Genesis RESEARCH
TEXAS
The University of Texas at Austin

Triangle Multiplication is All You Need for Biomolecular Structure Representations

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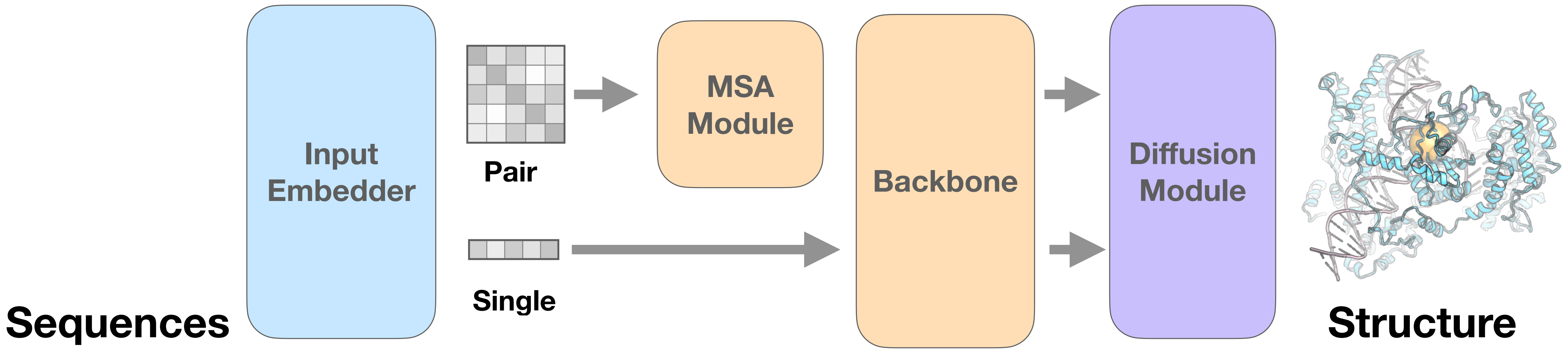
Overview

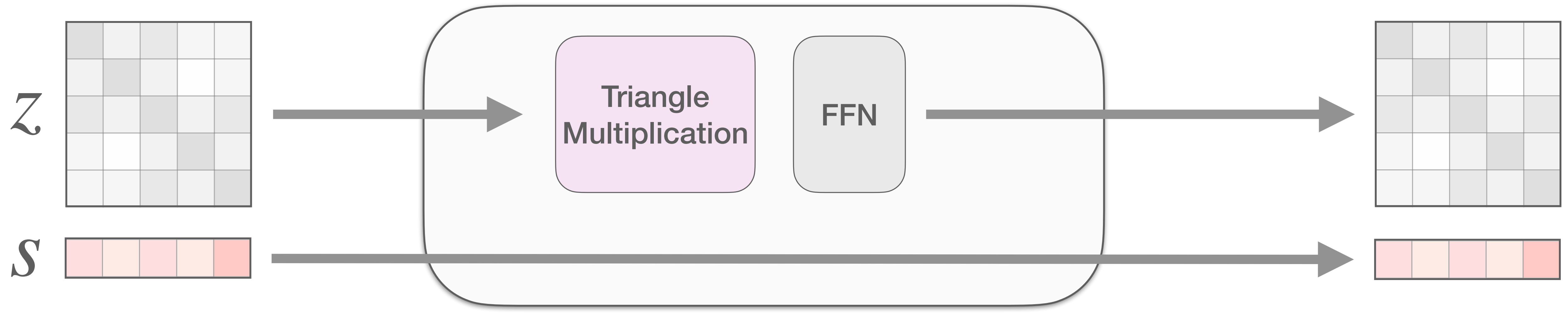
Biomolecular structure prediction



Sequences → Input Embedder → Pair → MSA Module → Backbone; Single → Backbone → Diffusion Module → Structure

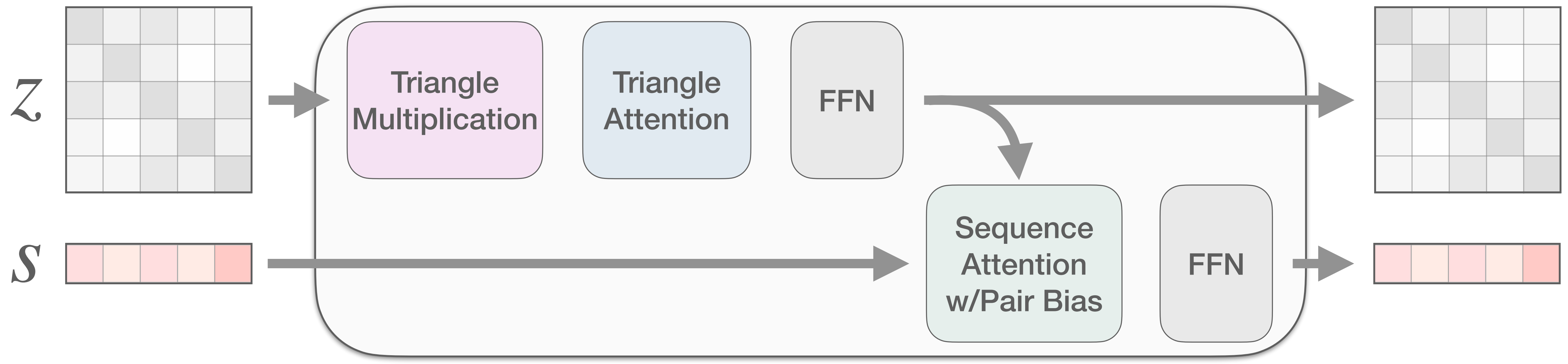
Method

Pairmixer - Efficient and equally effective backbone

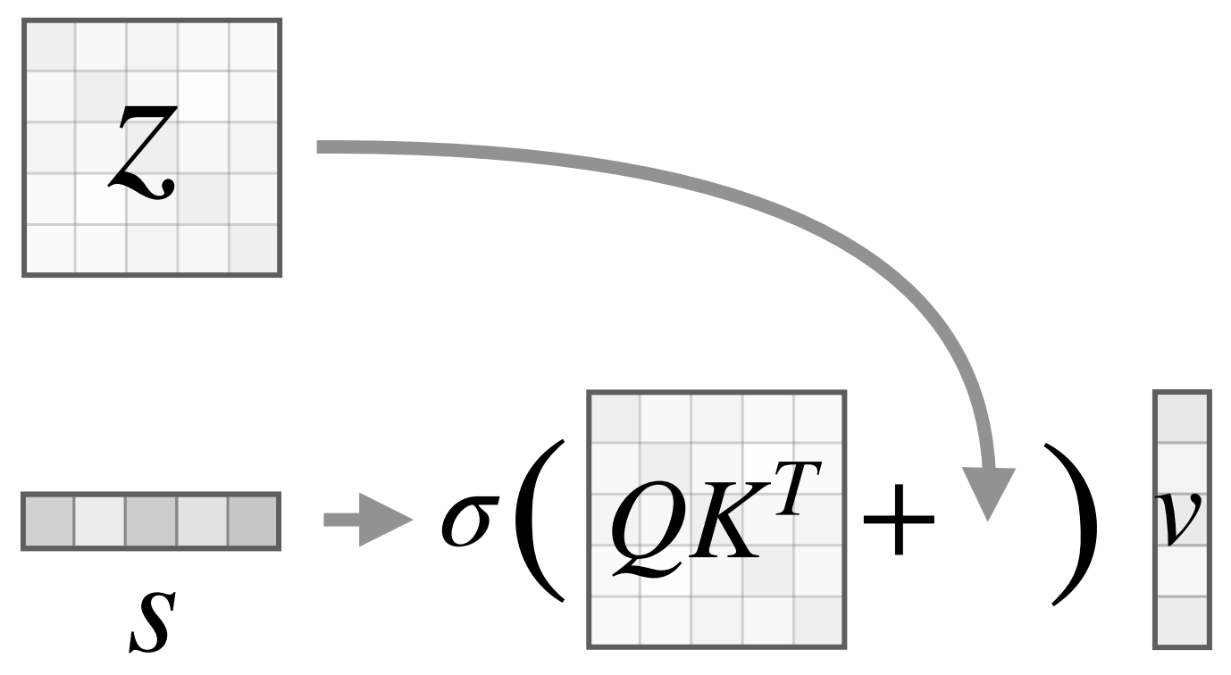


Preliminary

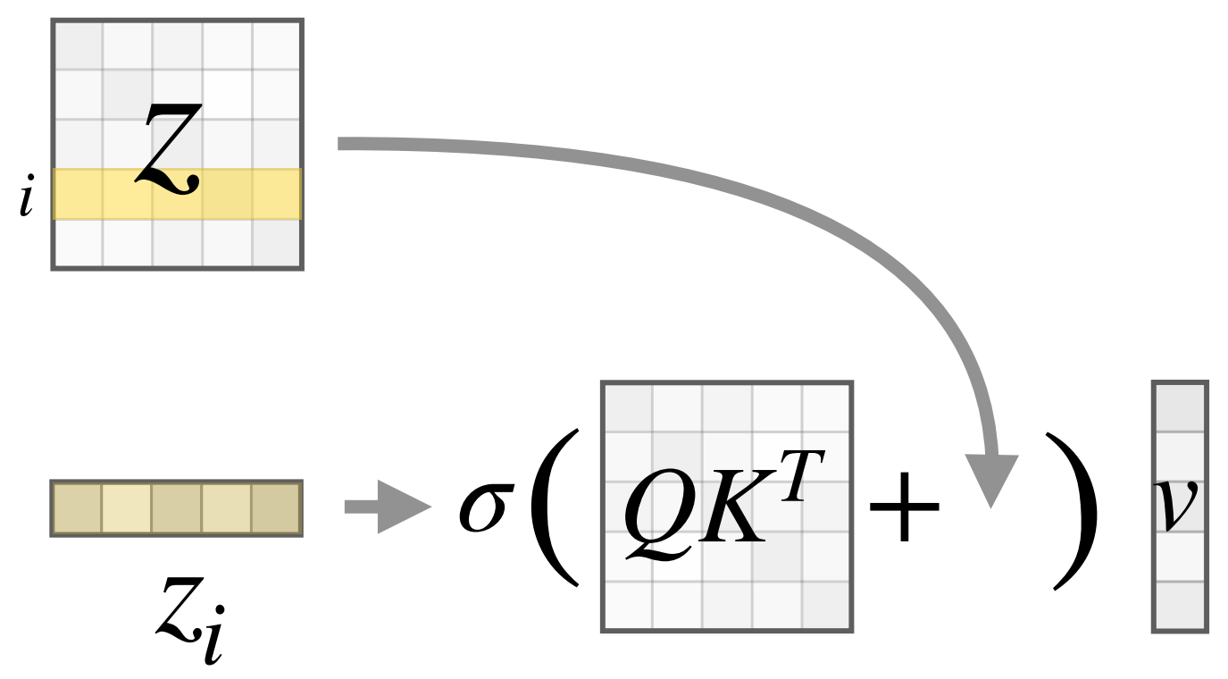
Pairformer - Highly effective backbone



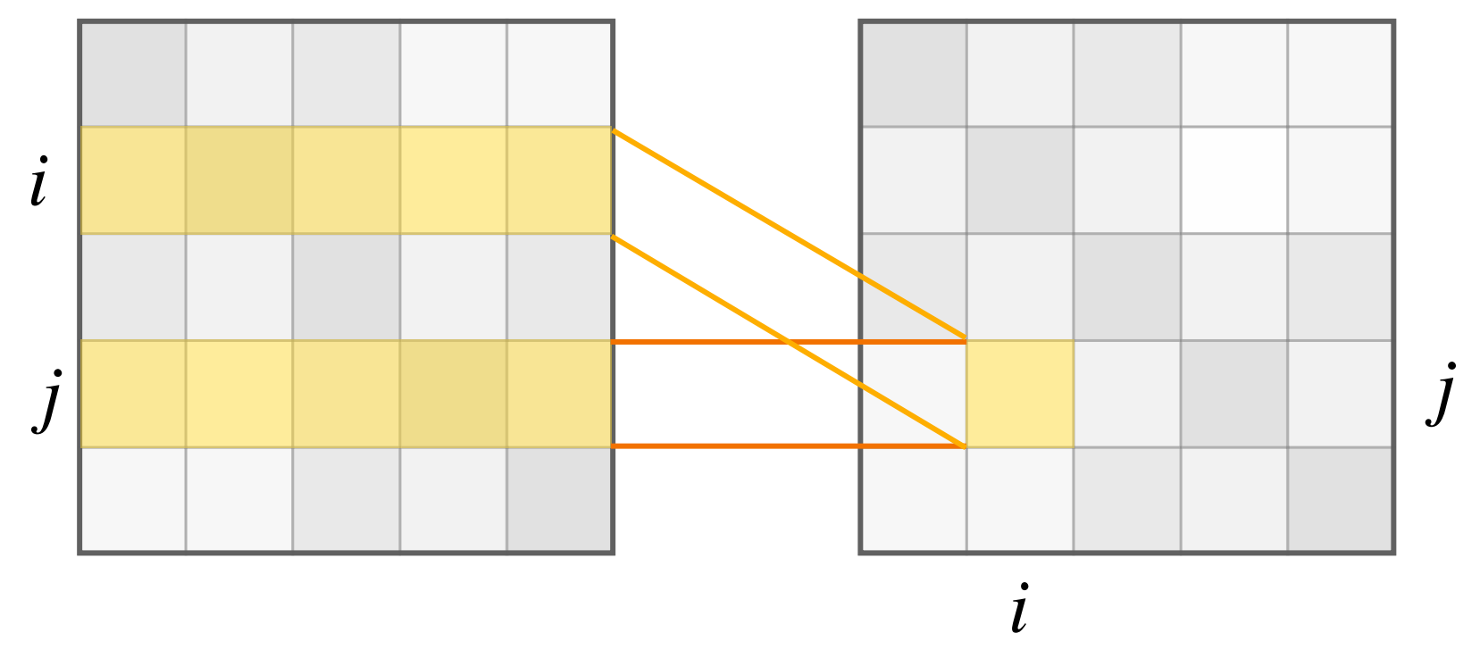
Sequence Attention



Triangle Attention

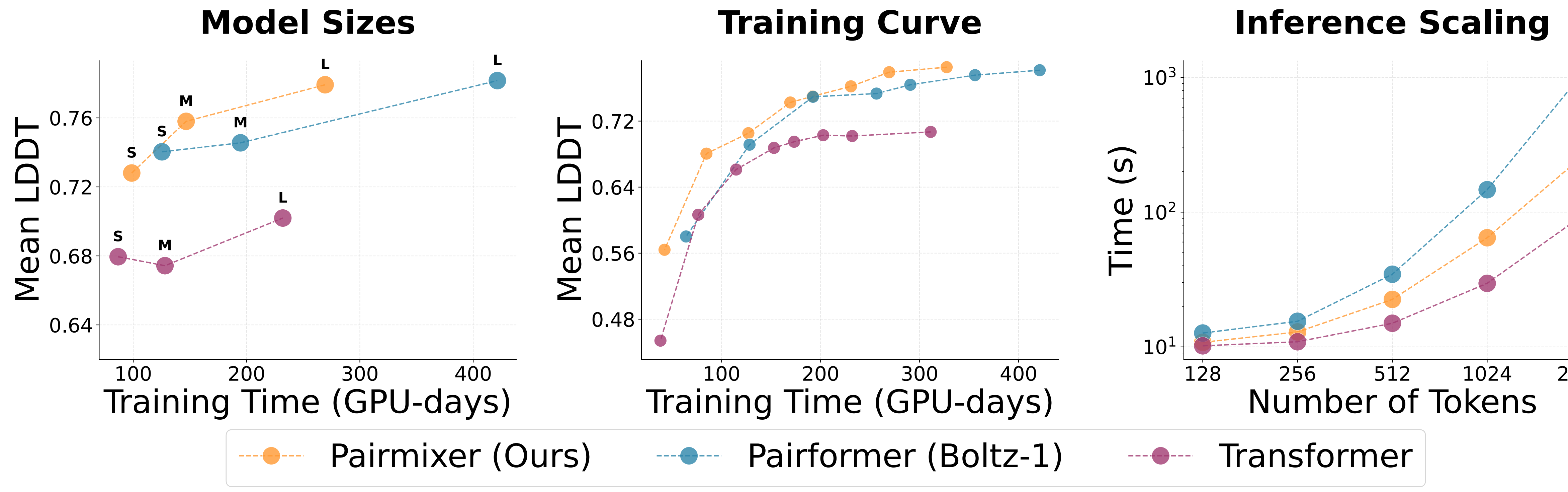


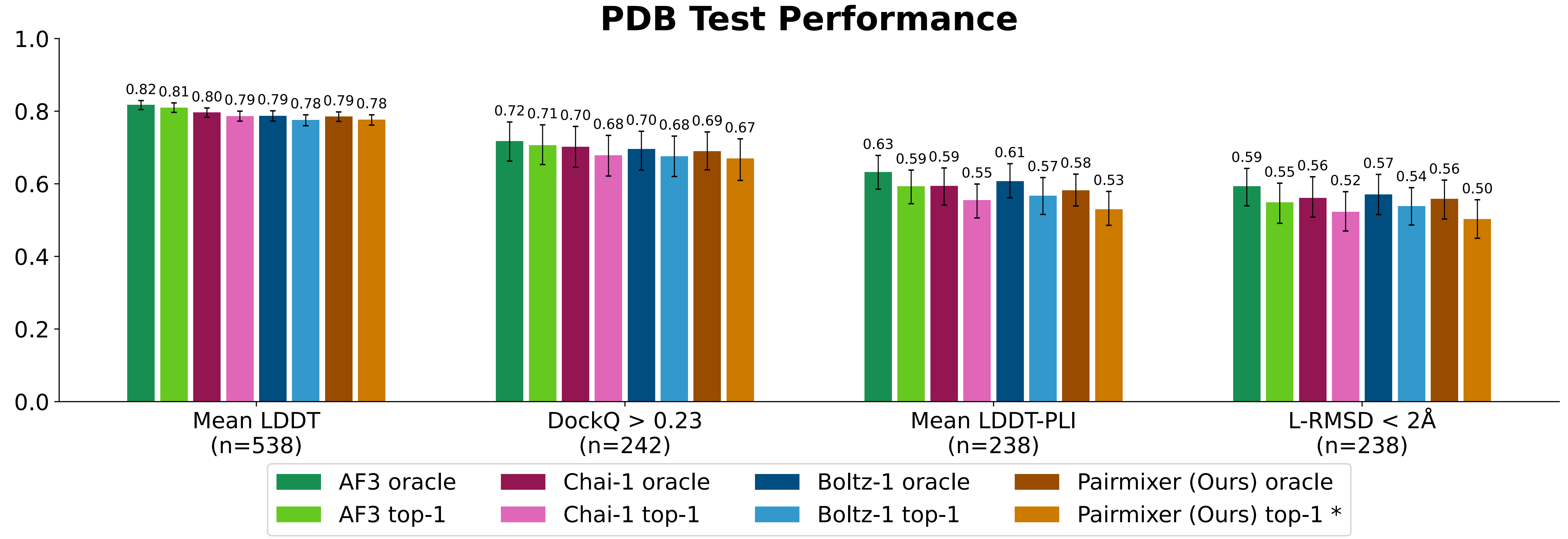
Triangle Multiplication



Results

Faster training, Faster inference, Same performance





PDB Test Performance

[1] Accurate structure prediction of biomolecular interactions with AlphaFold 3. Abramson et al. 2024.
[2] Boltz-1: Democratizing Biomolecular Interaction Modeling. Wohlwend et al. 2024.
[3] MiniFold: Simple, Fast, and Accurate Protein Structure Prediction. Wohlwend et al. 2025.