

*Graph Convolutional  
Policy Network (GCPN) for  
Goal-Directed Molecular  
Graph Generation*

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# The Problem

- *Drug discovery and material science are based on the principles of designing molecular structures with specific desired properties.*
- *The space is massive though ( $10^{23}$  -  $10^{60}$  drug-like molecules)*
- *Chemical space is discrete and molecular properties are highly sensitive to small changes in molecular structure.*



# *Progress in Molecular Design*

- Molecule generation has been achieved via DL models
- Achieving objectives of chemical and biological properties has been difficult because these are highly complex and non-differentiable goals.

# *The Solution: Graph Convolutional Policy Network*

- Combines 3 machine learning concepts:
  - Graph Representation: Used to obtain vector representation of the state of generated graphs
  - Reinforcement Learning: Trains the model end-to-end
  - Adversarial Training: adversarial loss used as reward to incorporate prior knowledge specified by dataset of example molecules

# *Graph Representation*

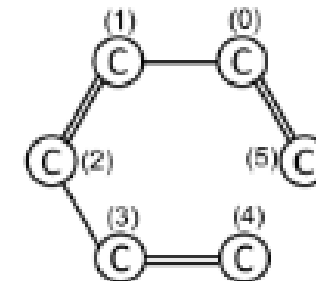
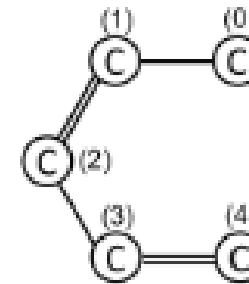
- Benefits over SMILE representation
  - Partial Graphs can be seen as substructures, but partial text-representations are not meaningful
  - If one character is changed in SMILE, it can change the entire structure or invalidate it.

# Graph Representation

- The graphs are represented as  $(A, E, F)$ 
  - $A \in \{0, 1\}^{n \times n}$  – Adjacency Matrix
  - $E \in \{0, 1\}^{b \times n \times n}$  - Edge-conditioned adjacency tensor where there are  $b$  possible edge types
    - $E_{i,j,k} = 1$  if  
there exists an edge of type  $i$  between nodes  $j$  and  $k$
  - $F \in \mathbb{R}^{n \times d}$  – Node Feature matrix where each node has  $d$  features

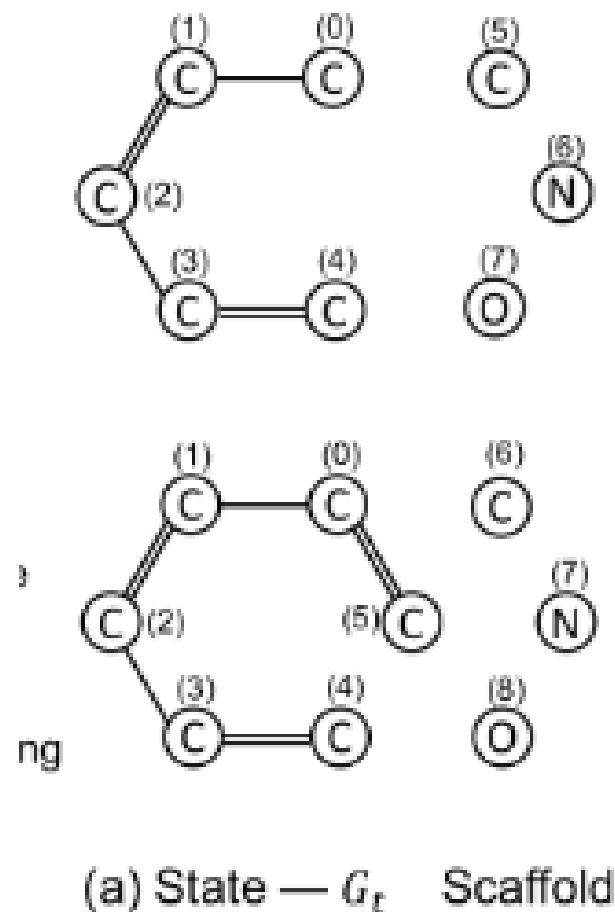
# Graph Generation: State Space

- An intermediate graph  $G_t$  at time step  $t$
- Initially starts as a single node that represents a carbon atom



# Graph Generation: Action Space

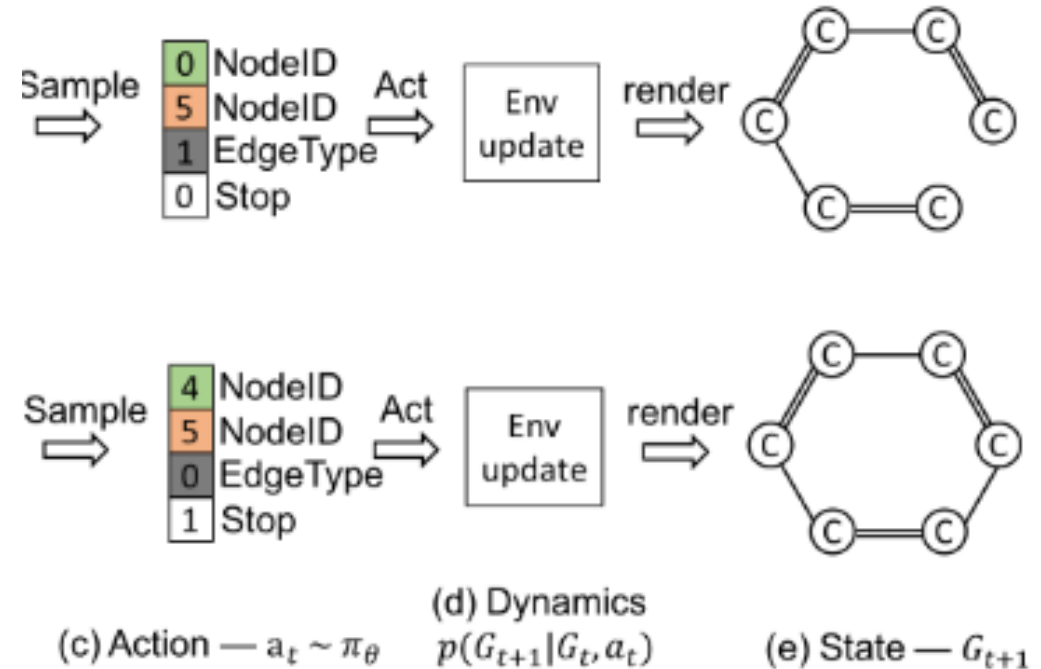
- Consists of a set of scaffold subgraphs  $\{C_1, \dots, C_s\}$
- An action can either consist of connecting a scaffold to the current graph  $G_t$  or connecting nodes already within the graph.
- A scaffold generally has single node representations of all the possible atoms desired for a molecule.





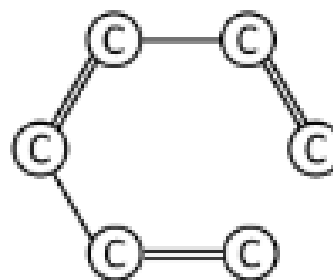
# Graph Generation: State Transition Dynamics

- This controls whether an action can be considered valid given a set of rules
- If an action results in an invalid state, that action is rejected and the state remains unchanged

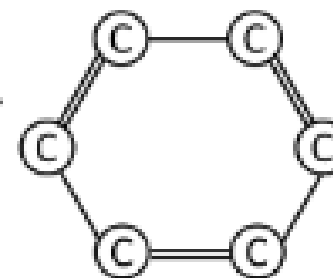


# Graph Generation: Reward

- Domain Specific rewards
  - Final property scores
    - octanol-water partition coefficient (logP), druglikeness (QED)
  - Unrealistic Molecule Penalties
- Intermediate Rewards
  - Step-wise validity rewards
  - Adversarial rewards (via Generative Adversarial Network)



0.1	Step reward
0	Final reward



0.1	Step reward
1	Final reward

(e) State —  $G_{t+1}$

(f) Reward —  $r_t$

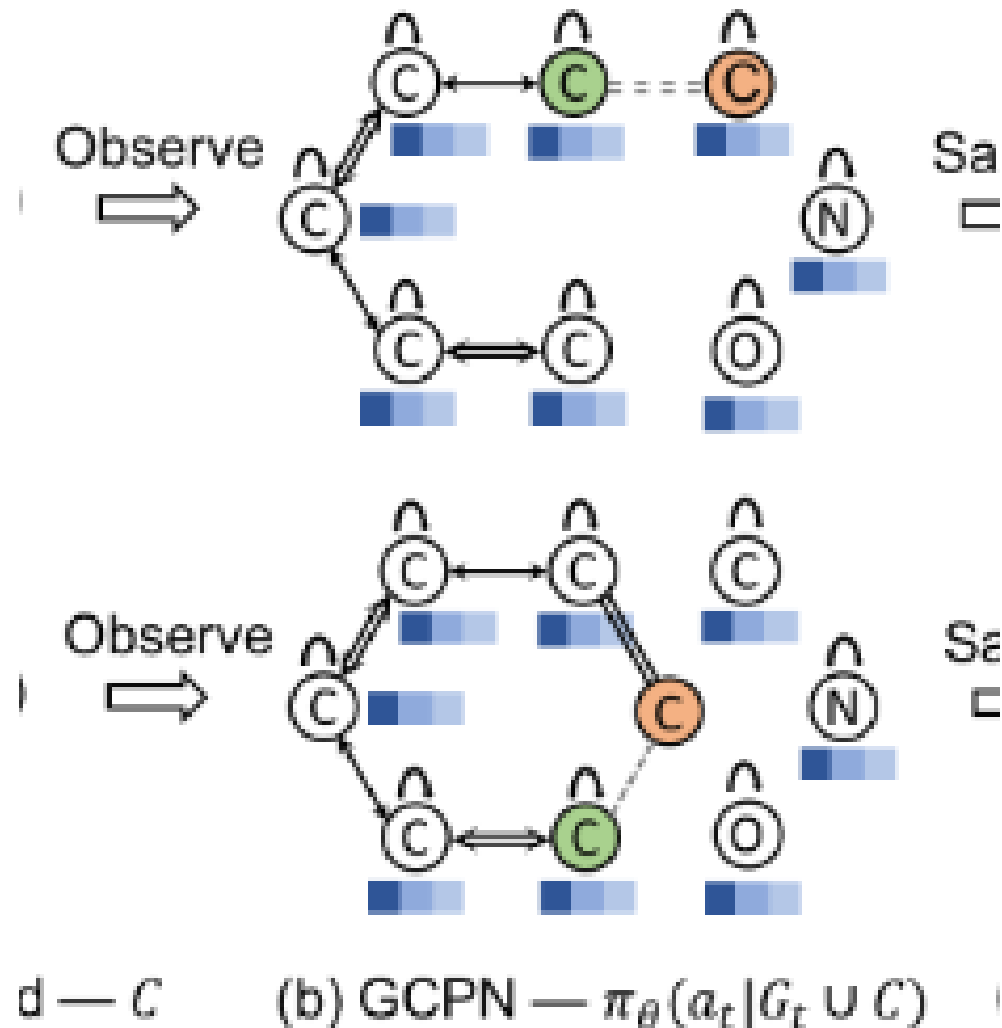
# Graph Convolutional Policy Network: Link Prediction

Node embeddings are computed via Graph Convolutional Networks using information from each edge type over  $L$  layers

These are aggregated at the  $l^{th}$  layer to compute the next layer node embedding.

Actions are then predicted by selection of two nodes and prediction if there will be an edge or termination

Multilayer Perceptrons (MLP) are used to achieve this



# Policy Gradient Training

- Allows for optimization of policy networks
- Specifically adopted Proximal Policy Optimization (PPO)
  - PPO computes an update at each step that minimizes the cost function while ensuring the deviation from the previous policy is relatively small
- Network can be pretrained on known molecules
  - A sampling of a graph  $G$  and randomly selecting one of its subgraphs  $G'$  results in a state  $s_t$
  - An action  $a_t$  can be defined as the addition of any atom or bond to the  $G'$  thus resulting in the pair  $(s_t, a_t)$

# *Experiments: Evaluation Tasks*

- Three tasks were used for evaluation of GCPN against state-of-the-art molecule generation algorithms
  - Property Optimization - Generate novel molecules whose specified molecular properties are optimized
  - Property Targeting – Generate novel molecules whose specified molecular properties are as close to the target scores as possible
  - Constrained Property Optimization - Generate novel molecules whose specified molecular properties are optimized, while also containing a specified molecular substructure

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# Experiments: Setup

- Dataset: ZINC250K which contains 250,000 drug like commercially available molecules
- Molecule Environment: OpenAI Gym using RDKit and adapted to ZINC250k (Max atom # = 38, 9 atom types, 3 edge types)
- Rewards
  - [-4, 4] for final chemical property reward
  - [-2, 2] for final chemical filter reward
  - [-1, 1] for final adversarial reward
  - [-1, 1] for intermediate adversarial reward
  - [-1, 1] for intermediate validity reward



# *Experiments: Baselines*

- Junction Tree VAE (JT-VAE) – Combines graph representation and a VAE framework
- ORGAN – RL-based molecule generation algorithm using a text-based representation of molecules



# Results

Table 1: Comparison of the top 3 property scores of generated molecules found by each model.

Method	Penalized logP				QED			
	1st	2nd	3rd	Validity	1st	2nd	3rd	Validity
ZINC	4.52	4.30	4.23	100.0%	0.948	0.948	0.948	100.0%
Hill Climbing	—	—	—	—	0.838	0.814	0.814	100.0%
ORGAN	3.63	3.49	3.44	0.4%	0.896	0.824	0.820	2.2%
JT-VAE	5.30	4.93	4.49	100.0%	0.925	0.911	0.910	100.0%
GCPN	<b>7.98</b>	<b>7.85</b>	<b>7.80</b>	<b>100.0%</b>	<b>0.948</b>	<b>0.947</b>	<b>0.946</b>	<b>100.0%</b>

# Results

Table 2: Comparison of the effectiveness of property targeting task.

Method	$-2.5 \leq \log P \leq -2$		$5 \leq \log P \leq 5.5$		$150 \leq MW \leq 200$		$500 \leq MW \leq 550$	
	Success	Diversity	Success	Diversity	Success	Diversity	Success	Diversity
ZINC	0.3%	0.919	1.3%	0.909	1.7%	0.938	0	—
JT-VAE	11.3%	<b>0.846</b>	7.6%	0.907	0.7%	0.824	16.0%	0.898
ORGAN	0	—	0.2%	<b>0.909</b>	15.1%	0.759	0.1%	0.907
GCPN	<b>85.5%</b>	0.392	<b>54.7%</b>	0.855	<b>76.1%</b>	<b>0.921</b>	<b>74.1%</b>	<b>0.920</b>

The diversity of a set of molecules is defined as the average pairwise Tanimoto distance between the Morgan fingerprints of the molecules

Table 3: Comparison of the performance in the constrained optimization task.

$\delta$	JT-VAE			GCPN		
	Improvement	Similarity	Success	Improvement	Similarity	Success
0.0	$1.91 \pm 2.04$	$0.28 \pm 0.15$	97.5%	<b><math>4.20 \pm 1.28</math></b>	<b><math>0.32 \pm 0.12</math></b>	<b>100.0%</b>
0.2	$1.68 \pm 1.85$	$0.33 \pm 0.13$	97.1%	<b><math>4.12 \pm 1.19</math></b>	<b><math>0.34 \pm 0.11</math></b>	<b>100.0%</b>
0.4	$0.84 \pm 1.45$	<b><math>0.51 \pm 0.10</math></b>	83.6%	<b><math>2.49 \pm 1.30</math></b>	$0.47 \pm 0.08$	<b>100.0%</b>
0.6	$0.21 \pm 0.71$	$0.69 \pm 0.06$	46.4%	<b><math>0.79 \pm 0.63</math></b>	<b><math>0.68 \pm 0.08</math></b>	<b>100.0%</b>