

Black Box Recursive Translations for Molecular Optimization

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Summary

- · We propose a new inference method for molecular optimization called Black Box Recursive Translation (BBRT).
- When generated molecules are iteratively fed back into the translator. properties improve with each step -- this finding is invariant to the choice of model.
- BBRT demonstrates results competitive with state-of-the-art for property optimization tasks using simple drop-in replacements with well-established models.
- We show BBRT generates samples with better properties relative to its nonrecursive peers across different decoding strategies and is highly interpretable.

Motivation

Molecular optimization as a translation problem. As in [1], we learn a mapping between sequence pairs $(x, y) \in (X, Y)$ with high chemical similarity, and where y scores higher on a prespecified property compared to x.

• We utilize Seq2Seq with an encoder-decoder framework [2], which learns parameters θ that estimate a conditional probability model $P(v|x,\theta)$, θ is estimated by maximizing the log likelihood:

$$L(\theta) = \sum_{(x,y)\in(X,Y)} \log P(y|x,\theta)$$

 We explore both deterministic (beam search) and stochastic decoding strategies that sample from the model at generation time. $y_t \sim q(y_t | y_{\leq t}, x, p_{\theta}).$

• We consider a top-k sampler [3] which restricts sampling to the k-most probable tokens at time-step t: a subset of vocabulary $U \subset V$ where U maximizes $\sum_{y \in U} p_{\theta}(y_t | y_{y < t}, x)$: (. .

$$q(y_t|y_{< t}, x, p_{\theta}) = \begin{cases} \frac{p_{\theta}(y_t|y_{< t}, x)}{Z} & y_t \in U\\ 0 & otherwise \end{cases}$$

initial seed compound.

Penalized logP: Choose compound with max. logP value

QED. Choose compound with max. QED value.

Max Δ **Sim**. Choose compound with highest chemical

Max Init Sim. Choose compound with highest similarity to

Min Mol Wt. Choose compound with min. molecular weight.

similarity to previous iteration's source compound.

Recursive Inference

- We recursively infer new sequences, where $\{y_i^k\}_{k=1}^{k}$ is a set of *K* outputs generated from $p(y_i|x)$ at i = 0.
- We introduce functions S (right) to score K output sequences to determine subsequent iteration's source sequence $\hat{y_i}$. We infer K outputs from $p(y_i|\hat{y_{i-1}})$ for n iterations.
- After n iterations, we ensemble the outputs $\{y_0, y_1, \dots, y_n\}_{k=1}^K$ and score the sequences on a desired objective. For property optimization, we return the argmax.



• We apply recursive translation to both		Penalized logP			QED		
	Method	1st	2nd	3rd	1st	2nd	3rd
sequence- and graph-	ZINC-250K	4.52	4.30	4.23	0.948	0.948	0.948
based translation models and report top 3	ORGAN JT-VAE	3.63 5.30	3.49 4.93	3.44 4.49	0.896 0.925	0.824 0.911	0.820
property scores on penalized logP and QED optimization tasks against baseline models.	GCPN JTNN Seq2Seq	7.98 5.97 4.65	7.85 4.96 4.53	7.80 4.71 4.49	0.948 0.948 0.948	0.947 0.948 0.948	0.946 0.948 0.948
	BBRT-JTNN BBRT-Seq2Seq	10.13 6.74	10.10 6.47	9.91 6.42	0.948 0.948	0.948 0.948	0.948 0.948

· We find stochastic decoding methods outperformed deterministic methods on average logP scores and average pairwise diversity for generated compounds as a function of recursive iteration.

Experiments

• We report top 100 logP generated compounds under both BBRT models, and nonrecursive counterparts (left and center) as well as diversity of top 100 generated compounds and training set (right).



 Top scoring compounds for logP and QED under both BBRT models below: for loaP. BBRT-JTNN produces compounds with higher property values and BBRT-Seq2Seq generates compounds with a richer molecular vocabulary.

 BBRT generates interpretable paths of optimization (left) that facilitate understanding of design trade-offs We highlight alternative translations for compound (2) below (right):



	Input	logP	QED	Mol Wt.	RB.	Sim.
(2) 3.146 sim = 0.77 (3) 3.303 (3) 3.00	Conditions and the	3.15	0.56	262.1	6	1.0
(5) 3549 (4) 3545	terteed0005kdeedFiedler1	3.59	0.53	340.0	6	0.44
	00	2.23	0.53	234.1	5	0.47
227 → → → → → → → ↓ → ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓		2.31	0.77	272.1	5	0.23
	Interest Constrained	3.52	0.53	340.0	6	0.77

References

[1] Wengong Jin, Kevin Yang, Regina Barzilay, and Tommi Jaakola. Learning multimodal graph-to-graph translation for molecule optimization. In International Conference on Learning Representations,

[2] Ilya Sutskever, Oriol Vinyals, and Quoc V. Le. Sequence to sequence learning with neural networks. In Proceedings of the 27th International Conference on Neural Information Processing Systems -Volume 2., pp. 3104-3112, 2014.

[3] Angela Fan, Mike Lewis, and Yann N. Dauphin. Hierarchical neural story generation. ACL, pp. 889-898, 2018.

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