Data and text mining

Enhancing Label Consistency on Document-level Named Entity Recognition

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Abstract

Summary: Named entity recognition (NER) is a fundamental part of extracting information from documents in biomedical applications. A notable advantage of NER is its consistency in extracting biomedical entities in a document context. Although existing document NER models show consistent predictions, they still do not meet our expectations. We investigated whether the adjectives and prepositions within an entity cause a low label consistency, which results in inconsistent predictions. In this paper, we present our method, ConNER, which enhances the label dependency of modifiers (e.g., adjectives and prepositions) to achieve higher label agreement. ConNER refines the draft labels of the modifiers to improve the output representations of biomedical entities. The effectiveness of our method is demonstrated on four popular biomedical NER datasets; in particular, its efficacy is proved on two datasets with 7.5–8.6% absolute improvements in the F1 score. We interpret that our ConNER method is effective on datasets that have intrinsically low label consistency. In the qualitative analysis, we demonstrate how our approach makes the NER model generate consistent predictions.

Availability and implementation: Our code and resources are available at https://github.com/dmis-lab/ConNER/.

Supplementary information: Supplementary data are available at Bioinformatics online.

1 Introduction

Named entity recognition (NER) is the task of determining entity boundaries and classifying categories of named entities. NER is a fundamental part of biomedical applications. Kim et al. 2019, Wei et al. 2019, Lee et al. 2020, Weber et al. 2021, Lewis et al. 2021, Sung et al. 2022. In the general domain, recent studies have attempted to train and evaluate NER models in a document-level context. Wei et al. 2020, Yamada et al. 2020, Wang et al. 2021, Guo et al. 2021. Likewise, the biomedical domain has shifted its focus on evaluating document contexts rather than sentence contexts. Wei et al. 2019, Wang et al. 2021, Weber et al. 2021.

There are several advantages of using document NER models: (1) The models suggest a better way to bridge the gap between research and application fields. Following previous studies, several researches have leveraged sentence NER models in biomedical domains. Cho and Lee 2019, Pérez et al. 2020, Jeong and Kang 2021. However, biomedical applications require an evaluation of the document rather than the sentence context. Wei et al. 2019, Kim et al. 2019, Weber et al. 2021, Sung et al. 2022. (2) Document NER models provide proper and consistent predictions owing to context completeness. Recent works Yamada et al. 2020, Wang et al. 2021, Guo et al. 2021 have shown that using document contexts improves the accuracy of the models. Although the authors of Guo et al. 2021 used powerful context representations such as BERT (Devlin et al. 2018) or ELMo (Peters et al. 2018), their inability to model document-level label consistency resulted in insufficient performance. Therefore, it is challenging to understand which factors contribute to creating document NER models that produce a consistent prediction in the same manner.

To tackle the above challenges, a series of studies Fu et al. 2020, 2021 have provided an interpretable evaluation to identify the attributes of datasets depending on their characteristics. Our intuitive motivation
is that entity-aware attributes are beneficial for achieving higher label consistency, which can also improve the accuracy of the NER models. In this paper, our goal is to develop a NER model that can be trained to predict an entity consistently in a document context.

We first clarify why we need the NER model to make consistent predictions. We provide our motivating example in Figure 1. For example, the mention ‘colorectal cancer’ is an entity of the disease type. Predicting such a mention is challenging in a sentence context owing to context incompleteness. As a result, the sentence model produces an error in predicting ‘non – FAP’ or ‘colorectal’. Meanwhile, the NER model trained on document contexts shows consistent predictions because the token ‘colorectal’ occurs frequently within the documents. Therefore, the document model provides sufficient label agreement to learn label representations of ‘colorectal’. Although the document NER model shows consistent predictions and much better performance than the sentence NER model (Table 1), it still falls behind our expectations. Models trained on document contexts continue to produce 64% errors that contain modifiers (i.e., prepositions or adjectives), such as primary, hereditary, and congenital (Table 1). Because modifiers are used as both entity and non-entity tokens depending on the context situation, they are difficult to predict. Therefore, the modifiers exhibit a low label consistency score and occur at short entity lengths (Figure 2).

To avoid the aforementioned errors, we present ConNER which enhances the label dependency of modifiers to achieve higher label agreement. An abstract of biomedical literature is fed into the biomedical pre-trained language model, BioBERT (Lee et al. 2020b), or BioLM (Liu et al. 2021a), to output context representation (Section 3.2). On top of the pre-trained language model, we propose label refinement to improve the label representations of uncertain tokens within entities (Section 3.3). We also support our loss term for biomedical entities to resemble the label representations on two different architectures: fully connected layers (MLP) and bidirectional long-short term memory (BiLSTM) architecture. We use MLP as the main classification layer to generate final output representations of raw text and use the BiLSTM architecture to generate label representations of biomedical entities. We adopt the notion that the MLP layer is more robust to long entities (multi-layer) and the BiLSTM layer is beneficial in improving label representations of biomedical entities. We employ the BiLSTM architecture to improve the label dependency of biomedical entities. We use four biomedical benchmarks. On three datasets, we achieve a higher F1 score than previous state-of-the-art models (Wang et al. 2011; Liu et al. 2016). To demonstrate the effectiveness of the proposed ConNER approach, we employ the BiLSTM architecture to improve the label dependency of biomedical entities. We use four biomedical benchmarks. On three datasets, we achieve a higher F1 score than previous state-of-the-art models (Wang et al. 2011; Liu et al. 2016). To demonstrate the effectiveness of the proposed ConNER approach, we employ the BiLSTM architecture to improve the label dependency of biomedical entities. We use four biomedical benchmarks. On three datasets, we achieve a higher F1 score than previous state-of-the-art models (Wang et al. 2011; Liu et al. 2016).

The contributions of this study are summarized as follows. (1) We investigate why document NER models make inconsistent predictions in biomedical domains. Based on our observations, we observe that modifiers (i.e., adjectives and prepositions) exhibit a low label consistency score and produce errors by making inconsistent predictions. (2) We present our method, ConNER, which enhances the label dependency of modifiers to generate improved label representations. (3) The results of the experiments show that our ConNER approach significantly improves the accuracy of document NER models, indicating that it can help achieve the highest level of label agreement. (4) For different tasks related to low label consistency, we show that ConNER outperforms various baselines, and we analyze the factors influencing its performance.

2 Background

2.1 Named Entity Recognition

The goal of NER is to find a word or phrase that corresponds to a specific instance, such as a person, location, organization, or any other miscellaneous entity. The NER task primarily involves the extraction and classification of named entities found in a corpus with pre-defined entity tags. We use BIO tagging (Ramshaw and Marcus 1999), where a B-
we define some training set-independent attribute functions as follows:

\[ \phi(x, \varphi) = \text{aggregate features to interpret the properties of tagged entities} \]

2.2 Attribute Definition

Following previous works [2020, 2021], we define the term attribute as a value that characterizes the properties of an entity that may be correlated with performance. The authors introduced attributes bridging the gap between the final performance (we use the F1 score) and interpretable evaluation based on model predictions. Assuming that one attribute is given, the test set of NER tasks naturally partitions into several performance bucket-wise.

Informally, we define notations to facilitate the definition of attributes. Given a set of documents \( D \), entity tagging aims to extract a set of entities \( \mathcal{E} \) as spans or tokens. We first denote a span set \( \mathcal{E}' \subset \mathcal{E} \) as an argument. Specifically, [2020] introduced a feature function \( \phi(\cdot) \) to aggregate features to interpret the properties of tagged entities \( \mathcal{E}' \):

\[ F(x, \phi(\cdot), D(\mathcal{E})) = \frac{|\{ i | \phi(c) = \phi(x), \forall c \in D(\mathcal{E}) \}|}{|D(\mathcal{E})|}, \quad (1) \]

where \( x \) denotes an entity span that can also replace it as token \( x \). Similarly, we define some training set-independent attribute functions as follows:

\[ \phi_{\text{tLen}}(x) = |x| : \text{token span length} \quad (2) \]
\[ \phi_{\text{eLen}}(x) = |x| : \text{entity span length} \quad (3) \]
\[ \phi_{\text{dLen}}(x) = |\text{doc}(x)| : \text{document length} \quad (4) \]
\[ \phi_{\text{eDen}}(x) = |\text{ent}(\text{doc}(x))| / \phi_{\text{dLen}}(x) : \text{entity density} \quad (5) \]
\[ \phi_{\text{OOV}}(x) = |\text{oov}(\text{doc}(x))| / \phi_{\text{dLen}}(x) : \text{OOV density} \quad (6) \]

Rather than using a sentence-level context, we provide a document-length attribute based on the usage of the document-level context. We use two functions to define the density of entity words, and the density of out-of-vocabulary words \( \text{oov}(\cdot) \), which counts the number of out of training set words. We also leverage the training set-dependent attribute functions, as follows:

\[ \phi_{\text{tFreq}}(x) = F(x, \phi_{\text{tDec}}(\cdot), D(\mathcal{E}')) : \text{token frequency} \quad (7) \]
\[ \phi_{\text{eFreq}}(x) = F(x, \phi_{\text{eDec}}(\cdot), D(\mathcal{E}')) : \text{entity frequency} \quad (8) \]
\[ \phi_{\text{trCons}}(x) = F(x, \phi_{\text{trLabel}}(\cdot), D(\mathcal{E}')) : \text{label consistency of token} \quad (9) \]
\[ \phi_{\text{cCons}}(x) = F(x, \phi_{\text{cLabel}}(\cdot), D(\mathcal{E}')) : \text{label consistency of entity} \quad (10) \]

where \( \phi_{\text{tDec}}(\cdot) \) and \( \phi_{\text{eDec}}(\cdot) \) denote a string and label of the corresponding argument, respectively, and \( \phi_{\text{trLabel}}(\cdot) \) and \( \phi_{\text{cLabel}}(\cdot) \) refer to measuring how consistently a certain token or entity span is assigned to a predefined label, respectively. Here, we define label consistency as the degree of label agreement of \( n \) tokens/entities in the training set. We use attribute functions to interpret which dataset attributes have an impact on performance improvement (Figure 3).

3 Method

In this section, we start by learning the document-level model through the supervision of named entity recognition tasks. Our goal is to learn how to enrich the label representations of biomedical entities by improving their label consistency (Section 3.1). We then introduce our label refinement on biomedical entities, which encourages label representations of uncertain tokens within entities (Section 3.2). Finally, we discuss the use of a loss term for biomedical entities to resemble the label representations of two different architectures. Figure 4 depicts the overall structure of ConNER approach.

3.1 Document Named Entity Recognition

ConNER consists of a pre-trained language model \( M_{LM} \) and label-refinement process, as shown in Figure 4. For document tagging, we use abstracts of biomedical literature as raw input and make predictions for each word. Let \( D_i = \{ T_{i1}, T_{i2}, \ldots, T_{iN} \} \) represent a sequence of tokens, where \( N \) denotes the total number of tokens in a document \( D_i \). First, we apply a biomedical pre-trained language model (e.g., BioBERT [Lee et al. 2020]) or BioLM [Lewis et al. 2020] to obtain contextualized word representations for each token \( T_{i1}, T_{i2}, \ldots, T_{iN} \in B^d \). Then, we represent a biomedical entity e as the concatenation of start-to-end vector

Fig. 2: Consistent score per entity length. The x-axis denotes the entity length (i.e., \( \phi_{\text{tLen}} \)), and the y-axis denotes the consistent score (i.e., \( \phi_{\text{Cons}} \)). Short lengths of entities show low consistent scores due to the low label agreement of the modifier tokens.

Fig. 3: Overview of Dataset Biases. Each dot denotes an attribute score of entities. Intuitively, these intrinsic differences in datasets explain what factors have a significant influence on improving performance.
Uncertainty (U) was analysed. The gene was analysed colorectal cancer. The APC gene was analysed colorectal cancer (3) colorectal cancer (2) colorectal cancer (1)

The independent decoder predicts well for longer entities, especially biomedical entities (Fu et al. 2020, 2021; Jeong and Kang, 2021). With the preceding observation, we find that the modifiers (i.e., prepositions or adjectives) are both used as entity and non-entity tokens. We also find that a low label consistency occurs at short lengths of entities (i.e., $|e|/|\text{Len}_LSTM| < 5$), which most modifiers consist of in this scope. As a result, we attempted to deal with long entities by employing the MLP layer and developing a label-refinement process to target those modifiers to be predicted consistently.

### 3.2 Label Refinement on Biomedical Entities

Overall, we propose a label-refinement process that depends on an entity-length attribute $\phi_{\text{Len}_LSTM}(E)$ to enrich the label representations of the entity spans. To encourage label representations, we add a loss term of entity uncertainty $L_{\text{class}}$ to improve the label consensus of entities that have low label agreement. On top of the fully connected layer, we compute an uncertainty score $U$ to determine which tokens need to be modified for their predicted label.

**Fig. 4**: Overview of ConNER performing label refinement on biomedical entities. The abstract of biomedical literature is fed into the pre-trained language model $\mathcal{M}_{LSTM}$ to output context representation. In the label-refinement process, we use a mask tensor $\text{MASK}$ to find the probability of biomedical entities and label it into the BiLSTM architecture $\mathcal{M}_{LSTM}$ to improve label dependency of modifiers within entities that induce low label agreement. On top of the fully connected layer, we compute an uncertainty score $U$ to determine which tokens need to be modified for their predicted label.

Representations, as follows:

$$\mathcal{M}_{LSTM}(e) = [T_{\text{start}}: T_{\text{end}}] \in \mathbb{R}^{\text{d} \times \text{Len}_LSTM}$$

where $T_{\text{start}}$ and $T_{\text{end}}$ denote the start and end of biomedical entity $e \in E$, respectively, and $d$ denotes the final hidden dimension of language model $\mathcal{M}_{LSTM}$. Note that we use the notation $e$ as an example to help understand our model ConNER. We use tag-independent decoding (i.e., MLP) on the model $\mathcal{M}_{LSTM}$ as the main classification layer, which is useful for predicting long-named entities (Fu et al. 2020). Formally, we can define our classification loss $L_{\text{class}}$ using cross-entropy objectives to optimize our model as follows:

$$L_{\text{class}} = -\frac{1}{N} \sum_{j=1}^{N} y_j \log(p_j)$$

where $y_j$ denotes the ground-truth label and $p_j$ denotes the probability of the main classification layer.

**Sentence vs. Document.** In our pilot experiments, we first observe that the label consistency of entity $\phi_{\text{Len}_LSTM}(E)$ is enhanced when we expand the context from sentences to documents. We also observe that using a larger context is helpful in achieving better performance (+1.4-1.8% in F1 score), as shown in Table [1]. Based on our positive observations, we hypothesize that one key reason for the performance gain is that biomedical entities are challenging to predict at the sentence level owing to context incompleteness. Learning from the limited context makes it difficult to predict a token within an entity such as ‘colorectal’ (see Figure [1]).

### 3.2 Label Refinement on Biomedical Entities

Overall, we propose a label-refinement process that depends on an entity-length attribute $\phi_{\text{Len}_LSTM}(E)$ to enrich the label representations of the entity spans. To encourage label representations, we add a loss term of entity uncertainty $L_{\text{class}}$ to improve label dependency of modifiers within entities that have low label agreement. On top of the fully connected layer, we compute an uncertainty score $U$ to determine which tokens need to be modified for their predicted label.

**Uncertainty.** We ask the natural question: *How can we decide what tokens should be refined?* We choose this criterion for the certainty of the draft label on token representations (Jeong et al. 2022). We calculate the uncertainty $U$ of the probability distributions of the MLP layer as follows:

$$U = H(p_i) = -\sum_{y \in C} p_i \log p_i.$$
where $C$ denotes the number of pre-defined entity types per dataset. We use the entropy of the probability distribution $p_i$ to define the uncertainty $U$. Given this uncertainty score, label refinement proposes a positive training signal to shift the draft label.

Label Refinement. We decide to improve the label dependency on modifiers (i.e., adjectives or prepositions) used in the entities during training. Specifically, we create an entity-aware mask tensor $M \text{MASK} \in \mathbb{R}^{B \times N \times N}$ to indicate the position of the padded indices such that our model does not attend to non-entities, where $B$ denotes the batch size. The mask tensor is applied to the BiLSTM layers $M_{\text{LSTM}}$ to obtain a label representation $l(e)$, as follows:

$$l(e) = M_{\text{LSTM}}(\text{MASK}(M_{\text{LSTM}}(e))) \in \mathbb{R}^{B \times L \times C}.$$  (14)

Then, $M_{\text{LSTM}}$ trains to softly assist the main classification layer in performing precise predictions with improved consistency. Note that we use the term softly assist to describe a process that assists the main classification layer in shifting its draft label during training. That is, the trained model $M_{\text{LSTM}}$ enhances the label dependency of an uncertain token and softly assists in refining the draft label of the uncertain token. Formally, we add element-wise to assist predictions before calculating a label loss $L_{\text{Label}}$, as shown below:

$$p = p \oplus l,$$  (15)

$$L_{\text{Label}} = -\frac{1}{N} \sum_{j=1}^{N} y_j \log(l_j)$$  (16)

where $y_j$ and $l_j$ denote the ground-truth label and probability of the $M_{\text{LSTM}}$ layer, respectively, and $p$ is used to compute the classification loss in Equation (15). Finally, we determine the criterion using the pre-computed uncertainty score $U$ in Equation (17). We set an uncertainty threshold $\Gamma$ to distinguish the tokens that should be refined within entities. For example, in Figure 2, a token 'cancer' of the entity 'colorectal cancer' is first predicted as an Outside tag. During training, the token 'cancer' is converted to a Beginning tag because of the high uncertainty score. We found that $\Gamma = 0.3$ worked well in practice. See Figure 2 for an ablation study.

Distillation. We propose improving the label representations of biomedical entities by distilling knowledge [Hinton et al., 2015] from our decoding layers. We minimize the Kullback-Leibler divergence between the probability distribution from the tag-independent layer (i.e., MLP) and the tag-dependent layer (i.e., BiLSTM) on top of the biomedical pre-trained language model. The distillation loss was computed as follows:

$$L_{\text{distill}} = \frac{K(L(p||l) + K(L(l||p))),}$$  (17)

where $p$ and $l$ denote the probability distributions of the MLP and BiLSTM layers, respectively. Note that distillation is computed before Equation (15).

3.3 Training Objective

We optimize the three losses altogether to improve the label agreement of the entity through label refinement and distilling knowledge while predicting on the tag-independent layer. Our final loss is computed as follows:

$$L = \lambda_1L_{\text{Label}} + \lambda_2L_{\text{Label}} + \lambda_3L_{\text{distill}},$$  (18)

where $\lambda_1, \lambda_2, \lambda_3$ scale the importance of each loss term. We observe that $\lambda_1 = 1, \lambda_2 = 1e^{-1}$, and $\lambda_3 = 1e^{-3}$ exhibit the best performance in our framework. See Table 3 for an ablation study of the other components.

### 4 Experimental Setup

#### 4.1 Dataset

We use four biomedical NER benchmarks across four entity types: NCBI-disease [Doğan et al., 2013], CDR [Xu et al., 2016], AnamEM [Füssel and Anamandu, 2014], and Gellus [Kaur et al., 2016], following the standard train/dev/test splits for biomedical NER evaluation. (1) NCBI-disease [Doğan et al., 2013] consists of 793 PubMed abstracts with manually annotated disease entities. (2) CDR [Xu et al., 2016] contains 1,500 PubMed abstracts manually annotated with disease and chemical entities in the same context. (3) AnamEM [Füssel and Anamandu, 2014] consists of 1,212 PubMed abstract and full-text extracts annotated with 12 anatomical entity types. (4) Gellus [Kaur et al., 2016] consists of annotating cell lines in 1,212 documents from PubMed abstracts and PMC full-text extracts. Half of the corpora were drawn from the Anem corpus [Ono et al., 2013], and the other half were drawn from the BioNLP ST’13 Cancer Genomics (CG) task documents [Füssel et al., 2017]. Table 2 shows the dataset statistics.

#### 4.2 Comparison Methods

We evaluate the sentence- and document-level contexts and compare ConNER with several neural network models commonly used in biomedical domains. (1) B-MTMT [Archiblame et al., 2017] developed a multi-task learning model using various biomedical sources annotated with different entity types. (2) BiLSTM-CRF [Rahbe et al., 2017] proposed a combination of word embeddings and LSTM with the CRF decoding strategy in the biomedical domain. (3) BioBERT [Lee et al., 2020b] introduced a biomedical-specific language representation model pre-trained on large-scale biomedical corpora. (4) BioLM [Lee et al., 2020d] suggested a biomedical-specific language representation model pre-trained on biomedical and clinical corpora. (5) CL-KL and CL-LA [Wang et al., 2021] proposed a method that can retrieve and select a semantically relevant context using a search engine to improve contextual representations, with the original sentence as a query.

#### 4.3 Implementation Details

We train ConNER using BioLM [Lee et al., 2020d] or BioBERT [Lee et al., 2020b] to treat biomedical entity types. These two pre-trained language models are commonly used as backbone models in the biomedical domain, and we adopt these models to generate contextualized
Table 4. Results on biomedical NER benchmarks. F1 score is reported. The best score is displayed in bold and the second-best score is underlined. 1numbers are estimated from the figures in the original papers.

| Context | Model | Evaluation (F1) |
|---------|-------|----------------|
|         | NCBI-disease | CDR | AnatEM | Gellus |
| Sentence | B-MTM [Crichton et al., 2017] | 80.4 | 89.2 | 82.2 | - |
|         | BiLSTM-CRF [Habib et al., 2017] | 84.6 | - | - | 75.6 |
|         | BioBERT [Lee et al., 2020] | 89.0 | 89.1 | 73.9 | 54.9 |
|         | BioLSTM [Lewis et al., 2020] | 88.3 | 89.5 | 74.9 | 55.9 |
|         | CL-L2 (w/o context) [Wang et al., 2021] | 89.2 | 90.7 | - | - |
|         | CL-KL (w/o context) [Wang et al., 2021] | 89.2 | 90.7 | - | - |
| Document | CL-L2 (w/ context) [Wang et al., 2021] | 89.2 | 91.0 | - | - |
|         | CL-KL (w/ context) [Wang et al., 2021] | 89.0 | 90.9 | - | - |
|         | ConNER (Ours) | 89.9 | 91.3 | 83.5 | 63.4 |

Table 5. An ablation study of ConNER components. We perform three different experiments: removing distillation (← \( L_{distill} \)), label refinement (← \( L_{label} \)), and both of these processes (← \( L_{distill}, L_{label} \)). We used our best hyperparameter setting on the BioLM [Lewis et al., 2020a] model equally. The best scores are displayed in bold.

| Model Description | Evaluation (P/R/F1) |
|-------------------|--------------------|
|                   | NCBI-disease | CDR | AnatEM | Gellus |
| ConNER \( \{
\} \) | 88.8 / 91.1 / 89.9 | 89.9 / 92.7 / 91.3 | 83.2 / 83.7 / 83.5 | 62.6 / 64.2 / 63.4 |
| ConNER \( \{ L_{distill} \} \) | 87.5 / 89.9 / 88.7 | 89.2 / 92.3 / 90.7 | 81.6 / 81.1 / 81.3 | 54.3 / 60.3 / 57.1 |
| ConNER \( \{ L_{label} \} \) | 87.4 / 90.4 / 88.8 | 89.4 / 92.1 / 90.7 | 81.0 / 81.9 / 81.5 | 54.2 / 61.2 / 57.5 |
| ConNER \( \{ L_{distill}, L_{label} \} \) | 87.4 / 89.7 / 88.5 | 89.8 / 90.7 / 90.2 | 80.3 / 80.4 / 80.3 | 54.8 / 59.1 / 56.9 |

representations. We set 128 tokens as the maximum sequence length for the sentence-level context and 512 tokens for the document-level context, and tokens with more than the maximum sequence length were truncated. The batch size was set to 32 for the sentence level and 6 for the document level. We select a learning rate in the range \( \{3e^{-5}, 5e^{-5}\} \). We search for a training epoch in the range \( \{30, 40, 50\} \). We suggest our total hyperparameter settings in Table 4. We train our model with a single NVIDIA Titan RTX (24GB) GPU for fine-tuning, and the training time took less than 2 hours.

4.4 Experimental Results

Table 4 reports the results of ConNER approach. To show the effectiveness of ConNER approach, we evaluate our model in the named entity recognition setting in four biomedical domains and compare its performance with that of other methods in different contexts. Compared to previous biomedical NER models, our approach achieves the best performance compared to all other baselines on three datasets: NCBI-disease [Dogan et al., 2014], CDR [Li et al., 2016], and AnatEM [Pyysalo et al., 2014]. This demonstrates that improving the label agreement of modifiers is effective in a document context. In addition, the performance gap between BioLM and ConNER on AnatEM (74.9 vs. 83.5) and Gellus (57.9 vs. 63.4) shows that the label refinement based on the dataset bias, which has low label consistency, is effective. Although it still lags behind the BiLSTM-CRF model, the gap is reduced. We provide additional ablation studies of ConNER approach in the following sections.

5 Analysis

5.1 Ablation studies

Table 5 shows our ablation result on four biomedical NER benchmarks. We evaluate our approach ConNER by removing its components: 1) distillation (← \( L_{distill} \)) and 2) the label-refinement process (← \( L_{label} \)) and both of these processes (← \( L_{distill}, L_{label} \)). The experiments show that ConNER is effective for all four benchmarks. Specifically, we observe that the AnatEM and Gellus datasets show significant improvement, demonstrating that our approach ConNER is effective for datasets with low label consistency on the entities shown in Figure 3. We also observe that adding each component consistently improves the recall metrics. These observations correspond to an advantage of ConNER approach, whereby it decides which token should be refined by relying on the uncertainty threshold \( \Gamma \).

Fig. 5: An analysis of uncertainty threshold \( \Gamma \). The x-axis refers to the threshold \( \Gamma \), and the y-axis denotes the F1 score. The overall results show that \( \Gamma = 0.3 \) results in stable performance on the four biomedical benchmarks.
ConNER

Table 6. A sample prediction of ConNER on the AnatEM and CDR datasets. yellow highlight refers to the correct prediction and red signifies to the wrong prediction.

| Dataset | AnatEM [Pysalos and Anamanioti, 2014] | CDR [Li et al., 2016] |
|---------|--------------------------------------|----------------------|
| PMID    | 10420526                             | 9158667              |

Title: [Histopathologic examination of rectal carcinoma\(^{(1)}\)]

Abstract: In patients with rectal carcinoma, the histopathological evaluation of the surgical specimen\(^{(2)}\) provides pivotal prognostic and therapeutic information. Important parameters are tumor size, depth of invasion, histological type and grade, pattern of invasion (diffusely infiltrating versus expanding margin\(^{(3)}\)), degree of peritumoral lymphocytic infiltration, and tumor involvement of surgical margin and lymph nodes\(^{(3)}\). Evaluation of the circumferential (deep, lateral) margin is of utmost importance. It should be labeled with ink in the gross specimen and should be examined histologically using several tissue blocks. The number of lymph node metastases and the total number of lymph nodes examined should be reported. A histological evaluation of the distal mesorectum in its entirety is recommended to detect discontinuous distal mesorectal tumor spread. The histopathological findings should be summarized using the TNM-classification.

Table 7. Case studies of inconsistent predictions in document NER models. We observe that BioLM\(^{(5)}\) predicts 'rectal carcinoma' as an entity only 11 times out of 100 times (i.e., we denote this 0.11 in Table 7). However, the corresponding token has 'rectal carcinoma' mention as an entity. Compared to ConNER prediction, a model without label refinement and distillation consistently predict 'rectal carcinoma' as an entity token in the first appearance and as a non-entity token in the second appearance. Another surprising example is the token 'surgical'. In the training dataset, the 'surgical' token achieved a consistency score of 92.3% in the entity dictionary. In other words, it was mostly used as an entity token, accounting for 92.3% of the total. The ConNER approach performs well in predicting the 'surgical' token as an entity token. As the intention was to enhance the label dependency of adjectives within entities, it surely works well as per our observations.

5.2 Qualitative analysis

Table [7] shows our ConNER prediction on the AnatEM dataset. We investigate which examples could show the advantages and disadvantages of our approach and find three different examples: (1) Our model consistently predict 'rectal carcinoma' mention as an entity. Compared to ConNER prediction, a model without label refinement and distillation process (i.e., ConNER — \(L_{distill}, L_{label}\)) predicts 'rectal' as an entity token in the first appearance and as a non-entity token in the second appearance. (2) Another surprising example is the token 'surgical'. In the training dataset, the 'surgical' token achieved a consistency score of 92.3% in the entity dictionary. In other words, it was mostly used as an entity token, accounting for 92.3% of the total. The ConNER approach performs well in predicting the 'surgical' token as an entity token. As the intention was to enhance the label dependency of adjectives within entities, it surely works well as per our observations.

However, ConNER still has several limitations in that it cannot generalize on out-of-density tokens such as 'mesorectum' or 'margin' that never occur in the training dataset. ConNER approach cannot predict these tokens as biomedical entities which is a common situation in real-world scenarios. On comparing the predictions 'peritumoral lymphocytic' and 'lymph nodes', we can see that the subtoken 'lymph' was predicted inconsistently even if they were composed of the same
lymph

et al.

Collobert, R.

Cho, H. and Lee, H. (2019). Biomedical named entity recognition using paragraphs but also utilizing retrieved contexts based on out-of-density that our solution will be more sophisticated by not only using golden datasets, which is a common situation in real-world scenarios. We expect our approach for biomedical NER applications. In our future work, we will performance on low-resource datasets, showing the possibility of adopting in three biomedical domains while providing a view of connecting contexts. We present a label-refinement process and encouragement of label representation to consistently predict biomedical entities. We expect that our solution will be more sophisticated by not only using golden paragraphs but also utilizing retrieved contexts based on out-of-density tokens.

6 Conclusion

In this paper, we present ConNER, an approach that enhances label dependency to construct consistent biomedical NER models in document contexts. We present a label-refinement process and encouragement of label representation to consistently predict biomedical entities. The ConNER approach outperforms existing biomedical NER methods in three biomedical domains while providing a view of connecting dataset attributes with a training framework. We also achieve a powerful performance on low-resource datasets, showing the possibility of adopting our approach for biomedical NER applications. In our future work, we will attempt to handle out-of-density tokens that never occur in the training dataset, which is a common situation in real-world scenarios. We expect that our solution will be more sophisticated by not only using golden paragraphs but also utilizing retrieved contexts based on out-of-density tokens.

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