
Context-Aware Regularization with Markovian Integration for Attention-Based Nucleotide Analysis

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Abstract

Transformers have revolutionized nucleotide sequence analysis, yet capturing long-range dependencies remains challenging. Recent studies show that autoregressive transformers often exhibit Markovian behavior by relying on fixed-length context windows for next-token prediction. However, standard self-attention mechanisms are computationally inefficient for long sequences due to their quadratic complexity and do not explicitly enforce global transition consistency.

We introduce CARMANIA (Context-Aware Regularization with Markovian Integration for Attention-Based Nucleotide Analysis), a self-supervised pretraining framework that augments next-token (NT) prediction with a transition-matrix (TM) loss. The TM loss aligns predicted token transitions with empirically derived n -gram statistics from each input sequence, encouraging the model to capture higher-order dependencies beyond local context. This integration enables CARMANIA to learn organism-specific sequence structures that reflect both evolutionary constraints and functional organization.

We evaluate CARMANIA across diverse genomic tasks, including regulatory element prediction, functional gene classification, taxonomic inference, antimicrobial resistance detection, and biosynthetic gene cluster classification. CARMANIA outperforms the previous best long-context model by at least 7%, matches state-of-the-art on shorter sequences (exceeding prior results on 20/40 tasks while running $\sim 2.5\times$ faster), and shows particularly strong improvements on enhancer and house-keeping gene classification tasks—including up to a 34% absolute gain in Matthews correlation coefficient (MCC) for enhancer prediction. The TM loss boosts accuracy in 33 of 40 tasks, especially where local motifs or regulatory patterns drive prediction. This enables more effective modeling of sequence-dependent biological features while maintaining robustness across non-coding and low-signal regions. Code available at <https://github.com/EESI/carmania>.

1 Introduction

Deoxyribonucleic acid (DNA), often referred to as the "language of life," encodes the genetic instructions essential for the development, functioning, and reproduction of all known living organisms and many viruses. The sequence of its four nucleotide bases—adenine (A), thymine (T), cytosine (C), and guanine (G)—forms the foundation of genetic information, dictating the synthesis of proteins and the regulation of various biological processes. Advancements in high-throughput sequencing technologies have exponentially increased genomic data availability.

Despite advances in sequencing, analyzing large-scale biological data remains challenging. Traditional methods—such as motif detection, sequence alignment, and Markov models—capture short-range dependencies well [Delcher et al. [2007], Steinegger and Söding [2017], Wood et al. [2019]], but often fail to represent complex or long-range patterns, especially in diverse or non-canonical sequences. Recent work has applied NLP techniques to biological sequences [Nguyen et al. [2024], Cahyawijaya et al. [2022], Schiff et al. [2024], Bo et al. [2025]], with large language models (LLMs) showing strong ability to capture complex dependencies. However, genomic sequences are often extremely long, making full attention computationally infeasible. To address this, transformer models use mechanisms like sliding window and sparse attention [Dong et al. [2025], Zaheer et al. [2020]], which expand the receptive field but may still struggle to capture long-range dependencies effectively in genomics.

In this work, we enhance transformers by incorporating Markovian priors, guiding them to follow long-range transition dynamics and better capture complex dependencies within the broader context of genomic sequences. Drawing on recent studies that interpret transformers’ capabilities through the lens of Markovian processes [Hu et al. [2024], Zekri et al. [2024]], we propose a novel pretraining strategy that explicitly enforces these Markovian properties.

Our approach, named CARMANIA (Context-Aware Regularization with Markovian Integration for Attention-Based Nucleotide Analysis), supplements the standard next-token prediction objective with an auxiliary loss. This loss aligns the model’s predicted first-order transition matrix with one derived from the full input sequence, encouraging consistency with its empirical token transition patterns. By doing so, CARMANIA captures the probabilistic structure of genomic sequences and improves context-awareness during next-token prediction.

To scale pretraining to long genomic sequences, we replace full attention with **sliding-window attention (SWA)**, a sparse mechanism that limits each token’s receptive field to a fixed-size window of preceding tokens, reducing complexity from $O(n^2)$ to $O(kn)$ ($k \ll n$) while preserving biologically meaningful local interactions. **TM loss** complements this by reinforcing short-range dependencies within the local window while promoting global consistency, since the transition matrix is computed over the entire input sequence. Together, these components enable a balance between local motif recognition and broader statistical alignment. *In practice, CARMANIA handles effective contexts up to 160 kbp, which makes it, to our knowledge, the longest-context transformer-based genomic language model to date.* An overview of our framework is illustrated in Figure 1.

In addition to improving context modeling, our pretraining approach supports efficient domain adaptation, as conserved transition patterns across species enable generalization with minimal fine-tuning [Bergeron et al. [2023]].

The main contributions of this work are:

- **A scalable architecture for long-context genomic modeling** that integrates sliding-window attention, RoPE-based positional encoding, FlashAttention, and a widened Transformer backbone, enabling efficient representation learning over extended DNA sequences.
- **A novel self-supervised objective based on Transition Matrix (TM) loss**, which regularizes the transformer model by aligning predicted token transitions with empirical n-gram distributions. This Markovian prior enhances memory retention, out-of-distribution generalization, and biological coherence across long genomic contexts.
- **Comprehensive evaluation across 40 genomic tasks**, including regulatory element prediction, functional gene classification, taxonomic inference, and biosynthetic gene cluster(BGC) prediction, where our model achieves consistent improvements—even in benchmarks where alternative inductive biases have previously dominated.

2 Related Work

2.1 Markovian Models in Genomics

Hidden Markov Models (HMMs) are widely used in genomics for modeling the probabilistic structure of biological sequences. They enable gene prediction, as in GeneMark [Lukashin and Borodovsky

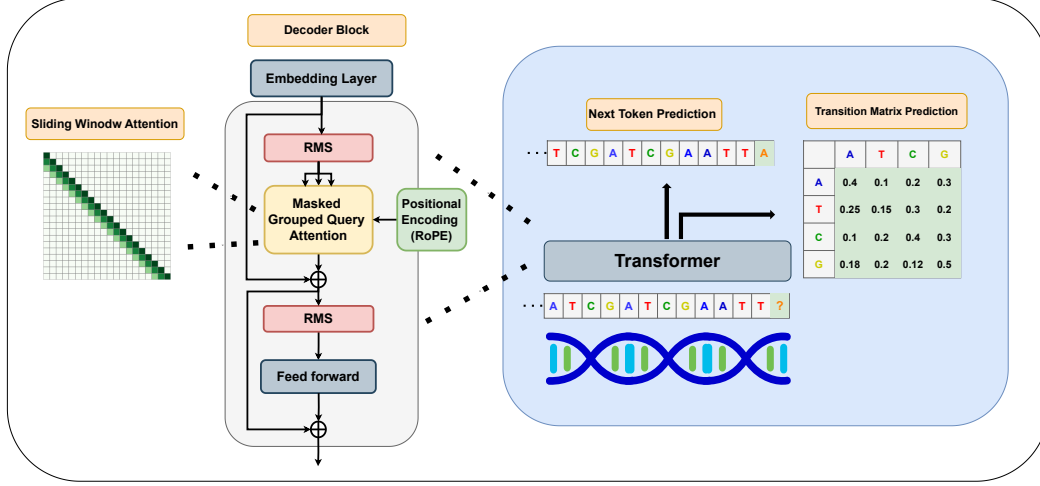


Figure 1: **Proposed Pretraining Framework.** We extend a LLaMA-style decoder with a transition matrix module to capture global nucleotide co-occurrence. The model uses sliding-window attention with rotary embeddings and local caching, reducing attention complexity from $O(n^2)$ to $O(n)$. The transition matrix complements local attention by preserving long-range dependencies efficiently.

[1998], and other methods for identifying coding regions Delcher et al. [2007]. Profile HMMs are commonly applied to protein family analysis, capturing conserved regions and domain variability Potter et al. [2018]. HMMs also power microbial classification tools like Clasnip Chuan et al. [2023], and Aphmm Firtina et al. [2024] improves the speed and efficiency of profile HMM computations. Their effectiveness depends on model structure, sequence length, and the biological complexity of the task.

2.2 Language Models in Genomics

The first breakthrough in genomic language models came with DNABERT Ji et al. [2021], which employed a BERT architecture with k-mer tokenization and sequence masking to learn DNA sequence representations. The Nucleotide Transformer Dalla-Torre et al. [2024] scaled this concept, training a 2.5 billion parameter model on 850 genomes. Other models like HyenaDNA Nguyen et al. [2024] used long convolutional blocks for efficient long-sequence handling, while BigBird Refahi et al. [2025, 2023] applied sparse and sliding window attention to capture long-range dependencies. Caduceus Schiff et al. [2024], built on Mamba, introduced a bi-directional model preserving reverse complement symmetry.

Together, these advances in tokenization, architecture, and representation learning have led to increasingly effective models for genomic analysis Cahyawijaya et al. [2022], Celikkanat et al. [2024].

2.3 The Markovian Core of Autoregressive Transformers

There has been significant research Edelman et al. [2024], Zekri et al. [2024], Ildiz et al. [2024], Hu et al. [2024] aimed at establishing an equivalence between autoregressive language models based on transformers and Markov chains. Specifically, findings emphasize the role of statistical induction heads, which adaptively learn in-context patterns, forming a foundation for next-token predictions. This perspective introduces a compelling connection between autoregressive architectures and Markov chains, paving the way for a nuanced understanding of in-context learning (ICL). Zekri et al. [2024], Edelman et al. [2024]. Zekri et al. [2024] demonstrates that an autoregressive model with a vocabulary size T and a context window of size K can be represented as a Markov chain with a state space of size $O(T^K)$.

In an autoregressive model, the probability of predicting the next token x_{t+1} given the previous K tokens $(x_t, x_{t-1}, \dots, x_{t-K+1})$ can be written as:

$$\Pr(x_{t+1} \mid x_t, x_{t-1}, \dots, x_{t-K+1}). \quad (1)$$

This conditional probability can be interpreted as a transition probability in a K -th order Markov chain, where each unique K -length token sequence defines a state. The transition matrix $Q \in \mathbb{R}^{T \times T}$ is defined as:

$$Q_{s,s'} = \Pr(x_{t+1} = x_{s'} \mid x_t = x_s), \quad (2)$$

where s and s' index sequences of K tokens. The rows of Q sum to 1, satisfying the Markov property. Thus, the model’s behavior approximates a Markov chain with T^K states, capturing dependencies within the fixed context window. Although self-attention is globally contextual and non-Markovian in theory, limited context in practice causes autoregressive Transformers to approximate Markovian behavior Ildiz et al. [2024].

3 Pretraining Long Sequences With Markovian Knowledge

We adopt a causal Transformer inspired by LLaMATouvron et al. [2023], where each layer computes hidden representations $\mathbf{h}^{(l)}$ from input tokens $\mathbf{x} = (x_1, x_2, \dots, x_n)$ and the previous layer’s outputs $\mathbf{h}^{(l-1)}$, using multi-head self-attention to predict the next token. To scale to long sequences, we replace full self-attention with SWA, where each token attends only to a fixed-size k window of preceding tokens, $x_{t-k}, \dots, x_{t-1}$, reducing complexity from $O(n^2)$ to $O(kn)$. This not only improves efficiency but also reflects the local nature of most biological dependencies in genomic sequences. We further improve efficiency with FlashAttention-2 Dao [2023] and enhance positional encoding via Rotary Positional Embeddings (RoPE) Su et al. [2024], enabling better extrapolation to long contexts.

3.1 Unified n -th Order Transition Tensor Formulation

To complement the next-token prediction objective, we introduce a unified probabilistic framework that captures higher-order dependencies through a transition tensor. Let $\mathbf{P}_t \in \mathbb{R}^V$ denote the model’s predicted probability distribution over the vocabulary $\mathcal{V}$ at position t , where $[\mathbf{P}_t]_i = \mathbb{P}(x_t = i \mid x_{<t})$.

We define the n -th order transition tensor $\mathcal{T}^{(n)} \in \mathbb{R}^{V^n}$ as:

$$\mathcal{T}_{i_1 i_2 \dots i_n}^{(n)} = \frac{1}{B(L-n+1)} \sum_{b=1}^B \sum_{t=1}^{L-n+1} \prod_{s=0}^{n-1} [\mathbf{P}_{t+s}^{(b)}]_{i_{s+1}}, \quad (3)$$

where B is the batch size, L is the sequence length, V is the vocabulary size, and $i_1, \dots, i_n$ index token values in the n -gram.

This formulation approximates the joint distribution over n consecutive model predictions, providing a global summary of sequential dynamics. In practice, we focus on the first-order case ($n = 2$), which corresponds to modeling bigram transitions. This strikes a balance between expressiveness and computational efficiency, and directly supports the TM loss introduced in the next section.

3.2 Pretraining Objective

Our pretraining objective combines two complementary components: next-token prediction and transition matrix alignment. The primary objective is the standard autoregressive language modeling loss, which minimizes the negative log-likelihood of predicting each token x_t given its preceding context:

$$\mathcal{L}_{\text{NT}} = - \sum_{t=1}^n \log P_\theta(x_t \mid x_1, \dots, x_{t-1}), \quad (4)$$

where P_θ denotes the model’s predicted token distribution.

To reinforce global sequence structure, we introduce a Transition Matrix (TM) loss that encourages the model to match the empirical token transition dynamics. Let p_{ij} and q_{ij} denote the smoothed n -gram distributions of the input and model outputs, respectively. The KL divergence between these distributions defines the TM loss:

$$\mathcal{L}_{\text{TM}} = \sum_{i,j} p_{ij} \log \frac{p_{ij}}{q_{ij}}. \quad (5)$$

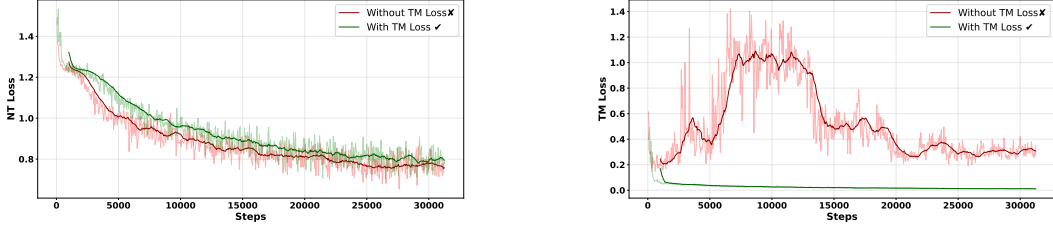


Figure 2: Comparison of training losses with and without explicit TM loss enforcement ($\beta = 1$ vs. $\beta = 0$). **Left:** Both models show similar reductions in next-token prediction loss. **Right:** Without TM loss ($\beta = 0$), the model partially learns transition structure—TM loss rises then stabilizes—indicating implicit alignment with n-gram patterns.

Table 1: Ablation study showing the impact of TM loss and attention type on model performance (F1 Macro, BLEU) and compute cost. All models are trained on the Scorpio-Gene-Taxa dataset. F1 Macro is evaluated on the Antimicrobial Resistance (AMR) classification tasks, while BLEU and Relative FLOPs are computed on the Human Genome-Short dataset using 10,000 fragments from the GRCh38/hg38 reference genome. Relative FLOPs are reported with respect to the Sliding Window attention baseline, which has an absolute compute cost of approximately 16.7×10^{12} FLOPs per sequence.

Model Setting	F1 Macro ($\uparrow$)	BLEU ($\uparrow$)	Relative FLOPs ($\downarrow$)
Transformer (SWA)	0.873 ± 0.130	0.73	1.00
+ TM Loss	0.882 ± 0.131	0.77	1.00
+ Full Attention + TM Loss	0.883 ± 0.131	0.71	1.58

The full loss combines both terms:

$$\mathcal{L}_{\text{Full}} = \mathcal{L}_{\text{NT}} + \beta \mathcal{L}_{\text{TM}}, \quad (6)$$

where β is a tunable hyperparameter controlling the influence of the TM loss.

4 Experiments

In this section, we evaluate CARMANIA across a range of genomic tasks. We first describe the pretraining datasets, model architecture, and training setup, followed by ablation studies assessing the impact of the TM loss and attention mechanism on convergence, efficiency, and long-range retention. Finally, we present comprehensive benchmark results demonstrating the model’s adaptability, generalization, and superior performance over existing methods.

4.1 Experimental Setup

Pre-training Datasets

We pre-train our model on three large-scale genomic datasets: (i) GRCh38 GRCh38 [2013], which provides $\sim 3\text{B}$ base pairs with 10 kbp and 160 kbp fragments; (ii) the Basic Genome Dataset Zhu et al. [2022], consisting of $\sim 10\text{B}$ base pairs across 4,600+ genomes with 10 kbp fragments; and (iii) the Scorpio Gene-Taxa Dataset Refahi et al. [2025], comprising $\sim 580\text{M}$ base pairs from 2,046 genomes with 4 kbp fragments. Additional details are in Appendix A.

Model and Training Details

Architecture: CARMANIA is a LLaMA-based causal Transformer tailored for genomic sequence modeling. It uses 16 attention heads (4 key-value), a window size of 128, and 5 custom Transformer layers with an embedding size of 1024 and intermediate dimension of 4608. The model uses SiLU activations and contains 83M parameters. We selected this wide architecture based on the comparative results in Supplementary Table 12, which demonstrate its superior performance and efficiency over deeper models in both in-domain and out-of-domain genomic tasks.

Tokenization and n-gram Frequency Calculation: We tokenize DNA sequences at the single-nucleotide level (A, T, C, G) to preserve fine-grained features such as SNPs and avoid disrupting open

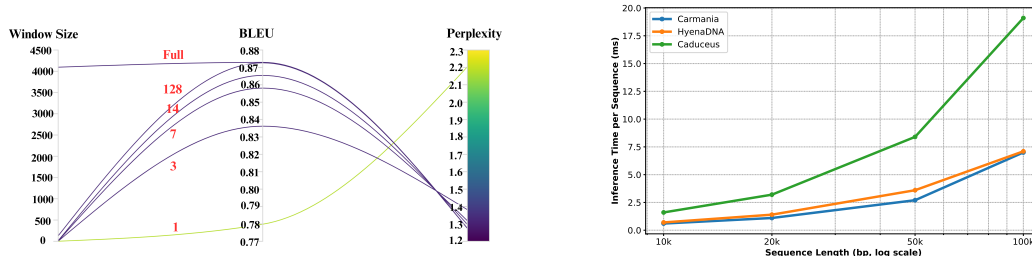


Figure 3: **Left:** Effect of window size on model performance. A window size of 128 achieves results comparable to full attention. **Right:** Inference time per sequence for CARMANIA(83M), HyenaDNA(1.6M), and Caduceus-PH(1.9M) across varying sequence lengths.

reading frames, as can occur with subword or non-overlapping k-mer methods. Additionally, during tokenization, we compute a normalized 4×4 first-order transition matrix for each sequence based on bigram frequencies, where each row defines a probability distribution over possible next nucleotides. This sequence-specific matrix acts as a self-supervised training signal, serving as ground truth for the transition-matrix loss and guiding the model to learn biologically meaningful transition patterns.

Training Parameters, and Hardware Specifics: The model was trained for two epochs using PyTorch on an NVIDIA A100 GPU (80GB). To fit within memory constraints, batch sizes were set based on sequence length: 35 for 4 kbp, 19 for 10 kbp, and 1 for 160 kbp inputs. We used a cosine annealing schedule with an initial learning rate of $5e-4$. Additional training details, including optimizer settings and gradient clipping, are listed in Supplementary Table 13. The training setup yields an efficiency of approximately 7.57×10^{-9} GPU-hours per token.

4.2 Ablation Studies

Effect of Transition Matrix Loss

We study the effect of adding first-order TM loss alongside the next-token (NT) loss by training on the Scorpio-Gene-Taxa dataset for 31k steps under two settings: with TM loss ($\beta = 1$) and without it ($\beta = 0$). In the $\beta = 0$ case, TM loss is computed but not used during training, allowing us to observe the model’s natural transition behavior. The left panel of Figure 2 shows NT loss decreases similarly for both models, indicating that adding TM loss does not hinder token-level learning. In contrast, the right panel reveals different TM loss patterns: for the $\beta = 0$ model, the TM loss initially increases then decreases as the model partially and passively captures transition structure, while for the $\beta = 1$ model, the TM loss consistently decreases from the start. However, as shown in supplementary results, convolution-based models like HyenaDNA require explicit TM regularization to exhibit this property.

Finally, as reported in Table 1, models trained with TM loss achieve higher macro F1 scores on downstream Antimicrobial Resistance (AMR) classification tasks (detailed in Supplementary Table 18) and improved BLEU scores on the human genome benchmark. We also evaluated this effect across all 40 downstream benchmarks and found that adding TM loss led to improved performance in 33 of them.

Higher-Order Transition Matrices. As shown in Supplementary Tables 10 and 11, applying second-order TM loss led to performance degradation across tasks compared to first-order TM or no TM. This drop is likely due to the sparsity of higher-order transitions in biological sequences, which makes the loss signal unstable. In contrast, first-order TM loss consistently improves performance by capturing reliable and biologically meaningful pairwise dependencies.

Effect of Windowed vs. Full Attention

We assess the effect of attention window size by training on a 100M bp subset of the Scorpio-Gene-Taxa dataset. As shown in Figure 3, larger windows improve BLEU scores and reduce perplexity, with full attention as an upper bound. Notably, a window size of 128 performs comparably to full attention, indicating that TM loss enables smaller windows to capture complex dependencies efficiently. Figure 3 also illustrates inference time comparisons across models on input sequences of varying lengths, up to 100k bases. Despite having 83M parameters, our model runs approximately

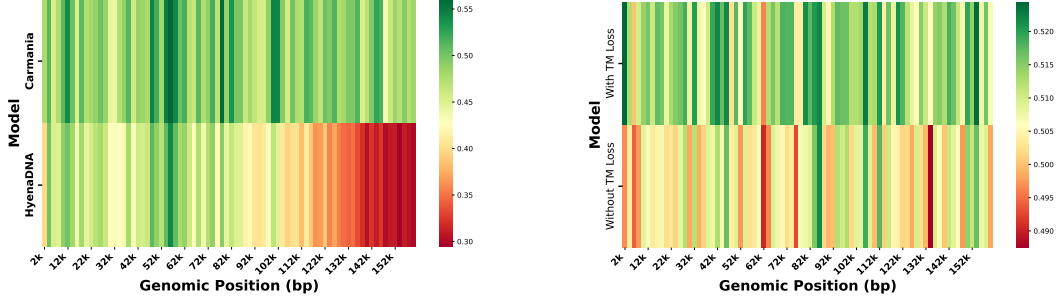


Figure 4: Heatmap of average sequence similarity across 50 independent 160 kbp genomic segments in 100 bp windows at 2000 bp intervals. **Left:** CARMANIA consistently maintains high similarity across all regions, demonstrating superior long-range memory, whereas HyenaDNA shows reduced sequence coherence in later segments. **Right:** Incorporating the TM loss improves memory retention in CARMANIA, yielding higher sequence similarity across extended contexts.

2.5 times faster than Caduceus becomes significantly slower as sequence length increases, while HyenaDNA (1.6M) maintains relatively fast inference but underperforms on long sequences and remains slower than our model. This demonstrates the practical efficiency of our architecture, and also highlights how windowed attention enables faster inference in Transformer-based models.

Table 1 compares the performance of models trained with full attention and windowed attention. While full attention achieves slightly better performance on downstream tasks, it results in a lower BLEU score. In addition, we evaluate the computational efficiency of windowed attention. As shown in Table 1, full attention requires 58% more computational resources compared to a window size of 128. This demonstrates the trade-off between accuracy and efficiency, as windowed attention reduces complexity from $O(n^2)$ in full attention to $O(k^2n)$, making it a more practical and scalable choice for large-scale sequence modeling.

4.3 Long-Range Sequence Retention

We evaluate each model’s ability to preserve long-range sequence structure by measuring internal consistency across extended human genome regions. Specifically, we analyze 50 independent 160 kbp genomic segments. Within each segment, we extract 100 bp windows using a fixed stride of 2000 bp and compare the model-predicted sequences against the corresponding regions in the original input sequence using Hamming similarity. This produces a position-wise similarity profile, which we average across all segments to assess how well each model maintains fidelity over increasing genomic distance.

As shown in Figure 4, HyenaDNA shows a marked drop in sequence similarity at distal positions. This likely reflects the limitations of its fixed-depth recurrence architecture, where information must propagate layer by layer without explicit token-to-token interaction Nguyen et al. [2024], making it harder to retain detailed signals over long spans. In contrast, CARMANIA maintains high similarity across the entire sequence due to its sliding-window attention and the TM loss, which encourages consistency in token transitions. The effect of the TM loss is further illustrated in Figure 4, where models trained without it show noticeably shorter retention spans, suggesting its role in supporting full-sequence memorization.

4.4 Downstream Task Evaluations

Genomics Benchmark: Supervised Adaptation

To evaluate task-specific adaptation, we fine-tuned our model on diverse genomics classification datasets. The Genomic Benchmarks collection includes tasks such as regulatory element prediction, enhancer detection, and binary species classification Grešová et al. [2023]. For a fair comparison, we fine-tuned the human-pretrained CARMANIA model using 5-fold cross-validation and compared its performance to other state-of-the-art models trained on the human genome. As shown in Table 2, CARMANIA achieves top performance in 4 out of 8 tasks and matches the best performance in 2 others, demonstrating its strong generalization ability in supervised downstream settings.

Table 2: Top-1 accuracy ($\uparrow$) across 5-fold cross-validation on Genomic Benchmark tasks. Results for CNN, HyenaDNA, Mamba, and both Caduceus variants are taken from the original Caduceus paper [Schiff et al., 2024]. Underlined values indicate second-best results.

Task	CNN	HyenaDNA	Mamba	Caduceus-PH	Caduceus-PS	CARMANIA	Baseline w/o TM
Mouse Enhancers	0.715 $\pm$ 0.087	<u>0.780 $\pm$ 0.025</u>	0.743 $\pm$ 0.054	0.754 $\pm$ 0.074	0.793 $\pm$ 0.058	0.761 $\pm$ 0.019	0.748 $\pm$ 0.020
Coding vs. Intergenic	0.892 $\pm$ 0.008	0.904 $\pm$ 0.005	0.904 $\pm$ 0.004	0.915 $\pm$ 0.003	0.910 $\pm$ 0.003	0.935 $\pm$ 0.001	<u>0.930 $\pm$ 0.001</u>
Human vs. Worm	0.942 $\pm$ 0.002	0.964 $\pm$ 0.002	0.967 $\pm$ 0.002	0.973 $\pm$ 0.001	<u>0.968 $\pm$ 0.002</u>	<u>0.968 $\pm$ 0.003</u>	0.966 $\pm$ 0.001
Human Enhancers Cohn	0.702 $\pm$ 0.021	0.729 $\pm$ 0.014	0.732 $\pm$ 0.029	0.747 $\pm$ 0.004	<u>0.745 $\pm$ 0.007</u>	0.724 $\pm$ 0.005	0.699 $\pm$ 0.005
Human Enhancer Ensembl	0.744 $\pm$ 0.122	0.849 $\pm$ 0.006	0.862 $\pm$ 0.008	0.893 $\pm$ 0.008	<u>0.900 $\pm$ 0.006</u>	0.916 $\pm$ 0.002	0.892 $\pm$ 0.001
Human Regulatory	0.872 $\pm$ 0.005	0.869 $\pm$ 0.012	0.814 $\pm$ 0.211	0.872 $\pm$ 0.011	0.873 $\pm$ 0.007	0.895 $\pm$ 0.002	<u>0.893 $\pm$ 0.002</u>
Human OCR Ensembl	0.698 $\pm$ 0.013	0.783 $\pm$ 0.007	0.815 $\pm$ 0.002	0.828 $\pm$ 0.006	<u>0.818 $\pm$ 0.006</u>	0.775 $\pm$ 0.002	0.763 $\pm$ 0.002
Human NonTATA Promoters	0.861 $\pm$ 0.009	0.944 $\pm$ 0.002	0.933 $\pm$ 0.007	0.946 $\pm$ 0.007	0.945 $\pm$ 0.010	0.963 $\pm$ 0.002	<u>0.961 $\pm$ 0.003</u>

Nucleotide Transformer Tasks: Supervised Adaptation

We benchmarked our model on 18 diverse genomics classification tasks introduced by Dalla-Torre et al. [2024], spanning histone modification prediction, regulatory annotation, and splice site detection. Following their evaluation protocol, we performed 10-fold cross-validation with early stopping, reporting the mean and standard deviation across different random seeds.

As shown in Table 3, CARMANIA achieves top-1 performance on 5 out of 18 tasks and outperforms the average of all baselines by over 3% across metrics. Notably, in enhancer classification tasks, CARMANIA achieves up to 34% absolute improvement in MCC over previous models Zhou et al. [2023], Avsec et al. [2021], Schiff et al. [2024], Nguyen et al. [2024], Dalla-Torre et al. [2024]. These results demonstrate the model’s strong ability to capture regulatory signals from sequence. A notable gain is observed on the H4ac histone mark, where adding the TM loss yields over 40.9% relative improvement in MCC. The benefit of the TM loss, however, is not uniform across all genomics tasks. In enhancer prediction, where positive and negative classes differ strongly in their local motif distributions (KL divergence = 9.28), the TM loss provides no measurable improvement ($\Delta = 0.0\%$). In splice-site donor prediction (KL = 0.99), it yields a modest 5.2% gain, and in the H4ac histone mark dataset (KL = 0.64), a substantial 40.9% improvement. These results demonstrate that TM-driven performance gains inversely track inter-class bigram separability, confirming that TM loss is most effective when local sequence features are ambiguous and long-range dependencies become critical. Biologically, this aligns with our understanding that enhancer regions possess clear, unique motifs that NT loss can easily learn, whereas splice sites rely on short, dispersed sequence cues. In contrast, H4 acetylation involves multiple lysine sites (K5, K8, K12, K16) on the H4 N-terminal tail that act cooperatively to regulate chromatin accessibility Dion et al. [2005], Ma et al. [2024]. Instead of strong individual motifs, these sites follow diffuse and combinatorial sequence patterns, making TM’s global co-occurrence modeling particularly advantageous.

Table 3: Performance comparison ($\uparrow$) on 10-fold cross-validation across 18 tasks, including histone marks, regulatory elements, and splice site prediction. We report MCC for histone/enhancer tasks, F1 for promoter/splice site, and accuracy for the “All” splice task. Baselines follow Caduceus Schiff et al. [2024] and Dalla-Torre et al. [2024]. CARMANIA achieves top performance on 5 tasks and remains competitive elsewhere. Underlined values denote second-best results.

	ENFORMER 252M	DNABERT-2 117M	NT-V2 500M	HYENADNA 1.6M	Caduceus-PH 1.9M	Caduceus-PS 1.9M	CARMANIA 83M	Baseline w/o TM 83M
Histone Markers								
H3	0.719 $\pm$ 0.048	0.785 $\pm$ 0.033	0.784 $\pm$ 0.047	0.779 $\pm$ 0.037	0.815$\pm$0.048	<u>0.799$\pm$0.029</u>	0.782 $\pm$ 0.023	0.785 $\pm$ 0.011
H3K14AC	0.288 $\pm$ 0.077	0.516 $\pm$ 0.028	0.551 $\pm$ 0.021	0.612 $\pm$ 0.065	0.631$\pm$0.026	0.541 $\pm$ 0.212	<u>0.627 $\pm$ 0.021</u>	0.631 $\pm$ 0.022
H3K36ME3	0.344 $\pm$ 0.055	0.591 $\pm$ 0.020	0.625 $\pm$ 0.013	0.613 $\pm$ 0.041	0.601 $\pm$ 0.129	0.609 $\pm$ 0.109	0.632 $\pm$ 0.011	<u>0.629 $\pm$ 0.017</u>
H3K4ME1	0.291 $\pm$ 0.061	0.511 $\pm$ 0.028	0.550$\pm$0.021	0.512 $\pm$ 0.024	<u>0.523$\pm$0.039</u>	0.488 $\pm$ 0.102	0.515 $\pm$ 0.017	0.516 $\pm$ 0.017
H3K4ME2	0.211 $\pm$ 0.069	0.336 $\pm$ 0.040	0.319 $\pm$ 0.045	0.455 $\pm$ 0.095	0.487 $\pm$ 0.170	0.388 $\pm$ 0.101	0.502 $\pm$ 0.025	<u>0.500 $\pm$ 0.038</u>
H3K4ME3	0.158 $\pm$ 0.072	0.352 $\pm$ 0.077	0.410 $\pm$ 0.033	0.549 $\pm$ 0.056	0.544 $\pm$ 0.045	0.440 $\pm$ 0.202	<u>0.565 $\pm$ 0.012</u>	0.586 $\pm$ 0.011
H3K79ME3	0.496 $\pm$ 0.042	0.613 $\pm$ 0.030	0.626 $\pm$ 0.026	0.672 $\pm$ 0.048	<u>0.697$\pm$0.077</u>	0.676 $\pm$ 0.026	0.699 $\pm$ 0.013	0.695 $\pm$ 0.018
H3K9AC	0.420 $\pm$ 0.063	0.542 $\pm$ 0.029	0.562 $\pm$ 0.040	0.581 $\pm$ 0.061	0.622$\pm$0.030	0.604 $\pm$ 0.048	<u>0.615 $\pm$ 0.013</u>	0.608 $\pm$ 0.010
H4	0.732 $\pm$ 0.076	0.796 $\pm$ 0.027	<u>0.799$\pm$0.025</u>	0.763 $\pm$ 0.044	0.811$\pm$0.022	0.789 $\pm$ 0.020	0.772 $\pm$ 0.010	0.769 $\pm$ 0.019
H4AC	0.273 $\pm$ 0.063	0.463 $\pm$ 0.041	0.495 $\pm$ 0.032	0.564 $\pm$ 0.038	0.621$\pm$0.054	0.525 $\pm$ 0.240	<u>0.606 $\pm$ 0.014</u>	0.197 $\pm$ 0.011
Regulatory Annotation								
ENHANCER	0.451 $\pm$ 0.108	0.516 $\pm$ 0.098	0.548 $\pm$ 0.144	0.517 $\pm$ 0.117	0.546 $\pm$ 0.073	0.491 $\pm$ 0.066	0.880$\pm$0.013	<u>0.878$\pm$0.013</u>
ENHANCER TYPES	0.309 $\pm$ 0.134	0.423 $\pm$ 0.051	0.424 $\pm$ 0.132	0.386 $\pm$ 0.185	0.439 $\pm$ 0.054	0.416 $\pm$ 0.095	0.724$\pm$0.013	<u>0.724$\pm$0.010</u>
PROMOTER: ALL	0.954 $\pm$ 0.006	0.971 $\pm$ 0.006	0.976$\pm$0.006	0.960 $\pm$ 0.005	<u>0.970$\pm$0.004</u>	0.967 $\pm$ 0.004	0.963 $\pm$ 0.001	0.960 $\pm$ 0.001
NOTATA	0.955 $\pm$ 0.010	0.972 $\pm$ 0.005	0.976$\pm$0.005	0.959 $\pm$ 0.008	<u>0.969$\pm$0.011</u>	0.968 $\pm$ 0.006	0.962 $\pm$ 0.002	0.960 $\pm$ 0.003
TATA	0.960 $\pm$ 0.023	0.955 $\pm$ 0.021	0.966$\pm$0.013	0.944 $\pm$ 0.040	0.953 $\pm$ 0.016	<u>0.957$\pm$0.015</u>	0.942 $\pm$ 0.008	0.940 $\pm$ 0.008
Splice Site Annotation								
ALL	0.848 $\pm$ 0.019	0.939 $\pm$ 0.009	0.983$\pm$0.008	0.956 $\pm$ 0.011	0.940 $\pm$ 0.027	0.927 $\pm$ 0.021	<u>0.967$\pm$0.008</u>	0.967 $\pm$ 0.004
ACCEPTOR	0.914 $\pm$ 0.028	0.975 $\pm$ 0.006	0.981$\pm$0.011	0.958 $\pm$ 0.010	0.937 $\pm$ 0.033	0.936 $\pm$ 0.077	<u>0.958$\pm$0.005</u>	0.943 $\pm$ 0.010
DONOR	0.906 $\pm$ 0.027	0.963 $\pm$ 0.006	0.985$\pm$0.022	0.949 $\pm$ 0.024	0.948 $\pm$ 0.025	0.874 $\pm$ 0.289	<u>0.973$\pm$0.002</u>	0.921 $\pm$ 0.018

Table 4: Performance comparison on the Scorpio-Gene-Taxa dataset.

	Test					Gene out				Taxa out
	Phylum	Class	Order	Family	Gene	Phylum	Class	Order	Family	Gene
MetaBERTa	0.712	0.584	0.426	0.322	0.282	0.640	0.471	0.290	0.204	0.074
HyenaDNA	0.764	0.636	0.447	0.292	0.846	0.449	0.265	0.113	0.058	0.674
Baseline w/o TM	0.860	0.765	0.589	0.417	0.845	0.547	0.401	0.222	0.145	0.608
CARMANIA	0.861	0.768	0.596	0.419	0.909	0.469	0.316	0.159	0.094	0.728

Task-Adaptive Pre-Training on the Scorpio-Gene-Taxa Dataset

We evaluated task-adaptive pre-training on the *Scorpio-Gene-Taxa* dataset [Refahi et al., 2025], which includes three evaluation splits: *Test* (seen genes and taxa), *Gene-out* (unseen gene labels), and *Taxa-out* (unseen phyla). All models were trained on the same data and evaluated using FAISS-based [Douze et al., 2024] embedding similarity to retrieve the best match from the training set.

As shown in Table 4, CARMANIA achieves the highest accuracy on both the main test set and the *Taxa-out* split, while also showing strong generalization on the *Gene-out* set. In contrast, MetaBERTa performs well on *Gene-out* but struggles on *Taxa-out*, suggesting it may rely more on taxonomic memorization than on learning a transferable mapping from gene sequence to taxonomy. This highlights a fundamental challenge in this dataset: there is often a trade-off between generalizing across gene identities and taxonomic groups. Most models struggle to do both simultaneously unless they explicitly capture the hierarchical structure linking genes to taxa [Refahi et al., 2025].

To further examine these results, we visualized the learned embeddings using t-SNE for the 10 most frequent genes (Figure 5). CARMANIA forms compact clusters that align well with both gene identity and taxonomic structure, suggesting it captures both levels of organization. HyenaDNA produces well-separated clusters based on gene identity but lacks alignment with taxonomic labels. In contrast, MetaBERTa embeddings show stronger alignment with taxonomy but weaker separation by gene, as also seen in Supplementary Figure 8.

This is further supported by additional results in Supplementary Table 5, where CARMANIA outperforms all other models on AMR gene classification tasks without fine-tuning, highlighting its strong domain adaptation capability.

Domain Adaptation and Generalization

We evaluated several pre-trained genomic models on the AMR dataset without fine-tuning. The dataset, derived from MEGARes Bonin et al. [2023] and CARD Jia et al. [2016], includes three classification tasks: Gene Family, Resistance Mechanism, and Drug Class Yoo et al. [2024]. Labels were assigned based on the closest match (best hit) in embedding space using FAISS Douze et al. [2024] on frozen representations.

As shown in Table 5, CARMANIA achieves the highest F1 Macro scores across all tasks, indicating that it produces more informative embeddings for AMR classification than prior models, including HyenaDNA Nguyen et al. [2024], Caduceus Schiff et al. [2024], MetaBERTa Refahi et al. [2025], and Nucleotide Transformers Dalla-Torre et al. [2024].

Table 5: F1 Macro scores for AMR classification on Gene Family, Resistance Mechanism, and Drug Class using FAISS-based best-hit embedding retrieval.

Model	GeneFamily	Resist-Mech	DrugClass
MetaBERTa (35.2M)	0.650	0.898	0.886
HyenaDNA (1.6M)	0.623	0.840	0.880
Caduceus-PH (1.9M)	0.597	0.823	0.839
NucleotideTrans (2.5B)	0.611	0.856	0.859
w/o TM (83M)	0.728	0.974	0.931
CARMANIA (83M)	0.733	0.975	0.942

Long Context Task: Biosynthetic Gene Cluster Classification

To evaluate the ability of genomic language models to capture functional patterns across extended DNA regions, we performed a large-scale classification task on biosynthetic gene clusters (BGCs) using the MiBiG database Kautsar et al. [2020], Liu et al. [2022], where each cluster is labeled by its

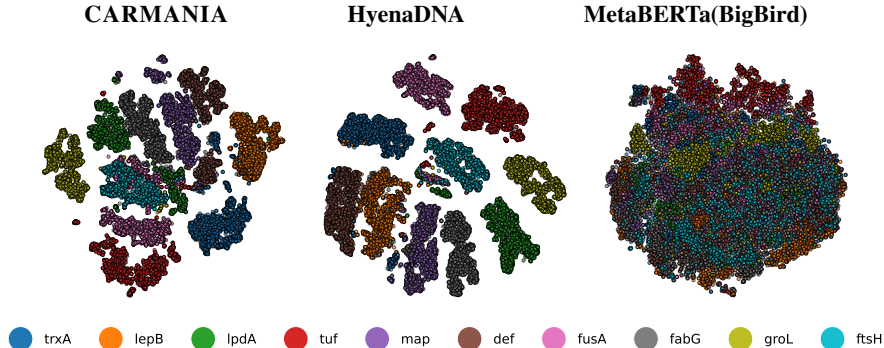


Figure 5: t-SNE visualization of the 10 most common genes in the Scorpio-Gene-Taxa dataset. CARMANIA effectively clusters genes while maintaining taxonomic coherence, leading to superior gene-to-taxonomy classification performance.

associated secondary metabolite class. This task was framed as multi-class classification using raw DNA sequences—without relying on protein translation or domain-level annotations. Since BGCs vary in length (average 377k bp), we truncated all sequences to 100k bp for model compatibility.

Unlike previous approaches that depend on external tools like Prodigal and HMMER Hannigan et al. [2019], Liu et al. [2022], our method directly operates on nucleotide sequences. We evaluated performance using 5-fold cross-validation. As shown in Table 6, CARMANIA, which incorporates TM loss, achieves the highest accuracy (48.4%), outperforming HyenaDNA by over 7% and significantly surpassing other baselines.

Table 6: 5-fold CV accuracy and standard deviation for BGC classification on 100,000 DNA sequences.

Model	Caduceus-Ph	HyenaDNA	Baseline w/o TM	CARMANIA
Accuracy $\pm$ Std	0.326 $\pm$ 0.119	0.412 $\pm$ 0.130	0.410 $\pm$ 0.240	0.484 $\pm$ 0.330

5 Conclusions

In this paper, we introduced CARMANIA, a novel pre-trained genomic model designed for long-sequence analysis and nucleotide-level processing. Unlike existing models, CARMANIA effectively captures both local and global sequence dependencies, making it highly suitable for diverse genomic tasks. Our evaluations demonstrate superior performance across multiple benchmarks, including AMR classification, gene-taxa association, regulatory element prediction, species classification, and biosynthetic gene cluster prediction.

Limitations and Future Work: While our method improves sequence representation learning, one limitation lies in the fixed scaling parameter β used to balance the next-token and TM losses. We set $\beta = 1$ and observed that the losses naturally aligned in scale, making this choice effective in practice. However, tasks involving rare but biologically important motifs may require more fine-grained or dataset-specific tuning. In cases where $H_{\text{emp}}(X) \neq H_{\text{model}}(X)$, a fixed β may lead to overfitting on common patterns while missing informative outliers. Future work could explore adaptive scaling strategies that dynamically adjust β based on the training loss distribution. Although the TM loss is computationally efficient due to its matrix-based formulation, memory usage increases with larger vocabulary sizes and batch dimensions. This can limit scalability, particularly in domains such as chemistry (e.g., SMILES representations) or natural language, where token sets are larger and sequence variability is higher. To address this, future work could explore memory-efficient approximations, sparse matrix operations, or gradient checkpointing to reduce the computational footprint. In addition, we aim to scale up both the model and the diversity of training datasets to improve generalization across a broader range of genomic and functional prediction tasks. Finally, we note that, like other predictive genomic models, this approach may raise concerns around potential misuse in synthetic biology or privacy-sensitive contexts, which should be addressed in future deployments.

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A Supplementary Material

A.1 Effect of TM Loss on Other Domains: Protein Modeling

While CARMANIA was primarily developed for genomic sequences, we further examined the generality of the proposed **TM loss** in other biological domains. In theory, TM loss should benefit any modeling task that relies on capturing long-range dependencies. To validate this hypothesis, we adapted the CARMANIA architecture for amino acid sequences and trained it on the **Scorpio-Gene-Taxa** protein dataset. Specifically, we constructed a 20×20 bigram frequency matrix representing pairwise transition statistics between standard amino acids and incorporated TM loss into the training objective.

As summarized in Table 7, incorporating TM loss consistently accelerated convergence and improved predictive accuracy across all hierarchical levels. These results confirm that TM loss generalizes beyond nucleotide modeling and effectively enhances protein-sequence representations.

Table 7: Performance comparison on the **Scorpio-Gene-Taxa** dataset using protein sequences.

Model	Test Set					Gene-Heldout				Taxa-Heldout
	Phylum	Class	Order	Family	Gene	Phylum	Class	Order	Family	Gene
Without TM Loss	91.1	84.9	70.6	51.3	99.5	19.8	10.9	3.3	1.1	98.4
With TM Loss	91.4	85.5	71.0	51.5	99.6	20.5	11.6	3.8	1.5	98.7

A.2 Effect of TM Loss on Convolution-Based Architecture: HyenaDNA

We trained HyenaDNA on the Scorpio-Gene-Taxa dataset with and without TM loss to investigate its effect on model performance. As shown in Figure 6, the model without TM loss demonstrates better convergence, with the training loss decreasing more effectively compared to the model with TM loss. Notably, the model without TM loss appears to struggle with learning the bigram frequency (transition matrix) inherent to the Markovian model. This observation suggests that convolution-based models, even in an autoregressive manner, may not capture Markovian dependencies as effectively as transformer-based models, which leverage attention mechanisms to model long-range dependencies more efficiently.

Additionally, we evaluated the models’ performance on the AMR detection tasks using the macro F1 score across all tasks. The results, Figure 7, indicate that incorporating TM loss improves performance in CARMANIA; however, the HyenaDNA model does not exhibit a similar performance gain. This suggests that convolution-based models may inherently struggle to learn embeddings and representations for tasks that rely on Markovian properties, highlighting a potential architectural limitation in such models for sequence modeling tasks.

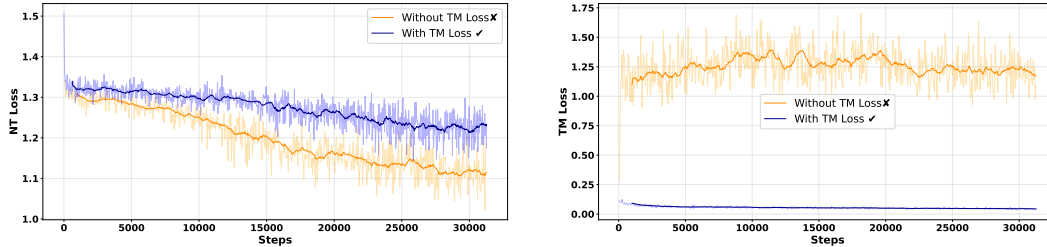


Figure 6: Left: Next-token loss; Right: TM loss for HyenaDNA. The convolution-based model struggles to learn the TM effectively, unlike the attention-based model, which better captures Markovian dependencies.

A.3 Effect of TM Loss on Mamba-Based Architecture: Caduceus

Caduceus Schiff et al. [2024] is a bi-directional, reverse-complement equivariant DNA language model built upon the MambaDNA architecture, which leverages selective state-space modeling for long-range sequence processing. While Caduceus is pretrained using a masked language modeling (MLM) objective distinct from our causal next-token prediction (NT) setup we incorporated the proposed TM loss into the MLM objective while keeping all other configurations unchanged. This modification allows us to assess whether TM loss provides additional benefits beyond the CARMANIA backbone.

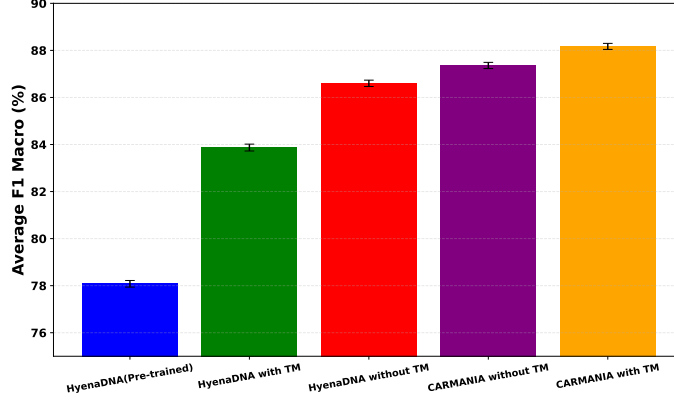


Figure 7: Effect of Transition Matrix Loss on HyenaDNA and CARMANIA : Pre-trained on Scorpio-gene-taxa

For this experiment, we used the largest available pretrained variant of Caduceus (approximately 7.7M parameters) and fine-tuned it on the **Scorpio Gene–Taxa** dataset with and without TM loss. Incorporating TM loss led to a notable performance boost, particularly on the gene classification task, yielding a +12% gain on the test set and +6% on the held-out set. These results suggest that TM loss provides a meaningful signal even in state-space models like Caduceus, although its impact remains more pronounced in transformer-based architectures such as CARMANIA.

Table 8: Effect of TM Loss on Caduceus Fine-Tuned on the Scorpio-Gene–Taxa Dataset. Performance (accuracy, %) across hierarchical taxonomic levels. Δ denotes the relative improvement when adding TM loss.

Model	Test Set					Gene-Heldout				Taxa-Heldout
	Phylum	Class	Order	Family	Gene	Phylum	Class	Order	Family	Gene
Δ (TM w/o TM)	+6.2	+7.0	+5.8	+4.0	+12.4	+0.3	+0.1	0.1	0.0	+6.6
Caduceus w/o TM	40.0	24.9	13.4	7.7	26.2	30.3	13.6	4.1	1.5	15.9
Caduceus + TM	46.2	31.9	19.2	11.7	38.6	30.6	13.7	4.0	1.5	22.5
CARMANIA	86.1	76.8	59.6	41.9	90.9	46.9	31.6	15.9	9.4	72.8

A.4 Sensitivity Analysis: Effect of β

The sensitivity analysis evaluates the impact of the hyperparameter β on model performance. As shown in Table 9, increasing β from 0 to 1.0 improves the macro F1 score (87.36% to 88.17%) and BLEU (0.73 to 0.77), suggesting that the TM loss helps capture Markovian dependencies. However, when β is increased to 5.0, performance significantly degrades, indicating that excessive TM loss disrupts the next-token objective. The best performance is achieved with $\beta = 1.0$, demonstrating a balanced contribution from both objectives.

Table 9: Comparison of β values with F1 Macro, BLEU, and Perplexity scores.

β	Average F1 Macro	BLEU	Perplexity
0	0.873	0.73	3.6
0.5	0.874	0.76	3.6
1.0	0.882	0.77	3.6
5.0	0.836	0.85	3.8

A.5 Higher-Order Transition Matrix

We explored the impact of incorporating TM loss at different Markov orders in CARMANIA, with results shown in Tables 10 and 11. Surprisingly, while the first-order TM consistently improves downstream classification performance across tasks, the second-order TM performs worse than both the first-order TM and the baseline without TM.

This performance degradation in the second-order setting can be attributed to the increased sparsity of higher-order transition patterns, particularly in biological sequence data. Since second-order

transitions require co-occurrence of triplets, many such patterns are infrequent or entirely missing from the training set, leading to unstable or noisy estimations. This sparsity reduces the model’s ability to generalize and can hinder the convergence of the transition-based objective Wu and Gleich [2017]. On the other hand, first-order transitions strike a balance by enforcing local smoothness and capturing robust pairwise dependencies that are both statistically reliable and biologically meaningful. This results in more stable training and improved generalization across domains.

Table 10: Comparison of F1 Macro scores across three AMR classification tasks with different TM orders. First-order TM improves performance across all tasks, while second-order TM leads to degradation.

Model Variant	GeneFamily	Resist-Mech	DrugClass
Without TM	0.728	0.974	0.931
1st-Order TM	0.733	0.975	0.942
2nd-Order TM	0.701	0.943	0.915

Table 11: Accuracy comparison on the Scorpio-Gene-Taxa test set across different taxonomic levels. First-order TM leads to consistent improvements, especially at the gene level. Second-order TM degrades performance across all levels.

Model Variant	Phylum	Class	Order	Family	Gene
Without TM	0.860	0.765	0.589	0.417	0.845
1st-Order TM	0.861	0.768	0.596	0.419	0.909
2nd-Order TM	0.810	0.703	0.520	0.371	0.690

A.6 Wide vs. Deep: Architectural Trade-offs for DNA Modeling

As shown in Table 12, our wide architecture reduces the number of layers while significantly increasing the hidden and intermediate sizes. This results in a network that is both more expressive and more efficient.

Most notably, the wide model achieves a substantially higher accuracy on the Scorpio-Gene-Taxa classification task ($71.05\% \pm 18.07$ vs. $63.87\% \pm 19.16$), demonstrating its superior ability to capture biologically meaningful patterns from genomic sequences. Furthermore, the wide model also outperforms the deep model on the AMR prediction task—an out-of-domain setting—with a higher macro F1 score ($88.32\% \pm 13.12$ vs. $85.22\% \pm 14.66$). These consistent gains across both in-domain and out-of-domain datasets highlight the robustness and generalization ability of the wide configuration.

The observed improvements can be attributed to three key factors:

First, wider layers with large hidden and MLP dimensions better capture motif-level and co-occurrence patterns, which are prevalent in DNA sequences. This capacity is especially critical for tasks such as gene classification and function prediction, where local patterns carry more signal than hierarchical abstractions.

Second, the reduced depth allows for better GPU utilization and faster convergence. With fewer sequential operations, the wide model completes training in nearly half the time while requiring fewer steps to achieve peak performance.

Third, by concentrating representational power within each layer, the wide network is better equipped to model long-range dependencies and subtle biological variations without needing deep hierarchical stacks. Given these advantages, we adopt the wide model as the backbone for the rest of our study. Its performance and efficiency make it a strong choice for DNA modeling tasks, especially when scaling to large or diverse datasets.

A.7 Model Size Scalability

We evaluate the effect of model scaling on performance and compute cost using the Basic Genome dataset. Table 14 compares a small 4M-parameter model trained on a 0.5B-token subset with the full 83M-parameter model trained on 10B tokens. Results show substantial gains in both F1 and BLEU scores, demonstrating that increased model capacity and training data size improve representation quality without disproportionately increasing relative FLOPs.

Table 12: Comparison of model configurations between deep and wide architectures. The wide model uses fewer layers but larger hidden and intermediate sizes.

Configuration	Deep Model (80M)	Wide Model (83M)
Number of Layers	24	5
Hidden Size	512	1024
Intermediate (MLP) Size	1664	4608
Attention Heads	8	16
Key/Value Heads	4	4
Attention Window	128	128
Activation Function	SiLU	SiLU
Training Steps	109,500	31,000
Epoch Time	6.1 hours	3.2 hours
Task	Performance Comparison	
Scorpio-Gene-Taxa Test (Accuracy%)	63.87 $\pm$ 19.16	71.05 $\pm$ 18.07
AMR (F1 Macro%)	85.22 $\pm$ 14.66	88.32 $\pm$ 13.12

Table 13: Parameter Ranges for Model Training

Parameter	Range / Value
Optimizer	AdamW
Batch Size	1, 19, 35
Num Epochs	2
Learning Rate	5e-4
Weight Decay	0.2
Adam Epsilon	1e-6
Adam Betas	(0.9, 0.999)
Warmup Steps	400
LR Scheduler Type	Cosine
Max Grad Norm	0.85, 2

A.8 Impact of Sequence Length Scaling

To evaluate the effect of input sequence length on model performance, we conducted an ablation study using the GRCh38 dataset, comparing models trained on 10 kbp and 160 kbp fragments. As shown in Table 15, increasing sequence length improves both macro F1 and BLEU score, while maintaining the same computational footprint (FLOPs). This suggests that access to longer genomic contexts enables the model to capture more distant dependencies, leading to more robust and informative sequence representations.

A.9 Comparison with Other Convolution-Based Models (ConvNova)

To contextualize CARMANIA’s performance with recent convolution-based models, we compared it against ConvNova Bo et al. [2025], a recently proposed architecture for long DNA modeling. Following their evaluation protocol, we used five random seeds on the same test benchmarks to ensure consistency. As shown in Table 16, CARMANIA achieves comparable or superior results on several tasks, demonstrating that its attention-based and Markovian design effectively captures long-range dependencies.

A.10 Pre-training Dataset

The pre-training phase utilizes large-scale genomic sequences to establish robust sequence embeddings, ensuring scalability, diversity, and compatibility with existing models trained on domain-specific datasets. We incorporate multiple datasets to support comprehensive learning and facilitate direct performance comparisons.

The Human Reference Genome (GRCh38 - hg38): This dataset comprises approximately 3 billion base pairs GRCh38 [2013]. From this genome, we extracted two non-overlapping sets of sequences to ensure coverage across diverse genomic regions. One set consists of long-range sequences with 160 kbp fragments, while the other contains shorter sequences of 10 kbp fragments.

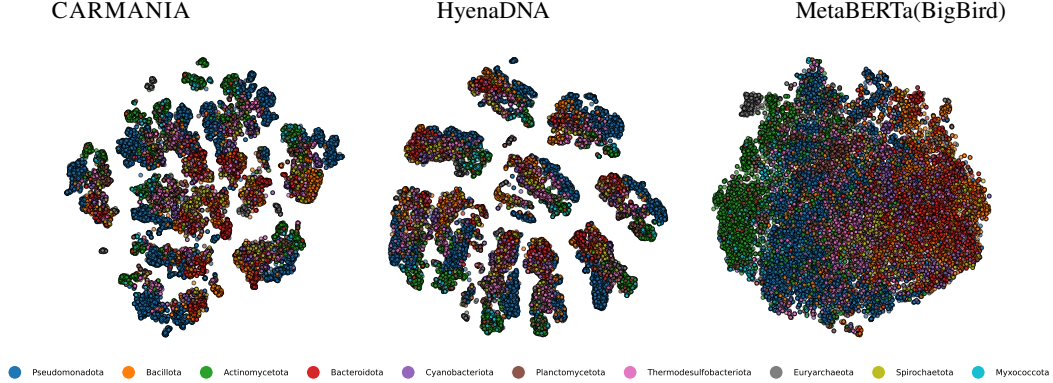


Figure 8: t-SNE visualization of the 10 most common phyla in the Scorpio-Gene-Taxa dataset. CARMANIA effectively captures the structure of inter-cluster taxonomy. As shown in Figure 5, the genes exhibit a clear global structure, with phylogenetic groups positioned near each other when colored based on phyla. This demonstrates that our model outperforms even MetaBERTa(BigBird) in preserving the taxonomy signal.

Table 14: Impact of model size on performance and compute cost.

Model Size / Dataset	F1 Macro(AMR) ($\uparrow$)	BLEU (Human dataset) ($\uparrow$)	Relative FLOPs ($\downarrow$)
4M params / 0.5B tokens	0.809 ± 0.114	0.41	0.07
83M params / 10B tokens	0.860 ± 0.130	0.82	1.00

The Basic Genome Dataset: Introduced by Zhu et al. [2022], this dataset includes 10 billion base pairs from 4,634 bacterial, archaeal, viral, and eukaryotic genomes. Sequences were extracted as 10 kbp fragments from each genome, ensuring representation across various species and evolutionary lineages.

The Scorpio Gene-Taxa Dataset: Developed by Refahi et al. [2025], this dataset spans 580 million base pairs from 2,046 bacterial and archaeal species, encompassing 497 distinct gene types. To maintain consistency, fragments of 4 kbp were extracted, with shorter sequences padded as needed. Table 17 summarizes the key statistics of pre-training datasets.

A.11 Downstream Datasets

We used five distinct datasets for fine-tuning and evaluation, covering a range of genomic classification tasks and label spaces. These include regulatory element prediction, gene function classification, taxonomic inference, antimicrobial resistance (AMR) detection, and biosynthetic gene cluster (BGC) prediction. Table 18 provides detailed statistics for each dataset.

AMR: The Antimicrobial Resistance classification dataset used in our evaluation is based on the benchmark introduced by Yoo et al. [2024]. It integrates sequences from two major sources: **MEGARes** Bonin et al. [2023], a manually curated database of antimicrobial resistance genes annotated by gene family and resistance mechanism; and **CARD** Jia et al. [2016], which provides detailed molecular annotations of AMR genes, mechanisms, and associated drugs.

BGC Dataset. To evaluate functional classification over extended DNA regions, we used the biosynthetic gene cluster (BGC) classification dataset derived from the MiBiG database Kautsar et al. [2020], Liu et al. [2022], where each cluster is labeled with a secondary metabolite class. Since BGCs vary in length (average 377k bp), we truncated all sequences to 100k bp for model compatibility.

Nucleotide Transformer Tasks. We evaluated our model on 18 genomic classification tasks introduced by Dalla-Torre et al. [2024], covering histone mark prediction, regulatory element annotation, and splice site detection. These tasks span a wide range of sequence-based regulatory functions, offering a comprehensive benchmark for assessing model generalization.

Table 15: Effect of sequence length on performance. Longer input improves both F1 and BLEU without increasing FLOPs.

Training Setup	F1 Macro ($\uparrow$)	BLEU ($\uparrow$)	Relative FLOPs ($\downarrow$)
Trained on 10k Sequences	0.765 ± 0.120	0.82	1.00
Trained on 160k Sequences	0.800 ± 0.138	0.84	1.00

Table 16: Genomics Benchmark Results. Top-1 accuracy ($\uparrow$) is reported for pretrained HyenaDNA, Caduceus-Ph, ConvNova, and CARMANIA, alongside the CNN baseline. The best result is in bold, and the second-best is underlined.

Task	CNN	HyenaDNA	Caduceus-Ph	ConvNova	CARMANIA
<i>Enhancers</i>					
Mouse Enhancers	0.730 ± 0.032	0.779 ± 0.013	0.754 ± 0.074	0.784 ± 0.009	0.795 ± 0.002
Human Enhancers (Cohn)	0.702 ± 0.021	0.718 ± 0.008	0.747 ± 0.004	<u>0.743 ± 0.005</u>	0.725 ± 0.002
Human Enhancers (Ensembl)	0.744 ± 0.122	0.832 ± 0.006	0.893 ± 0.008	0.900 ± 0.004	<u>0.895 ± 0.002</u>
<i>Species Classification</i>					
Coding vs. Intergenic	0.892 ± 0.008	0.904 ± 0.008	0.915 ± 0.003	0.943 ± 0.001	<u>0.930 ± 0.001</u>
Human vs. Worm	<u>0.942 ± 0.002</u>	0.961 ± 0.002	0.973 ± 0.001	0.967 ± 0.002	<u>0.970 ± 0.005</u>
<i>Regulatory Elements</i>					
Human Regulatory	0.872 ± 0.005	0.862 ± 0.004	0.872 ± 0.011	<u>0.873 ± 0.002</u>	0.894 ± 0.002
Human Non-TATA Promoters	0.861 ± 0.009	0.887 ± 0.005	0.946 ± 0.007	<u>0.951 ± 0.003</u>	0.965 ± 0.002
Human OCR (Ensembl)	0.698 ± 0.013	0.744 ± 0.019	0.828 ± 0.006	<u>0.793 ± 0.004</u>	0.778 ± 0.002

Genomics Benchmark Tasks. We evaluated supervised adaptation on the Genomic Benchmarks collection Grešová et al. [2023], which includes a range of classification tasks such as regulatory element prediction, enhancer detection, and binary species classification.

The Scorpio Gene-Taxa Dataset: Developed by Refahi et al. [2025], this dataset spans 580 million base pairs from 2,046 bacterial and archaeal species, encompassing 497 distinct gene types. To maintain consistency, fragments of 4 kbp were extracted, with shorter sequences padded as needed. The dataset features *Test*, *Gene Out*, and *Taxa Out* splits, carefully designed to assess both memorization and generalization—by holding out specific genes or entire taxonomic groups (e.g., phyla) while preserving hierarchical relevance. This enables robust evaluation of gene-level and taxonomy-level generalization.

B Confirming the Transition Matrix Implementation

The first-order transition probabilities for the next token given the current token are defined as:

$$P(w_{i+1} | w_i) = [P(A | w_i), P(T | w_i), P(C | w_i), P(G | w_i)]$$

Similarly, for the token after next:

$$P(w_{i+2} | w_{i+1}) = [P(A | w_{i+1}), P(T | w_{i+1}), P(C | w_{i+1}), P(G | w_{i+1})]$$

In our implementation, the bigram transition matrix for position i is computed as:

$$\mathbf{T}_i = P(w_{i+1} | w_i) \times P(w_{i+2} | w_{i+1})^T$$

Expanding this matrix explicitly:

$$\mathbf{T}_i = \begin{bmatrix} P(A | w_i)P(A | w_{i+1}) & P(A | w_i)P(T | w_{i+1}) & P(A | w_i)P(C | w_{i+1}) & P(A | w_i)P(G | w_{i+1}) \\ P(T | w_i)P(A | w_{i+1}) & P(T | w_i)P(T | w_{i+1}) & P(T | w_i)P(C | w_{i+1}) & P(T | w_i)P(G | w_{i+1}) \\ P(C | w_i)P(A | w_{i+1}) & P(C | w_i)P(T | w_{i+1}) & P(C | w_i)P(C | w_{i+1}) & P(C | w_i)P(G | w_{i+1}) \\ P(G | w_i)P(A | w_{i+1}) & P(G | w_i)P(T | w_{i+1}) & P(G | w_i)P(C | w_{i+1}) & P(G | w_i)P(G | w_{i+1}) \end{bmatrix}$$

Summing over the entire sequence of length N , we obtain the predicted (but not yet normalized) bigram matrix:

Table 17: Statistics of the Pre-training datasets.

Dataset	Number of Samples	Number of Tokens	Length range (bp)
Human Genome-long GRCh38 [2013]	19,029	3B	160k
Human Genome-short GRCh38 [2013]	303,921	3B	10k
Basic Genome Zhu et al. [2022]	1,010,237	10B	10k
Scorpio-Gene-Taxa Refahi et al. [2025]	547,523	580M	114–13,227 (4k for training)

Table 18: Statistics of the fine-tuning datasets.

Dataset	Number of Tasks	Classes	Length Range (bp)
Genomics Benchmark Grešová et al. [2023]	8	Binary (one multi-class)	70–4,776
Scorpio-Gene-Taxa Refahi et al. [2025]	10	Multi-class (497–1,929)	114–13,227
Antimicrobial Resistance Prediction Yoo et al. [2024]	3	Multi-class	211–5,274
Nucleotide Transformer Tasks Dalla-Torre et al. [2024]	18	Binary (one multi-class)	200–500
Biosynthetic Gene Cluster Prediction Kautsar et al. [2020]	1	8	204–8M (avg 377k; Truncated to 100k)

$$\mathbf{T}_{Pred} = \sum_{i=1}^N \mathbf{T}_i$$

To confirm equivalence with the bigram frequency matrix, consider the specific cell ($T \rightarrow A$):

$$\mathbf{T}_{Pred}(T \rightarrow A) = \sum_{i=1}^N P(T \mid w_i) P(A \mid w_{i+1})$$

If we replace probabilities with actual sequence counts, where $P(w_i = T) = 1$ if $w_i = T$ and 0 otherwise, and normalize each row to represent the transition probabilities, we get:

$$\mathbf{T}_{Pred}(T \rightarrow A) = \frac{\sum_{i=1}^N \mathbb{I}(w_i = T) \cdot \mathbb{I}(w_{i+1} = A)}{\sum_{x \in \{A, T, C, G\}} \sum_{i=1}^N \mathbb{I}(w_i = T) \cdot \mathbb{I}(w_{i+1} = x)}$$

This aligns with the actual bigram frequency:

$$P_{actual}(T \rightarrow A) = \frac{\text{count}(T \rightarrow A)}{\sum_{x \in \{A, T, C, G\}} \text{count}(T \rightarrow x)}$$

Both matrices are row-normalized, ensuring the sum of each row is 1:

$$\sum_{x \in \{A, T, C, G\}} \mathbf{T}_{Pred}(T \rightarrow x) = \sum_{x \in \{A, T, C, G\}} P_{actual}(T \rightarrow x) = 1$$

Thus, when probabilities are replaced with actual sequence values, the predicted transition matrix $\mathbf{T}_{Pred}$ is equivalent to the actual bigram frequency matrix P_{actual} , confirming that our method is inherently inspired by bigram frequency calculations while extending them with learnable model probabilities.

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Question: For crowdsourcing experiments and research with human subjects, does the paper include the full text of instructions given to participants and screenshots, if applicable, as well as details about compensation (if any)?

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