

Latent Bayesian Optimization via **Autoregressive Normalizing Flows**

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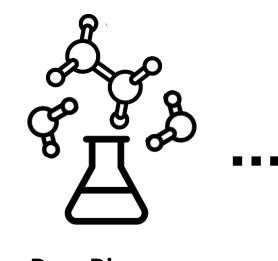


Goal: Optimize a Black-box Function Efficiently

$$\arg\max_{x\in\mathcal{X}}f(x)$$

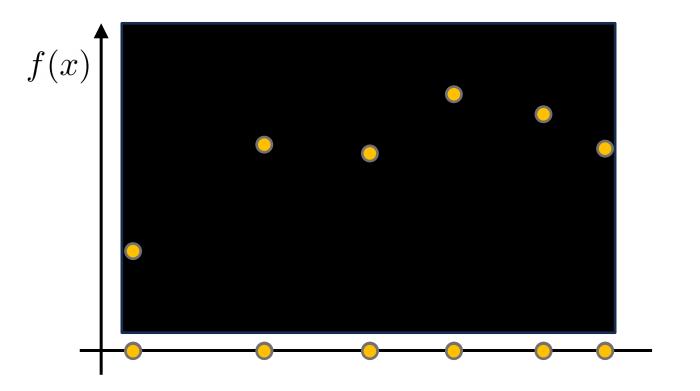


Applications



Drug Discovery

Goal: Optimize a Black-box Function Efficiently



$$\operatorname{arg} \max_{x \in \mathcal{X}} f(x)$$

Objective function f(x)

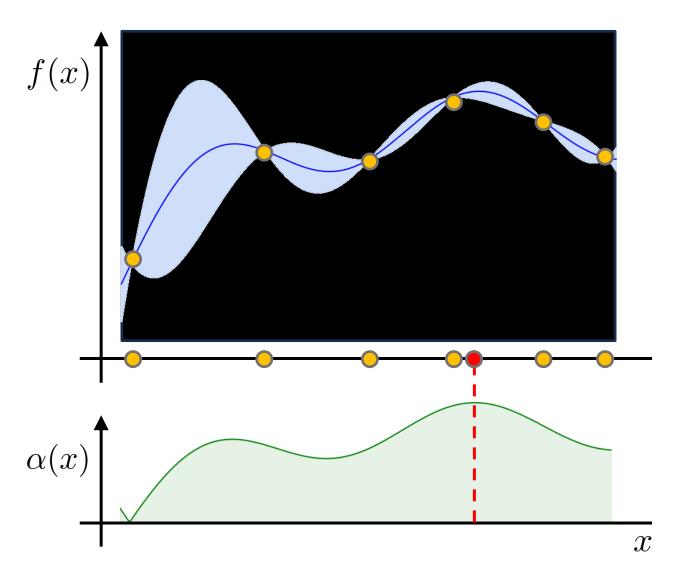
- → Expensive and complex
- → Black-box function

Function evaluation (0)

Derivative/gradient (X)

Goal: Optimize a Black-box Function Efficiently

$$\operatorname{arg} \max_{x \in \mathcal{X}} f(x)$$



Probabilistic surrogate model $\hat{f}(x)$

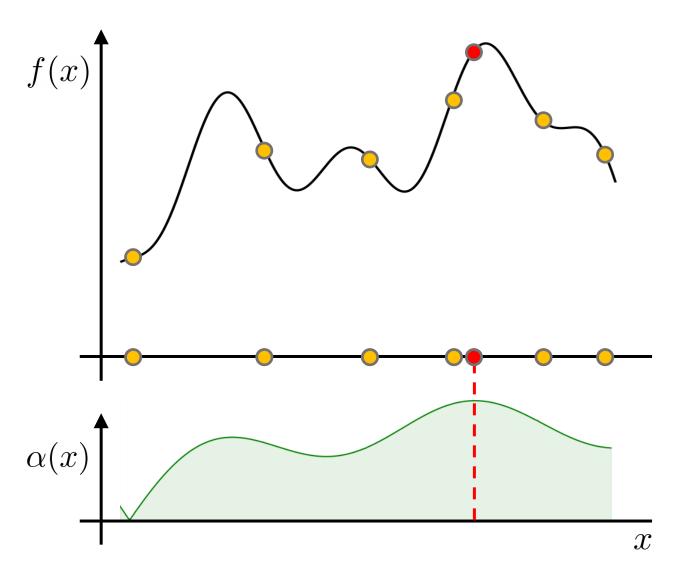
→ predicts objective with uncertainty

Acquisition function $\alpha(x)$

→ scores where to evaluate next

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Feasible set is often Complex

(structured/discrete)





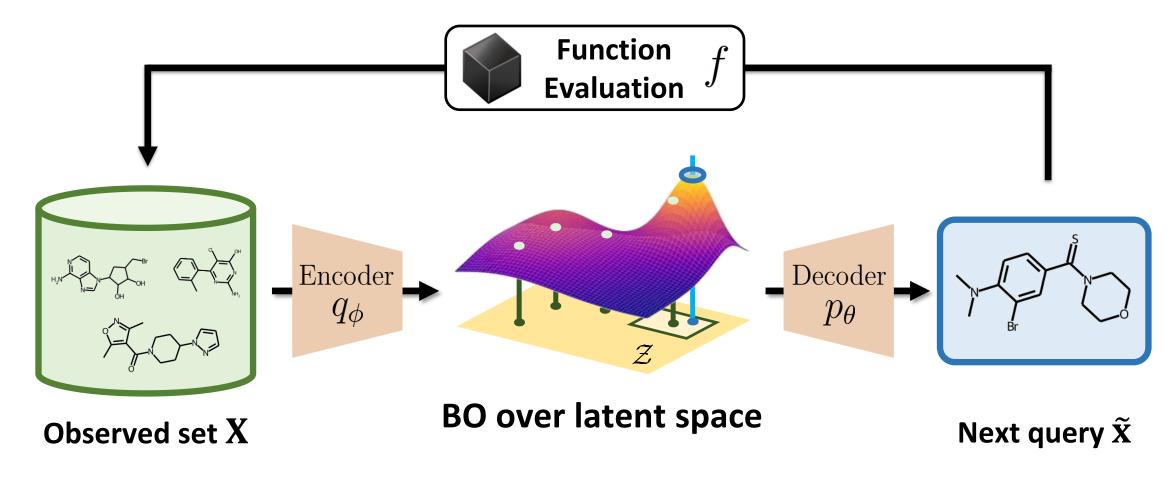
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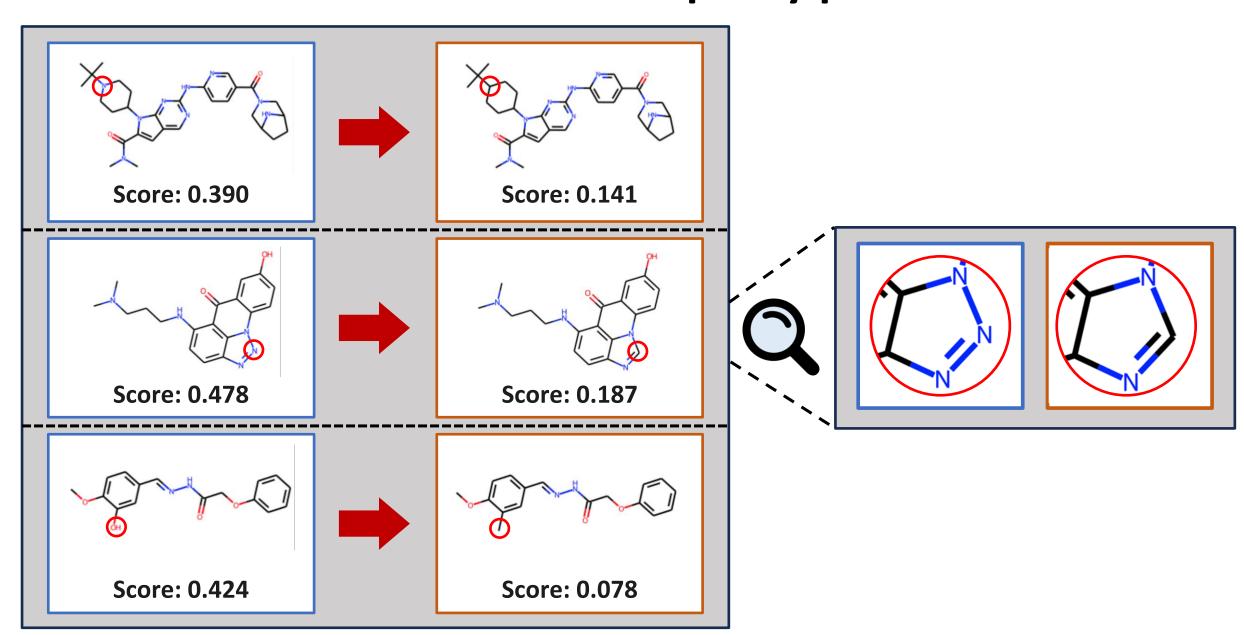
(structured/discrete)

→ Latent Bayesian optimization (LBO)

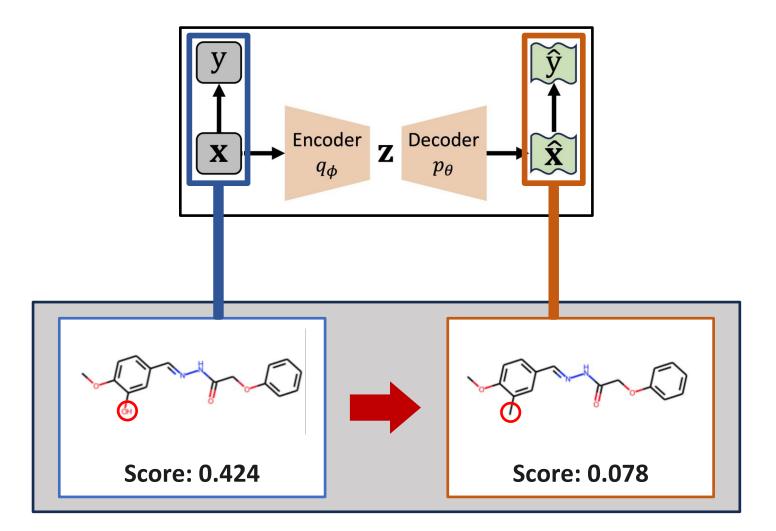
Latent Bayesian Optimization

• Using a generative model with an **encoder-decoder** structure (e.g., VAE), Bayesian Optimization efficiently **optimizes a black-box function** in the **latent space**.

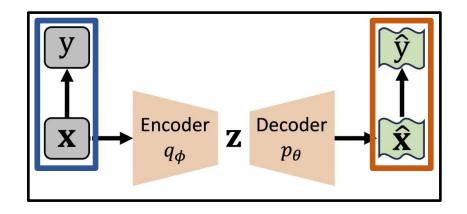


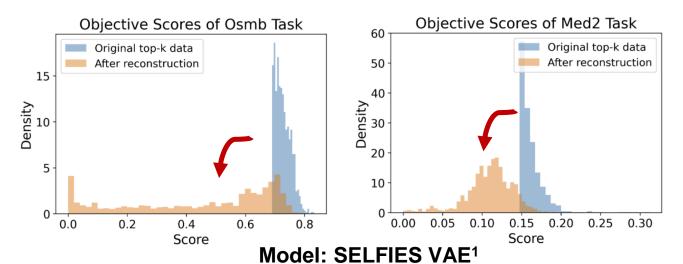


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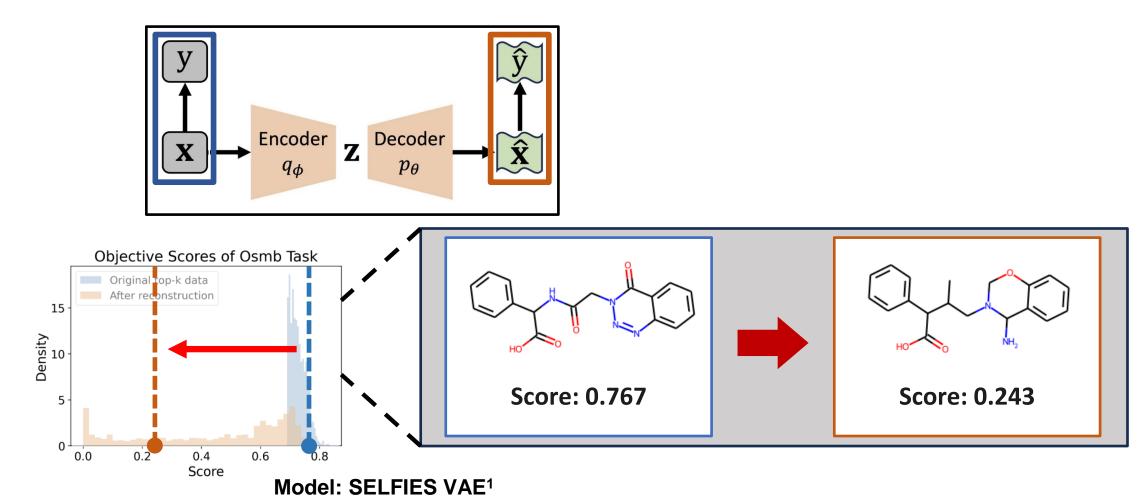




Objective score distribution

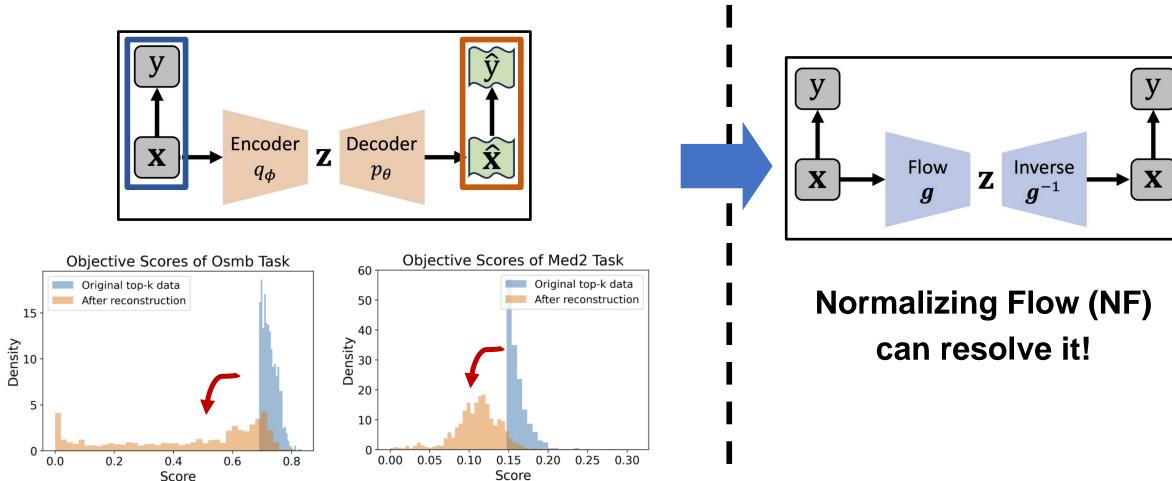
before and after reconstruction

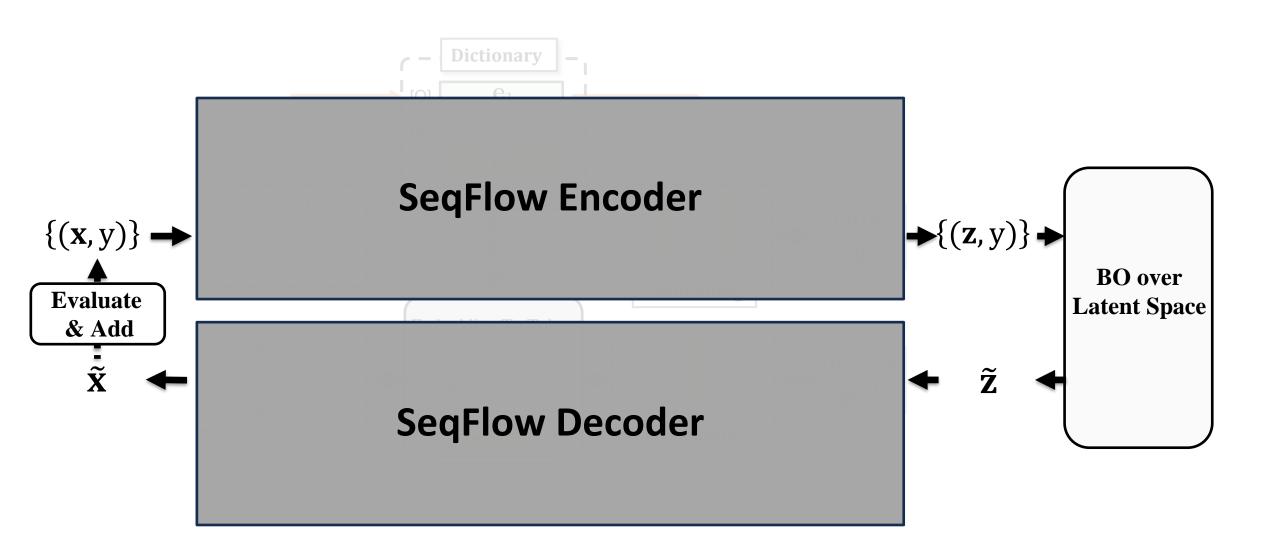
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Model: SELFIES VAE1

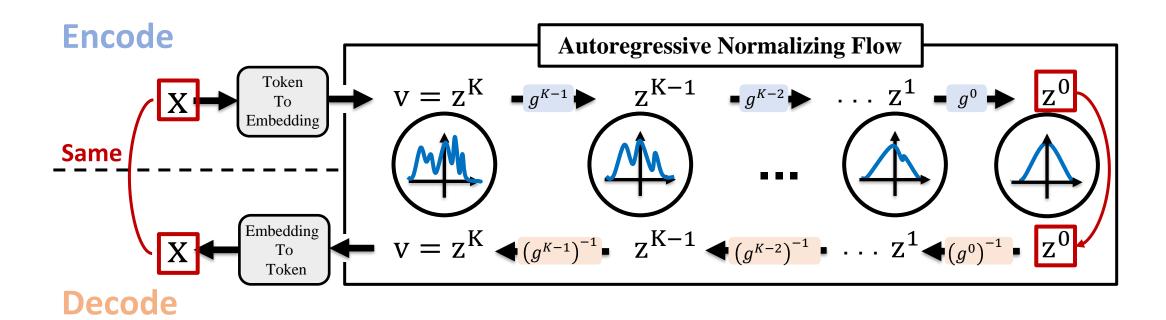
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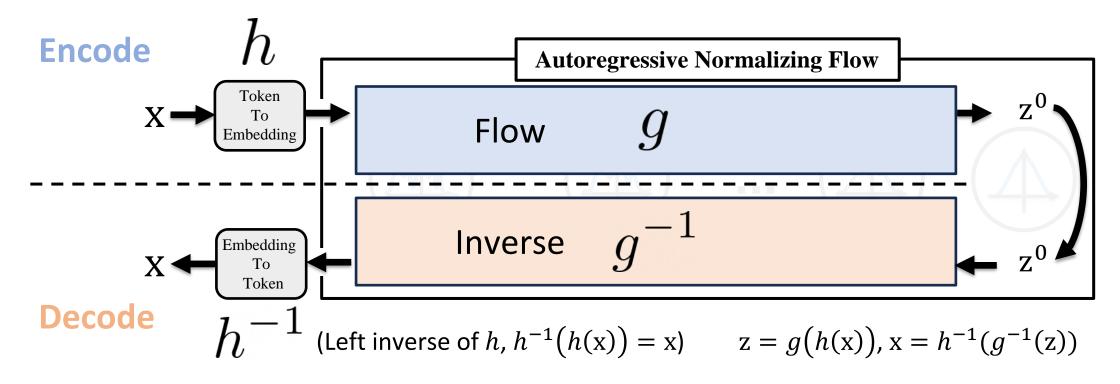


NF-BO: SeqFlow

- Prior Autoregressive Normalizing Flows are applied to continuous data or used with imperfect reconstruction on discrete sequences.
- We propose **SeqFlow**, which **perfectly reconstruct** discrete sequence data (e.g., text, SMILES).

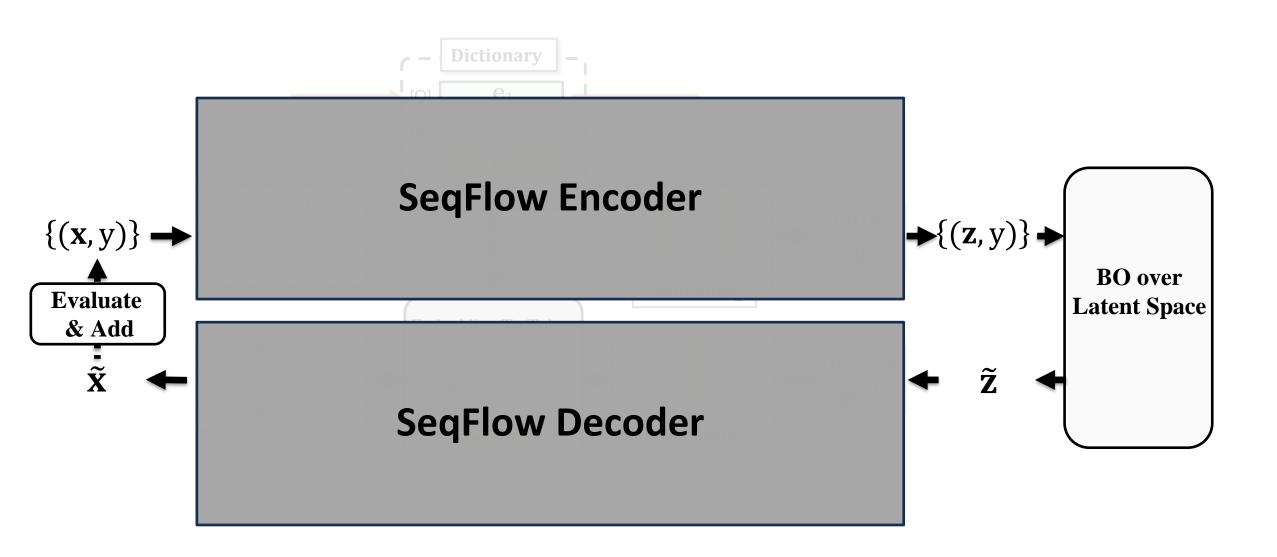


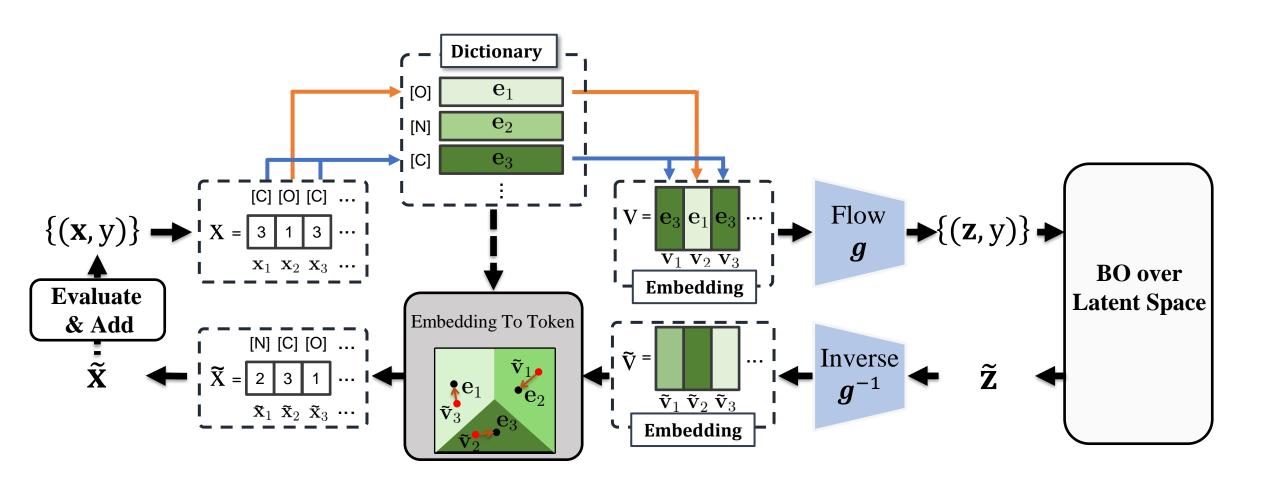
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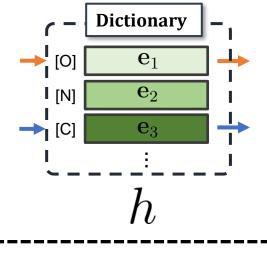


Proposition 1. If g is invertible and h is injective, then $f = g \circ h$ is left-invertible, i.e., $f^{-1} \circ f = id_X$, where $f^{-1} \coloneqq h^{-1} \circ g^{-1}$ and h^{-1} is the left inverse of h.

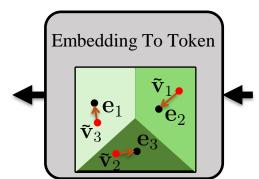
• This means X can be reconstructed exactly through these operations.





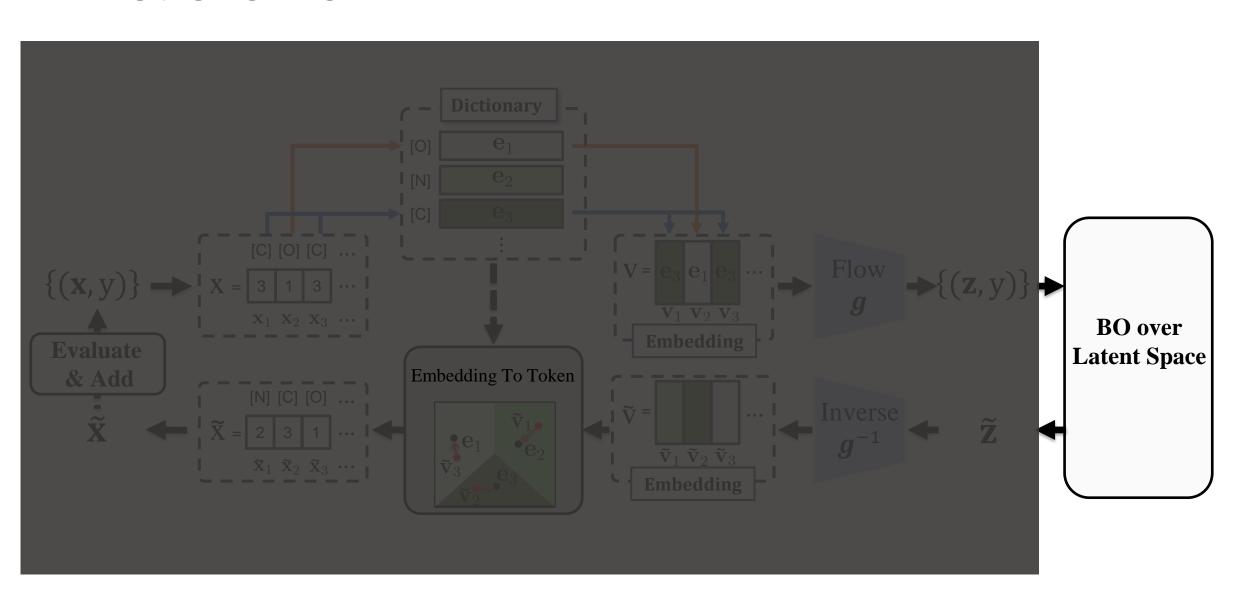


Proposition 2. Let the elements of embedding set $\mathcal{E} = \{e_1, e_2, ..., e_{|\mathcal{E}|}\}$ L2-normalized. Then $h(x) \coloneqq e_X$ is injective and its left-inverse is $h^{-1}(v) = [\arg\max_j \sin(v_i, e_j)]_{i=1}^L$, where $\sin(e_i, e_j) = e_i^T e_j$, i.e., $h^{-1}(h(x)) = x$.



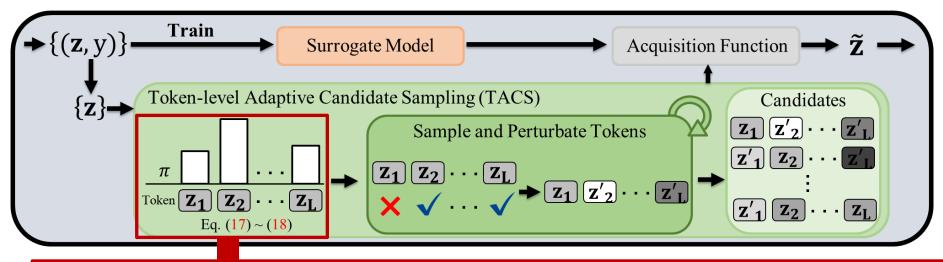
• Our token-to-embedding function and its left-inverse enable perfect reconstruction.

$$h^{-1}$$
 (Left inverse of h)



NF-BO: TACS - Token-level Adaptive Candidate Sampling

• We present a **Token-level Adaptive Candidate Sampling (TACS)** that utilize the **Pointwise Mutual Information (PMI)** between each token z_i and the sequence x.

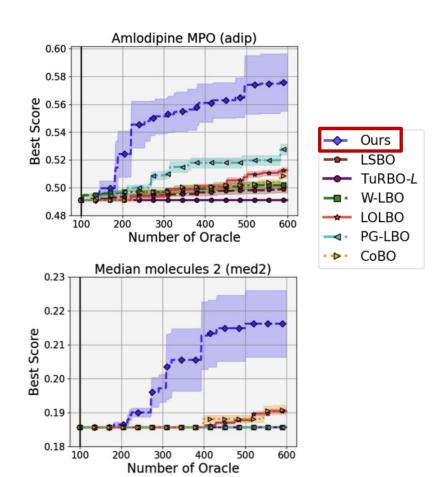


$$\omega_{i}(\mathbf{z}) = \text{PMI}(\mathbf{x}, \mathbf{z}_{i} | \mathbf{z}_{-i}) = \log \frac{p(\mathbf{x} | \mathbf{z})}{p(\mathbf{x} | \mathbf{z}_{-i})} = \log \frac{p(\mathbf{x} | \mathbf{z})}{\mathbb{E}_{\mathbf{z}_{i} \sim \mathcal{N}(\mathbf{0}, I)}(p(\mathbf{x} | \mathbf{z}))},$$

$$\pi_{i}(\mathbf{z}) = \min \left(\kappa s_{i}(\mathbf{z}), 1 \right), \quad s_{i}(\mathbf{z}) = \frac{\exp \left(\omega_{i}(\mathbf{z}) / \tau \right)}{\sum_{j} \exp \left(\omega_{j}(\mathbf{z}) / \tau \right)},$$

NF-BO: Experiments - Molecule design tasks

Methods	Assembly	Top-1 Score (Rank)	Top-10 Score (Rank)	Top-100 Score (Rank)	AUC Top-1 Score (Rank)	AUC Top-10 Score (Rank)	AUC Top-100 Score (Rank)
Bayesian Optimization							
NF-BO	SELFIES	18.095 (1)	17.692 (1)	17.037 (1)	15.539 (1)	14.737 (1)	13.423 (2)
GP BO	Fragments	15.345 (7)	14.940 (6)	14.365 (6)	13.798 (5)	13.156 (5)	12.122 (6)
VAE BO	SELFIES	11.423 (17)	9.788 (19)	7.622 (22)	10.589 (17)	8.887 (19)	6.899 (22)
VAE BO	SMILES	10.926 (21)	9.435 (21)	7.623 (21)	10.197 (19)	8.587 (21)	6.909 (21)
JT-VAE BO	Fragments	10.296 (23)	8.671 (24)	7.037 (24)	9.973 (22)	8.358 (24)	6.740 (23)
Reinforcement Learning							
REINVENT	SMILES	16.772 (2)	16.654 (2)	16.297 (2)	14.711 (2)	14.196 (2)	13.445 (1)
REINVENT	SELFIES	$\overline{16.059}$ (5)	$\overline{15.889}$ (4)	$\overline{15.377}$ (3)	$\overline{14.077}$ (4)	$\overline{13.471}$ (4)	12.475 (5)
MolDQN	Atoms	7.143 (26)	6.495 (26)	5.435 (26)	6.332 (26)	5.620 (26)	4.528 (26)
Genetic Algorithm							
Graph GA	Fragments	16.244 (4)	15.946 (3)	15.342 (4)	14.356 (3)	13.751 (3)	12.696 (3)
STONED	SELFIES	14.257 (8)	14.201 (8)	14.017 (7)	13.256 (7)	13.024 (6)	12.518 (4)
SMILES GA	SMILES	13.123 (11)	12.997 (9)	12.824 (9)	12.357 (10)	12.054 (8)	11.598 (7)
SynNet	Synthesis	13.105 (12)	12.279 (12)	10.768 (15)	12.425 (9)	11.498 (9)	9.914 (9)
GA+D	SELFIES	11.942 (16)	11.696 (15)	11.230 (13)	9.387 (24)	8.964 (18)	8.280 (15)
Hill Climbing							
LSTM HC	SMILES	16.754 (3)	15.880 (5)	14.621 (5)	13.611 (8)	12.223 (7)	10.365 (8)
LSTM HC	SELFIES	13.770 (9)	12.894 (10)	11.657 (12)	11.441 (14)	10.246 (15)	8.595 (13)
DoG-Gen	Synthesis	15.633 (6)	14.772 (7)	13.653 (8)	12.721 (8)	11.456 (10)	9.635 (12)
MIMOSA	Fragments	12.524 (15)	12.223 (13)	11.717 (11)	11.378 (15)	10.651 (13)	9.708 (11)



- Practical Molecular Optimization (PMO) benchmarks (Gao, Wenhao, et al.)
- Guacamol benchmarks (Brown, Nathan, et al.)

NF-BO: Analysis - SeqFlow

Compare SeqFlow to TextFlow¹

- We compare our base flow model, TextFlow, with our SeqFlow in two aspects:
- (1) Reconstruction ability, and (2) Optimization performance.
- Both models share the same Normalizing Flow (NF) component.

NF-BO: Analysis – SeqFlow

(1) Reconstruction ability.

- We evaluate **reconstruction ability** by measuring the **ratio of** $y \neq \hat{y}$.
- TextFlow¹ fails to reconstruct accurately due to its BiLSTM-based mapping, whereas
 our SeqFlow achieves perfect reconstruction with an invertible function.

Task	SeqFlow	TextFlow
Adip	0.000	0.548
Med2	0.000	0.609
Osmb	0.000	0.630
Pdop	0.000	0.502
Rano	0.000	0.814
Zale	0.000	0.750

The ratio of $y \neq \widehat{y}$

NF-BO: Analysis - SeqFlow

(2) Optimization performance

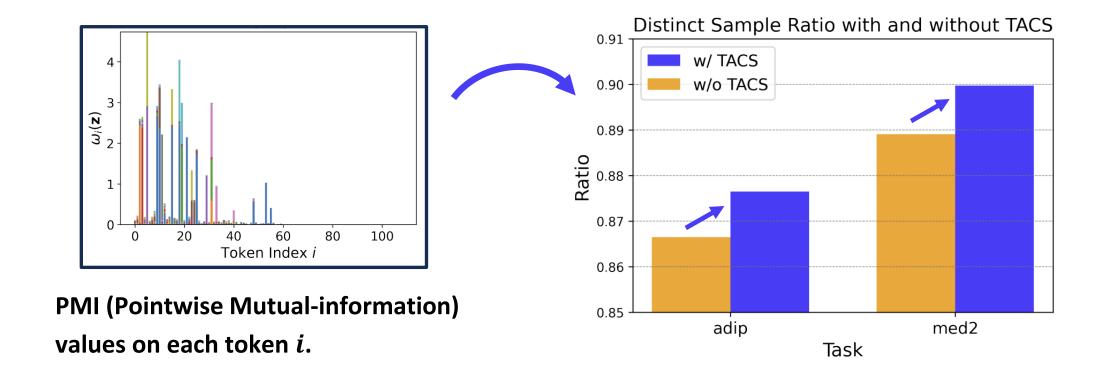
- Despite having more parameters, TextFlow¹ performs similarly to the baselines, as inaccurate reconstruction limits its effectiveness.
- SeqFlow, with fewer parameters and exact reconstruction, outperforms
 TextFlow in Bayesian Optimization tasks.

Method	SeqFlow	TextFlow	
Base NF	Autoregressive NF	Autoregressive NF	
Perfect Reconsturction	О	X	
# Params	31M	54M	
Adip Score	0.778	0.716	
Med2 Score	0.372	0.347	

NF-BO: Analysis - TACS

Impact of TACS (Token-level Adaptive Candidate Sampling)

• Model with TACS makes a higher ratio of distinct samples compared to those without TACS.



Conclusion

- **√Normalizing Flow-based Latent Bayesian Optimization (NF-BO)**
- ✓ Perfect reconstruction via invertible normalizing flows.
- ✓ Resolves value discrepancy problem in latent Bayesian optimization.

√Token-level Adaptive Candidate Sampling improves **local search efficiency**.

Thank you.

