Deep Generative Models for Graphs VAEs, GANs, and Reinforcement Learning for *de novo* drug discovery

Nicola De Cao

The University of Edinburgh and University of Amsterdam

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The drug design processes

Which problem do we want to solve?

• Drug design is the process of finding new drugs



- The first step is Drug Discovery
 - screening large compound libraries
 - designing of new unknown molecules (de novo)

How others proposed to study the problem?

- Generating SMILES representations [Gómez-Bombarelli et al., 2016]
- Generating labeled graphs [Simonovsky and Komodakis, 2018]

How do we study the problem?

- Using labeled graphs
- Likelihood-based vs. likelihood-free methods (VAE vs. GAN)
- Biasing the process using reinforcement learning

Background

Variational Auto-Encoders

Likelihood-based generative process [Kingma and Welling, 2013]



Image credit [Hafner, 2018]



Figure: Graphical model of a simple VAE.

Trained to maximize the log-evidence:

$$\log p_{ heta}(\mathbf{x}^{(i)}) = \log \int p_{ heta}(\mathbf{x}^{(i)}, \mathbf{z}) \, d\mathbf{z}$$

Training VAEs II



Figure: Graphical model of a simple VAE.

Evidence Lower Bound (ELBO)

Optimizing a lower bound of the loss makes the problem feasible:

$$\log p_{\theta}(\mathbf{x}^{(i)}) \geq \mathbb{E}_{q_{\phi}(\mathbf{z}|\mathbf{x}^{(i)})} \left[\log p_{\theta}(\mathbf{x}^{(i)}|\mathbf{z}) \right] - D_{KL} \left[\left. q_{\phi}(\mathbf{z}|\mathbf{x}^{(i)}) \parallel p_{\theta}(\mathbf{z}) \right. \right]$$

Likelihood-free generative process [Goodfellow et al., 2014]



Figure: Schema of GAN architecture.

Originally proposed loss:

$$\min_{\theta} \max_{\phi} \mathbb{E}_{\mathbf{x} \sim p_{data}(\mathbf{x})} \left[\log D_{\phi}(\mathbf{x}) \right] + \mathbb{E}_{\mathbf{z} \sim p_{\mathbf{z}}(\mathbf{z})} \left[\log (1 - D_{\phi}(G_{\theta}(\mathbf{z}))) \right]$$

but there are **better alternatives**:

- f-GAN [Nowozin et al., 2016];
- WGAN [Arjovsky et al., 2017];
- WGAN-GP [Gulrajani et al., 2017] (used in this work).

Can we train a **non-differentiable** generative process?



Figure: Reinforcement Learning loop schema.

How to learn a RL policy?

Deep deterministic policy gradient [Lillicrap et al., 2016]



Off-policy deterministic policy gradient

Update θ according to [Silver et al., 2014]:

$$\mathcal{L}(\mu_{ heta}) = \mathbb{E}_{s \sim
ho, s = \mu_{ heta}(s)} \left[Q_{\phi}(s, a)
ight]
onumber \
abla_{ heta} \mathcal{L}(\mu_{ heta}) = \mathbb{E}_{s \sim
ho, s = \mu_{ heta}(s)} \left[
abla_{s} Q_{\phi}(s, a) \
abla_{ heta} \mu_{ heta}(s)
ight]$$

and ϕ with:

$$\mathcal{L}(Q_{\phi}) = \mathbb{E}_{s \sim
ho, oldsymbol{a} = \mu_{ heta}(s)} \left[\| Q_{\phi}(s, oldsymbol{a}) - r(s, oldsymbol{a}) \|^2
ight]$$

Models

Vectorial representation of graphs I



Figure: The molecule (a) is represented as an labeled graph (b) which can be encoded into an adjacency tensor A and an annotation matrix X.

Vectorial representation of graphs II



Vectorial representation of graphs III



Technically:

$$(f*g)(t) = \int_{\mathbb{R}^n} f(\tau)g(t-\tau)d\tau$$

but in practice we do discrete convolutions:

$$(f * g)[n] = \sum_{m \in \mathbb{S}} f(m)g(n-m)$$

Graph Convolutional Networks II



Figure: Graph convolution on an image.

Graph Convolutional Networks III



- On images the topology is regular and neighbours are pixels
- On graphs the topology is arbitrary and neighbours are nodes

Edge-type-conditioned convolutions based on Relational-GCN [Schlichtkrull et al., 2018]:

$$\mathbf{h}_i^{(\ell+1)} = \tanh\left(f_s^{(\ell)}(\mathbf{h}_i^{(\ell)}, \mathbf{x}_i) + \sum_{j=1}^N \sum_{y=1}^{|\mathcal{X}_{\mathcal{E}}|} \frac{1}{|\mathcal{N}_i|} \, \mathbf{A}_{ijy} \, f_y^{(\ell)}(\mathbf{h}_j^{(\ell)}, \mathbf{x}_j)\right) \;,$$

and following [Li et al., 2016], we define a graph level representation vector as

$$\mathbf{h}_{\mathcal{G}} = \tanh\left(\sum_{i=1}^{N} \sigma\left(f_{g}\left(\mathbf{h}_{i}^{(L)}, \mathbf{x}_{i}\right)\right) \odot \tanh\left(f_{r}\left(\mathbf{h}_{i}^{(L)}, \mathbf{x}_{i}\right)\right)\right).$$

Molecular graph VAE



The reconstruction loss is a sum of two categorical cross entropy losses.

Molecular graph GAN



From generator to discriminator with **differentiable sampling** [Jang et al., 2017].

Molecular graph GAN with RL



Architecture from our previous work MolGAN [De Cao and Kipf, 2018]

Experiments

Which questions we would like to answer?

- likelihood-based vs. likelihood-free (VAEs vs. GANs)
- the effect of RL towards chemical objectives
- is generating a graph better than a SMILES representation?

Experiments on QM9 [Ramakrishnan et al., 2014].

VAEs train an encoder!



- VAE objective: reconstruction loss and divergence
- RL objective: sampled molecules should maximize a score

There is a mismatch between these two!

Synthetic accessibility score (SAS) distributions I



Figure: WGAN matches the data distribution of the synthetic accessibility score [Ertl and Schuffenhauer, 2009].

Synthetic accessibility score (SAS) distributions II



Figure: WGAN in combination with RL push the distribution of the synthetic accessibility score (SAS) to be as low as possible.

Trade-off between WGAN and RL

Method	validity	uniqueness	QED*
$\lambda = 0.0$ (full RL)	100.00	3.16	0.61
$\lambda = 0.125$	100.00	7.21	0.61
$\lambda = 0.25$	99.80	10.16	0.61
$\lambda = 0.375$	99.90	11.11	0.60
$\lambda = 0.5$	99.40	31.29	0.56
$\lambda = 0.625$	97.20	49.69	0.51
$\lambda = 0.75$	93.70	64.35	0.51
$\lambda = 0.875$	89.40	69.69	0.50
$\lambda=$ 1.0 (no RL)	90.10	63.91	0.50

Table: WGAN and RL objectives trade-off. *QED is the quantitative estimate of drug-likeness [Bickerton et al., 2012].

Evolution of the QED during training



Figure: Evolution of the QED during training with different λ values.

Comparison with VAE based methods

Method	validity	uniqueness	novelty
CharacterVAE	10.3	67.5	90.0
GrammarVAE	60.2	9.3	80.9
GraphVAE	55.7	76.0	61.6
GraphVAE/imp	56.2	42.0	75.8
GraphVAE NoGM	81.0	24.1	61.0
Our VAE	61.5	97.6	69.1
Our VAE with RL	89.1	11.1	92.3
Our WGAN	89.2	26.5	55.7
Our WGAN with RL	99.6	14.5	97.7

Table: Baseline results from [Gómez-Bombarelli et al., 2016, Kusner et al., 2017, Simonovsky and Komodakis, 2018]

Method	validity	SAS	time (h)
ORGAN	96.5	0.83	8.7
OR(W)GAN	97.6	0.75	9.6
Naive RL	97.7	0.83	10.6
Our VAE with RL	89.6	0.71	0.09
Our VAE with RL (full QM9)	94.0	0.86	2.2
Our WGAN with RL	100.0	0.70	0.15
Our WGAN with RL (full QM9)	99.8	0.92	3.3

Table: Baseline results from ORGAN [Guimaraes et al., 2017].

Best QED samples



Figure: Top four molecules with QED scores.

Conclusion and future work

Considering experimental, we identify these further contributions:

- recurrent SMILES generation is more computational expensive
- likelihood-based models are difficult to be optimized with RL
- ... but keeping in mind and those **limitations**:
 - we experimented using compounds of at most 9 atoms
 - models are susceptible to mode collapse

We identify four principal directions for future work:

- address mode collapse [Srivastava et al., 2017]
- combine variational approaches with adversarial learning to benefit from both approaches [Mescheder et al., 2017, Rosca et al., 2017]
- train our models on ChEMBL [Gaulton et al., 2011]
- more realistic reward functions [Li et al., 2018]

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