HARMONY: A MULTI-REPRESENTATION FRAMEWORK FOR RNA PROPERTY PREDICTION

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1 INTRODUCTION

RNA is a structurally and functionally versatile biomolecule, playing essential role in gene regulation, catalysis, and cellular processes (Sharp, 2009). Its properties emerge from the interplay of linear nucleotide sequences (1D), base-pair interactions forming secondary structures (2D), and intricate three-dimensional conformations (3D). Each of these representations captures different aspects of RNA function, and comprehensive modeling of RNA molecules requires combining the strengths of all three.

Existing ML approaches for RNA property prediction mainly use sequence-based representations (Chen et al., 2022; Yang et al., 2023; Penić et al., 2024; Wang et al., 2022; Yazdani-Jahromi et al., 2025; Prakash et al., 2024), while recent work shows that incorporating 2D or 3D structural information can enhance performance in certain scenarios (Xu et al., 2024; 2025). Though 2D and 3D models excel with high-quality structures—especially in low-data or partially labeled settings—3D methods are more sensitive to sequencing errors, whereas sequence-based models are more robust (Xu et al., 2024; 2025). Since data quality is often unknown in practice, adaptive models that dynamically integrate different RNA representations are needed.

To address this limitation, we introduce HARMONY, a framework that dynamically integrates 1D, 2D, and 3D RNA representations to handle varied real-world conditions. Instead of relying on a single representation, HARMONY leverages RNA's natural organization to systematically combine atomic, nucleotide, and molecular-scale information. We conduct experiments on multiple RNA datasets and demonstrate that HARMONY consistently achieves strong performance across diverse RNA property prediction tasks, including those with sequencing noise, limited training data, and out-of-distribution conditions. By eliminating the need for manual selection of the optimal RNA representation, HARMONY offers a robust and generalizable approach to RNA modeling.

2 METHODOLOGY: HARMONY

We introduce HARMONY, a multi-representational model that integrates 1D, 2D and 3D RNA representations. A figure is shown in Appendix A (Figure 2).

Each RNA is represented as: $\mathcal{G} = \{\mathcal{G}_{3D}, \mathcal{G}_{2D}, \mathcal{G}_{1D}\}$, where $\mathcal{G}_{3D} = \{X_{at}, R\}$ represents RNA 3D structure with atom features $X_{at} \in \mathbb{R}^{N_{at} \times F_{at}}$ and atom positions $R \in \mathbb{R}^{N_{at} \times 3}$ with N_{at} being the number of atoms. RNA 2D structure $\mathcal{G}_{2D} = \{X_{nt}, A\}$ consists of nucleotide features $X_{nt} \in \mathbb{R}^{N_{nt} \times F_{nt}}$ and an adjacency matrix $A \in \mathbb{R}^{N_{nt} \times N_{nt}}$. The 1D RNA sequence $\mathcal{G}_{1D} = \{X_{seq}\}$ encodes RNA's nucleotide sequence.

First, we apply a 3D encoder f_{3D} to extract atomic-level representations: $H_{3D} = f_{3D}(X_{at}, R)$. A nucleotide pooling layer maps atom-wise features to nucleotide-level representations mean pooling representations of atoms corresponding to each nucleotide: $H'_{3D} = \text{Nuc.Pooling}(H_{3D})$.

We concatenate the pooled 3D features H'_{3D} with nucleotide features X_{nt} and apply a 2D encoder f_{2D}: $H_{2D} = f_{2D}([X_{nt}, H'_{3D}], A)$. Since sequence tokens X_{seq} align with nucleotide positions, we concatenate them with H_{2D} and apply a 1D encoder f_{1D}: $H_{1D} = f_{1D}([X_{seq}, H_{2D}])$.

Finally, the representations from all dimensions are combined using a differentiable function σ, in our case an MLP: $H = \sigma([H_{3D}, H_{2D}, H_{1D}])$.

*This work was done while the author was an intern at Johnson & Johnson.

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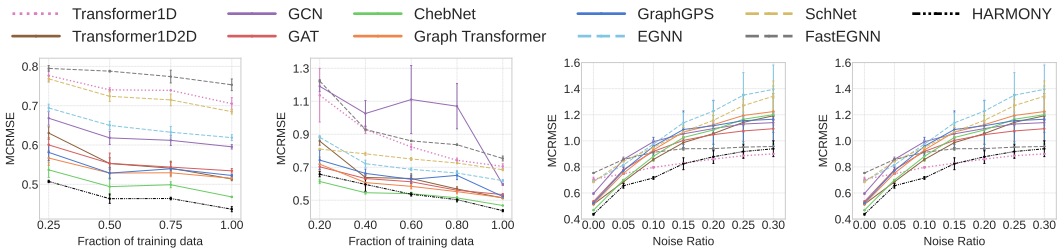

(a) Partial training data (b) Partial property (c) Robustness (d) Generalization

Figure 1: **Experiment results of 5 tasks on Ribonanza dataset.** Dotted, solid, and dashed lines denote 1D, 2D, and 3D methods, respectively.

We use EGNN (Satorras et al., 2021) for f_{3D}, the spectral 2D GNN ChebNet (Defferrard et al., 2016) for f_{2D}, and Transformer (Vaswani et al., 2017) for f_{1D}. This selection is based on prior findings (Xu et al., 2024; 2025), which identified these models as the strongest 3D, 2D, and 1D baselines for RNA property prediction, respectively.

3 Experiments

We followed the RNA property prediction tasks in prior work (Xu et al., 2024; 2025). These tasks reflect real-world challenges in computational RNA modeling and assess how different representations impact performance: **Task 1** Effect of Structural Information, **Task 2** Limited Training Data, **Task 3** Partial Sequence Labeling, **Task 4** Robustness to Sequencing Noise, and **Task 5** Generalization to Out-of-Distribution Data, which evaluate how different representations impact model performance. Details are provided in Appendix B.1.

We use the COVID, Ribonanza-2k, and Tc-Ribo datasets from (Xu et al., 2024; 2025), where each task involves regressing a RNA property of interest. Experiments follow the same baselines, hyperparameters, and evaluation protocol, using five random (70:15:15) train-val-test splits. Performance is reported as mean column-wise root mean squared error (MCRMSE) (Wayment-Steele et al., 2022; Xu et al., 2024; 2025) with standard deviation.

Table 1: **Comparison of 1D, 2D, and 3D models across datasets (MCRMSE ± std.).** The best results are bold. HARMONY consistently achieves state-of-the-art performance.

	Model	COVID	Ribonanza	Tc-Ribo
1D	Transformer1D	0.361±0.017	0.705±0.015	0.705±0.079
	RNA-FM	0.591±0.081	0.990±0.144	0.693±0.001
	SpliceBERT	0.588±0.077	1.022±0.144	0.708±0.003
2D	Transformer1D2D	0.305±0.012	0.514±0.004	0.633±0.001
	GCN	0.359±0.009	0.595±0.006	0.701±0.004
	GAT	0.315±0.006	0.534±0.006	0.685±0.024
	ChebNet	0.279±0.007	0.468±0.002	0.621±0.022
	Graph Transformer	0.318±0.008	0.515±0.001	0.710±0.041
	GraphGPS	0.332±0.013	0.523±0.003	0.715±0.012
3D	EGNN	0.480±0.025	0.808±0.023	0.725±0.002
	SchNet	0.499±0.003	0.843±0.004	0.696±0.008
	FAENet	0.486±0.010	0.834±0.003	0.703±0.011
	DimeNet	0.497±0.012	0.855±0.006	0.712±0.004
	GVP	0.467±0.010	0.797±0.012	0.744±0.004
	FastEGNN	0.477±0.005	0.816±0.014	0.753±0.001
Multi-dim	**HARMONY**	**0.271±0.003**	**0.437±0.006**	**0.554±0.004**

Table 1 presents the results for Task 1, which evaluates the impact of structural information on prediction performance. HARMONY outperforms all baselines relying on single-modality inputs, demonstrating that integrating 1D, 2D, and 3D representations leads to superior predictive performance.

Figure 1 summarizes results for Tasks 2–5 on the Ribonanza-2k dataset, with additional datasets provided in Appendix Section B. In Task 2 (model efficiency under limited training data), HARMONY consistently outperforms all baselines, indicating its strong sample efficiency in data-scarce scenarios. In Task 3 (performance with partial sequence labeling), where models must generalize beyond available labels, HARMONY achieves results comparable to the best single-modality ChebNet model, suggesting its ability to leverage incomplete annotations effectively.

For Task 4, where models are evaluated under stable noise conditions, HARMONY achieves the best overall performance, confirming its resilience to sequencing errors. In Task 5, which assesses adaptability to unseen noise variations, Transformer1D slightly outperforms HARMONY at high noise levels on Ribonanza, but HARMONY remains superior to all other baselines. Complete experimental results for other datasets are available in Appendix B. An ablation study (Appendix B.3) systematically evaluates the contribution of 1D, 2D, and 3D representations, demonstrating that removing any individual component leads to a performance drop, underscoring the importance of integrating all three modalities.

MEANINGFULNESS STATEMENT

A meaningful representation of life should capture the intricate relationships between structure and function at multiple biological scales. In RNA research, this requires integrating sequence, secondary structure, and 3D conformation to reflect its true biological complexity. HARMONY advances this direction by dynamically combining 1D, 2D, and 3D RNA representations, enabling robust and generalizable property prediction without prior assumptions about data quality. By bridging multiple levels of biological information, our approach provides a more holistic and adaptive framework for RNA modeling, facilitating deeper insights into RNA function and its role in cellular processes.

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A Framework Figure

The framework of the proposed HARMONY combines 1D, 2D, and 3D RNA representations in one model 2.

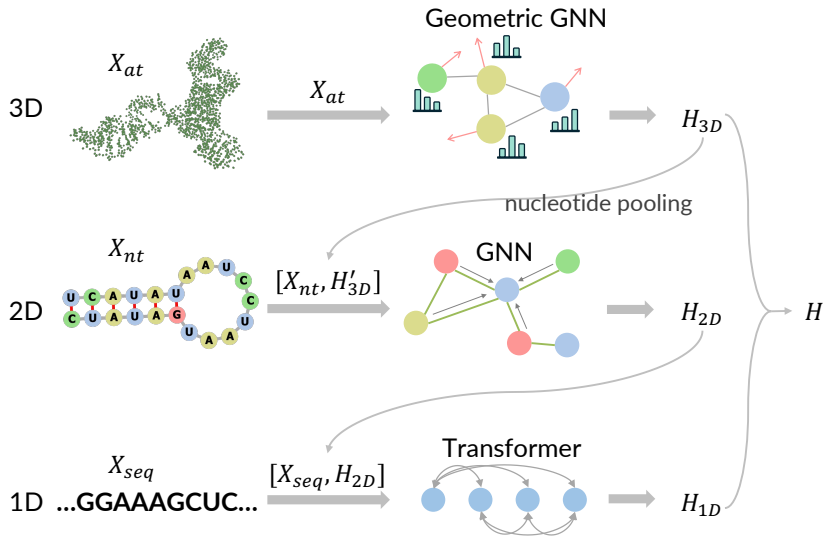


Figure 2: The HARMONY framework.

B More Experiments

B.1 Task Description

We first provide a brief overview of RNA property prediction tasks introduced in prior work (Xu et al., 2024; 2025). These tasks reflect real-world challenges in computational RNA modeling and assess how different representations impact performance:

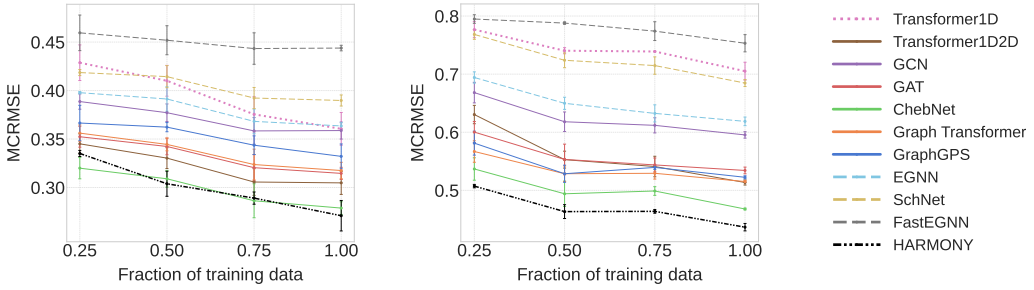
1. **Task 1 (Effect of Structural Information)** examines the impact of incorporating structural information (1D, 2D, and 3D) on predictive performance.
2. **Task 2 (Limited Training Data)** Since acquiring large labeled RNA datasets is challenging, we analyze model performance in data-scarce settings by progressively reducing training samples.
3. **Task 3 (Partial Sequence Labeling)** Real-world datasets often contain labels for only part of the sequence. We test model generalization when only partial annotations are available.
4. **Task 4 (Robustness to Sequencing Noise)** assesses robustness to sequencing noise by introducing controlled mutations during training and testing, simulating realistic sequencing error rates while keeping property labels clean.
5. **Task 5 (Generalization to Out-of-Distribution (OOD) Data)** evaluates generalization to out-of-distribution data by training models on clean, high-quality sequences and testing them on noisy data, reflecting deployment in different sequencing conditions or batch effects.

By considering these established tasks, we systematically analyze HARMONY's ability to dynamically integrate 1D, 2D, and 3D representations without requiring prior knowledge of task scenarios.

B.2 Results on other datasets

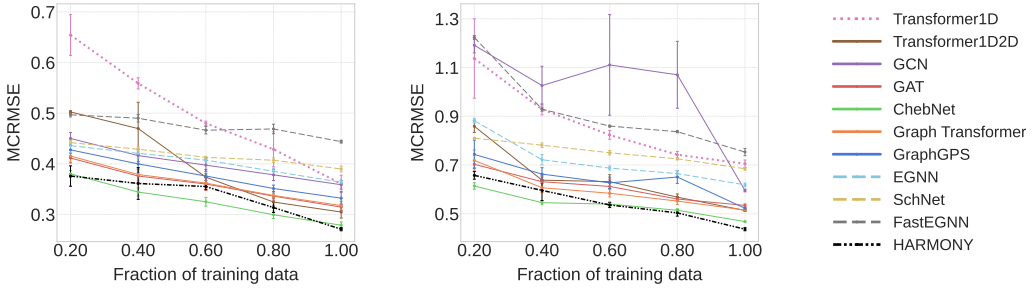
In this section, we provide the complete experiment results of Tasks 2 - 5 on each dataset. The results of Task 2 and Task 3 are presented in Fig.3 and Fig.4, respectively. In the limited data experiment (Task 2), HARMONY consistently outperforms all baselines, while in the partial sequence labeling task (Task 3), it achieves performance comparable to the best ChebNet model. The Tc-Ribo dataset

is excluded from Task 2 since varying the training ratio from 0.25 to 1 requires a larger dataset. Task 3 is conducted only on nucleotide-level prediction datasets (COVID and Ribonanza), where the labeled nucleotide ratio per sequence is varied from 0.2 to 1.



(a) COVID (b) Ribonanza

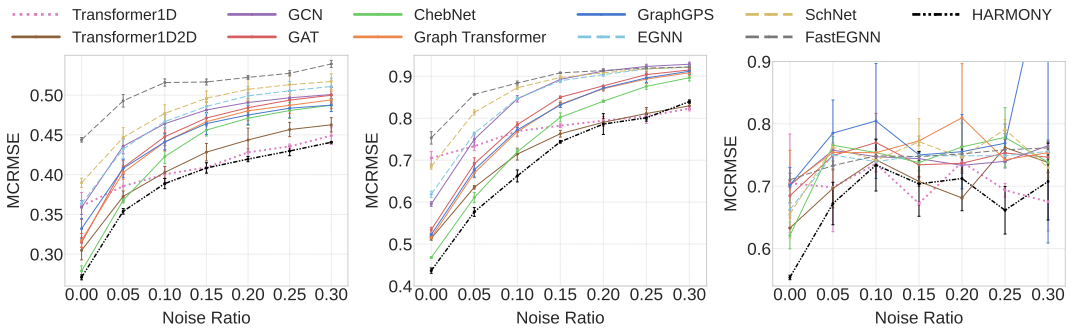
Figure 3: Performance vs. fraction of training data across various datasets.



(a) COVID (b) Ribonanza

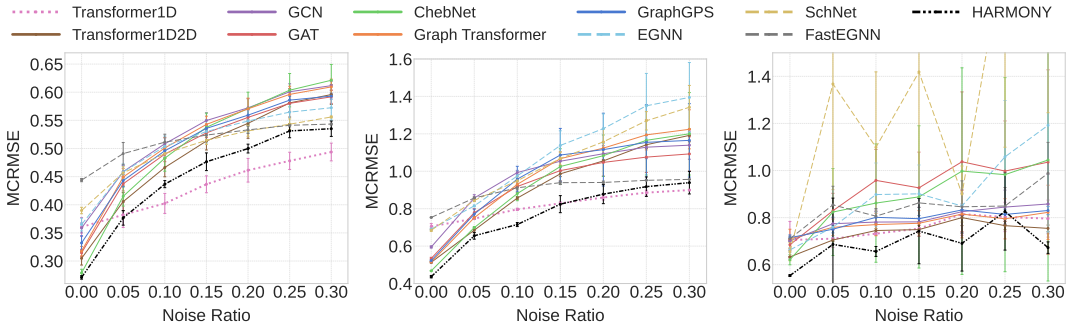
Figure 4: Performance vs. partial property labels on COVID and Ribonanza datasets.

The results of Task 4 (Robustness to Noise) and Task 5 (Generalization to Noisy Data) are presented in Fig.5 and Fig.6, respectively. In the robustness experiments, HARMONY achieves the best overall performance. For generalization, while Transformer1D slightly outperforms HARMONY at high noise levels on the COVID and Ribonanza datasets, HARMONY remains superior to all other baselines. HARMONY remains the top-performing model on Tc-Riboswithces dataset.



(a) COVID (b) Ribonanza (d) Tc-Riboswitches

Figure 5: Robustness experiments that train and test on noisy datasets.



(a) COVID (b) Ribonanza (d) Tc-Riboswitches

Figure 6: Generalization experiments train on clean datasets while test on noisy datasets.

B.3 Ablation Study

To assess the contribution of each dimension to the final performance, we conduct an ablation study by systematically removing 1D, 2D, and 3D information. The results, presented in Table 2, demonstrate that the full HARMONY model, which integrates all three types of information, achieves the best performance. Removing any individual component results in a noticeable performance drop, highlighting the importance of incorporating sequence, secondary structure, and tertiary structure features for RNA property prediction.

Table 2: Ablation study on the impact of 1D, 2D, and 3D information. The full HARMONY model performs the best, while removing any dimension degrades the performance.

	COVID	**Ribonanza**	**Tc-Ribo**
HARMONY	0.271±0.003	0.437±0.006	0.554±0.004
HARMONY w/o 1D	0.298±0.003	0.502±0.003	0.597±0.045
HARMONY w/o 2D	0.352±0.005	0.750±0.009	0.674±0.022
HARMONY w/o 3D	0.271±0.009	0.459±0.005	0.600±0.046

B.4 Training Details

All experimental protocols including dataset preprocessing, baselines and hyperparameter tuning are taken from Xu et al. (2024; 2025). All experiments were conducted on a single NVIDIA A100 GPU. For each baseline, hyperparameters were optimized using Optuna (Akiba et al., 2019), restricting the search to models with fewer than 10 million parameters that fit within the memory constraints of an 80GB NVIDIA A100 GPU. Most baseline implementations were sourced from PyTorch Geometric (Fey & Lenssen, 2019). The Transformer1D model was adapted to Transformer1D2D as detailed in the paper. For EGNN, we utilized the authors' implementation (Satorras et al., 2021), and for SchNet, the implementation from (Joshi et al., 2023) was used.

C Detailed Results

In this section, we present the additional results supporting Figures 3, 4, 5, and 6.

C.1 Impact of Data Availability

The detailed results of partial training data from Figure 3 are shown in Tables 3 and 4.

C.2 Impact of Partial Labeling

The detailed results of the partial labeling sequence from Figure 4 are shown in Tables 5 and 6.

C.3 Robustness to Sequencing Noise

The results of the robustness experiment from Figure 5 are shown in Tables 7, 8, and 9.

Table 3: Performance (MCRMSE) of different models across various training data (mean ± standard deviation) fractions on COVID dataset.

COVID	**0.25**	**0.50**	**0.75**	**1.00**
Transformer1D	0.429 ± 0.018	0.410 ± 0.016	0.375 ± 0.018	0.361 ± 0.017
Transformer1D2D	0.345 ± 0.010	0.330 ± 0.011	0.306 ± 0.014	0.305 ± 0.012
GCN	0.389 ± 0.008	0.377 ± 0.009	0.358 ± 0.014	0.359 ± 0.009
GAT	0.352 ± 0.011	0.342 ± 0.009	0.320 ± 0.014	0.315 ± 0.006
ChebNet	0.320 ± 0.011	0.309 ± 0.009	0.286 ± 0.018	0.279 ± 0.007
Graph Transformer	0.356 ± 0.008	0.344 ± 0.007	0.324 ± 0.016	0.318 ± 0.008
GraphGPS	0.367 ± 0.018	0.362 ± 0.005	0.344 ± 0.010	0.332 ± 0.013
EGNN	0.398 ± 0.001	0.391 ± 0.013	0.368 ± 0.013	0.364 ± 0.003
SchNet	0.419 ± 0.003	0.414 ± 0.011	0.392 ± 0.011	0.390 ± 0.006
FastEGNN	0.460 ± 0.018	0.452 ± 0.015	0.443 ± 0.016	0.444 ± 0.003
MultiDimGNN	0.335 ± 0.003	0.304 ± 0.013	0.289 ± 0.006	0.271 ± 0.016

Table 4: Performance (MCRMSE) of different models across various fractions of training data (mean ± standard deviation) on Ribonanza dataset.

Ribonanza	**0.25**	**0.50**	**0.75**	**1.00**
Transformer1D	0.777 ± 0.014	0.740 ± 0.005	0.739 ± 0.001	0.705 ± 0.015
Transformer1D2D	0.630 ± 0.016	0.553 ± 0.015	0.541 ± 0.018	0.514 ± 0.004
GCN	0.668 ± 0.018	0.618 ± 0.017	0.612 ± 0.013	0.595 ± 0.006
GAT	0.600 ± 0.018	0.553 ± 0.026	0.544 ± 0.012	0.534 ± 0.006
ChebNet	0.537 ± 0.019	0.494 ± 0.022	0.499 ± 0.007	0.468 ± 0.002
Graph Transformer	0.567 ± 0.019	0.529 ± 0.013	0.529 ± 0.010	0.515 ± 0.001
GraphGPS	0.581 ± 0.021	0.529 ± 0.015	0.540 ± 0.004	0.523 ± 0.003
EGNN	0.694 ± 0.010	0.650 ± 0.010	0.632 ± 0.015	0.619 ± 0.007
SchNet	0.768 ± 0.008	0.724 ± 0.013	0.715 ± 0.015	0.685 ± 0.006
FastEGNN	0.795 ± 0.007	0.788 ± 0.002	0.774 ± 0.016	0.753 ± 0.015
MultiDimGNN	0.507 ± 0.003	0.463 ± 0.012	0.464 ± 0.003	0.437 ± 0.006

C.4 Generalization to OOD data

The results of the generalization experiment from Figure 6 are shown in Tables 10, 11, and 12.

Table 5: Performance (MCRMSE) of different models across various fractions of sequence labeling (mean ± standard deviation) on COVID dataset.

COVID	**0.2**	**0.4**	**0.6**	**0.8**	**1.0**
Transformer1D	0.654 ± 0.040	0.559 ± 0.011	0.480 ± 0.004	0.429 ± 0.034	0.361 ± 0.017
Transformer1D2D	0.502 ± 0.002	0.470 ± 0.052	0.374 ± 0.007	0.325 ± 0.006	0.305 ± 0.012
GCN	0.450 ± 0.012	0.416 ± 0.012	0.397 ± 0.012	0.378 ± 0.011	0.359 ± 0.009
GAT	0.411 ± 0.010	0.376 ± 0.012	0.360 ± 0.012	0.336 ± 0.009	0.315 ± 0.006
ChebNet	0.380 ± 0.007	0.344 ± 0.008	0.325 ± 0.009	0.299 ± 0.007	0.279 ± 0.007
Graph Transformer	0.415 ± 0.012	0.379 ± 0.011	0.362 ± 0.011	0.338 ± 0.004	0.318 ± 0.008
GraphGPS	0.428 ± 0.015	0.400 ± 0.017	0.376 ± 0.013	0.351 ± 0.007	0.332 ± 0.013
EGNN	0.436 ± 0.014	0.421 ± 0.010	0.407 ± 0.004	0.385 ± 0.006	0.364 ± 0.003
SchNet	0.442 ± 0.004	0.429 ± 0.005	0.413 ± 0.001	0.407 ± 0.005	0.390 ± 0.006
FastEGNN	0.497 ± 0.004	0.490 ± 0.007	0.466 ± 0.007	0.469 ± 0.009	0.444 ± 0.003
MultiDimGNN	0.376 ± 0.020	0.361 ± 0.031	0.355 ± 0.006	0.314 ± 0.010	0.271 ± 0.003

Table 6: Performance (MCRMSE) of different models across various fractions of sequence labeling (mean ± standard deviation) on Ribonanza dataset.

Ribonanza	**0.2**	**0.4**	**0.6**	**0.8**	**1.0**
Transformer1D	1.137 ± 0.163	0.929 ± 0.023	0.823 ± 0.018	0.742 ± 0.013	0.705 ± 0.015
Transformer1D2D	0.859 ± 0.025	0.638 ± 0.013	0.632 ± 0.028	0.568 ± 0.013	0.514 ± 0.004
GCN	1.191 ± 0.031	1.026 ± 0.079	1.111 ± 0.206	1.070 ± 0.137	0.595 ± 0.006
GAT	0.703 ± 0.015	0.632 ± 0.025	0.612 ± 0.030	0.560 ± 0.010	0.534 ± 0.006
ChebNet	0.614 ± 0.013	0.546 ± 0.008	0.540 ± 0.008	0.514 ± 0.006	0.468 ± 0.002
Graph Transformer	0.719 ± 0.043	0.607 ± 0.020	0.584 ± 0.015	0.552 ± 0.013	0.515 ± 0.001
GraphGPS	0.743 ± 0.058	0.663 ± 0.026	0.627 ± 0.024	0.651 ± 0.026	0.523 ± 0.003
EGNN	0.882 ± 0.010	0.722 ± 0.021	0.687 ± 0.008	0.665 ± 0.013	0.619 ± 0.007
SchNet	0.810 ± 0.002	0.781 ± 0.009	0.750 ± 0.009	0.725 ± 0.004	0.685 ± 0.006
FastEGNN	1.223 ± 0.008	0.929 ± 0.008	0.860 ± 0.004	0.837 ± 0.004	0.753 ±0.015
MultiDimGNN	0.658 ± 0.016	0.596 ± 0.042	0.536 ± 0.011	0.504 ± 0.013	0.437 ± 0.006

Table 7: Performance (MCRMSE) of various models in **robustness** experiments on the **COVID** dataset (mean ± standard deviation).

Model	**0.00**	**0.05**	**0.10**	**0.15**	**0.20**	**0.25**	**0.30**
Transformer1D	0.361 ± 0.017	0.386 ± 0.015	0.400 ± 0.010	0.409 ± 0.006	0.428 ± 0.005	0.435 ± 0.003	0.449 ± 0.011
Transformer1D2D	0.305 ± 0.012	0.373 ± 0.007	0.403 ± 0.007	0.428 ± 0.011	0.444 ± 0.015	0.457 ± 0.009	0.463 ± 0.009
GCN	0.359 ± 0.009	0.436 ± 0.009	0.464 ± 0.011	0.481 ± 0.010	0.491 ± 0.012	0.497 ± 0.009	0.501 ± 0.009
GAT	0.315 ± 0.006	0.409 ± 0.009	0.448 ± 0.011	0.471 ± 0.010	0.484 ± 0.012	0.494 ± 0.011	0.500 ± 0.010
ChebNet	0.279 ± 0.007	0.368 ± 0.003	0.423 ± 0.009	0.456 ± 0.007	0.471 ± 0.009	0.481 ± 0.010	0.487 ± 0.008
Graph Transformer	0.318 ± 0.008	0.403 ± 0.008	0.441 ± 0.012	0.467 ± 0.011	0.480 ± 0.012	0.487 ± 0.010	0.494 ± 0.011
GraphGPS	0.332 ± 0.013	0.408 ± 0.012	0.441 ± 0.010	0.464 ± 0.014	0.475 ± 0.012	0.484 ± 0.012	0.487 ± 0.008
EGNN	0.364 ± 0.003	0.432 ± 0.012	0.467 ± 0.009	0.486 ± 0.009	0.499 ± 0.011	0.505 ± 0.012	0.511 ± 0.011
SchNet	0.390 ± 0.006	0.447 ± 0.012	0.477 ± 0.011	0.496 ± 0.009	0.507 ± 0.014	0.513 ± 0.012	0.517 ± 0.010
FastEGNN	0.444 ± 0.003	0.49283 ± 0.008	0.516 ± 0.005	0.516 ± 0.004	0.522 ± 0.002	0.527 ± 0.003	0.540 ± 0.004
MultiDimGNN	0.271 ± 0.003	0.354 ± 0.004	0.389 ± 0.006	0.408 ± 0.007	0.420 ± 0.003	0.430 ± 0.006	0.441 ± 0.001

Table 8: Performance (MCRMSE) of various models in **robustness** experiments on the **Ribonanza** dataset (mean ± standard deviation).

Model	**0.00**	**0.05**	**0.10**	**0.15**	**0.20**	**0.25**	**0.30**
Transformer1D	0.705 ± 0.015	0.733 ± 0.010	0.769 ± 0.014	0.782 ± 0.005	0.794 ± 0.010	0.805 ± 0.017	0.823 ± 0.005
Transformer1D2D	0.514 ± 0.004	0.635 ± 0.004	0.714 ± 0.014	0.763 ± 0.008	0.790 ± 0.009	0.811 ± 0.014	0.830 ± 0.008
GCN	0.595 ± 0.006	0.750 ± 0.014	0.846 ± 0.008	0.893 ± 0.003	0.912 ± 0.005	0.924 ± 0.005	0.929 ± 0.005
GAT	0.534 ± 0.006	0.691 ± 0.015	0.785 ± 0.006	0.850 ± 0.003	0.877 ± 0.001	0.904 ± 0.007	0.915 ± 0.007
ChebNet	0.468 ± 0.002	0.611 ± 0.012	0.720 ± 0.006	0.802 ± 0.011	0.841 ± 0.003	0.876 ± 0.007	0.897 ± 0.008
Graph Transformer	0.515 ± 0.001	0.670 ± 0.011	0.768 ± 0.011	0.833 ± 0.008	0.870 ± 0.006	0.893 ± 0.010	0.908 ± 0.007
GraphGPS	0.523 ± 0.003	0.677 ± 0.017	0.772 ± 0.006	0.832 ± 0.006	0.872 ± 0.004	0.896 ± 0.011	0.912 ± 0.006
EGNN	0.619 ± 0.007	0.764 ± 0.003	0.847 ± 0.003	0.889 ± 0.005	0.904 ± 0.003	0.917 ± 0.000	0.922 ± 0.002
SchNet	0.685 ± 0.006	0.814 ± 0.006	0.873 ± 0.004	0.897 ± 0.004	0.908 ± 0.004	0.918 ± 0.005	0.922 ± 0.005
FastEGNN	0.753 ± 0.015	0.857 ± 0.001	0.884 ± 0.005	0.908 ± 0.001	0.914 ± 0.004	0.920 ± 0.003	0.922 ± 0.003
MultiDimGNN	0.437 ± 0.006	0.577 ± 0.011	0.662 ± 0.014	0.744 ± 0.003	0.786 ± 0.025	0.801 ± 0.008	0.840 ± 0.004

Table 9: Performance (MCRMSE) of various models in **robustness** experiments on the **Tc-riboswitches** dataset (mean ± standard deviation).

Model	0.00	0.05	0.10	0.15	0.20	0.25	0.30
Transformer1D	0.705 ± 0.079	0.698 ± 0.071	0.736 ± 0.004	0.672 ± 0.003	0.739 ± 0.008	0.694 ± 0.011	0.675 ± 0.047
Transformer1D2D	0.633 ± 0.001	0.697 ± 0.031	0.742 ± 0.003	0.708 ± 0.008	0.681 ± 0.001	0.762 ± 0.022	0.738 ± 0.016
GCN	0.701 ± 0.004	0.758 ± 0.003	0.747 ± 0.005	0.744 ± 0.004	0.733 ± 0.013	0.740 ± 0.011	0.765 ± 0.009
GAT	0.685 ± 0.024	0.749 ± 0.017	0.770 ± 0.047	0.734 ± 0.021	0.737 ± 0.009	0.753 ± 0.001	0.747 ± 0.011
ChebNet	0.621 ± 0.022	0.766 ± 0.014	0.754 ± 0.021	0.738 ± 0.014	0.763 ± 0.039	0.778 ± 0.048	0.739 ± 0.004
Graph Transformer	0.703 ± 0.054	0.754 ± 0.005	0.754 ± 0.006	0.773 ± 0.008	0.810 ± 0.087	0.742 ± 0.004	0.754 ± 0.005
GraphGPS	0.702 ± 0.028	0.785 ± 0.053	0.805 ± 0.092	0.750 ± 0.006	0.755 ± 0.060	0.769 ± 0.031	1.078 ± 0.469
EGNN	0.663 ± 0.010	0.750 ± 0.001	0.739 ± 0.002	0.749 ± 0.005	0.749 ± 0.001	0.749 ± 0.001	0.756 ± 0.013
SchNet	0.655 ± 0.038	0.762 ± 0.005	0.742 ± 0.002	0.771 ± 0.037	0.746 ± 0.005	0.791 ± 0.016	0.730 ± 0.016
FastEGNN	0.710 ± 0.010	0.733 ± 0.007	0.749 ± 0.006	0.748 ± 0.006	0.752 ± 0.008	0.758 ± 0.017	0.761 ± 0.010
MultiDimGNN	0.554 ± 0.004	0.672 ± 0.034	0.734 ± 0.042	0.704 ± 0.052	0.712 ± 0.052	0.661 ± 0.038	0.708 ± 0.062

Table 10: Performance (MCRMSE) of various models in **generalization** experiments on the **COVID** dataset (mean ± standard deviation).

Model	0.00	0.05	0.10	0.15	0.20	0.25	0.30
Transformer1D	0.361 ± 0.017	0.382 ± 0.022	0.402 ± 0.018	0.436 ± 0.015	0.461 ± 0.021	0.478 ± 0.015	0.494 ± 0.016
Transformer1D2D	0.305 ± 0.012	0.406 ± 0.016	0.466 ± 0.017	0.513 ± 0.016	0.545 ± 0.027	0.581 ± 0.025	0.596 ± 0.018
GCN	0.359 ± 0.009	0.459 ± 0.011	0.508 ± 0.011	0.550 ± 0.014	0.572 ± 0.016	0.601 ± 0.014	0.612 ± 0.008
GAT	0.315 ± 0.006	0.437 ± 0.013	0.490 ± 0.013	0.528 ± 0.008	0.555 ± 0.013	0.580 ± 0.015	0.592 ± 0.012
ChebNet	0.279 ± 0.007	0.415 ± 0.017	0.483 ± 0.023	0.538 ± 0.025	0.571 ± 0.029	0.604 ± 0.030	0.621 ± 0.028
Graph Transformer	0.318 ± 0.008	0.449 ± 0.015	0.501 ± 0.018	0.543 ± 0.015	0.571 ± 0.019	0.596 ± 0.014	0.609 ± 0.014
GraphGPS	0.332 ± 0.013	0.443 ± 0.011	0.496 ± 0.006	0.536 ± 0.005	0.559 ± 0.010	0.586 ± 0.007	0.593 ± 0.005
EGNN	0.365 ± 0.011	0.458 ± 0.014	0.504 ± 0.018	0.530 ± 0.020	0.549 ± 0.021	0.565 ± 0.022	0.572 ± 0.022
SchNet	0.390 ± 0.006	0.457 ± 0.011	0.491 ± 0.008	0.515 ± 0.007	0.531 ± 0.010	0.543 ± 0.009	0.556 ± 0.002
FastEGNN	0.444 ± 0.003	0.491 ± 0.020	0.511 ± 0.014	0.524 ± 0.009	0.533 ± 0.006	0.541 ± 0.003	0.543 ± 0.001
MultiDimGNN	0.271 ± 0.003	0.377 ± 0.013	0.437 ± 0.006	0.476 ± 0.016	0.500 ± 0.008	0.531 ± 0.012	0.535 ± 0.014

Table 11: Performance (MCRMSE) of various models in **generalization** experiments on the **Ribonanza** dataset (mean ± standard deviation).

Model	0.00	0.05	0.10	0.15	0.20	0.25	0.30
Transformer1D	0.705 ± 0.015	0.747 ± 0.005	0.796 ± 0.006	0.828 ± 0.008	0.860 ± 0.013	0.886 ± 0.013	0.899 ± 0.003
Transformer1D2D	0.514 ± 0.004	0.685 ± 0.014	0.857 ± 0.008	0.986 ± 0.015	1.055 ± 0.007	1.142 ± 0.020	1.192 ± 0.034
GCN	0.595 ± 0.006	0.857 ± 0.018	0.993 ± 0.012	1.054 ± 0.034	1.094 ± 0.043	1.129 ± 0.061	1.139 ± 0.075
GAT	0.534 ± 0.006	0.778 ± 0.021	0.919 ± 0.030	1.003 ± 0.056	1.047 ± 0.073	1.076 ± 0.082	1.093 ± 0.091
ChebNet	0.468 ± 0.002	0.699 ± 0.005	0.881 ± 0.038	1.025 ± 0.095	1.083 ± 0.111	1.165 ± 0.185	1.200 ± 0.220
Graph Transformer	0.515 ± 0.001	0.752 ± 0.005	0.930 ± 0.013	1.067 ± 0.036	1.124 ± 0.033	1.194 ± 0.080	1.224 ± 0.104
GraphGPS	0.523 ± 0.003	0.771 ± 0.026	0.958 ± 0.068	1.087 ± 0.142	1.116 ± 0.195	1.154 ± 0.202	1.165 ± 0.196
EGNN	0.691 ± 0.006	0.815 ± 0.004	0.975 ± 0.026	1.138 ± 0.078	1.228 ± 0.079	1.350 ± 0.173	1.395 ± 0.187
SchNet	0.685 ± 0.006	0.844 ± 0.006	0.949 ± 0.022	1.068 ± 0.035	1.157 ± 0.069	1.270 ± 0.049	1.342 ± 0.117
FastEGNN	0.753 ± 0.015	0.857 ± 0.001	0.912 ± 0.007	0.939 ± 0.011	0.940 ± 0.010	0.952 ± 0.008	0.957 ± 0.001
MultiDimGNN	0.437 ± 0.006	0.655 ± 0.018	0.715 ± 0.011	0.824 ± 0.046	0.878 ± 0.051	0.918 ± 0.052	0.939 ± 0.060

Table 12: Performance (MCRMSE) of various models in **generalization** experiments on the **Tc-riboswitches** dataset (mean ± standard deviation).

Model	0.00	0.05	0.10	0.15	0.20	0.25	0.30
Transformer1D	0.705 ± 0.079	0.711 ± 0.038	0.732 ± 0.007	0.753 ± 0.019	0.815 ± 0.091	0.803 ± 0.062	0.796 ± 0.079
Transformer1D2D	0.633 ± 0.001	0.705 ± 0.007	0.745 ± 0.008	0.749 ± 0.017	0.800 ± 0.034	0.766 ± 0.017	0.754 ± 0.014
GCN	0.701 ± 0.004	0.774 ± 0.026	0.781 ± 0.051	0.782 ± 0.062	0.825 ± 0.093	0.845 ± 0.072	0.858 ± 0.126
GAT	0.685 ± 0.024	0.829 ± 0.074	0.958 ± 0.131	0.926 ± 0.152	1.037 ± 0.297	0.998 ± 0.213	1.036 ± 0.392
ChebNet	0.621 ± 0.022	0.824 ± 0.185	0.862 ± 0.251	0.888 ± 0.302	0.997 ± 0.439	0.983 ± 0.412	1.045 ± 0.514
Graph Transformer	0.710 ± 0.041	0.759 ± 0.035	0.770 ± 0.047	0.776 ± 0.054	0.815 ± 0.101	0.795 ± 0.085	0.822 ± 0.115
GraphGPS	0.715 ± 0.012	0.751 ± 0.016	0.801 ± 0.023	0.795 ± 0.014	0.833 ± 0.025	0.814 ± 0.022	0.830 ± 0.018
EGNN	0.663 ± 0.010	0.760 ± 0.043	0.898 ± 0.134	0.901 ± 0.123	0.849 ± 0.053	1.058 ± 0.239	1.192 ± 0.453
SchNet	0.655 ± 0.038	1.368 ± 0.449	1.099 ± 0.320	1.419 ± 0.491	0.900 ± 0.119	1.957 ± 0.858	2.025 ± 0.779
FastEGNN	0.710 ± 0.011	0.854 ± 0.079	0.806 ± 0.032	0.863 ± 0.020	0.846 ± 0.110	0.849 ± 0.079	0.988 ± 0.131
MultiDimGNN	0.554 ± 0.004	0.686 ± 0.197	0.656 ± 0.021	0.743 ± 0.139	0.691 ± 0.118	0.826 ± 0.164	0.672 ± 0.024