Abstract

The existing neural machine translation system has achieved near human-level performance in general domain in some languages, but the lack of parallel corpora poses a key problem in specific domains. In biomedical domain, the parallel corpus is less accessible. This work presents a new unsupervised sentence alignment method and explores features in training biomedical neural machine translation (NMT) systems. We use a simple but effective way to build bilingual word embeddings (BWEs) to evaluate bilingual word similarity and transferred the sentence alignment problem into an extended earth mover’s distance (EMD) problem. The proposed method achieved high accuracy in both 1-to-1 and many-to-many cases. Pre-training in general domain, the larger in-domain dataset and n-to-m sentence pairs benefit the NMT model. Fine-tuning in domain corpus helps the translation model learns more terminology and fits the in-domain style of text.

1 Introduction

Recent years have seen the neural machine translation (NMT) system reached near human-level performance on several language pairs in general domain or some specific domains (Wu et al., 2016; et al., 2018; Läubli et al., 2018). The reliance on large parallel corpora is the major challenge of training an NMT system, while in many domains the vast majority of language pairs have very little, if any, parallel data (Artetxe et al., 2019; Koehn and Knowles, 2017). Manually obtaining such parallel corpora is expensive and labor-intensive.

In biomedical domain, machine translation is essential. At the end of 2019, the outbreak of COVID-19 coronavirus had shown us the international medical communication and cross-language medical data sharing can help human beings around the world respond to medical emergencies (Liang et al., 2020; Koehn et al., 2020; Moorthy et al., 2020). A biomedical machine translation system facilitates the exchange of treatment experiences and research findings in a timely and efficient manner and promotes biomedicine development in countries with different languages. Moreover, a high-quality term translation model is also conducive to term normalization tasks, for which many models have been developed. Therefore, it makes sense to build a biomedical machine translation system.

The architecture of machine translation systems has developed over a long period of time. Statistical machine translation used to be the mainstream of machine translation (Brown et al., 1993; Koehn et al., 2003; Chiang, 2007), while NMT has become the de facto standard for large-scale machine translation in the past few years (Bahdanau et al., 2015; Cho et al., 2014; Vaswani et al., 2017; Stahlberg, 2019). The most popular machine translation model is the Transformer (Vaswani et al., 2017).
The first and most crucial step in constructing a translation model is to obtain a parallel corpus since the essence of Machine Translation (MT) is to use the knowledge mined from the existing corpora to translate new text (Tian et al., 2014). Most of the current works follow the pipeline to construct parallel corpus: text collection, text preprocessing, and sentence alignment (Sennrich and Volk, 2010; Tian et al., 2014; Ziemske et al., 2016). In the public domain of some dominant language, there are many large-scale parallel corpora containing tens of millions of sentence pairs publicly available. In contrast, the parallel corpus is less accessible in biomedical domain. On the other hand, the biomedical domain is well known for its complex nomenclature (Névéol et al., 2018) and massive sums of terminologies. Besides, matching the in-domain style of text is also meaningful for a biomedical translation model since the words and sentence patterns in the biomedical domain are different from those of the general domain. The translation model trained in the public domain is poorly (Zeng-Treitler et al., 2010) for these problems and leads to lower translation quality. The biomedical NMT model needs to learn how to translate texts in the biomedical domain from the related corpus. Therefore, domain-specific parallel corpora are fundamental to translate biomedical documents precisely. Some existing translation works provide bilingual biomedical corpus. These works construct bilingual corpus between majority languages such as fr/en, pt/en, es/en, de/en, it/en, and zh/en\(^1\), whose data size ranging from thousands to hundreds of thousands of sentence pairs (Neveol et al., 2018; Soares et al., 2019; Liu et al., 2020). Moreover, in zh/en case, such bilingual corpus is scarce, and the largest one is less than 100,000 sentence pairs (Ma et al., 2019; Liu et al., 2020) while we extracted more than 1 million sentence pairs in this work. The existing sentence alignment methods tend to rely on poorly available supervised data or lose many-to-many sentence pairs (Brown et al., 1991; Gale and Church, 1993; Moore, 2002; Varga et al., 2005; Adafre and de Rijke, 2006; Sennrich and Volk, 2010).

For the reasons mentioned above, we proposed a novel unsupervised sentence alignment method based on parallel documents only to extract biomedical sentence pairs. Then we train our biomedical NMT model with the resulting sentence pairs and existing biomedical knowledge: few existing Chinese-English sentence pairs from a cancer corpus ECCParaCorp\(^2\) and bilingual terms extracted from a medical dictionary. Firstly, the proposed sentence alignment method mixes the two corresponding Chinese and English documents into a pseudo document according to the relative position of words. These pseudo documents are used to train BWEs to evaluate bilingual word similarity by computing the cosine similarity between word embeddings (Vulic & Moens, 2015). The distance between sentences in a parallel document pair is evaluated by combining the word similarity and the relative position of sentences. Finally, each sentence is assigned a corresponding amount of information according to its length, such that the sentence alignment problem can be transferred into a problem of calculating the extended EMD between the sentences in a pair of parallel documents. To construct sentence-level parallel corpora, we crawled a medical corpus from UpToDate (Fox and Nashat, 2003) and a biomedical corpus from the abstracts of PubMed papers. Both corpora are English-Chinese document-level parallel corpora. Then we applied the proposed method to the corpora and finally extracted 992,112 one-to-one and 42,4051 many-to-many Chinese-English biomedical sentence pairs. For the biomedical NMT model, we reported a 17.72 (17.10) BLEU score gains in the fine-tuned Chinese-English (English-Chinese) model and found that the larger in-domain dataset and n-to-m sentence pairs are helpful for NMT model while the effect of dictionary is unstable.

2 Related Work

This section introduces BWEs, Sentence alignment tasks, and the basic concept of Earth Mover’s Distance (EMD).

2.1 Bilingual Word Embeddings

BWEs is a common vector space for words in two languages. BWEs usually maintains the semantic information of both languages, such as the word

\(^1\) fr=French, en=English, pt=Portuguese, es=Spanish, de=German, it=Italian, zh=Chinese.

\(^2\) http://www.phoc.org.cn/ECCParaCorp/
similarity that is usually computed by the cosine between their embeddings (Paula Czarnowska et al., 2019).

Current approaches for constructing BWEs can be divided into two categories: methods that train embeddings for two languages separately and learn a mapping to align two embedding spaces, e.g., with bilingual information (Mikolov et al., 2013; Zhang et al. 2016a; Artetxe et al., 2017) or by unsupervised approaches (Conneau et al., 2018; Dou et al., 2018), and methods that train BWEs by learning a shared embedding space for both languages (Hermann and Blunsom, 2014). Vulic et al. (2015) proposed an approach to learn BWEs from non-parallel document-aligned data by merging two aligned documents into one document which is shuffled later to generate a new pseudo-bilingual document. These pseudo-bilingual documents can be used to train BWEs. The corpora in this work are parallel document-aligned data, and we propose a method slightly different from Vulic et al. (2015) and use the word alignment information in parallel documents to train BEWs.

2.2 Sentence Alignment
Sentence alignment refers to the task of aligning sentences in a document pair, and the aligned sentence pairs express the same meaning in different languages. The most common alignment is 1-to-1 alignment. However, there are quite a proportion of complex alignment relationships such as 1-to-0, 1-to-2, 1-to-3, and 2-to-2, due to the characteristics of languages, translators’ personal reasons, or errors in sentence segmentation. Most of the previous work on sentence alignment can be divided into three categories: length-based (Brown et al., 1991; Gale and Church, 1993), word-based (Moore, 2002; Varga et al., 2005), and translation-based models (Adafre and de Rijke, 2006; Sennrich and Volk, 2010). Some of these models are supervised, depending on dictionaries or existing sentence pairs. Furthermore, strong assumptions about the alignment types are commonly seen in these models, e.g., assuming there are only specific types of alignment or the alignment must be ordinal. Most models are weak in the many-to-many case.

2.3 Earth Mover’s Distance
EMD is defined as the minimum cost of moving all mounds into holes, where the volume of the mounds and holes is known. The mounds and holds have an equal total amount of volume. The cost of moving the earth is the product of the moving distance and the moving amount. Calculating the EMD is equivalent to solving a linear programming problem (see more details in section 3.3), where a transport matrix and the minimum cost will obtain. EMD has been used in the bilingual lexicon induction task (Zhang et al. 2016a; Zhang et al. 2016b; Zhang et al. 2017a). Given the weight of words and the distance between words, the transport matrix obtained by calculating EMD infers the translation relation of words between two languages. We are inspired by these works and creatively applied extended EMD to the sentence alignment scenario.

3 Methods
In this section, we propose our approach to building a biomedical machine translation system. We trained BWEs by generating pseudo bilingual documents using parallel biomedical documents. Then we defined the distance between sentences and extended the EMD to align sentences. Finally, the biomedical machine translation model is trained with several corpora, including aligned sentences, in-domain knowledge, and out-of-domain corpus.

3.1 BWEs with Parallel Documents
The parallel documents contain information about the similarity between words in two languages. We assume that bilingual word pairs usually appear in a similar position in parallel documents, respectively. Based on this assumption, we mix two parallel documents into one document by re-ranking the words according to their relative position of words. If $S$ and $T$ are parallel documents, including $N$ words and $M$ words respectively, the relative position of the $i_{th}$ word in $S$ is $\frac{i}{N}$. Similarly, the relative position of the $j_{th}$ word in $T$ is $\frac{j}{M}$. We remove sentence boundaries and rearrange all the words in the parallel documents in descending order of their relative positions to generate new bilingual pseudo documents, from which BWEs are extracted with word2vec (Mikolov et al., 2013), skip-gram model. The similarity between words is defined as the cosine of two embeddings in BWEs.
3.2 Sentence Distance

The distance between two sentences in different languages is highly related to the words’ similarity and the relative position of sentences in the documents. We assume $S = \{s_i\}_{i=0}^n$, $T = \{t_j\}_{j=0}^m$, where $s_i$ and $t_j$ denotes the sentence in the parallel documents $S$ and $T$.

The word-level distance $d_1(s_i, t_j)$ is defined as

$$d_1(s_i, t_j) = \left( \frac{\sum_{w_k \in s_i} \max_{v_l \in t_j} \cos(w_k, v_l)}{\text{len}(s_i)} \right)^{-1},$$

where $w_k$ and $v_l$ are words in $s_i$ and $t_j$. $d_1(s_i, t_j)$ searches the most similar word in $t_j$ for each word in $s_i$ and averages the similarity to measure the word-level distance between sentences.

The distance based on relative position is defined as follows:

$$d_2(s_i, t_j) = |\text{posi}(s_i) - \text{posi}(t_j)|^3,$$

where,

$$\text{posi}(s_i) = \frac{\sum_{p < i} \text{len}(s_p)}{N},$$

$$\text{posi}(t_j) = \frac{\sum_{p < j} \text{len}(t_p)}{M}.$$ 

The definition of $N$ and $M$ is the same as in subsection 3.1.

In our experiments, the positional distance $d_2$ should be quite small when the relative position of the sentences is close since the relative positions of aligned sentences are not exactly the same. Therefore, the positional distance $d_2$ is defined as the third power of the difference of relative position.

Consequently, the distance between $s_i$ and $t_j$ can be defined as:

$$D_{ij} = d_1(s_i, t_j) + \alpha d_2(s_i, t_j).$$

The $\alpha$ is a hyper-parameter, which will be discussed in the later section.

3.3 Sentence Alignment

In this subsection, we make a hypothesis that in a pair of parallel documents $(S, T)$, $S$ and $T$ contain an equal amount of information, where the amount of information in one sentence is proportional to sentence relative length. We treat the sentences in $S$ as mounds and the sentences in $T$ as holes and take the distance from the mound to the hole as defined in 3.2. Furthermore, the volume of the mounds $s_i$ and the hole $t_j$ is $\text{len}(s_i)$ and $\text{len}(t_j)$, respectively, where,

$$\text{len}(s_i) = \frac{\#(w_k | w_k \in s_i)}{N},$$

$$\text{len}(t_j) = \frac{\#(w_k | w_k \in t_j)}{M}.$$ 

$D_{ij}$ is the known distance between $s_i$ and $t_j$. Then the problem of sentence alignment can be transferred into solving the EMD distance from $S$ to $T$:

$$\min_P \sum_{i,j} D_{ij} P_{ij},$$

s.t. $\sum_i P_{ij} \leq \text{len}(s_i), \forall i \in \{1,2,\ldots,n\}$,

$$\sum_j P_{ij} = \text{len}(t_j), \forall j \in \{1,2,\ldots,m\},$$

$$P_{ij} \geq 0, \forall i, j,$$

where $P$ is transport matrix and $P_{ij}$ denotes the transport quantity from $s_i$ to $t_j$. The first
constraint guarantees the amount of earth received by each hole does not exceed the volume of the hole, while the second constraint means the information is completely transported. Since \( \sum_{i,j} P_{ij} = \sum_{j} \text{len}(t_j) = 1 \), the "\( \leq \)" in the first constraint is equivalent to the "=".

However, in real data, the above strict constraints result in elements in \( P \) corresponding to some unaligned sentences to be non-zero since the amount of information contained in the sentence is not strictly proportional to sentence length. These non-zero elements in \( P \) lead to incorrect many-to-many sentence alignment. Therefore, we introduce a relaxation factor to transfer the problem into:

\[
\min \sum_{i,j} D_{ij} P_{ij},
\]

s. t. \( \sum_{i} P_{ij} \leq \text{len}(s_i) + \frac{\varepsilon}{n}, \forall i \in \{1, 2, \ldots, n\} \),

\[
\sum_{j} P_{ij} \leq \text{len}(t_j) + \frac{\varepsilon}{m}, \forall j \in \{1, 2, \ldots, m\},
\]

\[
P_{ij} \geq 0, \forall i, j,
\]

\[
\sum_{i,j} P_{ij} = 1,
\]

where the relaxation factor \( \varepsilon \) is a real number between 0 and 1. The relaxation factor effectively removes non-zero elements that should not appear in \( P \). Still, the selection of \( \varepsilon \) is a new problem. It is easy to find that \( \varepsilon = 0 \) will simplify the problem to the previous one, larger \( \varepsilon \) tends to reduce the number of non-zero elements, and if \( \varepsilon \) is large enough, the transport occurs only in one pair of sentences with the smallest distance. To address this problem, we propose a practical selection approach. The completely non-zero \( 2 \times 2 \) submatrixes in \( P \) may result in incorrect many-to-many alignments. We define \( Z_{\varepsilon}(P) \) as the sum of the smallest elements in all these completely non-zero \( 2 \times 2 \) submatrixes, and grid search \( \varepsilon \) to minimize \( Z_{\varepsilon}(P) + \gamma \varepsilon \), resulting in a small \( \varepsilon \) but can effectively reduce the alignment error. In our experiments, \( \gamma = 1 \) is a good choice.

So far, each non-zero element in \( P \) implies an alignment between sentences. In real data, the sentence alignment method occasionally bundles several alignments into one alignment group. We split the alignment groups containing a least three sentences in both languages by length-based approach, the Gale-Church algorithm (Gale and Church, 1993), to get the final alignments.

### 3.4 Biomedical NMT Model

We followed the traditional way in domain adaptation for NMT to pre-train the NMT model on general corpora and then fine-tune with in-domain parallel corpora. We use the base transformer model as our NMT model.\(^3\) Figure 1 illustrates the overall pipeline.

### 4 Results

#### 4.1 Data Collection

We crawled 8611 pairs of documents in both Chinese and English from UpToDate and 7137 pairs left after the cleaning process. As for PubMed abstracts, the Chinese abstracts come from a public website\(^4\) and are translated by workers in related fields. The English abstract is from the original paper. We crawled 60553 pairs of abstract. We applied preprocessing for both data, including punctuation standardization, sentence boundary

|       | UpToDate |       |       |       |       |       |       |
|-------|----------|-------|-------|-------|-------|-------|-------|
|       | Precision | Recall |       | F1    |       | Precision | Recall |       | F1    |
| 1-to-1| GC       | 69.10 | 74.05 | 71.49 |       | 89.21 | 78.47 | 83.50 |
|       | MS       | 94.41 | **94.41** | **94.41** |       | **99.49** | 45.14 | 62.10 |
|       | Bleu     | 87.50 | 90.83 | 89.13 |       | 87.01 | **93.06** | 89.93 |
|       | Ours     | **95.59** | 92.17 | 93.85 |       | 95.76 | 88.89 | **92.20** |
| n-to-m| GC       | 63.20 | 55.63 | 59.18 |       | 29.80 | 42.45 | 35.01 |
|       | MS       | 88.79 | 72.54 | 79.84 |       | 75.00 | 2.16  | 4.20  |
|       | Bleu     | 79.82 | 61.27 | 69.32 |       | 44.34 | 33.81 | 38.37 |
|       | Ours     | **89.55** | **84.51** | **86.96** |       | **75.49** | **55.40** | **63.90** |

Table 1: Precision, recall, and F1 scores of manually aligned sentence pairs. In n-to-m case, \( \max(n, m) > 1 \), \( n, m \neq 0 \). GC: Gale-Church (Gale and Church, 1993); MS: Microsoft Aligner (Moore, 2002); Bleu: Bleualign (Sennrich and Volk, 2010); Ours: the proposed method with \( \alpha = 1, \gamma = 1 \).

---

\(^3\) We implement the model on the open-source toolkit THUMT (Zhang et al., 2017b)

\(^4\) [http://www.chinapubmed.net/](http://www.chinapubmed.net/)
detection, truecasing, and Chinese word segmentation. 5

4.2 Quality of BWEs

We use the corpus of UpToDate and PubMed Abstract to trained BWEs, respectively, according to subsection 3.1. To test the quality of word similarity evaluated by BWEs, we retrieve all the medical terms in Xiangya Medical Dictionary and randomly selected 200 terms whose English and Chinese form appear in a pair of parallel documents and the difference of the relative position for both forms in the parallel documents is less than 0.1. For each selected Chinese term, we manually check if the most similar English term found by BWEs is correct. The top 1 and top 10 accuracy in cosine similarity is 66.8% and 86.0%. The 200 terms are divided into 4 quarters by word frequency in UpToDate (Figure 2). In addition, we found that the error mainly due to the inconsistency in the form of words and synonyms. For example, the most similar term in BWEs for “角膜 (cornea)” is “corneal”. Besides, the frequent terms (in the first quarter) are more likely to be common words whose meaning is diverse, which leads to low accuracy in this quarter.

4.3 Sentence Alignment Results

We compare the proposed method with three sentence alignment methods as mentioned: length-based method, Gale-Church (Gale and Church, 1993); word and length-based method, Microsoft Aligner (Moore, 2002); and translation-based method, Bleualign (Sennrich and Volk, 2010). We randomly select parallel documents in UpToDate and PubMed Abstract and manually aligned these documents as test sets. Figure 3 shows the details of the test set. The majority is 1-to-1 alignments, while the proportion of n-to-m alignments with min(n, m) ≥ 1, max(n, m) > 1 is not ignorable. During manual alignment, we also found

Table 3: In-domain and out-of-domain performance (BLEU) of NMT models. WMT18/None is the pre-trained model. "+" denotes the simple concatenation. WMT18 (small) is a subset of data in WMT18 with the same size as BioMed.
UpToDate data is better than PubMed Abstract in terms of translation quality. The precision, recall, and F1 scores are shown in Table 1. The evaluation metrics is calculated as:

\[
\text{precision} = \frac{\#(\text{correct extracted alignments})}{\#(\text{all extracted alignments})},
\]

\[
\text{recall} = \frac{\#(\text{correct extracted alignments})}{\#(\text{all manual alignments})},
\]

\[
F_1 = \frac{\text{precision} \times \text{recall}}{\text{precision} + \text{recall}}.
\]

For 1-to-1 alignment, our method and Microsoft Aligner are better, and our method achieves the best performance in n-to-m case for both data. After duplication elimination and cleaning, we finally extracted over 1.4 million sentence pairs (Table 2) by applying the proposed method.

4.4 NMT Model Results

We establish our biomedical domain corpus by merging the resulting 1.4 million sentence pairs from subsection 4.3 and the existing parallel corpus, ECCParaCorp, and bilingual terms extracted from a medical dictionary. ECCParaCorp is a Chinese-English parallel corpus in cancer information consisting of 412 pairs of words, 1083 pairs of phrases, and 5190 pairs of sentences. We extracted 59532 pairs of terms in a medical dictionary. The in-domain test set consists of the manually aligned sentence pairs (subsection 4.3) and 500 sentence pairs from ECCParaCorp. Thus, the in-domain training data is the remaining sentence pairs (denotes as BioMed).

We pre-trained the transformer model with over 24 million Chinese-English sentence pairs from WMT18 for 200,000 steps. Then, the base model was fine-tuned on in-domain training data for 40,000 steps. A model trained on in-domain training data and a model fine-tuned on a mixed corpus consisting of in-domain and out-of-domain (WMT18) data was used to explore the effect of pre-training and the in-domain and out-of-domain performance of models (Table 3). Pre-training is necessary since the model benefits in both directions by increasing 1.98 BLEU score for zh-en and 1.87 for en-zh. The model fine-tuned on in-domain data significantly improves in-domain translation quality (zh-en: +17.72 BLEU; en-zh: +17.02 BLEU), while fine-tuning decreases the quality of out-of-domain translation (zh-en: -9.93 BLEU; en-zh: -11.12 BLEU). As shown in Kocmi et al., 2017, simple concatenation of out-of-domain and in-domain data can be harmful for in-domain translation. A slight decrease is observed in both in-domain while the out-of-domain translate quality improved significantly when the model was fine-tuned in the mixture of in-domain and out-of-domain corpus (Table 3).

We found that even when the domain was limited to biomedicine, the different styles between sub-domains were not negligible. To probe this phenomenon, we compare the performance of en-zh models trained with different approaches on a small cancer corpus, ECCParaCorp (Table 4). The ECCParaCorp covers information in cancer prevention, cancer screening, and cancer treatment, but the UpToDate is a comprehensive clinical database. There are stylistic differences between the two corpora. Although the model fine-tuning on UpToDate training data outperform the pre-trained model, it was still far inferior to the model fine-tuning on ECCParaCorp training set. Moreover, compared to the model fine-tuned on ECCParaCorp, the model fine-tuned on UpToDate firstly significantly improve translation quality by 10.78 BLEU score, suggesting that a well-trained model in biomedical domain contribute to training a better model in a sub-domain with a small sub-domain parallel corpus. Besides, the model fine-tunes for single sub-domain (Table 4, Figure 4) and tested in corresponding sub-domain data gains higher BLEU score than for several sub-domains (Table 3).
We investigated the relationship between model performance and the size of sentence pairs use in fine-tuning. The linear growth of BLEU score requires approximately exponential growth of the size of fine-tuning data (Figure 4). Moreover, Figure 4 indicates that adding n-to-m sentence pairs improves the model performance consistently under the same number of parallel documents, even though their quality is not as good as 1-to-1 sentence pairs.

To illustrate the effect of fine-tuning on in-domain data, we analyze two examples showing that the model learned biomedical terms and fitted the in-domain text style after fine-tuning. Table 5 is an example in the zh-en direction. The source sentence contains medical terms such as “盐皮质激素”, “螺内酯”, “依普利酮”, “罗格列酮”, and “利尿剂”. In our fine-tuned model, these terms were correctly translated as “mineralocorticoid”, “spironolactone”, “eplerenone”, “rosiglitazone”, and “loop diuretic”, whereas the pre-trained model generated wrong translate. The common word “给予” is usually translated to “give”, while “administration” is more appropriate in medical domain when it means “the act of giving a drug to somebody”. Similar situations occurred in Table 6. Model learned the translation of “thiazolidinediones” after fine-tuning, and translate the term to “噻唑烷二酮类药物” correctly despite decoding different sub-word than the target sentence. As for the style of in-domain text, the word “retention” is better translated to the medical term “潴留” instead of the common word “滞留”. In-domain fine-tuning helps the model learn more terminology and fits the in-domain style in the phase of decoding.

In-domain sentence pairs do not cover all biomedical terms, a dictionary may alleviate the problem. In Table 7, “Aegyptianellosis”, “eperythrozoonosis”, “grahamelliosis” and “haemobartonellosis” never appear in sentence pairs in training data, but the last three terms appear as bilingual entries in training set. The Fine-tuning model correctly translates “grahamelliosis” and “haemobartonellosis” to “格雷汉体病” and “血巴尔通体病”, but wrongly translates the new term “Aegyptianellosis” and the term in corpus, “eperythrozoonosis”. Simply concatenating the in-domain dictionary and other in-domain data is potentially useful for NMT model but not very reliable.

| Source | Target |
|--------|--------|
| Administration of a mineralocorticoid receptor antagonist, such as spironolactone or eplerenone, is part of the standard medical regimen of many patients with HF and in a study of diabetic patients without HF who were treated with rosiglitazone, spironolactone produced more fluid removal than a loop diuretic [69]. | We investigate the effect of fine tuning data (Figure 4). Moreover, Figure 4 indicates that adding n-to-m sentence pairs improves the model performance consistently under the same number of parallel documents, even though their quality is not as good as 1-to-1 sentence pairs. |
| WMT18/BioMed | The administration of a mineralocorticoid receptor antagonist (eg, spironolactone or eplerenone) is part of the standard medical regimen for many patients with HF, and in a study of patients with diabetes mellitus without HF who were treated with rosiglitazone, spironolactone provided greater fluid removal than a loop diuretic [69]. Saline corticosteroid receptor antagonists were given as part of the standard internal therapy programme for many HF patients, a study of non-HF diabetic patients treated with rosiglitazone showed that LNE can remove liquids to a greater extent than cyclic diuretics. |
| WMT18/None | |

| Pre-train/Fine-tune | ECCParaCorp test set |
|---------------------|----------------------|
| None/ECC            | 7.13                 |
| WMT18/None          | 11.76                |
| WMT18/UpToDate       | 17.30                |
| WMT18/ECCParaCorp   | 34.90                |
| WMT18/UpToDate(first)+ECCParaCorp(later) | 45.68 |

Table 5: Fine-tuning model learns more terminology and fits the in-domain style in zh-en. The green words are the correct translation, the red words are wrong, and blue word shows the in-domain style of text.

Table 7: “Aegyptianellosis”, “eperythrozoonosis”, “grahamelliosis” and “haemobartonellosis” never appear in sentence pairs in training data, but the last three terms appear as bilingual entries in training set. The Fine-tuning model correctly translates “grahamelliosis” and “haemobartonellosis” to “格雷汉体病” and “血巴尔通体病”, but wrongly translates the new term “Aegyptianellosis” and the term in corpus, “eperythrozoonosis”. Simply concatenating the in-domain dictionary and other in-domain data is potentially useful for NMT model but not very reliable.
5 Conclusions

In this paper, we proposed a new unsupervised sentence alignment method that utilizes the bilingual word alignment information to evaluate word similarity and further evaluate sentence distance to alignment sentence in a linear programming way. The proposed method relaxes the assumption about the types of alignment and has better performance on n-to-m alignment. We used all obtained data to build the Chinese-English biomedical translation system. Pre-training NMT model in general domain, a larger amount of in-domain data, and n-to-m sentence pairs benefit the biomedical NMT model. In-domain fine-tuning improve quality of terms translation and helps NMT model fits the in-domain style in the phase of decoding. There are significant differences between the different sub-domains, while based on a well-trained in-domain model, a small amount of data, such as 6000 sentence pairs, is enough to improve the performance of NMT model in that sub-domain.

References

Adafre, S. F., & De Rijke, M. (2006). Finding similar sentences across multiple languages in Wikipedia. Proceedings of the Workshop on NEW TEXT Wikis and Blogs and Other Dynamic Text Sources.

Artetxe, M., Labaka, G., & Agirre, E. (2017). Learning bilingual word embeddings with (almost) no bilingual data. Proceedings of the 55th Annual Meeting of the Association for Computational Linguistics (Volume 1: Long Papers), 451–462.

Artetxe, M., Labaka, G., Agirre, E., & Cho, K. (2018). Unsupervised Neural Machine Translation. International Conference on Learning Representations.

Bahdanau, D., Cho, K., & Bengio, Y. (2014). Neural machine translation by jointly learning to align and translate. ArXiv Preprint ArXiv:1409.0473.

Brown, P. F., & Mercer, R. L. (1993). The mathematics of statistical machine translation: Parameter estimation. Computational Linguistics, 19(2), 263–311.

Brown, P. F., Della Pietra, V. J., & Mercer, R. L. (1993). The mathematics of statistical machine translation: Parameter estimation. Computational Linguistics, 19(2), 263–311.

Brown, P. F., Della Pietra, S. A., Della Pietra, V. J., & Mercer, R. L. (1993). The mathematics of statistical machine translation: Parameter estimation. Computational Linguistics, 19(2), 263–311.

Chiang, D. (2007). Hierarchical phrase-based translation. Computational Linguistics, 33(2), 201–228.

Cho, K., Van Merriënboer, B., Bahdanau, D., & Bengio, Y. (2014). On the properties of neural machine translation: Encoder-decoder approaches. ArXiv Preprint ArXiv:1409.1259.

Chu, C., & Dahre, R. (2018). Multilingual and multi-domain adaptation for neural machine translation. Proceedings of the 24st Annual Meeting of the Association for Natural Language Processing (NLP 2018), 909–912.

Czarnowska, P., Ruder, S., Grave, E., Cotterell, R., & Copestake, A. (2019a). Don’t Forget the Long Tail! A Comprehensive Analysis of Morphological Generalization in Bilingual Lexicon Induction. ArXiv Preprint ArXiv:1909.02855.

Czarnowska, P., Ruder, S., Grave, É., Cotterell, R., & Copestake, A. (2019b). Don’t Forget the Long Tail! A Comprehensive Analysis of Morphological Generalization in Bilingual Lexicon Induction. Proceedings of the 2019
Ma, H., Yang, F., Ren, J., Li, N., Dai, M., Wang, X., Liu, B., & Huang, L. (2020). Handbook of COVID-19 prevention and treatment. The First Affiliated Hospital, Zhejiang University School of Medicine. Compiled According to Clinical Experience, 68.

Liang, T. (2020). Handbook of COVID-19 prevention and treatment. The First Affiliated Hospital, Zhejiang University School of Medicine. Compiled According to Clinical Experience, 68.

Lample, G., Conneau, A., Ranzato, M., Denoyer, L., & Jé gou, H. (2018). Word translation without back translation. University of Southern California MARINA DEL REY INFORMATION SCIENCES INST.

Laurich, V., Restrepo, A. M. H., Preziosi, M.-P., & Swaminathan, S. (2020). Data sharing for novel coronavirus (COVID-19). Bulletin of the World Health Organization, 98(3), 150.

Névéol, A., Yepes, A. J., Neves, L., & Verspoor, K. (2018). Parallel corpora for the biomedical domain. International Conference on Language Resources and Evaluation.

Névéol, A., Yepes, A. J., Neves, M., & Verspoor, K. (2019). Parallel corpora for the biomedical domain. LREC 2018 - 11th International Conference on Language Resources and Evaluation, 286–291.

Sennrich, R., & Volk, M. (2010). MT-based sentence alignment for OCR-generated parallel texts. ArXiv:1309.4168.

Stahlberg, F. (2020). Neural machine translation: A review. Journal of Artificial Intelligence Research, 69, 343–418.

Tian, L., Wong, D. F., Chao, L. S., Quaresma, P., Oliveira, F., & Yi, L. (2014). UM-Paradigm: A Large English-Chinese Parallel Corpus for Statistical Machine Translation. LREC, 1837–1842.

Varghese, T., Halácsy, P., Kornai, A., Nagy, V., Németh, L., & Trón, V. (2007). Parallel corpora for medium density languages. Amsterdam Studies In The Theory And History Of Linguistic Science Series 4, 292, 247.

Vulic, I., & Moens, M.-F. (2015). Bilingual word embeddings from non-parallel document-
aligned data applied to bilingual lexicon induction. Proceedings of the 53rd Annual Meeting of the Association for Computational Linguistics (ACL 2015), 2, 719–725.

Wu, Y., Schuster, M., Chen, Z., Le, Q. V, Norouzi, M., Macherey, W., Krikun, M., Cao, Y., Gao, Q., & Macherey, K. (2016). Google’s neural machine translation system: Bridging the gap between human and machine translation. ArXiv Preprint ArXiv:1609.08144.

Zeng, J., Su, J., Wen, H., Liu, Y., Xie, J., Yin, Y., & Zhao, J. (2018). Multi-domain neural machine translation with word-level domain context discrimination. Proceedings of the 2018 Conference on Empirical Methods in Natural Language Processing, 447–457.

Zhang, J., Ding, Y., Shen, S., Cheng, Y., Sun, M., Luan, H., & Liu, Y. (2017). Thumt: An open source toolkit for neural machine translation. ArXiv Preprint ArXiv:1706.06415.

Zhang, M., Liu, Y., Luan, H., Liu, Y., & Sun, M. (2016). Inducing bilingual lexica from non-parallel data with earth mover’s distance regularization. Proceedings of COLING 2016, the 26th International Conference on Computational Linguistics: Technical Papers, 3188–3198.

Zhang, M., Liu, Y., Luan, H., & Sun, M. (2017). Earth mover’s distance minimization for unsupervised bilingual lexicon induction. Proceedings of the 2017 Conference on Empirical Methods in Natural Language Processing, 1934–1945.

Zhang, M., Liu, Y., Luan, H., Sun, M., Izuha, T., & Hao, J. (2016). Building Earth Mover’s Distance on bilingual word embeddings for machine translation. Proceedings of the Thirtieth AAAI Conference on Artificial Intelligence, 2870–2876.

Ziemski, M., Junczys-Dowmunt, M., & Pouliquen, B. (2016). The united nations parallel corpus v1. 0. Proceedings of the Tenth International Conference on Language Resources and Evaluation (LREC’16), 3530–3534.