







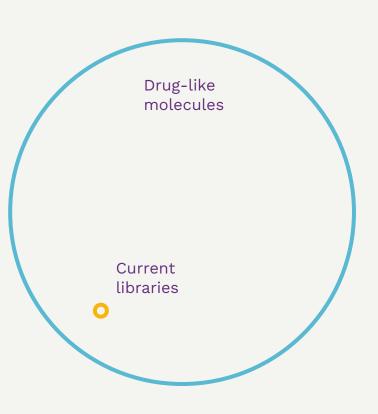
RGFN: Synthesizable Molecular Generation Using GFlowNets

Michał Koziarski*, Andrei Rekesh*, Dmytro Shevchuk*, Almer van der Sloot, Piotr Gaiński, Yoshua Bengio, Cheng-Hao Liu, Mike Tyers, Robert A. Batey

Why generative models?

The size of chemical space of drug-like molecules is often estimated at 10⁶⁰.

Generative models offer a promise of being able to explore that vast space **without** being limited to existing libraries.



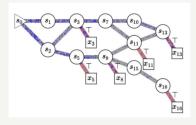
Why GFlowNets?

Generative Flow Networks (GFlowNets) are a relatively new family of generative models.

Goal: generating **high reward**, <u>diverse</u> samples in an **amortized** manner. All crucial in drug discovery!

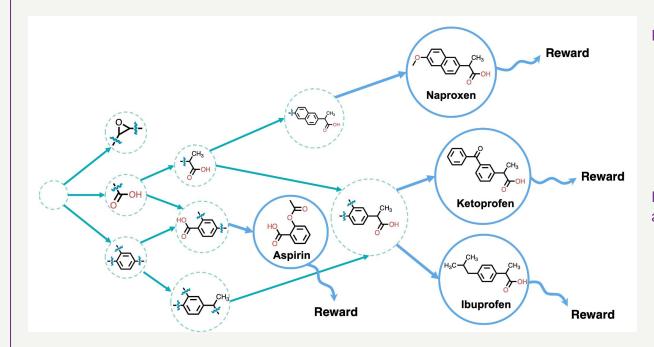
Shortcomings of the existing methods:

- MCMC lack of amortization,
- RL mean-seeking behaviour; mode collapse



How to do it? On high level: ensure that the probability of generating a sample is proportional to its reward: $p(x) \sim R(x)$. This can be done by training a <u>sampling policy</u> $\pi(x)$ (a machine learning model).

GFlowNets for Molecule Design



Key ingredients of GFlowNets:

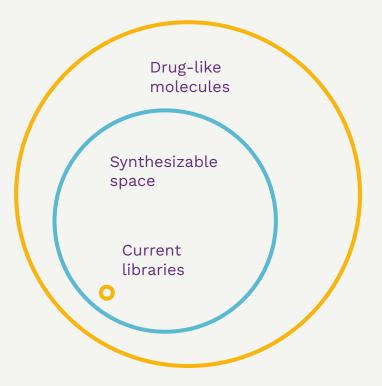
- **State** = current molecule
- Action space = fragments to add
- Reward function = property of interest

How do we ensure molecules are synthesizable?

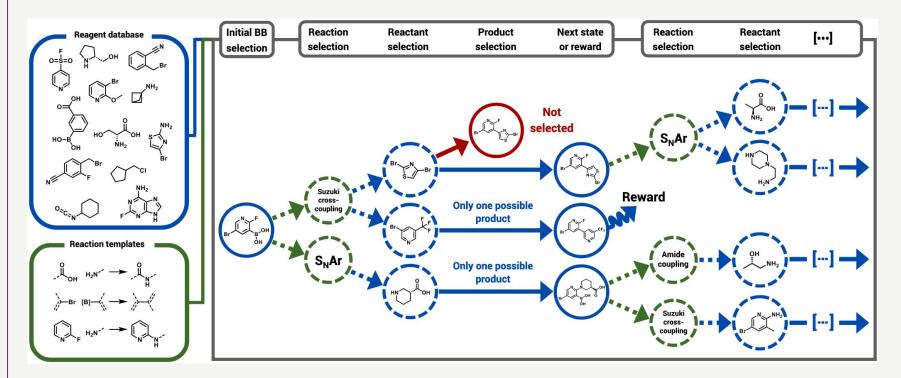
Constraint Trade-Off

The goal: constrain the searchable space to highly synthesizable compounds.

(while increasing the search space size as much as possible!)



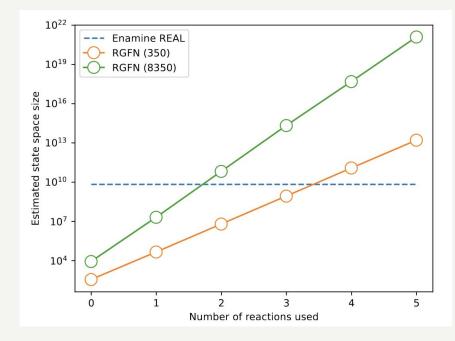
Reaction-GFlowNet

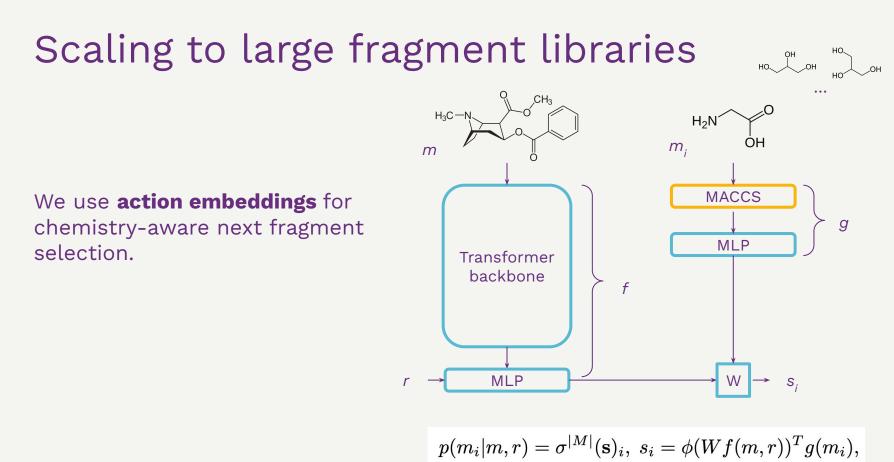


Chemical language

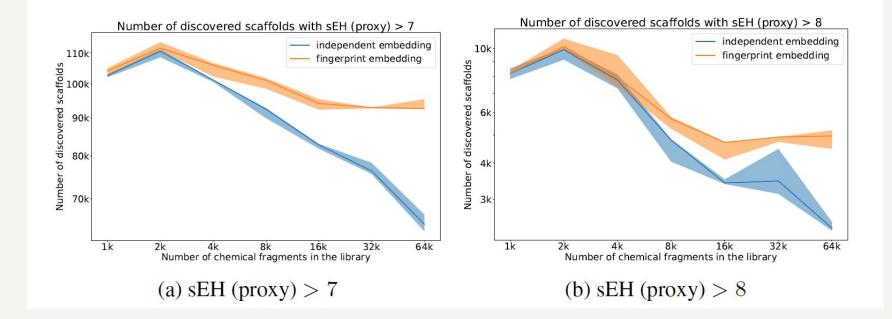
We select a total of **350** affordable reagents (≤\$200/g) **and 17** high-yield reactions.

Combinatorial space generated by this approach with depth 4 is **larger than most compound libraries.**



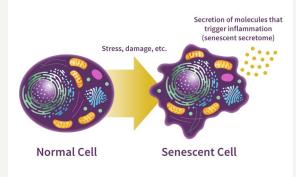


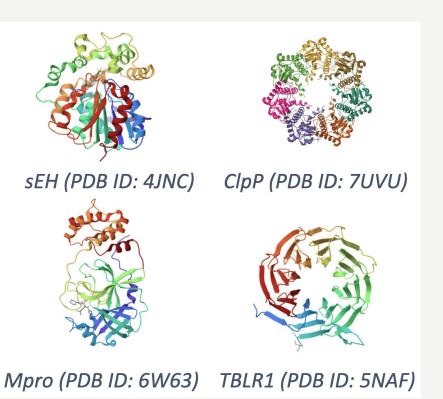
Scaling to large fragment libraries



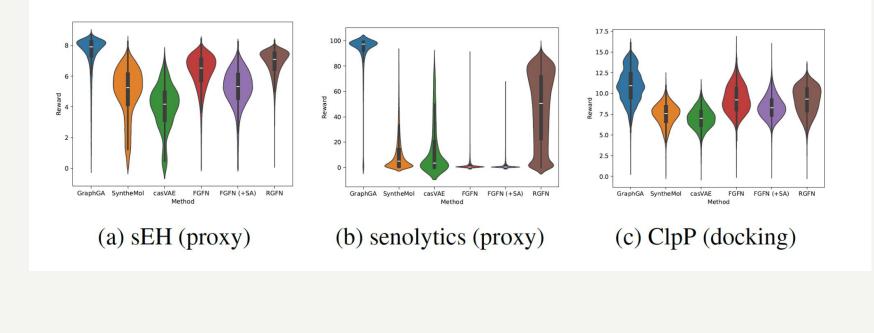
Experimental study

In addition to commonly used <u>sEH proxy</u>, we consider <u>GPU-accelerated docking</u> for several biologically relevant targets, and challenging activity-based <u>senolytic proxy</u>.

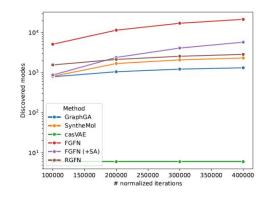


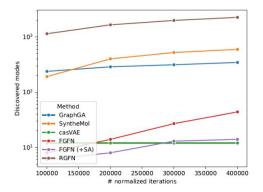


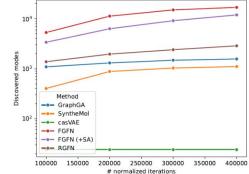
Reward distributions



Discovered modes







(a) sEH (proxy)

(b) senolytics (proxy)

(c) ClpP (docking)

Synthesizability

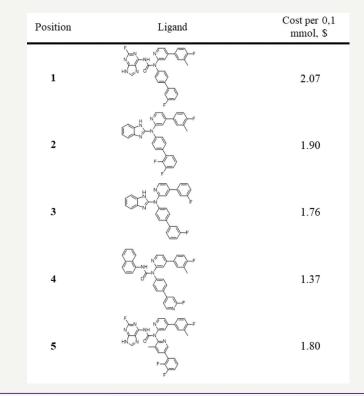
| Task | Method | Mol. weight \downarrow | QED ↑ | SAScore ↓ | AiZynth ↑ |
|-------|-----------|--------------------------|-----------------|-----------------|-------------|
| sEH | GraphGA | 528.6 ± 42.3 | 0.21 ± 0.06 | 3.87 ± 0.24 | 0.04 |
| | SyntheMol | 411.1 ± 66.7 | 0.57 ± 0.18 | 2.85 ± 0.55 | 0.80 |
| | casVAE | 421.6 ± 103.4 | 0.52 ± 0.23 | 2.41 ± 0.47 | 0.82 |
| | FGFN | 473.4 ± 58.9 | 0.39 ± 0.13 | 3.43 ± 0.48 | 0.14 |
| | FGFN+SA | 473.7 ± 62.2 | 0.36 ± 0.12 | 3.01 ± 0.50 | 0.27 |
| | RGFN | 495.2 ± 49.6 | 0.29 ± 0.10 | 3.09 ± 0.39 | 0.56 |
| Seno. | GraphGA | 485.7 ± 75.6 | 0.09 ± 0.05 | 2.92 ± 0.26 | 0.05 |
| | SyntheMol | 441.4 ± 83.5 | 0.48 ± 0.19 | 2.77 ± 0.40 | 0.53 |
| | casVAE | 431.5 ± 100.9 | 0.50 ± 0.19 | 2.82 ± 0.46 | 0.65 |
| | FGFN | 468.9 ± 47.7 | 0.42 ± 0.13 | 3.55 ± 0.52 | 0.02 |
| | FGFN+SA | 451.8 ± 54.5 | 0.32 ± 0.12 | 2.83 ± 0.44 | 0.13 |
| | RGFN | 558.7 ± 62.8 | 0.21 ± 0.09 | 3.24 ± 0.32 | <u>0.58</u> |
| ClpP | GraphGA | 521.0 ± 31.8 | 0.32 ± 0.07 | 4.14 ± 0.51 | 0.00 |
| | SyntheMol | 458.2 ± 60.7 | 0.45 ± 0.16 | 2.86 ± 0.56 | 0.56 |
| | casVAE | 423.0 ± 61.7 | 0.47 ± 0.17 | 2.44 ± 0.41 | 0.84 |
| | FGFN | 548.6 ± 42.9 | 0.22 ± 0.03 | 2.94 ± 0.54 | 0.25 |
| | FGFN+SA | 509.2 ± 52.4 | 0.24 ± 0.04 | 2.61 ± 0.49 | 0.33 |
| | RGFN | 526.2 ± 37.6 | 0.23 ± 0.04 | 2.83 ± 0.22 | 0.65 |

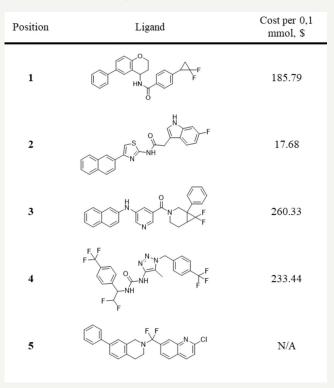
| | High reward | Diverse | Synthesizable |
|-----------|--|---|--|
| GraphGA | Image: A second s | | × |
| SyntheMol | | | \checkmark |
| CasVAE | | | Image: A second s |
| FGFN | Image: A second s | Image: A set of the set of the | |
| FGFN + SA | \checkmark | \checkmark | |
| RGFN | \checkmark | \checkmark | \checkmark |

Estimated synthesis cost

RGFN

SyntheMol





Summary

- RGFN guarantees synthesizability out-of-the-box.
- Chemical language used leads to ~100x lower cost of synthesis.
- Performs well and generates diverse candidates for a set of biologically relevant oracles.
- Flexible to the choice of fragments and reward functions.



Thank you!