
DiPol-GAN: Generating Molecular Graphs Adversarially with Relational Differentiable Pooling

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1 Problem Background and Methods

2 The extension of deep learning to graph data structures has become a popular research topic with
3 compelling applications to the field of chemistry [1]. Of particular interest is the impact of deep
4 generative models to *de novo* drug discovery. Drug discovery describes the process by which new
5 candidate medications are found with the goal of identifying a new target molecule with specific
6 desired properties. The key challenge presented is the vast size of the chemical space and the
7 discrete nature of molecular structures [2]. The drug discovery process is expensive as even *de novo*
8 approaches rely on some semblance of brute force. Improvements in methods to discover new drugs
9 with desired properties would have great impact. Our work presents a method to generate previously
10 undiscovered molecular graphs with specific desired properties.

11 Generative models have been making astounding progress in the field of computer vision and natural
12 language processing showing significant improvements in the quality of generated samples. Prominent
13 approaches to generative modeling are autoregressive models [3], variational autoencoders (VAEs)
14 [4], and generative adversarial networks (GANs) [5], each excelling in solving very specific types of
15 problems. For the task of image synthesis autoregressive models generate high quality images but
16 can be slow to evaluate and do not have a latent representation. VAEs train via maximum likelihood
17 estimation making them more numerically stable; however, they can produce lower quality results [6].
18 GANs implicitly learn model parameters without having to specify a likelihood [7] and are known
19 to produce higher quality results but are susceptible to generating lower diversity samples (a.k.a.
20 mode collapse), and are prone to numerical instability making them difficult to train even with recent
21 advances in adversarial training theory [8, 9, 10, 11].

22 Generative models have started to make their way into the domain of graphs with works such as
23 [7, 12, 13, 14, 15, 16]; however, learning to generate graphs presents problems for gradient based
24 learning due to the discrete nature of graphs because of their arbitrary connectivity [16]. Likelihood-
25 based models for graph generation are known to be stable but require expensive approximate graph
26 matching procedures as seen in GraphVAE [16] or require some fixed ordered representations of the
27 graph as seen in Junction Tree VAE (JT-VAE) [14], which often is not feasible. Autoregressive models
28 such as presented in GraphRNN [15] offer an interesting approach building a graph by conditionally
29 modeling sequences of nodes where the sequence generators are jointly aware of each other; however,
30 they lack a latent representation that would allow us to optimize for a desired chemical property.

31 GANs seem to present a clear advantage for the task of graph generation because they allow us
32 to implicitly learn the data generation distribution without having to formalize a likelihood that
33 necessitates a graph matching strategy as in the likelihood-based models (*e.g.* VAEs) while also
34 allowing for the optimization of the learned distribution towards a desired chemical property.

35 In this work we present DiPol-GAN, summarized in Figure 1, which is a GAN-based approach to
36 generating complete graph structures that are resistant to graph isomorphisms by learning to predict
37 discrete connections. Through the use of a reinforcement learning objective DiPol-GAN’s learned
38 generation distribution is encouraged towards a desired chemical property. DiPol-GAN implements

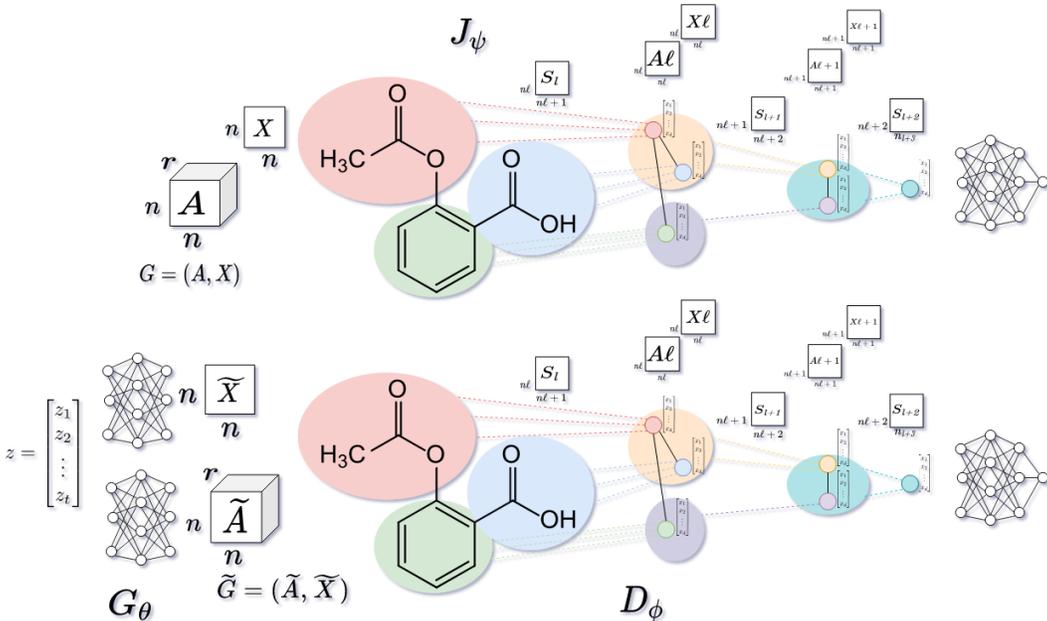


Figure 1: Proposed model architecture. J_ψ is a policy network, G_θ is the generator, and D_ϕ is the discriminator in a graph-based generative adversarial network. The generator is a graph $G = (\mathbf{A}, \mathbf{X})$ where \mathbf{A} is the adjacency matrix, and \mathbf{X} is the features matrix. The model implements a reinforcement learning reward mechanism.

39 Differentiable Pooling (DIFFPOOL) [17] in its discriminator, which learns to aggregate nodes on the
 40 molecular graph in a hierarchical way improving classification accuracy and the quality of learned
 41 graph embeddings. We believe that, through improving the discriminator’s architecture, it will
 42 encourage the generator to learn higher quality graph representations.

43 2 Results and Conclusions

44 Table 1 shows the results obtained with the proposed model on the QM9 dataset [18]. Reportedly,
 45 the proposed solutions are highly unique and diverse, which means that the molecules produced are
 46 not simply regurgitations of the existing (and known to be) valid molecules. However, in spite of the
 47 great results obtained, there are a few performance remarks that need to be noted. Using the QM9
 48 dataset for the task of goal directed molecular graph generation can be problematic in that there are
 49 134k molecular graph structures lacking software to calculate chemical properties on a GPU in a
 50 timely manner. However, nearly all related work reports lengthy training times with GraphVAE.

Table 1: Comparisons with related molecular graph generation work, presented are test results.

Algorithm	Valid (%)	Uniqueness	Diversity	Druglikeliness	Time (s)
MolGAN	77.5 \pm 42.0	0.098 \pm 0.16	0.877 \pm 0.21	0.513 \pm 0.22	16473 \pm 651
DiPo (WGAN)	100 \pm 0.0	0.883 \pm 0.01	0.999 \pm 0.45	0.648 \pm 0.21	19484 \pm 134

51 In summary, DiPOLGAN presents a method for generating molecular graphs with specific chemical
 52 properties via hierarchical differentiable pooling to improve discriminator performance while also
 53 optimizing towards a a reinforcement learning objective via the policy network. Through learning
 54 hierarchical graph representations it is our intuition from representation learning that our discriminator
 55 and policy networks are learning to hierarchically filter learned representations toward information
 56 present to improve each specific network’s objective and therefore implicitly encourage the generation
 57 of realistic molecular graphs.

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