

Introductions

Drug discovery is critical to modern healthcare but is hindered by traditional methods like molecular docking, free energy perturbation, and empirical modeling, which are time-consuming, costly, and often limited in scope. Deep learning has emerged as a transformative tool, enabling accurate predictions of protein structures and complex patterns while driving a shift toward data-driven approaches. Transformer-based models like ChatGPT demonstrate the promise of self-supervised learning, addressing the scarcity of labeled data in drug discovery. However, challenges remain in adapting these models to capture stereochemical intricacies in protein-ligand interactions. Addressing these limitations could revolutionize drug discovery, making it faster, more accurate, and cost-effective.

Methods

• <u>Hyperdigraph</u>

Definition 1: The hyperdigraph on finite vertex set *V* is defined by

 $\overrightarrow{\mathcal{H}} = \left(V, \overrightarrow{E}\right), \overrightarrow{E} = \{e : [k] \rightarrow V, [k] = \{0, 1, \dots, k\}\}$ E is a set of directed hyperedges. A k-directed hyperedge is a sequence including k + 1 distinct elements in V.



(a) Water molecule



(b) Graph representation

(c) Digraph representation







0-dimension, $\vec{\mathcal{H}}_0$



1-dimension, $\vec{\mathcal{H}}_1$

Hyperdigraph Laplacian

The chain complex $C_*(V; \mathbb{K}) = C_p(V; \mathbb{K})_{p \ge 1}$ with the boundary operator $\partial_k : C_k(V; \vec{\mathcal{H}}) \to C_{k-1}(V; \vec{\mathcal{H}})$ given by

$$\partial_k(x_0, x_1, \dots, x_k) = \sum_{i=0}^k (-1)^n (x_{0_i}, \dots, \hat{x_i}, \dots, x_k),$$

The infimum chain complex defined by

 $\Omega_k(\vec{\mathcal{H}};\mathbb{K}) = \{x \in C_k(\vec{\mathcal{H}};\mathbb{K}) | \partial_k x \in C_{p-1}(\vec{\mathcal{H}};\mathbb{K})\}$ **Definition 2**: The hyperdigraph Laplacian, $\Delta_k^{\overrightarrow{\mathcal{H}}} : \Omega_k(\overrightarrow{\mathcal{H}}; \mathbb{K}) \to \Omega_k(\overrightarrow{\mathcal{H}}; \mathbb{K})$ of $\overrightarrow{\mathcal{H}}$ is defined by $\Delta_k^{\mathcal{\vec{H}}} = \partial_k^* \circ \partial_k + \partial_{k+1} \circ \partial_{k+1}^*, k \ge 1 \quad \text{or} \quad L_k^{\mathcal{\vec{H}}} = B_k^T B_k + B_{k+1} B_{k+1}^T, k \ge 1$





Multiscale Topology-enabled AI for Drug Discovery

Dong Chen¹, Jana Shen², and Guo-Wei Wei^{1,3,4} ¹Mathematics, ³Biochemistry & Molecular Biology, and ⁴Electrical & Computer Engineering, Michigan State University ²Department of Pharmaceutical Sciences, University of Maryland



Drug Resistance Predictions



F140L



H172Y



(d) Hyperdigraph representation



2-dimension, $\vec{\mathcal{H}}_2$

 $n \geq 1$.



Binding Affinity Predictions



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References

- Advanced Science (2025).



• Achieved the best performance in binding affinity prediction on the PDBbind database, including the CASF-2007, CASF-2013, and CASF-2016 benchmarks.¹

1. <u>Chen, Dong</u>, et al. "Multiscale topology-enabled structure-to-sequence transformer for protein–ligand interaction predictions." Nature Machine Intelligence 6.7 (2024): 799-810. 2. Chen, Dong, et al. "Persistent hyperdigraph homology and persistent hyperdigraph Laplacians." Foundations of Data Science 5.4 (2023): 558.

3. <u>Chen, Dong</u>, et al. "Drug Resistance Predictions Based on a Directed Flag Transformer."