failing to leverage the unique structural properties and biological constraints inherent in genomic sequences, resulting in suboptimal compression and transmission efficiency.

Resource-Constrained Transmission Scenarios: Many genomic applications, particularly in remote sensing, field research, and point-of-care diagnostics, operate under severe bandwidth and power constraints. These scenarios demand communication systems that can achieve high compression ratios while maintaining the integrity of biologically relevant information, necessitating intelligent semantic extraction rather than brute-force data transmission approaches.

These motivating factors collectively highlight the need for a specialized semantic communication system that combines the computational efficiency of linear-complexity architectures with multi-task learning capabilities specifically tailored for genomic data transmission requirements.

C. Contributions

The main contributions of this paper are summarized as follows:

- We propose DNA-Mamba-DeepSC, a novel multi-task semantic communication system that leverages Mamba-2 architecture for efficient DNA sequence transmission. The system addresses the computational challenges of processing extremely long genomic sequences while simultaneously performing semantic reconstruction and classification tasks.
- We introduce a joint optimization framework that enables simultaneous DNA sequence reconstruction and class prediction. This multi-task approach preserves both sequence-level fidelity and high-level semantic information during wireless transmission, making the system suitable for genomic applications requiring both data integrity and classification accuracy.
- We demonstrate through comprehensive experiments that DNA-Mamba-DeepSC achieves superior performance compared to existing baselines across multiple metrics, including significant improvements in edit distance reduction, classification accuracy, and processing latency, while maintaining biological constraints essential for DNA sequence validity.

II. Proposed System

Fig. 1 presents an overview of the proposed multi-task semantic communication system for DNA transmission. In this system, a DNA sequence is first semantically encoded and then transmitted through a wireless channel. At the receiver, the transmitted sequence is decoded to reconstruct the original DNA sequence while simultaneously predicting its associated class labels through the multi-task learning framework.

A. Proposed System Architecture

The proposed system architecture is illustrated in Fig. 2. The system consists of two main components: encoder side and decoder side. Firstly, the DNA sequence has length L which $X_{\text{DNA}} \in \mathbb{R}^{N \times L_{\text{DNA}}}$, is fed into DNA tokenizer to convert the DNA sequence into a sequence of tokens $X_{\text{tok}} \in \mathbb{R}^{N \times L_{\text{tok}} \times VS}$, where $L_{\text{tok}} \ll L_{\text{DNA}}$ is the length of the tokenized sequence and VS represents for the vocabulary size of tokenizer. Then, the tokenized sequence is fed into the encoder side which consists of three main blocks: embedding, semantic encoder and channel encoder. The embedding convert the tokenized sequence to a latent representation $X_{\text{embedding}} \in \mathbb{R}^{N \times L_{\text{tok}} \times D_{\text{sem}}}$ where D_{sem} represents the the size of semantic features. After that, it go through semantic encoder which consists of 3 blocks of Mamba-2 to extract semantic features, express as follows:

$$X_{\text{sem}} = \text{Mamba-2}^3(X_{\text{embedding}}) \in \mathbb{R}^{N \times L_{\text{tok}} \times D_{\text{sem}}} \quad (1)$$

After that, it go through the channel encoder to compress the features into symbols suitable for transmission over the noisy

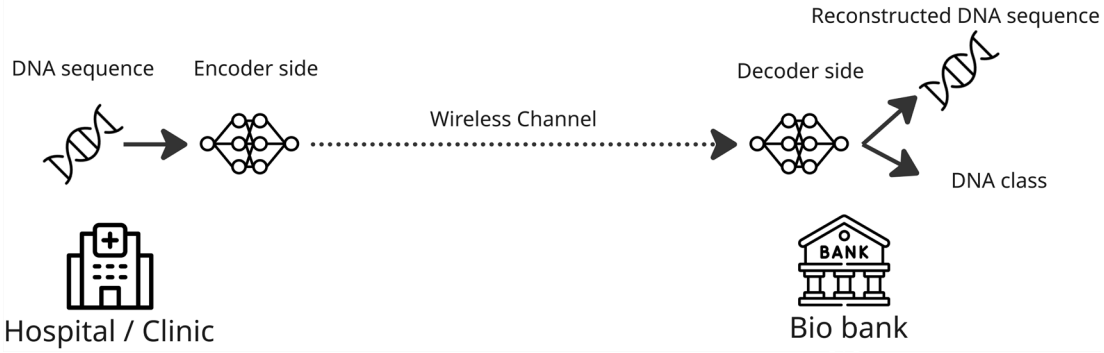

Fig. 1. Overview about Multi-task Semantic Communication System for DNA transmission

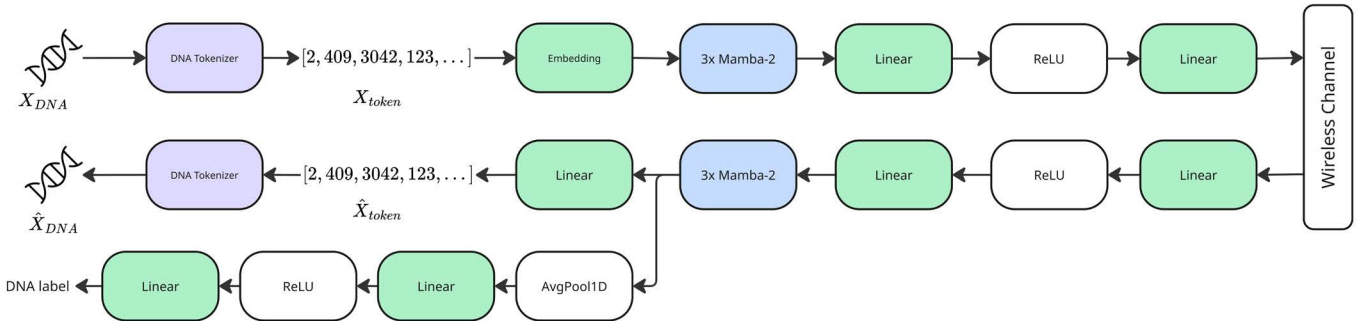

Fig. 2. Proposed DNA-Mamba-DeepSC architecture showing the multi-task semantic communication system with Mamba-2 blocks for joint DNA sequence reconstruction and classification

satellite channel. This transformation is achieved through a non-linear projection

$$Y = Linear2(ReLU(Linear1(X_{\text{sem}}))) \in \mathbb{R}^{N \times L_{\text{tok}} \times D_{\text{chan}}} \tag{2}$$

where Y is channel symbol features; D_{chan} represents for the number of channel hidden size. The encoded symbols traverse a wireless channel subject to atmospheric. The encoded symbols traverse a wireless channel subject to atmospheric interference and distance-related degradation. We model this as an Additive White Gaussian Noise (AWGN) channel:

$$Z = Y + \mathcal{N}(0, \sigma_n^2) \in \mathbb{R}^{N \times L_{\text{tok}} \times D_{\text{chan}}} \tag{3}$$

where Z represents the received symbols at the ground station, and $\mathcal{N}(0, \sigma_n^2)$ denotes AWGN with variance σ_n^2 determined by the signal-to-noise ratio (SNR). The ground station begins processing with channel decoding, which mirrors the encoding structure to recover the semantic features:

$$\hat{X}_{\text{sem}} = Linear4(ReLU(Linear5(Z))) \in \mathbb{R}^{N \times L_{tok} \times D_{\text{sem}}} \tag{4}$$

The semantic decoder performs the heavy computational lifting on the ground station side, where resources are more abundant. The decoded features undergo progressive refinement through three Mamba-2 blocks:

$$X_{decoded} = \text{Mamba-2}^3(\hat{X}_{\text{sem}}) \tag{5}$$

The decoded features X_{decoded} are then processed in parallel through two specialized task branches:

- **DNA Reconstruction Branch:** This branch recovers the original DNA sequence from the semantic features:

$$\hat{X}_{\text{DNA}} = \text{TokenizerDecode}(\text{Linear}(X_{\text{decoded}})) \tag{6}$$

  where $\hat{X}_{\text{DNA}} \in \mathbb{R}^{N \times L_{\text{DNA}}}$ represents the reconstructed DNA sequence with N being the batch size and L_{DNA} the sequence length.
- **DNA Classification Branch:** This branch predicts the class labels associated with the DNA sequences:

$$\text{Cls} = \text{Linear}(\text{ReLU}(\text{Linear}(\text{AvgPool1D}(X_{\text{decoded}})))) \tag{7}$$

  where $\text{Cls} \in \mathbb{R}^{N \times C}$ represents the classification logits and C denotes the total number of classes.

This dual-branch architecture enables the system to simultaneously preserve sequence-level information for accurate DNA reconstruction while extracting high-level semantic features for robust classification, thereby supporting both data fidelity and semantic understanding in genomic applications.

B. Mamba-2 Block

The Mamba-2 block architecture is illustrated in Fig. 3. The Mamba-2 block begins by applying dual linear transformations to the normalized input signal:

$$\begin{aligned} x &= \text{Linear}(i) \in \mathbf{R}^{L \times (E \times D)} \\ z &= \text{Linear}(i) \in \mathbf{R}^{L \times (E \times D)} \end{aligned} \tag{8}$$

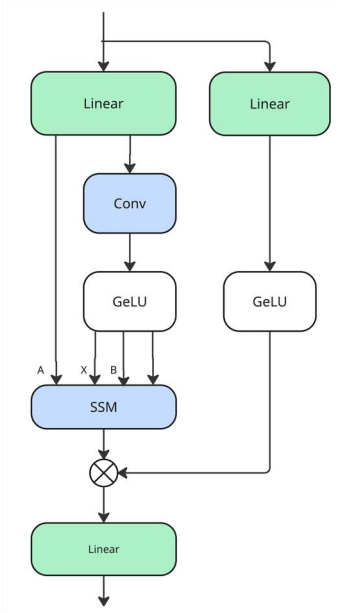

Fig. 3. Mamba-2 Block Architecture

where E indicating the expansion ratio. Subsequently, the primary pathway undergoes depthwise convolution processing:

$$x_c = Conv(x) \in \mathbf{R}^{L\times(E\times D)} \tag{9}$$

The core computation involves processing through the state space model:

$$y = SSM_{A,B,C,\Delta}(GeLU(x_c)) \in \mathbf{R}^{L\times(E\times D)} \tag{10}$$

where A, B, C, and Δ constitute the trainable SSM parameters. Following this, the gate pathway modulates the SSM results through element-wise multiplication:

$$y_{\text{merged}} = y \cdot GeLU(z) \in \mathbf{R}^{L\times(E\times D)} \tag{11}$$

Finally, the block produces its output via a linear transformation combined with skip connection:

$$out = Linear(y_{\text{merged}}) + i \in \mathbf{R}^{L\times D} \tag{12}$$

The integration of Mamba-2 blocks in our DNA-DeepSC system offers significant advantages for genomic sequence processing. Unlike traditional transformer architectures that exhibit quadratic complexity with sequence length, Mamba-2 provides linear computational complexity, making it particularly suitable for handling extremely long DNA sequences that can span millions of base pairs. The state space model architecture excels at capturing long-range dependencies inherent in genetic data, such as regulatory relationships between distant genomic regions and structural patterns that extend across entire chromosomes. Furthermore, Mamba-2's selective attention mechanism enables the model to focus on biologically relevant motifs and conserved sequences while efficiently processing redundant regions, thereby preserving critical genetic information during semantic compression. This selective processing capability is crucial for DNA transmission tasks where maintaining the integrity of functional genomic elements is paramount for downstream biological applications.

C. Training Loss Function

The proposed multi-task system optimizes two complementary objectives simultaneously through a weighted combination of reconstruction and classification losses. The total loss function is formulated as:

$$L_{\text{total}} = \lambda_{\text{recon}} L_{\text{recon}} + \lambda_{\text{cls}} L_{\text{cls}} \tag{13}$$

where λ_{recon} and λ_{cls} represent the weighting coefficients for reconstruction and classification tasks respectively.

The reconstruction loss measures the fidelity between the predicted and original DNA sequences using cross-entropy:

$$L_{\text{recon}} = -\frac{1}{N \times L_{\text{DNA}}} \sum_{i=1}^{N} \sum_{j=1}^{L_{\text{DNA}}} \sum_{k=1}^{4} y_{i,j,k} \log(\hat{y}_{i,j,k}) \tag{14}$$

where $y_{i,j,k}$ denotes the ground truth one-hot encoding for the k-th nucleotide at position j in sequence i, and $\hat{y}_{i,j,k}$ represents the corresponding predicted probability.

Similarly, the classification loss employs cross-entropy to measure the accuracy of DNA sequence classification:

$$L_{\text{cls}} = -\frac{1}{N} \sum_{i=1}^{N} \sum_{c=1}^{C} t_{i,c} \log(p_{i,c}) \tag{15}$$

where $t_{i,c}$ is the ground truth label for class c in sequence i, $p_{i,c}$ is the predicted probability for that class, and C represents the total number of classes. This joint optimization enables the model to preserve both sequence-level details and high-level semantic information during transmission.

III. Numerical Results

A. Simulation Setup

Experiments utilize an Intel Core Intel(R) Xeon(R) Platinum 8462Y and a NVIDIA H100 GPU. We adopted the DNA sequence dataset [13] include 6880 sequences in 7 classes. Table I lists training parameters. To compare performance with DNA-DeepSC, we adopt two baseline: DeepSC represents for standard deep-learning-enabled sematnic communication and UTF-8+Turbo represents for conventional method which uses UTF-8 as source coding and Turbo as channel coding

TABLE I
Simulation Parameters and Configuration Settings

Parameter	Value	Parameter	Value
Batch Size	8	Tokenizer	DNABERT-2-117M
Learning Rate	1.00E-04	D_{Sem}	128
Training Epoch	15	Vocab Size	4096
λ_{recon}	1	D_{Chan}	16
λ_{cls}	0.2		

B. Evaluation Metrics

We employ two evaluation metrics to assess the performance of the proposed system against two baseline methods:

1) Edit distance, formally defined as the Levenshtein distance, constitutes a fundamental string similarity metric quantifying the minimum number of elementary operations—insertions, deletions, and substitutions—required to transform one string into another. For strings S_1 and S_2 of lengths m and n respectively, the edit distance $\mathcal{D}(S_1, S_2)$ is computed through dynamic programming with recurrence relation:

$$\mathcal{D}[i,j] = \min \begin{cases} \mathcal{D}[i-1,j] + 1(\text{deletion}) \\ \mathcal{D}[i,j-1] + 1(\text{insertion}) \\ \mathcal{D}[i-1,j-1] + \delta(i,j)(\text{substitution}) \end{cases} \tag{16}$$

where $\delta(i,j) = 0$ if characters match, 1 otherwise. This metric satisfies essential mathematical properties including non-negativity, symmetry, and triangle inequality, establishing it as a true distance function in metric space theory. The algorithm achieves $\mathcal{O}(mn)$ time complexity with $\mathcal{O}(\min(m,n))$ space optimization through rolling array implementation.

2) Classification accuracy quantifies the proportion of correctly predicted DNA sequence class labels relative to the total number of predictions. For a dataset containing N DNA sequences with ground truth labels $\{y_1, y_2, \ldots, y_N\}$ and corresponding predictions $\{\hat{y}_1, \hat{y}_2, \ldots, \hat{y}_N\}$, the classification accuracy $\mathcal{A}$ is defined as:

$$\mathcal{A} = \frac{1}{N} \sum_{i=1}^{N} \mathbb{I}(y_i = \hat{y}_i) \times 100\% \tag{17}$$

where $\mathbb{I}(\cdot)$ denotes the indicator function that equals 1 when the condition is true and 0 otherwise. This metric provides a direct measure of the multi-task system's capability to preserve semantic class information during DNA sequence transmission and reconstruction.

C. Performance Comparison

The edit distance performance comparison in Fig. 4 demonstrates the superior reconstruction accuracy of the proposed DNA-DeepSC system across various SNR conditions. At low SNR (-6 dB), DNA-DeepSC achieves an edit distance of 2.16, outperforming DeepSC (2.25) by 4% and UTF-8 + Turbo (129.41) by 98.3%, highlighting the robustness of Mamba-2 based semantic encoding under harsh channel conditions. At moderate SNR (0 dB), DNA-DeepSC maintains superiority with 0.125 edit distance compared to DeepSC (0.177) and UTF-8 + Turbo (72.45), representing 29.4% and 580× improvements respectively. Even at high SNR (18 dB), DNA-DeepSC (0.003) consistently outperforms both DeepSC (0.005) and UTF-8 + Turbo (0.008) by 40% and 62.5% respectively. The consistent performance advantage across all SNR ranges validates the effectiveness of the multi-task learning framework and Mamba-2 architecture in preserving DNA sequence integrity for reliable genomic information transmission.

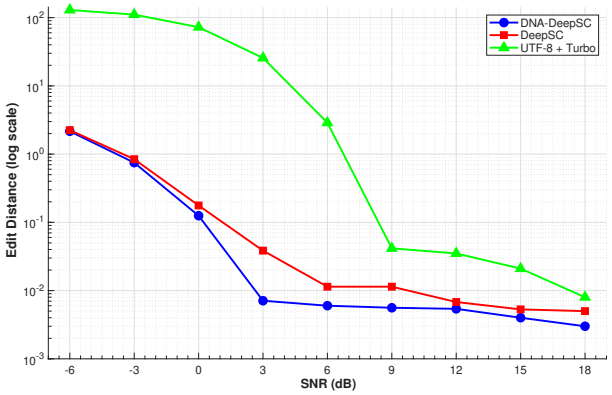

Fig. 4. Edit Distance Performance Comparison across Different SNR Values

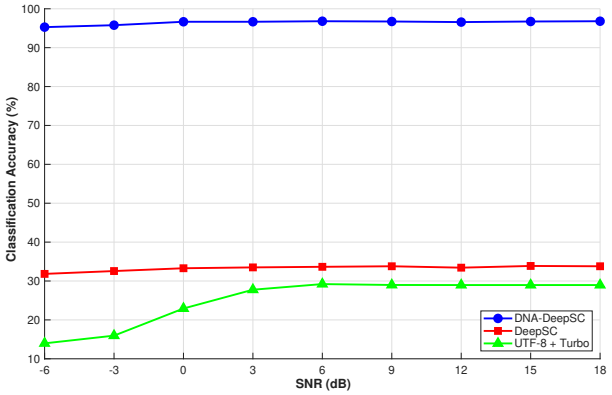

Fig. 5. Classification Accuracy Performance Comparison across Different SNR Values

The classification accuracy results in Fig. 5 demonstrate the exceptional performance of the proposed DNA-DeepSC system in the multi-task learning scenario. DNA-DeepSC achieves consistently high classification accuracy ranging from 95.28% at -6 dB to 96.8% at high SNR conditions, significantly outperforming both baseline methods across all channel conditions. In contrast, DeepSC achieves only 31.83-33.87% accuracy, representing approximately 3× lower performance, while UTF-8 + Turbo shows the poorest results with 13.97-29.21% accuracy. The remarkable stability of DNA-DeepSC's classification performance (less than 2% variation across SNR range) compared to the baseline methods highlights the effectiveness of the joint optimization strategy in the multi-task framework, where the classification task benefits from the semantic representations learned during DNA sequence reconstruction, enabling robust class prediction even under severe channel impairments.

D. Model Complexity Analysis

Table II demonstrates that DNA-DeepSC achieves superior performance with only 1,866,207 parameters, represent-

TABLE II
MODEL PARAMETER COMPARISON

Model	Number of Parameters
DeepSC	12,697,553
DNA-DeepSC	1,866,207
UTF-8+Turbo	-

ing an 85.3% reduction compared to DeepSC's 12,697,553 parameters. This efficiency stems from Mamba-2's linear complexity architecture, which eliminates the quadratic scaling of transformer-based attention mechanisms. The reduced parameter count enables deployment in resource-constrained environments while maintaining lower memory requirements, faster inference, and reduced energy consumption.

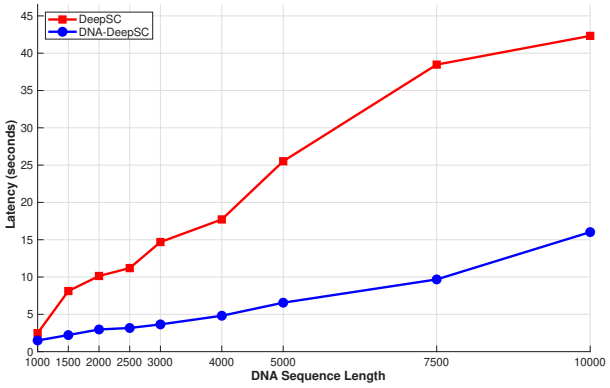

Fig. 6. Processing Latency Comparison for Different DNA Sequence Lengths

The sequence latency analysis in Fig. 6 demonstrates the computational efficiency advantage of the proposed DNA-DeepSC system over DeepSC across varying DNA sequence lengths. DNA-DeepSC consistently exhibits lower processing latency, with particularly significant improvements at longer sequences: at 1000 nucleotides, DNA-DeepSC requires 1.5ms compared to DeepSC's 2.48ms (39.5% reduction), while at 10,000 nucleotides, the latency gap widens dramatically with DNA-DeepSC achieving 16.02ms versus DeepSC's 42.32ms (62.1% reduction). This superior scalability stems from Mamba-2's linear computational complexity O(L) compared to the quadratic complexity $O(L^2)$ of transformer-based architectures in DeepSC, making DNA-DeepSC particularly suitable for processing extremely long genomic sequences that are common in real-world DNA transmission applications.

IV. CONCLUSION

This paper presented DNA-Mamba-DeepSC, a novel multi-task semantic communication system that leverages Mamba-2 architecture for efficient DNA sequence transmission with simultaneous reconstruction and classification capabilities. Experimental results demonstrate significant performance improvements including up to 98.3% edit distance reduction compared to conventional methods, consistently high classification accuracy of 95-96% across various SNR conditions, and 62.1% latency reduction for long sequences due to linear computational complexity. The proposed multi-task learning framework successfully preserves both sequence-level fidelity and semantic information during transmission, making it highly suitable for genomics research, personalized medicine, and biotechnology applications requiring reliable DNA data exchange.

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