An Alignment-based Approach to Text Segmentation Similarity Scoring

Anonymous EMNLP submission

Abstract

Text segmentation is a natural language processing task with popular applications, such as topic segmentation, element discourse extraction, and sentence tokenization. Much work has been done to develop accurate segmentation similarity metrics, but even the most advanced metrics used today, B, and WindowDiff, exhibit incorrect behavior due to their evaluation of boundaries in isolation. In this paper, we present a new segment-alignment based approach to segmentation similarity scoring and a new similarity metric A. We show that A does not exhibit the erratic behavior of B and WindowDiff, quantify the likelihood of B and WindowDiff misbehaving through simulation, and discuss the versatility of alignment-based approaches for segmentation similarity scoring. We make our implementation of A publicly available in the hope that it will encourage the community to explore more sophisticated approaches for text segmentation similarity scoring.

1 Introduction

Text segmentation is a natural language processing (NLP) task that consists of dividing a sequence of text elements into segments.

Let $T = e_1, e_2, e_3...e_n$ be a sequence of text elements (e.g. words, sentences, paragraphs, etc...). A segmentation S of T is given by a binary string $Q = [0|1]^{n-1}$ that encodes boundaries between the elements of T. The ith character of Q codifies the presence of a boundary (1) or lack thereof (0) between e_i and e_{i+1} in S. S contains $m - 1$ boundaries and partitions T into m segments[1].

Measuring similarity between segmentations is not simple. The most straightforward approach is to frame a segmentation as a series of decisions made at every *potential boundary position* (PBP), which exist between every pair of elements in T, and to calculate the average PBP agreement, but this does not match human intuition well.

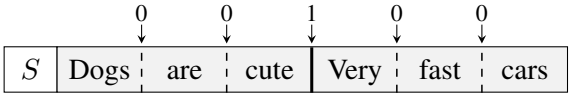


Figure 1: Example segmentation with $Q = 00100$.

Consider how S in Figure 1 compares with $h1$ and $h2$ in Figure 2: h_1 agrees with S in 4 out of 5 positions (one missing boundary), while h_2 agrees with S in only 3 out of 5 positions (one missing and one "extra" boundary). Yet it is easy to agree that h_2 is actually closer to S, as it has simply "shifted" the boundary in S one unit to the right.

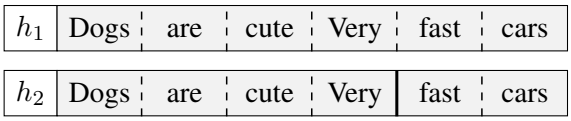


Figure 2: Alternate segmentations to S from Figure 1.

To address this, researchers have proposed a variety of similarity metrics that distinguish "soft" and "hard" errors (shifted versus missing/extra boundaries). However, existing metrics look at boundary errors in isolation; they do not consider the impact that errors have on segments around them.

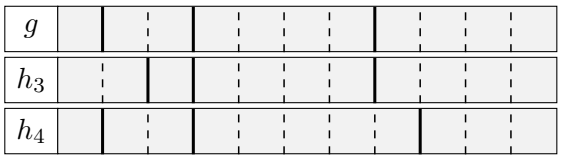


Figure 3: Three similar segmentations.

Consider how hypothesis segmentations h_3 and h_4 compare to a reference segmentation r in Figure 3. Both have a boundary that is shifted one PBP to the right, which results in an"extra" element in the segment to the left of the PBP and a missing

[1]This definition corresponds to *single-type* segmentation. A *multi-type* version also exists where different boundary types are considered, enabling the encoding of different types of segments and even hierarchical relations between them.

element in the segment to the right. However, the resulting segment distortion is not the same. In h_3, only $1/2$ of the elements in the the first segment are correct, while $1/2$ of the reference elements are missing from the second segment; in h_4, the third segment has $4/5$ correct elements, and the fourth segment has $1/4$ missing elements. It is easy to argue then that h_4 is closer to r than h_3, but current metrics are unable to distinguish between them.

We propose a new similarity metric based on segment alignment, which scores segmentations based on how well their *segments* match, rather than their boundaries (Section 3). We show that our metric aligns more closely with human intuition than existing metrics (Section 4) and quantify the errors encountered by those metrics (Section 5).

2 Existing Metrics

Current segmentation similarity metrics fall into two categories: **window-based** metrics try to capture errors by sliding a window across the element sequence T and comparing the boundaries in both segmentations; in contrast, **edit-based** metrics try to find a sequence of boundary edit operations that would make both segmentations equal.

2.1 Window-Based Metrics

WindowDiff (Pevzner and Hearst, 2002) and P_k (Beeferman et al., 1999) are the most popular similarity metrics currently used.

$\mathbf{P_k}$ is defined as "the probability that a random pair of elements, k elements apart, will be classified inconsistently by two segmentations as belonging/not belonging in the same segment." Given an element sequence T of length n, a reference segmentation r, and an alternate segmentation h, a window of size $k+1$ is slid across the elements(k is recommended to be half the average segment size in r); at every window position, the segmentations are compared based on the elements at the edges of the window, e_i and e_{i+k}; if the segmentations disagree on whether the elements belong in the same segment, a penalty of 1 is added; finally, the penalty sum is divided by the number of windows:

$$P_k(r,h) = \frac{1}{n-k} \sum_{i=1,j=i+k}^{i=n-k} \delta(r_{i,j}) \neq \delta(h_{i,j})$$

where $\delta(x_{i,j})$ is true iff e_i, e_j are in the same segment in segmentation x.

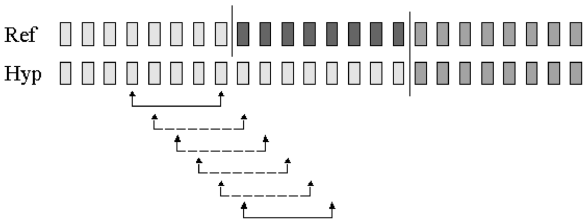


Figure 4: Illustration of P_k and WindowDiff with $k = 4$ (Pevzner and Hearst, 2002). Penalized windows indicated by dashed lines.

There are a variety of situations where P_k penalizes errors inconsistently (Pevzner and Hearst, 2002): it penalizes missing boundaries more than extra boundaries, fails to penalize extra boundaries that are in close proximity to correct boundaries, and is also quite sensitive to the window size k.

WindowDiff improves on P_k by using a different penalty criteria. Instead of comparing the elements at the window edges, WindowDiff counts the number of boundaries contained within the window and assigns a penalty of 1 if the number is inconsistent between segmentations:

$$\mathrm{WD}(r,h) = \frac{1}{n-k} \sum_{i=1,j=i+k}^{i=n-k} b(r_{i,j}) \neq b(h_{i,j})$$

where $b(x_{i,j})$ is the boundary count between e_i and e_j in segmentation x.

WindowDiff solves some of P_k's inconsistency problems, but still produces unintuitive scores and penalizes errors at the edges of the element sequence less than those towards the middle (a weakness shared with P_k). WindowDiff is usually reported along with P_k rather than instead of it.

Lamprier et al. (2007) present a simple correction to WindowDiff: adding $k-1$ extra elements at the beginning and end of the sequence T ensures that errors at every PBP are penalized an equal number of times. Further, they argue that WindowDiff is unfair because the expected score of a random segmenter depends on the number of boundaries in the reference r. To address this, they present two normalized versions of WindowDiff, **NWin** and **TNWin**, which take into account the expected WindowDiff scores of two random segmentations with the same cardinality as the reference and hypothesis segmentations being evaluated.

Finally, Scaiano and Inkpen (2012) propose **WinPR**, which uses the element padding correction from (Lamprier et al., 2007) and categorizes the

errors at each window into true positives (correct boundaries), false positives (extra boundaries), true negatives (correct empty PBPs), and false negatives (missing boundaries), allowing for finer-grained error analysis and the calculation of F1 scores.

Although WinPR is an improvement on WindowDiff, it has not been widely adopted by the community and, like NWin, depends on the correctness of WindowDiff. Thus, throughout the rest of this paper, we will limit our discussion of window-based metrics to WindowDiff and P_k.

2.2 Edit-Based Metrics

Edit-based segmentation similarity metrics are based on ideas introduced by Damerau-Levenshtein string edit distance (Damerau, 1964; Levenshtein, 1966) and partially replicated by Generalized Hamming Distance (Bookstein et al., 2002). The general idea is that every segmentation can be framed as a sequence of boundaries, each placed at a specific position. If we define a set of edit operations (with costs) that can modify any sequence of boundaries, the distance between two segmentations can be measured as the cost of the optimal sequence of edit operations required to make the two segmentations equal. The optimal sequence of edit operations is equivalent to a boundary alignment between the segmentations.

Segmentation Similarity (Fournier and Inkpen, 2012) and Boundary Similarity (Fournier and Inkpen, 2012) are both based on the same set of boundary edit operations:

- Match: Mark a boundary as correct (no cost).
- Addition/Deletion: Insert or delete a boundary.
- K-Transposition: Shift a boundary to the left or right by a max of k units[2]. Default $k = 1$[3].
- Substitution: Replace a boundary with one of a different type[4].

Segmentation Similarity (S) (Fournier and Inkpen, 2012) assigns a constant cost to all edit operations and normalizes the resulting distance based on the total number of possible boundaries for the given element sequence. The idea behind this normalization is to scale the cost based on the potential complexity of the segmentation in question; the intuition is that a constant cost is less impactful on a longer/more complex sequence than it is on a shorter/simpler one.

[2]If a boundary can not be transposed, it must be deleted and a new boundary must be inserted at the new location.

[3]When $k > 1$, Segmentation Similarity and Boundary Similarity allow transpositions across existing boundaries.

[4]Only required for multi-type segmentation.

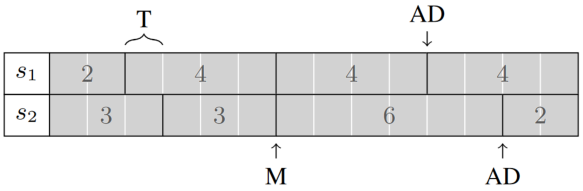


Figure 5: Example segmentation alignment with boundary edit operations (Fournier, 2013).

Let A_e, T_e S_e be the sets of the optimal boundary addition/deletion, transposition, and substitution operations required to align a pair of segmentations, h_1 and h_2, over a sequence of elements T. Further, let b be the number of boundary types (in the case of multi-type segmentation) available.

$$S(h_1, h_2, T) = 1 - \frac{|A_e| + |T_e| + |S_e|}{b(|T| - 1)}$$

Fournier and Inkpen show that S a) produces scores that align favorably with human judgment compared to WindowDiff in three key examples, b) has reduced sensitivity to variations in segment sizes compared to WindowDiff, and c) produces more accurate inter-annotator agreement scores than WindowDiff in one dataset. It is also noted that S can be used for multi-type segmentation, where traditional window-based methods can not.

Boundary Similarity (B) (Fournier, 2013) improves S by introducing weighted-costs transpositions/substitutions, improving the edit distance normalization factor, and producing a confusion matrix from the edit operations to calculate F1 scores.

$$B(h_1, h_2, T) = 1 - \frac{|A_e| + t(T_e, k) + s(S_e, B_t)}{|A_e| + |T_e| + |S_e| + |M|}$$

where k is the maximum transposition distance, $|M|$ is the number of matching boundary pairs between the two segmentations, B_t is the set of boundary types, and t and s are functions that return the weighted sums of T_e (transpositions) and S_e (substitutions). The normalization factor in B produces behavior that aligns more closely with human judgement than in S.

When comparing the scores generated by WindowDiff, P_k, S, and B on a handful of key examples, Fournier argues that B produces behavior that is more correct. B is further shown on one dataset to produce more reliable inter-annotator agreement

scores when compared to S, which over-estimates, and also to overcome WindowDiff's bias towards segmentations with few or tightly-clustered boundaries when evaluating three segmenters.

As we will demonstrate Section 4, however, B (and WindowDiff) disregards the impact of individual mistakes on the surrounding segments, which leads to scores that do not align well with human judgement in key scenarios.

3 An Alignment-Based Approach to Segmentation Similarity Scoring

In Section 1, Figure 2, we presented an example that showcased the importance of weighing boundary differences in terms of the impact they have on their corresponding segments. None of the current metrics attempt to do this, and they can not be easily modified to do so.

We propose to measure similarity between a pair of segmentations by comparing the segments defined in them. The intuition is straightforward: two segmentations are similar iff the segments defined by them are similar. Inspired by alignments from machine translation and string comparison, our approach measures segmentation similarity by *finding the maximum likelihood segment alignment and scoring its correctness*.

The concept of the most likely alignment is based on two key observations. First, it only makes sense to align overlapping segments. Second, the overlap between two segments is a good indicator for their "closeness", which tells us if they should be aligned. Thus, the maximum likelihood alignment (MLA) is one where every segment is aligned to its closest other segment.

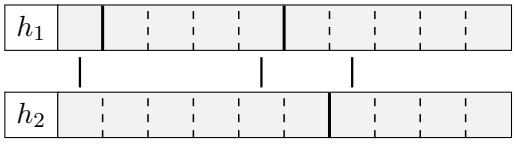


Figure 6: Sample maximum likelihood alignment.

Consider the example alignment in Figure 6: h_2 has fuzzily merged the first two segments in h_1 into a single segment, which results in the third segment from h_1 having a slightly shifted boundary in h_2. Here, it does not make sense to align the third segment in h_1 with the first segment in s_h; even if they overlap, the third segment in s_h overlaps mainly with the second segment in s_h.

The MLA can be found greedily in $O(m_1 + m_2)$ time, where m_1 and m_2 are the number of segments in h_1 and h_2, respectively. We only need to find the closest segment for any given segment. Figure 7 shows pseudocode for generating the MLA[5].

```
MLA(h1,h2,fn: c):
  for each segment p in h1:
   for each segment q in h2, overlapping p:
      closeness = c(p,q)
    r = segment in h2 with max c(p,r)
    align p (source) to r (target)
  repeat for h2
  return list of alignment edges
```

Figure 7: Maximum likelihood alignment algorithm.

The MLA depends on the closeness function c. For a generic alignment, where all elements in the element sequence are considered equal, we recommend a simple intersect ratio function i between two segments, x and y:

$$i(x, y) = \frac{\text{intersect}(x, y)}{|x|}$$

The MLA explains the differences between a pair of segmentations in terms of boundaries: in Figure 8, missing/extra boundaries are indicated by the existence of segments with more than one aligned segment. The first segment in h_3 is aligned to two segments in h_4 because h_4 contains an extra boundary; similarly, the third segment in h_4 is aligned to two segments in h_3 because the third segment in h_4 is missing a boundary present in h_3. Furthermore, the existence of pairs of aligned segments with no alignments to any other segments are indicators of matches or transpositions, such as the last segments in h_3 and h_4.

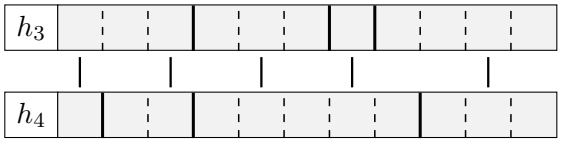


Figure 8: Maximum likelihood alignment.

Once the MLA has been generated, a function should be chosen to map the MLA to a similarity score. A simple approach is to assign a weight to every alignment edge, using a function g, and

[5]This version is not strictly $O(m_1 + m_2)$ but is presented for brevity.

normalize by the number of edges in the MLA. This generic similarity score A is defined as

$$A(h_1, h_2, c, g) = \frac{\sum_{\text{edge} \in \text{MLA}(h_1,h_2,c)} g(\text{edge})}{\text{\# edges in MLA}(h_1, h_2, c)}$$

A variety of edge weighting functions can be used: clustering similarity functions such as the rand index, or set similarity metrics such as the overlap coefficient, the Sørensen–Dice coefficient, or the Jaccard index[6]. Both symmetric and asymmetric weighting functions can be used, as the edges generated by the MLA function are directed; we recommend the Jaccard index, since it guarantees a symmetrical segmentation similarity score. Further, the Jaccard version of A can be easily modified to distinguish between "soft" and "hard" mistakes by penalizing edges with weights under some threshold t. The Jaccard index, $J \in [0, 1]$, between two sets S and T is defined as

$$J(S, T) = \frac{|\text{intersect}(S, T)|}{|\text{union}(S, T)|}$$

The MLA approach with similarity score function A compares favorably to WindowDiff, B, and similar metrics in terms of error analysis, as the MLA structure and edge weights provide information about segmentation differences in terms of both boundaries and segments.

Further, the separation between the MLA algorithm and the similarity score function A makes our approach quite versatile, as the MLA may instead be scored with a different, task-specific similarity scoring function. Consider the reference segmentation r and candidate segmentations h_1 and h_2 in Figure 9: h_1 and h_2 produce the same score under A with Jaccard (0.58), B, and WindowDiff. However, for a task like topic segmentation, h_2 may be preferred, as it contains "meta" topics that consistently match two topics each in r, whereas h_1 contains two correct topics, but one really bad third topic, which is a mixture of four topics in r. Conversely, for a task like sentence segmentation, h_1 may be preferred, as it correctly identifies two sentences, where h_2 contains only incorrect sentences. The MLA could be used in conjunction with a similarity scoring function that imposes exponentially increasing penalties on segments with many alignments to favor h_2, while a scoring function that considers only the highest weighted edge for any given segment would favor h_1.

[6]Different weight functions for each reference segment type could be used to score multi-type segmentations.

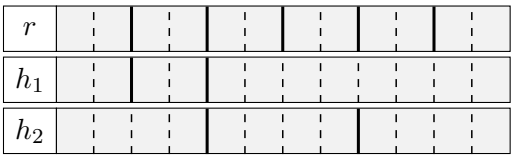


Figure 9: Reference segmentation and two candidates.

Finally, as we show in the following section, a straightforward implementation of A using the intersect ratio i as the closeness function and the Jaccard index J as the edge weight function behaves favorably compared to current metrics in a key set of examples, as it takes into account the impact of boundary differences on surrounding segments.

4 Similarity Metric Behavior

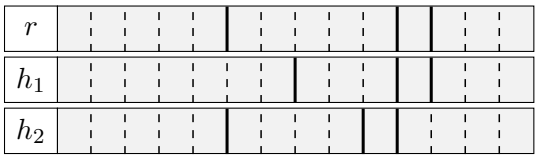
In this section, we outline three erratic behaviors from B and WindowDiff, and compare these metrics against A in a series of example segmentations.

4.1 Cross-Boundary Transpositions

Since B and WindowDiff look at each boundary in isolation, they consider all boundary shifts with the same distance to be equally bad, resulting in a *pseudo-transposition*, where one boundary crosses over another, being penalized the same as a standard transposition. It is easy to argue against this, as a boundary shift that crosses another boundary is not a true transposition, but rather a pair of over- and under-segmentations. This is illustrated in Figure 10, where h_1 is clearly closer to the reference segmentation r than is h_2. h_1 transposes the leftmost boundary of r two units to the right, while h_2 pseudo-transposes the rightmost boundary two units to the left, crossing over the middle boundary. h_2 results in an oversegmentation of the second segment and undersegmentation of the third and fourth segments of r. A correctly identifies this behavior because it works on segment alignments; B and WindowDiff, however, incorrectly score h_1 and h_2 as being equally close to r.

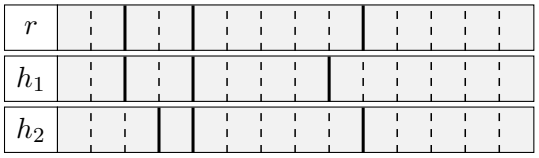
4.2 Constant Cost Transpositions

B and WindowDiff measure the cost of a transposition based on its absolute distance, without considering the impact it has on the surrounding segments. This quickly leads to problematic behavior, as any given pair of segmentations that contain transpositions with the same distance will get the same score (assuming all other boundary operations are the same). Figure 11 illustrates this prob-



Pair	A	B (k=1)	$1-$WD (k=2)
(r, h_1)	0.83	0.50	0.67
(r, h_2)	0.60	0.50	0.67

Figure 10: Cross-boundary pseudo-transposition.



Pair	A	B (k=1)	$1-$WD (k=2)
(r, h_1)	0.91	0.83	0.83
(r, h_2)	0.79	0.83	0.83

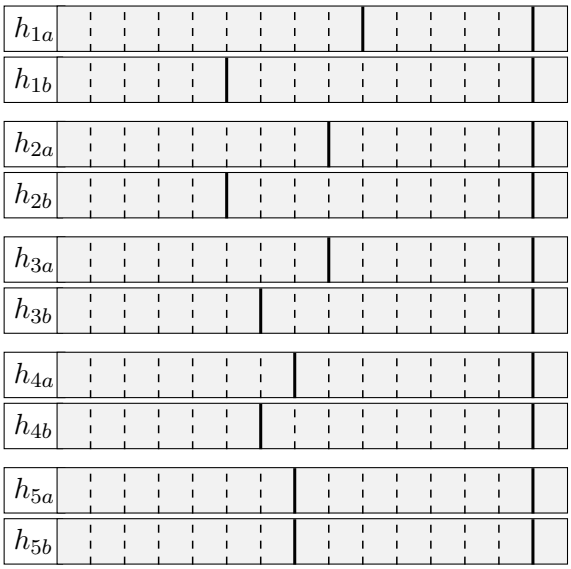
Figure 11: Constant cost transpositions.

lem: B and WindowDiff scores both segmentations equally, even though the impact of the transposed boundaries is not the same. Both h_1 and h_2 transpose a boundary by one unit, but in h_1 this results in a single extra/missing token in segments originally of size five, while in h_2, the extra/missing token affects segments originally of size two, impacting them more significantly. A produces proper behavior here, weighing the distance of the transposition in relation to the corresponding segment sizes.

4.3 Vanishing Transpositions

Unlike A, the sensitivity of B and WindowDiff to "near-misses" (transpositions) is regulated by constants. B defines a maximum transposition distance, while WindowDiff utilizes a fixed window size. This causes problematic behavior, as boundary shifts beyond the maximum transposition distance for each metric look the same, which is compounded with the disregard for segment sizes mentioned in the previous subsection.

The five segmentation pairs in Figure 12 illustrate this behavior. Although the pairs are ordered by increasing similarity, B and WindowDiff score three out of five pairs equally using their default maximum transposition distance values of 1. The behavior of B is particularly concerning, as it jumps from a relatively high score of 0.75 for the fourth pair, to a very low score of 0.33 for the third pair. In contrast, A correctly matches the first



Pair	A	B (k=1)	$1-$WD (k=2)
(h_{1a}, h_{1b})	0.70	0.33	0.69
(h_{2a}, h_{2b})	0.76	0.33	0.69
(h_{3a}, h_{3b})	0.83	0.33	0.69
(h_{4a}, h_{4b})	0.91	0.75	0.85
(h_{5a}, h_{5b})	1	1	1

Figure 12: Vanishing Transpositions

segments and second segments in each pair and considers the relative impact of the transposition given the size of the segments involved.

5 Error Quantification

We quantify the likelihood of WindowDiff and B behaving erroneously through simulation[7]. For the three main error types described in Section 4, we first instantiate every possible reference segmentation r for sequences of length $n \in [3, 20]$. We then try to find two alternate segmentations h_1 and h_2 that B or WindowDiff score as equally similar to r, but in fact are not. Finally, for both B and WindowDiff, we present the ratio of reference segmentations r of length n for which such error-producing pairs h_1 and h_2 exist.

To simplify our analysis, we use the Lamprier-corrected version of WindowDiff (Lamprier et al., 2007), which pads the beginning and end of the sequence with $k-1$ elements. The number of errors produced by this version is a lower bound on the number of errors produced by the original WindowDiff, which penalizes boundary mismatches at

[7]We use the implementation of B from the segeval Python 3 package (Fournier, 2013) and WindowDiff from the Python 3 NLTK package (Bird et al., 2009).

the edges less than those at the center.

5.1 Cross-Boundary Transpositions

We consider B and WindowDiff to behave erroneously if a pair of segmentations h_1 and h_2 are judged equally similar to r, where h_2 pseudo-transposes a boundary by x units, crossing an existing boundary from r, and h_1 performs a standard transposition of a boundary, also by x units. For fairness, we only consider h_1 where the two segments on either side of the transposed boundary have Jaccard > 0.5 with the corresponding original segments from r, i.e. the transposition can reasonably be considered a "soft" mistake where the affected segments are still more similar to the originals than not, in contrast to the pseudo-transposition in h_2, where, by crossing a boundary, h_2 effectively oversegments one reference segment and undersegments another (Figure 10).

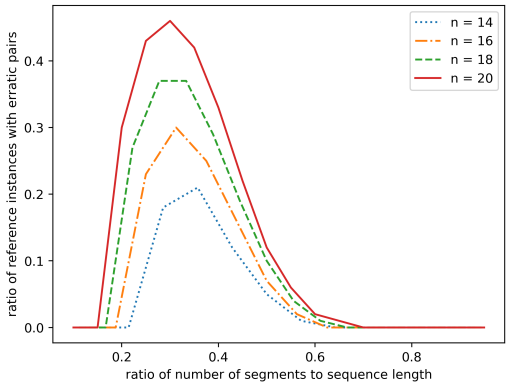


Figure 13: Ratio of potential cross-transposition errors for B and WindowDiff.

Figure 13 shows the percentage of the reference segmentation space for which such erroneous pairs h_1 and h_2 exist, for both B and WindowDiff with various sequence lengths n. Varying the number of segmentations m for a given n, we notice an interesting trend: when the number of segmentations is too low or too high, it is impossible to construct erroneous pairs. For example, it is impossible for $m = 2$ because there is no other boundary to transpose across; similarly, when the m approaches n, segments become unit-sized, and can no longer be involved either pseudo- or standard transpositions.

5.2 Vanishing Transpositions

Here, B and WindowDiff behave erroneously if a pair of segmentations h_1 and h_2 are judged equally similar to r, where h_1 transposes a boundary by x units and h_2 transposes the same boundary by $x + 1$ units. Again, we only consider "soft" transpositions, where the two segments on either side of the transposed boundary have Jaccard > 0.5 with the corresponding original segments from r.

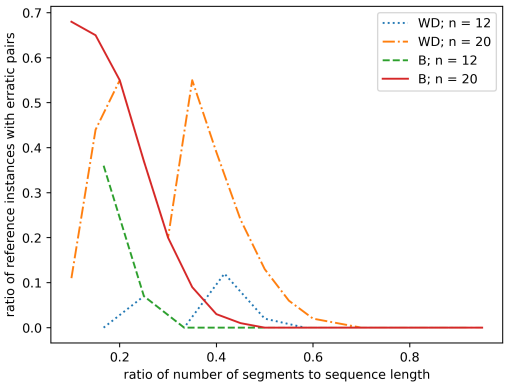


Figure 14: Ratio of potential vanishing transposition errors for B and WindowDiff.

Figure 14 differs from Figures 13 and 15 in that WindowDiff and B behave differently. In fact, it is Figures 13 and 15 that are unusual; as we have seen in previous examples, B and WindowDiff often behave differently. In this case, WindowDiff calculates its window size and maximum transposition range based on the reference segmentation, while B has a fixed maximum transposition range of one unit by default. Thus, the maximum distance beyond which transpositions "vanish" varies for WindowDiff, but not for B.

5.3 Constant Cost Transpositions

Finally, B and WindowDiff behave erroneously if a pair of segmentations h_1 and h_2 are judged equally similar to r, where h_1 "soft" transposes a boundary by one unit, and h_2 "hard"transposes a different boundary by one unit, i.e. the segments on either side of the hard-transposed boundary have Jaccard < 0.5 with the corresponding original r segments.

The trend in Figure 15 is as follows: if the ratio between the number of segments m and the sequence length n is two low, the segments are so large that it is hard to find a pair of segments such that transposing their boundary results in a "hard" error; conversely, when the ratio is too high, all segments are small, and it is hard to find a pair such that transposing by one unit is still "soft."

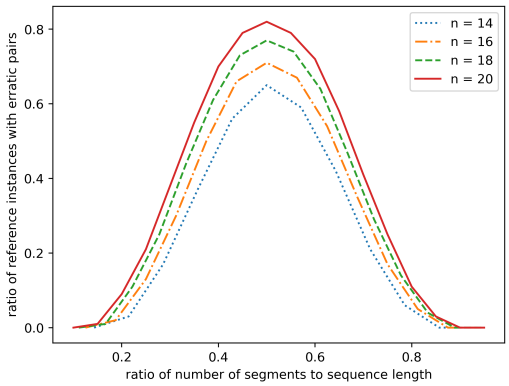
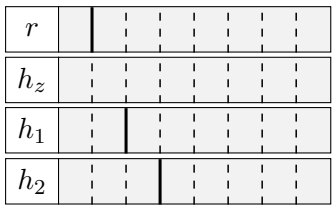


Figure 15: Ratio of potential "hard" transposition errors for B and WindowDiff.

6 Limitations

While we have seen that A performs favorably when compared to B and WindowDiff, more investigation may be warranted on the general MLA approach. First, the space of potential alignments for a given pair of segmentations can be quite large, and while a simple greedy intersection ratio approach generates sensible alignments, there may very well exist edge cases that exhibit undesirable behavior for specific applications.



Pair	A	B (k=1)	$1 - \text{WD}$ (k=2)
(r, h_0)	0.67	0.50	0.88
(r, h_1)	0.79	0.75	0.88
(r, h_2)	0.58	0.33	0.62

Figure 16: Intricate Behavior of A.

Consider Figure 16. h_0 deletes a boundary from r, while h_1 and h_2 transpose it different distances. However, A gives h_2 a worse score than h_0; this behavior is explained by the MLA between r and h_2 containing a diagonal alignment between the first segment in h_2 and the second segment in r, due to the first segment in r being very small — so small that transposing its boundary by two units is considered worse than deleting it. The intersect ratio closeness function in A uses segment size to distinguish "soft" and "hard" transpositions; as we saw in Figure 12, when the segments are longer, A will match the left and right segments of a two-unit transposition with the original segments in r, resulting in a similarity score greater than h_0.

However, it may be that application-specific requirements push in the direction of favoring of soft transpositions over deletions regardless of segment size, which would require a) a different segment-to-segment closeness function c, or b) maximizing some global MLA function, such as Maximum Spanning Tree or another graph algorithm.

Second, in Figure 9, we presented a reference segmentation r and two different candidate segmentations h_1 and h_2 that are scored equally by A, B, and WindowDiff. Here, the fact that A can not distinguish between them is not due to the MLA, as there is only one possible alignment between each candidate and r. Thus, it may be of interest to develop more sophisticated ways of scoring the MLA, rather than simply averaging utilizing Jaccard-weighted edges, in order to be able to distinguish between h_1 and h_2.

7 Conclusion

In this paper, we present a new alignment-based approach to text segmentation similarity scoring and present a new similarity metric A. We compare A with the most commonly used existing metrics in text segmentation, B and WindowDiff, and explain key scenarios where they do not produce correct behavior, unlike A. We comment on the potential versatility of alignment-based approaches when paired with different alignment-generating and alignment-scoring functions, and show that A, B, and WindowDiff exhibit intricate behaviors that should be carefully explored in the future. We make our implementation of A publicly available and hope that it encourages the NLP community to explore more sophisticated approaches for text segmentation similarity scoring.

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