

Deep Retrosynthetic Reaction Prediction using Local Reactivity and Global Attention

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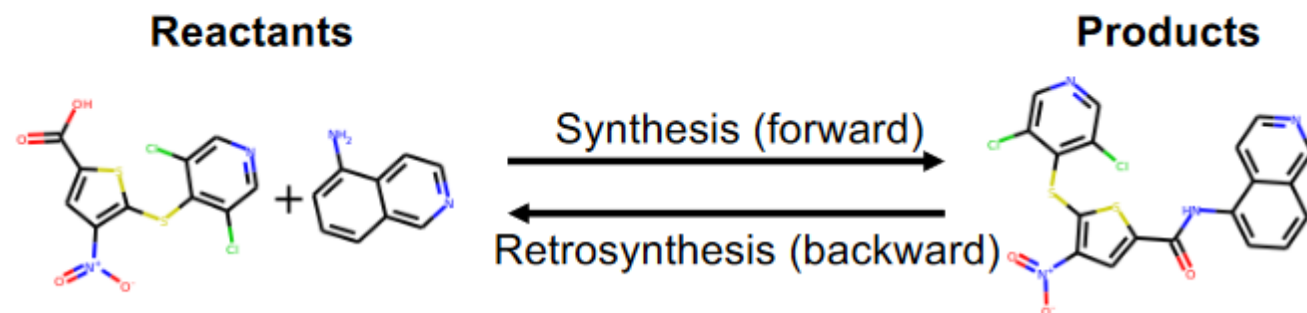


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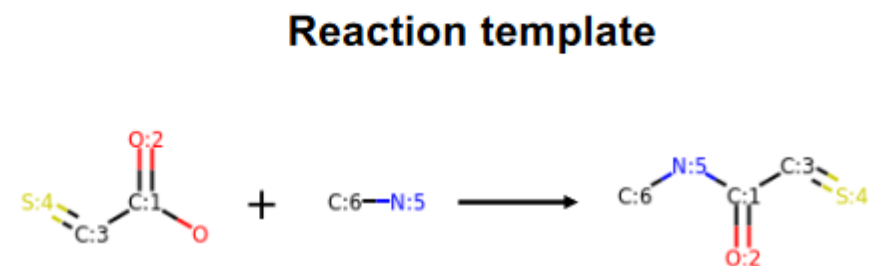


Read Online

Background

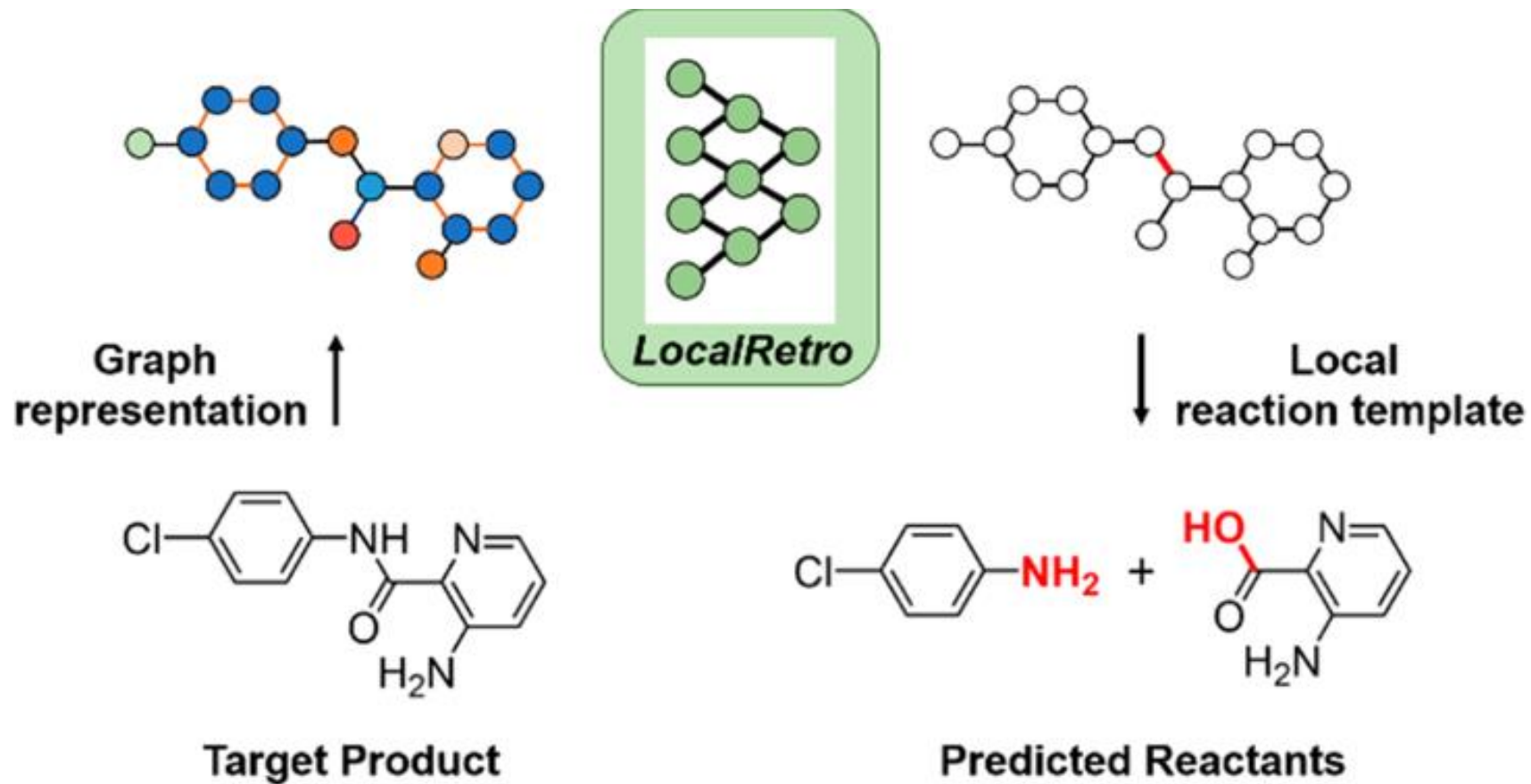


(a) Chemical reaction



(b) Reaction template

Overview



Motivation

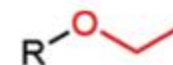
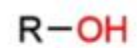
- All existing methods suggest reactants based on the global structures of the molecules.
- However, only local structure are edited in reaction.

Atom reaction template

Retro-reaction

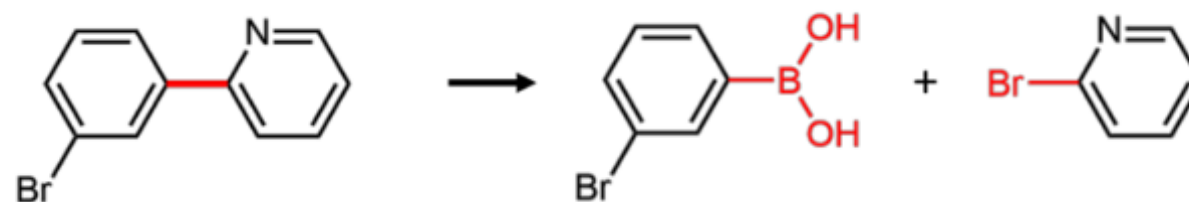


Local reaction template

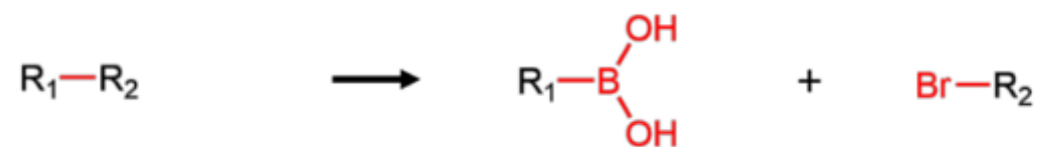


Bond reaction template

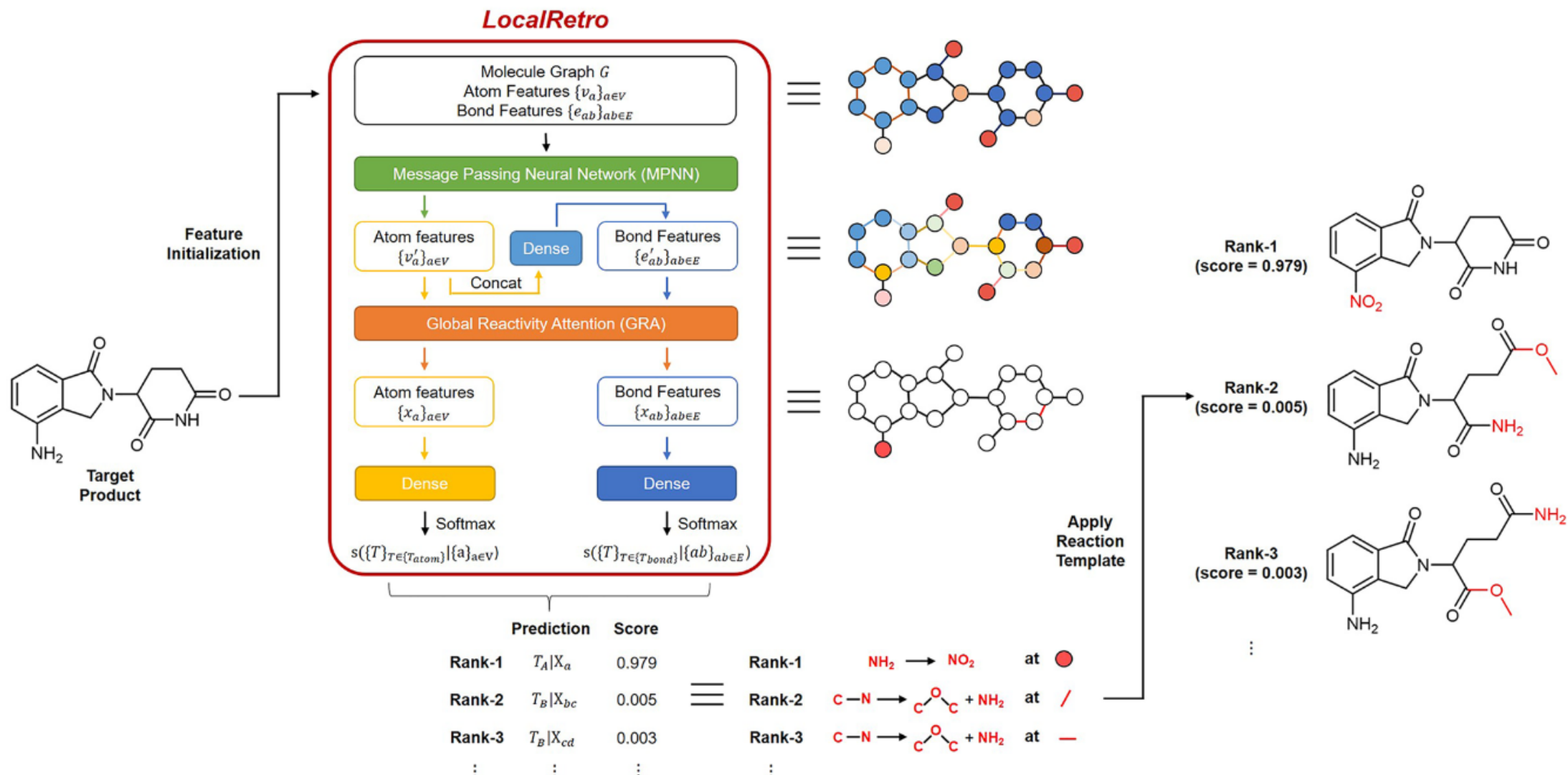
Retro-reaction



Local reaction template



System



Implementation details

- MPNN:

$$v'_a = \text{MPNN}(v_a, \{v_b\}, \{e_{ab}\})$$

$$e'_{ab} = w(v'_a \| v'_b) + c$$

- Graph attention (GRA):

$$x_a = \text{GRA}(v'_a, \{v'_a\}_{a \in V}, \{e'_{ab}\}_{ab \in E})$$

$$x_{ab} = \text{GRA}(e'_{ab}, \{v'_a\}_{a \in V}, \{e'_{ab}\}_{ab \in E})$$

- Output

$$o_a = u_A^T (\sigma(w_A x_a + c_A))$$

$$o_{ab} = u_B^T (\sigma(w_B x_{ab} + c_B))$$

$$s(T|a) = \text{Softmax}(o_a), T \in \{T_{\text{atom}}\}$$

$$s(T|ab) = \text{Softmax}(o_{ab}), T \in \{T_{\text{bond}}\}$$

Results

Table 1. Top- k Exact Match Accuracy on USPTO-50K Dataset and USPTO-MIT Dataset without Given Reaction Class^a

dataset	model	top- k accuracy (%)				
		$K = 1$	3	5	10	50
USPTO-50K	<i>GLN</i> ¹⁴	52.5	69.0	75.6	83.7	92.4
	<i>G2G</i> ¹⁵	48.9	67.6	72.5	75.5	
	<i>GraphRetro</i> ¹⁶	53.7	68.3	72.2	75.5	
	<i>Augmented Transformer</i> ²⁵	53.5	69.4	81.0	85.7	
	<i>MEGAN</i> ¹⁷	48.1	70.7	78.4	86.1	93.2
	<i>LocalRetro</i> wo/ GRA (this work)	49.8	75.8	84.0	91.3	97.7
	<i>LocalRetro</i> (this work)	53.4	77.5	85.9	92.4	97.7
USPTO-MIT	<i>LocalRetro</i> wo/ GRA (this work)	49.9	70.7	77.0	83.1	89.8
	<i>LocalRetro</i> (this work)	54.1	73.7	79.4	84.4	90.4

^aThe best top- k exact match accuracy is highlighted with bold font.

Results

Table 2. Top- k Exact Match Accuracy on USPTO-50K Dataset with Given Reaction Class^a

dataset	model	top- k accuracy (%)				
		$K = 1$	3	5	10	50
USPTO-50K	<i>GLN</i> ¹⁴	64.2	79.1	85.2	90.0	93.2
	<i>G2G</i> ¹⁵	61.0	81.3	86.0	88.7	
	<i>GraphRetro</i> ¹⁶	63.9	81.5	85.2	88.1	
	<i>MEGAN</i> ¹⁷	60.7	82.0	87.5	91.6	95.3
	<i>LocalRetro</i> wo/ GRA (this work)	62.3	86.1	91.8	96.0	97.9
	<i>LocalRetro</i> (this work)	63.9	86.8	92.4	96.3	97.9

^aThe best top- k exact match accuracy is highlighted with bold font.

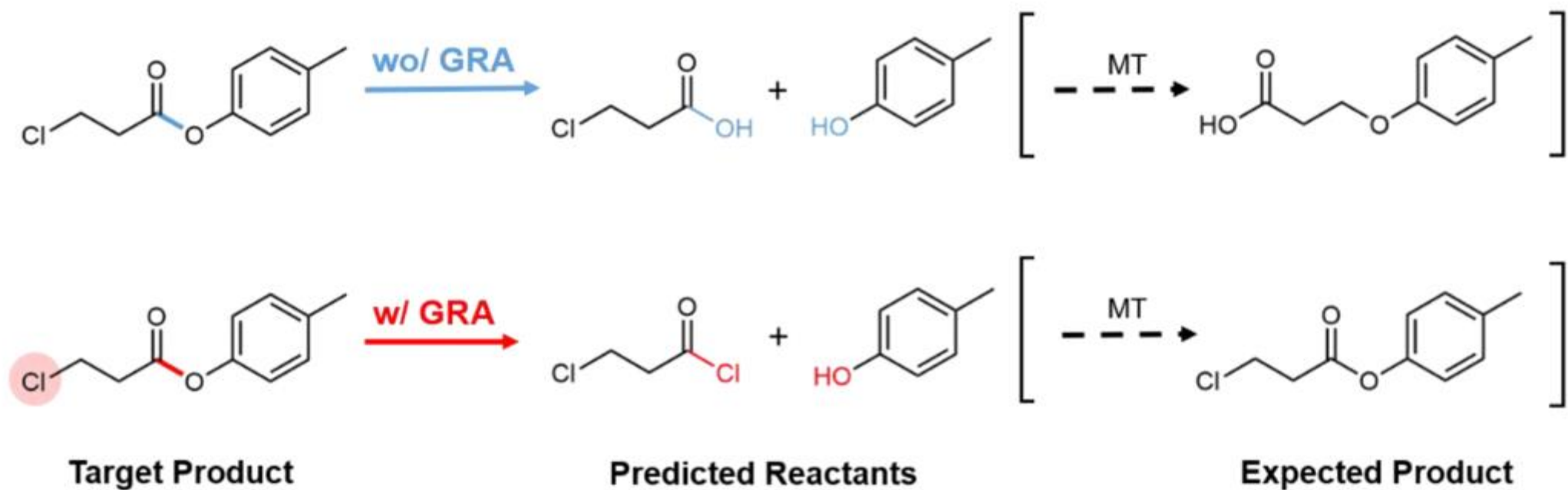
Results

Table 3. Top- k Round-Trip Accuracy on the USPTO-50K Dataset and USPTO-MIT Dataset^a

dataset	model	top- k accuracy (%)		
		$K = 1$	3	5
USPTO-50K	<i>GLN</i> ¹⁴	88.4	95.0	97.1
	<i>LocalRetro</i> wo/GRA (this work)	88.2	97.8	98.9
	<i>LocalRetro</i> (this work)	89.5	97.9	99.2
USPTO-MIT	<i>LocalRetro</i> wo/GRA (this work)	85.7	95.7	97.3
	<i>LocalRetro</i> (this work)	87.0	95.9	97.4

^aThe best top- k round-trip accuracy is highlighted with bold font.

Study of GRA



Case study

Case study on considered in various retrosynthesis and inverse design works in the literature: lenalidomide, salmeterol, kinase inhibitors, etc.

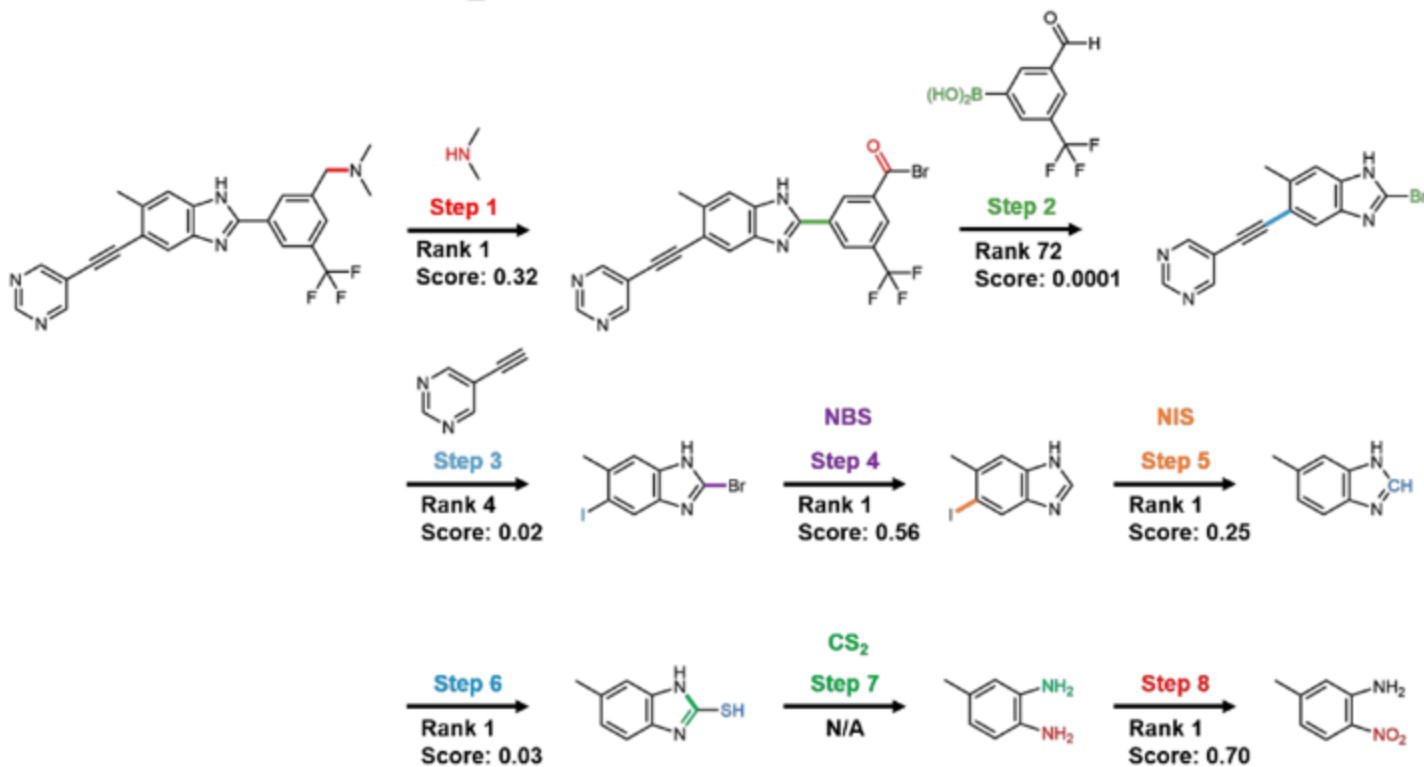
a. Lenalidomide



Identical as reported in literature

Case study

e. DDR1 kinase inhibitor INS015_032



Identical as reported in literature

Take home message

- Local reactivity is essential for retrosynthesis.

RETCCL: A Selection-based Approach for Retrosynthesis via Contrastive Learning

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IJCAI21

Motivation

- Formulate the retrosynthesis as a retrieval task rather than generation task, therefore:
 - Can consider the availability.
 - Generalize to unseen templates.

Compare different paradigms

- Template free methods: choose from whole space of (possibly unavailable) molecules.
- Template based methods: choose from reactants extracted from known reaction templates.
- This work: choose from expert defined template library, which can be updated during inference.

Overview

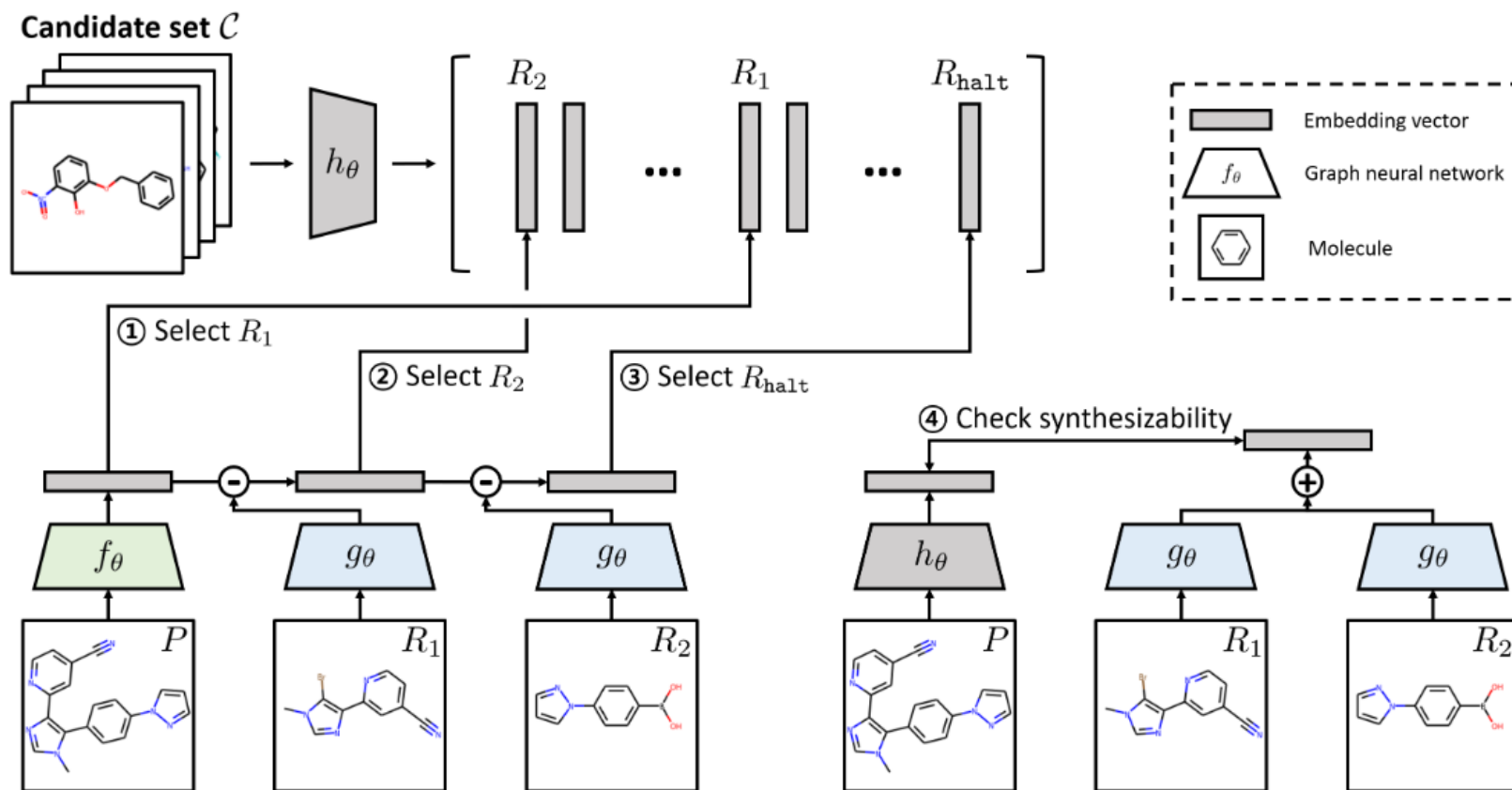


Figure 2: Illustration of the search procedure in RETCL. It first (1-3) selects reactants sequentially based on $\psi(R|P, \mathcal{R}_{\text{given}})$, and then (4) check the synthesizability of the selected reactant-set based on $\phi(P|\mathcal{R})$. The overall score is the average over all scores from (1) to (4).

The score function

The diagram illustrates the components of the score function formula. Arrows point from descriptive boxes to parts of the equation:

- Product** points to P .
- Reactants** points to \mathcal{R} .
- Backward scoring** points to $\psi(R_{\pi(i)} | P, \{R_{\pi(1)}, \dots, R_{\pi(i-1)}\})$.
- Forward scoring** points to $\phi(P | \mathcal{R})$.
- #reactants + EOS + Forward score** points to the denominator $n + 2$.
- All reactants permutation** points to the maximization over $\pi \in \Pi$.

$$\text{score}(P, \mathcal{R}) = \frac{1}{n + 2} \left(\max_{\pi \in \Pi} \sum_{i=1}^{n+1} \psi(R_{\pi(i)} | P, \{R_{\pi(1)}, \dots, R_{\pi(i-1)}\}) + \phi(P | \mathcal{R}) \right)$$

The score function

$$\psi(R|P, \mathcal{R}_{\text{given}}) = \text{CosSim} \left(f_{\theta}(P) - \sum_{S \in \mathcal{R}_{\text{given}}} g_{\theta}(S), h_{\theta}(R) \right),$$
$$\phi(P|\mathcal{R}) = \text{CosSim} \left(\sum_{R \in \mathcal{R}} g_{\theta}(R), h_{\theta}(P) \right),$$

f_{θ} Query of product

g_{θ} Query of reactant

h_{θ} Key of a molecule

Contrastive learning

$$p(R|P, \mathcal{R}_{\text{given}}, \mathcal{C}) = \frac{\exp(\psi(R|P, \mathcal{R}_{\text{given}})/\tau)}{\sum_{R' \in \mathcal{C} \setminus \{P\}} \exp(\psi(R'|P, \mathcal{R}_{\text{given}})/\tau)},$$

$$q(P|\mathcal{R}, \mathcal{C}) = \frac{\exp(\phi(P|\mathcal{R})/\tau)}{\sum_{P' \in \mathcal{C} \setminus \mathcal{R}} \exp(\phi(P'|\mathcal{R})/\tau)},$$

$$\mathcal{L}_{\text{backward}}(P, \mathcal{R}|\theta, \mathcal{C}) = -\max_{\pi \in \Pi} \sum_{i=1}^{n+1} \log p(R_{\pi(i)}|P, \{R_{\pi(1)}, \dots, R_{\pi(i-1)}\}, \mathcal{C}),$$

$$\mathcal{L}_{\text{forward}}(P, \mathcal{R}|\theta, \mathcal{C}) = -\log q(P|\mathcal{R}, \mathcal{C}),$$

Contrastive learning

It's costly to use all ($6 \cdot 10^5$) negative examples

$$\mathcal{C}_{\mathcal{B}} = \{M \mid \exists (\mathcal{R}, P) \in \mathcal{B} \text{ such that } M = P \text{ or } M \in \mathcal{R}\},$$

$$\mathcal{L}(\mathcal{B}|\theta) = \frac{1}{|\mathcal{B}|} \sum_{(\mathcal{R}, P) \in \mathcal{B}} \left(\mathcal{L}_{\text{backward}}(P, \mathcal{R}|\theta, \mathcal{C}_{\mathcal{B}}) + \mathcal{L}_{\text{forward}}(P, \mathcal{R}|\theta, \mathcal{C}_{\mathcal{B}}) \right).$$

Hard negative mining

$$\tilde{\mathcal{C}}_{\mathcal{B}} = \mathcal{C}_{\mathcal{B}} \cup \bigcup_{M \in \mathcal{C}_{\mathcal{B}}} \{\text{Top-}K \text{ nearest neighbors of } M \text{ from } \mathcal{C}\},$$

Category	Method	Top-1	Top-3	Top-5	Top-10	Top-20	Top-50
Reaction type is unknown							
Template-free	Transformer (Karpov et al., 2019)	37.9	57.3	62.7	-	-	-
	SCROP (Zheng et al., 2019)	43.7	60.0	65.2	68.7	-	-
	Transformer (Chen et al., 2019)	44.8	62.6	67.7	71.1	-	-
	G2Gs (Shi et al., 2020)	48.9	67.6	72.5	75.5	-	-
Template-based	retrosim (Coley et al., 2017b)	37.3	54.7	63.3	74.1	82.0	85.3
	neuralsym (Segler & Waller, 2017)	44.4	65.3	72.4	78.9	82.2	83.1
	GLN (Dai et al., 2019)	52.5	69.0	75.6	83.7	89.0	92.4
Selection-based	Bayesian-Retro (Guo et al., 2020)	47.5	67.2	77.0	80.3	-	-
	RETCL (Ours)	71.3	86.4	92.0	94.1	95.0	96.4
Reaction type is given as prior							
Template-free	seq2seq (Liu et al., 2017)	37.4	52.4	57.0	61.7	65.9	70.7
	Transformer [†] (Chen et al., 2019)	54.1	70.0	74.2	77.8	80.4	83.3
	SCROP (Zheng et al., 2019)	59.0	74.8	78.1	81.1	-	-
	G2Gs (Shi et al., 2020)	61.0	81.3	86.0	88.7	-	-
Template-based	retrosim (Coley et al., 2017b)	52.9	73.8	81.2	88.1	91.8	92.9
	neuralsym (Segler & Waller, 2017)	55.3	76.0	81.4	85.1	86.5	86.9
	GLN (Dai et al., 2019)	64.2	79.1	85.2	90.0	92.3	93.2
Selection-based	Bayesian-Retro (Guo et al., 2020)	55.2	74.1	81.4	83.5	-	-
	RETCL (Ours)	78.9	90.4	93.9	95.2	95.8	96.7

Results

Table 2: The top- k exact match accuracy (%) of our RETCL, Transformer (Chen et al., 2019) and GLN (Dai et al., 2019) with discarding predictions not in the candidate set \mathcal{C} .

Category	Method	Top-1	Top-5	Top-10	Top-50	Top-100	Top-200
Reaction type is unknown							
Template-free	Transformer (Chen et al., 2019)	59.6	74.3	77.0	79.4	79.5	79.6
	RETCL (Ours)	71.3	92.0	94.1	96.4	96.7	97.1
Template-based	GLN (Dai et al., 2019)	77.3	90.0	92.5	93.3	93.3	93.3
Reaction type is given as prior							
Template-free	Transformer (Chen et al., 2019)	68.4	82.4	84.3	85.9	86.0	86.1
	RETCL (Ours)	78.9	93.9	95.2	96.7	97.1	97.5
Template-based	GLN (Dai et al., 2019)	82.0	91.7	92.9	93.3	93.3	93.3

Case study

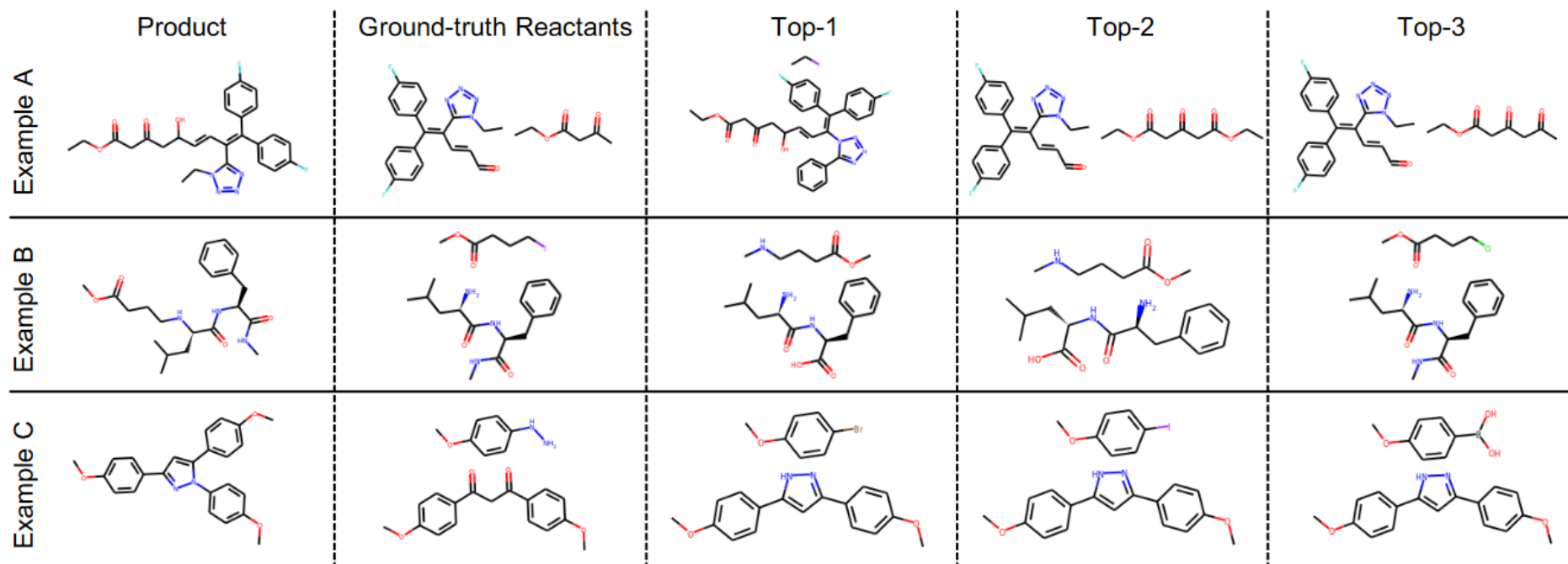


Figure 3: Failure cases of RETCL.

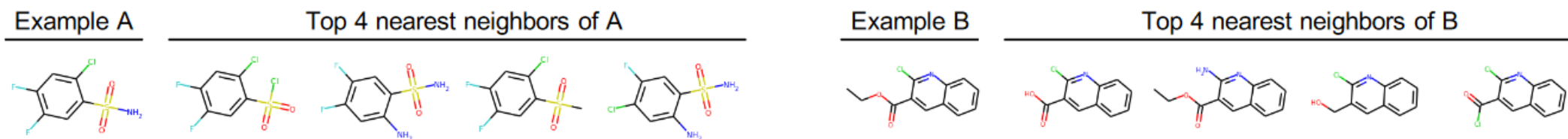


Figure 4: The top-4 nearest neighbors of two randomly sampled molecules in \mathcal{C} .

Ablation

Table 3: Ablation study.

$\phi(P \mathcal{R})$	K	sum	Top-1	Top-10
✓			59.5	79.8
✓	1		69.6	92.2
✓	2		70.9	92.7
✓	4		71.1	92.9
	4		69.8	90.3
✓	4	✓	71.3	94.1

Generalization to unseen templates

Table 4: The top-10 exact match accuracy (%) of our RETCL and GLN (Dai et al., 2019) trained on USPTO-50k without reaction types from 6 to 10. The average column indicates the average of class-wise accuracy for each reaction type.

Method	Average	Reaction type									
		1	2	3	4	5	6	7	8	9	10
GLN (Dai et al., 2019)	39.7	84.3	92.2	70.7	59.3	89.7	0.0	0.0	0.0	0.5	0.0
RETCL (Ours)	55.6	93.9	97.6	86.4	67.0	95.6	59.1	11.9	18.3	26.1	0.0

Generalization to larger dataset

Table 5: Generalization to USPTO-full.

Method	Top-1	Top-10	Top-50
Transformer (Chen et al., 2019)	29.9	46.6	51.0
GLN (Dai et al., 2019)	26.7	42.2	46.7
RETCL (Ours)	39.9	57.1	60.9

Generalization to unseen candidates

Table 6: Generalization to unseen candidates.

$ \mathcal{C}_{\text{train}} $	Top-1	Top-5	Top-10	Top-20	Top-50
91,297	69.0	88.1	91.0	92.8	94.4
671,518	71.3	92.0	94.1	95.0	96.4

Multi-step retrosynthesis

Table 7: Multi-step retrosynthesis.

Single-step model	Single		Hybrid	
	MLP	TF	TF+TF	RETCL+TF
Succ. rate (%)	86.84	91.05	90.54	96.84
Avg. length	-	4.30	4.31	3.90

Take home message

- Retrieval based methods may be a new direction.