Group Meeting - November 12, 2020

Paper review & Research progress

Truong Son Hy *

*Department of Computer Science
The University of Chicago

Ryerson Physical Lab

Content

Content:

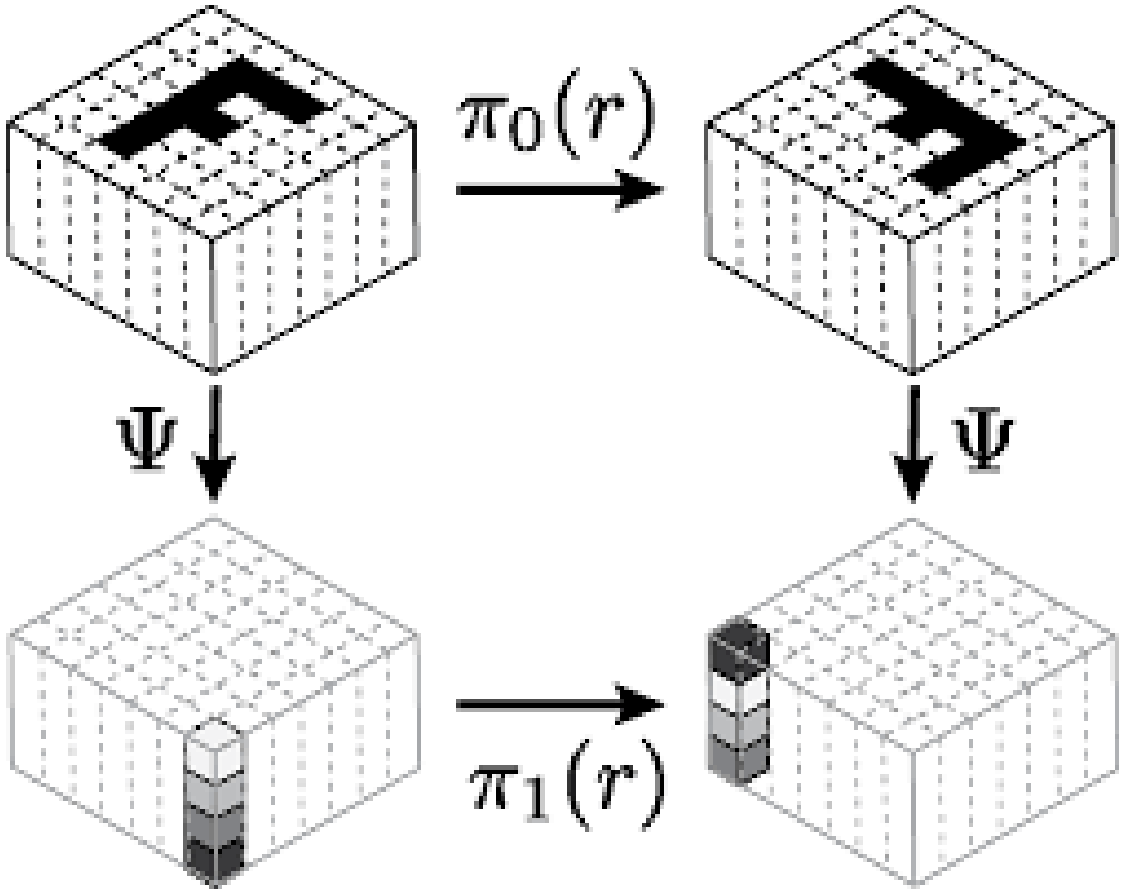
1. Permutation equivariance for graph neural networks
2. A brief overview in the field of graph/molecule generation
3. Current and future work

Slides (search for the date – November 12):
`http://people.cs.uchicago.edu/~hytruongson/Discussions-2020/`

Part 1: Permutation equivariance for graph neural networks

- **Covariant compositional networks for learning graphs** (ICLR 2018 workshop), `https://arxiv.org/pdf/1801.02144.pdf`
- **Predicting molecular properties with covariant compositional networks** (Journal of Chemical Physics), `http://people.cs.uchicago.edu/~risi/papers/CCN-JCP18.pdf`

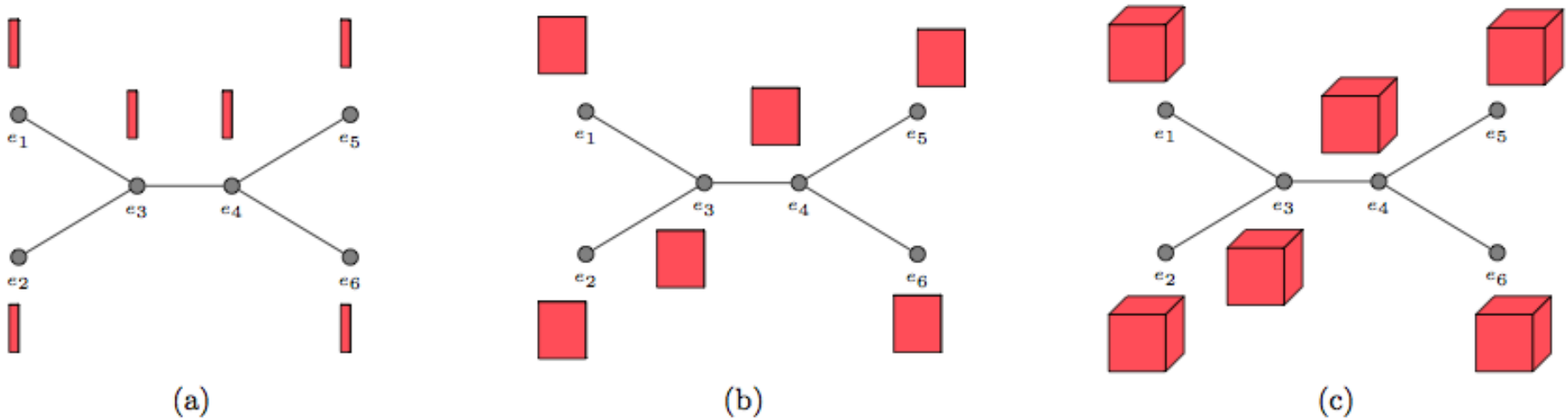
Permutation equivariance on images



Steerable CNNs, Taco S. Cohen, Max Welling,
`https://arxiv.org/abs/1612.08498`

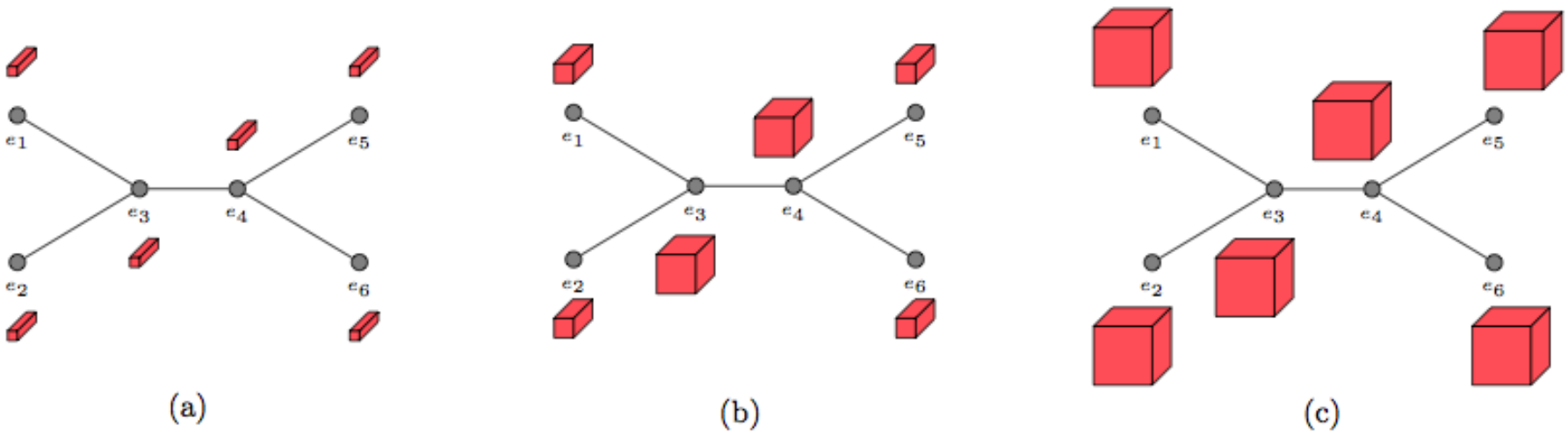
Higher order message passing (1)

Molecular graph of C_2H_4:



Geometry of the tensor activations in zeroth (CCN 0D or MPNN), first (CCN 1D), and second (CCN 2D) order message passing algorithms. Vertices have a vector (zeroth order), matrix (first order), and second order tensor representations corresponding as shown in (a), (b), and (c).

Higher order message passing (2)



Tensor activations for our CCN-2D architecture applied to a C_2H_4 molecular graph. The tensor activations of each vertex in a CCN 2D model are shown after 0, 1, and 2 rounds of message passing in (a), (b) and (c). Here the rows and columns correspond to the size of the receptive field, whereas the depth of the tensor is determined by the number of channels.

Permutation equivariance on graphs (1)

Definition

For a graph G with the comp-net $\mathcal{N}$, and an isomorphic graph G' with comp-net $\mathcal{N}'$, let ν be any neuron of $\mathcal{N}$ and ν' be the corresponding neuron of $\mathcal{N}'$. Assume that:

$$\mathcal{P}_\nu = (e_{p_1}, .., e_{p_m})$$

while:

$$\mathcal{P}_{\nu'} = (e_{q_1}, .., e_{q_m})$$

and let $\pi \in \mathbb{S}_m$ be the permutation that aligns the orderings of the two receptive fields, i.e., for which $e_{q_{\pi(a)}} = e_{p_a}$. We say that $\mathcal{N}$ is **equivariant to permutations** if for any π, there is a corresponding function R_π such that:

$$f_{\nu'} = R_\pi(f_\nu)$$

Permutation equivariance on graphs (2)

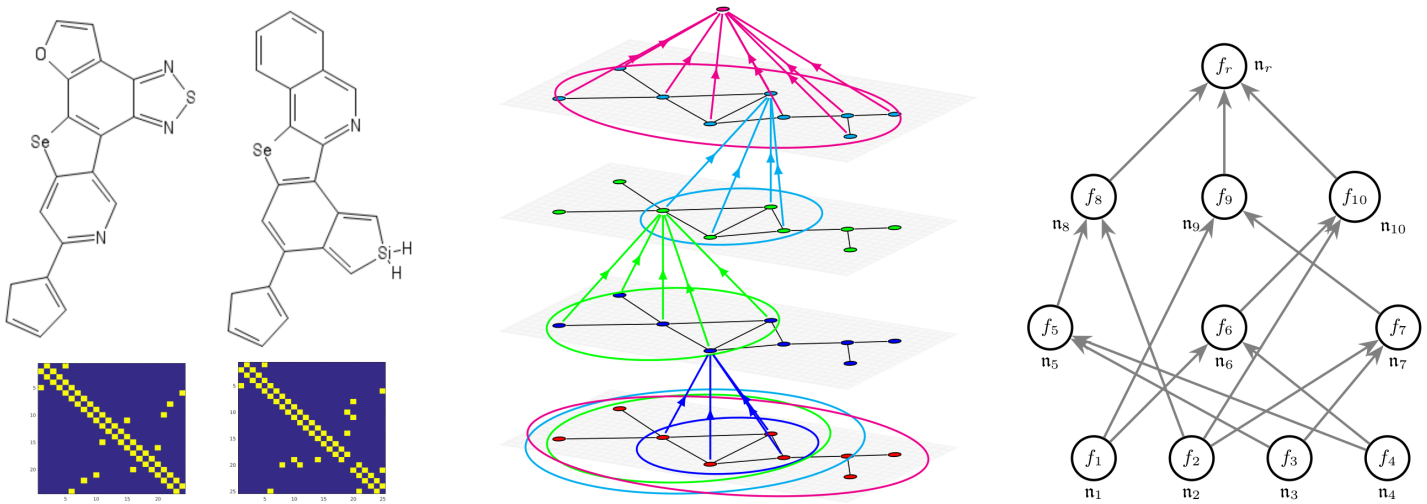
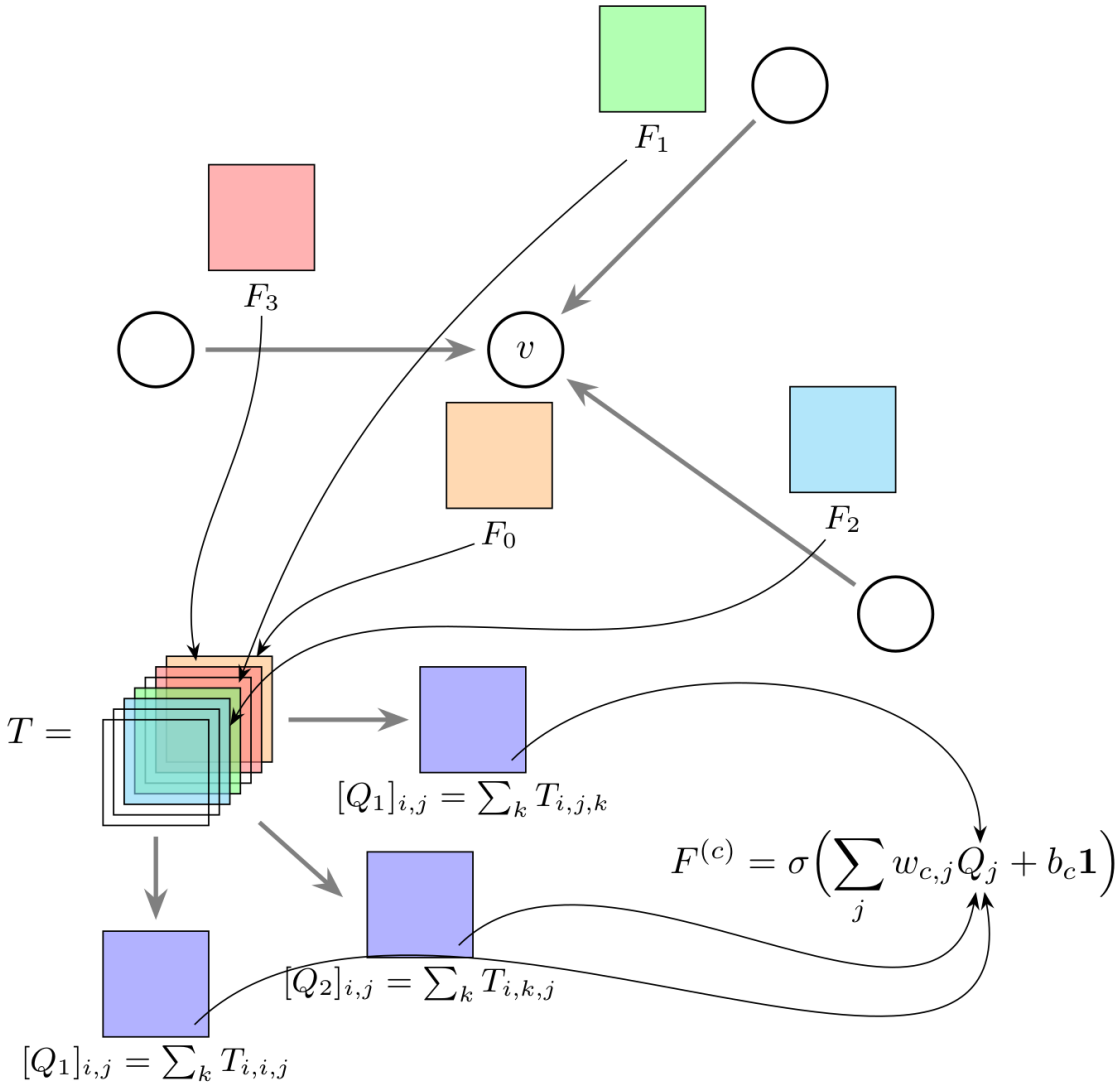


FIG. 1. **Left:** Molecular graphs for $C_{18}H_9N_3OSSe$ and $C_{22}H_{15}NSeSi$ from the Harvard Clean Enery Project (HCEP)[4] dataset with corresponding adjacency matrices. **Center and right:** The comp-net of a graph $\mathcal{G}$ is constructed by decomposing $\mathcal{G}$ into a hierarchy of subgraphs $\{\mathcal{P}_i\}$ and forming a neural network $\mathcal{N}$ in which each "neuron" $\mathfrak{n}_i$ corresponds to one of the $\mathcal{P}_i$ subgraphs, and receives inputs from other neurons that correspond to smaller subgraphs contained in $\mathcal{P}_i$. The center pane shows how this can equivalently be thought of as an algorithm in which each vertex of $\mathcal{G}$ receives and aggregates messages from its neighbors. To keep the figure simple, we only marked aggregation at a single vertex in each round (layer).

Permutation equivariance on graphs (3)



Part 2: Graph/Molecule Generation

1. Traditional graph generation approaches:
   - Erdös-Rényi (ER) Model
   - Stochastic Block Models (SBM)
2. Deep generative models:
   - VAEs
   - GANs
   - Auto-regressive methods (RNNs)

Traditional graph generation approaches (1)

Erdös-Rényi (ER) Model:

$$p(\boldsymbol{A}_{u,v} = 1) = r, \qquad \forall u, v \in \mathcal{V}, \qquad u \neq v$$

where $r \in [0, 1]$ is parameter controlling the density of the graph. Edges are generated **independently**.

Traditional graph generation approaches (2)

Stochastic Block Models (SBM):

- We specify a number γ as the number of different blocks $\{C_1, .., C_\gamma\}$.
- Every node $u \in \mathcal{V}$ has a probability p_i of belonging to block i:

$$p_i = p(u \in \mathcal{C}_i), \qquad \sum_{i=1}^{\gamma} p_i = 1$$

- Block-to-block edge probabilities are specified by a matrix $\boldsymbol{C} \in [0,1]^{\gamma \times \gamma}$ where $C_{i,j}$ is the probability of an edge occuring between a node in block $\mathcal{C}_i$ and a node in block $\mathcal{C}_j$.
- SBM is able to generate graphs that exhibit community structure.

Traditional graph generation approaches (3)

Preferential Attachment (PA) [Albert and Barabási, 2002]:

- **Assumption**: Real-world graphs exhibit **power law** degree distribution. The probability of a node u having degree d_u is:

$$p(d_u = k) \propto k^{-\alpha}, \qquad \alpha > 1$$

Intuitively, the **heavy tailed** power distribution leads to a large number of nodes with small degrees, but a small number of nodes with extremely large degrees.

Traditional graph generation process (4)

Preferential Attachment (PA) [Albert and Barabási, 2002]:

- **Generative process**:
  1. Initialize a fully connected graph with m_0 nodes.
  2. Iteratively add $n - m_0$ nodes to this graph. At iteration t, we add a new node u to the graph, and we connect u to $m < m_0$ existing nodes according to the following distribution:

$$p(\boldsymbol{A}_{u,v} = 1) = \frac{d_v^{(t)}}{\sum_{v' \in \mathcal{V}^{(t)}} d_{v'}^{(t)}}$$

  where $d_v^{(t)}$ denotes the degree of node v at iteration t and $\mathcal{V}^{(t)}$ denotes the set of nodes that have been added to the graph up to iteration t.

- The generation process is **autoregressive** (iterative approach). I think it is similar to Dirichlet Process in which high-degree nodes tend to have more connections.

Deep Generative Models

Traditional methods

Limitation:

1. Rely on a fixed, hand-crafted generation process.
2. Lack the ability to learn a generative model from data.

Generative models

Goal: Design models that can observe a set of graphs $\{\mathcal{G}_1, .., \mathcal{G}_n\}$ and learn to generate graphs with similar characteristics as this training set.

- **All-at-once**: VAEs, GANs.
- **Autoregressive** (generate a graph *incrementally*): LSTM-based language models, GRNN, GRANs, etc.

Variational Autoencoder Approaches (1)

Main components:

1. **Probabilistic encoder** $q_\theta(\boldsymbol{Z}|\mathcal{G})$ defines a distribution over *latent representations*. We specify the latent conditional distribution as $\boldsymbol{Z} \sim \mathcal{N}(\mu_\theta(\mathcal{G}), \sigma_\theta(\mathcal{G}))$, where μ_θ and σ_θ are neural networks that generate the mean and variance parameters for a normal distribution (that we sample latent embeddings $\boldsymbol{Z}$ from).
2. **Probabilistic decoder** $p_\theta(\boldsymbol{A}|\boldsymbol{Z})$, from which we can sample realistic graphs (i.e. adjacency matrices) $\hat{\boldsymbol{A}} \sim p_\theta(\boldsymbol{A}|\boldsymbol{Z})$ by conditioning on a latent variable $\boldsymbol{Z}$.
3. **Prior distribution** $p(\boldsymbol{Z})$ over the latent space. Assume $\boldsymbol{Z} \sim \mathcal{N}(0, 1)$.

Variational Autoencoder Approaches (2)

Motivation

Motivated from the theory of variational inference **[Wainwright and Jordan, 2008]**.

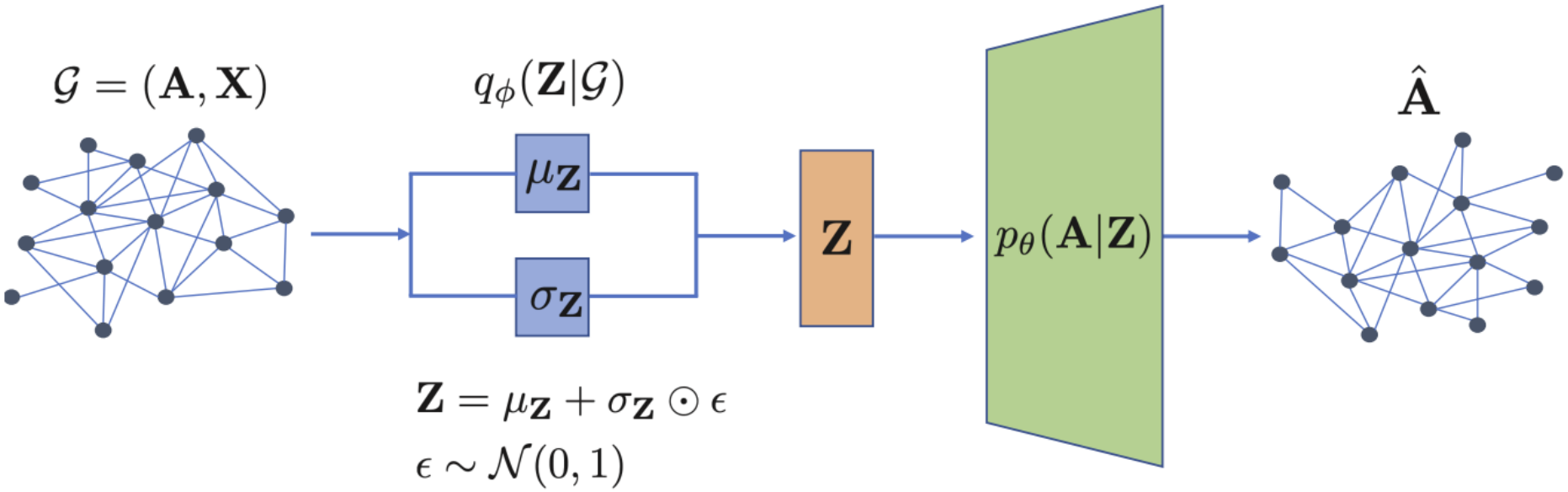
Given a set of training graphs $\{\mathcal{G}_1, .., \mathcal{G}_n\}$, we can train a VAE model by minimizing the evidence likelihood lower bound (ELBO):

$$\mathcal{L} = \sum_{\mathcal{G}_i \in \{\mathcal{G}_1, .., \mathcal{G}_n\}} \mathbb{E}_{q_\theta(\boldsymbol{Z}|\mathcal{G}_i)}[p_\theta(\mathcal{G}_i|\boldsymbol{Z})] - \mathrm{KL}(q_\theta(\boldsymbol{Z}|\mathcal{G}_i)||p(\boldsymbol{Z}))$$

Basic idea:

- Maximize the reconstruction ability of our decoder $\mathbb{E}_{q_\theta(\boldsymbol{Z}|\mathcal{G}_i)}[p_\theta(\mathcal{G}_i|\boldsymbol{Z})]$.
- Minimize the KL-divergence between our posterior latent distribution $q_\theta(\boldsymbol{Z}|\mathcal{G}_i)$ and the prior $p(\boldsymbol{Z})$.

Variational Autoencoder Approaches (3)



Graph Representation Learning, William L. Hamilton (McGill University, 2020) `https://www.cs.mcgill.ca/~wlh/grl_book/`

Node-level Latents – VGAE (1)

Key idea:

- First proposed by **[Kipf and Welling, 2016]**: Variational Graph Autoencoder (VGAE).
- However, the authors proposed VGAE model as an approach to generate node embeddings, but they did not intend it as a generative model to sample new graphs.
- The encoder generates latent representations for each node in the graph.
- The decoder takes pairs of embeddings as input and uses these embeddings to predict the likelihood of an edge between the two nodes.

Node-level Latents – VGAE (2)

The encoder has two separate GNNs to generate mean and variance parameters, conditioned on the input:

$$\mu_{\boldsymbol{Z}} = \text{GNN}_{\mu}(\boldsymbol{A}, \boldsymbol{X}) \in \mathbb{R}^{|\mathcal{V}| \times d}$$

$$\log \sigma_{\boldsymbol{Z}} = \text{GNN}_{\sigma}(\boldsymbol{A}, \boldsymbol{X}) \in \mathbb{R}^{|\mathcal{V}| \times d}$$

Reparameterization trick to sample a set of latent node embeddings:

$$\boldsymbol{Z} = \epsilon \odot \exp(\log(\sigma_{\boldsymbol{Z}})) + \mu_{\boldsymbol{Z}} \in \mathbb{R}^{|\mathcal{V}| \times d}, \qquad \epsilon \sim \mathcal{N}(0, 1)$$

[Kipf and Welling, 2016] employs a simple dot-product decoder:

$$p_{\theta}(\boldsymbol{A}_{u,v} = 1 | \boldsymbol{z}_u, \boldsymbol{z}_v) = \gamma(\boldsymbol{z}_u^T \boldsymbol{z}_v)$$

$$p_{\theta}(\mathcal{G} | \boldsymbol{Z}) = \prod_{(u,v) \in \mathcal{V}^2} p_{\theta}(\boldsymbol{A}_{u,v} = 1 | \boldsymbol{z}_u, \boldsymbol{z}_v)$$

Graph-level Latents – GraphVAE (1)

Proposed by **[Simonovsky and Komodakis, 2018]**:

- GraphVAE only has a single graph - level embedding:

$$\boldsymbol{z}_{\mathcal{G}} \sim \mathcal{N}(\mu_{\boldsymbol{z}_{\mathcal{G}}}, \sigma_{\boldsymbol{z}_{\mathcal{G}}})$$

- In contrast, VGAE defines a posterior distributions for each node.

The encoder:

$$\mu_{\boldsymbol{z}_{\mathcal{G}}} = \text{POOL}_{\mu}(\text{GNN}_{\mu}(\boldsymbol{A}, \boldsymbol{X})) \in \mathbb{R}^{|\mathcal{V}| \times d}$$

$$\sigma_{\boldsymbol{z}_{\mathcal{G}}} = \text{POOL}_{\sigma}(\text{GNN}_{\sigma}(\boldsymbol{A}, \boldsymbol{X})) \in \mathbb{R}^{|\mathcal{V}| \times d}$$

where $\text{POOL} : \mathbb{R}^{|\mathcal{V}| \times d} \to \mathbb{R}^{d}$ denotes a pooling function that maps a matrix of node embeddings $\boldsymbol{Z} \in \mathbb{R}^{|\mathcal{V}| \times d}$ to a graph - level embedding vector $\boldsymbol{z}_{\mathcal{G}} \in \mathbb{R}^{d}$.

Graph-level Latents – GraphVAE (2)

With a Bernoulli distributional assumption, the decoder uses an MLP to map the latent vector $\boldsymbol{z}_{\mathcal{G}}$ to a matrix $\hat{\boldsymbol{A}} \in [0,1]^{|\mathcal{V}|\times|\mathcal{V}|}$ of edge probabilities:

$$\hat{\boldsymbol{A}} = \gamma(\text{MLP}(\boldsymbol{z}_{\mathcal{G}}))$$

The posterior distribution:

$$p_\theta(\mathcal{G}|\boldsymbol{z}_{\mathcal{G}}) = \prod_{(u,v)\in\mathcal{V}\times\mathcal{V}} \hat{\boldsymbol{A}}_{u,v}\boldsymbol{A}_{u,v} + (1-\hat{\boldsymbol{A}}_{u,v})(1-\boldsymbol{A}_{u,v})$$

where $\boldsymbol{A}$ denotes the true adjacency, and $\hat{\boldsymbol{A}}$ denotes the predicted edge probabilities.

Graph-level Latents – GraphVAE (3)

Key challenges:

1. Assumption of independent Bernoulli distributions for each edge $\rightarrow$ Graphical models!
2. Assumption of a fixed number of nodes $\rightarrow$ Specify empirical distribution of graph sizes from the training data.
3. We do not know the correct ordering (graph matching):

$$p_\theta(\mathcal{G}|\boldsymbol{z}_\mathcal{G}) = \max_{\pi \in \Pi} \prod_{(u,v) \in \mathcal{V} \times \mathcal{V}} \hat{\boldsymbol{A}}^\pi_{u,v} \boldsymbol{A}_{u,v} + (1 - \hat{\boldsymbol{A}}^\pi_{u,v})(1 - \boldsymbol{A}_{u,v})$$

Specify a particular ordering function π:

$$p_\theta(\mathcal{G}|\boldsymbol{z}_\mathcal{G}) \approx \prod_{(u,v) \in \mathcal{V} \times \mathcal{V}} \hat{\boldsymbol{A}}^\pi_{u,v} \boldsymbol{A}_{u,v} + (1 - \hat{\boldsymbol{A}}^\pi_{u,v})(1 - \boldsymbol{A}_{u,v})$$

or a bit smarter:

$$p_\theta(\mathcal{G}|\boldsymbol{z}_\mathcal{G}) \approx \sum_{\pi_i \in \{\pi_1, .., \pi_n\}} \prod_{(u,v) \in \mathcal{V} \times \mathcal{V}} \hat{\boldsymbol{A}}^{\pi_i}_{u,v} \boldsymbol{A}_{u,v} + (1 - \hat{\boldsymbol{A}}^{\pi_i}_{u,v})(1 - \boldsymbol{A}_{u,v})$$

Adversarial Approaches (1)

Basic idea of GAN-based generative models:

- Define a trainable **generator network** $g_\theta : \mathbb{R}^d \to \mathcal{X}$ that takes a random seed $\boldsymbol{z} \in \mathbb{R}^d$ as input, and generates realistic (but fake) data samples $\hat{\boldsymbol{x}} \in \mathcal{X}$.
- Define a **discriminator network** $d_\phi : \mathcal{X} \to [0, 1]$ that outputs the probability a given input is fake (distinguishing between real data samples $\boldsymbol{x} \in \mathcal{X}$, and samples generated by the generator $\hat{\boldsymbol{x}} \in \mathcal{X}$).

Both the generator and discriminator optimized jointly in an **adversarial game**:

$$\min_\theta \max_\phi \mathbb{E}_{\boldsymbol{x} \sim p_{\text{data}}(\boldsymbol{x})}[\log(1 - d_\phi(\boldsymbol{x})] + \mathbb{E}_{\boldsymbol{z} \sim p_{\text{seed}}(\boldsymbol{z})}[\log(d_\phi(g_\theta(\boldsymbol{z})))]$$

where $p_{\text{data}}(\boldsymbol{x})$ denotes the empirical distribution of real data samples, and $p_{\text{seed}}(\boldsymbol{z})$ denotes the random seed distribution (e.g. standard multivariate normal).

Adversarial Approaches (2)

[De Cao and Kipf, 2018] (less successful than VAE-based methods) The generator generates a matrix of edge probabilities given a seed vector $\boldsymbol{z}$:

$$\hat{\boldsymbol{A}} = \gamma(\text{MLP}(\boldsymbol{z}))$$

Given this matrix of edge probabilities, we generate a discrete adjacency matrix $\boldsymbol{A} \in \mathbb{Z}^{|\mathcal{V}|\times|\mathcal{V}|}$ by sampling independent Bernoulli variables for each edge $\boldsymbol{A}_{u,v} \sim \text{Bernoulli}(\hat{\boldsymbol{A}}_{u,v})$. The discriminator is any GNN-based graph classification model.

Advantage and Disadvantage:

1. GAN-based models do not require any node ordering (vs. VAE-based models).
2. Training minimax optimization is difficult.

Autoregressive Models (1)

To model edge dependencies, we define the likelihood of a graph given a latent representation $\boldsymbol{z}$ by decomposing the overall likelihood into a set of independent edge likelihoods:

$$p(\mathcal{G}|\boldsymbol{z}) = \prod_{(u,v)\in\mathcal{V}\times\mathcal{V}} p(\boldsymbol{A}_{u,v}|\boldsymbol{z})$$

In autoregressive approach, we assume that edges are generated sequentially and that the likelihood of each edge can be conditioned on the edges that have been previously generated:

$$p(\mathcal{G}|\boldsymbol{z}) = \prod_{i=1}^{|\mathcal{V}|} p(\boldsymbol{L}_{v_i}|\boldsymbol{L}_{v_1}, .., \boldsymbol{L}_{v_{i-1}}, \boldsymbol{z})$$

where $\boldsymbol{L}$ denotes the lower-triangle portion of the adjacency matrix $\boldsymbol{A}$.

Autoregressive Models (2)

[You et al., 2018] GraphRNN:

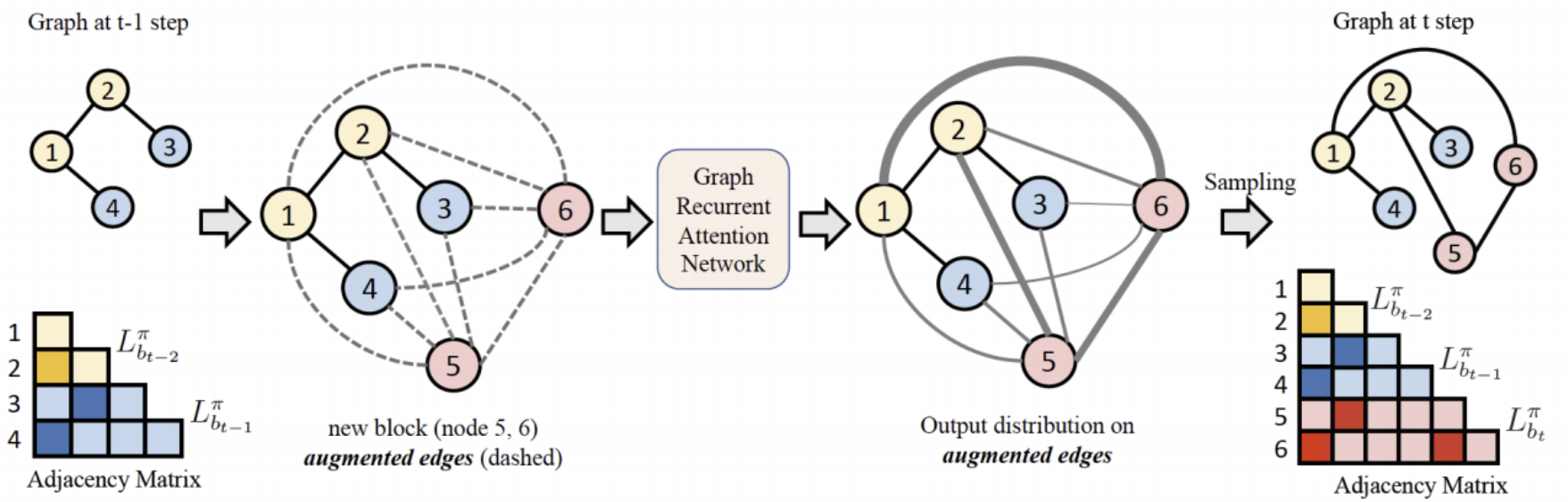
1. Graph-level RNN maintains a hidden state $\boldsymbol{h}_i$, which is updated after generating each row of the adjacency matrix $\boldsymbol{L}_{v_i}$:

$$\boldsymbol{h}_{i+1} = \text{RNN}_{\text{graph}}(\boldsymbol{h}_i, \boldsymbol{L}_{v_i})$$

2. Node-level RNN generates the entries of $\boldsymbol{L}_{v_i}$ in an autoregressive manner. RNN_{node} takes the graph-level hidden state $\boldsymbol{h}_i$ as an initial input, and then sequentially generates the binary values of $\boldsymbol{L}_{v_i}$ assuming a conditional Bernoulli distribution for each entry.

Autoregressive Models (3)

[Lieo et al., 2019] GRAN (graph recurrent attention networks) models the conditional distribution of each row of the adjacency matrix by running a GNN on the graph that has been generated so far.



Autoregressive Models (4)

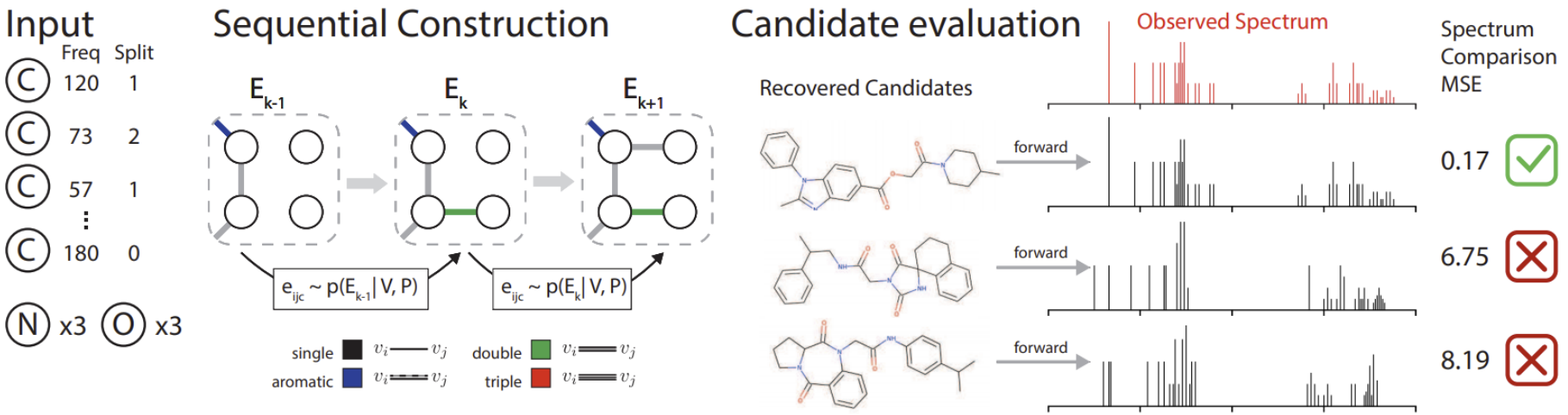


Figure 2: a.) Our input is a molecular formula indicating the number of atoms (vertices) of each element (color) along with per-vertex properties P measured for a subset of those vertices (in this case, carbon nuclei). b.) We sequentially construct a molecule by sampling the next edge (i, j) and edge label c conditioned on the existing edge set as well as vertices V and vertex properties P. c.) We end up with a sampled collection of candidate molecules, which we can then pass back through our forward model to compute their spectra, and validate against the true (observed) spectrum.

Deep imitation learning for molecular inverse problems (NeurIPS 2019), Eric Jonas, `https://papers.nips.cc/paper/8744-deep-imitation-learning-for-molecular-inverse-problems`

Evaluating graph generation (1)

[Liao et al., 2019] The current practice is to analyze different statistics of the generated graphs, and to compare the distribution of statistics for the generated graphs to a test set.

Assume we have a set of graph statistics $\mathcal{S} = (s_1, s_2, .., s_n)$ where each of these statistics $s_{i,\mathcal{G}} : \mathbb{R} \to [0, 1]$ is assumed to define a univariate distribution over $\mathbb{R}$ for a given graph $\mathcal{G}$. For example:

- Degree distribution
- Distribution of clustering coefficients
- Distribution of different motifs or graphlets

Evaluating graph generation (2)

Given a particular statistic s_i, total variance distance betwen the statistics of a test graph $s_{i,\mathcal{G}_{test}}$ and a generated graph $s_{i,\mathcal{G}_{gen}}$:

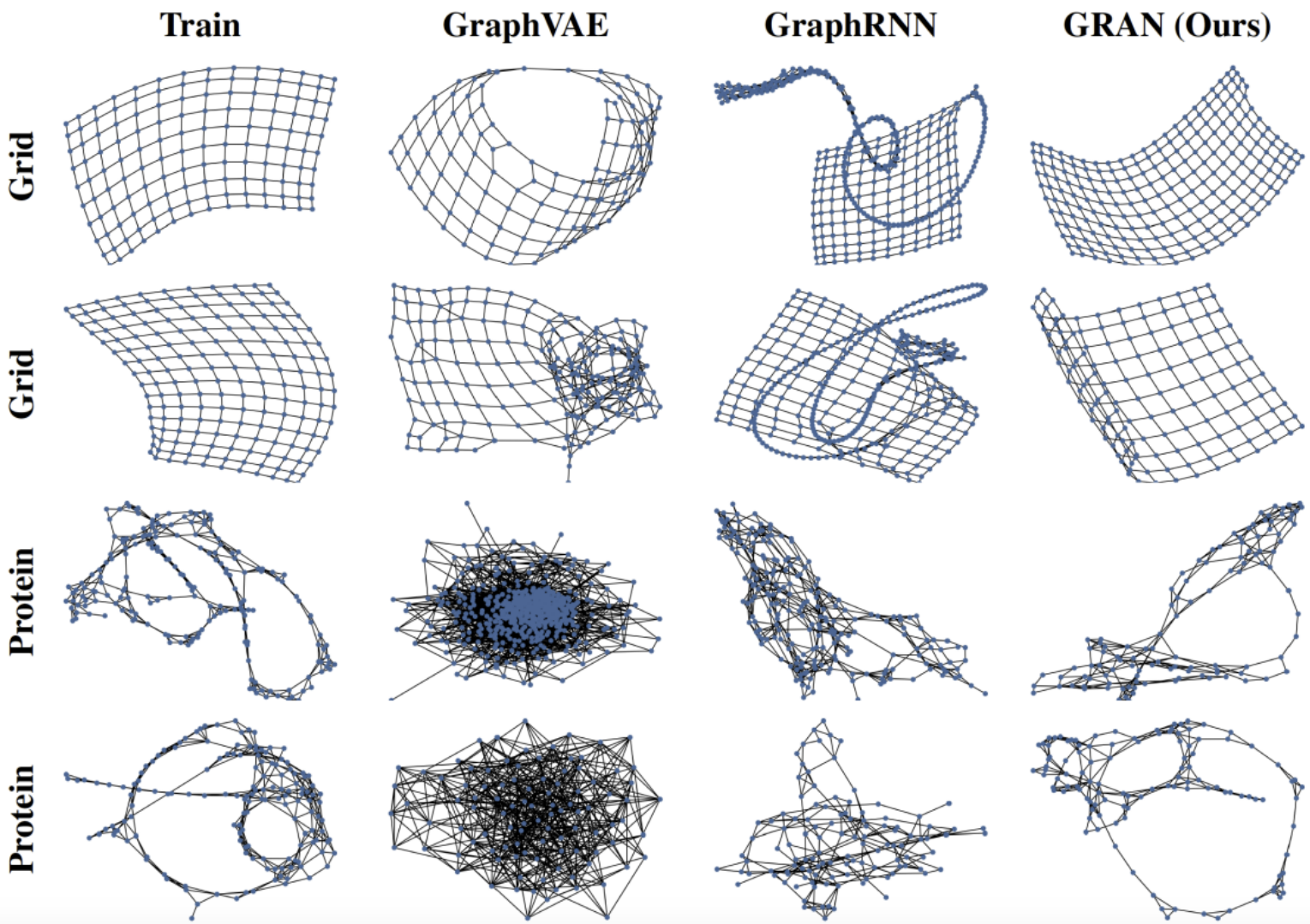
$$d(s_{i,\mathcal{G}_{test}}, s_{i,\mathcal{G}_{gen}}) = \sup_{x \in \mathbb{R}} |s_{i,\mathcal{G}_{test}} - s_{i,\mathcal{G}_{gen}}|$$

To measure the performance, we compute the average pairwise distributional distance between a set of generated graphs and graphs in a test set (e.g. Wasserstein distance).

Molecule generation (special case):

- Graph structures need to be both valid (e.g. chemically stable), and ideally have some desirable properties (e.g. medicinal properties, or solubility).
- Unlike general graph generation, molecule generation can benefit substantially from domain-specific knowledge for both model design and evaluation strategies.

Evaluating graph generation (3)



Part 3: Current and Future work

The general theory of permutation equivarant neural networks and higher order graph variational encoders

Erik Henning Thiede, Truong Son Hy, Risi Kondor

`https://arxiv.org/pdf/2004.03990.pdf`

Link prediction

Method	AUC	AP
SC	84.6 $\pm$ 0.01	88.5 $\pm$ 0.00
DW	83.1 $\pm$ 0.01	85.0 $\pm$ 0.00
GAE	91.0 $\pm$ 0.02	92.0 $\pm$ 0.03
VGAE	91.4 $\pm$ 0.01	92.6 $\pm$ 0.01
GraphStar	95.65 $\pm$?	96.15 $\pm$?
2nd order VGAE (our method)	**96.1** $\pm$ 0.07	**96.4** $\pm$ 0.06

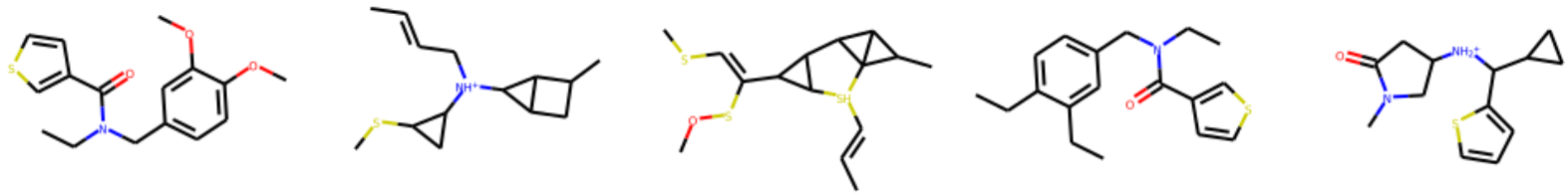
Table 1: Cora link prediction results (AUC & AP)

Method	AUC	AP
SC	80.5 $\pm$ 0.01	85.0 $\pm$ 0.01
DW	80.5 $\pm$ 0.02	83.6 $\pm$ 0.01
GAE	89.5 $\pm$ 0.04	89.9 $\pm$ 0.05
VGAE	90.8 $\pm$ 0.02	92.0 $\pm$ 0.02
GraphStar	**97.47** $\pm$?	**97.93** $\pm$?
2nd order VGAE (our method)	95.3 $\pm$ 0.02	94.3 $\pm$ 0.02

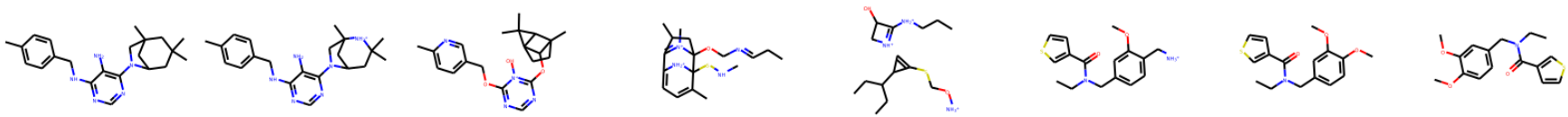
Table 2: Citeseer link prediction results (AUC & AP)

Molecular generation

Generated examples (model trained on ZINC):



Interpolation on the latent:



Brainstorm

Existing problems:

1. The model can generate something-similar-to molecules.
2. Generated examples are still **not** chemical useful.
3. Some sub-structures don't exist in Nature. Why?
4. Computationally expensive.

Potential future direction:

1. Goal-oriented molecular generation to optimize a specific molecular property.
2. Drug discovery datasets? Self-supervised learning?
3. **Looking forward for your suggestions! Thanks.**