

Constrained Sequence-to-Tree Generation for Hierarchical Text Classification

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ABSTRACT

Hierarchical Text Classification (HTC) is a challenging task where a document can be assigned to multiple hierarchically structured categories within a taxonomy. The majority of prior studies consider HTC as a flat multi-label classification problem, which inevitably leads to "label inconsistency" problem. In this paper, we formulate HTC as a sequence generation task and introduce a sequence-to-tree framework (Seq2Tree) for modeling the hierarchical label structure. Moreover, we design a constrained decoding strategy with dynamic vocabulary to secure the label consistency of the results. Compared with previous works, the proposed approach achieves significant and consistent improvements on three benchmark datasets.

CCS CONCEPTS

Computing methodologies → Natural language processing;
 Information extraction; Natural language generation.

KEYWORDS

text representation, text classification, sequence-to-sequence

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1 INTRODUCTION

Hierarchical text classification (HTC) is a particular multi-label text classification problem, which aims to assign each document to a set of relevant nodes of a taxonomic hierarchy as depicted in Figure 1(a). HTC has many applications, such as product categorization[4], fine-grained entity typing [22] and news classification [8].

Existing approaches can be compartmentalized into two groups: local approaches and global approaches. Local approaches tend to construct multiple local classifiers and usually ignore the holistic

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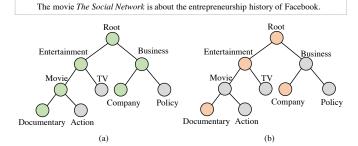


Figure 1: An example of taxonomic hierarchy for HTC. (a) The ground truth labels of the input document. (b) An illustration for "label inconsistency".

structural information of the taxonomic hierarchy. As the mainstream for HTC in recent years, global approaches utilize one single model to deal with all classes and introduce various strategies to capture the hierarchical information of the label space, such as dynamic routing [20], hyperbolic label embedding [5], Tree-LSTM and GCN [24]. However, since all these approaches consider HTC as a flat multi-label classification (MLC) task, the classification results will suffer from "label inconsistent" problem.

As depicted in Figure 1 (a), the ground truth labels of the input document should be the green nodes and these nodes belong to two paths, while traditional MLC approaches may lead to the prediction results as shown in Figure 1 (b), where isolated nodes such as *Documentary* and *Company* are produced and they will even be regarded as a valid positive prediction according to traditional evaluation metrics of HTC. In fact, due to the nature of HTC, the prediction of each node should not be in conflict with the results of its ancestors within a path. The isolated predictions and the "inconsistent paths" can not meet the needs in many actual application scenarios. In this paper, we aim to address this "label inconsistent" problem of HTC.

In order to make the classification results satisfy the "label consistency", we should focus on the label dependency within paths in the taxonomic hierarchy instead of each individual node. We associate this with the depth-first traverse algorithm (DFS) [17] for tree-structure, which is able to ensure that the nodes within the same path could be visited in the top-down order. Inspired by some previous works [12, 16, 18, 19] resorting to sequence generation to address various NLP tasks, we propose a sequence to tree (Seq2Tree) framework for HTC. Specifically, we firstly leverage DFS to transform hierarchical labels to a linearized label sequence, then we map the document text and corresponding label sequence in a traditional seq2seq manner. Furthermore, we design a constrained

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decoding strategy (CD), which can guide the generation process using hierarchical label dependency. In this way, the candidate labels generated at each time step will be limited to the children of the parent node generated at the last time step. In addition to ensuring the label consistency of the results, our approach could make full use of both semantic and structural information of the hierarchical labels during the training process.

In summary, our main contributions are as follows:

- We devise a sequence-to-tree generation framework with a constrained decoding strategy for HTC, which effectively guarantees the label consistency of the results.
- We propose two new evaluation metrics for HTC task: C-MicroF1 and C-MacroF1, which are more reasonable and more in line with actual application scenarios for HTC.
- We conduct experiments on three benchmark datasets and the results demonstrate that our method outperforms strong baselines on both traditional evaluation metrics and our new proposed metrics.

2 METHODOLOGY

We aim to leverage sequence generation architecture to address HTC task. To this end, we need to convert the taxonomic hierarchy into a sequence (label linearization). In this section, we start with the problem definition, and then introduce the method for label linearization (*LL*) and the model architecture with constrained decoding strategy (*CD*) in following subsections, respectively.

2.1 Problem Definition

We formulate HTC task as $F:(X,T) \to \mathcal{Y}$, where $X=\{X_1,...,X_N\}$ refers to the set of input documents, $T=\{V,E\}$ is a predefined taxonomic hierarchy, V is the set of label nodes and E denotes the parent-child relations between them. $\mathcal{Y}=\{Y_1,...,Y_N\}$ is the target label sets of X. Our task is to learn a model F that maps a new document $X_i=\{x_1,...,x_{|X_i|}\}$ to its target label set $Y_i=\{y_1,...,y_{k_i}\}$ within T, where k_i is the number of labels and $k_i \leq |V|$.

2.2 DFS-based Label Linearization

We achieve label linearization (LL) in a very straightforward way following DFS algorithm. As depicted in Figure 2, the target labels Y_i of the document make up a subtree of T. According to DFS algorithm, these labels could be linearized as \hat{Y}_i { $Root\text{-}Entertainment\text{-}Movie\text{-}Documentation\text{-}POP\text{-}POP\text{-}Business\text{-}Company\text{-}POP\text{-}POP\text{-}}POP\text{-}Business\text{-}Company\text{-}POP\text{-}POP\text{-}}POP\text{-}POP\text{-}Business\text{-}Company\text{-}POP\text{-}POP\text{-}}POP\text{-}POP\text{-}Business\text{-}Company\text{-}POP\text{-}POP\text{-}}POP\text{-}POP\text{-}Business\text{-}Company\text{-}}POP\text{-}POP\text{-}POP\text{-}}POP\text{-}Business\text{-}Company\text{-}} is visited, it is necessary to perform three consecutive POP operations to return to <math>Root$ node for starting a new path { $Root\text{-}Business\text{-}Company\text{-}}$ }. Since DFS algorithm is invertible, DFS-based LL is equivalent to inject the structure information of the hierarchy into the label sequence.

2.3 Seq2Tree with Constrained Decoding

As conventional Seq2Seq paradigm, Seq2Tree is also composed of two components: **Encoder** and **Decoder**. The architecture is depicted in Figure 3.

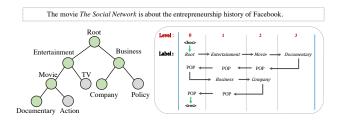


Figure 2: An example of DFS-based label linearization

Encoder: Given the input sequence X_i , the encoder part is to encode X_i into hidden vector representation $H_i = \{h_1, ..., h_{|X_i|}\}$ as follows:

$$H_i = Encoder(x_1, ..., x_{|X_i|})$$
(1)

Decoder: After the input sequence is encoded, the decoder part predicts the DFS label sequence step by step. Specifically, at time step i of generation, the decoder predicts the i-th token $\hat{y_i}$ in the linearized DFS label sequence and its corresponding decoder state h_i^d as:

$$\hat{y_i}, h_i^d = Decoder_c([H_i, h_{< i}^d], \hat{y_{i-1}}, T)), \quad \hat{y_i} \in DV_{\hat{y_i}}$$
 (2)

where $Decoder_c$ denotes decoder with CD, $h_{< i}^d$ denotes decoder state at previous time steps, $y_{\hat{i}-1}$ is the token generated at the last time step. The output sequence starts from the token " $\langle bos \rangle$ " and ends with the token " $\langle eos \rangle$ ". $DV_{\hat{y}_i}$ denotes the dynamic vocabulary for generating \hat{y}_i , its generation process is elabrated in Algorithm 1:

Algorithm 1: Dynamic Vocabulary Generation.

```
Input: Generated tokens \hat{y_1}, ..., \hat{y_{i-1}}, Taxonomic hierarchy T

Output: Dynamic vocabulary DV_{\hat{y_i}}

NodeStack = ();

for j = 0 to i - 1 do

| if \hat{y_j} is POP then
| NodeStack.pop();
| else
| NodeStack.add(\hat{y_j});
| end

end

y_{cur} = \text{NodeStack.}pop();

if \hat{y_{cur}} is Leaf Node then
| DV_{\hat{y_i}} = \{POP\};

else
| DV_{\hat{y_i}} = \{child_T(\hat{y_{cur}}), POP\};

end

return DV_{\hat{y_i}};
```

When predicting $\hat{y_i}$, the *CD* strategy with dynamic vocabulary will be executed. In most cases, the candidate tokens are limited to the child-nodes of $\hat{y_{cur}}$ within T due to the label dependency. As illustrated in Figure 3, the model needs to determine which

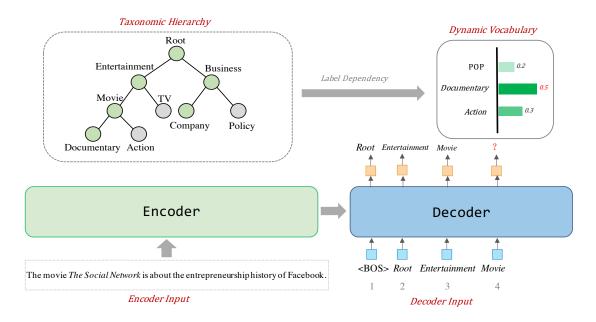


Figure 3: The proposed Seq2Tree framework.

label should be generated at the 4-th decoding time step. Since the model has generated "Movie" at the last time step, due to the label dependency from T, the candidate vocabulary is limited as {POP, Documentary, Action} rather than the whole vocabulary. In this way, we could secure the label consistency during decoding process.

For the training phase, each instance is a (text sequence, linearized label sequence) pair, we define the training object as following negative log likelihood loss:

$$L = -\sum_{(X,\hat{Y})\in(X,\hat{\mathcal{Y}})} log(P_{\theta}(\hat{Y}|X,T))$$
 (3)

$$P_{\theta}(\hat{Y}|X,T) = \prod_{i}^{|\hat{Y}|} P_{\theta}(\hat{y}_{i}|\hat{y}_{< i},X,T) \tag{4}$$

where θ is model parameters, $\hat{y_{< i}}$ denotes the previous generated labels. $P_{\theta}(\hat{y_i}|\hat{y_{< i}},X,T)$ is the probability distribution over the dynamic candidate vocabulary $DV_{\hat{y_i}}$, which is normalized by $softmax(\cdot)$.

For the inference phase, we resort to beam search strategy to generate the output label sequence as:

$$\hat{Y}^{*} = \underset{\hat{Y}}{\arg \max} log(P_{\theta^{*}}(\hat{Y}|X,T))
= \underset{\hat{Y}: \{\hat{y}_{1}, \dots, \hat{y}_{\hat{k}_{i}}\}}{\arg \max} log \prod_{i}^{|\hat{Y}|} P_{\theta^{*}}(\hat{y}_{i}|\hat{y}_{< i}, X, T)$$
(5)

Finally, we obtain $\hat{Y}^* = \{\hat{y}_1^*, ..., \hat{y}_{k_i}^*\}$ as the predicted label sequence. We adopt T5-Base [13] as the backbone to implement Seq2Tree. More implementation details are reported in **Section 3.1**.

3 EXPERIMENT

3.1 Experimental Settings

Datasets: We evaluate our method on three widely used datasets for HTC, including RCV1-V2¹, WOS² and BGC³. The categories of these datasets are all structured as a tree-like hierarchy. We keep exactly the same data splits as reported in the previous works [6, 24]. It is worth noting that WOS is for single-path HTC while RCV1-V2 and BGC are both for multi-path HTC. Please refer to Table 2 for the detailed statistics of the datasets.

Baseline: We compare our method with following HTC models: SGM [23], HMC-capsule [1], HiLAP-RL [10], HiAGM [24], HTCInfoMax [7], HiMatch and HiMatch-BERT [6]⁴. Since SGM is also a generative method for HTC, we implement a variant (SGM-T5) of SGM for a fair comparison, which replaced its LSTM-based encoder-decoder backbone with T5. Among these baselines, HiMatch-BERT is the state-of-the-art model. Besides, HiLAP-RL [10] is the only method that attempts to address the "label inconsistency" problem, which leverages deep reinforcement learning to tackle this issue. In [10], the authors also mention that "label inconsistency" problem could be solved through post processing operation, i.e., simply assign the ancestors of the isolated nodes to the prediction results of corresponding isolated nodes. Therefore, we also implement this post processing on HiMatch-BERT to validate its effectiveness.

Evaluation Metrics: Besides Micro-F1 and Macro-F1, which are widely adopted evaluation metrics in existing HTC studies [1, 6, 7, 24], we propose two new metrics: path-constrained MicroF1

 $^{^{1}} http://www.ai.mit.edu/projects/jmlr/papers/volume5/lewis04a/lyrl2004_rcv1v2_README.htm$

 $^{^2} https://data.mendeley.com/datasets/9 rw3 vkcfy 4/2 \\$

 $^{^3\}mbox{https://www.inf.uni-hamburg.de/en/inst/ab/lt/resources/data/blurb-genre-collection.html}$

⁴Please refer to Section 4 for introduction of these baseline methods.

Table 1: Results of different methods on three datasets. The results of SGM and HiLAP-RL are reported by Zhou et al. [24]. The results of other baselines are from corresponding original papers. "-" means not available in the original paper. Our implementation results are marked by "*". "HiMatch-BERT+pp" is an abbreviation of "HiMatch-BERT+post processing". Since HiLAP-RL, HiMatch-BERT+pp and our method have guaranteed the label consistency, the results of them on each metric and its corresponding path constrained variant are always the same. "↑" indicates the improvement of our method compared with HiMatch-BERT.

Model	RCV1-V2				wos				BGC			
	Micro F1	C-Micro F1	Macro F1	C-Macro F1	Micro F1	C-Micro F1	Macro F1	C-Macro F1	Micro F1	C-Micro F1	Macro F1	C-Macro F1
HMC-Capsule	-	-	-	-	-	-	-	-	74.37	-	-	-
SGM	77.30	-	47.49	-	-	-	-	-	-	-	-	-
HiLAP-RL	83.30	83.30	60.10	60.10	-	-	-	-	-	-	-	-
HTCInfoMax	83.51	-	62.71	-	85.58	-	80.05	-	-	-	-	-
SGM-T5	84.39*	83.75*	65.09*	64.55*	85.83*	85.14*	80.79*	79.95*	77.84*	76.72*	60.91*	59.97*
HiAGM	83.96	83.05	63.35	59.64	85.82	85.35	80.28	79.84	77.22*	76.16*	57.91*	56.61*
HiMatch	84.73	83.49	64.11	60.64	86.20	85.61	80.53	79.32	76.57*	75.23*	58.34*	56.31*
HiMatch-BERT	86.33	85.25	68.66	67.15	86.70	85.74	81.06	79.86	78.89*	78.01*	63.19*	62.23*
HiMatch-BERT + pp	85.37*	85.37*	67.01*	67.01*	85.86*	85.86*	80.18*	80.18*	77.59*	77.59*	62.05*	62.05*
Seq2Tree(Ours)	86.88 $^{\uparrow 0.55}$	86.88 $^{\uparrow 1.63}$	70.01 $^{\uparrow 1.35}$	70.01 $^{\uparrow 2.86}$	87.20 ^{↑0.50}	87.20 $^{\uparrow 1.46}$	82.50 $^{\uparrow 1.44}$	$82.50^{\uparrow 2.64}$	79.72 ^{↑0.83}	$79.72^{\uparrow 1.71}$	63.96 ^{↑0.77}	63.96 $^{\uparrow 1.73}$

(C-MicroF1) and path-constrained MacroF1 (C-MacroF1). The difference between these path-constrained variants and traditional metrics is that, the prediction result for a node will be regarded as "true" only when all its ancestor nodes have been predicted as "true". Take Figure 1(b) as an example, although the model has made correct predictions for *Documentary* and *Company*, the output results for these two nodes are still regarded as "false" due to mistakes happened on their parent nodes.

Implementation Details: For all datasets, the batch size is set to 16 and we optimize the model with label smoothing [11] and AdamW [9] with a learning rate of 5e-5. The results reported in our experiments are all based on the average score of 5 runs with different random seeds. For baseline models (HiAGM, HiMatch and HiMatch-Bert), we use the implementations provided by the authors to produce the experimental results on BGC dataset, the hyperparameters of these baseline models are manually tuned on the standard validation set provided in BGC. Our experiments are all conducted on a single Tesla V100M32 GPU. Besides, during the decoding stage, the tokens already generated previously are also excluded in subsequential dynamic vocabularies.

3.2 Main Results

The experimental results are elaborated in Table 1 and our proposed Seq2Tree consistently outperforms previous approaches across all the datasets. Compared with SGM-T5, Seq2Tree also outperforms it with a large margin, which validates that the improvement of our method is mainly brought by our design on the framework rather than T5. In general, the performance improvements on C-MicroF1 and C-MacroF1 are more remarkable than on MicroF1 and MacroF1. The reason is that Seq2Tree is able to guarantee the label consistency on each path through the *CD* strategy. It is also notable that the performance of post-processing does not improved but decreased. The reason is that HiMatch-BERT cannot guarantee the prediction accuracy of the isolated nodes, and simply assigning ancestor nodes for documents has introduced a lot of noise, which causes the performance degradation of HiMatch-BERT+pp.

Table 2: The statistics of datasets. |V| is the total number of labels. *Depth* is the maximum level of the label hierarchy. Avg(|V|) is the average number of labels in each sample.

Dataset	V	Depth	Avg(V)	Train	Validation	Test
RCV1-V2	103	4	3.24	20833	2316	781265
WOS	141	2	2	30070	7518	9397
BGC	146	4	3.01	58715	14785	18394

3.3 Ablation Study

To reveal the individual effects of label linearization (LL) and constrained decoding strategy (CD), we implement different variants of Seq2Tree by removing CD and LL sequentially. The experimental results on RCV1-V2 are reported in Table 3. Removing CD results in significant performance degradation, which validates its effectiveness. The performance will further decrease when we remove both CD and LL, which illustrating the importance of incorporating the holistic tree-structural information of the taxonomic hierarchy through DFS.

Table 3: Ablation study results on RCV1-V2. When both *CD* and *LL* are removed, Seq2Tree is equivalent to SGM-T5.

Model	Micro F1	C-Micro F1	Macro F1	C-Macro F1
Seq2Tree	86.88	86.88	70.01	70.01
w/o CD	85.31	84.98	66.23	65.15
w/o CD&LL	84.39	83.75	65.09	64.55

4 RELATED WORK

Existing works for HTC could be categorized into local and global approaches. Local approaches [2, 3, 15] tend to construct multiple local classifiers and usually ignore the holistic structural information of the taxonomic hierarchy. As the mainstream for HTC in recent years, global approaches utilize one single model to deal with all classes and introduce various strategies to capture the hierarchical information of the label space. For instance, [20] adopt a

hierarchical network to extract the concepts and model the sharing process via a modified dynamic routing algorithm. HMC-Capsule [1] employs capsule networks to classify documents into hierarchical structured labels. HiLAP-RL [10] formulates HTC as a Markov decision process and propose to learn a label assignment policy via deep reinforcement learning. HTCInfoMax [7] utilizes text-label mutual information maximization algorithm and label prior matching strategy for capturing hierarchical information between labels. In HiAGM [24], two structure encoders (Tree-LSTM and GCN) are introduced for modeling hierarchical label in both top-down and bottom-up manners. HiMatch [6] proposes a hierarchy-aware label semantics matching network to learn the text-label semantics matching relationship in a hierarchy-aware manner. HVHMC [21] introduces loosely coupled graph convolutional neural network as the representation component for capturing vertical and horizontal label dependencies simultaneously. Although the methods mentioned above have been successful to a certain extent, most of them suffer from the "label inconsistency" problem.

It is worth mentioning that there are two previous works also resort to sequence-to-sequence paradigm to address HTC task, one is SGM [23], the other is [14]. However, these two works are limited to single path scenarios which can not tackle the multi-path cases. Moreover, since these two methods generate hierarchical labels sequence uncontrollably, which will also suffer from "label inconsistent" problem.

5 CONCLUSION

In this paper, we propose Seq2Tree method for addressing the "label inconsistency" limitation of prior HTC approaches. Seq2Tree formulates HTC as a sequence generation problem and adopts a T5-based seq2seq architecture to generate a DFS-styled label sequence for each document. In this simple but effective manner, Seq2Tree is able to capture the structural information of the taxonomic hierachy. It secures the consistency of generated labels through the constrained decoding strategy with dynamic vocabulary. The experimental results on three benchmark datasets demonstrate the effectiveness of Seq2Tree.

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