# PARD: Permutation-invariant AutoRegressive Diffusion for Graph Generation

Lingxiao Zhao, Xueying Ding, Leman Akoglu

## **AR vs Diffusion for Graph Generation**

- Autoregressive approach
  - Simple, efficient, and fast inference
  - Permutation sensitive, sample inefficient
- Diffusion method
  - Permutation invariant, sample efficient
  - Slow inference with ~1000 steps, requiring additional domain-specific features (DiGress)

## How to Get the Full Benefits of Both?

- ???
  - Simple, efficient, and fast inference
  - Permutation invariant, sample efficient



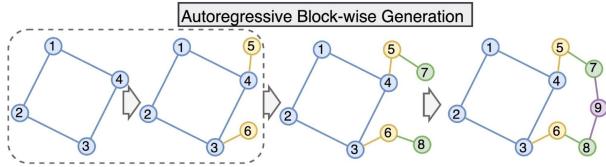


### From AR to PARD

- Why is AR permutation sensitive?
  - Finding unique node/edge ordering is impossible (graph canonization, NP-intermediate)
    Vikraman Arvind, Bireswar Das, and Johannes Köbler. The space complexity of k-tree isomorphism. Springer, 2007.
  - Non-unique, non-deterministic
- However, graphs are not set, as nodes are not completely unordered.
  - Nodes are not "fully equivalent" considering edges.

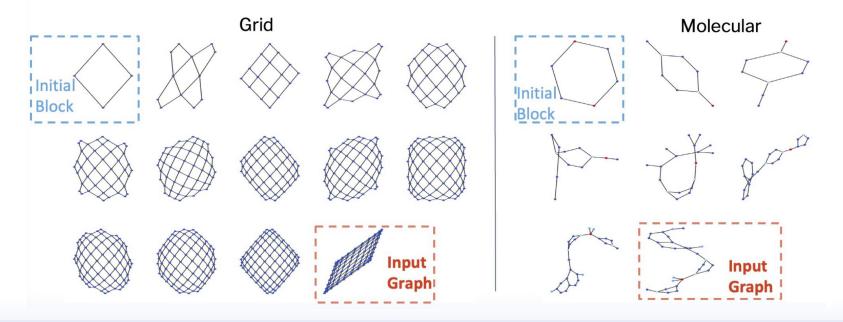
### **Permutation-equivariant Partial Order**

- No unique node order
- Unique **partial** order can be easily defined!
  - Why partial: structurally-equivalent nodes <u>MUST</u> have the same rank/order.
- Structural partial ordering: sequence of blocks
  - Unique, deterministic, permutation-equivariant.



### **The Structural Partial Order**

**Thm.** For any G, structural partial order  $\phi$  is deterministic, unique, and permutation equivariant:  $\phi(\mathbf{P} \star \mathbf{G}) = \mathbf{P} \star \phi(\mathbf{G})$ 



### **Blockwise Autoregression**

• Let block  $\mathcal{B}_j = \{i \in \mathcal{V}(G) | \phi(i) = j\}$  and  $\mathcal{B}_{1:i} := \cup_{j=1}^i \mathcal{B}_j$ , can decompose the joint distribution of G with AR

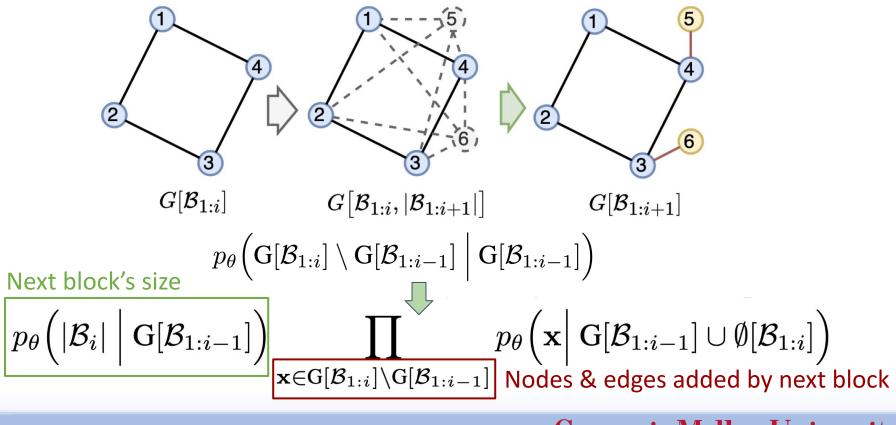
$$p_{\theta}(\mathbf{G}) = \prod_{i=1}^{K_B} p_{\theta} \left( \underbrace{\mathbf{G}[\mathcal{B}_{1:i}] \setminus \mathbf{G}[\mathcal{B}_{1:i-1}]}_{\text{All nodes and edges in block i,}} \middle| \mathbf{G}[\mathcal{B}_{1:i-1}] \right)$$

Each block's conditional distribution is <u>easier</u> to model

**Carnegie Mellon University** 

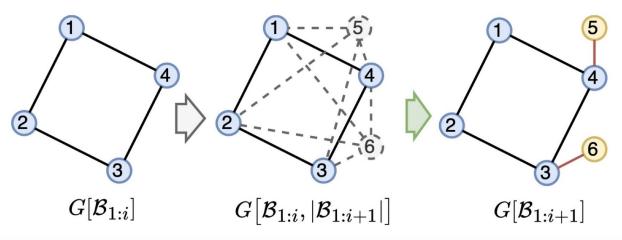
 Permutation invariant under certain condition of block's conditional distribution

### **Modeling Block Conditional Distribution**



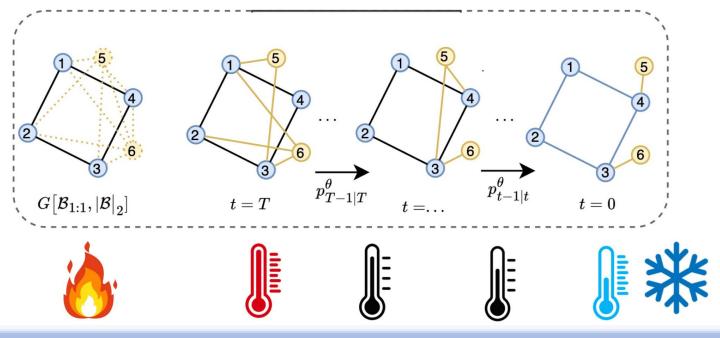
### Issue

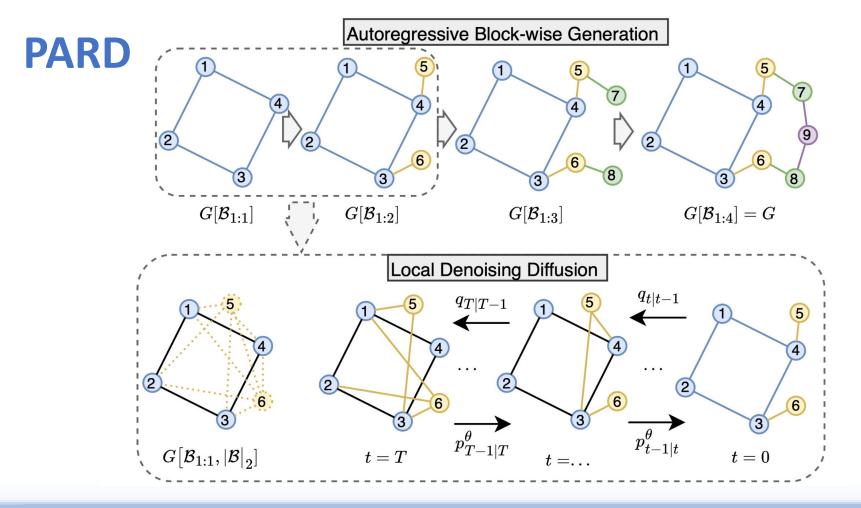
- Thm.: next block prediction cannot be solved directly with <u>any</u> equivariant GNN
  - due to structural equivalences: all dashed edges (middle) will receive SAME prediction



# **Solution: Annealing / Diffusion**

To "increase energy", **add random noise** to nodes edges (heat), then reduce noise (cool) to attain desired target





### **Important Techniques for Training PARD**

- Efficient and expressive architecture
  - PPGN + transformer (reduce memory cost)
- **<u>Parallel</u>** training of diffusion for ALL blocks
  - Similar as causal transformer
  - Non-trivial (for PPGN). See paper for the detail.
- Simple discrete diffusion framework
  - Zhao, Lingxiao, et al. "Improving and Unifying Discrete&Continuous-time Discrete Denoising Diffusion." *arXiv preprint arXiv:2402.03701* (2024).

## **Experiments: SoTA**

Table 1: Generation quality on QM9 with explict hydrogens.

Model	Valid. $\uparrow$	Uni. †	Atom.↑	Mol. $\uparrow$
Dataset (optimal)	97.8	100	98.5	87.0
ConGress	86.7	98.4	97.2	69.5
DiGress (uniform)	89.8	97.8	97.3	70.5
DiGress (marginal)	92.3	97.9	97.3	66.8
DiGress (marg. + feat.)	95.4	97.6	98.1	79.8
PARD (no feat.)	97.5	95.8	98.4	86.1

Model	Validity <b>†</b>	$\mathbf{FCD}\downarrow$	Uni. ↑	Model Size
EDP-GNN	82.97	16.74	99.79	0.09M
GraphEBM	5.29	35.47	98.79	-
SPECTRE	90.20	18.44	67.05	-
GDSS	97.01	14.66	99.64	0.37M
GraphArm	88.23	16.26	99.46	-
DiGress	91.02	23.06	81.23	18.43M
SwinGNN-L	90.68	1.99	99.73	35.91M
Pard	95.23	1.98	99.99	4.1M

Generation quality on MOSES. The top three methods use hard-coded rules

Model	Val. ↑	Uni. ↑	Novel. ↑	<b>Filters ↑</b>	$\mathbf{FCD}\downarrow$	$\mathbf{SNN}\uparrow$	Scaf. ↑
VAE	97.7	99.8	69.5	99.7	0.57	0.58	5.9
JT-VAE	100	100	99.9	97.8	1.00	0.53	10.0
GraphINVENT	96.4	99.8	-	95.0	1.22	0.54	12.7
ConGress	83.4	99.9	<b>96.4</b>	94.8	1.48	0.50	<b>16.4</b>
DiGress	85.7	<b>100</b>	95.0	97.1	1.19	0.52	14.8
Pard	86.8	100	78.2	99.0	1.00	0.56	2.2

### **Ablation**

Table 5: Ablation study on QM9 with varying maximum hops while keeping the total diffusion steps fixed (first two parts). The last part examines the effect of increasing steps for the no AR case.

Setting	No AR	With AR    No AR, † step			R, † steps	
Total diffusion steps	140		140		280	490
Maximum hops	0	1	2	3	0	0
Average number of blocks	1	4.3	5.6	7.75	1	1
Diffusion steps per block	140	32	25	20	280	490
Validity	93.8	97.1	96.7	97.0	94.3	95.2
Uniqueness	96.9	96.5	96.2	96.1	96.5	96.9
Mol stability	76.4	86.1	85.4	86.3	79.3	79.2
Atom Stability	97.7	98.3	98.3	<b>98.4</b>	97.9	98.0

# **Thank You**

Code: <a href="https://github.com/LingxiaoShawn/Pard">https://github.com/LingxiaoShawn/Pard</a>



15