

VIDY Reading Group Drug Discovery

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GEOLDM

Algorithm 2 Sampling Algorithm of GEOLDM

- 1: **Input:** decoder network \mathcal{D}_{ξ} , denoising network ϵ_{θ}
- 2: $\mathbf{z}_{x,T}, \mathbf{z}_{h,T} \sim \mathcal{N}(\mathbf{0}, I)$
- 3: **for** t in T, T-1, ..., 1 **do**
- 4: $\epsilon \sim \mathcal{N}(0, I)$ {Latent Denoising Loop}
- 5: Subtract center of gravity from ϵ_x in $\epsilon = [\epsilon_x, \epsilon_h]$
- 6: $\mathbf{z}_{t-1} = \frac{1}{\sqrt{1-\beta_t}} (\mathbf{z}_t \frac{\dot{\beta}_t}{\sqrt{1-\alpha_t^2}} \epsilon_{\theta}(\mathbf{z}_t, t)) + \rho_t \epsilon$
- 7: end for
- 8: $\mathbf{x}, \mathbf{h} \sim p_{\xi}(\mathbf{x}, \mathbf{h} | \mathbf{z}_{\mathbf{x},0}, \mathbf{z}_{\mathbf{h},0})$ {Decoding}
- 9: return x, h

☐ About the experiments, how to select an optimal value for T (timestep) to balance the model's performance and computational cost?



GEOLDM

☐ Why is Gaussian distribution chosen in the diffusion model, can it be effectively replaced by alternative distributions?

☐ How does latent modeling in the proposed method contribute to controllable molecule generation?

