Who Should Go First? A Self-Supervised Concept Sorting Model for Improving Taxonomy Expansion

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ABSTRACT
Taxonomies have been widely used in various machine learning and text mining systems to organize knowledge for facilitating downstream tasks. One critical challenge is that, as data and business scope grow in real applications, existing taxonomies need to be expanded to incorporate new concepts. Previous work on taxonomy expansion assumes those concepts are independent and process them one after another. As a result, they ignore the potential relationships among new concepts. However, in reality, those new concepts tend to be correlated and form hypernym-hyponym structures. In such a scenario, ignoring the relations among new concepts and inserting them into the taxonomy in an arbitrary order may trigger error propagation. For example, previous taxonomy expansion systems may insert hyponyms to existing taxonomies before their hypernyms, leading to sub-optimal expanded taxonomies.

To complement existing taxonomy expansion systems, we propose TaxoOrder, a novel self-supervised framework that simultaneously discovers hypernym-hyponym relations among new concepts and decides their insertion order. TaxoOrder can be directly plugged into any taxonomy expansion system and improve the quality of expanded taxonomies. Experiments on two real-world datasets validate the effectiveness of TaxoOrder to enhance taxonomy expansion systems, leading to better-resulting taxonomies with comparison to baselines under various evaluation metrics.

CCS CONCEPTS
• Information systems → Ontologies; • Theory of computation → Semi-supervised learning; • Applied computing → Enterprise ontologies, taxonomies and vocabularies; • Computing methodologies → Machine learning.

KEYWORDS
Taxonomy Expansion; Self-supervised Learning

1 INTRODUCTION
Taxonomies, represented as Direct Acyclic Graphs (DAGs), have been used to organize knowledge and information for centuries [24]. High-quality taxonomies can benefit many downstream applications such as query understanding [7, 27], content browsing [28], personalized recommendation [8, 33], and user-behavior modeling [15]. In the past, the majority of taxonomies are manually curated by human experts. Such curation is time-consuming and labor-intensive. To reduce the burden of human experts, many automatic taxonomy construction methods [13, 21, 31] have been proposed. With the growth of human knowledge comes the increasing demand for expanding the existing taxonomies to incorporate new concepts.

Driven by this demand, previous studies [12, 14, 20, 32] on taxonomy expansion aim to rank the candidate hypernyms in existing taxonomies and insert new concepts as hyponyms of the most likely hypernym. In reality, the order of inserting operations for new concepts is critical for existing taxonomy expansion systems. Suppose that a hyponym concept is inserted before its hypernyms, existing taxonomy expansion systems can hardly recover the ground truth hypernym-hyponym structure, because later concepts can only be added as leaf nodes in taxonomy. For example, considering a hypernym-hyponym pair of concepts (“geometry”, “rectangle”), if “rectangle” is first inserted into the existing taxonomy, then when processing “geometry”, we can only insert it as a hyponym of “rectangle”, which is incorrect. Figure 1 (Bottom) illustrates how inserting order determines the quality of expanded taxonomy. For an optimal taxonomy expansion model which always outputs the “correct” hypernym concept, if the inserting order is sub-optimal (1-3-2 or 3-1-2), it can never recover ground truth taxonomy.

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To address this issue, we instead study the order-aware taxonomy expansion system that bypasses the problem by dividing the task of inserting k new concepts into k independent tasks, each with a single element. This strategy ignores the potential dependencies among concepts and converts one new concept into an independent expansion task. We introduce a novel sorting model, TaxoOrder, which determines the order of insertion for new concepts. Within this model, hypernyms are ranked based on their frequency, and when hyponyms are inserted, the potential parent nodes are already included in the expanded taxonomy. TaxoOrder first learns the hypernym-hyponym relations from the existing taxonomy and then utilizes the learned model to iteratively insert each individual concept into the existing taxonomy.

In this section, we first define a taxonomy and then formulate the problem of taxonomy expansion. We consider a directed acyclic graph (DAG) where each node represents a concept and each directed edge indicates a hypernym-hyponym relation. The goal is to insert all new concepts into the existing taxonomy in an optimal order to improve the performance of the taxonomy expansion system. To achieve this, we introduce TaxoOrder, which can generate high-quality concept orders and benefit taxonomy expansion models.
and learning details. Finally, we explain how to expand the taxonomy with expansion models\textsuperscript{3} based on the order of new concepts generated by TaxoOrder. The overall illustration of the proposed TaxoOrder framework is shown in Figure 2.

### 3.1 Pattern-based Concept Graph

For the new concept set $C$, we first generate some hypernyms relations by patterns in surface names (e.g., "science" is a hypernym of "computer science", "text mining" is a hypernym of "biotext mining"). Such surface matching process provides a set of high-quality hypernym-hyponym edges ($\mathcal{E}_{\text{pattern}}$). The generated edges, as well as the set of new concepts $C$, lead to the concept graph $G_{\text{concept}} = (C, \mathcal{E}_{\text{pattern}})$. However, such graph contains minor noisy edges and potentially forms cycles within graph which prevents the graph to be sorted. Then to provide an order for each concept and to best preserve the high-quality order pairs mined by the rule-based surface matching, cycles are cut in decreasing order of cycle size to form $T_{\text{concept}}$, which is guaranteed to be a DAG. Such pattern-based concept graph generation enjoys high precision but has low recall: the coverage of valid hypernym-hyponym pairs is far from satisfactory. To leverage the existing taxonomy, we then model the concept pairs and learn a concept pair sorting algorithm to further enhanced the order relation among new concepts.

### 3.2 Modeling Concept Pairs

The concept sorting model we aim to learn is a scoring function $f$ (as shown in Figure 2), which inputs a pair of concepts $(a, c)$ and outputs their relative order score. Higher score $f(a, c)$ indicates higher confidence to have pair $(a, c)$ ordered as $a$ in front of $c$. In other words, $a$ is a more general concept than $c$ and therefore should be inserted into taxonomy first.

Following the previous work \cite{20}, we assume each new concept has an initial feature vector learned from the associated corpus. Concept $c_i$ is represented using its initial feature vector $\mathbf{c}_i \in \mathbb{R}^d$.

For each candidate concept pair $(a, c)$, we generate four sub-features:

- $a$: Embedding of concept “a”;
- $c$: Embedding of concept “c”;
- $a-c$: Difference between embedding of concept “a” and concept “c”;
- $a \odot c$: Element-wise multiplication of embedding of concept “a” and concept “c”.

The feature vector $\text{Feature}(a, c)$ is the concatenation of four sub-features mentioned above:

$$\text{Feature}(a, c) = [\mathbf{a} \parallel \mathbf{c} \parallel a-c \parallel a \odot c].$$

(1)

Then we parameterize the scoring function $f$ as a multi-layer perceptron (MLP), which inputs the feature vector $\text{Feature}(\cdot, \cdot)$ of a pair of concepts. Section 4.4.2 describes the detailed implementation of the scoring function.

### 3.3 Self-supervision Generation

To learn the concept sorting model, we generate self-supervisions as shown in Figure 2. Given one edge $(n_p, n_c)$ in the existing taxonomy $\mathcal{T}$, we construct N negative pairs by fixing the child node $n_c$ and randomly selecting N concept nodes $n_1, n_2, \ldots, n_N$, which are not ancestors of $n_c$. For example, as illustrated in the “Self-Supervision” part in Figure 2, for a query concept “Label Propagation”, there is a real edge (Semi-Supervised Learning, Label Propagation) in the taxonomy. This real edge corresponds to a positive sample. Then to generate the negative samples, we fix “Label Propagation” and select “Integrated Circuit” and “GPU” as negative samples. Here, the node “Machine Learning” will not be sampled because it is the ancestor of “Label Propagation”. These $N+1$ pairs collectively consist of one training instance $X = \{(n_p, n_c), (n_1, n_c), (n_2, n_c), \ldots, (n_N, n_c)\}$. We repeat the process above for each edge in the existing taxonomy $\mathcal{T}$ to generate the full self-supervision data $X = \{X_1, X_2, \ldots, X_{|E|}\}$.
3.4 Model Training

In self-supervised learning settings, contrastive loss is widely adopted and Noise Contrastive Estimation (NCE) [5] provides great discriminative learning power. Since in TaxoOrder settings, the negative samples are readily available in a large number, we learn our TaxoOrder on $X$ using the InfoNCE loss [25] as follows:

$$L(\Theta) = -\frac{1}{|X|} \sum_{x \in X} \log \frac{f(n_p, n_c)}{\sum_{(n_j, n_c) \in X} f(n_j, n_c)},$$  \tag{2}

where, the subscript $j \in [p, 1, 2, ..., N]$. If $j = p$, $(n_j, n_c)$ is a positive pair, otherwise it is a negative pair. The above loss is the cross entropy of classifying positive pair $(n_p, n_c)$ correctly, with $f(n_p, n_c)$ as the model prediction.

Algorithm 1: Self-supervised learning of TaxoOrder

**Input:** A taxonomy $T^0$; negative size $N$, batch size $B$; model $f(\cdot|\Theta)$.

**Output:** Learned model parameters $\Theta$.

1. Randomly initialize $\Theta$;
2. while $L(\Theta)$ in Eq. (2) not converge do
3. Enumerate nodes in $T^0$ and sample $B$ nodes without replacement;
4. $D = \emptyset$ # current batch of training instances;
5. for each sampled node $n_q$ do
6. Select one of its parents $n_p$ to construct one positive pair $(n_p, n_q)$;
7. Generate $N$ negative pairs $\{n^1_p, n_q \}, \ldots , \{n^N_p, n_q \}$;
8. $D \leftarrow D \cup \{(n_p, n_q), (n^1_p, n_q), \ldots , (n^N_p, n_q)\}$;
9. Update $\Theta$ based on $D$;
10. Return $\Theta$;

3.5 Candidate Concept Pair Generation

At the inference stage, we are given a set of new query concepts $C$ and aim to apply the learned model $f(\cdot|\Theta)$ to predict the pair-wise ordering of concepts in $C$. Notably, we only need to correctly sort relevant concepts. That is, we aim to place hyponym concept in the front of its hyponyms, while for irrelevant concept pairs, their ordering will not affect the resulting taxonomy. Thus, we first examine the semantic similarity between each pair of new concepts and only consider the pairs with high semantic similarity scores as candidate concept pairs, because they are more likely to have hypernym-hyponym relations. To achieve this goal, we perform straightforward threshold-based filtering to get high quality candidate pairs. Such threshold is learned from the existing taxonomy. The details about the threshold setting is illustrated in Section 4.4.1.

3.6 Pattern-enhanced Concept Sorting

Our TaxoOrder learns a relative score for each concept pair which indicates the relative ranking order within the new concept set. Thus, we generate the pseudo-edges $(n_p, n_c)$ with weight $f(n_p, n_c)$ to order the set with confidence learned in TaxoOrder.

Finally, we generate the order leveraging both pattern-based concept graph $T_{\text{concept}}$ and pseudo-edges $(n_p, n_c)$. To maintain the DAG property, pseudo-edges are iteratively appended to $T_{\text{concept}}$ in the descent order of their weights. During the $i$th iteration, if pseudo-edge $e_i$ forms cycle in current $T_{\text{order}}$, it will be discarded. After appending all pseudo-edges, the $T_{\text{concept}}$ finally becomes $T_{\text{order}}$. The order $O_C$ is obtained by applying topological sort on $T_{\text{order}}$.

$$O_C = \text{TopologicalSort}(T_{\text{order}}) \tag{3}$$

That enforces the output order $O_C$ follow the pair-wise ordering given by the edges in $T_{\text{order}}$. An illustrative example for the whole pattern-enhanced concept sorting process is provided in Figure 3.

3.7 Iterative Taxonomy Expansion

For expanding existing taxonomies, we adopt TaxoExpan [20] and Arborist [12], two state-of-the-art taxonomy expansion systems. We iteratively insert new concepts following the order $O_C$ given by Eq. 3. Specifically, at iteration $t$, we update the current taxonomy $T^{t-1} = (N^{t-1}, E^{t-1})$ by attaching the $t$-th concept $(c^t)$ to the concept $n^* \in N^{t-1}$ with the highest matching score:

$$T^t = (N^t = N^{t-1} \cup \{n^*\}, E^t = E^{t-1} \cup (n^*, c^t)) \tag{4}$$

where $(n^*)$ is output by the expansion model.

| Dataset | $|N|$ | $|E|$ | $|D|$ | $|C|$ |
|---------|------|------|------|------|
| MAG-CS  | 24,754 | 42,329 | 6 | 3,765 |
| MAG-Full| 355,808 | 638,674 | 6 | 37,804 |

4 EXPERIMENTS

In this section, we discuss the information about the dataset and then make comparisons between different methods for our task.

4.1 Dataset

We evaluate TaxoOrder on the public Field-of Study (FoS) Taxonomy\(^2\) in Microsoft Academic Graph (MAG) [23]. We modify the dataset from TaxoExpan in separation to fit our task. As shown

\(^2\)https://docs.microsoft.com/en-us/academic-services/graph/reference-data-schema
in Figure 4, we only mask leaf nodes for validation. For testing, if some node concept $c$ is sampled, we mask the whole DAG rooted at $c$ to construct the testing set. Table 1 shows the statistics of the two datasets mentioned above.

In detail, the FoS taxonomy contains more than 660k scientific concepts and over 700k taxonomic relations. Although it is constructed in a semi-automatic manner, the previous study [22] shows that this taxonomy is of high quality. We remove all concepts that have no relation in the original FoS taxonomy and then randomly mask 20% of concepts (along with their relations) for validation and testing. The remaining FoS taxonomy is then treated as the input existing taxonomy. We refer to this dataset as MAG-Full. Based on MAG-Full, we construct another dataset called MAG-CS focusing on the computer science domain. Specifically, we first select a subgraph consisting of all descendants of the “computer science” node and then mask around 10% of concepts in this subgraph for testing and then mask another 10% leaf concepts for validation.

As discussed in Section 3.2, each concept within our task has an initial feature vector. To obtain such feature vectors, we first construct a corpus that consists of all paper abstracts mentioning at least one concept in the original MAG dataset. Specifically, each concept should be treated as a single token for embedding learning (e.g., for multi-word expression “data mining”, it will be converted to “data_mining”). Then, we learn 250-dimension word embedding as initial feature vectors using the skip-gram model word2vec [16].

4.2 Evaluation Metrics

- Error Node Count (ENC) is the number of query concepts whose parent is not present in the existing taxonomy when it is inserted.
- Hit@$k$ is the number of query concepts whose parent is ranked in the top-$k$ positions, divided by the total number of queries.

4.3 Compared Methods

We compare our TaxoOrder concept sorting algorithm with several baselines. All these methods are used to determine the inserting order for new concepts. We examine the effectiveness of these methods with two taxonomy expansion modules. Note that taxonomy expansion module is independent to our concept sorting problem, thus make our TaxoOrder compatible with other original expansion work.

1. Random: This method simply inserts new concepts in random order which applies the EXPANSION model directly to the new task.
2. Affinity: The EXPANSION model assigns affinity scores for the candidate $(n_p, n_q)$ pair. Such affinity scores can be interpreted as the level of confidence that $n_p \in \mathcal{T}$ is the hypernym of $n_q \in C$. Affinity inserts new concepts based on the affinity scores from the Expansion module. Affinity sorts the new concepts by the highest affinity score available for each query $n_q$: the new concept node with the highest affinity score with the existing taxonomy node gets inserted first.
3. MLP: This is the proposed TaxoOrder without pattern guidance, the DAG $\mathcal{T}_{ordw}$ is generated by applying pruning algorithm (Minimum Spanning Tree) on $\mathcal{G}_\text{order}$.
4. Pattern: This method first performs TOPOLOGICALSORT on $\mathcal{T}_{pattern}$ to determine the order $O$. Then it inserts the new concepts using the topological order $O$ of $\mathcal{T}_{pattern}$.
5. TaxoOrder: Proposed pattern-enhanced TaxoOrder method.
Table 2: Overall results on MAG-CS datasets with TaxoExpan and Arborist. Note that smaller ENC indicates better model performance. For all other metrics, larger values indicate better performance. We highlight the best two models in terms of the performance under each metric.

| Methods             | ENC  | MRR   | Hit@1 | Hit@3 | Pred F1 | Edge F1 | Ancestor F1 |
|---------------------|------|-------|-------|-------|---------|---------|-------------|
| TaxoExpan +Ground Truth | 0    | 0.2702| 0.1934| 0.2576| 0.1427  | 0.9026  | 0.9345      |
| TaxoExpan +Random    | 1208 | 0.2113| 0.1450| 0.2109| 0.1070  | 0.8985  | 0.9328      |
| TaxoExpan +Affinity  | 966  | 0.2169| 0.1498| 0.2157| 0.1105  | 0.8989  | 0.9329      |
| TaxoExpan +MLP       | 794  | 0.2320| 0.1610| 0.2117| 0.1188  | 0.8987  | 0.9326      |
| TaxoExpan +Pattern   | 1892 | 0.1662| 0.1116| 0.1687| 0.0823  | 0.8957  | 0.9327      |
| TaxoExpan +TaxoOrder | 437  | 0.2595| 0.1782| 0.2534| 0.1315  | 0.9013  | 0.9332      |
| Arborist +Ground Truth | 0   | 0.2272| 0.2024| 0.2619| 0.1493  | 0.9034  | 0.9315      |
| Arborist +Random     | 1208 | 0.1877| 0.1450| 0.2135| 0.1070  | 0.8994  | 0.9305      |
| Arborist +Affinity   | 966  | 0.1919| 0.1482| 0.2183| 0.1150  | 0.8995  | 0.9305      |
| Arborist +MLP        | 794  | 0.2035| 0.1620| 0.2316| 0.1250  | 0.9006  | 0.9304      |
| Arborist +Pattern    | 1892 | 0.1514| 0.1222| 0.1740| 0.0902  | 0.8966  | 0.9309      |
| Arborist +TaxoOrder  | 437  | 0.2258| 0.1780| 0.2584| 0.1313  | 0.9013  | 0.9300      |

4.4 Implementation Details

4.4.1 Threshold for Semantic Similarity. As described in Section 3.5, we only consider concept pairs whose semantic similarity is higher than a threshold \( \alpha \). Here, we adopt cosine similarity, and the threshold \( \alpha \) is set based on the existing taxonomy to avoid heavy tuning. To set the threshold \( \alpha \), we compare the cosine similarity distribution between (1) real edges in existing taxonomy \( \mathcal{T}^0 \) and (2) randomly sampled node pair from \( N^0 \). Figure 6 shows that there is a clear difference between the distribution of similarity scores of real edges and that of randomly generated node pairs. Hence, we simply use the mean of the similarity scores of real edges 0.7 as our threshold \( \alpha \).

4.4.2 MLP Details. We simply use one hidden layer MLP and the structure is described by formula 7 below,

\[
f_{\text{MLP}}(a, c) = \sigma(W_1 f(\text{feature}(a, c) + B_1) + B_2)
\]

where \( W_1, W_2, B_1 \) and \( B_2 \) are learnable parameters, \( \sigma \) is a sigmoid function, and \( \gamma \) is ReLU activation function.

Empirically, we use 512-dimensional hidden layer and 250-dimensional embedding for node feature, which gives us \( 4 \times 250 \times 512 + 512 \times 1 + 512 + 1 = 513025 \) parameters. We even further studied a deeper MLP with 2.5M parameters. They end up with similar performances. Hence we do not go further here.

Table 3: Average run-time analysis (hr/epoch)

|          | TaxoOrder | TaxoExpan | Arborist |
|----------|-----------|-----------|---------|
| Memory   | 0.15      | 0.25      | 0.1     |

4.4.3 Code Reproducibility and Runtime Analysis. For taxonomy expansion modules, we modified TaxoExpan\(^3\) and Arborist\(^4\) to fit the new task. For the TaxoOrder module, we use PyTorch [18] as the basic framework. For TaxoExpan and TaxoOrder, we train, validate, and test the model on a Linux Host with Intel(R) Core(TM) i7-8700K CPU @ 3.70GHz CPU, 48G DDR4 Memory, and Nvidia GeForce RTX 2080 GPU. For the Arborist module, we run on a Linux Server with Intel(R) Xeon(R) CPU E5-2680 v2 @ 2.80GHz CPU and 256G Memory. The average run-time per epoch for each sub-module is listed in Table 3.

Figure 6: embedding cosine similarity distribution between (a) real edges in existing taxonomy \( \mathcal{T}^0 \) and (b) random sampled node pair from \( N(\mathcal{T}^0) \)

4.5 Experimental Results

Overall Performance. Table 2 shows the overall result of all compared methods. First, by comparing the correlation between ENC and other metrics, it can be concluded that the taxonomy expansion performance is highly sensitive to the inserting order: the lower the ENC, the higher the expansion performance can achieve. And the ground truth inserting order gives the best expansion performance since its ENC is zero. Among all the methods compared in both expansion modules in experiments, the TaxoOrder outperforms the baseline methods and is distinguished out by a large margin. Even compared with the ground truth order, the TaxoOrder performs relatively well in terms of most of the evaluation metrics. Comparing Affinity with Random, the ENC has dropped a lot, but in the
expansion quality evaluation, there is only a small improvement from Random to Affinity. That is because the Affinity score is not tailored to this sorting task. Although it represents the hypernym-hyponym relation to some extent, the lack of learning process on this sorting task limits its capability to get better expansion results.

**Ablation Study.** We perform the ablation study by comparing TaxoOrder with MLP and Pattern respectively. For the MLP model, the ENC is significantly smaller than randomly assigned order, which demonstrates the feasibility of the proposed learning framework, however, the MLP model produces extra noisy data which also violates the real edge in the new concepts. These noisy data make the inserting result worse than TaxoOrder. By comparing between TaxoOrder and Pattern, the Pattern method provides many high-quality potential hypernym relations but not all parent-children concepts have this surface name matching rule. That leaves many concepts orphan in the DAG created in Pattern. The TOPOLOGICALSORT has no control over the order of these orphan concepts, thus making the ENC of the Pattern even worse than Random. Other evaluation metrics follow the same logic, higher ENC gives worse expansion results. But the Pattern model does contain high-quality order information for the concepts with matching results. TaxoOrder model makes a big step and benefits both from the pattern-based method for high-quality order extraction and also covers most of the new concepts such that decrease the ENC and achieve nearly comparable with ground truth order.

5 RELATED WORK

**Taxonomy Construction.** Traditional taxonomy construction methods use lexical features from the resource corpus such as lexical-patterns [1, 6, 9, 17] or embedding-based distribution methods [10, 11, 19, 26]. Later work CRIM [2] utilized word-embedding, negative sampling, fine-tuning, and multiple projection matrices to achieve the best performance in the SemEval 2018 hypernym discovery task.

**Taxonomy Expansion.** Arborist [12] follows the framework in piecewise projection-learning on word-embeddings [4] and designed a training objective with a marginal loss which enforces the projection matrix learning the hypernym-hyponym relationship [3]. With graph neural networks being introduced, TaxoExpan [20] utilizes a position-enhanced graph neural network (GNN) that captures the local structure of a concept node in the existing taxonomy and at the same time trains a matching module to find the matching score for each anchor-query concepts pair measuring the confidence that the anchor is the hypernym of this query. And they claim a noise-robust training objective that enables the learned model to be insensitive to the label noise in the self-supervision data. STEAM [30] further explores on top of the GNN based method and proposes to utilize semantic mini-paths in the existing taxonomy to further capture the hypernym-hyponym relations. TMN [32] investigates such a problem in an alternative way, instead of one-to-one matching in the existing taxonomy expansion work, it proposes one-to-pair matching and introduces a channel-wise gating function to capture the hypernym and hyponym of query concepts.

**Lexical Memorization.** The lexical memorization does matter in the taxonomy expansion task. Some “super-hypernym” nodes may absorb many new concepts as children. Although TaxoOrder is learned on the existing taxonomy, it is applied to new concepts only. It won’t get in touch with the existing taxonomy for data leakage. It can be argued that the learned model somehow memorized the existing taxonomy structure. It also learned how relative generality is for a given concept pair. Memorizing the existing taxonomy structure won’t directly affect the prediction of the order in new concepts. The experiments also support this argument; the model didn’t learn a perfect expansion model. Instead, it only learned a relative generality score function. And the output order shows that this order benefits the expansion model a lot.

6 CONCLUSIONS

This work extends the taxonomy expansion task from discovering the hypernym-hyponym relations between existing concepts and new concepts to a more general form: discovering the additional relation within new concepts. To solve this extended task, a novel sorting framework is proposed that leverages self-supervision from the existing taxonomy and learns a pattern-enhanced taxonomy ordering model TaxoOrder which helps capture the hypernym relations within new concepts. Combined with taxonomy expansion modules, TaxoOrder is able to provide high-quality inserting order and discover the hypernym-hyponym relations within new concepts. The experiment results and the ablation study showed the overall superiority of the proposed method and the effectiveness of each sub-module in the TaxoOrder model design. Interesting future work may include using the ordering function with expansion models to clean the existing taxonomy.

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