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

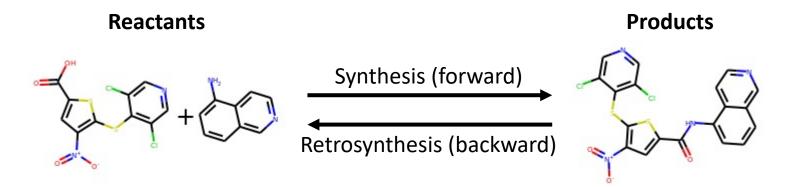
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What Is Retrosynthesis?

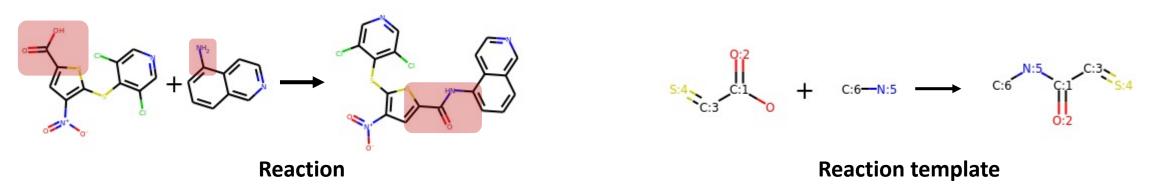
 Retrosynthesis aims at finding a synthetic route starting from commercially available reactants to synthesize a target product



- It plays an essential role in practical applications by finding a new synthetic path, which can be more costeffective or avoid patent infringement
- Challenges:
 - One molecule could be synthesized by different combinations of reactants
 - Some complex compounds require more than 100 synthesis steps
 - The number of reaction types (or rules) is very huge
 - Hence, the search space is too vast

Existing Approaches for Retrosynthesis

- 1. Template-based approaches [1-3]
 - A reaction template describes how the chemical reaction occurs among reactants
 - Reaction templates can be extracted from a reaction database automatically or encoded by experts



- How do template-based approaches perform retrosynthesis?
 - 1. Construct a set of templates $\mathcal{T} = \{T_1, T_2, \dots, T_{|\mathcal{T}|}\}$ by automatic tools or experts
 - 2. Given a product molecule *P*, find a well-matched template $T \in \mathcal{T}$
 - 3. Obtain a set of reactants by applying the template *T* to the product *P*

• Limitation: they limit the search space to known templates and cannot discover novel synthetic routes

^[1] Coley et al., Computer-assisted retrosynthesis based on molecular similarity. ACS central science, 3(12):1237–1245, 2017.

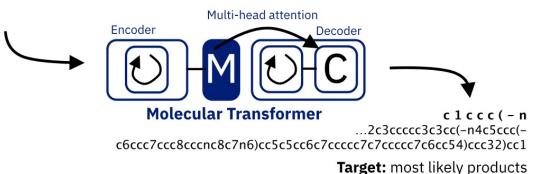
^[2] Segler & Waller, Neural-symbolic machine learning for retrosynthesis and reaction prediction. Chemistry–A European Journal, 23(25):5966–5971, 2017.

^[3] Dai et al., Retrosynthesis prediction with conditional graph logic network, NeurIPS, 2019.

Existing Approaches for Retrosynthesis

- 2. Template-free approaches [1-4]
 - They generate the reactants from scratch without knowledge of reaction templates
 - In other words, they consider retrosynthesis as a conditional generation problem such as machine translation
 - Note. Molecules can be encoded by graph or string format (SMILES)

Input: reactants-reagents (atom-wise tokenization) Br c 1 c c c 2 ...c(c1)c1cc3c4ccccc4c4ccccc4c3cc1n2-c1ccc2c(c1)c1ccccc1n2-c1ccccc1.CCO. Cc1ccccc1.OB(O)c1ccc2ccc3cccnc3c2n1.c1ccc([PH](c2ccccc2)(c2cccc2)[Pd]([PH](c2cccc2)(c2ccc2)(c2cccc2)(c2cccc2)(c2ccc2)(c2cccc2)(c2cccc2)(c2ccc



• Limitation: they require to search the entire molecular space, and their predictions could be either unstable or commercially unavailable

^[1] Liu et al., Retrosynthetic reaction prediction using neural sequence-to-sequence models. ACS central science, 3(10): 1103–1113, 2017

^[2] Karpov et al., A transformer model for retrosynthesis. In International Conference on Artificial Neural Networks, pp. 817–830. Springer, 2019.

^[3] Zheng et al., Predicting retrosynthetic reactions using self-corrected transformer neural networks. Journal of Chemical Information and Modeling, 2019.

^[4] A graph to graphs framework for retrosynthesis prediction. ICML, 2020.

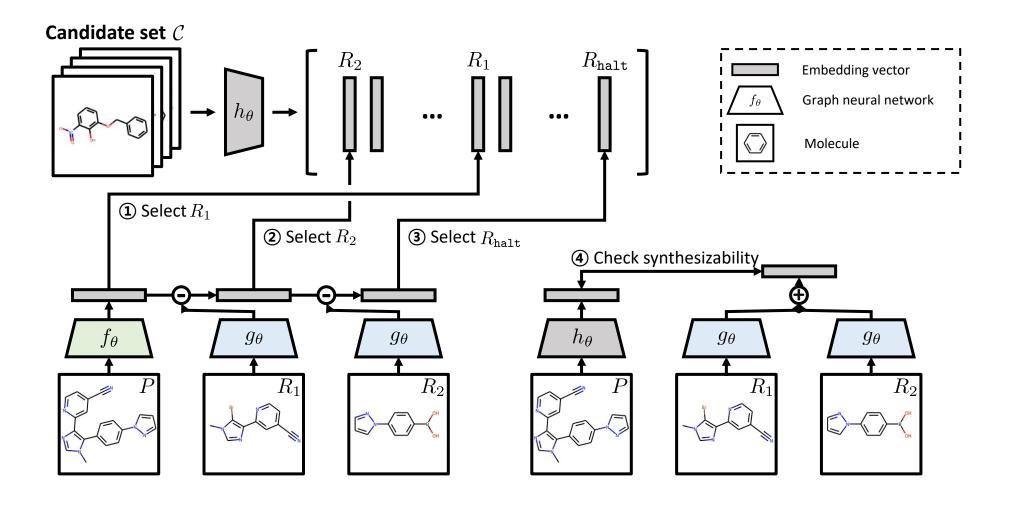
Proposed Method: Selection-based Approach

- **Recall.** Existing approaches have fundamental limitations:
 - Template-based ones cannot generalize to unseen templates
 - Template-free ones does not consider the availability of reactants
- We propose a new selection-based approach considering the availability of reactants
 - Assumption: we have a candidate set of commercially available reactants ${\cal C}$
 - We reformulate retrosynthesis as the following selection problem:

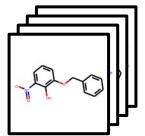
Given a target product P, our goal is to select a set of reactants $\mathcal{R} = \{R_1, \dots, R_{|\mathcal{R}|}\}$ from the candidate set \mathcal{C} (i.e., $\mathcal{R} \subset \mathcal{C}$) for synthesizing the product P

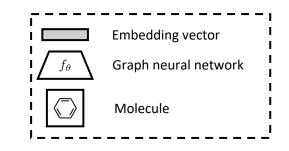
Benefits over the existing approaches:

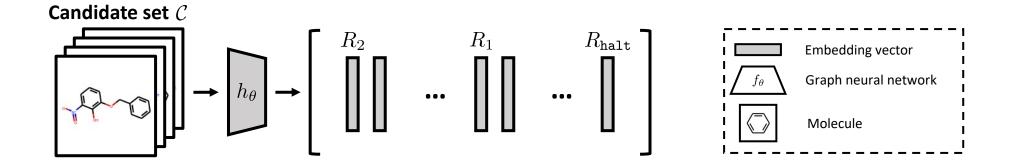
- It guarantees the **commercial availability** of the selected reactants
- It can generalize to unseen reaction templates and find novel synthetic routes

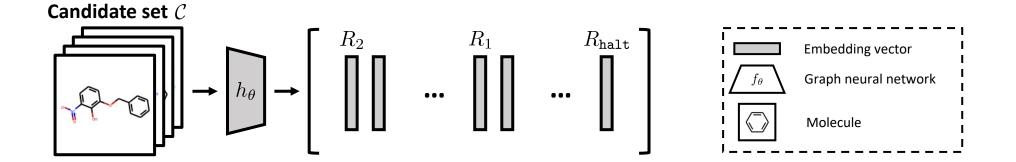


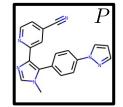
Candidate set C

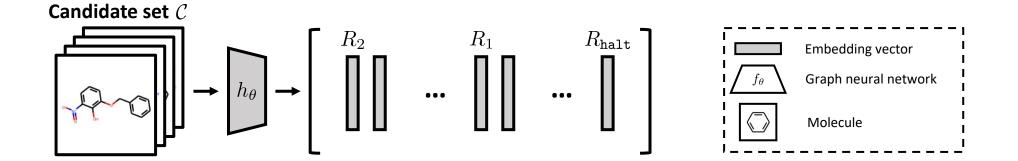


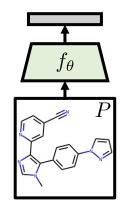




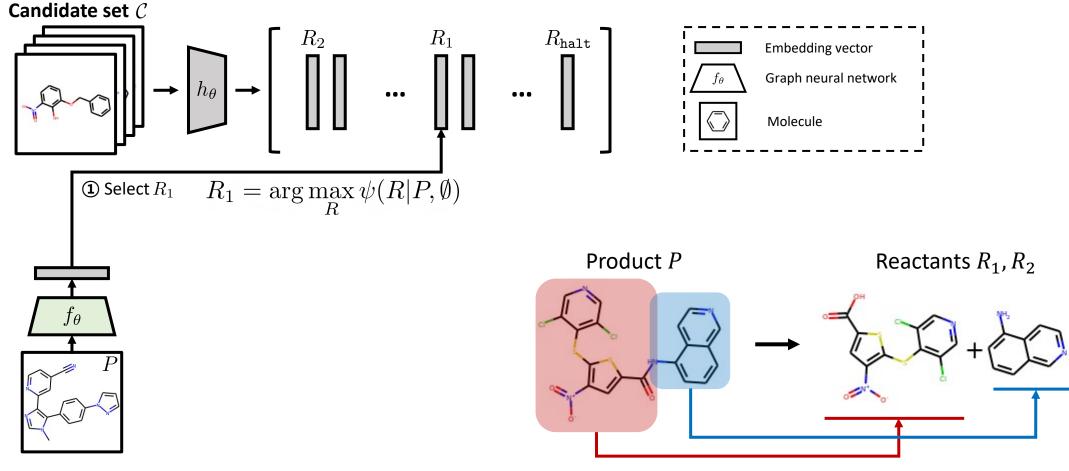




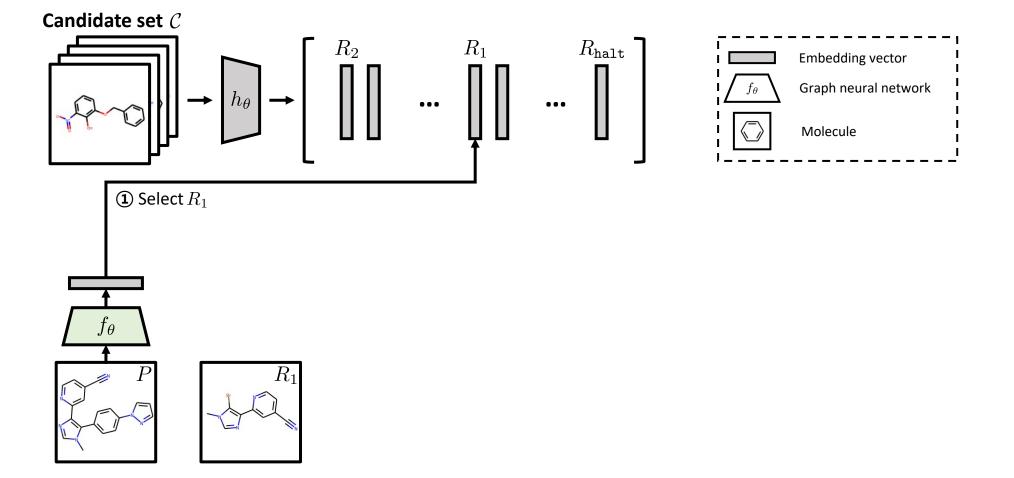




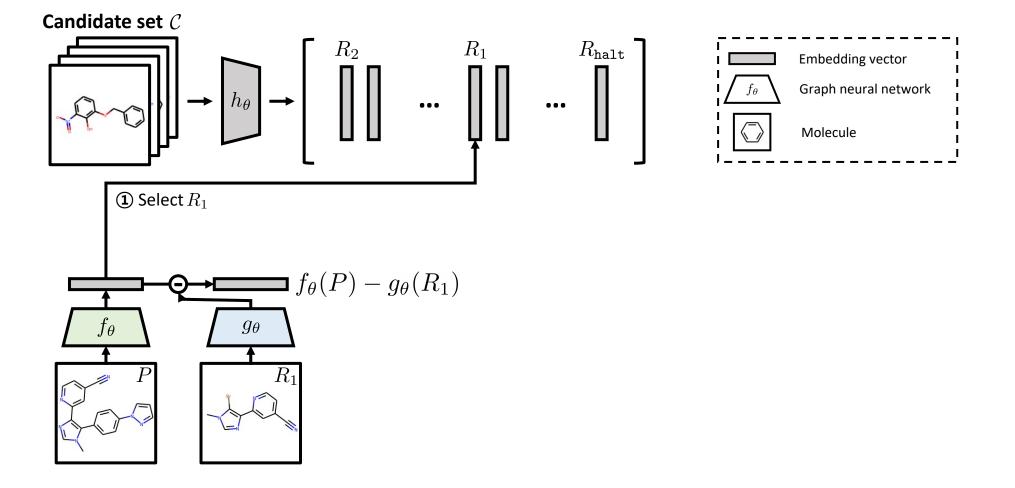
Backward Selection Score:
$$\psi(R|P, \mathcal{R}_{given}) = \text{CosSim}\left(f_{\theta}(P) - \sum_{S \in \mathcal{R}_{given}} g_{\theta}(S), h_{\theta}(R)\right)$$



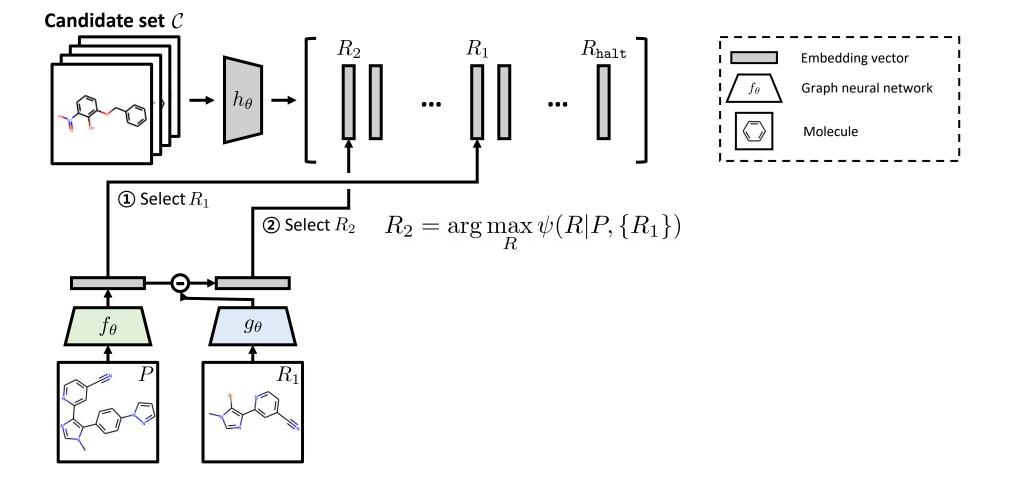
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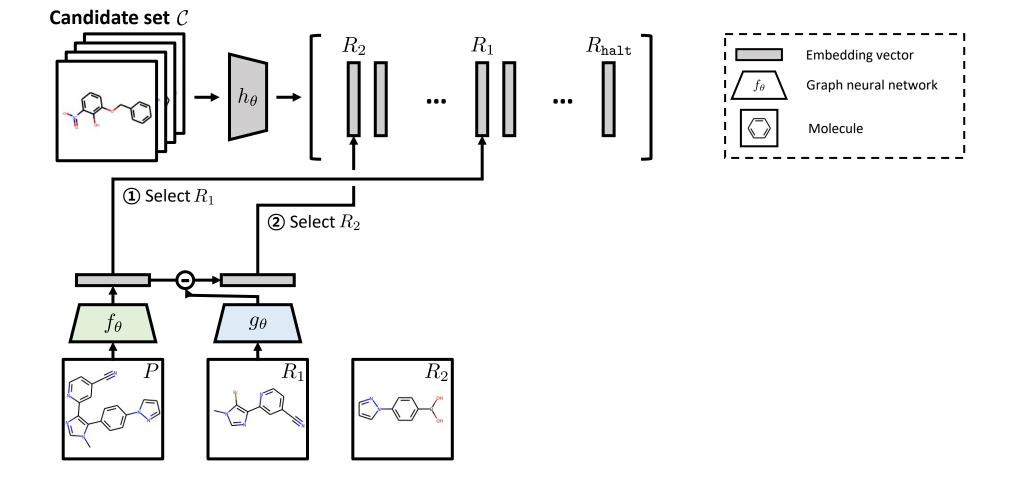
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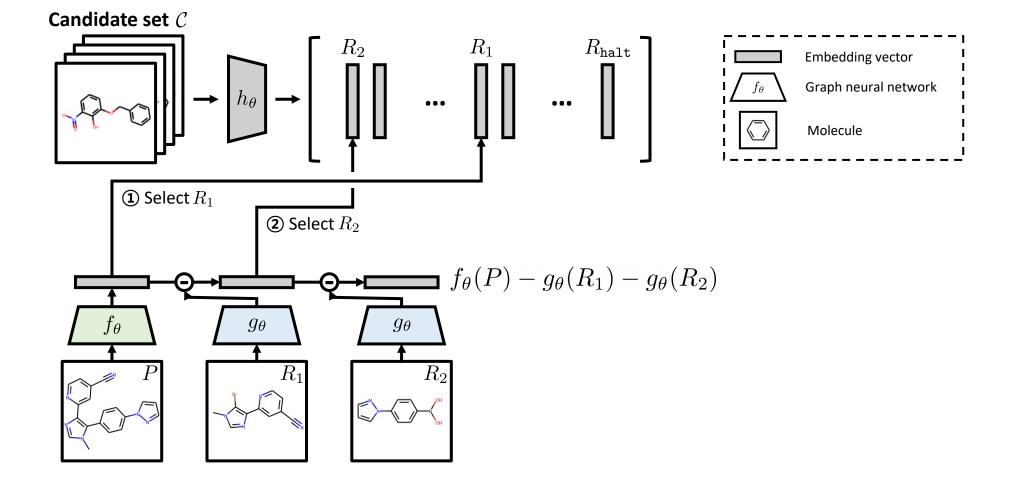
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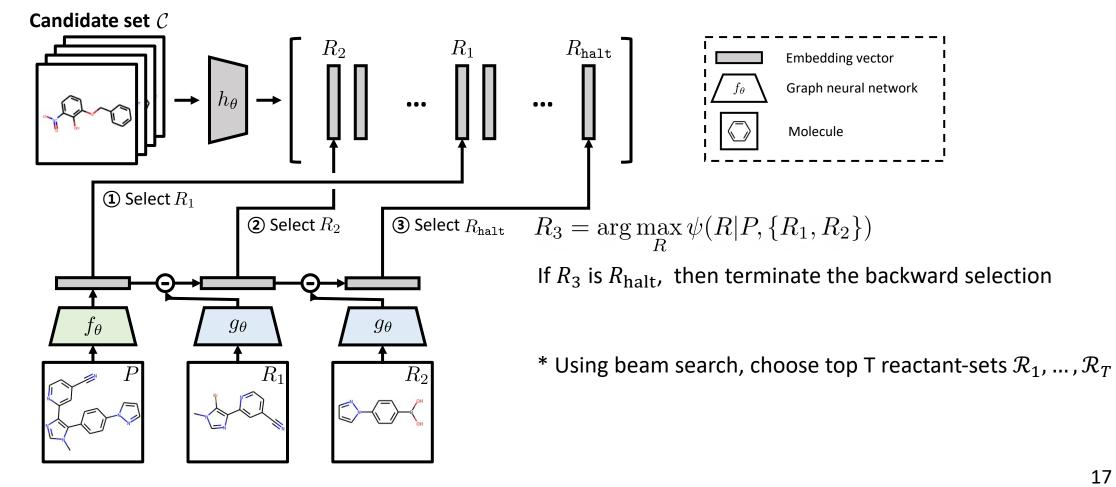
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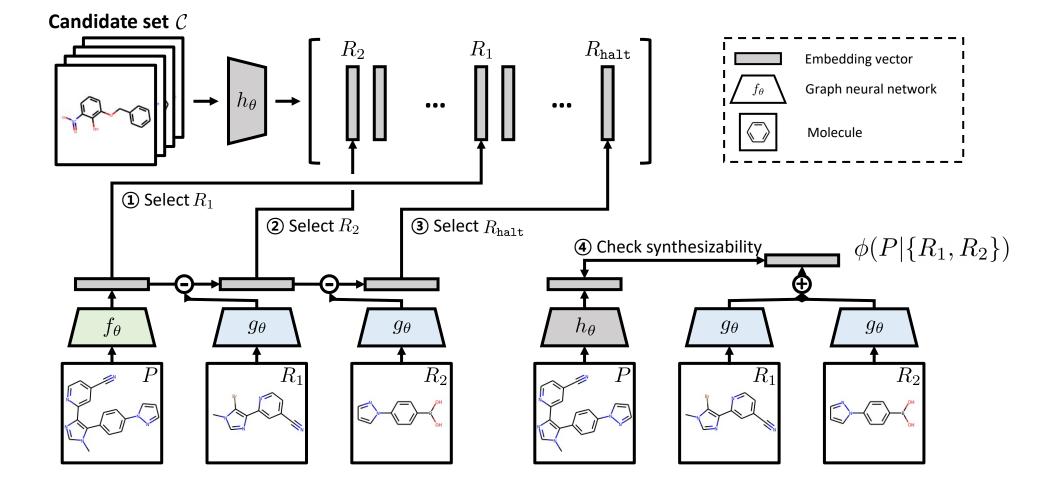
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Backward Selection Score:
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Forward Selection Score:
$$\phi(P|\mathcal{R}) = \operatorname{CosSim}\left(\sum_{R \in \mathcal{R}} g_{\theta}(R), h_{\theta}(P)\right)$$



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 R_1

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 $g_{ heta}$

 R_2

 h_{θ}

P

 $g_{ heta}$

 R_1

 g_{θ}

 R_2

- **Recall.** We design two selection scores:
 - $\psi(R|P, \mathcal{R}_{given})$: score of a reactant R given a product P and a set of previously selected reactants \mathcal{R}_{given}
 - $\phi(P|\mathcal{R})$: score of a product *P* given a set of reactants \mathcal{R}
- How to learn the scores?
 - The score functions resemble the classification scores of selecting a reactant or a product
 - Given a reaction (\mathcal{R}, P) in a database, we consider two **classification tasks**:

$$\begin{array}{ll} \mbox{Backward } P \to \mathcal{R} & \mbox{Forward } \mathcal{R} \to P \\ p(R|P,\mathcal{R}_{\texttt{given}},\mathcal{C}) = \frac{\exp(\psi(R|P,\mathcal{R}_{\texttt{given}})/\tau)}{\sum_{R' \in \mathcal{C} \setminus \{P\}} \exp(\psi(R'|P,\mathcal{R}_{\texttt{given}})/\tau)} & q(P|\mathcal{R},\mathcal{C}) = \frac{\exp(\phi(P|\mathcal{R})/\tau)}{\sum_{P' \in \mathcal{C} \setminus \mathcal{R}} \exp(\phi(P'|\mathcal{R})/\tau)} \\ \mathcal{L}_{\texttt{backward}}(P,\mathcal{R}|\theta,\mathcal{C}) = -\max_{\pi \in \Pi} \sum_{i=1}^{n+1} \log p(R_{\pi(i)}|P,\mathcal{R}_{$$

$$\mathcal{L}_{\texttt{total}} = \mathcal{L}_{\texttt{backward}}(P, \mathcal{R} | \theta, \mathcal{C}) + \mathcal{L}_{\texttt{forward}}(P, \mathcal{R} | \theta, \mathcal{C})$$

- How to learn the scores? (Cont.)
 - The optimization is intractable since ${\mathcal C}$ contains a large number of candidate molecules
 - To resolve this, we approximate ${\mathcal C}$ with the set of molecules in a mini-batch ${\mathcal B}$

$$\mathcal{C}_{\mathcal{B}} = \{ M \mid \exists (\mathcal{R}, P) \in \mathcal{B} \text{ such that } M = P \text{ or } M \in \mathcal{R} \}$$
$$\mathcal{L}(\theta | \mathcal{C}_{\mathcal{B}}) = \frac{1}{|\mathcal{B}|} \sum_{(\mathcal{R}, P) \in \mathcal{B}} \mathcal{L}_{\text{backward}}(P, \mathcal{R} | \theta, \mathcal{C}_{\mathcal{B}}) + \mathcal{L}_{\text{forward}}(P, \mathcal{R} | \theta, \mathcal{C}_{\mathcal{B}})$$

• To further improve approximation, we add hard negatives (i.e., nearest neighbors) into the candidate set

$$\widetilde{\mathcal{C}}_{\mathcal{B}} = \mathcal{C}_{\mathcal{B}} \cup \bigcup_{M \in \mathcal{C}_{\mathcal{B}}} \{ \text{Top-}K \text{ NN of } M \text{ from } \mathcal{C} \}$$

- The nearest neighbors (NN) are defined with respect to the cosine similarity on $\{h_{\theta}(M)\}_{M \in \mathcal{C}}$
- Since computing all embeddings for every iteration is time-consuming, we update the information periodically
- We found that this hard negative mining significantly improves the performance of RetCL

- Experimental setup
 - Our models are evaluated on **USPTO-50k**, which is a standard benchmark for retrosynthesis
 - For the candidate set C, we use **all reactants in the entire USPTO database (671k molecules)**
 - For molecule encoders f_{θ} , g_{θ} , h_{θ} , we use a single shared structure2vec [1] and separate residual layers
 - For evaluation, we use top-k exact match accuracy, which is widely used in the retrosynthesis literature

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

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- Effects of components
 - Hard negative mining is crucial in contrastive learning

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- Effects of components
 - Hard negative mining is crucial in contrastive learning
 - Considering the forward direction is important in retrosynthesis

$\phi(P \mathcal{R})$	K	sum	Top-1	Top-10
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• Effects of components

- Hard negative mining is crucial in contrastive learning
- Considering the forward direction is important in retrosynthesis
- Sum-pooling is more effective than mean-pooling

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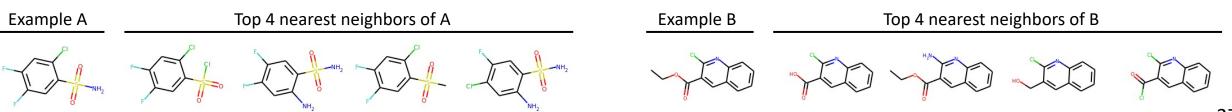
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• Nearest neighbors based on molecule embeddings $h_{\theta}(M)$

Considering the forward direction is important in retrosynthesis

Hard negative mining is crucial in contrastive learning

• Sum-pooling is more effective than mean-pooling



• Single-step retrosynthesis

• **<u>Note</u>**. Different categories = different assumptions about prior knowledge

Category	Method	Top-1	Top-3	Top-5	Top-10	Тор-20	Top-50	
Reaction type is unknown								
	Transformer [Karpov et al., 2019]	37.9	57.3	62.7	-	-	-	
Template-free	SCROP [Zheng et al., 2019]	43.7	60.0	65.2	68.7	<u>_</u>	-	
Template-free	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	-	-	
	retrosim [Coley et al., 2017]	37.3	54.7	63.3	74.1	82.0	85.3	
Template-based	neuralsym [Segler and 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	
Calastian based	Bayesian-Retro [Guo et al., 2020]	47.5	67.2	77.0	80.3	-	-	
Selection-based	RETCL (Ours)	71.3	86.4	92.0	94.1	95.0	96.4	
	Reaction type i	s given a	s prior					
	seq2seq [Liu et al., 2017]	37.4	52.4	57.0	61.7	65.9	70.7	
Tomplete free	Transformer [†] [Chen et al., 2019]	54.1	70.0	74.2	77.8	80.4	83.3	
Template-free	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	_	-	
	retrosim [Coley et al., 2017]	52.9	73.8	81.2	88.1	91.8	92.9	
Template-based	neuralsym [Segler and 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	
Calastian based	Bayesian-Retro [Guo et al., 2020]	55.2	74.1	81.4	83.5	-	-	
Selection-based	RETCL (Ours)	78.9	90.4	93.9	95.2	95.8	96.7	

- Single-step retrosynthesis
 - **<u>Note</u>**. Different categories = different assumptions about prior knowledge
 - It is hard to fairly compare between methods operating under different assumptions
 - To alleviate such a concern, we incorporate our prior knowledge of candidates C into the baselines
 - How? we simply filter out reactants outside the candidates C from the predictions made by the baselines

Prior knowledge	Category	Method	Top-1	Top-5	Top-10	Top-50	Top-100	Тор-200
	Reaction type is unknown							
Candidates ${\mathcal C}$	Template-free	Transformer [Chen <i>et al.</i> , 2019] RETCL (Ours)	59.6 71.3	74.3 92.0	77.0 94.1	79.4 96.4	79.5 96.7	79.6 97.1
templates $\mathcal T$ + Candidates $\mathcal C$	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 <i>et al.</i> , 2019] RETCL (Ours)	68.4 78.9	82.4 93.9	84.3 95.2	85.9 96.7	86.0 97.1	86.1 97.5
	Template-based	GLN [Dai et al., 2019]	82.0	91.7	92.9	93.3	93.3	93.3
coverage of known terr						wn tem	plates, i.e	

coverage of known templates, i.e.,

upper bound of template-based approaches

Conclusion

- We propose a selection-based approach considering the commercial availability of reactants
 - We reformulate the task of retrosynthesis as a problem where reactants are selected from a candidate set of available molecules
 - We design two effective selection scores in synthetic and retrosynthetic manners using graph neural networks
 - We propose a novel contrastive learning scheme with hard negative mining to overcome a scalability issue while handling a large-scale candidate set
 - We demonstrate the effectiveness of our framework in various single- and multi-step retrosynthesis experiments based on the USPTO database

Thank you for your listening!