

# Constrained Graph Variational Autoencoders for Molecule Design

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<https://qdata.github.io/deep2Read>

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# Motivation

- Generate graphs representing distribution in training data
- Generate graphs that obey hard constraints specific to the task
- generating and optimizing chemical molecules : important real-world application

- Constrained Graph Variational Autoencoder: Graph as input and Graph as output
- encoder-decoder are Gated Graph Neural Nets in a variational autoencoder (VAE)
- incorporate hard domain-specific constraints

Key Challenge: sampling directly from a joint distribution over all configurations of labeled nodes and edges is intractable for reasonably sized graphs. Related Work:

- Uncorrelated generation
- Sequential generation

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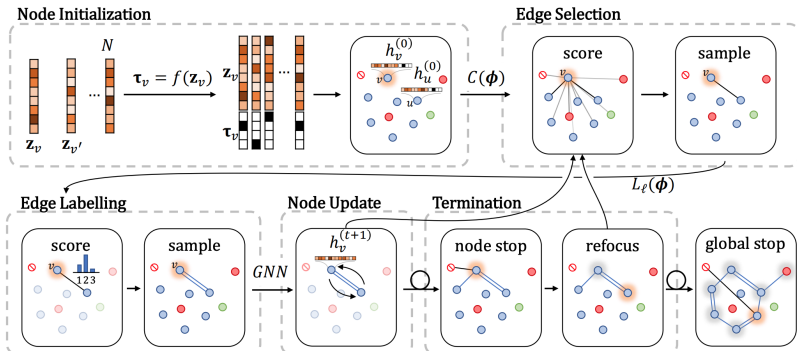
- Uncorrelated generation
- Sequential generation :
  - lose permutation symmetry
  - challenging to marginalize out the construction trace when computing the log-likelihood of a graph in the VAE objective.

## Related Work: Uncorrelated generation

- The Erdos-Rnyi  $G(n, p)$  random graph model
- each edge exists with independent probability  $p$ .
- GraphVAEs : where the decoder emits independent probabilities governing edge and node existence and labels.

- generating a graph from an auxiliary stream of information that imposes an order on construction steps.
- an autoregressive model for graphs without the auxiliary stream.
  - good results, but each decision is conditioned on a full history of the generation sequence
  - stability and scalability problems

# Method





# Method: Generative Model/Decoder

- process is seeded with  $N^1$  vectors  $z_v$
- form a latent specification for the graph to be generated
- generation of edges between nodes:
  - focus : zoom into one node
  - focus: deterministic queue using breadth first search
  - expand: chooses edges to add from the focus node.

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<sup>1</sup> $N$  is an upper bound on the number of nodes in the final graph

## Method: *expand* function

- ideally, make expand condition upon the full history of the generation.
- learned model is likely to learn to reproduce generation traces
- underlying data usually only contains fully formed graphs: trace is an artifact
- this would lead to extremely deep computation graphs, as even small graphs easily have many dozens of edges;
- makes training of the resulting models very hard

## Method: *expand* function

- **Solution:** condition expand only upon the partial graph structure  $G^t$  generated so far
- intuitively, learning how to complete a partial graph without using any information about how the partial graph was generated.

# Method: Node Initialization

- state  $h_v^{(t=0)}$  with each node  $v$
- $z_v$  is drawn from the  $d$ -dimensional standard normal  $N(0, I)$
- $h_v^{(t=0)}$  is the concatenation  $[z_v, \tau_v]$
- $\tau_v$  is an interpretable one-hot vector : the node type.
- $\tau_v$  is derived from  $z_v$  by sampling from the softmax output of a learned mapping  $\tau_v : f(z_v)$ <sup>2</sup>
- The interpretable component of  $h_v^{(t=0)}$ :  $\tau_v$  gives us a means to enforce hard constraints during generation.
- node-level variables, to global representations  $H(t)$  and  $H_{init}$ ,
- also initialize a special stop node to a learned representation  $h_\phi$  for algorithm termination

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<sup>2</sup> $f$  is an NN

# Method: Node Update

- Whenever we obtain a new graph  $G^{(t+1)}$ , discard  $h_v^{(t)}$  and compute new representations  $h_v^{(t+1)}$  for all nodes taking their (possibly changed) neighborhood into account.
- This is implemented using a standard gated graph neural network (GGNN)  $G_{dec}$  for  $S$  steps

$$\mathbf{m}_v^{(0)} = \mathbf{h}_v^{(0)} \quad \mathbf{m}_v^{(s+1)} = \text{GRU} \left[ \mathbf{m}_v^{(s)}, \sum_{v \leftrightarrow u} E_\ell(\mathbf{m}_u^{(s)}) \right] \quad \mathbf{h}_v^{(t+1)} = \mathbf{m}_v^{(S)}$$

- the sum runs over all edges in the current graph and  $E$  is an edge-type specific neural network
- since  $h_v^{(t+1)}$  is computed from  $h_v^{(0)}$  rather than  $h_v^{(t)}$ , the representation  $h_v^{(t+1)}$  is independent of the generation history of  $G^{(t+1)}$

# Method: Edge Selection and Labeling

- first pick a focus node  $v$  from our queue
- function `expand` then selects edges  $v \overset{l}{\leftrightarrow} u$  from  $v$  to  $u$  with label  $l$  as follows.
- For each non-focus node  $u$ , we construct a feature vector where  $d_{v,u}$  is the graph distance between  $v$  and  $u$ .
- We use these representations to produce a distribution over candidate edges:

$$p(v \overset{l}{\leftrightarrow} u | \phi_{v,u}^{(t)}) = p(l | \phi_{v,u}^{(t)}, v \overset{l}{\leftrightarrow} u) \cdot p(\overset{l}{\leftrightarrow} u | \phi_{v,u}^{(t)}). \quad (1)$$

- The factors are calculated as softmax outputs from neural networks  $C$  (determining the target node for an edge) and  $L$  (determining the type of the edge):

$$p(v \leftrightarrow u | \phi_{v,u}^{(t)}) = \frac{M_{v \leftrightarrow u}^{(t)} \exp[C(\phi_{v,u}^{(t)})]}{\sum_w M_{v \leftrightarrow w}^{(t)} \exp[C(\phi_{v,w}^{(t)})]}, \quad p(l | \phi_{v,u}^{(t)}) = \frac{m_{v \overset{l}{\leftrightarrow} u}^{(t)} \exp[L_l(\phi_{v,u}^{(t)})]}{\sum_k m_{v \overset{k}{\leftrightarrow} u}^{(t)} \exp[L_k(\phi_{v,u}^{(t)})]}.$$

- $M(t)v \overset{u}{\leftarrow}$  and  $m(t)v \overset{l}{\leftarrow} u$  are binary masks that forbid edges that violate constraints.
- New edges are sampled from these distributions
- any nodes that are connected to the graph for the first time are added to the focus queue.
- only consider undirected edges in this paper, extension to directed graphs

## Method: Generative: Termination

- keep adding edges to a node  $v$  using `expand` and  $G_{dec}$  until an edge to the stop node is selected.
- Node  $v$  then loses focus and becomes closed (mask  $M$  ensures that no further edges will ever be made to  $v$ ).
- The next focus node is selected from the focus queue.
- a single connected component is grown in a breadth-first manner.
- Edge generation continues until the queue is empty



## Method: training the generative model: Encoder

- The encoder of our VAE is a GGNN  $G_{enc}$  that embeds each node in an input graph  $G$  to a diagonal normal distribution in  $d$ -dimensional latent space parametrized by mean  $\mu_v$  and standard deviation  $\sigma_v$  vectors.
- The latent vectors  $z_v$  are sampled from these distributions
- VAE regularizer term measuring the KL divergence between the encoder distribution and the standard Gaussian prior:

$$L_{latent} = \sum_{v \in G} \text{KL}(N(\mu, \text{diag}_{\sigma_v}^2) \| N(0, I)) \quad (2)$$

# Training the Decoder

- decoder: generative procedure described previously
- condition generation on a latent sample from the encoder distribution during training

# Node Initialization

- first sample a node specification  $z_v$  for each node  $v$
- independently for each node generate the label  $\tau_v$  using the learned function  $f$ .
- The probability of re-generating the labels  $\tau^*_v$  observed in the encoded graph is given by a sum over node permutations

$$p(\mathcal{G}^{(0)} | \mathbf{z}) = \sum_{\mathcal{P}} p(\boldsymbol{\tau} = \mathcal{P}(\boldsymbol{\tau}^*) | \mathbf{z}) > \prod_v p(\tau_v = \tau^*_v | \mathbf{z}_v).$$

- This inequality provides a lower bound given by the single contribution from the ordering used in the encoder

# Edge Selection and Labelling

- During training, provide supervision on the sequence of edge additions based on breadth-first traversals of each graph in the dataset  $D$ .
- to learn a distribution over graphs (and not graph generation traces), we would need to train with an objective that computes the log-likelihood of each graph by marginalizing over all possible breadth-first traces.
- computationally intractable: only compute a Monte-Carlo estimate of the marginal on a small set of sampled traces.
- expand model is not conditioned on full traces, and instead only considers the partial graph generated so far.

# Edge Selection and Labeling

- Jensen's inequality to show that the log-likelihood of a graph  $G$  is loosely lower bounded by the expected log-likelihood of all the traces  $\Pi$  that generate it.

$$\log p(G | \mathcal{G}^{(0)}) = \log \sum_{\pi \in \Pi} p(\pi | \mathcal{G}^{(0)}) \geq \log(|\Pi|) + \frac{1}{|\Pi|} \sum_{\pi \in \Pi} \log p(\pi | \mathcal{G}^{(0)})$$

- decompose each full generation trace  $\pi \in \Pi$  into a sequence of steps of the form  $(t, v, \epsilon)$ , where  $v$  is the current focus node and  $\epsilon = v/u$  is the edge added at step  $t$ :

$$\log p(\pi | \mathcal{G}^{(0)}) = \sum_{(t,v,\epsilon) \in \pi} \left\{ \log p(v | \pi, t) + \log p(\epsilon | \mathcal{G}^{(t-1)}, v) \right\}$$

# Edge Selection and Labeling

- first term corresponds to the choice of  $v$  as focus node at step  $t$  of trace  $\pi$ .
- focus function is fixed: this choice is uniform in the first focus node and then deterministically follows a breadth-first queuing system.
- A summation over this term thus evaluates to the constant  $\log(1/N)$ .

# Edge Selection and Labeling

- the second term only conditioned on the current graph (and not the whole generation history  $G^{(0)} \dots G^{(t-1)}$ ).
- consider the set of generation states  $S$  of all valid state pairs  $s = (G^{(t)}, v)$  of a partial graph  $G^{(t)}$  and a focus node  $v$ .
- We use  $|s|$  to denote the multiplicity of state  $s$  in  $\prod$ , i.e., the number of traces that contain graph  $G^{(t)}$  and focus on node  $v$ .
- Let  $E_s$  denote all edges that could be generated at state  $s$  (the edges from the focus node  $v$  that are present in the graph  $G$  from the dataset, but are not yet present in  $G^{(t)}$ .)

# Edge Selection and Labeling

- Then, each of these appears uniformly as the next edge to generate in a trace for all  $|s|$  occurrences of  $s$  in a trace from  $\Pi$
- rearrange a sum over paths into a sum over steps

$$\begin{aligned}\frac{1}{|\Pi|} \sum_{\pi \in \Pi} \sum_{(t,v,\epsilon) \in \pi} \log p(\epsilon | s) &= \frac{1}{|\Pi|} \sum_{s \in \mathcal{S}} \sum_{\epsilon \in \mathcal{E}_s} \frac{|s|}{|\mathcal{E}_s|} \log p(\epsilon | s) \\ &= \mathbb{E}_{s \sim \Pi} \left[ \frac{1}{|\mathcal{E}_s|} \sum_{\epsilon \in \mathcal{E}_s} \log p(\epsilon | s) \right]\end{aligned}$$

- $|s|/|\Pi|$ : the probability of observing state  $s$  in a random draw from all states in  $\Pi$
- $L_{recon} = \sum_{G \in \mathcal{D}} \log[p(G|G^{(0)}) \cdot p(G^{(0)}|z)]$



# Optimizing Graph Properties

- perform (local) optimization of these graphs with respect to some numerical property,  $Q$ .
- gradient ascent in the continuous latent space using a differentiable gated regression model  
 $R(z_v) = \sum_v \sigma(g_1(z_v))g_2(z_v)$ , where  $g_1$  and  $g_2$  are neural networks
- During training, L2 distance loss  $L_Q$  between  $R(z_v)$  and the labeled properties  $Q$ .
- at test time, we can sample an initial latent point  $z_v$  and then use gradient ascent to a locally optimal point  $z_v^*$  subject to an L2 penalty that keeps the  $z_v^*$  within the standard normal prior of the VAE.
- Decoding from the point  $z_v^*$  then produces graphs with an optimized property  $Q$ .

$$L = L_{recon.} + \lambda_1 L_{latent} + \lambda_2 L_Q, \quad (3)$$

## Datasets

- QM9: 134k samples with 9 atoms, the molecules in this dataset only reflect basic structural constraints.
- ZINC: 250k drug compounds 23 atoms, molecules are bigger (23 heavy atoms) and structurally more complex than the molecules in QM9.
- CEPDB: 250k organic molecules 28 heavy atoms, structurally very complex, containing six to seven rings each

In the encoder, molecular graphs are presented with nodes annotated with onehot vectors  $\tau_v$  indicating their atom type and charge.

- edge types: single, double, triple covalent bonds
- Encoder Inputs: node one hot vector that indicate atom type and charge

# Experiments: Valency Masking

- valency : the number of bonds that that atom can make in a stable molecule
- valency rules : some atoms can only make certain types of bonds
- valency of 2: 2 bonds
- Mask: the number of bonds  $b_v$  never exceeds the valency  $b_v^*$  of the node
- if bonds less than the valency: add hydrogen atoms
- this generates valid molecules: parse the graph to SMILES string using RDKitParser
- also handle avoidance of edge duplication and self loops

$$M_{v \leftrightarrow u}^{(t)} = \mathbb{1}(b_v < b_v^*) \times \mathbb{1}(b_u < b_u^*) \times \mathbb{1}(\text{no } v \leftrightarrow u \text{ exists}) \times \mathbb{1}(v \neq u) \times \mathbb{1}(u \text{ is not closed})$$

- DeepGAR: DeepAutoregressive model
- GrammarVAE
- ChemVAE
- GraphVAE
- random graph models

train on the three datasets and then sample 20k molecules from the trained models

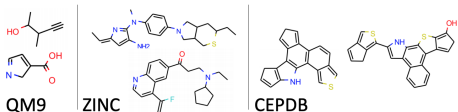
- Novelty: fraction of molecules not appearing in the training data
- syntactic validity
- uniqueness: ratio of sample set size before and after deduplication of identical molecules
- average atom type
- average bond type
- the average number of 3-, 4-, 5-, and 6-membered cycles in each molecule.

# Results

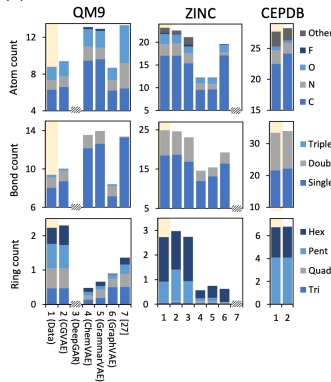
(a)

	Measure	2: CGVAE	3: [21]	4: [8]	5: [17]	6: [29]	7: [27]
QM9	% valid	100	-	10.00	30.00	61.00	98.00
	% novel	94.35	-	90.00	95.44	85.00	100
	% unique	98.57	-	67.50	9.30	40.90	99.86
ZINC	% valid	100	89.20	17.00	31.00	14.00	-
	% novel	100	89.10	98.00	100	100	-
	% unique	99.82	99.41	30.98	10.76	31.60	-
CEPDB	% valid	100	-	8.30	0.00	-	-
	% novel	100	-	90.05	-	-	-
	% unique	99.62	-	80.99	-	-	-

(c)









(b)





# Results: Directed Molecule Generation

- predict the Quantitative Estimate of Drug-Likeness (QED) directly from latent space
- generate molecules with very high QED values by performing gradient ascent in the latent space using the trained QED-scoring network.

						
Pred. QED	0.5686	0.6685	0.7539	0.8376	0.9013	0.9271
Real QED	0.5345	0.6584	0.7423	0.8298	0.8936	0.9383