Generative AI for Synthesizable Antibiotic Design

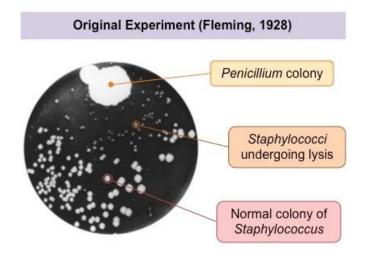
Kyle Swanson, Gary Liu, Denise Catacutan, Autumn Arnold, James Zou, Jonathan Stokes

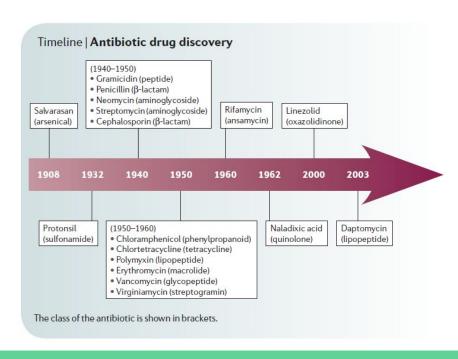
Brief history of antibiotics

1928: Alexander Fleming discovers penicillin

1940-60: Many new antibiotics discovered

1960-now: Few structurally novel antibiotics





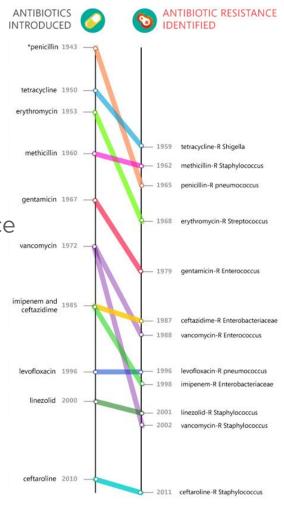
Drug resistant bacteria

Bacteria develop resistance to antibiotics

2019: 1.27 million people likely died from antibiotic resistance

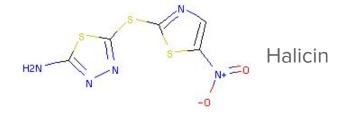
2050: 10 million people may die from resistance annually

Takeaway: We need new antibiotics!



A Deep Learning Approach to Antibiotic Discovery, Stokes, et al., Cell, 2020

Train GNN on 2.5K molecules with known *E. coli* inhibition (5% active)

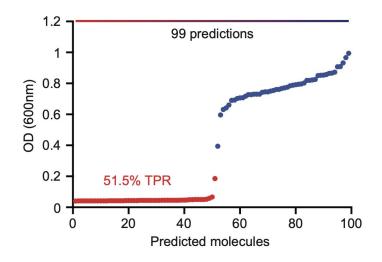


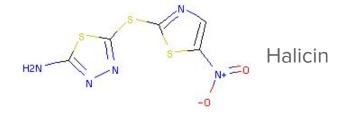
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Predict on 6K molecules

- 51.5% active among top 99 predictions
- Halicin targets multi-drug resistant bacteria





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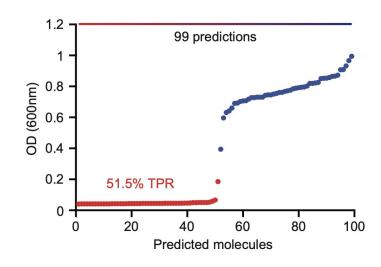
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Predict on 107M molecules

- 4 days of computation
- 8 structurally novel antibiotics among top 23





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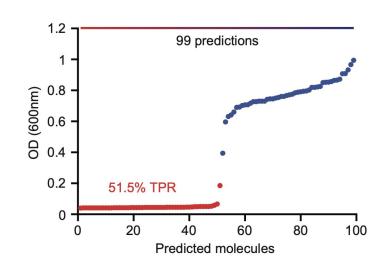
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Limitation: No intelligent search ⇒ scales poorly to larger chemical spaces

Generative models

Model: Generative models directly design molecules with desirable properties

$$\begin{cases} x_{\star}^{\mathcal{G}} \\ X_$$

Benefit: Rapid design of good molecules without slow search

Limitation: Generated molecules are difficult to synthesize ⇒ practically useless

Synthesis-aware generative model

Goals

- 1) Build a generative model that guarantees synthesizability
- 2) Generate, synthesize, and experimentally validate generated molecules

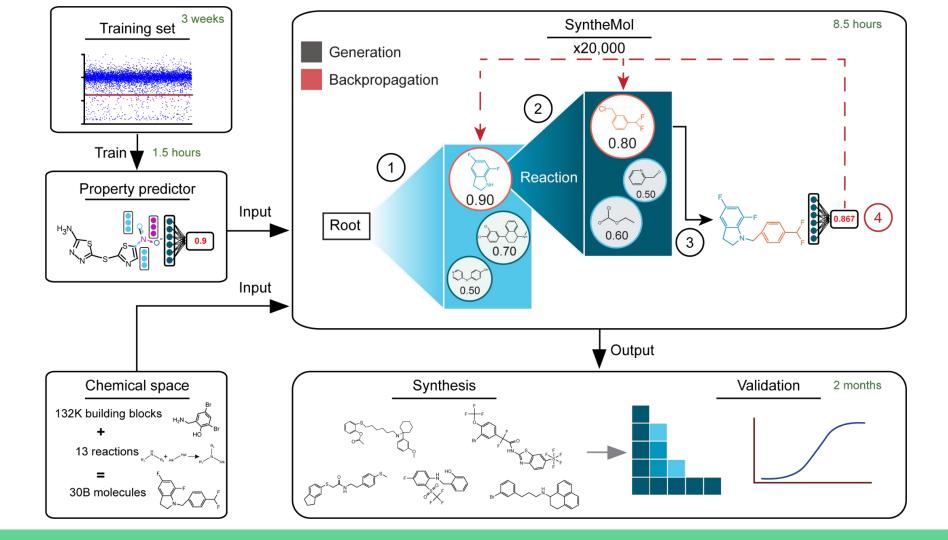
Synthesis-aware generative model

Goals

- 1) Build a generative model that guarantees synthesizability
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Idea: Design molecules with off-the-shelf building blocks + easy chemical reactions

Application: Generate structurally novel antibiotics



Training set

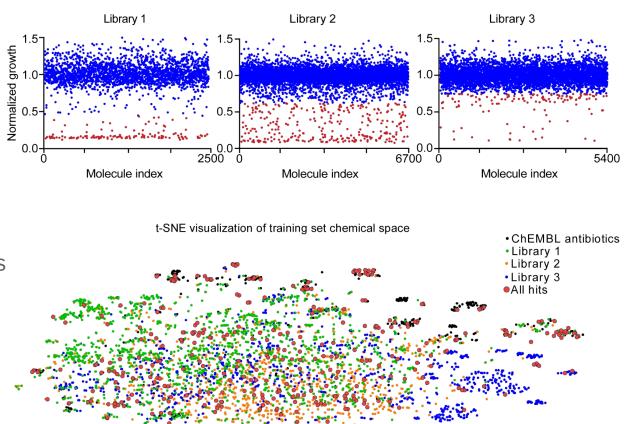
Target: *A. baumannii*

3 libraries

- 2 drug repurposing
- 1 synthetic compounds

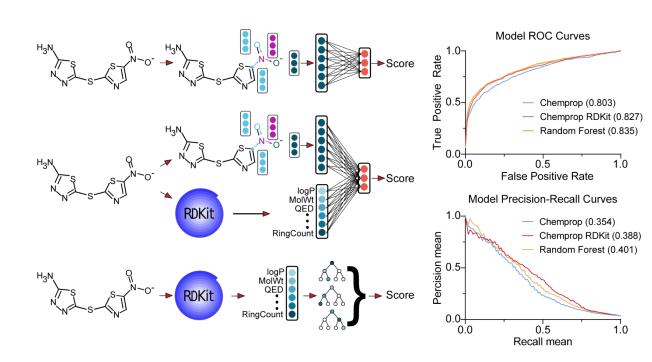
13,524 molecules

- 470 active
- 13,054 inactive



Three models

- 1) Chemprop
 - a) GNN
- 2) Chemprop RDKit
 - a) GNN + 200 features
- 3) Random Forest
 - a) RF on 200 features

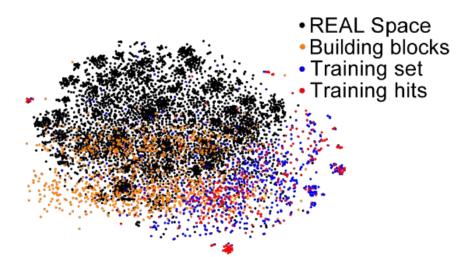


Performance: ROC-AUC = 0.80–0.84 and PRC-AUC = 0.35–0.40 on 10-fold CV

Chemical space

Enamine REAL Space: 31 billion molecules

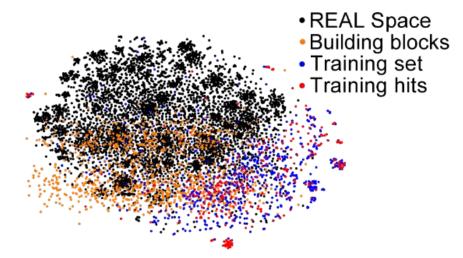
- 138,000 building blocks
- 169 chemical reactions



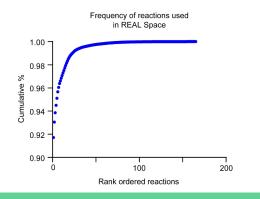
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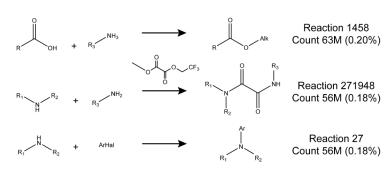
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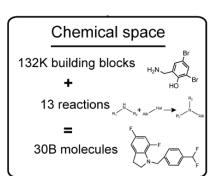
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Simplification: 96.6% of molecules with 13 reactions





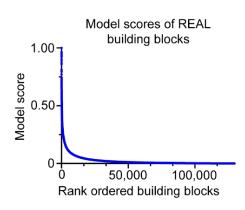


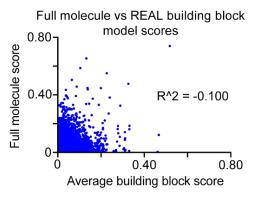
Generative model

Greedy: build molecules with highest scoring building blocks

Problems

- Few building blocks have high scores ⇒ low diversity
- Building block scores not correlated with full molecule





Generative model

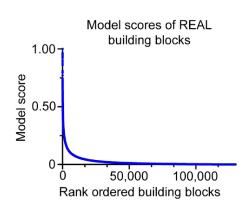
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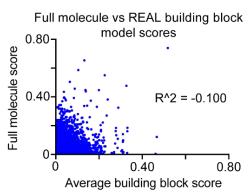
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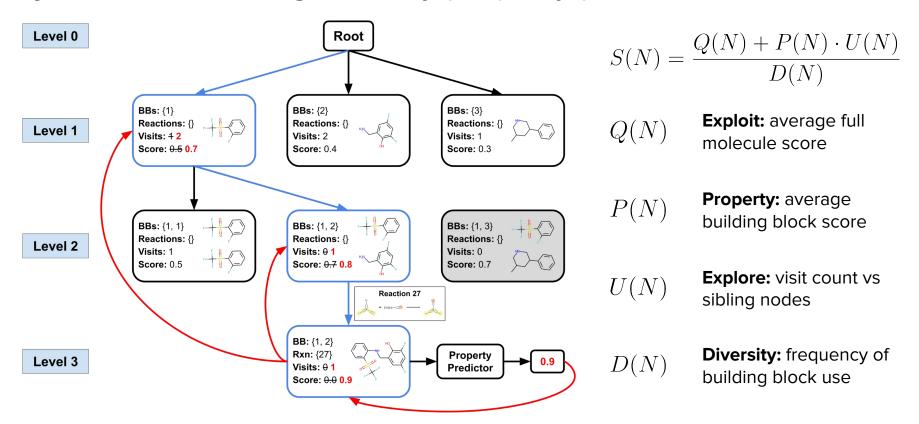
Monte Carlo tree search (MCTS)

- **Exploration:** construct diverse molecules
- **Exploitation:** use full molecule scores to guide search





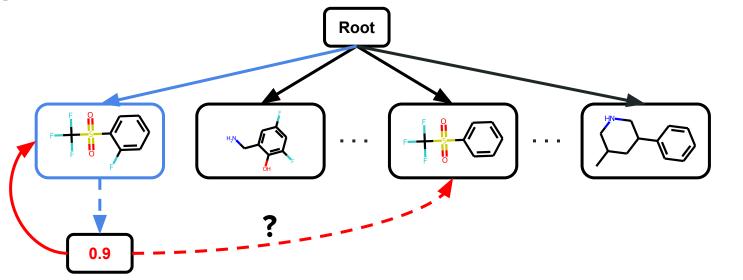
SyntheMol: MCTS guided by property predictor



Limitations of MCTS

Independence: MCTS treats nodes independently, ignoring chemical similarity

Coverage: First level alone has 132k nodes ⇒ cannot test all with 20k rollouts

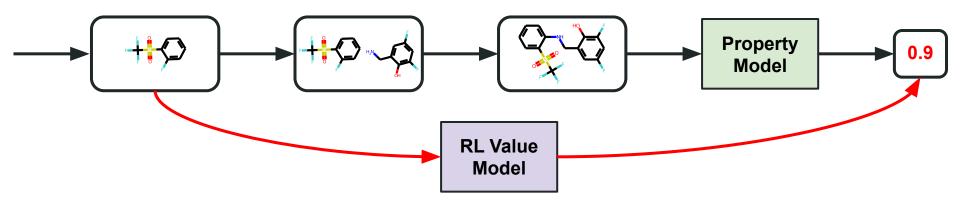


Result: MCTS is not an efficient value function for building blocks

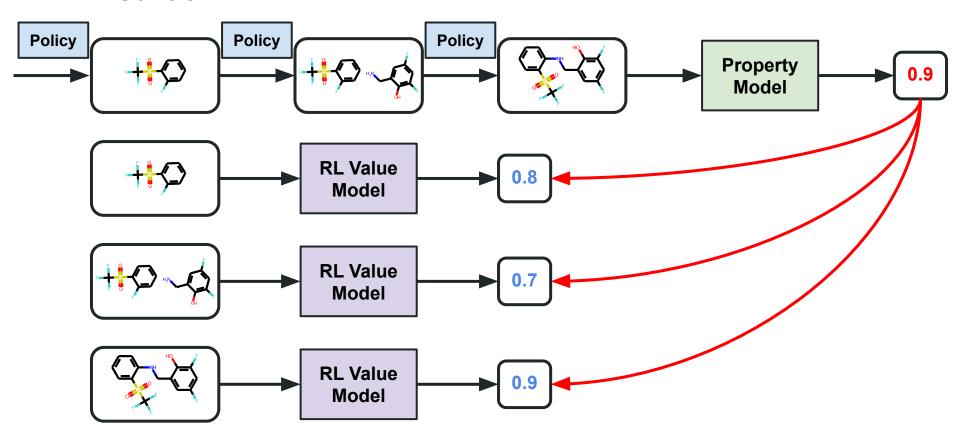
$MCTS \Rightarrow RL$

Idea: Use reinforcement learning (RL) in place of MCTS

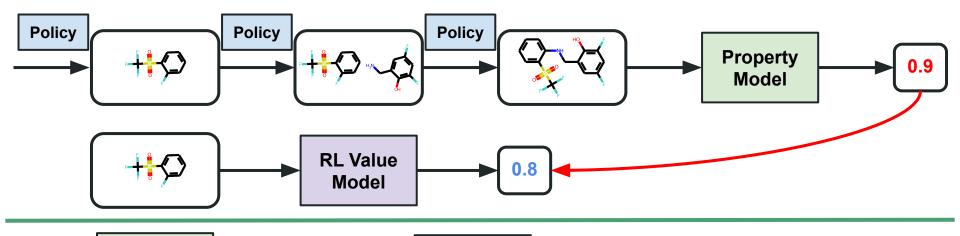
- MCTS computes a value for each BB separately
- **RL** learns a value function that generalizes to chemically similar BBs



RL method



RL method



GNN pretrained to predict molecular property (fixed)

Property

Model

GNN trained to predict full molecule score from building block(s)

RL Value

Model

Sample building blocks proportional to their score with temperature control $P(BB) \propto e^{\mathrm{value}(BB)/T}$

Policy

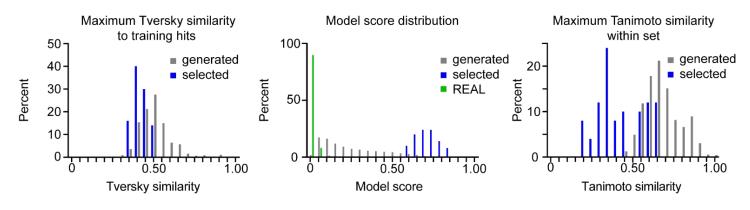
SyntheMol: antibiotic design

Generations: SyntheMol-MCTS for 20,000 rollouts guided by 3 property predictors

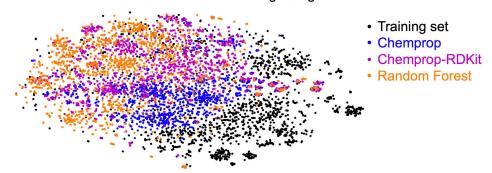
Filters to select optimal molecules

- 1) **Novel:** avoid analogs of known antibiotics
 - a) Tversky similarity(generated, antibiotic) ≤ 0.5
- 2) **Effective:** high property prediction score
 - a) Top 20% of molecules by score
- 3) Diverse: avoid analogs of the same compound
 - a) K-means clustering with Tanimoto similarity

SyntheMol: antibiotic generations



t-SNE visualization of training and generated sets



Synthesis

Selected: 150 molecules (50 each from three models)

Requested: 70 molecules

- Not all 150 molecules are available from Enamine
- Reaction templates are overly simple ⇒ not all matches are synthesizable

Synthesized: 58 molecules (83% success) in four weeks

• 26 Chemprop, 22 Chemprop RDKit, 10 random forest

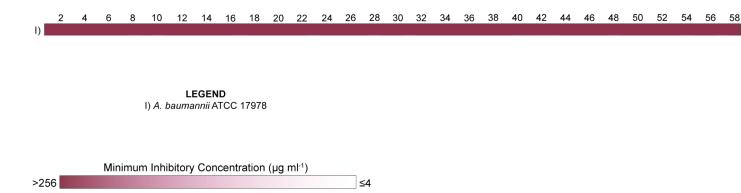
Experiment: Test generated molecules against *A. baumannii*

Same growth inhibition assay as training set creation

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Same growth inhibition assay as training set creation

Result: No molecules worked



Challenge: Killing Gram-negative bacteria like A. baumannii requires two abilities

- 1) Permeability: Pass through double cell wall
- 2) Activity: Inhibit an essential component (e.g., protein)

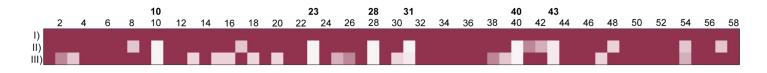
Idea: What if our molecules have activity but lack permeability?

Experiment: Couple generated molecules with a permeabilizer

>256

Experiment: Couple generated molecules with a permeabilizer

Result: Six of the molecules are extremely potent



LEGEND

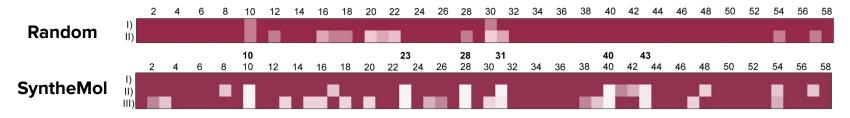
I) A. baumannii ATCC 17978 II) A. baumannii 17978 + 16μg/mL SPR 741 III) A. baumannii 17978 + 0.125 μg/mL Colistin

Minimum Inhibitory Concentration (μg ml⁻¹)
≤4

Experiment: Test randomly selected molecules for comparison

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Result: Generated compounds are more effective than random ones



LEGEND

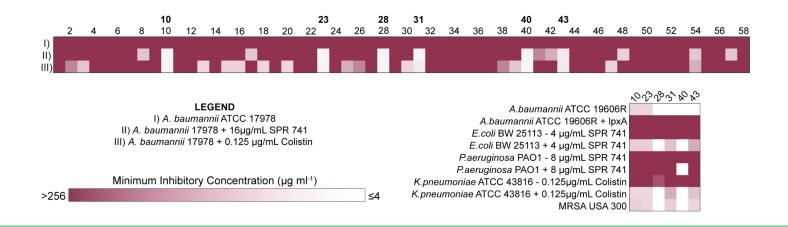
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Minimum Inhibitory Concentration (μg ml⁻¹) >256

Experiment: Test generated molecules against other bacterial species

Experiment: Test generated molecules against other bacterial species

Result: Six potent molecules are broad spectrum (with permeabilizer)



GFlowNet comparison

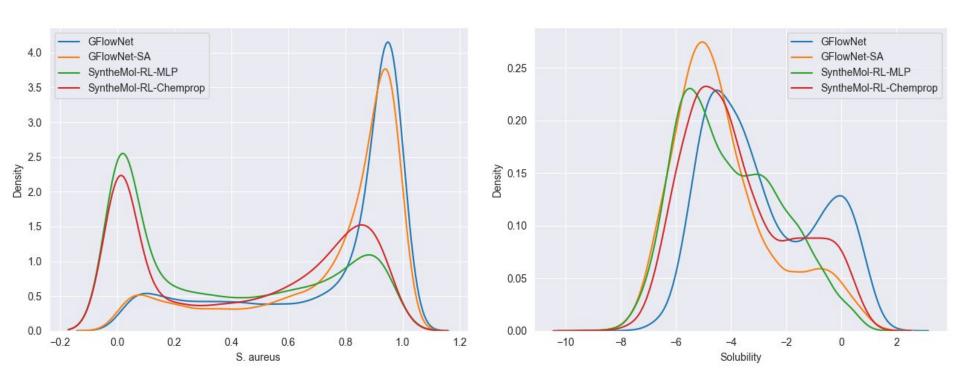
Question: How does SyntheMol compare to other generative models?

Multi-Objective GFlowNets (ICML, 2023)

- GFlowNets use RL + temperature scaling for diverse molecule generation
- Uses arbitrary molecular fragments not from known synthetic routes

Experiment: Modified GFlowNet to optimize for antibiotic efficacy (*S. aureus*), solubility, and optionally SAScore (synthesizability)

GFlowNet vs SyntheMol: generated



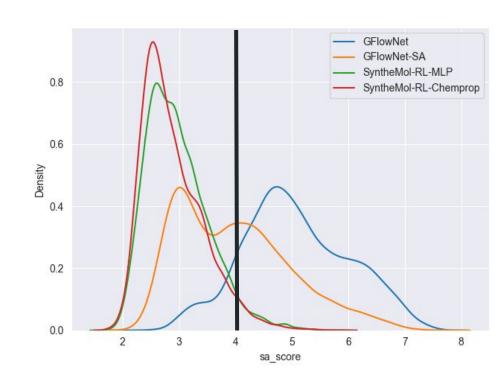
Takeaway: Appears that GFlowNet >> SyntheMol for generating antibiotics

GFlowNet vs SyntheMol: filtering

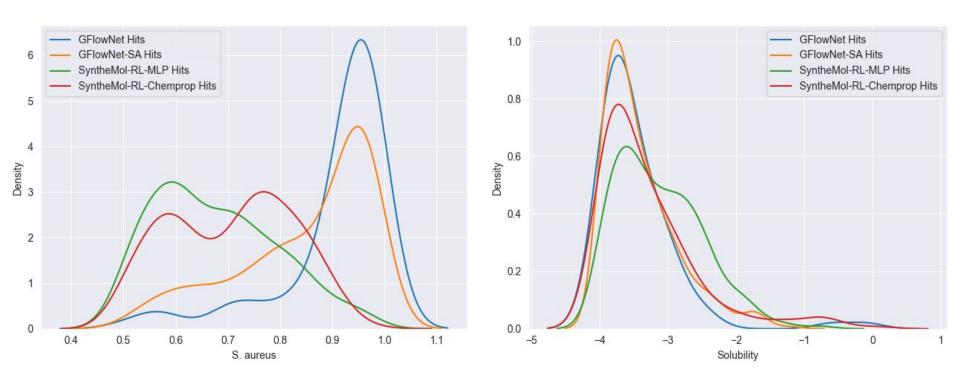
Limitation: GFlowNet molecules are less synthesizability based on SAScore

Synthesis filter: Need synthesizable compounds so filter by SAScore ≤ 4

Selection: Then, apply typical filters for hits, novelty, and diversity

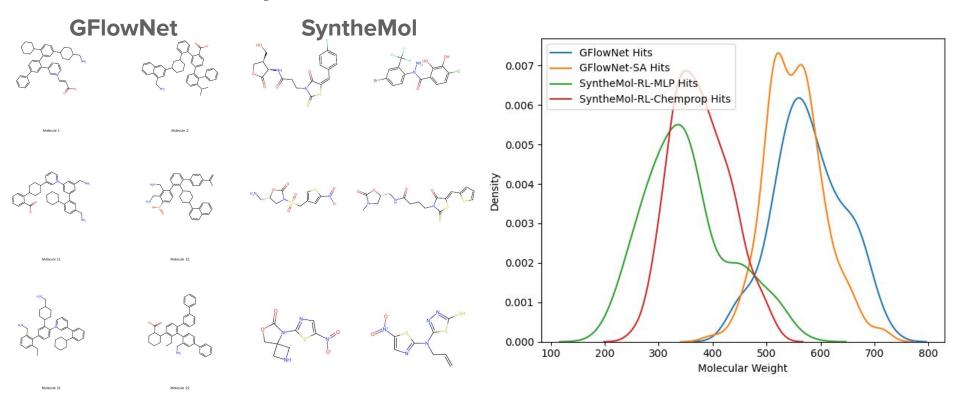


GFlowNet vs SyntheMol: selected



Takeaway: Appears that GFlowNet >> SyntheMol for generating *synthesizable* antibiotics

GFlowNet vs SyntheMol: selected



Takeaway: GFlowNet molecules are bulky, not drug-like, and look difficult to synthesize

GFlowNet: synthesis

Test: Sent 300 GFlowNet compounds to Enamine

Enamine: "...our chemistry group has reviewed list of cpds...and, unfortunately, we are not able to propose a synthesis. Our apologies for the inconvenience caused."

Takeaway: GFlowNet designs impressive molecules according to ML-based objectives, but they are **not easily synthesizable** ⇒ need SyntheMol!

Conclusion

SyntheMol is a synthesis-aware generative model for drug design

⇒ property predictor + MCTS/RL to explore vast chemical spaces

Filters select for novel, effective, and diverse generated molecules

We synthesized and experimentally validated 58 generated molecules

We discovered six highly potent and structurally novel antibiotic candidates

Questions?

