



Explore Deep Graph Generation

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Abstract

We explore deep graph generation from two directions:

- 1) we use CNN GANs to model the whole adjacency matrix directly after sorting the nodes;
- 2) we built upon the very recent Graph Recurrent Attention Networks (GRANs), proposed a graph completeness judger network and improved its attention mechanism.

The first direction works on small grid graphs to some extent but fails to work on large graphs and we analyze its failure.

For the second direction, experiments on the Grid and Protein datasets show that our improved version outperforms the original approach and the completeness judger is effective.

Motivation

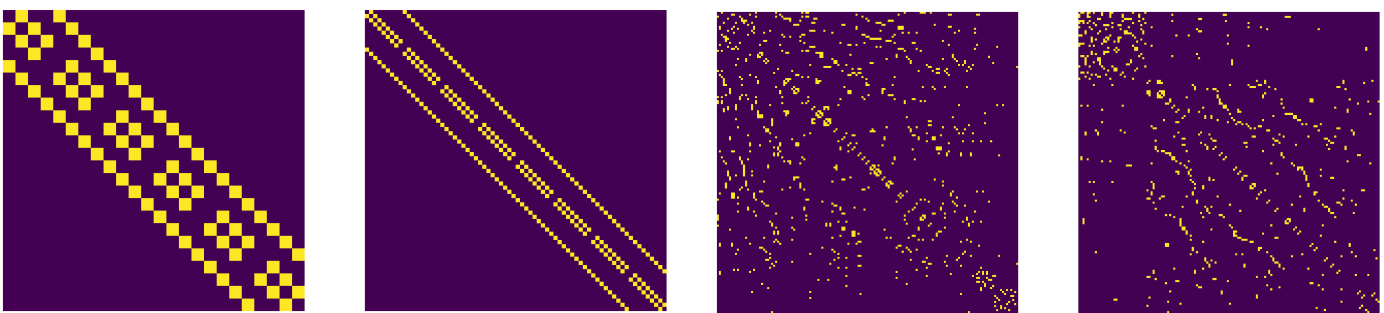
- “What I cannot create, I do not understand.” -- Richard Feynman.
- Twofold advantages: 1) discover new realistic graphs and benefit downstream applications, e.g., drug design, protein study; 2) better null models for network analysis.
- Deep generative models enjoy success in CV and NLP.
- 3 categories: autoregressive, VAEs, GANs.

Dataset

- **Grid:** 100 standard 2D grid graphs. $100 \leq |V| \leq 400$.
- **Protein:** 918 protein graphs. Two nodes (amino acids) are connected if < 6 Angstroms away. $100 \leq |V| \leq 500$.
- Plot of adjacency matrices after sorting nodes:

Grid, default ordering
m = 6 n = 4

Protein, k-core ordering
m = 8 n = 9

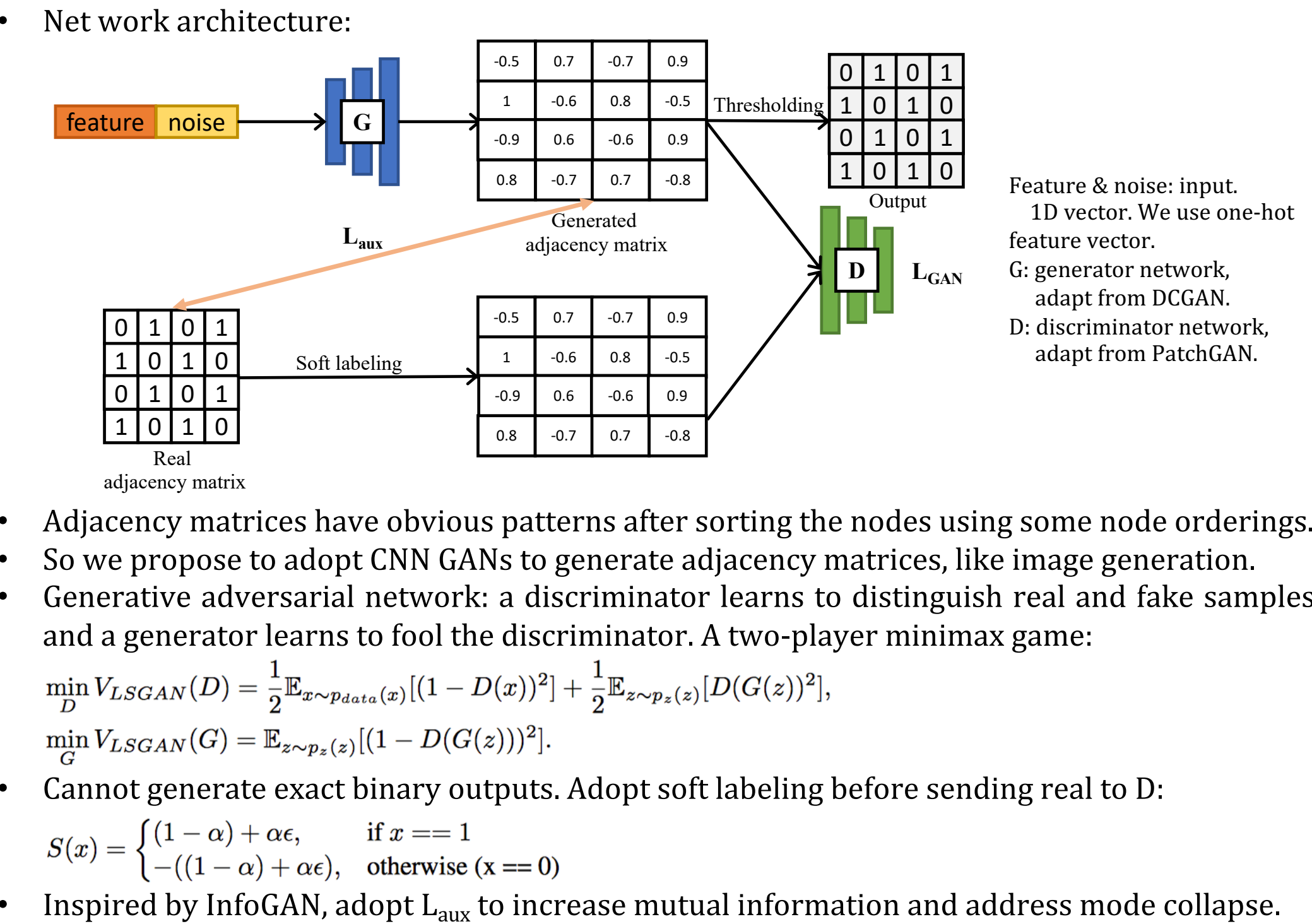


Future work

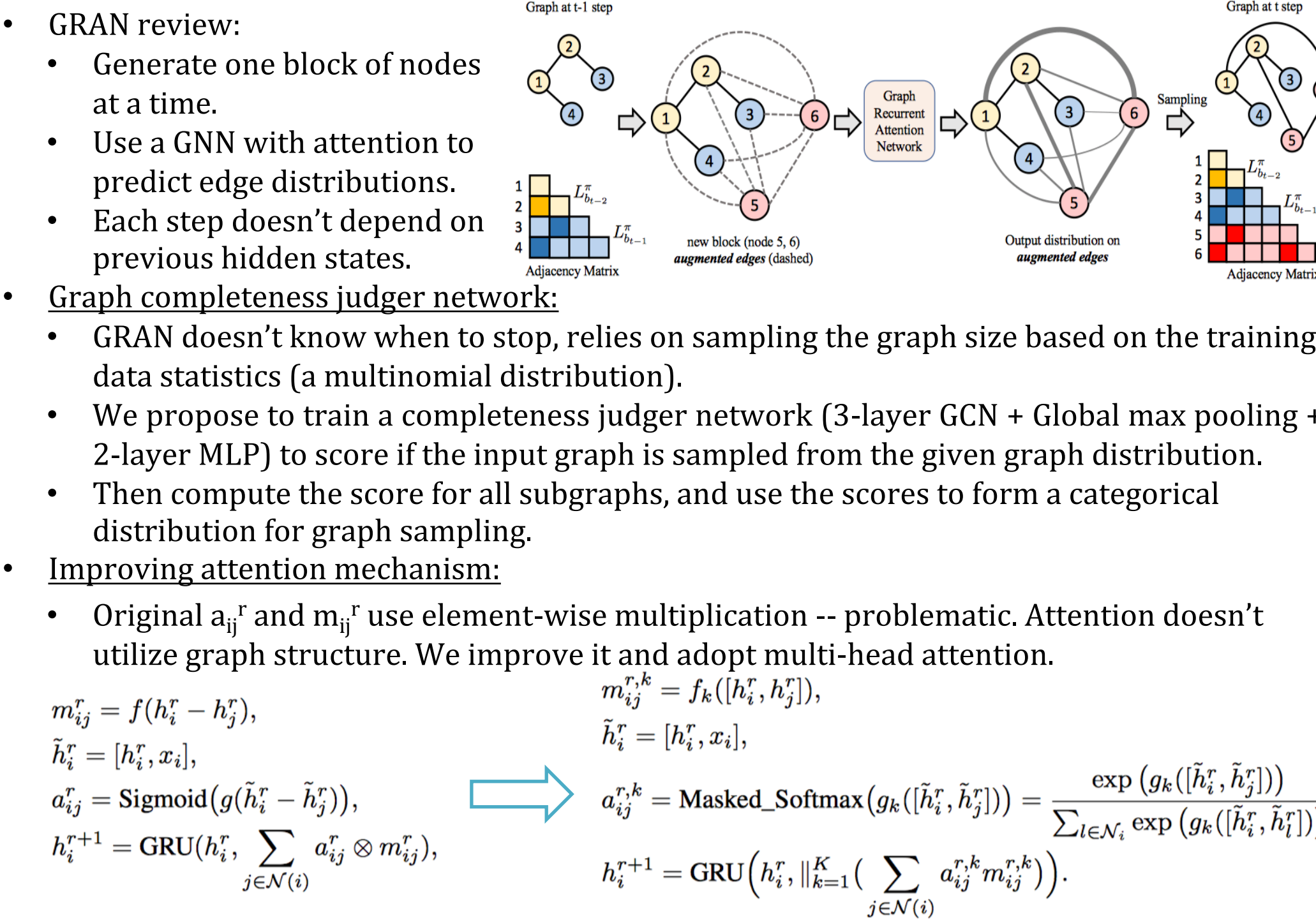
There is still a long way to go on deep generative models for graphs. It's less successful than generative models on images and texts/audios. Generation on graphs are much harder due to complex topological structure.

Because of the inherent limitations of auto-regressive models, though our first GAN approach failed, for future work we think combining the advantages of the two approaches is worthwhile, for example, GANs with a GNN generator and a GNN discriminator.

First direction: CNN GANs on adjacency matrices

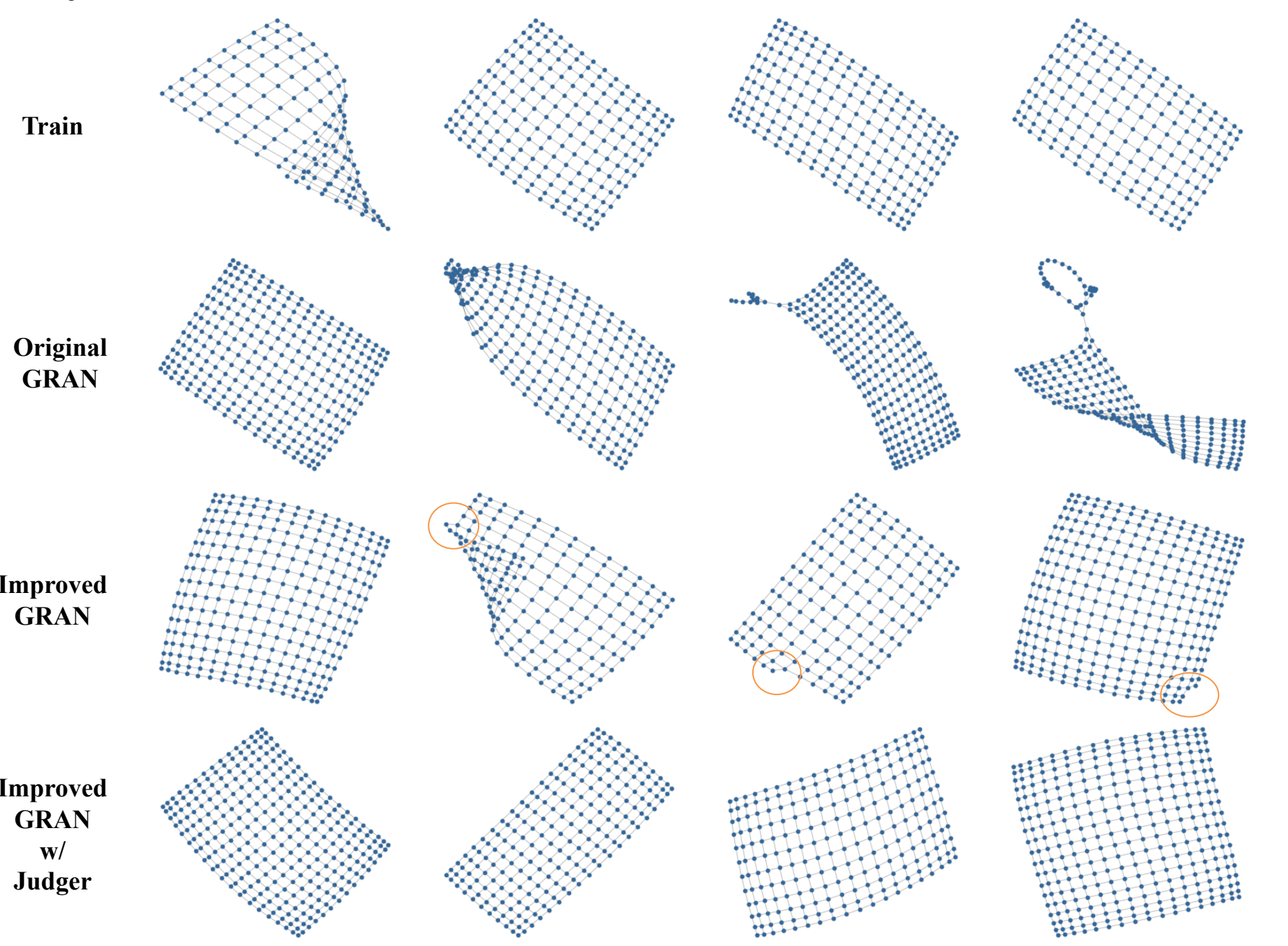


Second direction: Improving GRAN

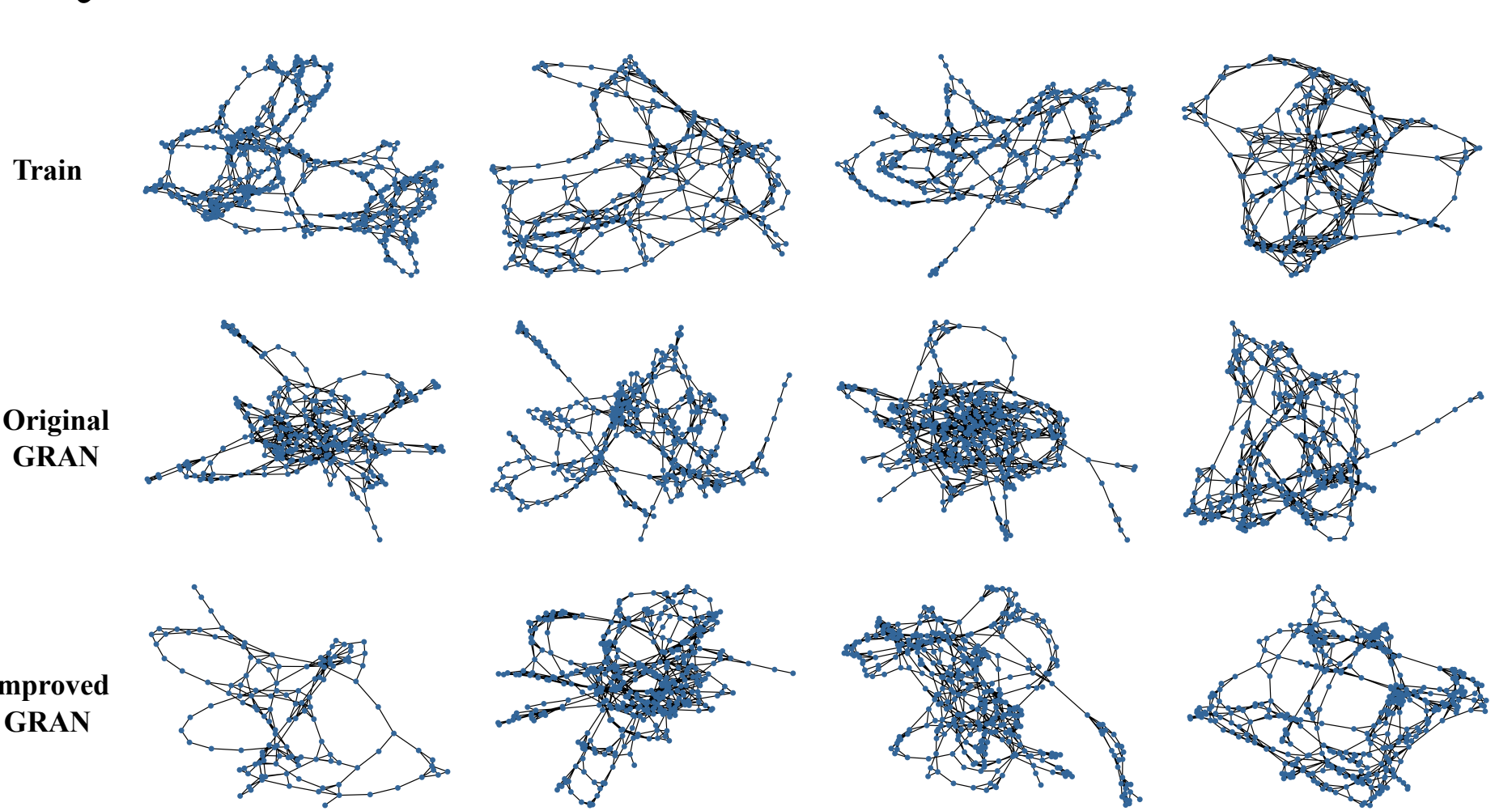


Results

Qualitative results on Grid



Qualitative results on Protein



Maximum mean discrepancy (MMD) over graph statistics

	Grid				Protein				Deg.: degree distribution. Clus.: clustering coefficients. Orbit: the number of 4-node orbits. Spec.: spectrum of graph Laplacian. All metrics the smaller the better.
	Deg.	Clus.	Orbit	Spec.	Deg.	Clus.	Orbit	Spec.	
GRAN	$6.84e^{-4}$	0	$1.45e^{-3}$	$1.50e^{-2}$	$6.91e^{-3}$	$9.30e^{-2}$	$7.75e^{-2}$	$4.74e^{-3}$	
Improved	$1.42e^{-4}$	0	$2.41e^{-4}$	$8.48e^{-3}$	$6.57e^{-3}$	$7.44e^{-2}$	$5.92e^{-2}$	$4.71e^{-3}$	
w/ Judger	$4.33e^{-6}$	$2.71e^{-5}$	$3.19e^{-6}$	$1.35e^{-2}$	-	-	-	-	