

Deep Generative Models for Graphs

VAEs, GANs, and reinforcement learning for *de novo* drug discovery

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MSc Thesis presentation

① Introduction

- Drug design processes
- Our contributions

② Background

- VAEs and GANs

③ Models

④ Experiments

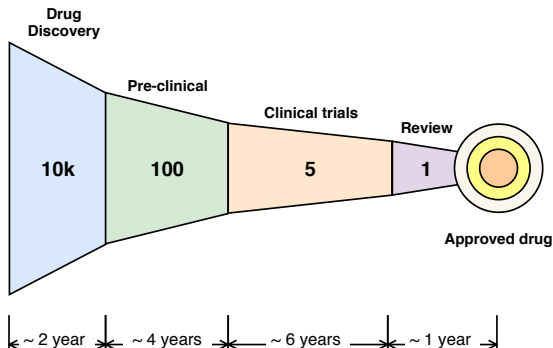
- Analysis of VAE vs. (W)GAN
- Combination with RL
- Comparison with literature

⑤ Conclusion and future work

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]

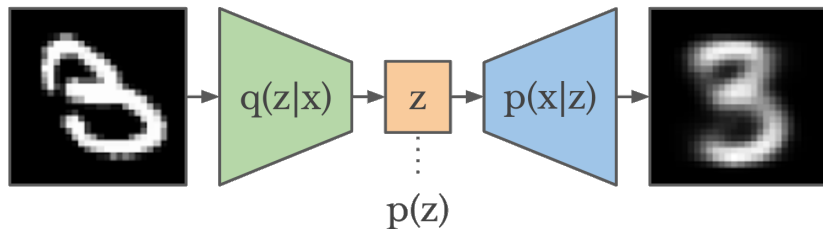
How do we study the problem?

- 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]



[Hafner, 2018]

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

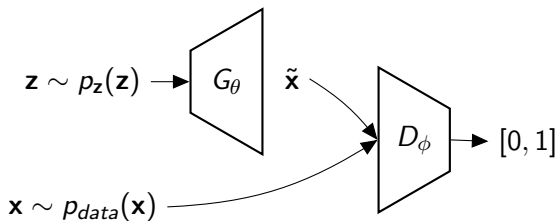


Figure: Schema of **GAN** architecture.

Models

Vectorial representation of graphs

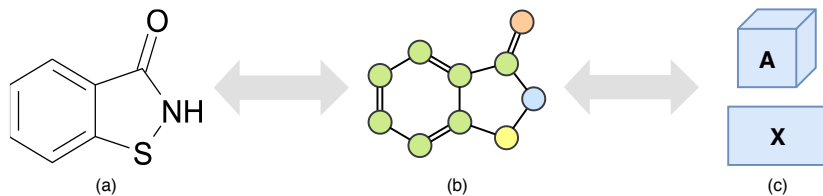
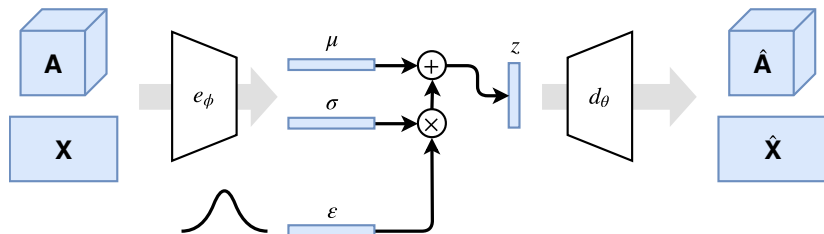


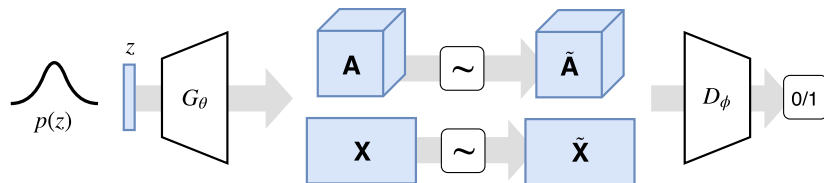
Figure: The **molecule** (a) is represented as an **labeled graph** (b) which can be encoded into an **adjacency tensor \mathbf{A}** and an **annotation matrix \mathbf{X}** .

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**.

Molecular graph GAN with RL

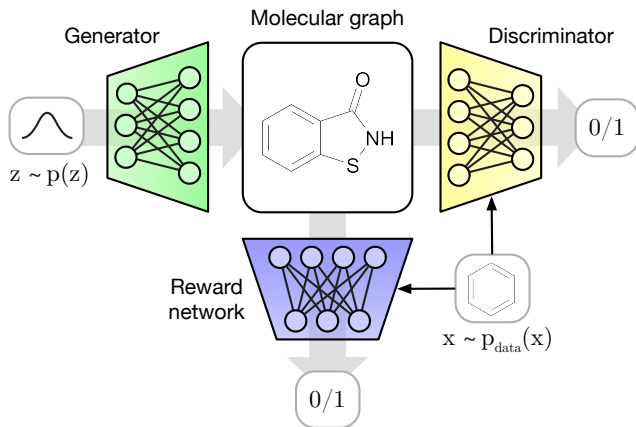


Figure: Schema of **MoIGAN** from our previous work [De Cao and Kipf, 2018].

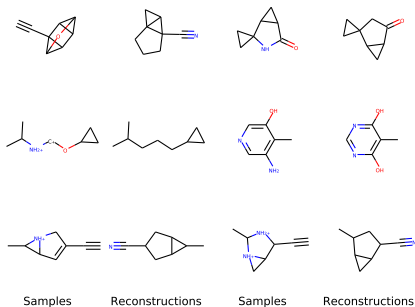
Experiments

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?

VAE advantages and disadvantages

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!**

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.

Synthetic accessibility score (SAS) distributions I

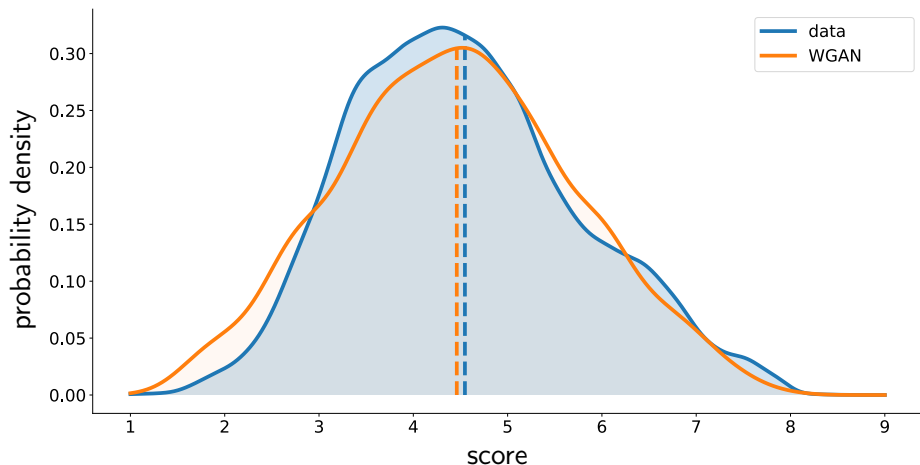


Figure: WGAN matches the data distribution of the synthetic accessibility score.

Synthetic accessibility score (SAS) distributions II

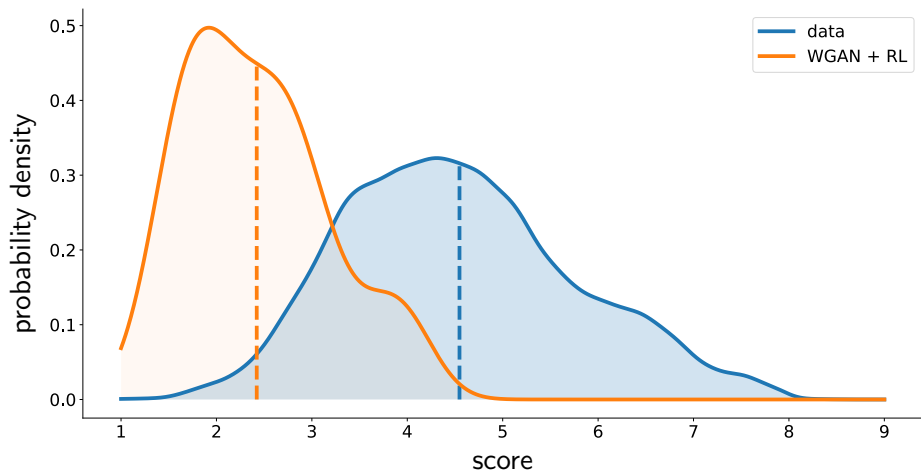


Figure: WGAN in combination with RL push the distribution of the synthetic accessibility score (SAS) to be as low as possible.

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 GraphVAE [Simonovsky and Komodakis, 2018].

Comparison with a GAN based method

Method	validity	SAS	time
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].

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 these **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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