STEAM: Self-Supervised Taxonomy Expansion with Mini-Paths

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ABSTRACT

Taxonomies are important knowledge ontologies that underpin numerous applications on a daily basis, but many taxonomies used in practice suffer from the low coverage issue. We study the taxonomy expansion problem, which aims to expand existing taxonomies with new concept terms. We propose a self-supervised taxonomy expansion model named STEAM, which leverages natural supervision in the existing taxonomy for expansion. To generate natural self-supervision signals, STEAM samples mini-paths from the existing taxonomy, and formulates a node attachment prediction task between anchor mini-paths and query terms. To solve the node attachment task, it learns feature representations for query-anchor pairs from multiple views and performs multi-view co-training for prediction. Extensive experiments show that STEAM outperforms state-of-the-art methods for taxonomy expansion by 13.4% in accuracy and 7.0% in mean reciprocal rank on three public benchmarks. The implementation of STEAM can be found at https://github.com/yueyu1030/STEAM.

KEYWORDS

Taxonomy Expansion, Mini-Paths, Self-supervised Learning

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INTRODUCTION

Taxonomies, as hierarchical organizations of concepts, play a central role in a wide spectrum of applications. On a daily basis, ecommerce websites like Amazon heavily rely on their product

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taxonomies to support billions of product navigations, searches, and recommendations [45]; the usage of scientific taxonomies (e.g., MeSH¹) makes it much quicker for scientists to identify relevant information from massive scientific papers, and the concept taxonomies in knowledge bases (e.g., Freebase [5]) underpin many question answering systems [14]. Such importance has nurtured various taxonomies in general and specific domains (e.g., WordNet [27], Wikidata [40], MeSH, Amazon Product Taxonomy [17]).

One bottleneck that hinders the performance of existing taxonomies for different applications is the low coverage problem. This problem arises mainly due to two reasons. First, many existing taxonomies are curated by domain experts. As the curation process is expensive and time-consuming, the result taxonomies often include only the most frequent and coarse-grained terms. Consequently, the curated taxonomies often have high precision, but limited coverage. Second, domain-specific knowledge is constantly growing in most applications. New concepts arise continuously, but it is too expensive to rely on human curation to maintain and update the existing taxonomies accordingly. The low coverage issue can largely hurt the performance of downstream tasks that require concept taxonomies. To address this issue, an automatic taxonomy expansion and enrichment method is urgently in need of development.

Existing methods for automatic taxonomy construction follow two lines. One direction is to construct taxonomies in an unsupervised way [23, 29, 41, 43]. This is achieved by either grouping concept terms into a hierarchy (e.g., by hierarchical clustering or topic modeling), or leveraging syntactic patterns (e.g., the Hearst pattern [15]) to derive *parent-child* pairs for taxonomy discovery. The other direction is to adopt supervised approaches [13, 19, 25]. They first detect hypernymy pairs (i.e., term pairs with the "is-a" relation) and then organize these pairs into a tree structure. The key step of hypernymy pair detection typically relies on a large amount of positive and negative pairs that are manually annotated. Despite the success of existing methods, they encounter several limitations while dealing with the taxonomy expansion task. First, most of the existing methods attempt to construct taxonomies from scratch. Their output taxonomies can rarely preserve the initial taxonomy structures curated by domain experts [34]. Second, most of those methods merely rely on single-view information as supervision signals. For instance, [13, 19, 29] merely consider lexico-syntactic

¹https://www.nlm.nih.gov/mesh/meshhome.html

patterns and [34, 43] only consider distributed representations. Consequently, such methods fail to simultaneously model multiple types of information, which hinders their performance.

We address the taxonomy expansion problem with a self-supervised model named STEAM, which is short for Self-supervised Taxonomy ExpAnsion with Mini-Paths. As shown in Figure 1, the self-supervised taxonomy expansion task aims to insert the new concepts into the existing taxonomy without requiring extra labels. In order to automatically generate self-supervision signals, the core idea of STEAM is sampling mini-paths to connect terms in different layers (e.g. "Pollutant"-"Atmospheric Pollutant"-"Dust" in Figure 1) as well as query terms to from query-anchor pairs from the existing taxonomy (Section 3.1). With these query-anchor pairs, we learn a model to pinpoint the correct position for a query term in the mini-path. Based on the model, we attempt to figure out the correct position for new concepts and insert them into the existing taxonomy. Compared with previous methods [25, 34, 37, 39] which train binary classifiers using single terms as query-anchor pairs, STEAM can better preserve the taxonomy structural information since fixedlength snippets contain richer information from different levels of the taxonomy compared with a single node.

Another unique design in our mini-path classification framework is to use multi-view information (Section 3.2). To allot query terms to the correct positions in the existing taxonomy, STEAM uses three complementary sources of information between terms: (1) distributed features that capture the similarity between terms' distributed representations (i.e. word embeddings); (2) contextual features, i.e. information from two terms' co-occurring sentences; (3) *lexico-syntactic information* extracted from the string features between terms. To fuse the three views more effectively, we propose a multi-view co-training procedure. In this procedure, the three views lead to different branches for predicting the positions of the query term, and the predictions from these three views are encouraged to agree with each other. Such a co-training procedure can better integrate the complementary signals from different views and improve the overall performance of taxonomy expansion with mini-paths.

We have conducted extensive experiments on three public benchmarks for taxonomy construction in different domains. The results show that STEAM outperforms state-of-the-art methods for taxonomy expansion by 13.4% in accuracy and 7.0% in mean reciprocal rank on three public benchmarks. Moreover, ablation studies demonstrate the effect of mini-path for capturing structural information from the taxonomy as well as the multi-view co-training for utilizing the complementary signals from all views.

Our main contributions are: 1) a self-supervised framework that performs taxonomy expansion with natural supervision signals from existing taxonomies and text corpora; 2) a mini-path-based anchor format that better captures structural information in taxonomies for expansion; 3) a multi-view co-training procedure that integrates multiple sources of information in an end-to-end model; and 4) extensive experiments verifying the efficacy of our method.

2 PROBLEM DESCRIPTION

We focus on the taxonomy expansion task for *term-level* taxonomies, which is formally defined as follows.

Definition 2.1 (Taxonomy). A taxonomy $\mathcal{T} = (\mathcal{V}, \mathcal{E})$ is a tree structure where 1) \mathcal{V} is a set of terms (words or phrases); and 2) \mathcal{E} is a set of edges representing *is-a* relations between terms. Each directed edge $\langle v_i, v_j \rangle \in \mathcal{E}$ represents a hypernymy relation between term v_i and term v_j , where v_i is the hyponym (child) and v_j is the hypernym (parent).

The problem of taxonomy expansion (Figure 1) is to enrich an initial taxonomy by inserting new terms into it. These new terms are often automatically extracted and filtered from a text corpus. Formally, we define the problem as below:

Definition 2.2 (Taxonomy Expansion). Given 1) an existing taxonomy $\mathcal{T}_0 = (\mathcal{V}_0, \mathcal{E}_0)$, 2) a text corpus \mathcal{D} , and 3) a set of candidate terms \mathcal{C} , the goal of taxonomy expansion is to insert the term $q \in \mathcal{C}$ into the existing taxonomy \mathcal{T}_0 and expand it into a more complete taxonomy $\mathcal{T} = (\mathcal{V}, \mathcal{E})$ where $\mathcal{V} = \mathcal{V}_0 \cup \mathcal{C}, \mathcal{E} = \mathcal{E}_0 \cup \mathcal{R}$ with \mathcal{R} being the newly discovered relations between terms in \mathcal{C} and \mathcal{V}_0 .

3 THE STEAM METHOD

In this section, we describe our proposed method STEAM. We first give an overview of our method, and then detail the two key modules: mini-path-based prediction and multi-view co-training. Finally, we discuss the model learning and inference procedures.

3.1 Self-Supervised Learning by Mini-Path Attachment

The central task of taxonomy expansion is to attach a query term $q \in C$ into the correct position in the existing taxonomy \mathcal{T}_0 . STEAM learns to attach query terms using natural supervision signals from the seed taxonomy. Its self-supervised learning procedure aims to preserve the structure of the seed taxonomy by creating a learning task that pinpoints the anchor positions for the terms already seen in the seed taxonomy. The training data for this self-supervised learning task can be easily obtained from the seed taxonomy, thereby facilitating learning a model that performs query attaching at inference time.

3.1.1 Query-Anchor Matching with Mini-Paths. To instantiate the self-supervised learning paradigm [22, 34, 38], an intuitive idea is to find the best hypernym for the query term q. Most existing works [25, 34, 39] follow this idea and model the taxonomy expansion problem as finding the optimal hypernym pairs for test terms. They usually design a binary classifier trained by determining whether $\langle p_i, p_j \rangle$ $(p_i, p_j \in \mathcal{V}_0)$ is a hypernymy pair.

Unlike the binary classification formulation, STEAM learns to match query terms with anchors with richer structural information. The core of STEAM's self-supervised learning procedure is *mini-paths*, which are snippets sampled from the seed taxonomy. These mini-paths, containing the term pairs from different layers of taxonomy, can preserve the hierarchical relations among different terms. Below, we introduce the notion of *mini-path* and formulate the self-supervised learning task based on mini-paths.

Definition 3.1 (Mini-path). A mini-path $P = [p_1, p_2, ..., p_L]$ consists of several terms $\{p_1, p_2, ..., p_L\} \subset \mathcal{V}_0$, where L is the length of P. Each term pair $\langle p_i, p_{i+1} \rangle$ $(1 \le i \le L - 1)$ corresponds to an edge in \mathcal{E}_0 .

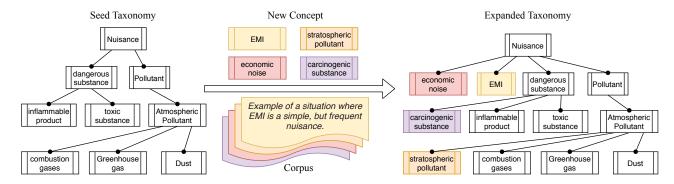


Figure 1: Illustration of the expansion procedure for an environment taxonomy. The goal is to train an expansion model with the existing taxonomy and auxiliary corpus to insert incoming terms to correct positions.

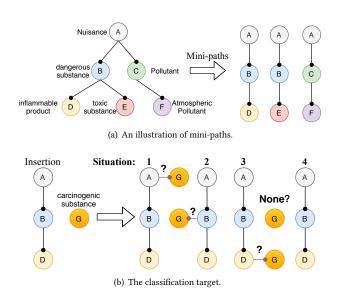


Figure 2: An illustration of the proposed self-supervised data structure, including the construction of mini-paths and the learning target during the term-insertion process.

The mini-paths are fixed-length branchless sub-graphs of the existing taxonomy \mathcal{T}_0 , as shown in Figure 2(a), which maintain part of the parent-child relationships between terms. To keep the hierarchical information in the taxonomy with the self-supervised training set, we design the training task as a multi-class classification problem. As shown in Figure 2(b), given a 3-terms mini-path as anchor and a new term as query, STEAM predicts the probabilities of the query being attached to the three terms or none of them.

Compared with the simple task of binary hypernymy classification, matching query terms with mini-paths has two major advantages: 1) When attaching a query term q into an anchor minipath P, we consider the collection of all terms $p_i \in P$ as a whole, rather than attend to them separately. This not only provides richer information for query attachment but also results in larger training data for self-supervised learning. 2) Compared with the binary classification, this task is more challenging—the matching module needs to judge not only whether q should be matched to P but

also which specific position to attach. Learning from this more challenging self-supervised task allows STEAM to better leverage the structural information of the existing taxonomy and perform better for anchor term deduction and taxonomy expansion.

3.1.2 Sampling Mini-Paths from the Seed Taxonomy. To facilitate the learning problem, we need to sample mini-paths from the existing taxonomies as anchors, as well as the query terms that should be attached to different positions in anchor mini-paths. This can be achieved by randomly sampling mini-paths in the seed taxonomy, along with positive and negative query terms for each mini-path.

The detailed procedure for training data creation is described as follows. Given one mini-path $P \in \mathcal{P}$ where \mathcal{P} is the collection of all mini-paths in the existing taxonomy, we first generate positive training set \mathcal{X}^{pos} by sampling all the child terms $a_{i,l} \in A$ of $P \in \mathcal{P}$, where $a_{i,l}$ is the i-th child of the l-th anchor term $p_l \in P$ and A contains all child terms attached to the mini-path, and a positive pair is represented as $X_{i,l}^{\text{pos}} = \langle a_{i,l}, p_j, l \rangle$. Once \mathcal{X}^{pos} is obtained, we augment the training set by adopting the negative sampling strategy to generate negative set \mathcal{X}^{neg} by randomly selecting $|\mathcal{X}^{\text{neg}}| = r \times |\mathcal{X}^{\text{pos}}|$ terms $\{n_i\}_{i=1}^{|\mathcal{X}^{\text{neg}}|}$ with sampling ratio r, each constituting a negative pair with one term that is not its parent in a anchor. Since these negative terms do not directly associate with the minipath P, we assign a relative position L+1 for them to indicate no connection exists. Combining \mathcal{X}^{pos} and \mathcal{X}^{neg} together we obtain the final training set \mathcal{X} .

After obtaining query-anchor pairs, we need to learn a model using such data. Given the set of training pairs X, we denote each pair as $X = \langle q, P, l \rangle \in X$ where q is the query term, P is the mini-path, and y is the relative position and aim to learn a model $f(q, P|\Theta)$ to identify the correct position (represented by the true label y). The training objective is to optimize the negative log likelihood $\ell = -\sum_X \sum_{i=1}^{L+1} y_i \log \hat{y_i}$ where \hat{y} is the predicted position.

3.2 Multi-View Co-Training with Mini-Paths

Now the question is how to obtain feature representations for each query-anchor pair (q, P). In STEAM, we learn feature representations for query-anchor pairs from three different views and integrate them with a multi-view co-training procedure.

3.2.1 Multi-View Feature Extraction. STEAM learns representations of query-anchor pairs from three views: (1) the distributed representation view, which captures their correlation from pre-trained word embeddings; (2) the contextual relation view, which captures their correlation from the sentences where the query term and anchor terms co-occur; and (3) the lexico-syntactic view, which captures their correlation from the linguistic similarities between the query and the anchor.

Each of the three views has its own advantages and disadvantages: (1) Distributed features have a high coverage over the term vocabulary, but they do not explicitly model pair-wise relations between a query term and an anchor term; (2) Contextual features can capture the relation between two terms from their co-occurred sentences, but have limited coverage over term pairs. For example, only less than 15% of hypernym pairs have co-occurred in the scientific corpus of the SemEval dataset; (3) Lexico-Syntactic features encode linguistic information between terms and can work well for matched term pairs, but these features are too rigid to cover all the linguistic patterns, and may also have limited coverage.

Given a query term q and an anchor mini-path $P = [p_1, p_2, \cdots, p_L]$, we describe the details of how we learn representations for the query-anchor pair (q, P) from the three different views.

(1) Distributed Features. The first view extracts distributed features for both the query q and the anchor mini-path P. For the query term q and the anchor terms in the mini-path P, we use pre-trained BERT embeddings [9] to initialize their distributed representations due to its superior expressive power [16, 21]. While it is feasible to directly use such initial embeddings for similarity computation, recent work [34] shows that the neighboring terms of an anchor term are also useful for taxonomy expansion. We follow [34] to use a position-enhanced graph attention network (PGAT) to propagate the embeddings for the terms in the seed taxonomy by considering the taxonomy as a directed graph—this will lead to updated embeddings for the anchor terms in the mini-path P. For each anchor term $p_l \in P$, we use $\mathbf{w}(p_l)$ to denote its PGAT-propagated embedding and use $\mathbf{w}(q)$ to denote the embedding of the query term q, then we concatenate these embeddings and obtain the distributed representation for the query-anchor pair (q, P):

$$\mathbf{h}_d(q, P) = [\mathbf{w}(q) \oplus \mathbf{w}(p_1) \oplus \cdots \oplus \mathbf{w}(p_L)]. \tag{1}$$

(2) Contextual Features. When two terms co-occur in the same sentence, the contexts of their co-occurrence can often indicate the relation of the two terms. Our second view thus harvests the sentences from the given corpus D to extract features for the query term q and the mini-path P. Given the query term q and any anchor term $p_l \in P$, we fetch all the sentences where q and p_l have co-occurred from corpus D. Similar to [37], we process these sentences to extract the dependency paths between q and p_l in these sentences, denoted as \mathcal{D}_{q,p_l} . For each dependency path $d_{q,p_l} \in \mathcal{D}_{q,p_l}$, it is a sequence of context words that lead q to p_l in the dependency tree:

$$d_{q,p_l} = \{v_{e_1}, v_{e_2}, \cdots, v_{e_k}\},\tag{2}$$

where k is the length of the dependency path. Each edge v_e in the dependency path contains 1) the connecting term v_l , 2) the part-of-speech tag of the connecting term v_{pos} , 3) the dependency label v_{dep} , and 4) the edge direction between two subsequent terms v_{dir} . Formally, each edge v_e is represented as: $v_e = [v_l, v_{pos}, v_{dep}, v_{dir}]$.

Now in order to encode each extracted dependency path d_{q,p_l} , we feed the multi-variate sequence d_{q,p_l} into an LSTM encoder. The representation of the LSTM's last hidden layer, denoted as LSTM (d_{q,p_l}) , is then used as the representation the path d_{q,p_l} . As the set $\mathcal{D}(q,p_l)$ contains multiple dependency paths between q and p_l , we aggregate them with the attention mechanism to compute the weighted average of these path representations:

$$\hat{\alpha}_{d} = \mathbf{u}^{T} \tanh \left(\mathbf{W} \cdot \text{LSTM}(d_{q,p_{l}}) \right),$$

$$\alpha_{d} = \frac{\exp \left(\hat{\alpha}_{d} \right)}{\sum_{d' \in \mathcal{D}_{q,p_{l}}} \exp \left(\hat{\alpha}_{d'} \right)},$$

$$\mathbf{d}(q, p_{l}) = \sum_{d \in \mathcal{D}(q, p_{l})} \alpha_{d} \cdot \text{LSTM}(d_{q,p_{l}}),$$
(3)

where α_d denotes attention weight for the dependency path d_{q,p_I} ; **W**, **u** are trainable weights for the attention network.

The final contextual features between q and P is thus given by

$$\mathbf{h}_c(q, P) = [\mathbf{d}(q, p_1) \oplus \cdots \oplus \mathbf{d}(q, p_L)]. \tag{4}$$

- (3) Lexical-Syntactic Features. Our third view extracts lexical-syntactic features between terms. Such features encode the correlations between terms based on their surface string names and syntactic information [25, 29, 44]. Given a term pair (x, y), we extract the following lexical-syntactic features between them:
- **Ends with**: Identifies whether *y* ends with *x* or not.
- **Contains**: Identifies whether *y* contains *x* or not.
- **Suffix match**: Identifies whether the *k*-length suffixes of *x* and *y* match or not.
- LCS: The length of longest common substring of term x and y.
- **Length Difference**: The normalized length difference between x and y. Let the length of term x and y be L(x) and L(y), then the normalized length difference is calculated as $\frac{|L(x)-L(y)|}{\max(L(x),L(y))}$.
- Normalized Frequency Difference: The normalized frequency of (x, y) in corpus D with min-max normalization. Specifically, follow [13], we consider **two types of** normalized frequency based on the noisy hypernym pairs obtained in [29]: (1) the normalized frequency difference. Given a term pair (x, y), their normalized frequency is defined as $nf(x, y) = \frac{freq(x, y)}{\max_{x \in V} freq(x, z)}$ where freq(x, y) defines the occurrence frequency between term (x, y) in the hypernym pairs given by [29] and $V = V_0 \cup C$ which is all terms in the existing taxonomy and test set. Then the first normalize frequence difference is defined as f(x, y) = nf(x, y) nf(y, x). (2) the generality difference. For term x, the normalized generality score ng(x) = log(1+h), where h is defined as the logarithm of the number of its distinct hyponyms. Then the generality difference of term pair g(x, y) is defined as the difference in generality between (x, y) as g(x, y) = ng(x) ng(y).

Given the query term q and the mini-path $P = [p_1, p_2, \cdots, p_L]$, we compute the lexico-syntactic features for each pair (q, p_l) $(1 \le l \le L)$, denoted as $s(q, p_l)$ and concatenate the features derived from all the term pairs as the lexical-syntactic features for (q, P):

$$\mathbf{h}_{s}(q, P) = [\mathbf{s}(q, p_{1}) \oplus \cdots \oplus \mathbf{s}(q, p_{L})]. \tag{5}$$

3.2.2 The Multi-View Co-Training Objective. As the three views provide complementary information to each other, it is important to aggregate the three views for the query-anchor matching. To this

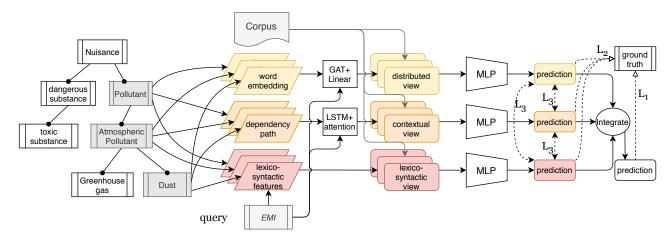


Figure 3: Illustration of the proposed co-training model architecture. The grey terms in the existing taxonomy on the left is an anchor path to attach the new term to. L_1 , L_2 and L_3 corresponds to the log-likelihood loss and Euclidean loss calculated in Equation (8), (9) and (10) respectively.

end, one may simply stack three different sets of features and train one unified classifier [25]. However, such feature-level integration can lead to suboptimal results due to two reasons: (1) one view can provide dominant signals over the other two, making it hard to fully unleash the discriminative power of each view; (2) the three views can have different dimensionality and distributions, making learning a unified classifier from concatenated features difficult.

To more effectively harvest the information from the three dif-

ferent views, we propose a multi-view co-training procedure. This

co-training procedure (see Figure 3) uses the three views to learn three different classifiers, and then derives an aggregated classifier from the three classifiers and also encourages their predictions to be consistent. The entire model can be trained in an end-to-end manner. Below, we first describe the base classifiers designed for the three different views, and then present the co-training objective. **Base Classifiers from Multiple Views.** Based on three sets of feature \mathbf{h}_d , \mathbf{h}_c , \mathbf{h}_s derived from different views, we design three neural classifiers for the query-anchor matching task, *i.e.*, the multiclass classification problem formulated in Section 3.1. For each of the three views, we use a multi-layer perceptron (MLP) with one hidden layer for this prediction task, denoted as f_d , f_s , and f_r . Then

the predictions from the three views are given by:

$$\mathbf{y}^{d} = f_{d}(\mathbf{h}_{d}) = \mathbf{W}_{2}^{d}(\sigma(\mathbf{W}_{1}^{d}\mathbf{h}_{d} + \mathbf{b}_{1}^{d}) + \mathbf{b}_{2}^{d}),$$

$$\mathbf{y}^{c} = f_{c}(\mathbf{h}_{c}) = \mathbf{W}_{2}^{c}(\sigma(\mathbf{W}_{1}^{c}\mathbf{h}_{c} + \mathbf{b}_{1}^{c}) + \mathbf{b}_{2}^{c}),$$

$$\mathbf{y}^{s} = f_{c}(\mathbf{h}_{s}) = \mathbf{W}_{2}^{s}(\sigma(\mathbf{W}_{1}^{s}\mathbf{h}_{s} + \mathbf{b}_{1}^{s}) + \mathbf{b}_{2}^{s}),$$
(6)

where $\{\mathbf{W}_1^k, \mathbf{W}_2^k, \mathbf{b}_1^k, \mathbf{b}_2^k\}$ $k \in \{d, s, c\}$ are trainable parameters for the three MLP classifiers, and $\sigma(\cdot)$ is the activation function for which we use ReLU in our experiments.

The Co-Training Objective. Figure 3 shows the co-training model that integrates the three base classifiers. From the three base classifiers f_d , f_s , and f_r , we design an aggregated classifier for the final

output. This aggregated classifier, which we denote as f_{agg} , integrates the three base classifiers by averaging over their predictions²:

$$\mathbf{y}^{\text{agg}} = f_{\text{agg}}\left(\mathbf{y}^d, \mathbf{y}^c, \mathbf{y}^s\right) = \operatorname{softmax}\left(\frac{1}{3}\left(\mathbf{y}^d + \mathbf{y}^s + \mathbf{y}^r\right)\right).$$
 (7)

To jointly optimize the base classifiers as well as the aggregated classifier, we develop a co-training procedure that not only learns the classifiers to fit the self-supervised signals but also promotes consistency among these classifiers. The co-training objective involves three types of supervision, as detailed below.

The first loss ℓ_1 is defines for the aggregated classifier f^{agg} , which produces the final output. Let $\{(\mathbf{x}_i, \mathbf{y}_i)_{i=1}^N \text{ be the training dataset, where } \mathbf{x}_i \text{ is a query-anchor pair and } \mathbf{y}_i \text{ is the label indicating the correct position of the query term in the anchor mini-path. Then <math>\ell_1$ is defined as the negative log-likelihood loss:

$$\ell_1 = -\sum_{i=1}^{N} \sum_{j=1}^{C} \mathbf{y}_{ij} \log \mathbf{y}_{ij}^{\text{agg}},$$
 (8)

where C = L + 1 is the number of labels for query-anchor matching. The second loss ℓ_2 is defined for three base classifiers corresponding to the three views:

$$\ell_2 = -\sum_{u \in \{d,c,s\}} \sum_{i=1}^{N} \sum_{j=1}^{C} \mathbf{y}_{ij} \log \mathbf{y}_{ij}^u.$$
 (9)

The third loss ℓ_3 is a *consistency loss* that encourages the prediction results from different views to agree with each other. We use L2-distance to measure the difference between the classifiers and define ℓ_3 as:

$$\ell_3 = \sum_{u,v \in \{d,s,r\}} \sum_{i=1}^{N} \|\mathbf{y}_i^u - \mathbf{y}_i^v\|^2.$$
 (10)

The overall objective of our model is then:

$$\ell = \ell_1 + \lambda \ell_2 + \mu \ell_3,\tag{11}$$

where $\lambda > 0$, $\mu > 0$ are two pre-defined balancing hyper-parameters.

 $^{^2\}mathrm{We}$ have also tried to use attention mechanism to aggregate the score but didn't see an obvious performance gain.

3.3 Model Learning and Inference

During training, we can minimize the total loss ℓ with the model parameter Θ using stochastic gradient-style optimization techniques, such as Adam [18]. During inference, given a new query term $q \in C$, we traverse all the mini-paths $P \in \mathcal{P}$ and calculate the scores for all anchor terms $p \in P$ based on the aggregated final prediction score $y_{q,p}^P$ in Eq. (7). Specifically, for any anchor term \hat{p} , we calculate the overall score for being the parent of query q as

$$y_{\hat{p}} = \frac{1}{|\hat{\mathcal{P}}|} \sum_{P \in \hat{\mathcal{P}}} y_{q,\hat{p}}^{P}, \tag{12}$$

where \hat{P} is the set of mini-paths which contain term \hat{p} . Then, we rank all anchor terms and select the term p* with the highest score as the predicted parent of the query q:

$$p^* = \arg\max_{p \in \mathcal{V}_0} y_p. \tag{13}$$

3.4 Complexity Analysis

At the training stage, our model uses $|\mathcal{P}|$ training instances every epoch and thus scales linearly to the number of mini-paths in the existing taxonomy. From above we have listed the number of mini-paths in our training, and the number of such mini-paths is linear to $O(|\mathcal{V}_0|)$ (i.e. the number of terms in the existing taxonomy). At the inference stage, for each query term, we calculate $L|\mathcal{P}|$ matching scores, where L is the length of the mini-path. To accelerate the computation, we use GPU for matrix multiplication and pre-calculate distributional and lexico-syntactic features and store the dependency paths for faster evaluation.

4 EXPERIMENTS

In this section, we evaluate the empirical performance of our proposed STEAM method. Our experiments are designed to answer the following three research questions:

- RQ1: How well does STEAM perform for the taxonomy expansion task compared with state-of-the-art methods?
- **RQ2**: How effective are the two key components in STEAM: mini-path-based prediction and multi-view co-training?
- RQ3: What are the effects of different parameters on the performance of STEAM?

4.1 Experiment Setup

4.1.1 Datasets. We evaluate the performance of our taxonomy construction method using three public benchmarks. These datasets come from the shared task of taxonomy construction in SemEval 2016 [6]. We use all the three English datasets in SemEval 2016, which correspond to three human-curated concept taxonomies from different domains: environment (EN), science (SCI), and food (Food). The statistics of these three benchmarks are presented in table 1. For each taxonomy, we start from the root term and randomly grow in a top-down manner until 80% terms are covered. We use the randomly-growed taxonomies as seed taxonomies for self-supervised learning, and the rest 20% terms as our test data. Our STEAM method and several baselines also require external text corpora to model the semantic relations between concept terms.

4.1.2 Baselines. We compare with the following baselines:

Table 1: The statistics of the three datasets for evaluation.

Dataset	Environment	Science	Food
# of Terms	261	429	1486
# of Edges	261	452	1576
# of Layers	6	8	8

- TAXI³ [29] is a taxonomy induction method that reached the first
 place in the SemEval 2016 task. It first extracts hypernym pairs
 based on substrings and lexico-syntactic patterns with domainspecific corpora and then organizes these terms into a taxonomy.
- HypeNet⁴ [37] is a strong hypernym extraction method, which uses an LSTM-CNN model to jointly model the distributional and relational information between term pairs.
- BERT+MLP is a distributional method for hypernym detection based on pre-trained BERT embeddings. For each term pair, it first obtains term embeddings from a pre-trained BERT model, and then feeds them into a Multi-layer Perceptron to predict whether they have the hypernymy relationship⁵.
- TaxoExpan⁶ [34] is state-of-the-art self-supervised method for taxonomy expansion. It adopts graph neural networks to encode the positional information and uses a linear layer to identify whether the candidate term is the parent of the query term. For fair comparison, we also use BERT embeddings for TaxoExpan instead of the word embeddings as in the original paper.
- 4.1.3 Variants of STEAM. We also compare with several variants of STEAM to evaluate the effectiveness of its different modules: Concat directly concatenates the three features and feeds it into an MLP for prediction; Concat-D concatenates only the context and lexico-syntactic views; Concat-C concatenates the distributed and the lexico-syntactic features; Concat-L concatenates the distributed and the context features; STEAM-Co directly uses the aggregated classifier for prediction instead of the co-training objective (i.e., $\lambda = \mu = 0$); STEAM-D co-trains without the distributed view; STEAM-C co-trains without the contextual view and STEAM-L co-trains without the lexico-syntactic view.
- 4.1.4 Implementation Details. All the baseline methods, except for BERT-MLP, are obtained from the code published by the original authors. The others (BERT-MLP, our model, and its variants) are all implemented in PyTorch. When learning our model, we use the ADAM optimizer [18] with a learning rate of 1e-3. On all the three datasets, we train the model for 40 epochs as we observe the model has converged after 40 epochs. To prevent overfitting, we used a dropout rate of 0.4 and a weight decay of 5e-4. For encoding context features, we follow [37] and set the dimensions for the POS-tag vector, dependency label vector, and edge direction vector, to 4, 5, and 1, respectively; and set the dimension for hidden units in the LSTM encoder to 200. For the three base MLP classifiers, we set the dimensions of the hidden layers to 50. For sampling negative minipaths, we set the size of negative samples r=4. In the co-training module, there are two key hyper parameters: λ and μ for controlling

³https://github.com/uhh-lt/taxi

⁴https://github.com/vered1986/HypeNET

⁵For combining term embeddings, we experimented with Concat, Difference, and SUM as different fusing functions and report the best performance.

 $^{^6} https://github.com/mickeystroller/TaxoExpan\\$

Table 2: Comparision of STEAM against the baseline methods on the three datasets (in %). To reduce the randomness, we ran all methods for three times and report the average performance. TAXI outputs an entire taxonomy instead of ranking lists, so we are unable to obtain the MRRs for it.

Dataset	En	viron	ment	Science			Food		
Metric	Acc	MRR	Wu&P	Acc	MRR	Wu&P	Acc	MRR	Wu&P
BERT+MLP	11.1	21.5	47.9	11.5	15.7	43.6	10.5	14.9	47.0
TAXI	16.7	-	44.7	13.0	-	32.9	18.2	-	39.2
HypeNet	16.7	23.7	55.8	15.4	22.6	50.7	20.5	27.3	63.2
TaxoExpan	11.1	32.3	54.8	27.8	44.8	57.6	27.6	40.5	54.2
STEAM	36.1	46.9	69.6	36.5	48.3	68.2	34.2	43.4	67.0

the strength for training base classifiers and the consistency among classifiers. By default, we set $\lambda=0.1, \mu=0.1$. We will study how these parameters affect the performance of our model later.

4.1.5 Evaluation Protocol. At test time, pinpointing the correct parent for a query term is a ranking problem. Specifically, given n test samples, let us use $\{\hat{y}_1, \hat{y}_2, \cdots, \hat{y}_n\}$ to denote their ground truth positions, $\{y_1, y_2, \cdots, y_n\}$ to denote model predictions. Follow existing works [24, 34, 39], we use multiple metrics as follows:

(1) **Accuracy (Acc)** measures the exact match accuracy for terms in the test set. It only counts the cases when the prediction equals to the ground truth, calculated as

$$Acc = \frac{1}{n} \sum_{i=1}^{n} \mathbb{I}(y_i = \hat{y}_i).$$

(2) **Mean reciprocal rank (MRR)** is the average of reciprocal ranks of a query concept's true parent among all candidate terms. Specifically, it is calculated as

$$MRR = \frac{1}{n} \sum_{i=1}^{n} \frac{1}{rank(y_i)}.$$

(3) Wu & Palmer similarity (Wu&P) calculates the semantic similarity between the predicted parent term y and the ground truth parent term \hat{y} as

$$\omega(\hat{y}, y) = \frac{2 \times \operatorname{depth}(\operatorname{LCA}(\hat{y}, y))}{\operatorname{depth}(\hat{y}) + \operatorname{depth}(y)}$$

where "depth(·)" is the depth of a term in the taxonomy and "LCA(·,·)" is the least common ancestor of the input terms in the taxonomy. Then, the overall Wu&P score is the mean Wu & Palmer similarity for all terms in the test set written as Wu&P = $\frac{1}{n}\sum_{i=1}^{n}\omega(y_i,\hat{y}_i)$.

4.2 Experimental Results

4.2.1 Comparison with baselines. Table 3 reports the performance of STEAM and the baseline methods on the three benchmarks. From the results, we have the following observations:

• STEAM consistently outperforms all the baselines by large margins on the three datasets. In particular, STEAM improves the performance of the state-of-the-art taxonomy expansion method (Taxo-Expan) by 25.0%, 8.7% and 6.6% for Acc, MRR and Wu&P on average. Such huge performance gains clearly show the merits of STEAM in using mini-paths for capturing the holistic structure of the seed

Table 3: Overall results of all variants of our methods on three datasets (in %).

Dataset	Environment				Science			Food			
Metric	Acc	MRR	Wu&P	Acc	MRR	Wu&P	Acc	MRR	Wu&P		
Concat	25.0	40.3	64.2	20.4	25.8	51.1	15.5	23.8	49.6		
Concat-D	30.6	38.6	63.7	11.1	20.1	48.1	23.1	28.9	55.4		
Concat-C	27.7	37.4	57.8	13.5	25.7	53.3	25.3	31.2	58.3		
Concat-L	11.1	31.4	57.7	13.5	23.7	39.1	8.30	13.4	40.1		
STEAM-Co	25.0	41.0	66.3	32.7	45.3	64.4	31.1	40.7	65.1		
STEAM-D	13.8	32.0	54.3	23.1	32.9	60.0	20.1	31.5	60.8		
STEAM-C	11.1	26.8	49.2	32.7	44.5	67.2	19.3	29.7	59.3		
STEAM-L	11.1	27.5	51.6	23.1	36.5	62.1	12.7	22.6	56.7		
STEAM	36.1	46.9	69.6	36.5	48.3	68.2	34.2	43.4	67.0		

taxonomy and harvesting multi-view information based on the co-training procedure.

- Among the baselines, TaxoExpan achieves the strongest overall performance. The key advantage of TaxoExpan compared with other baselines is that it propagates the embeddings among neighbors in the taxonomy via graph neural networks. From the results, we can see that embedding propagation is effective in improving the MRR, making it achieve close MRRs with STEAM. However, TaxoExpan is largely outperformed by STEAM in accuracy. This phenomenon shows that while distributed features are useful for finding relevant concepts, contextual and lexico-syntactic features are important for pinpointing the exact hypernymy relationships.
- Pre-trained BERT embeddings have remarkable expressive power. However, BERT embeddings alone can yield limited performance in the taxonomy expansion task since BERT does not well capture the contextual relations and between terms. STEAM is based on BERT embedding, but it integrates contextual and pattern information, which are highly useful for improving the performance.
- TAXI underperforms other methods on all three datasets. The major drawback of TAXI and other taxonomy construction methods is that they fail to use self-supervision signals in the existing taxonomy. This hinders them from learning the hierarchical and semantic information during the training process. Moreover, they simply use lexico-syntactic patterns and neglect other distributional features, which is important for taxonomy expansion.
- HypeNet outperforms BERT and TAXI since it combines the contextual and distributed features. However, it neglects the structural information during training and does not consider lexico-syntactic features, rendering it less effective than STEAM.
- 4.2.2 Ablations Studies. We perform ablation studies to study the effectiveness of the different components in STEAM: 1) mini-path-based self-supervised learning; 2) the multi-view information; and 3) the co-training procedure.

The Effect of Mini-Paths. To study the effectiveness of mini-path-based self-supervised expansion, we vary the length L of mini-paths. Note that, when L=1, the model is reduced to performing hypernymy prediction. Figure 4 shows the performance of STEAM on the three datasets when L varies. Generally, when L is small, the performance of STEAM stably increases with L. Such results show that mini-paths can effectively capture the structural information

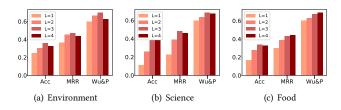


Figure 4: The result for different length of mini-paths ${\cal L}$ over three datasets.

in the seed taxonomy—apart from the 'parent' of the query term, the grandparents and siblings contain additional information to improve expansion performance. The mini-paths connect terms from different layers of the taxonomy and carry such information to make the model pinpoint the correct position. However, when L increases from 3 to 4, we observe slight performance drops. This is because the size of the training data shrinks for smaller taxonomies when L becomes larger. Take the environment dataset as an example: It contains 185 training samples when L=3 while 83 when L=4. As a result, the final performance decreases by 3.2% for accuracy.

The Effect of Multi-view Information. We study the contributions of different views by comparing STEAM with its variants (STEAM-D, STEAM-C, STEAM-L). Table 3 shows the results on the three datasets. As shown, it is clear that all three types of features contribute significantly to the overall performance. When eliminating one of the three views, the average performance drops by 6.07%, 8.10% and 4.67% for the three metrics.

The Effect of Co-training. Now we proceed to study the effectiveness of the co-training procedure. While integrating multiple views is important, *how* to integrate multi-view information is equally important. From the results in Table 3, one can see STEAM outperforms Concat by 15.3%, 16.2% and 13.3% for three metrics on average. This verifies the effectiveness of co-training compared with concatenation: the simple concatenation strategy cannot fully harvest the information from each view and could make the learning problem more difficult. Interestingly, the performance for Concat is even worse than Concat-D and Concat-C in accuracy on Food and Environment, which implies that simple concatenation can even hurt the performance with more views.

The co-training objective in STEAM involves two loss terms that encourage better learning of the base classifiers and the consistency among them. From Table 3, the performance gap between STEAM and STEAM-Co shows the effectiveness of these two terms. STEAM-Co only uses the aggregated classifier for prediction and underperforms STEAM by large margins. The reason is that two loss terms explicitly require *every* base classifier is sufficiently trained and mutually enhances each other; without these two terms, certain views may not be fully leveraged, which limit the effectiveness in leveraging multi-view information for training.

4.2.3 Parameter Studies. In this subsection, we study the effects of different parameters on the performance of STEAM. We have already studied the effect of the path length in the ablation study, now we study the effects of two key parameters in the co-training

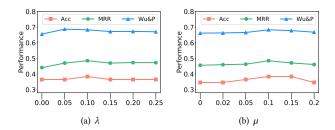


Figure 5: The performance of our model when varying different parameters.

Gold Parent: Physics			Gold Pare	nt: Fruit	Juice	Gold Parent: Mamma			
View	Score	Rank	View	Score	Rank	Ī	View	Score	Rank
Distributed	0.812	11	Distributed	0.720	25	į	Distributed	0.416	116
Contextual	0.947	12	Contextual	0.921	14	i	Contextual	0.987	1
Lexico-syntactic	0.640	15	Lexico-syntactic	0.656	15	i	Lexico-syntactic	0.615	31
STEAM Output	0.799	_1_	STEAM Output	0.765	1	i	STEAM Output	0.672	1
(a) term Electrostatics (SCI)			(b) term N	ectar (F	ood)	_	(c) term Whale Marine (EN		
Gold Parent: Medicine							Gold Parent: Sea Bed		
Gold Pare	nt: Med	icine	Gold Pare	nt: Red	Vine	I L	Gold Pare	nt: Sea	Bed
Gold Pare	nt: Med Score	icine Rank	Gold Pare View	nt: Red \	Wine Rank		Gold Parei	nt: Sea	Bed Rank
View	Score	Rank	View	Score	Rank		View	Score	Rank
View Distributed	Score 0.741	Rank 51	View	Score 0.468	Rank 169		View Distributed	Score 0.387	Rank 35
View Distributed Contextual	Score 0.741 0.959	Rank 51 2	View Distributed Contextual	Score 0.468 0.493	Rank 169 24		View Distributed Contextual	Score 0.387 0.568	Rank 35 22

Figure 6: Prediction result for several test terms from different datasets.

procedure: 1) the weight of the prediction loss of the three base classifiers λ , and 2) the weight of the consistency loss μ . When evaluating one parameter, we fix other parameters to their default values and report the results. Due to the space limit, we only report the results on parameters on Science dataset as the tends and findings are similar for the three datasets.

Effect of λ . Figure 5(a) shows the effect of λ on the Science dataset. We can observe that as λ increases, the performance improves for all three metrics. This is because larger λ will add more weight to learning base classifiers and enforce each base classifier to achieve good prediction performance. As the base classifiers become stronger, the derived aggregated classifier can also become stronger. However, when $\lambda \geq 0.15$, the performance decreases with λ . We suspect the reason is each single view can be one-sided and noisy to yield biased predictions, when λ is too large, the biased information from each single view can no longer be effectively eliminated during integration, which can hurt the overall performance.

Effect of μ . Figure 5(b) shows the effect of μ . Similarly, as μ increases, the performance of STEAM first increases and then decreases when μ is too large. The reason for this phenomenon is that: 1) when μ is too small, the three models cannot regularize each other well, which hinders them from sharing the result with others; 2) when the μ is too large, then the output will be close to optimizing Equation 11. When one model does not perform well, it will negatively affect the other two models, which will deteriorate the performance of the overall model.

4.3 Case Studies and Error Analysis

Figure 6 shows multiple cases to illustrate the efficacy of STEAM. It reports the final prediction score of STEAM for the ground-truth parent, as well as the prediction scores from the three base classifiers. Based on the scores, we calculate the rank of the ground truth parent. From Figure 6(a), (b), we can find that there are cases when the predictions from all the three views are inadequate, but the final prediction can integrate the weak signals to rank the ground-truth to the top. Such cases verify the power of multi-view co-training in STEAM, which can utilize the complementary signals from all views and improve the final performance. Besides, Figure 6(c), (d) shows two cases when the predictions of one specific view are poor (e.g. Distributed view for term Whale Marine), yet STEAM can rectify the mistakes by leveraging the information from the other two views. Figure 6(e) and (f) show two random examples on which our model fails to provide the correct predictions. Through in-depth analysis, we found that one common case when our model cannot perform well is that all views cannot make accurate predictions. In such cases, the information from the three views is insufficient to capture the hypernymy relationships between the test term and its parent.

5 RELATED WORK

Taxonomy Construction. There have been many methods on automatic taxonomy construction. One line of works constructs taxonomies using cluster-based methods. They group terms into a hierarchy based on hierarchical clustering [1, 33, 43] or topic models [10, 23]. These methods can work in an unsupervised way. However, they cannot be applied to our taxonomy expansion problem, because they construct topic-level taxonomies where each node is a collection of topic-indicative terms instead of single terms. More relevant to our work are the methods developed for constructing term-level taxonomies. Focused on taxonomy induction, these methods organize hypernymy pairs into taxonomies. Graph optimization techniques [3, 8, 13, 19] have been proposed to organize the hypernymy graph into a hierarchical structure, and Mao et al. [25] utilize reinforcement learning to organize term pairs by optimizing a holistic tree metric over the training taxonomies. Very recently, Shang et al. [32] design a transfer framework to use the knowledge from existing domains for generating taxonomy for a new domain. However, all these methods attempt to construct taxonomies from *scratch* and cannot preserve the structure of the seed taxonomy.

Hypernymy Detection. Hypernym detection aims at identifying hypernym-hyponym pairs, which is essential to taxonomy construction. Existing methods for hypernymy detection mainly fall into two categories: pattern-based methods and distributed methods. Pattern-based methods extract hypernymy pairs via pre-defined lexico-syntactic patterns [15, 29, 31]. One prominent work in this branch is the Hearst patterns [15], which extract hypernymy pairs based on a set of hand-crafted is-a patterns (e.g., "X is a Y"). Pattern-based methods achieve good precision, but they suffer from low recall [42] and are prone to idiomatic expressions and parsing errors [20]. Distributed methods detect hypernymy pairs based on the distributed representations (e.g. word embeddings [9, 26, 30]) of terms. For a term pair $\langle x, y \rangle$, their embeddings are used for learning a binary classifier to predict whether it has the hypernymy relation

[4, 7, 12, 36]. As embeddings are directly learned from the corpora, distributed methods eliminate the needs of designing hand-crafted patterns and have shown strong performance. However, their performance relies on a sufficient amount of labeled term pairs, which can be expensive to obtain.

Taxonomy Expansion. Taxonomy expansion is less studied than taxonomy construction. Most existing works on taxonomy expansion aims to find new is-a relations and insert new terms to their hypernyms. For example, Aly et al. [2] refine existing taxonomy by adopting hyperbolic embeddings [28] to better capture hierarchical lexical-semantic relationships, [35, 39] design various semantic patterns to determine the position to attach new concepts for expanding taxonomies, and Fauceglia et al. [11] use a hybrid method to take advantage of linguistic patterns, semantic web and neural networks for taxonomy expansion. However, the above methods simply adopt fail to capture the global structure of the existing taxonomy thus cannot fully harvest self-supervision signals. To better exploit self-supervision signals, Manzoor et al. [24] study expanding taxonomies by jointly learning latent representations for edge semantics and taxonomy concepts. Recently, Shen et al. [34] propose position-enhanced graph neural networks to encode the relative position of terms and improve the overall quality of taxonomy. However, the above two approaches only consider distributional features such as word embeddings but neglect other types of relationships among terms. Compared with these methods, STEAM is novel in two aspects. First, it inserts new terms with mini-pathbased classification instead of simple hypernym attachment, which models different layers to better preserve the holistic structure. Second, it considers multiple sources of features for expansion and integrates them with a multi-view co-training procedure.

6 CONCLUSION

We proposed STEAM, a self-supervised learning framework with novel mini-path-based prediction and a multi-view co-training objective. The self-supervised learning nature enables our model to optimize the utilization of the knowledge in the existing taxonomy without labeling efforts. Compared with the traditional node-to-node *query-anchor* pairs, the adoption of mini-paths captures more structural information thus facilitates the inference of a query's attachment position. The multi-view co-training objective effectively integrates information from multiple input sources, including PGAT-propagated word embeddings, LSTM-embedded dependency paths and lexico-syntactic patterns. Comprehensive experiments on three benchmarks show that STEAM consistently outperforms all baseline models by large margins, which demonstrates its superiority for taxonomy expansion.

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APPENDIX-EXTERNAL SOURCES OF CORPUS

STEAM (our method) and several baselines require external text corpora to model the semantic relations between concept terms. For all the three benchmarks, we collect the following public corpora:

1) the Wikipedia dump⁷, 2) the UMBC web-based corpus⁸; 3) the One Billion Word Language Modeling Benchmark⁹.

We directly match the terms with the corpus with tools available online (*i.e.* WikiExtractor¹⁰) and only preserve the sentences that term pairs co-occur. In this way, for each dataset, we obtain a tailored corpus which preserves the co-occurrence between terms. The information for these corpora are summarized as:

- **Environment**: The corpus size is 824MB with 1.51M sentences.
- Science: The corpus size is 1.36GB with 2.07M sentences.
- Food: The corpus size is 2.00GB with 3.42M sentences.

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- 7 We use the 20190801 version of wikidump during our experiments.
- $^8 https://ebiquity.umbc.edu/resource/html/id/351$
- 9https://www.statmt.org/lm-benchmark/
- ¹⁰https://github.com/attardi/wikiextractor

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