Combining Multiple Alignments to Improve Machine Translation

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Abstract

Word alignment is a critical component of machine translation systems. Various methods for word alignment have been proposed, and different models can produce significantly different outputs. To exploit the advantages of different models, we propose three ways to combine multiple alignments for machine translation: (1) *alignment selection*, a novel method to select an alignment with the least expected loss from multiple alignments within the minimum Bayes risk framework; (2) *alignment refinement*, an improved algorithm to refine multiple alignments into a new alignment that favors the consensus of various models; (3) *alignment compaction*, a compact representation that encodes all alignments generated by different methods (including (1) and (2) above) using a novel calculation of link probabilities. Experiments show that our approach not only improves the alignment quality, but also significantly improves translation performance by up to 1.96 BLEU points over single best alignments, and 1.28 points over merging rules extracted from multiple alignments individually.

KEYWORDS: alignment combination, minimum Bayes risk, alignment refinement, weighted alignment matrix.

Alignments	GIZA++	Berkeley	Vigne
GIZA++	–	70.29%	75.17%
Berkeley	70.29%	–	73.25%
Vigne	75.17%	73.25%	–

Table 1: Agreement of alignment links between different alignment models. Here we use three different alignment models: GIZA++ (Och and Ney, 2003), the unsupervised Berkeley aligner (Liang et al., 2006), and a discriminative aligner Vigne (Liu et al., 2010).

1 Introduction

Word alignment is a preliminary step for statistical machine translation (SMT). Most SMT systems, not only phrase-based models (Och and Ney, 2004; Koehn et al., 2003; Chiang, 2005; Xiong et al., 2006), but also syntax-based models (Galley et al., 2006; Shen et al., 2008; Liu et al., 2006; Huang et al., 2006), rely heavily on word-aligned bilingual corpora.

Various methods for word alignment, including generative methods (Brown et al., 1993; Vogel et al., 1996; Liang et al., 2006) and discriminative methods (Moore et al., 2006; Taskar et al., 2005; Blunsom and Cohn, 2006; Liu et al., 2010), have been proposed in the literature. Different models produce significantly different alignments. [1] Table 1 shows the *agreement* between each pair of alignments on 1.5M Chinese-English parallel sentence pairs. Here *agreement* is computed by using one alignment model's output as a gold standard to evaluate the other alignment model's output in terms of F1 score (Xiao et al., 2010). The higher the agreement score is, the more similar two alignments are. Table 1 shows that the agreement scores are always below 76%.

Therefore, it is natural to combine multiple alignments to improve both alignment quality and translation quality. In this paper, we propose three ways to exploit multiple alignments for machine translation: alignment selection, refinement and compaction. Alignment selection chooses high quality alignments while refinement generates new and more reliable alignments. Alignment compaction encodes multiple possible alignments. We show that these methods work well together: alignment refinement e.g. offers high quality alignment choices, that can be exploited by alignment compaction.

2 Related Work

Our research builds on previous work in the field of minimum Bayes risk (MBR) decision, system combination and model compaction. MBR decision aims to find the candidate hypothesis that has the least expected loss under a probability model when the true reference is not known (Brickel and Doksum, 1977). Diverse loss functions have been described by using different evaluation criteria for loss calculation, e.g. edit distance and sentence-level BLEU in SMT (Kumar and Byrne, 2004; Tromble et al., 2008; González-Rubio et al., 2011). In our work, we select an alignment within the MBR framework using a number of loss functions at both alignment and phrase levels.

System combination, the process which integrates fragment outputs from multiple systems, has produced substantial improvements in many natural language processing tasks, including parsing (Henderson and Brill, 1999; Sagae and Lavie, 2006; Fossum and Knight, 2009), word segmentation (Sun and Wan, 2012) and machine translation (Rosti et al., 2007; He et al.,

[1] These alignments have equivalent qualities compared to a true gold standard (see in Table 2).

2008; Feng et al., 2009), just to name a few. Alignment combination has also been explored previously (Och and Ney, 2003; Koehn et al., 2003; Ayan et al., 2005; DeNero and Macherey, 2011). We draw inspiration from (Och and Ney, 2003; Koehn et al., 2003) but our technique differs from previous work in that (1) they require exactly two bidirectional alignments while our approach can use an arbitrary number of alignments; (2) we take into account the occurrences of potential links, which turns out to be important.

Previous research has demonstrated that compact representations can produce improved results by offering more alternatives, e.g. using forests over 1-best trees (Mi and Huang, 2008; Tu et al., 2010), word lattices over 1-best segmentations (Dyer et al., 2008), and weighted alignment matrices (WAMs) over 1-best alignments (Liu et al., 2009; Tu et al., 2011). Instead of using k-best alignments from the same model, as in (Liu et al., 2009; Tu et al., 2011), here we construct WAMs from multiple alignments generated by different models (including MBR-based and refined models). As the alignment probabilities are generally incomparable between different alignment models, we propose a novel calculation of link probabilities in WAMs.

3 Approach

3.1 Alignment Selection

Alignment selection refers to selecting one alignment from multiple alignments using minimum Bayes risk. If the reference alignment a was known, we could measure each alignment a_i using the loss function $\mathscr{L}(a_i, a)$. In the MBR framework, although the true reference alignment is unknown, we assume that the individual alignment models' output forms a reasonable distribution over possible reference alignments. The MBR decision aims to find the candidate alignment that has the least expected loss under the distribution (Brickel and Doksum, 1977).

3.1.1 MBR Decision

MBR decision has the following form:

$$\hat{a} = \arg\min_{a_i \in A} \mathscr{R}(a_i) = \arg\min_{a_i \in A} \sum_{a_j \in A} \mathscr{L}(a_i, a_j) \cdot p(a_j|f, e) \tag{1}$$

where $\mathscr{R}(a_i)$ denotes the Bayes risk of candidate alignment a_i under loss function $\mathscr{L}$, A indicates the set of alignments generated by different models. In general, for different alignment models, the probabilities $p(a|f, e)$ are not directly comparable. For simplicity, in our work below we assume that they are in fact comparable and have the same value. [2]

3.1.2 Loss Functions

The loss function $\mathscr{L}(a_i, a_j)$ is used to measure the quality of alignments. Here we introduce a set of metrics for the evaluation of alignments at both alignment and phrase levels.

AER

Alignment error rate (Och and Ney, 2003) has been used as the official evaluation criterion in most alignment shared tasks (Liu et al., 2009). AER scores are given by:

$$AER(S, P, A) = 1 - (|A \cap S| + |A \cap P|)/(|A| + |S|) \tag{2}$$

[2] Alignment probabilities can be set empirically based on (expected overall) performance (Fossum and Knight, 2009), or uniformly without any bias (Xiao et al., 2010; Duan et al., 2010). We tried a few other settings and found them to be less effective.

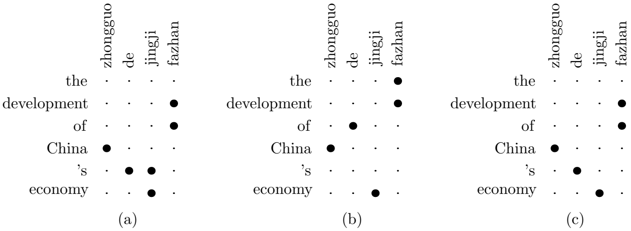


Figure 1: (a) Alignment of a sentence pair generated by GIZA++ (a_1), (b) alignment of the same sentence by Berkeley aligner (a_2), (c) another alignment by Vigne (a_3).

where S and P are sets of sure and possible links in a hand-aligned reference alignment respectively, and A is a candidate alignment. Note that S is a subset of P: $S \subseteq P$. As there is no reference alignment that is hand-aligned by human experts in our work, we cannot distinguish sure links from possible links. Therefore, we regard all links to be sure links: $S = P$. With this, the AER score is calculated by:

$$AER(a_i, a_j) = 1 - (2 \times |a_i \cap a_j|)/(|a_i| + |a_j|) \tag{3}$$

CPER

Although widely used, AER is criticized for correlating poorly with translation performance (Ayan and Dorr, 2006; Fraser and Marcu, 2007). Therefore, Ayan and Dorr (2006) have proposed *constituent phrase error rate* (CPER) for evaluating word alignments at the phrase level instead of the alignment level. CPER can be computed as:

$$CPER(a_i, a_j) = 1 - (2 \times |P_{a_i} \cap P_{a_j}|)/(|P_{a_i}| + |P_{a_j}|) \tag{4}$$

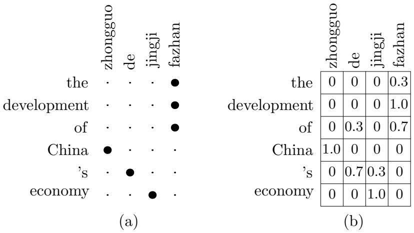
where P_a denotes the set of phrases that are consistent with a given alignment a. Compared with AER, CPER penalizes dissimilar alignment links more heavily. As a dissimilar link reduces the number of intersected links of two alignments by 1 in AER, it might lead to more than one different phrase pair added to or removed from the set of phrases (Ayan and Dorr, 2006).

CHER

As CPER evaluates word alignments in the context of phrase-based MT, we propose a similar metric called *constituent hierarchical-phrase error rate* (CHER) for hierarchical-phrase models. The difference between them is that we use H_a instead of P_a, where H_a denotes the hierarchical phrases extracted. Hierarchical phrases are more sensitive to word alignments because they are sensitive to inside (i.e. subtracted) phrases.

3.2 Alignment Refinement

Alignment refinement refers to extracting parts of multiple alignments and constructing a new alignment instead of selecting the best one from existing alignments. A simple way to refine multiple alignments is to employ their intersection or union. However, using intersection will result in a high-precision but low-recall alignment, while using union will result in a high-recall but low-precision alignment. Koehn et al. (2003) show performance improvements by finding a balance between the intersection and union with the *grow-diag-final* algorithm.



	zhongguo	de	jingji	fazhan
the	·	·	·	●
development	·	·	·	●
of	·	·	·	●
China	●	·	·	·
’s	·	●	·	·
economy	·	·	●	·

(a)

	zhongguo	de	jingji	fazhan
the	0	0	0	0.3
development	0	0	0	1.0
of	0	0.3	0	0.7
China	1.0	0	0	0
’s	0	0.7	0.3	0
economy	0	0	1.0	0

(b)

Figure 2: (a) The refined alignment generated from multiple alignments in Figure 1, (b) the resulting weighted alignment matrix that samples the same alignments, where the number in the cells are the probabilities of the corresponding link.

Unfortunately, this algorithm cannot be applied to our approach. This is because the *grow-diag-final* algorithm requires exactly two bidirectional alignments, while we would use more than two alignments. Therefore, we propose a variation of the *grow-diag-final* algorithm named *grow-diag-final-rank* adapted for multiple alignments. The difference between the two algorithms is that we take into account the occurrences of *conflicting links*. Conflicting links refer to triples <l_i, l_j, l_k>, in which l_i and l_j are the links that share the same source side, and l_j and l_k share the same target side. For example, the triple < (*de*, *’s*), (*de*, *of*), (*fazhan*, *of*)> is conflicting because the first two share the same source side while the latter two share the same target side.

Alignment refinement chooses the links with the most occurrences when there are conflicting links. Intuitively, our approach is motivated by the following observation: the links that occur more often in different alignments frequently have a higher confidence than those that occur less often. Our algorithm favors the links that occur frequently. As an example, consider the conflicting links < (*de*, *’s*), (*de*, *of*), (*fazhan*, *of*)>: without considering the number of their occurrences, we would retain the first two links if we run grow-diag-final greedily. In contrast, considering that the links (*de*, *’s*) and (*fazhan*, *of*) occur twice while (*de*, *of*) only occurs once, we prefer to retain (*de*, *’s*) and (*fazhan*, *of*). Figure 2(a) shows the refined alignment generated from the three alignments in Figure 1 using the *grow-diag-final-rank* algorithm.

3.3 Alignment Compaction

Given the original alignments and the alignments generated by alignment refinement, it is quite natural to try to encode them in a compact representation. In this paper, we use weighted alignment matrices for this purpose. A weighted alignment matrix (Liu et al., 2009) is a matrix to encode the probabilities of k-best alignments of the same sentence pair. Each element in the matrix stores a link probability which is estimated from a k-best list.

$$p_m(j,i) = \frac{\sum_{k=1}^{K} p(a_k|f,e) \cdot \delta(a_k,j,i)}{\sum_{k=1}^{K} p(a_k|f,e)} \tag{5}$$

where

$$\delta(a_k,j,i) = \begin{cases} 1 & (j,i) \in a_k \\ 0 & \text{otherwise} \end{cases} \tag{6}$$

Here $a_k \in \mathscr{K}$ is a k-best list, $p(a_k|f,e)$ is the probability of an alignment a_k in the k-best list. Intuitively, a higher link probability $p_m(j,i)$ indicates high agreement between different alignments, thereby high quality.

(Liu et al., 2009; Tu et al., 2011) have shown that WAMs yield encouraging results by making good use of k-best alignments from a single alignment model. Unlike in this previous work, in our approach we construct WAMs from alignments generated by different models (including MBR-based and refined models). In a k-best list, each alignment is weighted using their probabilities since they are obtained from the same model, and a higher weight denotes that the alignment model has higher confidence in the output. In contrast, the alignments in our work are generated by different models and their probabilities are generally incomparable. As noted above, we assume that all the alignments have the same probabilities. Then, we obtain:

$$p_m(j,i) = \frac{\sum_{k=1}^{N} \delta(a_k, j, i)}{N} \tag{7}$$

Figure 2(b) shows the WAM that captures the three alignments in Figure 1.[3]

We then follow (Tu et al., 2011) to extract hierarchical phrases from WAM and calculate their translation and lexical probabilities. Instead of extracting phrase pairs that respect the word alignment, Tu et al. (2011) enumerate all potential phrase pairs and calculate their fractional counts. As they soften the alignment consistency constraint, there exists a massive number of phrase pairs extracted from the training corpus. To maintain a reasonable phrase table size, they discard any phrase pair that has a fractional count lower than a threshold t. For further details, see (Tu et al., 2011).

4 Experiments

4.1 Setup

We carry out our experiments using a reimplementation of the hierarchical phrase-based system (Chiang, 2005) on the NIST Chinese-English translation tasks. Our training data contains 1.5M sentence pairs from LDC dataset.[4] We train a 4-gram language model on the Xinhua portion of the GIGAWORD corpus using the SRI Language Toolkit (Stolcke, 2002) with modified Kneser-Ney Smoothing (Kneser and Ney, 1995). We use minimum error rate training (Och, 2003) to optimize the feature weights on the MT02 testset, and test on the MT03/04/05 testsets. For evaluation, case-insensitive NIST BLEU (Papineni et al., 2002) is used to measure translation performance.

Three alignment models are chosen for our experiments with default settings: GIZA++ (Och and Ney, 2003), the unsupervised Berkeley aligner (Liang et al., 2006), and the linear modeling alignment Vigne (Liu et al., 2010). We use the three baseline alignments to select MBR alignments and to generate a refined alignment. We use all three baseline alignments, as well as all of the MBR and refined alignments in the WAM-based compaction approach. When extracting rules from WAM, we follow (Tu et al., 2011) to set the pruning threshold t=0.5.

[3] In practice, alignment compaction encodes both baseline alignments and the new alignments in Section 3.1 and 3.2.

[4] The corpus includes LDC2002E18, LDC2003E07, LDC2003E14, Hansards portion of LDC2004T07, LDC2004T08 and LDC2005T06.

Alignments	AER	BAER	CPER	CHER
GIZA++	22.50	27.92	24.11	33.23
Berkeley	21.11	26.41	23.35	34.44
Vigne	19.13	24.05	23.54	34.02
Selection$_{AER}$	**17.93**	**23.29**	22.10	31.47
Selection$_{CPER}$	18.32	23.72	**21.53**	30.56
Selection$_{CHER}$	18.52	23.93	21.68	30.84
Refinement	18.79	24.43	**21.50**	**30.31**

Table 2: Evaluation of alignment quality. Here "Selection$_{\mathscr{L}}$" indicates the alignment selected from multiple single alignments using MBR decision under the loss function $\mathscr{L}$ (e.g. AER, CPER and CHER). For all metrics, the lower the score is, the better the alignment quality is.

4.2 Evaluation of Alignment Quality

In this section, we investigate the quality of different alignments on the Chinese-English language pair data. We annotated 1007 sentences with annotations that distinguish between sure and possible links.[5] We used 502 sentences as the tuning set, and 505 sentences as the test set. We run GIZA++ and the Berkeley aligner on the training corpus as well as the test set. We tune the feature weights of Vigne on the tuning set using AER as the optimization criterion. We evaluate alignments in terms of AER, CPER and CHER as described in Section 3.1.2. Inspired by Fraser and Marcu (2007), we also employ a new metric called **balanced AER** (BAER) that considers only the sure links in the reference alignments:

$$BAER(S,A) = 1 - (2 \times |A \cap S|)/(|A| + |S|) \tag{8}$$

For all metrics, lower score indicates better alignment quality.

Table 2 lists the alignment quality results for different alignment strategies. We find that both selection and refinement methods outperform single alignments at all metrics, indicating that our methods improve the quality of alignment in a certain way. One finding is that the selection method usually achieves the best score at the metric it uses as loss function. For example, the selection method using AER as loss function outperforms other alignments at the AER and BAER metrics while underperforming at other metrics. This is intuitive, since the method always selects the alignment with the minimum expected loss under the metric.

4.3 Evaluation of Translation Quality

Table 3 summaries the results of translation performance with different alignment methods.

- **Baseline results**. We have three baseline systems: GIZA++, Berkeley and Vigne. The results show that GIZA++ achieves the best performance among the baseline systems. Therefore, we compare our methods with GIZA++ system in the following analysis.
- **Rule Merging**. Different alignments generally result in very different sets of hierarchical rules. As one would expect, merging them outperforms using any of them individually through enlarging the rule coverage. Experimental results show that merging rules indeed outperforms using single best alignments, at the cost of a much larger rule table.

[5] available at http://nlp.ict.ac.cn/~tuzhaopeng/.

Alignments	Links	Rules	DEV	MT03	MT04	MT05	Avg.
GIZA++	45.4M	143M	35.07	33.11	35.06	32.98	33.72
Berkeley	33.7M	270M	34.72	32.64	34.93	32.58	33.38
Vigne	35.6M	140M	34.64	33.16	34.29	32.45	33.30
Rule Merging	–	553M	35.55	34.12**	35.88**	33.66*	34.55
Inter	24.5M	178M	34.10	32.35	34.17	32.47	33.00
Union	55.6M	94M	34.83	33.42	35.04	33.05	33.84
Selection$_{AER}$	37.9M	175M	35.35	33.65**	35.82**	33.56*	34.34
Selection$_{CPER}$	38.9M	187M	35.36	34.21**	36.05**	33.71**	34.66
Selection$_{CHER}$	39.1M	182M	35.71	34.16**	35.88**	33.94**	34.66
Refinement	45.5M	210M	35.44	33.81**	35.98**	33.95**	34.58
Compaction	55.6M	319M	**36.64**	**35.01****	**36.81****	**34.94****	**35.59**

Table 3: Evaluation of translation quality. "Links" denotes the number of links in the alignment and "Rules" denotes the number of rules (Chiang, 2005) extracted from the corresponding alignment. "Avg." is the average BLEU score on the three test sets. Significance tests are done against GIZA++ on test sets following the *sign-test* approach (Collins et al., 2005), and "**" and "*" denote p-value less than 0.01 and 0.05, respectively. Furthermore, Compaction is significantly better than Rule Merging for p-value less than 0.01 on all test sets.

- **Alignment Selection**. Concerning selection methods, the results show that using loss functions at phrase level (i.e. CPER and CHER) outperforms loss function at alignment level (i.e AER). One possible reason is that CPER and CHER relate more tightly to the translation performance, because they care about the phrases which are used directly in machine translation. In brief, using selection methods with different loss functions improves translation performance in BLEU score by up to 0.92 points on average.

- **Alignment Refinement**. Table 3 shows that simply using the intersection (Inter) or union (Union) does not achieve any improvement. This is in accord with intuition, because intersection discards many useful links while union includes many incorrect links. By contrast, alignment refinement finds a good balance between them, and achieves significant improvement in BLEU score ranging from 0.70 to 0.97 points.

- **Alignment Compaction**. Alignment compaction encodes all alignments and achieves the best result, which improves BLEU scores by between 1.75 and 1.96 points. Compared with rule merging, alignment combination produces substantial improvements in both translation performance and rule table size.

5 Conclusion

In this paper, we have presented three simple and effective methods to make use of multiple alignments. First, we select the alignments with minimum Bayes risk using different loss functions at both alignment and phrase levels. Then, we refine multiple alignments using an improved *grow-diag-final-rank* algorithm that considers the occurrences of alignment links. Finally, we use a compact representation named weighted alignment matrix to represent all alignments (including MBR-based and refined alignments) and propose a novel calculation of link probabilities. Experimental results show that our method not only improves the alignment quality, but also significantly improves translation performance over both single best alignments and merging rules extracted from different single alignments individually.

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