A supervised approach to taxonomy extraction using word embeddings

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Abstract

Large collections of texts are commonly generated by large organizations and making sense of these collections of texts is a significant challenge. One method for handling this is to organize the concepts into a hierarchical structure such that similar concepts can be discovered and easily browsed. This approach was the subject of a recent evaluation campaign, TExEval, however the results of this task showed that none of the systems consistently outperformed a relatively simple baseline.In order to solve this issue, we propose a new method that uses supervised learning to combine multiple features with a support vector machine classifier including the baseline features. We show that this outperforms the baseline and thus provides a stronger method for identifying taxonomic relations than previous methods.

Keywords: taxonomy extraction, word embeddings, supervised learning, terminology

1. Introduction

When confronted with a large collection of texts a key challenge is to organize these texts into a structure that makes it easy to discover the information that is behind these texts. For example, it is common that large organizations will collect many documents generated by their staff into a content management system, with only limited organization such as tags. One of the most widely used methodologies for organizing text collections is that of the taxonomic structure, where a set of topics (defined by a set of terms) are organized into a tree structure and individual documents are then clustered under these topics. This method, as exemplified in bibliothecal classification schemes such as the Dewey Decimal Classification scheme, has been widely employed by libraries to organize large collections of texts for over one hundred years. Such schemes are still widely employed by organizations such as the ACM[1] or the IEEE (IEEE, 2017) to organize contributions to major conferences and other research contributions.
The task of organizing topics into a hierarchy is called taxonomy extraction and consists of two key steps. Firstly, in the *term extraction* step the set of terms that are relevant can be extracted from a collection of texts and secondly, in the *taxonomy learning* step these terms are grouped into a hierarchical structure. The first step is well explored and recent strong results have been shown on this task (Astrakhantsev, 2016; Buitelaar et al., 2013) and as such we shall not focus on it in the course of this article. The second task is however much less well-explored and this is the focus of this article, and so we assume that the terms have already been identified by an approach such as those outlines above. The task of taxonomy extraction is closely related to tasks such as *hypernym detection* (Hearst, 1992) or *ontology learning* (Buitelaar et al., 2005), in which a structured representation of concepts should be learned. However, the task of taxonomy extraction does not have the formal nature that either of these tasks in that the terms only need to be loosely associated. For examples, taxonomies frequently place terms under broader concepts that do not match the strict requirements of ontological subsumption (Gangemi et al., 2002) that would be required from an ontology, e.g., grouping “Kalman Filter” is under “Filtering” in the IEEE taxonomy, where a type of filter is grouped under the concept of filtering. Moreover, often concepts are grouped in a way that does not conform to a strict hypernym or broader/narrower relationship, such as “Google” which is grouped under “Computer Networks” in the IEEE taxonomy. As such, this task is subtly yet importantly different to the other tasks.
Recently the TExEval task (Bordea et al., 2016) was created to provide an open forum for evaluating the performance of systems on this task. For this task, a simple method based on whether one term was a substring of another string was proposed as a baseline, while competitors in the shared task took many methods inspired from hypernym extraction and ontology learning. Surprisingly, the results of the task showed that none of the competitors consistently outperformed this very simple baseline. This underlines the highly distinct nature of this task, when compared to hypernym extraction and the need for novel approaches. In this context, we approach the problem as a supervised learning task, where individual features can be extracted from the label as well as word embeddings associated with these labels and these features can be weighted by means of a support vector machine (Cortes and Vapnik, 1995). We show that while none of theses features outperform the baseline of the TExEval baseline, the combination of these features with the baseline can provide a stronger result than the baseline.

2. Related Work

While taxonomy extraction is not simply the task of hypernym identification, this is one of the most important goals of such research and several methods going back to (Hearst, 1992) have been proposed for this task. A recent such system to use this is the TAXI system (Panchenko et

[1]http://www.acm.org/publications/class-2012

al., 2016), which combined simple string substring metrics with Hearst-like patterns learned from text, which are then constructed into a taxonomy using Tarjan's algorithm (Tarjan, 1972).
A different approach, by (Tan et al., 2016), used the *endocentricity* of a term, that is if a term contains another term, e.g., 'fish' in 'goldfish', whether this indicates a hypernym-like relationship. The QASSIT system (Cleuziou and Moreno, 2016) used the genetic algorithm in order to learn taxonomic relations, however performance across domains was poor.
BabelNet (Navigli and Ponzetto, 2012), a wide coverage dictionary, has been used both as a source of information about taxonomic relations (Maitra and Das, 2016) and also itself was constructed using automatic taxonomy learning (Navigli et al., 2011). However, the focus of this has been mostly on single words as would be found in a dictionary and less on the kind of multi-word terminology that can be used to describe specialist domains as in this paper.
Finally, there has been some work on the use of word embeddings to predict hypernym relations, such as in (Fu et al., 2014), where a linear project function from a word embedding to its hypernym was constructed. The possibility of combining this with syntactic patterns for hypernym discovery has also been investigated (Shwartz et al., 2016).

3. Methodology

Our methodology is based on the use of multiple features that can be extracted from the labels or an associated corpus. We then learn to combine these using a supervised learning approach. In this section we will present the methodology for the features we used.

3.1. Data

While, the TexEval task has recently given a baseline, by which performance on this task can be measured. There are some weaknesses with this baseline in particular that most of the sources are resources such as WordNet (Fellbaum, 1998), which are primarily databases of hypernyms. As such using these datasets does not distinguish the task well from that of hypernym detection. In fact, taxonomies are not intended to be strict hypernym graphs but may in fact contain other relations. However, we use this as the basis for our experiments as this dataset is established and has been used by other systems. In addition, to these datasets, we also make use of a large background corpus for our experiments. In this case, we use the English Wikipedia [2]. The Wikipedia dump file of English language which contains 2,976,828 number of articles with 1,940,620,295 unique terms. This is used particularly for the Jaccard similarity (see below) where we consider the articles that contain a given term. In addition, we use the Word2Vec vectors pre-trained on Google News [3] for calculating word similarity. As several of our methods use supervised learning, for these experiments we simply held-out one of the TExEval datasets as the test set and used the remaining datasets for training.

[2]http://en.wikipedia.org/

[3]https://code.google.com/archive/p/word2vec/

3.2. Term substring

Following the baseline of the TExEval task (Bordea et al., 2016), we use a baseline that counts a string if it is a substring of the other string. Following discussions with the TExEval organizers, we exactly implement this as in the task, that is we introduce a link in the taxonomy graph if either term is equal (ignoring case), or one term starts with another term and then a word boundary, or one term ends with another term (not considering word boundaries)[4].

3.3. Jaccard similarity

To extract relations, we can use Jaccard similarity between two terms to develop the taxonomy tree. To find the Jaccard similarity between two terms, we count the number of articles which contain both the terms and divide it by the number of articles which contain at least one of the two terms. Mathematically this can be defined as:

$$JS(A, B) = \frac{|W_{A \cap B}|}{|W_{A \cup B}|}$$

After calculating the scores for every possible pair of terms, we sort the terms on the basis of their Jaccard scores and then greedily select the pairs on the basis of their Jaccard similarity such that loops are not formed in the tree. We continue this process until all the terms are present in the final tree. The final tree obtained using this method will contain all the term nodes present in the dataset.

3.4. Word2Vec Min-Max

In this approach, we use word embeddings to extract similarity between two terms. Word2Vec (Mikolov et al., 2013) is a machine learning technique to obtain numerical representation of words in the form of word vectors. Using this method, we can obtain vector representation of each word present in the corpus. For each word in a given term, we obtain a vector of fixed size K (we choose $K = 100$). To obtain a vector representation of the entire term, we use the Min-Max combination technique of combining word vectors.
Min-Max technique: We form 2 vectors for the term. The first is known as the Min vector. It is constructed by taking the minimum value at each index position of its constituent words by comparing the values present in that index position of the vectors of its word constituents. The second vector is constructed in a similar manner by taking the maximum value at each index position.
The final vector of the term is obtained by concatenating the minimum vector with the maximum vector to obtain a vector of size $2K$ (200 in our case). The similarity between two terms is calculated by first normalizing the word vectors of both the terms and then taking the cosine similarity of the two vectors. The final tree is constructed in a similar manner as the tree constructed in Section 3.3.

3.5. Word2Vec averaged

In this method we again use word vectors to compute similarity between two terms. However, to construct the word vector of the term, we take the average of the word vectors

[4]This implementation exactly follows that of TExEval

Corpus	Number of terms
Environment (Eurovoc)	261
Food (WordNet)	1486
Food (EN)	1555
Science (Eurovoc)	125
Science (Wordnet)	370
Science (EN)	452

Table 1: The size of datasets used in these experiments

of its constituent words. We again find the similarity between two terms using cosine similarity of the two vectors And follow the greedy approach to construct the tree.

3.6. SVD classification

Let $\mathbf{V}$ be the matrix of vectors obtained using the methods of Section 3.4. and 3.5. We form the matrix by with each row representing the word vectors of the terms and let $\mathbf{B}$ be the matrix representing the relations between the terms. So, for any two terms a and b of the matrix $\mathbf{B}$,

$$R(a,b) = \begin{cases} 1 & \text{if } a \subset b \\ -1 & \text{if } a \supset b \\ 0 & \text{otherwise} \end{cases}$$

Thus is we have $\mathbf{v}_i$, $\mathbf{v}_j$ as the vectors corresponding to the words w_i,w_j then we choose to estimate our similarity using a linear function with a matrix, $\mathbf{A}$, as follows:

$$R'(w_i, w_j) = \mathbf{v}_i^{\mathrm{T}} \mathbf{A} \mathbf{v}_j^{\mathrm{T}}$$

We find the matrix $\mathbf{A}$ that minimizes the Euclidean error between our training data across all word pairs, e.g.,

$$\text{error} = \sqrt{\sum_{i=1,\ldots,|v|} \sum_{i=1,\ldots,|v|} (R(w_i,w_j) - R'(w_i,w_j))^2}$$

We can rewrite this in terms of matrices:

$$\text{error} = ||\mathbf{B} - \mathbf{V}^{\mathrm{T}}\mathbf{A}\mathbf{V}||_{\mathcal{F}}$$

We shall assume that $\mathbf{V}$ is a $m \times n$ network and that $m > n$, in other words that the number of words is greater than the length of the Word2Vec vectors. We can then assume that we can minimize the error by finding the point where

$$\frac{\partial \text{error}^2}{\partial \mathbf{A}} = 0$$

We derive this using identities proven in the Matrix Cookbook (Petersen et al., 2008), readers are recommended to refer to this text to better understand the derivation here:

$$\frac{\partial ||\mathbf{B} - \mathbf{V}^{\mathrm{T}}\mathbf{A}\mathbf{V}||^2_{\mathcal{F}}}{\partial \mathbf{A}}$$

$$= \frac{\partial}{\partial \mathbf{A}} \text{tr}(\mathbf{B} - \mathbf{V}^{\mathrm{T}}\mathbf{A}\mathbf{V})^{\mathrm{T}}(\mathbf{B} - \mathbf{V}^{\mathrm{T}}\mathbf{A}\mathbf{V})$$

$$= \frac{\partial}{\partial \mathbf{A}} \text{tr}[\mathbf{B}^{\mathrm{T}}\mathbf{B} - \mathbf{B}^{\mathrm{T}}\mathbf{V}^{\mathrm{T}}\mathbf{A}\mathbf{V} -$$

$$\mathbf{V}^{\mathrm{T}}\mathbf{A}^{\mathrm{T}}\mathbf{V}\mathbf{B} + \mathbf{V}^{\mathrm{T}}\mathbf{A}\mathbf{V}\mathbf{V}^{\mathrm{T}}\mathbf{A}\mathbf{V}]$$

$$= 2\mathbf{V}\mathbf{V}^{\mathrm{T}}\mathbf{A}\mathbf{V}\mathbf{V}^{\mathrm{T}} - 2\mathbf{V}\mathbf{B}\mathbf{V}^{\mathrm{T}}$$

Thus:

$$\mathbf{V}\mathbf{V}^{\mathrm{T}}\mathbf{A}\mathbf{V}\mathbf{V}^{\mathrm{T}} = \mathbf{V}\mathbf{B}\mathbf{V}^{\mathrm{T}}$$

We can easily find a matrix $\mathbf{V}^+$ that satisfies [5]

$$\mathbf{V}^+\mathbf{V} = \mathbf{I}$$

In particular this can be achieved by using the singular value decomposition of $\mathbf{V}$ in order to find

$$\mathbf{V} = \mathbf{U}\mathbf{\Sigma}\mathbf{W}^{\mathrm{T}}$$

Such that Σ is a diagonal matrix and the following hold

$$\mathbf{U}^{\mathrm{T}}\mathbf{U} = \mathbf{I}$$

$$\mathbf{W}\mathbf{W}^{\mathrm{T}} = \mathbf{W}^{\mathrm{T}}\mathbf{W} = \mathbf{I}$$

Then

$$\mathbf{V}^+ = \mathbf{W}\mathbf{\Sigma}^{-1}\mathbf{U}^{\mathrm{T}}$$

It is clear that a solution to find $\mathbf{A}$ is:

$$\mathbf{A} = (\mathbf{V}^+)^{\mathrm{T}}\mathbf{B}\mathbf{V}^+$$

To obtain the $\mathbf{A}$ matrix, we used all but one of the taxonomies as training data and evaluated on the rest of the taxonomies. As such, our evaluation is cross-domain, which potentially further impacts our baseline results. After obtaining the $\mathbf{A}$ vector using the above method, The vectors $\mathbf{V}$ for the remaining datasets were obtained and then the $\mathbf{B}$ matrix for the terms was generated.

3.7. Using SVM to identify relations

Finally, we treat this task as a multi class classification problems, with the numerical representations of the relations as follow:

$$R(A,B) = \begin{cases} +1 & \text{if } A \subset B \\ -1 & \text{if } A \supset B \\ 0 & \text{otherwise} \end{cases}$$

We deploy a SVM classifier to classify the relations. The training data for the SVM was constructed holding one dataset out as above and we used different features to obtain our improved results. The features are as follow:

Baseline feature : Since the baseline method has a better recall and F-measure as compared to other methods, we choose this to be one of the features.

Word overlap : We also consider the number of words that are present in both the terms. We then divide the number of words overlapping by the number of words present in the term containing more number of terms.

Longest common subsequence : For the two terms in consideration, we find the length of the longest common subsequence present and divide it by the length of the longest term.

[5]This is the Moore-Penrose pseudo-inverse of $\mathbf{V}$

Features		Environment (Eurovoc)	Food (EN)	Science (EuroVoc)	Food (Wordnet)	Science (EN)	Science (Wordnet)
Baseline: String matching	Precision	0.500	0.536	0.576	0.501	0.668	0.783
	Recall	0.199	0.177	0.153	0.244	0.269	0.213
	F-measure	0.285	0.266	0.242	0.328	0.383	0.335
	F&M	0.000	0.000	0.006	0.002	0.004	0.000
Jaccard Similarity	Precision	0.038	0.023	0.095	0.037	0.053	0.081
	Recall	0.019	0.011	0.048	0.022	0.026	0.050
	F-measure	0.026	0.015	0.064	0.027	0.035	0.062
	F&M	0.000	0.000	0.000	0.022	0.000	0.050
Word2Vec Min-Max	Precision	0.100	0.016	0.127	0.053	0.085	0.109
	Recall	0.050	0.007	0.065	0.025	0.039	0.052
	F-measure	0.066	0.010	0.086	0.034	0.053	0.071
	F&M	0.000	0.000	0.000	0.000	0.000	0.000
Word2Vec Averaged	Precision	0.099	0.016	0.127	0.053	0.090	0.109
	Recall	0.050	0.007	0.065	0.025	0.041	0.052
	F-measure	0.066	0.010	0.086	0.034	0.056	0.071
	F&M	0.000	0.000	0.000	0.000	0.000	0.000
SVD Min-Max Classification	Precision	0.008	0.328	0.532	0.000	0.571	0.000
	Recall	0.007	0.112	0.202	0.000	0.069	0.000
	F-Measure	0.008	0.175	0.292	0.000	0.123	0.000
	F&M	0.001	0.104	0.000	0.000	0.011	0.000
SVD Averaged Classification	Precision	0.000	0.031	0.021	0.002	0.018	0.008
	Recall	0.000	0.011	0.008	0.001	0.002	0.005
	F-Measure	0.000	0.017	0.012	0.001	0.004	0.006
	F&M	0.000	0.000	0.000	0.000	0.000	0.014
SVM	Precision	0.341	0.683	0.391	0.515	0.474	0.463
	Recall	0.735	0.301	0.605	0.498	0.735	0.735
	F-Measure	0.577	0.418	0.475	0.506	0.577	0.568
	F&M	0.083	0.019	0.072	0.018	0.286	0.072

Table 2: Comparison of Unsupervised and Unsupervised Taxonomy Construction

SVD scores : We use the SVD scores from Section 3.6. between terms as one of the features for the SVM classifier since the tree obtained using this method had a higher F&M measure.

Word2Vec scores : We also use the word2vec scores as one of the features since word2vec scores between terms capture semantic similarity quite well.

Jaccard similarity scores : We use this as another feature since the this captures the co-occurrence of terms which gives an indication of their relatedness.

We used radial basis function(RBF) kernel and obtained the Cost(C) and Gamma(G) using grid search and ten fold cross validation.

We applied an ablation analysis, where we consider the effect of removing a single feature from the classifier and this analysis is presented in Table 3, where we present the average precision, recall and F-Measure over all results. We found that the there was a statistically significant improvement using McNemar's test at 5% (McNemar, 1947), by using all features except for the baseline and a non-significant improvement using the Word2Vec scores.

3.8. Taxonomy Construction

Once we have developed a function for each pair of terms in the taxonomy, which estimates whether it is likely to be a taxonomic relation and the direction of this relation, we need to extract a complete taxonomy. For these experiments we assume that the extracted structure should be a tree (acyclic graph) that contains all the topics that are candidates for this learning task. Initially, following earlier proposed solutions to the task (Navigli et al., 2011) we attempted to find a maximal spanning tree using Kruskal's algorithm (Kruskal, 1956). However we found that these results were disappointing and that a stronger and simpler approach was to greedily construct a tree by taking the highest scoring edges and adding them to the current graph, unless this would lead to a cycle. This process continues until all topics are included in the taxonomy.

4. Evaluation

We use the dataset used in the Taxonomy Extraction Evaluation (Bordea et al., 2016) which was a part of the International Workshop on Semantic Evaluation organized by ACL SIGLEX. The datasets consists of a set of terms from different corpora and the statistics of the datasets are given in Table 1.

	Precision	Recall	F-Measure
All features	0.676	0.478	0.429
- Baseline feature	0.550	0.478	0.462
- Word Overlap	0.694	0.471	0.416
- LCS	0.722	0.464	0.405
- Jaccard	0.682	0.473	0.425
- Word2Vec	0.693	0.479	0.429

Table 3: Ablation study of performance of features for SVM classification

We evaluated the taxonomy extraction procedure in two stages: firstly, we evaluated the results for the individual features using the greedy taxonomy construction procedure as described above. The results for this are given in Table 2, where we present the edge precision, recall and F-Measure based on the number of edges that match those in the taxonomy we are trying to create. In addition, we present the Fowlkes and Mallows metric (Fowlkes and Mallows, 1983) following the TExEval task as it "measures level by level how well a target taxonomy clusters similar nodes compared to a gold standard taxonomy" (Bordea et al., 2016).

In Table 2 the baseline features, Jaccard similarity (Section 3.3.), and Word2Vec similarities (Section 3.4. and 3.5.) are obtained in an unsupervised manner. The supervised results for the SVD and the combination of features with an SVM are also given in this table, where we held out the evaluation dataset and trained on all other datasets.

5. Conclusion

Taxonomy learning is a task that has up until now not achieved satisfactory results. In particular, research on terminology extraction using has not produced a higher F-Measure than for a very simple baseline of whether a substring is included in the term. While the TExEval results did show that these methods can improve in terms of the Modified Fowlkes and Mallows methods, this metric is very sensitive to the topology of the hierarchy, such as the depth of the network and the average number of children of a node. We present a new method that uses word embeddings in order to calculate the taxonomic relationship between two concepts in a directed manner. We compare this to the baseline used in the recent TExEval task, and show that while this metric itself does not outperform the baseline, it can easily be combined by means of a SVM classifier to produce a model that does outperform the baseline consistently in terms of F-Measure, proving a state-of-the-art result above the results of the TExEval task. While the improvements in F-Measure are significant and show the effectiveness of our methodology, we do not see the same improvements in the Fowlkes and Mallows score suggesting that the overall structure of our networks is not as good. This is likely due to the way the network has been constructed with a greedy algorithm and future work will look into the way that the network is constructed in order to produce a better overall taxonomy.

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