



Bias Mitigation in Graph Diffusion Models

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Those who wish to succeed must ask the right preliminary questions. —Aristotle



Bias Mitigation in Graph Diffusion Models

- 1 Graph Diffusion models
- 2 Correct Method
- 3 Result



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Graph Diffusion models

- Given the constraints of graph data scale and network learning capacity, these models truncate the forward diffusion process to enhance performance, preventing it from fully reaching the standard Gaussian distribution.
- However, during sampling, they have to start from the standard Gaussian distribution without employing any specific strategy.
- This mismatch is a critical issue and including exposure bias.



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Graph diffusion models

Model	GDSS	GSDM	HGDM	MOOD
Dataset	Comm.	Enz	QM9	ZINC250k
Type	Edge	Eigen	Edge	Node
SDE	VPSDE	VPSDE	VESDE	VPSDE
$\beta_{\min} \sigma_{\min}$	0.1	0.1	0.1	0.1
$\beta_{\max} \sigma_{\max}$	1.0	1.0	1.0	1.0
u_T	0.7596	0.7596	1.0	0.7596
σ_T^2	0.4231	0.4231	1.0	0.4231

Figure: (a) starting bias

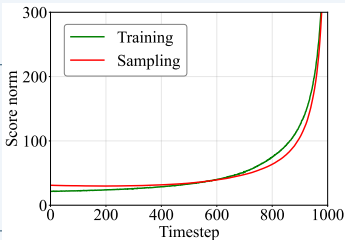


Figure: (b) Baseline

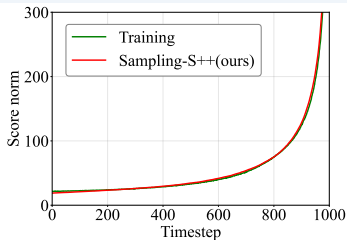


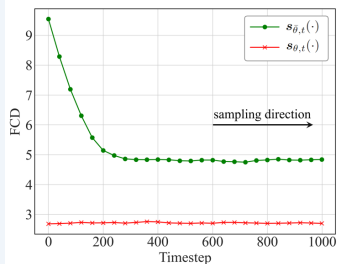
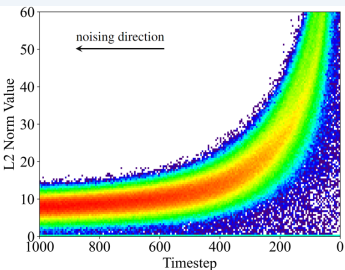
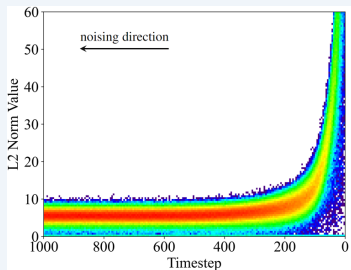
Figure: (c) corrected

$$p(\mathbf{z}_t|\mathbf{x}) = \mathcal{N}\left(\mathbf{z}_t \middle| e^{-\frac{1}{4}t^2(\beta_{\max}-\beta_{\min})} - \frac{1}{2}t\beta_{\min}\mathbf{x}, (1 - e^{-\frac{1}{2}t^2(\beta_{\max}-\beta_{\min})} - t\beta_{\min})\mathbf{I}\right) = \mathcal{N}(u_t\mathbf{x}, \sigma_t^2\mathbf{I}).$$



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Why baselines are truncated?





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How to correct these bias?

- If we known the inference model $\mathbf{s}(\hat{\mathbf{z}}_t, t, \mathbf{w}^*)$, and its β_{\min} and β_{\max} , we can use Langevin sampling to correct the reverse-starting bias. Moreover, we already have a pretrained score network $\mathbf{s}(\hat{\mathbf{z}}_t, t, \mathbf{w}^*) \approx \nabla \log p(\mathbf{z}_t | \mathbf{x})$. This score guides Langevin sampling to obtain samples from the distribution $p(\hat{\mathbf{z}}_T) \approx q(\mathbf{z}_T | \mathbf{x})$:

$$\hat{\mathbf{z}}_T = \hat{\mathbf{z}}_T + \gamma \mathbf{s}(\hat{\mathbf{z}}_T, T, \mathbf{w}^*) + \sqrt{2\gamma} \epsilon$$

Here, we use Tweedie formula and have the following equations,

$$\begin{aligned} \nabla_{\mathbf{z}_t} \log p(\mathbf{z}_t) &= -\frac{\epsilon_t}{\sqrt{1 - \alpha_t}} \\ \mathbf{s} &= -\frac{\mathbf{g}}{\sqrt{1 - \alpha_t}} \end{aligned}$$



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Algorithm

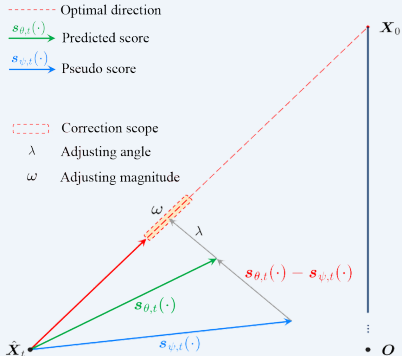
for $j = 1$ to M do

$$\mathbf{s} = \left(\mathbf{s} + \lambda(\mathbf{s} - \mathbf{s}(\mathbf{z}_T, \psi^*, T)) \right) / \omega$$

$$\epsilon \sim \mathcal{N}(\mathbf{0}, \mathbf{I})$$

$$\mathbf{z}_N \leftarrow \mathbf{z}_N + \gamma \mathbf{s} + \sqrt{2\gamma} \epsilon$$

end for





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Ablation

Method	QM9		
	Val. w/o corr. \uparrow	NSPDK MMD \downarrow	FCD \downarrow
GDSS-OC	73.5	0.0157	4.58
GDSS-w/o Correction in sampling	94.8	0.0037	2.65
GDSS-w/o Reverse-starting Alignment	89.8	0.0031	2.01
GDSS-OC-S++	94.0	0.0014	1.67



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Results

Dataset Info.	Community-small Synthetic, $12 \leq V \leq 20$				Enzymes Real, $10 \leq V \leq 125$				Grid Synthetic, $100 \leq V \leq 400$			
	Deg.↓	Clus.↓	Orbit↓	Avg.↓	Deg.↓	Clus.↓	Orbit↓	Avg.↓	Deg.↓	Clus.↓	Orbit↓	Avg.↓
GDSS-OC	0.050	0.132	0.011	0.064	0.052	0.627	0.249	0.309	0.270	0.009	0.034	0.070
GDSS-OC-S++	0.021	0.061	0.005	0.029	0.067	0.099	0.007	0.058	0.105	0.004	0.061	0.066
GDSS-WC	0.045	0.088	0.007	0.045	0.044	0.069	0.002	0.038	0.111	0.005	0.070	0.070
GDSS-WC-S++	0.019	0.062	0.004	0.028	0.031	0.050	0.003	0.028	0.105	0.004	0.061	0.057
HGDM-OC	0.065	0.119	0.024	0.069	0.125	0.625	0.371	0.374	0.181	0.019	0.112	0.104
HGDM-OC-S++	0.021	0.034	0.005	0.020	0.080	0.500	0.225	0.268	0.023	0.034	0.004	0.020
HGDM-WC	0.017	0.050	0.005	0.024	0.045	0.049	0.003	0.035	0.137	0.004	0.048	0.069
HGDM-WC-S++	0.021	0.024	0.004	0.016	0.040	0.041	0.005	0.029	0.123	0.003	0.047	0.058
GSDM-OC	0.142	0.230	0.043	0.138	0.930	0.867	0.168	0.655	1.996	0.0	1.013	1.003
GSDM-OC-S++	0.011	0.016	0.001	0.009	0.012	0.087	0.011	0.037	1.2e-4	0.0	1.2e-4	0.066
GSDM-WC	0.011	0.016	0.001	0.009	0.013	0.088	0.013	0.038	0.002	0.0	0	7.2e-5
GSDM-WC-S++	0.011	0.016	0.001	0.009	0.011	0.086	0.010	0.036	5.0e-5	0.0	1.1e-5	0.066