

Energy-Inspired Molecular Conformation Optimization

ICLR 2022

Jiaqi Guan¹, Wesley Wei Qian¹, Qiang Liu², Wei-Ying Ma³, Jianzhu Ma⁴, Jian Peng^{1,3,5}

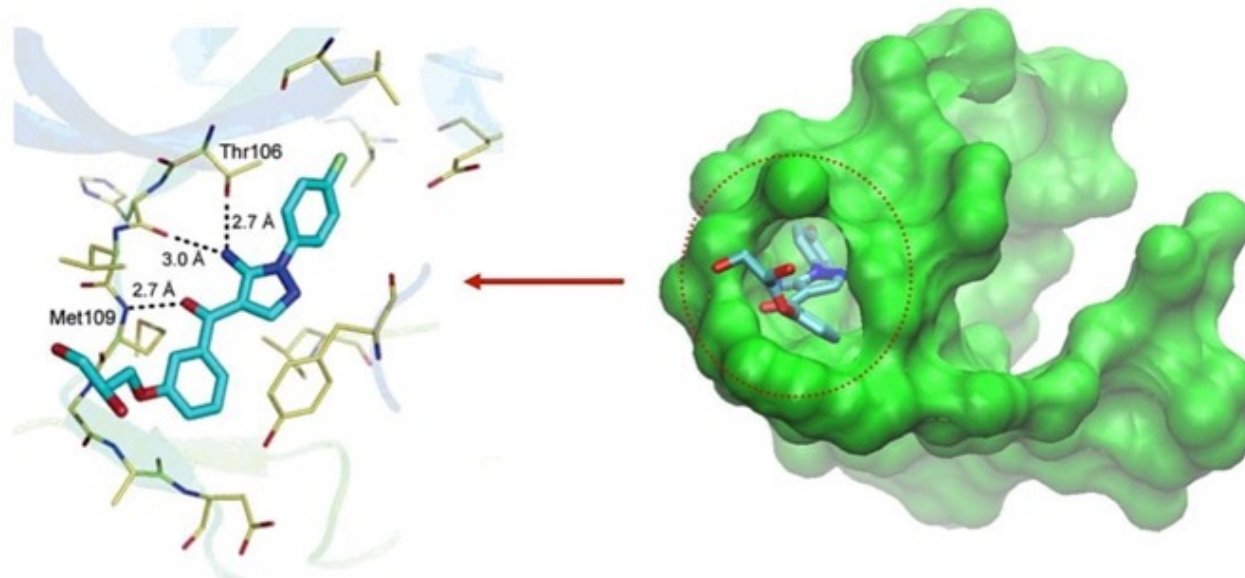
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Code: https://github.com/guanjq/confopt_official

Background

- Molecular conformer determines the steric and electronic properties of the molecules
- Efficiently and accurately generate molecular conformation can unlock lots of new opportunities including screening for protein targets



Previous Work

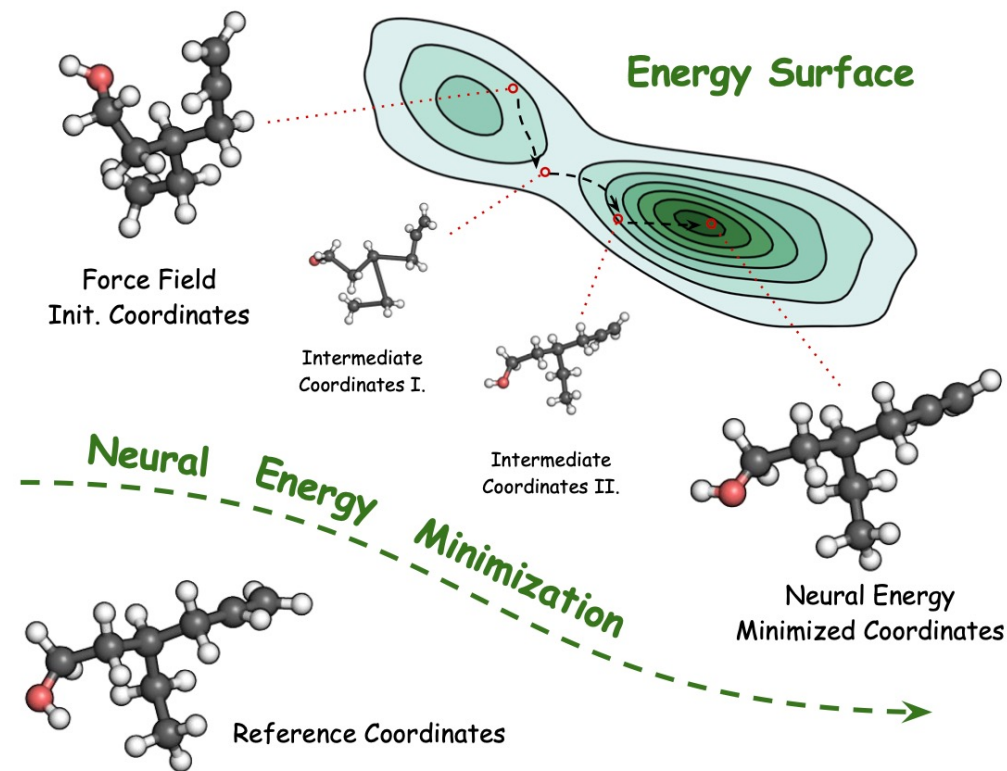
- **Molecular Dynamics Simulation**
 - Accuracy and efficiency trade-off
 - DFT based / FF based methods
- **Two-Stage Deep Generative Models** (First generate pairwise distances)
 - GraphDG (VAE based) [1]
 - CGCF (Continuous Normalizing Flow based) [2]
- **One-Stage Deep Generative Models**
 - ConfGF (Score-Matching based) [3]

1. Mansimov, E., Mahmood, O., Kang, S., & Cho, K. (2019). Molecular geometry prediction using a deep generative graph neural network. *Scientific reports*.
2. Xu, M., Luo, S., Bengio, Y., Peng, J., & Tang, J. (2021). Learning neural generative dynamics for molecular conformation generation. *ICLR 2021*.
3. Shi, C., Luo, S., Xu, M., & Tang, J. (2021). Learning gradient fields for molecular conformation generation. *ICML 2021*.

Motivation

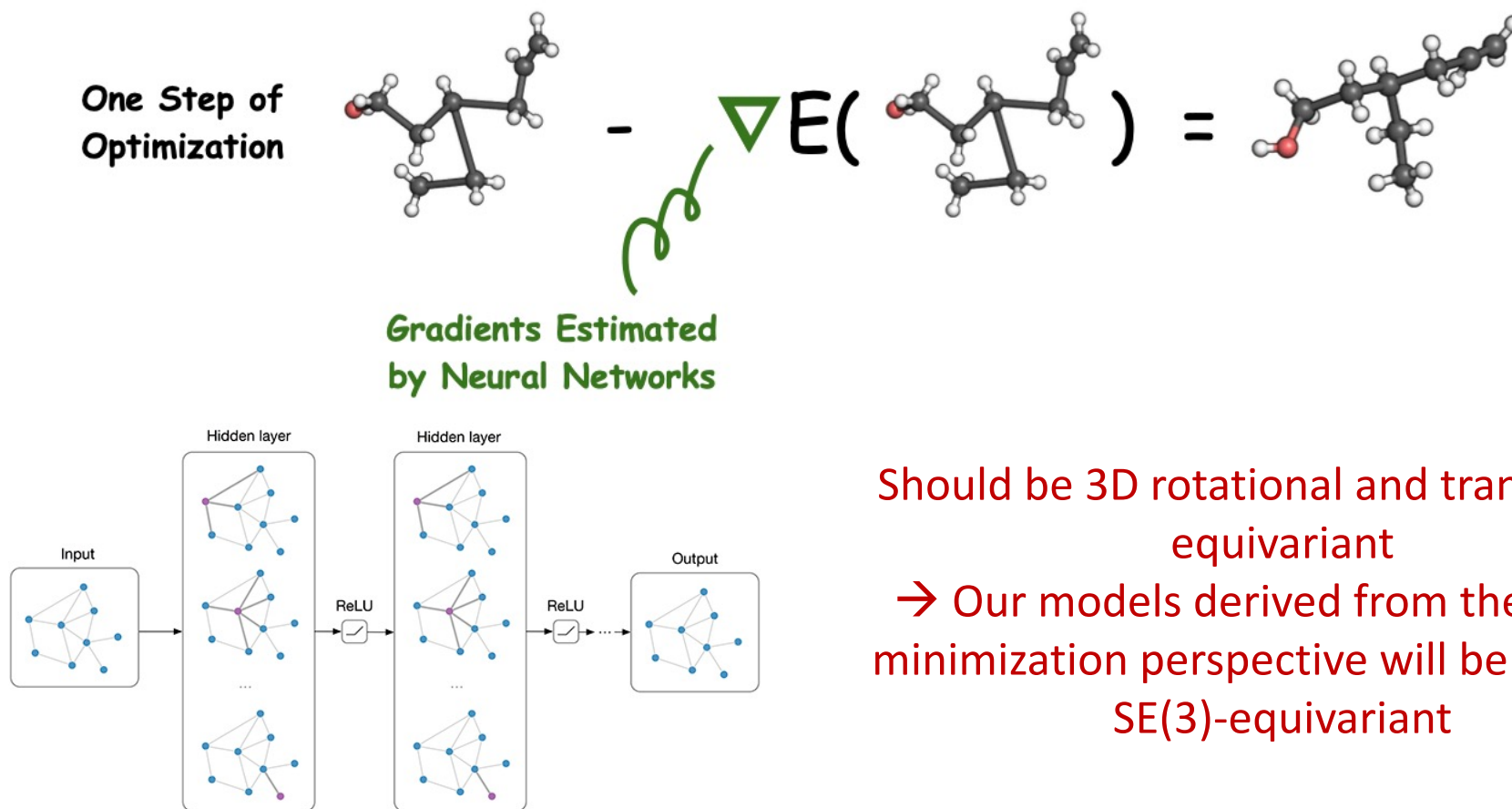
- Nature has an energy function for conformer
- The energy function governs an energy surface
- Stable equilibrium conformer corresponds a local minimum on the potential energy surface

To get a conformer with lowest energy, we can **navigate** the energy surface (**perform gradient descent**) by updating the 3D coordinates



Motivation

Use a graph neural network to learn the gradient field of conformational energy from data



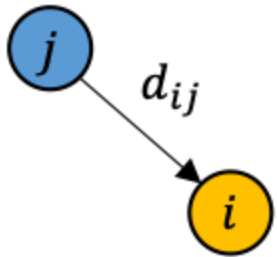
Should be 3D rotational and translational equivariant

→ Our models derived from the energy minimization perspective will be naturally SE(3)-equivariant

Recipe For Deriving Energy-Inspired Models

- Assume an underlying energy function

I. Energy Function

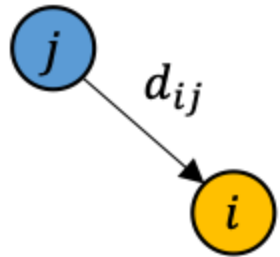


$$E(\mathbf{x}; G) = \sum_{i \in \mathcal{V}} \sum_{j \neq i} \phi(d_{ij}; G)$$

Recipe For Deriving Energy-Inspired Models

- Assume an underlying energy function
- Take gradients of the energy function w.r.t conformation \mathbf{x}

I. Energy Function



$$E(\mathbf{x}; G) = \sum_{i \in \mathcal{V}} \sum_{j \neq i} \phi(d_{ij}; G)$$

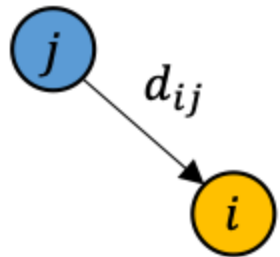
II. Energy Gradients w.r.t \mathbf{x}

$$\begin{aligned} f_{\theta}(\mathbf{x}; G)|_{x_i} &= \frac{\partial E(\mathbf{x}; G)}{\partial x_i} = \sum_{j \neq i} \frac{\partial \phi(d_{ij}; G)}{\partial x_i} \\ &= \sum_{j \neq i} \frac{\partial d_{ij}}{\partial x_i} \frac{\partial \phi(d_{ij}; G)}{\partial d_{ij}} \\ &= \sum_{j \neq i} \frac{(x_i - x_j)}{d_{ij}} \frac{\partial \phi(d_{ij}; G)}{\partial d_{ij}} \\ &= \sum_{j \neq i} (x_i - x_j) g_{\theta}(d_{ij}; G) \end{aligned}$$

Recipe For Deriving Energy-Inspired Models

- Assume an underlying energy function
 - Take gradients of the energy function w.r.t conformation \mathbf{x}
- Obtain a SE(3)-equivariant network naturally

I. Energy Function



$$E(\mathbf{x}; G) = \sum_{i \in \mathcal{V}} \sum_{j \neq i} \phi(d_{ij}; G)$$

II. Energy Gradients w.r.t \mathbf{x}

$$\begin{aligned} f_{\theta}(\mathbf{x}; G)|_{x_i} &= \frac{\partial E(\mathbf{x}; G)}{\partial x_i} = \sum_{j \neq i} \frac{\partial \phi(d_{ij}; G)}{\partial x_i} \\ &= \sum_{j \neq i} \frac{\partial d_{ij}}{\partial x_i} \frac{\partial \phi(d_{ij}; G)}{\partial d_{ij}} \\ &= \sum_{j \neq i} \frac{(x_i - x_j)}{d_{ij}} \frac{\partial \phi(d_{ij}; G)}{\partial d_{ij}} \\ &= \sum_{j \neq i} (x_i - x_j) g_{\theta}(d_{ij}; G) \end{aligned}$$

Result: a SE(3)-Equivariant model

Each update is a SE(3)-equivariant operation

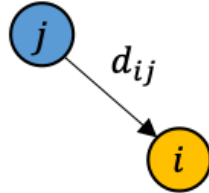
Proof:

Assume input \mathbf{x} is $\hat{\mathbf{x}} = R\mathbf{x} + \mathbf{t}$ and translate with \mathbf{t} :

$$\begin{aligned} \hat{\mathbf{x}}^{t+1} &= \hat{\mathbf{x}}^t - f_{\theta}(\hat{\mathbf{x}}^t; G) \\ &= R\mathbf{x}^t + \mathbf{t} - Rf_{\theta}(\mathbf{x}^t; G) \\ &= R(\mathbf{x}^t - f_{\theta}(\mathbf{x}^t; G)) + \mathbf{t} \\ &= R\mathbf{x}^{t+1} + \mathbf{t} \end{aligned}$$

More Variants

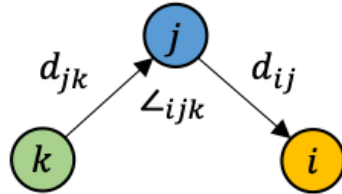
Two-Atom Model



$$E(\mathbf{x}; G) = \sum_{i \in \mathcal{V}} \sum_{j \neq i} \phi(d_{ij}; G)$$

$$x_i^{l+1} = x_i^l + \sum_{j \neq i} (x_i^l - x_j^l) f_{h \rightarrow x}(\|x_i^l - x_j^l\|, h_i^l, h_j^l; e_{ij})$$

Three-Atom Model



$$E(\mathbf{x}; G) = \sum_{i \in \mathcal{V}} \sum_{j \neq i} \sum_{k \neq i, j} \phi(d_{ij}, d_{ik}, \angle_{jik}; G)$$

$$x_i^{l+1} = x_i^l + \sum_{jk} (x_i - x_j) g_{\psi}(d_{ij}, d_{ik}, r_{ij}^T r_{ik}) + (x_i - x_k) h_{\omega}(d_{ij}, d_{ik}, r_{ij}^T r_{ik})$$

Benefits:

- Instead of proposing a model heuristically based on MPNN (like EGNN), the derived model is SE(3)-equivariant naturally and aligns the underlying physical assumption
- Avoid complicated spherical-harmonics-based techniques, like SE(3)-Transformer
- One-stage; Faster sampling compared to ConfGF

Experiments – Setup

- **Molecular Conformation Optimization**

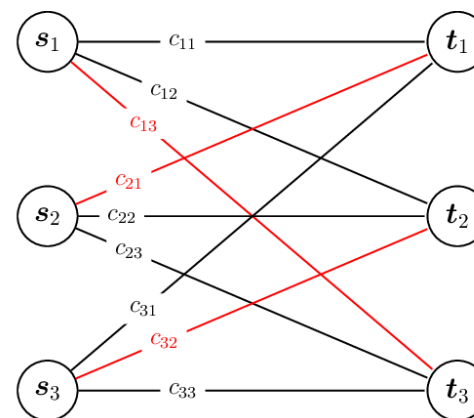
- L2 Loss on pairwise distance matrix
- Datasets: QM9 and lowest energy conformer in GEOM-Drug
- Baselines: RDKit, EGNN, SE(3)-Transformer
- Metrics: mean / median RMSD

- **Molecular Conformation Generation**

- Apply the optimal transport loss

$$L_{OT} = \min_{\pi \in \Gamma} \sum_{i,j} \pi_{i,j} \mathbf{C}(\mathbf{X}_i^*, \mathbf{X}_j)$$

- Datasets: GEOM-QM9 and GEOM-Drug (multiple conformers)
- Baselines: RDKit, multiple deep generative models
- Metrics: Coverage rate (COV), Mismatching rate (MIS), Matching score (MAT)



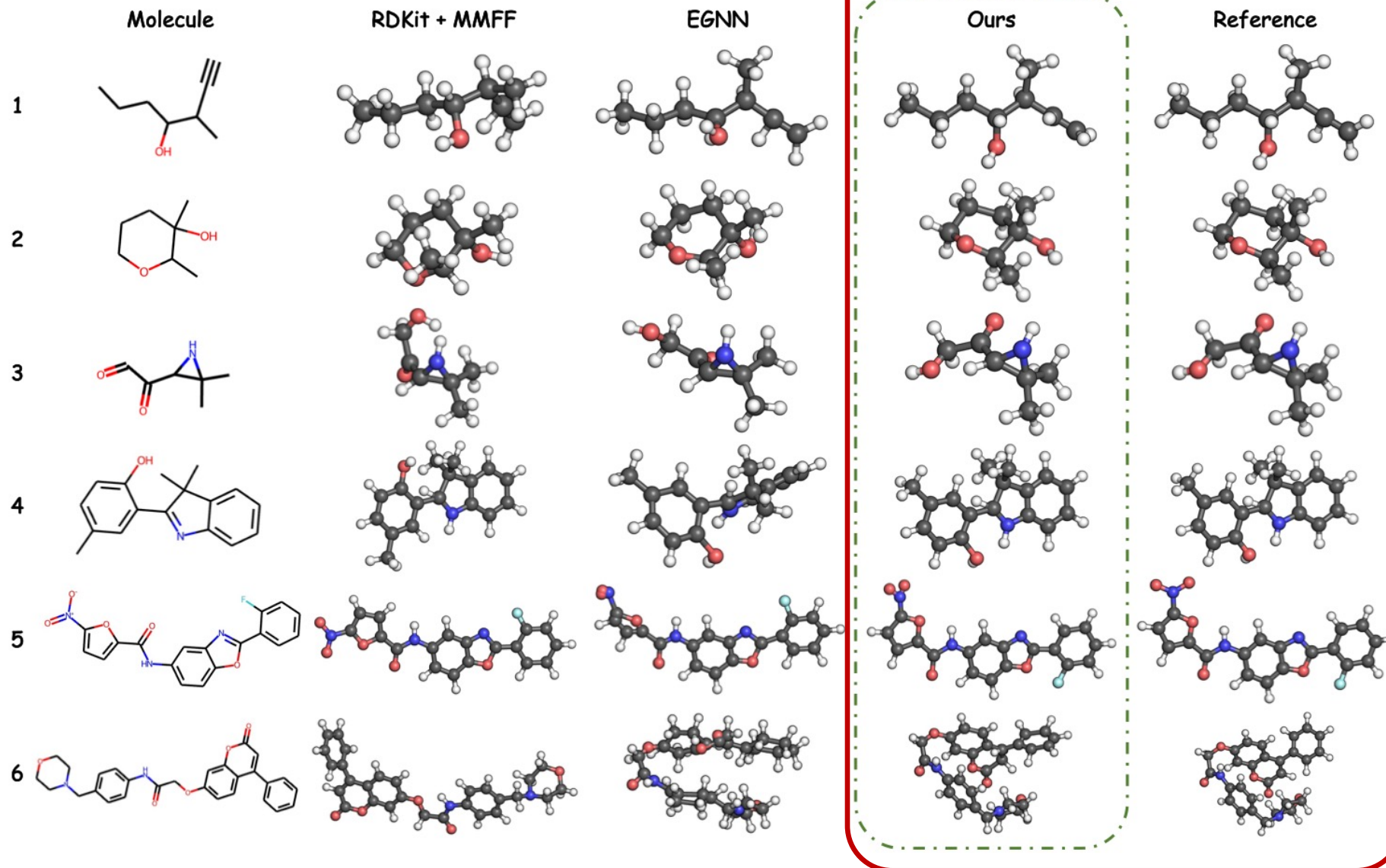
Experiments – Optimization Results

Molecular Conformation Optimization

- Better RMSD

Model \ Dataset	QM9		GEOM-Drug	
	mean RMSD (↓)	median RMSD (↓)	mean RMSD (↓)	median RMSD (↓)
RDKit+MMFF	0.3872 ± 0.0029	0.2756 ± 0.0075	1.7913 ± 0.0030	1.6433 ± 0.0097
SE(3)-Tr. [8]	0.2476 ± 0.0021	0.1657 ± 0.0022	1.0050 ± 0.0022	0.9139 ± 0.0041
EGNN [34]	0.2101 ± 0.0009	0.1356 ± 0.0013	1.0405 ± 0.0018	0.9598 ± 0.0038
Ours-TwoAtom	0.1415 ± 0.0004	0.0534 ± 0.0002	0.8839 ± 0.0014	0.7733 ± 0.0026
Ours-Ext _v	0.1383 ± 0.0005	0.0505 ± 0.0001	0.8691 ± 0.0015	0.7535 ± 0.0028
Ours-ThreeAtom	0.1374 ± 0.0004	0.0522 ± 0.0002	0.8567 ± 0.0014	0.7192 ± 0.0024

Experiments – Visualization



Experiments – Generation Results

Molecular Conformation Generation

- Evaluate with different initialization
- Better precision and recall

Dataset Metric	GEOM-QM9						GEOM-Drugs					
	COV(%) (↑)		MIS(%) (↓)		MAT(Å) (↓)		COV(%) (↑)		MIS(%) (↓)		MAT(Å) (↓)	
	Mean	Median	Mean	Median	Mean	Median	Mean	Median	Mean	Median	Mean	Median
RDKit	83.26	90.78	8.13	1.00	0.3447	0.2935	60.91	65.70	27.95	12.07	1.2026	1.1252
CVGAE	0.09	0.00	-	-	1.6713	1.6088	0.00	0.00	-	-	3.0702	2.9937
GraphDG	73.33	84.21	56.09	64.66	0.4245	0.3973	8.27	0.00	97.92	100.00	1.9722	1.9845
CGCF	78.05	82.48	63.51	64.66	0.4219	0.3900	53.96	57.06	78.32	86.28	1.2487	1.2247
ConfGF	88.49	94.13	53.56	56.59	0.2673	0.2685	62.15	70.93	76.58	84.48	1.1629	1.1596
Ours-Random	88.83	93.18	30.21	30.74	0.3778	0.3736	76.50	83.78	31.40	23.03	1.0694	1.0583
Ours-RDKit	86.68	91.34	5.46	0.00	0.2667	0.2125	67.72	75.30	21.52	2.66	1.0739	1.0372

Thanks for watching!

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