Graph Generative Pre-trained Transformer

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Abstract

Graph generation is an essential task across various domains, such as molecular design and social network analysis, as it enables the modeling of complex relationships and structured data. While many modern graph generative models rely on adjacency matrices, this work revisits an approach that represents graphs as sequences of node and edge sets. We argue that this method offers more efficient graph encoding and then devise a method representing graphs as token sequences. Leveraging this representation, we present the Graph Generative Pre-trained Transformer (G2PT), an auto-regressive model designed to learn graph structures through next-token prediction. To extend G2PT's utility as a general-purpose foundation model, we explore fine-tuning techniques for two downstream tasks: goal-oriented generation and graph property prediction. Comprehensive experiments across multiple datasets demonstrate that G2PT delivers state-of-the-art generative performance on both generic graph and molecular datasets. Moreover, G2PT showcases strong adaptability and versatility in downstream applications, ranging from molecular design to property prediction.

1. Introduction

Graph generation has emerged as a vital task across diverse fields, including chemical discovery and social network analysis, due to its capacity to capture complex relationships and generate realistic, structured data (Du et al., 2021; Zhu et al., 2022).

Early generation methods such as DeepGMG (Li et al., 2018) and GraphRNN (You et al., 2018b) model graphs with sequential models. These approaches employed sequential frameworks (e.g., RNNs or LSTMs (Sherstinsky, 2020)) to generate graphs sequentially. For instance, GraphRNN generates adjacency matrix entries step-by-step, and for undirected graphs, it only needs to generate the lower triangular part of the adjacency matrix. DeepGMG frames graph generation as a sequence of actions (e.g., add-node, add-edge), and utilizes an agent-based model to learn the action trajectories.

Recent advances in graph generative models primarily focus on permutation-invariant methods leveraging diffusion-based approaches (Ho et al., 2020; Austin et al., 2021). For example, models like EDP-GNN (Niu et al., 2020) and GDSS (Jo et al., 2022a) represent graphs using continuous adjacency matrices. DiGress (Vignac et al., 2022) and EDGE (Chen et al., 2023) employ discrete diffusion, treating node types and all node pairs (edges) as categorical variables. These models start from a random or a fixed adjacency matrix and run "denoising" steps to sample an adjacency matrix from the target graph distribution. These models assign the same probability to adjacency matrices of the same graph and thus specify exchangeable distributions over graphs. However, achieving the permutation-invariant property has a price. The underlying neural network needs to be permutation-invariant as well, limiting the architecture choice to graph neural networks only. Furthermore, each denoising step needs to sample entries of the adjacency matrix independently, which creates difficulties in learning the true distribution and requires increasing the number of denoising steps Lezama et al. (2022); Campbell et al. (2022).

In recent years, the revolutionary success of large language models (Achiam et al., 2023; Dubey et al., 2024) shows the power of autoregressive transformers and also inspired the application of these models in other fields such as image generation [citations]. In this work, we revisit the sequential approach and consider autoregressive transformers for the problem of graph generation. Instead of simply replacing previous RNNs with a transformer, we design a new framework for graph generation and use tokens to encode sparse representations of graphs. Our newly designed encoding unlocks the potential of the transformer for graph generation by enabling it to predict token sequences to generate graphs, leading to our new method called Graph Generative Pre-trained Transformer (G2PT). Although this new model is not permutation-invariant, we hypothesize that its ability to learn accurate distributions from large-scale data outweighs the benefit of being permutation-invariant. Table 1 gives a comparison of diffusion-based models, sequential models

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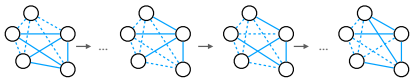
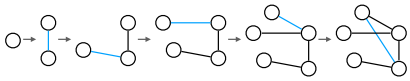
Model (Rep.)	Likelihood	Illustration	#Network Calls	#Variables	$p(\mathbf{A})$ or $p(E)$
Diffusion($\mathbf{A}$)	$p(\mathbf{A}^T)\prod_{t=1}^{T} p(\mathbf{A}^{t-1}\|\mathbf{A}^t)$		T	$O(Tn^2)$	Intractable
Sequential($\mathbf{A}$)	$\prod_{i=2}^{n}\prod_{j=1}^{i-1} p(\mathbf{A}_{i,j}\|\mathbf{A}_{<i,<i-1}, \mathbf{A}_{i,<j})$		$O(n^2)$	$O(n^2)$	Full factorization
Sequential(E)	$p(e_1)\prod_{i=2}^{m} p(e_i\|e_{<i})$		$O(m)$	$O(m)$	Full factorization

Table 1. Overview of graph generative model families combined with the used data representation (Rep.). n: number of nodes. m: number of edges. In the illustration, we use solid line for edges and dash line for non-edges, (non-)edges generated at current step are colored in blue. **Our proposed G2PT is an auto-regressive model that learns on E representation.**

based on adjacency matrices, and our model based on edges.

The new approach has an additional advantage: it enables the utilization of recently developed training methods for transformers in NLP applications. In particular, we use our new model to perform goal-oriented generation and optimize molecule properties in molecule generation tasks. We explore the rejection sampling fine-tuning and the reinforcement learning approaches, where both methods elevate the probability mass of graphs of interest in the pre-trained model distribution. Furthermore, our model can also learn a graph representation when the entire graph is used as the input. In this context, our model serves as a representation learning method, which is impossible for diffusion-based generative models. Combined with fine-tuning and a supervised objective, our model can also perform graph-level learning tasks such as graph classification.

We evaluate G2PT on a series of graph generation tasks: generic graph generation, molecule generation, and goal-oriented molecular generation. Without excessive architectural engineering or reliance on small training tricks, G2PT performs better than or on par with previous state-of-the-art (SOTA) baselines over seven datasets. By fine-tuning G2PT towards generating molecules with target properties, we showcase that G2PT can be easily adapted to various generative tasks that require additional alignment. We also fine-tune G2PT for molecular property prediction on MoleculeNet datasets. The results demonstrate the effectiveness of G2PT's learned representations for prediction tasks. Finally, we analyze the G2PT model and show its performance with data augmentation.

Contributions. Our main contributions are as follows:

- We propose a novel sequence-based representation that efficiently encodes graphs;
- We introduce G2PT, a transformer decoder trained on the new graph representation to model sequence distributions via next-token prediction;
- We explore fine-tuning techniques to adapt G2PT for downstream tasks, such as goal-oriented graph generation and graph property prediction;
- We conduct an extensive empirical study of G2PT, which achieves strong performance across diverse graph generation and prediction tasks

2. Related work

Permutation-invariant vs sequential models. Neural graph generative models are first developed as auto-regressive models. These models represent graphs as sequences and learn to generate such representations. A variety of models such as GraphRNN (You et al., 2018a), GRAN (Liao et al., 2019), GraphDF (Luo et al., 2021), and DAGG (Han et al., 2023) generate entries of the lower triangular of the adjacency matrix of the target graph, while DeepGMG (Li et al., 2018) and BiGG (Dai et al., 2020) directly generate edges through node representations learned from partially generated graphs.

In parallel, another research direction considers permutation-invariant models to predict logits of adjacency matrices and then sample the adjacency matrix in one-shot (Madhawa et al., 2019; Liu et al., 2019). These models define exchangeable distributions over graphs. This approach has been further advanced with diffusion-based methods (Ho et al., 2020; Austin et al., 2021), which can be divided into continuous diffusion models (Niu et al., 2020; Jo et al., 2022b) and discrete diffusion models (Vignac et al., 2022; Chen et al., 2023; Qin et al., 2024). Among these, discrete diffusion models have shown superior performance due to their alignment with the discrete nature of graphs. These models begin with a fixed or random adjacency matrix and iteratively update matrix entries over multiple steps to converge to the target adjacency matrix. Each update step, referred to as a "denoising" step, independently modifies a subset of the adjacency matrix entries.

Despite the superior performance, discrete diffusion graph models typically require a large number of denoising steps

for graph sampling. This is because for each step, entries are sampled independently conditioned on the previous step. Such sampling scheme introduces the compounding decoding error (Lezama et al., 2022), leading to a poor approximation to the true distribution (Campbell et al., 2022).

Generating adjacency matrices vs edge lists. Most graph generative models including most of the sequential models (You et al., 2018b; Liao et al., 2019) and all diffusion-based models (Jo et al., 2022b; Niu et al., 2020; Vignac et al., 2022; Chen et al., 2023; Qin et al., 2024) generate (the lower triangular of) an adjacency matrix. And only a few models (Li et al., 2018; Dai et al., 2020) generates the edge list of a target graph.

Despite the popularity, learning adjacency matrices requires modeling all node pairs in a graph, which is quadratic of the number of nodes n. For auto-regressive models, it creates long sequences for the model to learn, making it a challenging learning problem (Hihi & Bengio, 1995). For diffusion-based models, it requires many denoising steps to generate all those entries accurately. That is, generating adjacency matrices are computationally intensive for both kinds of models. In contrast, edge lists only define variables over actual edges. When graphs are sparse, both learning and sampling complexities are reduced.

Despite these advantages, modeling the edge set has received limited attention compared to adjacency matrix-based methods. This is because previous works utilize a action-based framework to model a sequence of specialized operations, such as "add-node" and "add-edge". Such modeling requires using different networks for different actions, posing challenges to the optimization (Li et al., 2018). Additionally, since nodes are incrementally added to the graph, the logits' length for edge prediction changes dynamically. Previous methods rely on a edge prediction model that uses node representations as input. However, these models are often shallow networks, limiting their expressiveness. In this work, we show that with proper sequence design and model architecture choice, modeling edge lists can achieve superior performance while being efficient.

3. Graph Generative Pre-trained Transformer

3.1. Representing Graph as Sequence

We consider modeling a graph as a sequence of actions that first generates all nodes of a graph, then the edges among them. Denote a feature graph $G = (V, E)$ Here $v \in V$ is represented as a tuple $v := (v^{\text{c}}, v^{\text{id}})$, where $v^{\text{id}} \in \mathbb{Z}^+$ is the node index and $v^{\text{c}} \in \{1, \dots, K_v\}$ is the node type. And $e \in E$ is represented as a triple $e := (v^{\text{id}}_{\text{src}}, v^{\text{id}}_{\text{dest}}, e^{\text{c}})$, where the first two elements define the edge connection and $e^{\text{c}} \in \{1, \dots, K_e\}$ is the edge type. For a featureless graph, the above representation can be simplified by removing the node and edge type definitions. A graph G with n nodes and m edges can be represented as

$$[\underbrace{v^{\text{c}}_1, v^{\text{id}}_1, \dots, v^{\text{c}}_n, v^{\text{id}}_n}_{n\times 2}, a_\Delta, \underbrace{v^{\text{id}}_{\text{src}}, v^{\text{id}}_{\text{dest}}, e^{\text{c}}_1, \dots, v^{\text{id}}_{\text{src}}, v^{\text{id}}_{\text{dest}}, e^{\text{c}}_m}_{m\times 3}].$$

Here a_Δ is used to denote a transition from node generation to edge generation. We illustrate it in Figure 1.

Algorithm 1 Degree-Based Edge Removal Process

Input: Graph $G = (V, E)$, neighborhood function $\text{Nei}(\cdot)$
Output: Sequence of removed edges σ_E
Initialize $\sigma_E \leftarrow [\,]$
while $E \neq \emptyset$ **do**
  Select $v_{\text{src}} \in V$ with the minimum degree.
  Select $v_{\text{dest}} \in \text{Nei}(v_{\text{src}})$ with the minimum degree.
  Remove edge $e = (v_{\text{src}}, v_{\text{dest}})$ from E; append e to σ_E.
  Update the degrees of v_{src} and v_{dest}.
end while

Since a graph can be encoded into different sequences by varying the node permutation and the edge generation ordering. For node orderings, we index the node using a random permutation. Based on the node indices, we obtain the edge generation orderings via the reverse of a degree-based edge-removal process shown in Alg. 1. Intuitively, the reverse of such a process first constructs an "initial seed graph" and grows it by iteratively attaching nodes to it. We also explore the effectiveness of using other canonical edge orderings such as breadth-first search (BFS) and depth-first search (DFS) (details are presented in Appendix D.1).

3.2. Learning Graph Sequences via Transformer

We utilize a transformer decoder (Vaswani, 2017) for modeling the graph sequences. Unlike language models, our defined graph sequence contains tokens from different action spaces. Here we consider using a tokenizer that unifies all types of actions into one vocabulary.

Tokenization. Let n_{max} be the maximum number of nodes of a graph dataset. The unified vocabulary lookup is then defined as

$$\begin{aligned}
&\text{tokenize}(v^{\text{id}}) = v^{\text{id}}, \quad v^{\text{id}} \in \{1, \dots, n_{\text{max}}\};\\
&\text{tokenize}(v^{c}) = v^{c} + n_{\text{max}}, \quad v^{c} \in \{1, \dots, K_v\};\\
&\text{tokenize}(e^{c}) = e^{c} + n_{\text{max}} + K_v, \quad e^{c} \in \{1, \dots, K_e\};\\
&\text{tokenize}(a_\Delta) = n_{\text{max}} + K_v + K_e + 1.
\end{aligned}$$

We additionally introduce special tokens [SOG] and [EOG], representing the start and the end of the sequence generation. We denote the tokenized sequence $\mathbf{s} = [s_1, \dots, s_L]$, which is used in the following sections.

Training objective. With the auto-regressive transformer, we minimize the the sequence negative log-likelihood.

$$\mathcal{L}_{\text{pt}}(\mathbf{s}; \theta) := -\log p_\theta(\mathbf{s}) = \sum_{l=1}^{L} -\log p_\theta(s_l | \mathbf{s}_{<l}),$$

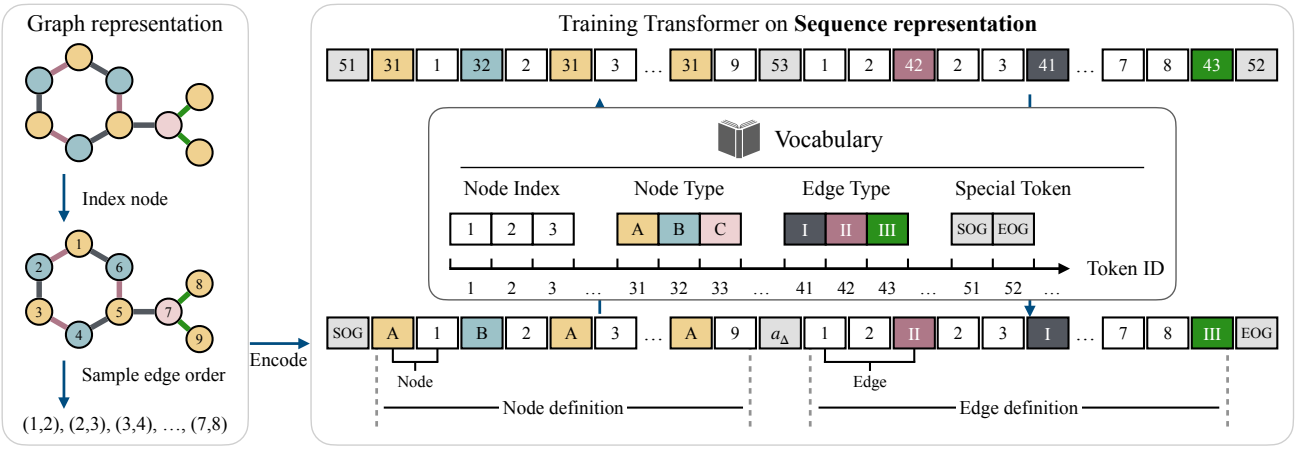


Figure 1. Illustration of our proposed graph sequence representation. This representation can be viewed as a sequence of actions: first generating all nodes (node type, node index), then explicitly adding edges (source node index, destination node index, edge type) step by step until completion. A unified vocabulary is used to map different types of actions into a shared token space.

where θ is the parameters of the model. Since the tokens in sequence are arranged based on the defined rule, the action space for each decoding step is limited to a subset. For example, when the current input token is one of the node type, its output token can only be one of the node indices. One can impose such constraint on the output logits vector at each step to improve the modeling accuracy. In our experiment, we find that an unconstrained logits space can also yield a superior performance due to the expressiveness of transformers.

Relationship with graph likelihood. We show that maximizing the sequence likelihood maximizes a lower bound of the graph likelihood. Denote a training set of N graphs $\{G_1, \ldots, G_N\}$. The log-likelihood of the graph dataset is $\mathcal{L}(\theta) = \sum_{i=1}^{N} \log p_\theta(G_i)$. Let $p_{\mathrm{d}}(G)$ denote the data distribution, and $p_{\mathrm{d}}(\mathbf{s}|G)$ denote the distribution of drawing sequences from a graph G. We have

$$\begin{aligned}
&\mathcal{L}(\theta) + \mathbb{H}[p_{\mathrm{d}}(G)] = -\mathrm{KL}\big(p_d(G)\|p_\theta(G)\big) \\
&\geq -\mathrm{KL}\big(p_d(G)\|p_\theta(G)\big) - \mathbb{E}_{p_{\mathrm{d}}}\Big[\mathrm{KL}\big(p_{\mathrm{d}}(\mathbf{s}|G)\|p_\theta(\mathbf{s}|G)\big)\Big] \\
&= -\mathrm{KL}\big(p_{\mathrm{d}}(\mathbf{s})\|p_\theta(\mathbf{s})\big) = \sum_{i=1}^{N} -\mathcal{L}_{\mathrm{pt}}(\mathbf{s};\theta) + \mathbb{H}[p_{\mathrm{d}}(\mathbf{s})].
\end{aligned}$$

In the second line, we use the fact that $p(G, \mathbf{s}) = p(\mathbf{s})$ because $\mathbf{s}$ determines G. And both the entropy terms are constant with regard to the model parameters θ.

From the lower bound, we see that an accurate approximation $p_\theta(\mathbf{s}|G)$ can tighten the bound. Although $p_\theta(\mathbf{s}|G)$ is not directly compute, providing more sequences from the same graph G can reduce the condition KL. Intuitively, increasing the number of sequences increases the diversity of the training data, thus improving model's generalization.

4. Fine-tuning

After pre-training a model, we further fine-tune it for downstream tasks. We consider generative (§4.1) and predictive (§4.2) downstream tasks, where the former aims to generate graphs with desired properties, and the latter utilizes the graph embeddings learned from the transformer to predict properties.

4.1. Goal-oriented Generation

Let $z(\cdot)$ be the function that estimates property z of a graph G. In goal-oriented generation, we are interested in obtaining a new model that generates graphs whose properties are close to z^* more often then the pre-trained model. Such a setup has a broad application in the graph generation community such as drug discovery. In this work, we explore obtaining such distribution by fine-tuning the pre-trained model. We consider rejection sampling fine-tuning (RFT) and reinforcement learning (RL) approaches.

Rejection sampling fine-tuning. This approach fine-tunes the model using its own generated samples that satisfy the desired property z^*. We consider the case where the property is a scalar, and an acceptance function $m_\omega^{z^*}(G) = \mathbb{1}_{|z^* - z(G)| < \omega}$ is controlled by an distance threshold ω.

The algorithm for generating the fine-tuning dataset $\mathcal{D}_\omega^{y^*} = \{G_b\}_{b=1}^{B}$ via rejection sampling is shown in Alg. 2. Note that we expect the learned pre-trained model is able to generate graphs with desired property.

When the graph of interest has a low density in the model distribution, RFT becomes inefficient as it rejects most of the samples. To address this, we further propose to self-bootstrap (SBS) the RFT model to approach the target distribution. Specifically, we first define a sequence with τ thresholds $\omega_1 > \omega_2 > \ldots > \omega_\tau$, where $\omega_\tau = \omega$. Then we

Algorithm 2 RFT Dataset Construction

Input: Model p_θ, acceptance function $m_\omega^{z^*}$, data size B.
Output: Fine-tuning dataset $\mathcal{D}_\omega^{z^*}$
Initialize $\mathcal{D}_\omega^{z^*} \leftarrow \{\,\}$
while $|\mathcal{D}_\omega^{z^*}| \neq B$ **do**
  Generate $G \sim p_\theta$.
  if G is valid **and** $m_\omega^{z^*}(G) = 1$ **then**
    Append G to $\mathcal{D}_\omega^{z^*}$.
  end if
end while

Algorithm 3 SBS$^\tau$ combined with RFT

Input: Model p_θ, thresholds list $[\omega_1 \ldots, \omega_\tau]$, data size B.
Output: Fine-tuned model p_{θ_τ}
Set $\theta_0 = \theta$.
for $i = 1, \ldots, \tau$ **do**
  Use $p_{\theta_{i-1}}$ as input model, obtain $\mathcal{D}_{\omega_i}^{z^*} \leftarrow$ Alg. 2.
  Fine-tune θ_{i-1} on $\mathcal{D}_{\omega_i}^{z^*}$, obtain new parameters θ_i.
end for

can obtained a sequence of fine-tuned models by iteratively constructing fine-tuned datasets using model trained from previous threshold. The SBS algorithm combined with RFT is shown in Alg. 3.

Reinforcement learning. Denote a target-relevant reward function $r_{z^*}(G)$, we consider a KL-regularized reinforcement learning problem:

$$\phi^* = \arg\max_\phi \mathbb{E}_{p_{\phi(\mathbf{s})}}\big[r_{z^*}(\mathbf{s}) - \rho_1 \mathrm{KL}\big(p_\phi(\cdot|\mathbf{s}) \| p_\theta(\cdot|\mathbf{s})\big)\big].$$

We use the notation $\mathbf{s}$ and G interchangeable as the mapping from $\mathbf{s}$ to G is deterministic. The KL divergence $\mathrm{KL}(\cdot\|\cdot)$ prevents the target model from deviating too much from the pre-trained model.

We choose Proximal Policy Optimization (PPO) (Schulman et al., 2017) to effectively train the target policy (actor model) without sacrificing stability. We first define the token-level reward:

$$R([\mathbf{s}_{<l}, s_l]) = \begin{cases} 0 & s_l \neq [\mathrm{EOG}] \\ r([\mathbf{s}_{<l}, s_l]) & s_l = [\mathrm{EOG}] \end{cases}.$$

Here $\mathbf{s}_{<l}$ is the state of the l-th step in a finite trajectory (sequence). We only assign a reward when the generation is completed. The value function of state $\mathbf{s}_{<l}$ under a model p is the expectation of the undiscounted future return:

$$V^p(\mathbf{s}_{<l}) = \mathbb{E}_{p(\mathbf{s}_{\geq l}|\mathbf{s}_{<l})}\big[r(\mathbf{s})\big].$$

A critic model $V_\psi(\mathbf{s}_{<l})$ is then learned to approximate the true value function $V^p(\mathbf{s}_{<l})$ via minimizing the mean absolute error $\mathcal{L}_{\text{critic}}(\psi)$. We parameterize the critic model with a transformer that is the same architecture as the pre-trained model, except the logits head is replaced by a value head. The parameters of the critic model are also initialized from the pre-trained model.

We use the clipped surrogate objective $\mathcal{L}_{\text{pg-clip}}(\phi)$ in PPO to optimize the actor model. Moreover, to mitigate possible model degradation, we incorporate the pre-training loss $\mathcal{L}_{\text{pt}}(\phi)$ following Zheng et al. (2023); Liu et al. (2024).

All terms combined, we minimize the objective:

$$\mathcal{L}_{\text{ppo}}(\phi, \psi; \theta) = \mathcal{L}_{\text{pg-clip}}(\phi) + \rho_2 \mathcal{L}_{\text{critic}}(\psi) + \rho_3 \mathcal{L}_{\text{pt}}(\phi).$$

Here ρ_1, ρ_2, ρ_3 are loss coefficients. We provide preliminaries of PPO and details of each loss term in Appendix A.

4.2. Property Prediction

Assume a labeled graph dataset $\mathcal{C}$, where each instance consists a graph G along with a label y. We fine-tune the pre-trained model on it to learn to predict y given G. After the sequence $\mathbf{s}$ is generated from G, we extract the activation $\mathbf{h}$ of the final token $\mathbf{s}_L$ output by the last transformer block as the graph representation. The rationale is that the model must have learned the information of the entire input graph in order to expand it with further edges. To predict y, we then feed $\mathbf{h}$ into a dropout layer followed by a linear layer:

$$p(y|\mathbf{s}) = \mathrm{Softmax}(\mathrm{Dropout}(\mathrm{Linear}(\mathbf{h}))).$$

We minimize the cross-entropy loss $-\mathbb{E}_{(G,y)\sim\mathcal{C}} \log p(y|G)$ to fine-tune the model. Compared to freezing the whole transformer during training and only update parameters of the linear layer, we found that unlocking the latter half of the transformer blocks significantly enhances performance.

5. Experiments

5.1. Setup

Datasets. We consider both generative tasks and predictive tasks in our experiments. In generative tasks, we consider training transformer decoders on molecular datasets and generic graph datasets. For molecular datasets, we use QM9 (Wu et al., 2018b), MOSES (Polykovskiy et al., 2020), and GuacaMol (Brown et al., 2019). For generic graph datasets, we adapted the widely used datasets: Planar, Tree, Lobster, and stochastic block model (SBM). In predictive tasks, we fine-tune models pre-trained from GuacaMol datasets on various molecular property tasks using MoleculeNet (Wu et al., 2018a), detailed in Appendix B.4, to verify the usefulness of the learned graph representations.

Model specifications. We train transformers with three different sizes: (1) the small transformer has 6 transformer layers and 6 attention head, with $d_{\text{model}} = 384$, leading to approximately 10M parameters; (2) the base transformer has 12 transformer layers and 12 attention head, with $d_{\text{model}} = 768$, leading to approximately 85M parameters; (2) the large transformer has 24 transformer layers and 16 attention head, with $d_{\text{model}} = 1024$, leading to approximately

Model	Planar						Tree					
	Deg.↓	Clus.↓	Orbit↓	Spec.↓	Wavelet↓	V.U.N.↑	Deg.↓	Clus.↓	Orbit↓	Spec.↓	Wavelet↓	V.U.N.↑
GRAN (Liao et al., 2019)	7e-4	4.3e-2	9e-4	7.5e-3	1.9e-3	0	1.9e-1	8e-3	2e-2	2.8e-1	3.3e-1	0
BiGG (Dai et al., 2020)	7e-4	5.7e-2	3.7e-2	1.1e-2	5.2e-3	5	1.4e-3	**0.00**	**0.00**	1.2e-2	5.8e-3	75
DiGress (Vignac et al., 2022)	7e-4	7.8e-2	7.9e-3	9.8e-3	3.1e-3	77.5	2e-4	**0.00**	**0.00**	1.1e-2	4.3e-3	90
BwR (Diamant et al., 2023)	2.3e-2	2.6e-1	5.5e-1	4.4e-2	1.3e-1	0	1.6e-3	1.2e-1	3e-4	4.8e-2	3.9e-2	0
HSpectre (Bergmeister et al., 2023)	**5e-4**	6.3e-2	1.7e-3	7.5e-3	**1.3e-3**	95	**1e-4**	**0.00**	**0.00**	1.2e-2	4.7e-3	**100**
DeFoG (Qin et al., 2024)	**5e-4**	5e-2	6e-4	**7.2e-3**	1.4e-3	99.5	2e-4	**0.00**	**0.00**	1.1e-2	4.6e-3	96.5
$G2PT_{small}$	4.7e-3	**2.4e-3**	**0.00**	1.6e-2	1.4e-2	95	2e-3	**0.00**	**0.00**	7.4e-3	**3.9e-3**	99
$G2PT_{base}$	1.8e-3	4.7e-3	**0.00**	8.1e-3	5.1e-3	**100**	4.3e-3	**0.00**	1e-4	**7.3e-3**	5.7e-3	99

Model	Lobster						SBM					
	Deg.↓	Clus.↓	Orbit↓	Spec.↓	Wavelet↓	V.U.N.↑	Deg.↓	Clus.↓	Orbit↓	Spec.↓	Wavelet↓	V.U.N.↑
GRAN (Liao et al., 2019)	3.8e-2	**0.00**	1e-3	2.7e-2	-	-	1.1e-2	5.5e-2	5.4e-2	**5.4e-3**	2.1e-2	25
BiGG (Dai et al., 2020)	**0.00**	**0.00**	**0.00**	9e-3	-	-	1.2e-3	6.0e-2	6.7e-2	5.9e-3	3.7e-2	10
DiGress (Vignac et al., 2022)	2.1e-2	**0.00**	4e-3	-	-	-	1.8e-3	4.9e-2	4.2e-2	4.5e-3	**1.4e-3**	60
BwR (Diamant et al., 2023)	3.2e-1	**0.00**	2.5e-1	-	-	-	4.8e-2	6.4e-2	1.1e-1	1.7e-2	8.9e-2	7.5
HSpectre (Bergmeister et al., 2023)	-	-	-	-	-	-	1.2e-2	5.2e-2	6.7e-2	6.7e-3	2.2e-2	45
DeFoG (Qin et al., 2024)	-	-	-	-	-	-	**6e-4**	5.2e-2	5.6e-2	**5.4e-3**	8e-3	90
$G2PT_{small}$	2e-3	**0.00**	**0.00**	5e-3	**8.5e-3**	**100**	3.5e-3	1.2e-2	7e-4	7.6e-3	9.8e-3	**100**
$G2PT_{base}$	1e-3	**0.00**	**0.00**	**4e-3**	1e-2	**100**	4.2e-3	**5.3e-3**	**3e-4**	6.1e-3	6.9e-3	**100**

Table 2. Generative performance on generic graph datasets.

300M parameters. We use different specifications for different experiments according to the task complexity.

5.2. A Proof-of-Concept using Planar Graph

We first validate the effectiveness of our proposed graph sequence representation compared to the adjacency matrix. To achieve this, we train transformer decoders on planar graphs using both representations and evaluate their generative performance. For the adjacency representation, planar graphs are encoded as sequences of 0s and 1s derived from the strictly lower triangular matrix, with rows and columns permuted using BFS orderings to augment the training dataset. Table 3 presents the quantitative and qualitative results of the generated samples. Our proposed representation demonstrates superior generative performance with a much smaller set of tokens, while model learning adjacency matrices struggles to capture the topological rules of the training graphs.

5.3. Generic Graph Generation

We evaluate G2PT on four generic datasets using Maximum Mean Discrepancy (MMD) to compare the graph statistics distributions of generated and test graphs. The evaluation considers degree (Deg.), clustering coefficient (Clus.), orbit counts (Orbit), spectral properties (Spec.), and wavelet statistics. Moreover, we report the percentage of valid, unique, and novel samples (V.U.N.) (Vignac et al., 2022). For this task, we trained the $G2PT_{small}$ and $G2PT_{base}$ models.

As shown in Table 2, G2PT demonstrates superior performance compared to the baselines. The details about baseline and metric are introduced in appendix B.5 The base model achieves 11 out of 24 best scores and ranks in the top two for 17 out of 24 metrics. The small model also demonstrates competitive results, indicating that a lightweight model can effectively capture the graph patterns in the datasets.

Rep.	#Tokens↓	Deg.↓	Clus.↓	Orbit↓	Spec.↓	Wavelet↓	V.U.N.↑
A	2018	8.6e-3	1e-1	8e-3	3.2e-2	6.1e-2	94
s (Ours)	**737**	**4.7e-3**	**2.4e-3**	**0.00**	**1.6e-2**	**1.4e-2**	**95**

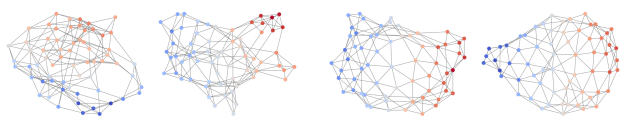


Table 3. Generative performance comparison between the proposed edge sequence and adjacency matrix representations.

5.4. Molecule Generation

De novo molecular design is a key real-world application of graph generation. We assess G2PT's performance on the QM9, MOSES, and GuacaMol datasets. For the QM9 dataset, we adopt the evaluation protocol in Vignac et al. (2022). For MOSES and GuacaMol, we utilize the evaluation pipelines provided by their respective toolkits (Polykovskiy et al., 2020; Brown et al., 2019).

The quantitative results are presented in Table 4. On MOSES, G2PT surpasses other state-of-the-art models in validity, uniqueness, FCD, and SNN metrics. We introduce the details for metrics in appendix B.6. Notably, the FCD, SNN, and scaffold similarity (Scaf) evaluations compare generated samples to a held-out test set, where the test molecules have scaffolds distinct from the training data. Although the scaffold similarity score is relatively low, the overall performance indicates that G2PT achieves a better goodness of fit on the training set. G2PT also delivers strong performance on the GuacaMol and QM9 datasets. We additionally provide qualitative examples from the MOSES and GuacaMol datasets in the table.

Model	MOSES							GuacaMol				
	Validity↑	Unique.↑	Novelty↑	Filters↑	FCD↓	SNN↑	Scaf↑	Validity↑	Unique.↑	Novelty↑	KL Div.↑	FCD↑
DiGress (Vignac et al., 2022)	85.7	**100**	95.0	97.1	1.19	0.52	14.8	85.2	**100**	**99.9**	92.9	68
DisCo (Xu et al., 2024)	88.3	**100**	**97.7**	95.6	1.44	0.5	15.1	86.6	86.6	86.5	92.6	59.7
Cometh (Siraudin et al., 2024)	90.5	99.9	92.6	99.1	1.27	0.54	**16.0**	98.9	98.9	97.6	96.7	72.7
DeFoG (Qin et al., 2024)	92.8	99.9	92.1	**99.9**	1.95	**0.55**	14.4	**99.0**	99.0	97.9	**97.9**	73.8
$G2PT_{small}$	95.1	**100**	91.7	97.4	1.10	0.52	5.0	90.4	**100**	99.8	92.8	86.6
$G2PT_{base}$	96.4	**100**	86.0	98.3	**0.97**	**0.55**	3.3	94.6	**100**	99.5	96.0	**93.4**
$G2PT_{large}$	**97.2**	**100**	79.4	98.9	1.02	**0.55**	2.9	95.3	**100**	99.5	95.6	92.7

Model	QM9		
	Validity↑	Unique.↑	FCD↓
DiGress (Vignac et al., 2022)	99.0	96.2	-
DisCo (Xu et al., 2024)	**99.6**	96.2	0.25
Cometh (Siraudin et al., 2024)	99.2	96.7	0.11
DeFoG (Qin et al., 2024)	99.3	96.3	0.12
$G2PT_{small}$	99.0	96.7	**0.06**
$G2PT_{base}$	99.0	**96.8**	**0.06**
$G2PT_{large}$	98.9	96.7	**0.06**

MOSES			GuacaMol		
Train	$G2PT_{small}$	$G2PT_{base}$	Train	$G2PT_{small}$	$G2PT_{base}$

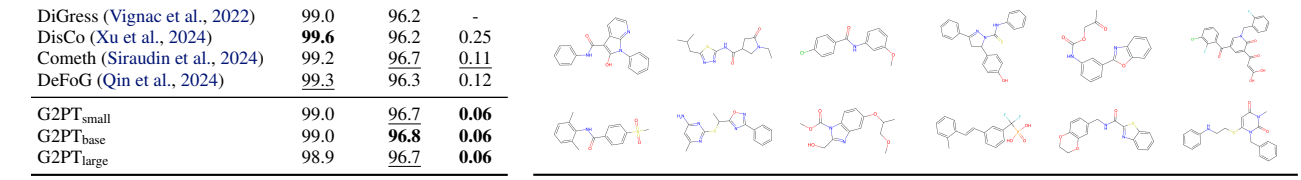
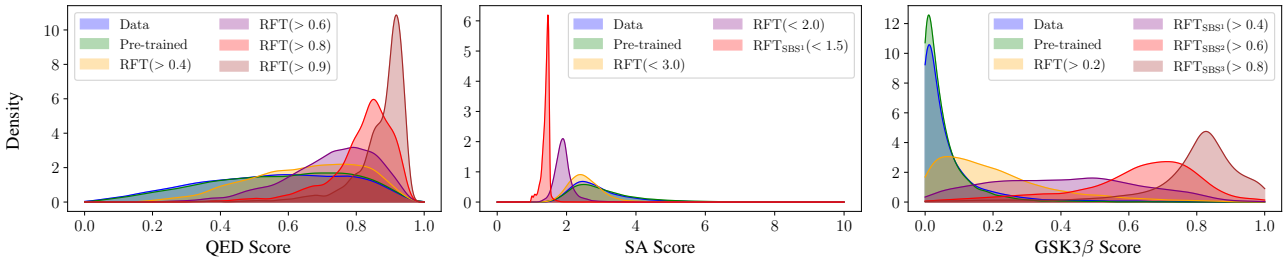
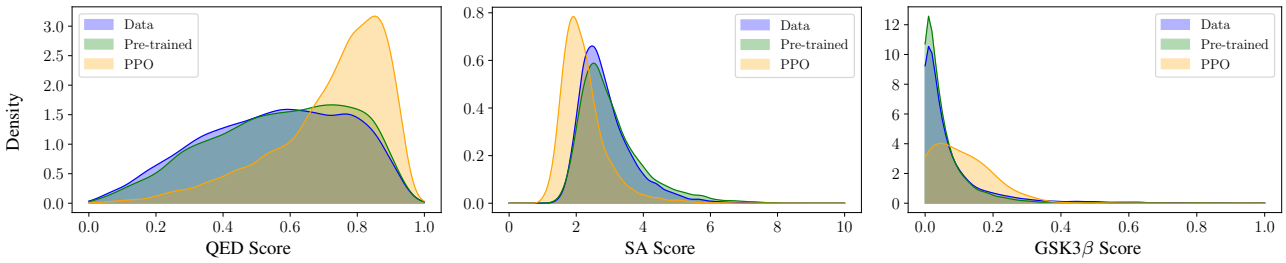


Table 4. Generative performance on molecular graph datasets



(a) Rejection sampling fine-tuning (with self-bootstrap)



(b) Reinforcement learning framework (PPO)

Figure 2. Goal-oriented molecule generation using QED, SA and GSK3β scores. Top row (a) shows the results using RFT, and bottom row (b) shows the results using RL.

5.5. Goal-oriented Generation

In addition to distribution learning which aims to draw independent samples from the learned graph distribution, goal-oriented generation is a major task in graph generation that aims to draw samples with additional constraints or preferences and is key to many applications such as molecule optimization (Du et al., 2024).

We validate the capability of G2PT on goal-oriented generation by fine-tuning the pre-trained model. Practically, we employ the model pre-trained on GuacaMol dataset and select three commonly used physiochemical and binding-related properties: quantitative evaluation of druglikeness (QED), synthesis accessibility (SA), and the activity against target protein Glycogen synthase kinase 3 beta (GSK3β), detailed in Appendix B.3. The property oracle functions are provided by the Therapeutics Data Commons (TDC) package (Huang et al., 2022).

As discussed in §4.1, we employ two approaches for fine-tuning: (1) rejection sampling fine-tuning and (2) reinforcement learning with PPO. Figure 2 shows that both methods can effectively push the learned distribution to the distribution of interest. Notably, RFT, with up to three rounds of SBS, significantly shifts the distribution towards a desired one. In contrast, PPO, despite biasing the distribution, suffers from the over-regularization from the base policy, which aims for training stability. In the most challenging

	BBBP	Tox21	ToxCast	SIDER	ClinTox	MUV	HIV	BACE	Avg.
AttrMask (Hu et al., 2020a)	70.2±0.5	74.2±0.8	62.5±0.4	60.4±0.6	68.6±9.6	73.9±1.3	74.3±1.3	77.2±1.4	70.2
InfoGraph (Sun et al., 2020)	69.2±0.8	73.0±0.7	62.0±0.3	59.2±0.2	75.1±5.0	74.0±1.5	74.5±1.8	73.9±2.5	70.1
ContextPred (Hu et al., 2020a)	**71.2±0.9**	73.3±0.5	62.8±0.3	59.3±1.4	73.7±4.0	72.5±2.2	75.8±1.1	78.6±1.4	70.9
GraphCL (You et al., 2021)	67.5±2.5	**75.0±0.5**	62.8±0.2	60.1±1.3	78.9±4.2	**77.1±1.0**	75.0±0.4	68.7±7.8	70.6
GraphMVP (Liu et al., 2022a)	68.5±0.2	74.5±0.0	62.7±0.1	**62.3±1.6**	79.0±2.5	75.0±1.4	74.8±1.4	76.8±1.1	71.7
GraphMAE (Hou et al., 2022b)	70.9±0.9	**75.0±0.4**	**64.1±0.1**	59.9±0.5	81.5±2.8	76.9±2.6	**76.7±0.9**	81.4±1.4	**73.3**
$G2PT_{small}$ (No pre-training)	60.7±0.3	66.4±0.5	57.0±0.3	61.6±0.2	67.8±1.1	45.8±8.5	70.1±7.5	68.8±1.3	62.3
$G2PT_{base}$ (No pre-training)	56.5±0.2	67.4±0.4	57.9±0.1	60.2±2.8	71.0±5.6	60.1±1.3	72.7±1.1	73.4±0.3	64.9
$G2PT_{small}$	68.5±0.5	74.7±0.2	61.2±0.1	61.7±1.0	**82.3±2.2**	74.9±0.1	75.7±0.4	81.3±0.5	72.5
$G2PT_{base}$	71.0±0.4	**75.0±0.3**	63.0±0.5	61.9±0.2	82.1±1.1	74.5±0.3	76.3±0.4	**82.3±1.6**	**73.3**

Table 5. Results for molecule property prediction in terms of ROC-AUC. We report mean and standard deviation over three runs.

case (GSK3β), PPO fails to sampling data with high rewards. Conversely, RFT overcomes the barrier in the second round (RFT_{SBS^1}), where its distribution becomes flat across the range and quickly transitions to a high-reward distribution.

5.6. Predictive Performance on Downstream Tasks

We conduct experiments on eight graph classification benchmark datasets from MoleculeNet (Wu et al., 2018a), strictly following the data splitting protocol used in GraphMAE (Hou et al., 2022a) for fair comparison. A detailed description of these datasets is provided in Appendix B.4.

For downstream fine-tuning, we initialize G2PT with parameters pre-trained on the GuacaMol dataset, which contains molecules with up to 89 heavy atoms. We also provide results where models are not pre-trained.

As summarized in Table 5, G2PT's graph embeddings demonstrate consistently strong (best or second-best) performance on seven out of eight downstream tasks, achieving an overall performance comparable to GraphMAE, a leading self-supervised learning (SSL) method. Notably, while previous SSL approaches leverage additional features such as 3D information or chirality, G2PT is trained exclusively on 2D graph structural information. Overall, these results indicate that G2PT not only excels in generation but also learns effective graph representations.

5.7. Scaling Effects

We analyze how scaling the model size and data size will affect the model performance using the three molecular datasets. We use the validity score to quantify the model performance. Results are provided in Figure 3.

For model scaling, we additionally train G2PTs with 1M, 707M, and 1.5B parameters. We notice that as model size increases, validity score generally increases and saturates at some point, depending on the task complexity. For instance, QM9 saturates at the beginning (1M parameters) while MOSES and GuacaMol require more than 85M (base) parameters to achieve satisfying performance.

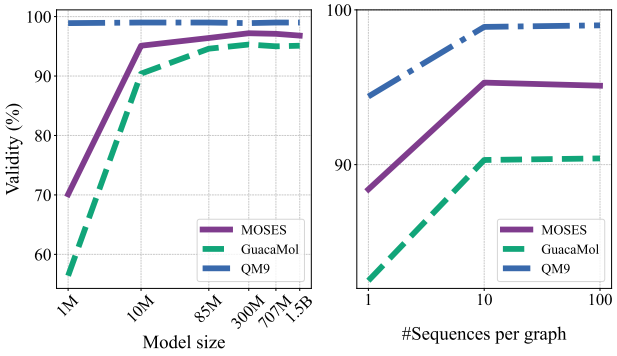


Figure 3. Model and data scaling effects.

For data scaling, we generating multiple sequences from the same graph to improve the diversity of the training data. The number of augmentation per graph is chosen from $\{1, 10, 100\}$. As shown, one sequence per graph is insufficient to train transformers effectively, and improving data diversity helps improve model performance. Similar to model scaling, performance saturated at some point when enough data are used.

6. Conclusion

This work revisits the sequential approach to graph generation and proposes a novel token-based representation that efficiently encodes graph structures via node and edge tokens. This representation serves as the foundation for the proposed Graph Generative Pre-trained Transformer (G2PT), an auto-regressive model that effectively models graph sequences using next-token prediction. Extensive evaluations demonstrated that G2PT achieves remarkable performance across multiple datasets and tasks, including generic graph and molecule generation, as well as downstream tasks like goal-oriented graph generation and graph property prediction. The results highlight G2PT's adaptability and scalability, making it a versatile framework for various applications. One limitation of our method is that G2PT is order-sensitive, where different graph domains may prefer different edge orderings. Future research could be done by exploring edge orderings that are more universal and expressive.

Impact Statement This paper introduces a framework that models graphs in a similar vein to GPT (Generative Pre-trained Transformer). The G2PT framework allows seamless plantation of training techniques that have developed in other domains based on GPT. Besides performing generative tasks such as drug discovery, G2PT also can be easily extended for discriminative tasks such as graph property prediction. We hope this work will advance the field of graph learning. As a powerful tool, G2PT may also be used as one step in a complex system to create molecule structures harmful to humans or the environment, but we don't see immediate hazards from our study.

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A. Reinforcement Learning Details

A.1. Preliminaries on Proximal Policy Optimization (PPO)

Generalized Advantage Estimation. In reinforcement learning, the Q function $Q(\mathbf{s}_{<l}, s_l)$ captures the expected returns when taking an action s_l at current state $\mathbf{s}_{<l}$, and the value function $V(\mathbf{s}_{<l})$ captures the expected return following the policy from a given state $\mathbf{s}_{<l}$.

The advantage function $A(s_l, \mathbf{s}_{<l})$, defined as the difference between the Q function and the value function, measures whether taking action s_l is better or worse than the policy's default behavior. In practice, the Q function is estimated using the actual rewards r_l and the estimated future returns (the value function). There are two commonly used estimators, one is the one-step Temporal Difference (TD):

$$\hat{Q}(\mathbf{s}_{<l}, s_l) = r_l + \gamma V(\mathbf{s}_{<l+1}),$$
$$\hat{A}(\mathbf{s}_{<l}, s_l) = r_l + \gamma V(\mathbf{s}_{<l+1}) - V(\mathbf{s}_{<l}),$$

and the full Monte Carlo (MC):

$$\hat{Q}(\mathbf{s}_{<l}, s_l) = \sum_{l'=l}^{L} \gamma^{l'-l} r_{l'},$$
$$\hat{A}(\mathbf{s}_{<l}, s_l) = \sum_{l'=l}^{L} \gamma^{l'-l} r_{l'} - V(\mathbf{s}_{<l}),$$

assuming finite trajectory with L steps in total. However, the TD estimator exhibits high bias and the MC estimator exhibits high variance. The Generalized Advantage Estimation (GAE) (Schulman et al., 2015) effectively balances the high bias and high variance smoothly using a trade-off parameter γ. Let $\delta_l = r_t + \gamma V(\mathbf{s}_{<l+1}) - V(\mathbf{s}_{<l})$, the definition of GAE is:

$$\hat{A}^{\gamma}(\mathbf{s}_{<l}, s_l) = \sum_{l'=l}^{L} (\gamma\lambda)^{l'-l} \delta_{l'} = \delta_l + \hat{A}^{\gamma}(\mathbf{s}_{<l+1}, s_{l+1}).$$

GAE plays an important role in estimating the policy gradient, and will be used in the PPO algorithm.

Proximal Policy Optimization. PPO (Schulman et al., 2017) is a fundamental technique in reinforcement learning, designed to train policies efficiently while preserving stability. It is built on the principle that gradually guides the policy towards an optimal solution, rather than applying aggressive updates that could compromise the stability of the learning process.

In traditional policy gradient methods, the new policy should remain close to the old policy in the parameters space. However, proximity in parameter space does not indicate similar performance. A large update step in policy may lead to falling "off the cliff", thus getting a bad policy. Once it is stuck in a bad policy, it will take a very long time to recover.

PPO introduces two kinds of constraints on policy updates. The first kind is to add an KL-regularization term to the policy gradient "surrogate" objective

$$\mathcal{L}_{\text{pg-penalty}}(\phi) = \hat{\mathbb{E}}_l \left[\frac{p_\phi(s_l|\mathbf{s}_{<l})}{p_{\phi_{\text{old}}}(s_l|\mathbf{s}_{<l})} \hat{A}_l \right] - \beta \text{KL}(p_{\phi_{\text{old}}}(\cdot|\mathbf{s}_{<l}) \| p_\phi(\cdot|\mathbf{s}_{<l})).$$

Here $\hat{\mathbb{E}}_l[\cdot]$ is the empirical average over a finite batch of samples where sampling and optimization alternates. β is the penalty factor. $\hat{A}_l := \hat{A}^{\gamma}(\mathbf{s}_{<l}, s_l)$ is GAE, which is detailed in last section.

The second type is the **clipped surrogate objective**, expressed as

$$\mathcal{L}_{\text{pg-clip}}(\phi) = \hat{\mathbb{E}}_l \left[\min \left(\frac{p_\phi(s_l|\mathbf{s}_{<l})}{p_{\phi_{\text{old}}}(s_l|\mathbf{s}_{<l})} \hat{A}_l, \text{clip}\left(\frac{p_\phi(s_l|\mathbf{s}_{<l})}{p_{\phi_{\text{old}}}(s_l|\mathbf{s}_{<l})}, 1-\epsilon, 1+\epsilon \right) \hat{A}_l \right) \right],$$

where $\frac{p_\phi(s_l|\mathbf{s}_{<l})}{p_{\phi_{\text{old}}}(s_l|\mathbf{s}_{<l})}$ is the probability ratio between the new and the old policy. And ϵ decides how much the new policy can deviate from the one policy. The clipping operations prevent the policy from changing too much from the older one within one iteration. In the following, we elaborate on how the critic model is optimized.

	QM9	MOSES	GuacaMol	Planar	Tree	Lobster	SBM
#Node Types	4	8	12	1	1	1	1
#Edge Types	4	4	4	1	1	1	1
Avg. #Nodes	8.79	21.67	27.83	64	64	55	104.01
Min. #Nodes	1	8	2	64	64	10	44
Max. #Nodes	9	27	88	64	64	100	187
#Training Sequences	9,773,200	141,951,200	111,863,300	12,800,000	10,000,000	12,800,000	12,800,000
Vocabulary Size	27	60	120	73	73	110	195
Max Sequence Length	85	207	614	737	383	599	3950

Table 6. Dataset statistics.

Value Function Approximation. The critic model $V_\psi(\mathbf{s}_{<l})$ in PPO algorithm is used to approximate the actual value function $V^p(\mathbf{s}_{<l})$. We use the mean absolute value loss to minimize the difference between the predicted values and the actual return values. Specifically, the objective is

$$\mathcal{L}_{\text{critic}}(\psi) = \hat{\mathbb{E}}_l\left[|V_\psi(\mathbf{s}_{<l}) - \hat{V}(\mathbf{s}_{<l})|\right].$$

Here the actual return value is estimated using GAE to balance the bias and variance:

$$\hat{V}(\mathbf{s}_{<l}) = \hat{A}(\mathbf{s}_{<l}, s_l) + V_{\psi_{\text{old}}}(\mathbf{s}_{<l}),$$

where $V_{\psi_{\text{old}}}(\mathbf{s}_{<l})$ is collected during the sampling step in PPO. The critic loss is weight by a factor ρ_2.

A.2. KL-regularization

As mentioned in §4.1, we adopt a KL-regularized reinforcement learning approach. Unlike the KL penalty in $\mathcal{L}_{\text{pg-penalty}}(\phi)$, this regularizer ensures that the policy model p_ϕ does not diverge significantly from the reference model p_θ. Instead of optimizing this term directly, we incorporate it into the rewards r_l. Specifically, we define:

$$r_l^{\rho_1} = r_l - \rho_1 \text{KL}(p_\phi(\cdot|[\mathbf{s}_{<l}, s_l]) \| p_\theta(\cdot|[\mathbf{s}_{<l}, s_l])),$$

where ρ_1 is the penalty factor. In practice, ρ_1 is set to a small value, such as 0.03, to promote exploration.

A.3. Pre-training loss

Following Zheng et al. (2023) and Liu et al. (2024), we incorporate the pre-training loss $\mathcal{L}_{\text{pt}}(\phi)$ o mitigate potential degeneration in the model's ability to produce valid sequences. This is particularly beneficial for helping the actor model recover when it "falls off the grid" during PPO. The pre-training data is sourced from the dataset used to train the reference model, and the loss $\mathcal{L}_{\text{pt}}(\phi)$ is weighted by the coefficient ρ_3.

B. Additional Experimental Details

B.1. Graph Generative Pre-training

Generative pre-training leverages graph-structured data to learn foundational representations that can be fine-tuned for downstream tasks.

Sequence conversion. We convert graphs into sequences of tokens that represent nodes and edges. This transformation involves encoding the molecular structure in a sequential format that captures both the composition and the order of assembly. For instance, we iteratively process the nodes and edges, and insert special tokens to mark key points in the sequence, such as the start and end of generation. Additionally, we apply preprocessing steps like filtering molecules by size, removing hydrogens, or addressing dataset-specific constraints to ensure consistency and suitability for the target tasks.

Data splitting. We divide generic datasets into training, validation, and test sets based on splitting ratios 6:2:2. For the molecular datasets, we follow the default settings of the datasets.

	10M	85M	300M
Architecture			
#layers	6	12	24
#heads	6	12	16
d_{model}	384	768	1024
dropout rate		0.0	
Training			
Lr		1e-4	
Optimizer		AdamW (Loshchilov & Hutter, 2019)	
Lr scheduler		Cosine	
Weight decay		1e-1	
#iterations		300000	
Batch size	60	60	30
#Gradient Accumulation	8	8	16
Grad Clipping Value		1	
#Warmup Iterations		2000	

Table 7. Hyperparameters for graph generative pre-training.

Dataset statistics. The vocabulary size, maximum sequence length, and other parameters vary across datasets due to their distinct molecular characteristics. We summarize the specifications in Table 6, which includes details on the number of node types, edge types, and graphs for each dataset.

Hyperparameters. Table 7 provides hyperparameters used for training three distinct model sizes, corresponding to approximately 10M, 85M, and 300M parameters, respectively.

B.2. Demonstration Experiment

We elaborate on how to represent adjacency matrix as sequence and train a transformer decoder on it. We choose planar graphs as the investigation object as it requires a model to be able to capture the rule embedded in the graph. We use $\text{G2PT}_{\text{small}}$ for this experiment.

Sequence conversion. We convert a 2-D adjacency matrix into a 1-D sequence before training the models. Similar to GraphRNN (You et al., 2018b), we consider modeling the strictly lower triangle of the adjacency matrix. To obtain sequence, we flatten the triangle by concatenating the rows together. The i-th row has $i-1$ entries, where each entry is either 0 or 1. We employ BFS to determine the node orderings, which is used to permute the rows and columns of the adjacency matrix to reduce the learning complexity (as uniform orderings are generally harder to fit (Chen et al., 2021)).

Training transformers on adjacency matrices. After obtaining the sequence representation, we prepend and append two special tokens, [SOG] and [EOG], to mark the start and end of the generation of each sequence. The sequence is then tokenized using a vocabulary of size 4, and the transformer is trained on these sequences. Note that no additional token is needed to indicate transitions between rows, as the flattened sequence maintains a fixed correspondence between positions and the referenced node pairs. Specifically, the original row and column indices in the adjacency matrix for the i-th entry in the sequence can be determined as:

$$\text{row} = \left\lceil \frac{1+\sqrt{1+8i}}{2} \right\rceil, \text{col} = i - \frac{(\text{row}-1)(\text{row}-2)}{2}.$$

Here $\lceil \cdot \rceil$ is the ceiling operation. Such correspondence is agnostic to graph size and can be inferred by transformers by using positional embeddings.

	QED	SA	GSK3β
γ		1.0	
λ		1.0	
ρ_1		0.5	
ρ_2	0.03	0.03	0.05
ρ_3		0.03	
Advantage Normalization and Clipping	Yes	No	No
Reward Normalization and Clipping	No	Yes	Yes
Ratio Clipping (ϵ)		[0.2]	
Critic Value Clipping		[0.2]	
Entropy Regularization		No	
Gradient Clipping Value		1.0	
Actor Lr		1.0	
Critic Lr	0.5	0.5	1.0
#Iterations		6000	
Batch size		60	

Table 8. Hyperparameters used for PPO training.

B.3. Fine-tuning G2PT for Goal-oriented Generation

For the goal-oriented generation, we fine-tune G2PT to generate molecules with desired characteristics. Specifically, we consider three properties that are commonly used for molecule optimization whose functions are easily accessed through the Therapeutics Data Commons (TDC) package (Huang et al., 2022).

- Quantitative evaluation of druglikeness (QED): range 0-1, the higher the more druglike.
- Synthesis accessibility (SA) score: range 1-10, the lower the more synthesizable.
- GSK3β: activity against target protein Glycogen synthase kinase 3 beta, range 0-1, the higher the better activity.

We use the 85M model pre-trained on GucaMol dataset for all experiments. Below we elaborate on how the RFT and RL algorithms implement each optimization task (property).

Rejection-sampling fine-tuning. For RFT algorithm without SBS, we begin by generating samples using the pre-trained model and retain only those that meet the criteria defined by the acceptance function $m_\omega^{z^*}(\cdot)$. We collect 200,000 qualified samples from the generations. Then, we fine-tune the model by initializing it with pre-trained parameters. When combining RFT with SBS, we repeat this process iteratively, using the fine-tuned model from the previous iteration for both sampling and parameter initialization.

For QED score, we retain samples with scores exceeding thresholds of 0.4, 0.6, 0.8, or 0.9. We do not use the SBS algorithm here, as the pre-trained model generates samples efficiently across all QED score ranges.

For SA score, we consider thresholds of $\{< 3.0, < 2.0, < 1.5\}$. We find that the pre-trained model efficiently generates molecules with SA scores below 2.0 and 3.0 but struggles with scores below 1.5. To address this, we bootstrap the fine-tuned model from the 2.0 threshold to the 1.5 threshold.

For GSK3β, we consider thresholds in $\{> 0.2, > 0.4, > 0.6, > 0.8\}$. We observe that the pre-trained model's score distribution is skewed towards 0, making it challenging to generate satisfactory samples. To resolve this, we fine-tune the model at the 0.2 threshold and progressively bootstrap it through intermediate thresholds (0.4, 0.6) up to 0.8, performing three bootstrapping steps in total.

All models are trained for 6000 iterations, with batch size of 120 and learning rate of 1e-5. The learning rate gradually decay to 0 using Cosine scheduler.

Reinforcement learning. We use the PPO algorithm to further optimize the pre-trained model. In practice, the token-level reward $R([\mathbf{s}_{<l}, s_l])$ is set to 0 except when $s_l = [\text{EOG}]$. The final reward $r(\mathbf{s})$ for the three properties are designed as follow:

$$r^{\text{QED}}(\mathbf{s}) = \mathbb{1}_{s \to G} \max(0.2, 2 \times (\text{QED}(G) - 0.5)), \tag{1}$$

$$r^{\text{SA}}(\mathbf{s}) = \mathbb{1}_{s \to G} \max(0.2, 0.2 \times (5 - \text{SA}(G)), \tag{2}$$

$$r^{\text{GSK3}\beta}(\mathbf{s}) = \mathbb{1}_{s \to G}(5 \times (\text{GSK3}\beta(G)). \tag{3}$$

The indicator function $\mathbb{1}_{s \to G}$ assigns 0 to the final reward when the generated sequence $\mathbf{s}$ is invalid. We show the PPO hyperparameters for each targeted task in Table 8.

B.4. Fine-tuning G2PT for Graph Property Prediction

Datasets. We use eight classification tasks in MoleculeNet (Wu et al., 2018a) following Zhu et al. (2024) to validate the predictive capability of our learned representations.

The datasets cover two types of molecular properties: biophysical and physiological properties.

- Biophysical properties include (1) the HIV dataset for HIV replication inhibition, (2) the Maximum Unbiased Validation (MUV) dataset for virtual screening with nearst neighbor search, (3) the BACE dataset for inhibition of human β-secretase 1 (BACE-1), and (4) the Side Effect Resource (SIDER) dataset for grouping the side effects of marketed drugs into 27 system organ classes.

- Physiological properties include (1) the Blood-brain barrier penetration (BBBP) dataset for predicting barrier permeability of molecules targeting central nervous system, (2) the Tox21, (3) the ClinTox, and (4) the ToxCast datasets that are all associated with certain type of toxicity of the chemical compounds.

We adopt the scaffold split that divides train, validation and test set by different scaffolds, introduced by Wu et al. (2018b).

Fine-tuning details. We fine-tune $\text{G2PT}_{\text{small}}$ and $\text{G2PT}_{\text{base}}$ pre-trained on GuacaMol dataset for the downstream tasks. We setup the dropout rate to 0.5 and use a learning rate of 1e-4 for training the linear layer. For the half transformer blocks, we use a learning rate of 1e-6. We use a batch size of 256 and train the models for 100 epochs. Test result with best validation performance is reported.

B.5. Baselines

We evaluate our proposed method against a variety of baselines across different datasets. The baselines include models that span diverse methodologies, ranging from graph neural networks to transformer-based architectures.

Generic graph datasets. The performance of baseline models on Planar, Tree, Lobster, and SBM datasets is shown in Table 2. We consider baselines mainly from two categories: auto-regressive and diffusion graph models. Among them, GRAN (Liao et al., 2019), BiGG (Dai et al., 2020), and BwR (Diamant et al., 2023) are auto-regressive models that sequentially generate graphs. GRAN uses attention-based GNNs to perform block-wise generation, focusing on dependencies between components within the graph. In contrast, BiGG addresses the challenges of efficiency by leveraging the sparsity of real-world graphs to avoid constructing dense representations. Unlike GRAN and BiGG, BwR simplifies the generation process further by restricting graph bandwidth. On the other hand, DiGress (Vignac et al., 2022) and HSpectra (Bergmeister et al., 2023) are built based on diffusion frameworks. DiGress is the first approach that uses a discrete diffusion model to iteratively modify graphs, while HSpectra focuses on multi-scale graph construction by progressively generating graphs through localized denoising diffusion.

Molecule generation datasets. We compare G2PT against four baselines: DiGress (Vignac et al., 2022), DisCo (Xu et al., 2024), Cometh (Siraudin et al., 2024), and DeFoG (Qin et al., 2024). Among them, DisCo and Cometh are both based on a continuous-time discrete diffusion framework, with Cometh additionally incorporating positional encoding for nodes and separate noising processes for nodes and edges. DeFoG adopts a discrete flow matching approach with a linear interpolation noising process.

Graph pre-training methods. We compare against several pre-training approaches for molecular property prediction, as summarized in Table 5. The goal ofGraph pre-training methods is to learn robust graph representations via exploiting the structural information. AttrMask (Hu et al., 2020a) uses attribute masking at both node and graph levels to capture local and global features simultaneously. ContextPred (Hu et al., 2020a) builds on this idea by predicting subgraph contexts, enabling the model to understand patterns beyond individual attributes. Similarly, InfoGraph (Sun et al., 2020) focuses on multi-scale graph representations by maximizing mutual information between graph-level embeddings and substructures. Moving to contrastive learning approaches, GraphCL (You et al., 2021) applies graph augmentations to generate positive and negative samples for representation learning. Building on this idea, GraphMVP (Liu et al., 2022a) incorporates both 2D molecular topology and 3D geometric views, aligning them within a contrastive framework to enhance feature representation. In contrast to these methods, GraphMAE (Hou et al., 2022b) adopts a generative approach, using a masked graph auto-encoder to reconstruct node features and capture structural information.

B.6. Evaluation

Metrics for molecule datasets. As MOSES and GuacaMol are established benchmarking tools, they provide predefined metrics for evaluating and reporting results. These metrics are briefly outlined as follows: Validity assesses the percentage of molecules that satisfy basic valency constraints. Uniqueness evaluates the fraction of molecules represented by distinct SMILES strings, indicating non-isomorphism. Novelty quantifies the proportion of generated molecules absent from the training dataset. The filter score represents the percentage of molecules that satisfy the same filtering criteria applied during test set construction. The Frechet ChemNet Distance (FCD) (Preuer et al., 2018) quantifies the similarity between molecules in the training and test sets based on neural network-derived embeddings. SNN computes the similarity to the nearest neighbor using the Tanimoto distance. Scaffold similarity compares the distributions of Bemis-Murcko scaffolds, and KL divergence measures discrepancies in the distribution of various physicochemical descriptors.

For QM9 dataset, the validity metric reported in this study is calculated by constructing a molecule using RDKit and attempting to generate a valid SMILES string from it, as this approach is commonly employed in the literature. However, as explained by Jo et al. (2022b), this method has limitations, as it may classify certain charged molecules present in QM9 as invalid. To address this, they propose a more lenient definition of validity that accommodates partial charges, offering a slight advantage in their computations.

Metrics for generic graph datasets. We adopt the evaluation framework outlined by (Martinkus et al., 2022) and (Bergmeister et al., 2024), incorporating both dataset-agnostic and dataset-specific metrics. The dataset-agnostic metrics evaluate the alignment between the distributions of the generated graphs and the training data by analyzing general graph properties. Specifically, we characterize graphs based on their node degrees (Deg.), clustering coefficients (Clus.), orbit counts (Orbit), eigenvalues of the normalized graph Laplacian (Spec.), and statistics derived from a wavelet graph transform (Wavelet). To quantify the alignment, we compute the distances between the empirical distributions of these statistics for the generated and test graphs using Maximum Mean Discrepancy (MMD).

Subsequently, we evaluate the generated graphs using dataset-specific metrics under the V.U.N. framework, which measures the proportions of valid (V), unique (U), and novel (N) graphs. Validity is determined by dataset-specific criteria: graphs must be planar, tree-structured, or statistically consistent with a Stochastic Block Model (SBM) for the planar, tree, and SBM datasets, respectively. Uniqueness evaluates the proportion of non-isomorphic graphs among the generated samples, while novelty quantifies the proportion of generated graphs that are non-isomorphic to any graph in the training set.

B.7. Computation Resources.

We ran all pre-training tasks and all goal-oriented generation fine-tuning tasks run on 8 NVIDIA A100-SXM4-80GB GPU with distributed training. For PPO training and graph property prediction tasks, we ran experiments using a A100 GPU.

C. Extended Related works

C.1. Auto-regressive Graph Generative Models

Even though graph is naturally an unordered set, auto-regressive models generate graphs sequentially, one node, edge, or substructure at a time. GraphRNN and DeepGMG (You et al., 2018b; Li et al., 2018) prefix a canonical ordering (e.g., breath-first search) for the nodes and edges and generates nodes and edges associated with them step by step. On the contrary,

Algorithm 4 Depth-First search edge order generation

Input: Graph $G = (V, E)$, neighborhood function Nei.$(\cdot)$.
Output: Sequence of traversed edges σ_E.
Initialize $\sigma_E \leftarrow [\,]$, sample v_0 from V.

DFS_helper (v):
for $v' \in$ Nei(v) **do**
  $e = (v, v')$.
  if v' is not visited **then**
    Append e to σ_E.
    Call **DFS_helper**(v').
  else
    if $e \notin \sigma_E$ **then**
      Append e to σ_E.
    end if
  end if
end for

Run **DFS_helper**(v_0).

Algorithm 5 Breadth-First Search edge order generation

Input: Graph $G = (V, E)$, neighborhood function Nei$(\cdot)$.
Output: Sequence of traversed edges σ_E.
Initialize $\sigma_E \leftarrow [\,]$, sample v_0 from V, initialize queue $\leftarrow [v_0]$.
while queue is not empty **do**
  $v \leftarrow$ queue.popfirst()
  for $v' \in$ Nei(v) **do**
    $e = (v, v')$.
    if v is not visited **then**
      append e to σ_E, append v' to queue.
    else
      if $e \notin \sigma_E$ **then**
        append e to σ_E.
      end if
    end if
  end for
end while

Bacciu et al. (2020) propose to generate edges first then the connected nodes subsequently. These auto-regressive models are also broadly adapted into applications such as molecule generation. GCPN (You et al., 2018a), and REINVENT (Olivecrona et al., 2017) both leverage pre-trained auto-regressive models to fine-tune with a reward model to generate molecules with desired properties.

C.2. Non-auto-regressive Graph Generative Models

In addition to auto-regressive models, non-auto-regressive graph generative models can be categorized into two branches: (1) one-shot generation and (2) iterative refinement. One-shot generation aims to generate a graph in a single step including methods such as generative adversarial networks (De Cao & Kipf, 2018), variational auto-encoders (Simonovsky & Komodakis, 2018; Liu et al., 2018) and normalizing flows (Madhawa et al., 2019; Zang & Wang, 2020). Nevertheless, one-shot graph generative models often suffer from the decoding strategies such that it requires an expressive decoder to map from latent vectors to graphs. On the other side, iterative refinement methods generate the entire graph in the first step and then iteratively refine the generated graph to be close to a realistic graph, including diffusion (Niu et al., 2020; Jo et al., 2022a; Vignac et al., 2022; Chen et al., 2022b; 2023; Jo et al., 2023; Haefeli et al., 2022; Wu et al., 2023; Siraudin et al.,

Algorithm 6 Uniform edge order genration

Input: Graph $G = (V, E)$
Output: Sequence of edge ordering σ_E
Initialize $\sigma_E \leftarrow [\,]$
while E is not empty **do**
  sample e from E, append e to σ_E
  Remove e from E
end while

Model	Edge Orderings	Validity↑	Unique.↑	Novelty↑	Filters↑	FCD↓	SNN↑	Scaf↑
$G2PT_{small}$	Degree-based	95.1	**100**	91.7	97.4	1.1	0.52	5.0
	DFS	91.6	**100**	87.1	98.0	1.2	**0.55**	8.9
	BFS	**96.2**	**100**	86.8	**98.3**	**1.0**	**0.55**	**10.6**
	Uniform	62.9	**100**	**99.4**	52.0	7.0	0.38	9.5
$G2PT_{base}$	Degree-based	96.4	**100**	86.0	98.3	**0.97**	**0.55**	3.3
	DFS	91.9	**100**	83.7	98.1	1.13	**0.55**	7.5
	BFS	**96.9**	**100**	84.6	**98.7**	0.98	**0.55**	**11.1**
	Uniform	80.9	**100**	**97.0**	83.9	2.14	0.46	10.3

Table 9. Sensitivity analysis on edge orderings.

2024; Xu et al., 2024; Wang et al., 2025) and flow matching models (Qin et al., 2024; Eijkelboom et al., 2024; Lipman et al., 2022; Liu et al., 2022b; Campbell et al., 2024; Gat et al., 2024). As discussed in **??**, they often require a prefixed number of refinement steps and they need to maintain an adjacency matrix over the trajectory which is computationally intensive.

C.3. Pre-training Transformers for Graphs

Transformers are now dominating domains of natural language processing (NLP) and computer vision (CV) (Radford, 2018; Devlin, 2018; Dosovitskiy, 2020). Several works also attempt to applying transformers in the field of graph learning (Ying et al., 2021; Hu et al., 2020b; Dwivedi & Bresson, 2020; Rampášek et al., 2022; Chen et al., 2022a; Wu et al., 2021; Kreuzer et al., 2021; Min et al., 2022; Chen et al., 2024; Gao et al., 2024). Those approaches propose several methods to encode the graph structure information into sequences, specifically, the key research problem lies in how to add identifiers to nodes and tokenize the edges. For instance, Kim et al. (2022) uses positional embedding to help transformer to identify nodes, and type embeddings to distinguish node and edge tokens. A more recent work, Gao et al. (2024), which focuses on molecule representation learning, uses a vocabulary to store all atom types and all possible bond types (same bonds with different atoms as endpoints are considered as different type in their case). In contrast, by introducing node index into the vocabulary, G2PT easily implements the edge tokenizations and node identifications.

D. Additional Results

D.1. Sensitivity Analysis of Edge Orderings

We investigate how the employed edge orderings will affect the generative performance of G2PT. Specifically, we consider four orderings: the reverse of edge-removal process (Alg. 1), DFS ordering (Alg. 4), BFS ordering (Alg. 5), and uniform ordering (Alg. 6). We train $G2PT_{small}$ and $G2PT_{base}$ on MOSES dataset and evaluate the performance.

Result. Table 9 reports the performance of different edge orderings. BFS and degree-based edge-removal orderings both exhibit superior results, while DFS orderings show moderate performance. Particularly, uniform ordering shows poor performance in capturing the sequence distribution. This result highlights the importance of choosing the right ordering families for generating sequences.

D.2. Additional Visualizations

We further visualize the generic graph in Figure 4, and molecular graph in Figure 5. The results show that both $G2PT_{small}$ and $G2PT_{base}$ have the ability to capture the topological rules of the training graphs.

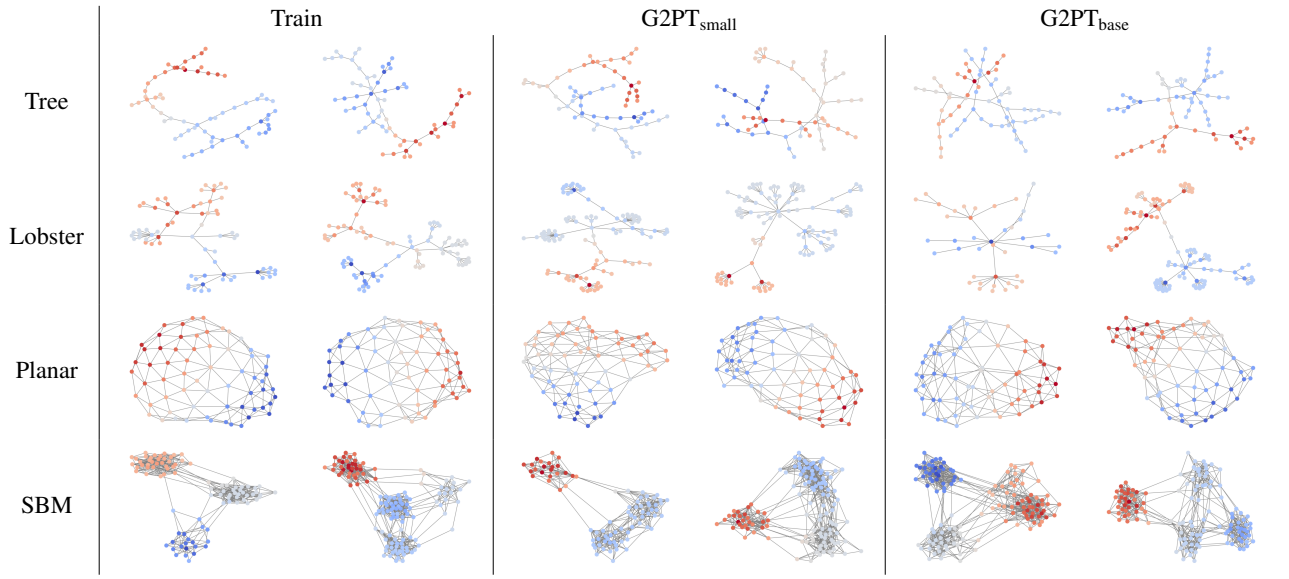

Figure 4. The visualization of generic graph datasets

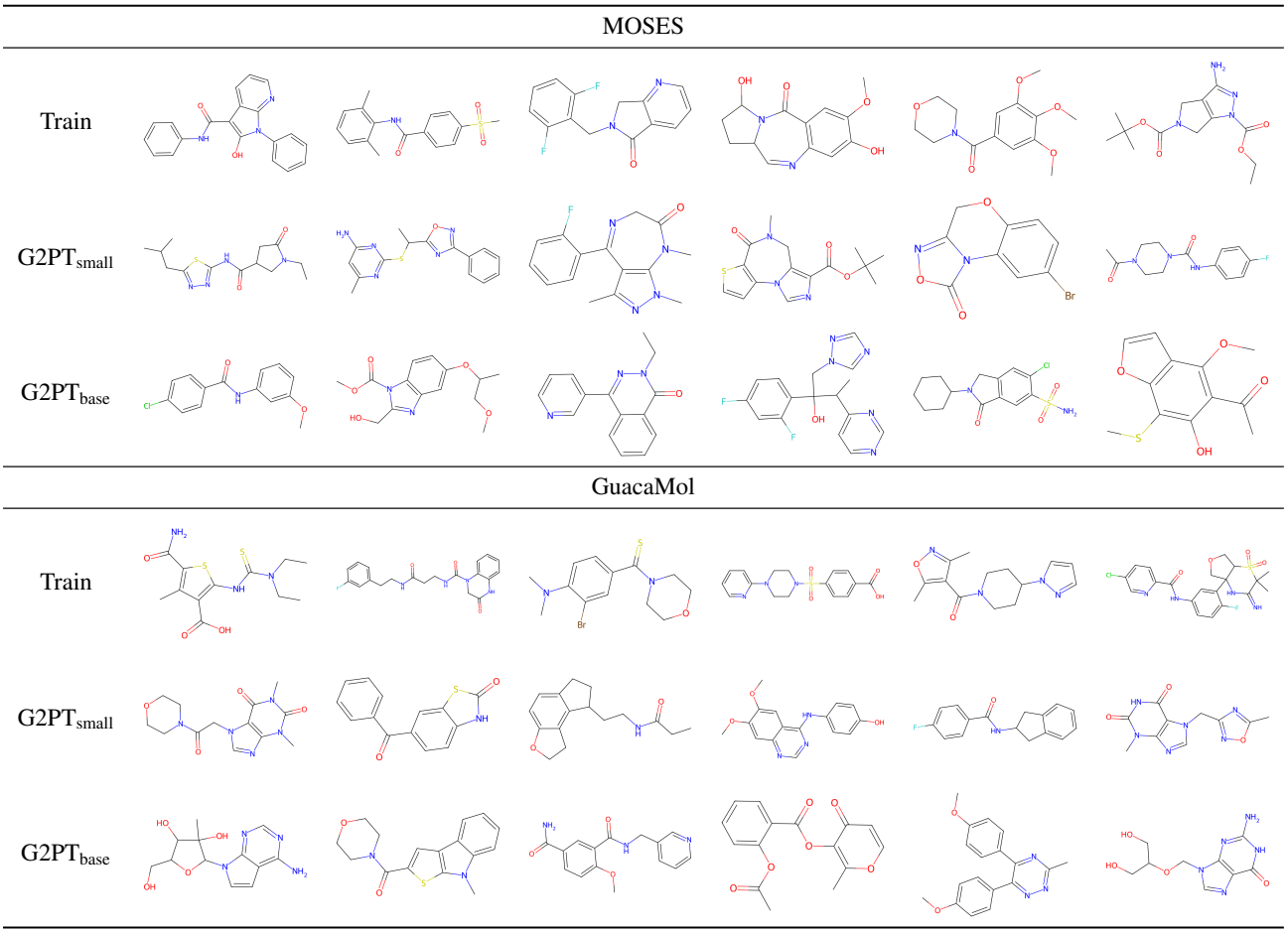

Figure 5. The visualization of molecular datasets