GNAT: A General Narrative Alignment Tool

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Abstract

Algorithmic sequence alignment identifies similar segments shared between pairs of documents, and is fundamental to many NLP tasks. But it is difficult to recognize similarities between distant versions of narratives such as translations and retellings, particularly for summaries and abridgements which are much shorter than the original novels.

We develop a general approach to narrative alignment coupling the Smith-Waterman algorithm from bioinformatics with modern text similarity metrics. We show that the background of alignment scores fits a Gumbel distribution, enabling us to define rigorous p-values on the significance of any alignment. We apply and evaluate our general narrative alignment tool (GNAT) on four distinct problem domains differing greatly in both the relative and absolute length of documents, namely summary-to-book alignment, translated book alignment, short story alignment, and plagiarism detection—demonstrating the power and performance of our methods.

1 Introduction

Algorithmic sequence alignment is a fundamental task in string processing, which identifies similar text segments shared between a pair of documents. Sequence alignment is a common operation in many NLP tasks, with representative applications including identifying spelling (Darg̀is et al., 2018) and OCR (Yalniz and Manmatha, 2011) errors in documents, quantifying post-publication edits in news article titles (Guo et al., 2022), and plagiarism detection (Potthast et al., 2013). Text alignment has been used to create datasets for text summarization tasks (Chaudhury et al., 2019), by loosely aligning summary paragraphs to the chapters of original stories and documents. Textual criticism is the study of the transmission of text (Abbott and Williams, 2014), typically for religious and historically significant texts such as the Bible. The collation task in textual criticism examines textual variations across different versions of a text through alignment (Yousef and Janicke, 2020). Text alignment is often deployed in literary research, e.g., analyzing how books are adapted for young adults (Sulzer et al., 2018), translated (Bassnett, 2013), and how the gender of the translator affects the translated work (Leonardi, 2007).

However, sequence alignment in NLP research is largely done on an ad hoc basis, serving small parts of bigger projects by relying on hand-rolled tools. This is in contrast to the field of bioinformatics, where the alignment of nucleotide and protein sequences plays a foundational role. Popular tools such as BLAST (Altschul et al., 1990) running on large sequence databases are used to identify even distant homologies (similarites) with rigorous statistical measures of significance. Such tools facilitate meaningful analyses over vast differences in scale, from short gene-to-gene comparisons to full genome-to-genome alignment or gene-to-database searches.

The overarching goal of our work is to extend the rigorous sequence analysis techniques from bioinformatics to the world of narrative texts. Sequence alignment can be computed using the widely-used edit distance algorithm for Leveinshtein disance (Levenshtein et al., 1966), which aligns texts by computing the minimum number of deletions, insertions, substitutions, and/or transpositions. However, edit distance fails when applied to distant narrative texts that are semantically but not textually similar, since neither character nor word-level changes capture the semantic meaning of the text. Consider comparing two independent translations of a particular novel, or two different retellings of a classic fable. We anticipate very little in terms of long common text matches, even though the documents are semantically identical, and it is not obvious how to quantify the significance of whatever matches we do happen to find.

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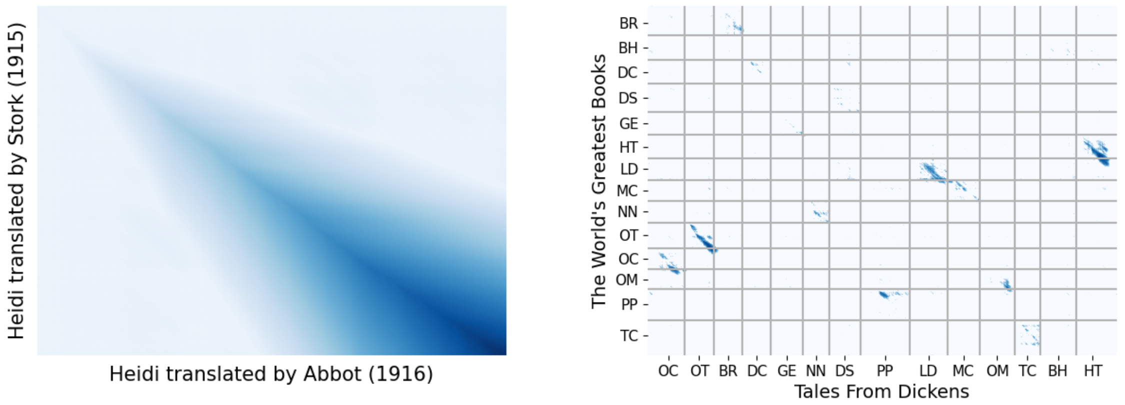

(a) Heidi Alignment by SW + SBERT

(b) Aligning versions of Dickens' tales by SW + SBERT

Figure 1: Heat maps representing Smith-Waterman alignments in two distinct narrative domains. On left, two different English translations of the novel *Heidi* are aligned: the bright main diagonal correctly indicates that they follow the same sequence of events. On right, two different story collections of abridged novels are aligned: the disjoint diagonal patterns correctly identify different versions of the same novels (represented using acronyms) shared across the collections.

Aligning large text documents is a difficult task, for reasons beyond measuring distance in semantic space versus simple text-based edits. Often the proper interpretation consists of multiple local alignments instead of one sequential global alignment. For instance, consider a document that plagiarizes disjoint parts of a second document in a different order. While local sequence alignments are successfully used in the bioinformatics domain to align genome and protein sequences (Smith et al., 1981), they have been underutilized in NLP. A second issue is scale mismatch: aligning a short book summary to an unabridged novel requires mapping single sentences to pages or even chapters of the larger text. A final concern is the statistical rigor of an alignment: every pair of completely unrelated texts has an optimal alignment, but how can we tell whether such an alignment exhibits meaningful measures of similarity?

Although text alignment is used in a NLP tasks across multiple domains, much of the existing work has been domain-specific or focused on global alignments. In this paper, we develop and evaluate a general purpose tool (GNAT) for the efficient and accurate alignment of pairs of distant texts. We propose a method for adapting the classical Smith-Waterman (SW) local alignment algorithm with affine gap penalties for NLP tasks by employing multiple textual similarity scoring functions and perform comparative analysis.

Our major contributions[1] [2] are as follows:

- *Local Alignment Methods for Narrative Texts* – We develop and evaluate sequence alignment methods for distant but semantically similar texts, and propose a general method for computing statistical significance of text alignments in any domain. Specifically, we demonstrate that alignment scores of unrelated pairs of narrative texts are well-modelled by a Gumbel distribution (Altschul and Gish, 1996). Fitting the parameters of this distribution provides a rigorous way to quantify the significance of putative alignments.

- *Distance Metrics for Narrative Alignment* – We propose and evaluate five distinct distance metrics for the alignment of narrative documents over a range of relative and absolute sizes. We demonstrate that neural similarity measures like SBERT generally outperform other metrics, although the simpler and more efficient Jaccard similarity measure proves surprisingly competitive on task like identifying related pairs of book translations (0.94 AUC vs. 0.99 AUC for SBERT). However, we show that Jaccard similarity loses sensitivity over larger (chapter-scale) text blocks.

[1] All codes and datasets are available at `https://github.com/tanzir5/alignment_tool2.0`

[2] An associated web interface can be found at `https://www.aligntext.com/`

The Dodger and Charley Bates had taken Oliver out for a walk, and after sauntering along, they suddenly pulled up short on Clerkenwell Green, at the sight of an old gentleman reading at a bookstall. So intent was he over his book that he might have been sitting in an easy chair in his study. To Oliver's horror, the Dodger plunged his hand into the gentleman's pocket, drew out a handkerchief, and handed it to Bates. Then both boys ran away round the corner at full speed. Oliver, frightened at what he had seen, ran off, too; the old gentleman, at the same moment missing his handkerchief, and seeing Oliver scudding off, concluded he was the thief, and gave chase, still holding his book in his hand. The cry of "Stop thief!" was raised. Oliver was knocked down, captured, and taken to the police-station by a constable. The magistrate was still sitting, and Oliver would have been convicted there and then but for the arrival of the bookseller.	You can imagine Oliver's horror when he saw him thrust his hand into the old gentleman's pocket, draw out a silk handkerchief and run off at full speed. In an instant Oliver understood the mystery of the handkerchiefs, the watches, the purses and the curious game he had learned at Fagin's. He knew then that the Artful Dodger was a pickpocket. He was so frightened that for a minute he lost his wits and ran off as fast as he could go. Just then the old gentleman found his handkerchief was gone and, seeing Oliver running away, shouted "Stop thief!" which frightened the poor boy even more and made him run all the faster. Everybody joined the chase, and before he had gone far a burly fellow overtook Oliver and knocked him down. A policeman was at hand and he was dragged, more dead than alive, to the police court, followed by the angry old gentleman.

Table 1: Excerpts from two distinct abridgements of *Oliver Twist*. The highlighted areas indicate pairs of segments aligned by our text alignment tool.

- *Performance Across Four Distinct Application Domains* –To prove the general applicability of GNAT, we evaluate it in four application scenarios with text of varying absolute and relative sizes:
  - *Summary-to-book alignment:* Our alignment methods successfully match the summary with the correct book from the set of candidates with 90.6% accuracy.
  - *Translated book alignment:* We have constructed a dataset of 36 foreign language books represented in Project Gutenberg by two independent, full-length translations into English. Our alignment methods achieve an AUC score of 0.99 in distinguishing duplicate book pairings from background pairs.
  - *Plagiarism detection:* Experiments on the PAN-13 dataset (Potthast et al., 2013) demonstrate the effectiveness of our alignment methods on a vastly different domain outside our primary area of interest. Our F_1 score of 0.85 on the summary obfuscation task substantially outperforms that of the top three teams in the associated competition (0.35, 0.46, and 0.61, respectively).
  - *Short story alignment:* We conduct experiments on a manually annotated dataset of 150 pairs of related short stories (Aesop's fables), aligning sentences of independently written versions of the same underlying tale. Sentence-level Smith-Waterman alignments using SBERT ($F_1 = 0.67$) substanially outperform baselines of sequential alignments and a generative one-shot learner model (0.40 and 0.46, respectively).

This paper is organized as follows. Section 2 provides an overview of related works on sequence alignments in NLP and bioinformatics. Section 3 formally defines the problem of text alignment and presents our alignment method with the different metrics for scoring textual similarities. Section 4 details our method for computing the statistical significance of text alignments. We describe our experimental results in Section 5 before concluding with future directions for research in Section 6.

2 Related Work

The literature on sequence alignment algorithms and applications is vast. Here we limit our discussion to representative applications in NLP and bioinformatics, and prior work on measuring the statistical significance of alignments.

2.1 Algorithmic Sequence Alignment

Dynamic programming (DP) is a powerful technique widely used in sequence alignment tasks, closely associated with dynamic time warping (DTW) (Müller, 2007). Everingham et al. (2006) and Park et al. (2010) used DTW to align script dialogues with subtitles. Thai et al. (2022) used the Needleman-Wunstch DP algorithm with an embedding-based similarity measure to create pairwise global alignments of English translations of the same foreign language book. Apart from DP, Naim et al. (2013) uses weighted A^* search for aligning multiple real-time caption sequences.

2.2 Representative NLP Applications

Statistical Machine Translation (MT) (Lopez, 2008) and neural MT models (Bahdanau et al., 2014) learn to compute word alignments using large corpora of parallel texts. However, these models are limited to word-level alignment and face computational inefficiencies for longer texts (Udupa and Maji, 2006). Multiple works (Mota et al., 2016, 2019; Sun et al., 2007; Jeong and Titov, 2010) have proposed joint segmentation and alignment can create better text segmentations via aligning segments sharing the same topic and having lexical cohesion. Paun (2021) uses Doc2Vec embeddings for alignment and creates monolingual parallel corpus.

By using text alignment tools to automate the alignment process, researchers can streamline their analyses and uncover new insights in a more efficient manner. For example, Janicki et al. (2022) performs large scale text alignment to find similar verses from ∼90,000 old Finnic poems by using clustering algorithms based on cosine similarity of character bigram vectors. Janicki (2022) uses embeddings of texts and proposes optimizations for simpler modified versions of the DP-based Needleman-Wunstch algorithm.

Pial et al. (2023) extends the methods proposed for GNAT for book-to-film script alignment and do analysis on the scriptwriter's book-to-film adaptation process from multiple perspectives such as faithfulness to original source, gender representation, importance of dialogues.

Foltỳnek et al. (2019) categorizes the extrinsic plagiarism detection approach as aligning text between a pair of suspicious and source document. Potthast et al. (2013) notes that many plagiarism detection algorithms employ the seed-and-extend paradigm where a seed position is first found using heuristics and then extended in both directions. Plagiarism detection tools can align different types of text, including natural language document, source codes (Bowyer and Hall, 1999), and mathematical expressions (Meuschke et al., 2017).

2.3 Sequence Alignment in Bioinformatics

DNA and protein sequence alignment have been extensively used in bioinformatics to discover evolutionary differences between different species. Smith et al. (1981) modified the global Needleman-Wunstch algorithm (Needleman and Wunsch, 1970) to compute optimal local alignments and created the Smith-Waterman (SW) algorithm. In this paper, we use the SW algorithm as our choice of alignment method, but adapt it to the NLP domain.

These algorithms are quadratic in both time and space complexity. Hirschberg (1975) and Myers and Miller (1988) brought down the space complexity of these algorithms to linear. Nevertheless, pairwise alignment between a query sequence and a vast database remains a computationally intensive task. Altschul et al. (1990) proposed a faster but less accurate algorithm called BLAST for protein searches in database. We argue that with appropriate similarity metrics and modifications, these algorithms can be applied to narrative alignment.

2.4 Statistical Significance of Alignments

For ungapped nucleotide alignments where a single alignment must be contiguous without gaps, Karlin and Altschul (1990) proposed an important method for computing the statistical significance of an alignment score. The distribution of scores of ungapped alignments between unrelated protein or genome sequences follows an extreme-value type I distribution known as Gumbel distribution (Ortet and Bastien, 2010). For gapped alignments, no such analytical method is available but many empirical studies have demonstrated that the gapped alignment scores also follow an extreme value distribution (Altschul and Gish, 1996), (Pearson, 1998), (Ortet and Bastien, 2010). Altschul and Gish (1996) proposes a method to estimate the statistical significance of gapped alignment scores empirically. We adapt and empirically evaluate these methods for computing the statistical significance of narrative alignments.

3 Methods for Alignment

Text alignment involves matching two text sequences by aligning their smaller components, such as characters, words, sentences, paragraphs, or even larger segments like chapters. The best component size depends on the task and the user's intent. For example, aligning a summary with a book requires comparing sentences from the summary with paragraphs or chapters, while aligning two book translations requires comparing paragraphs, pages, or larger units.

Formally, we define text alignment as follows:

given text sequences $X = (x_0, x_1, ..., x_{m-1})$ and $Y = (y_0, y_1, ..., y_{n-1})$, we seek to identify a set of alignments where an alignment $a = \langle x_i, x_j, y_p, y_q \rangle$ indicates that the text segment x_i to x_j corresponds to the text segment y_p to y_q.

3.1 The Smith-Waterman (SW) Algorithm

Here we use the local alignment method proposed by Smith et al. (1981), defined by the recurrence relation $H(i, j)$ in Equation 1 that attempts to find the maximal local alignment ending at index i and index j of the two sequences.

$$H(i,j) = \max \begin{cases} H(i-1, j-1) + S(X_i, Y_j), \\ H(i-1, j) + g, \\ H(i, j-1) + g, \\ 0 \end{cases} \tag{1}$$

$S(a, b)$ is a function for scoring the similarity between components a and b and g is a linear gap penalty. However, we employ the more general affine gap penalty (Altschul, 1998) with different penalties for starting and extending a gap as the deletion of a narrative segment is often continuous, therefore extending an already started gap should be penalized less than introducing a new gap. The time complexity of the SW algorithm is $O(mn)$, where m and n are the lengths of the two sequences. We discuss how we obtain multiple local alignments based on the DP matrix created by SW in Apppendix A.

3.2 Similarity Scoring Functions

The key factor that distinguishes aligning text sequences from other types of sequences is how we define the similarity scoring function $S(a, b)$ in Equation 1. An ideal textual similarity function must capture semantic similarity. This section describes several similarity scoring functions as Section 5.2 evaluates their comparative performance.

SBERT Embeddings: Reimers and Gurevych (2019) proposed SBERT to create semantically meaningful text embeddings that can be compared using cosine similarity. SBERT creates embeddings of texts of length up to 512 tokens, which is roughly equivalent to 400 words (Gao et al., 2021). Usually this limit works for all sentences and majority of paragraphs. For texts longer than 400 words, we chunk the text into segments of 400 words and do a mean pooling to create the embedding following Sun et al. (2019). SBERT has previously been used in computing semantic overlap between summary and documents (Gao et al., 2020).

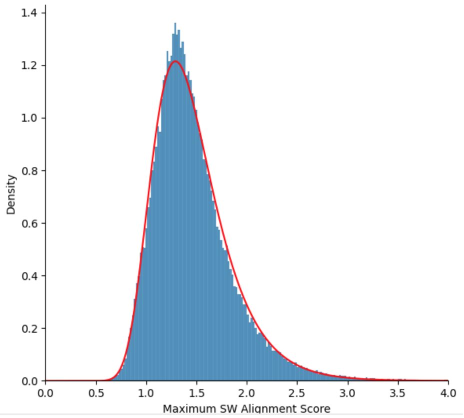

Figure 2: The distribution of maximum SW alignment scores from 2.5×10^5 pairs of unrelated books, where the red curve is the Gumbel distribution estimated from this data using maximum likelihood estimation (location $\mu = 1.29$, scale $\beta = 0.30$).

Jaccard: The Jaccard index treats text as a bag-of-words, and computes similarity using the multiset of words present in both text segments:

$$J(a, b) = \frac{a \cap b}{a \cup b} \tag{2}$$

Jaccard has the caveat that it is not suitable for computing similarity between two texts of different lengths. Diaz and Ouyang (2022) has used Jaccard index for text segmentation similarity scoring.

TF-IDF: The Term Frequency Inverse Document Frequency (TF-IDF) measures text similarity using the frequency of words weighted by the inverse of their presence in the texts, giving more weight to rare words. Here the set of documents is represented by the concatenated set of text segments from both sequences. Chaudhury et al. (2019) uses TF-IDF to align summaries to stories.

GloVe Mean Embedding: Following Arora et al. (2017), we represent a text by the average of GloVe (Pennington et al., 2014) embeddings of all the words in the text, and compute cosine similarity.

Hamming Distance: Given two text segments containing $n \geq m$ words, we decompose the longer text into chunks of size n/m. The Hamming distance $h(.,.)$ is the fraction of chunks where chunk i does not contain word i from the shorter text. We then use $1 - h(.,.)$ as the similarity score.

3.3 Unifying Similarity Scoring Functions

The diverse ranges and interpretations of similarity scores from different scoring functions make

	# of pairs	Total # of words	Avg. # of sentences per book/summary/fable	Avg. # of paragraphs per book/summary/fable	Human Annotation
RelBook	36	6.56 Million	4668	1953.7	×
Classics Stories	14	146.9K	271.1	114.5	×
(S)ummary(B)ook	464	542K (S)	61.5 (S)	11.6 (S)	×
	464	47.35 Million (B)	5166.1 (B)	1843 (B)	×
Fables	152	39K	7.1	-	✓

Table 2: Statistics of the datasets employed in this study. For the Fables dataset, alignments between sentence pairs are manually annotated.

it challenging to compare alignment results. To unify these metrics, we generate a distribution of similarity scores for a large set of unrelated text components. We then calculate the similarity score between two text components, x and y as follows:

$$S(x,y) = \sigma(Z(x,y)) - th_s) \times 2 - 1 \qquad (3)$$

where $\sigma(.)$ is the logistic sigmoid function, $Z(x,y)$ is the z-score of the similarity between x and y, and th_s is a threshold for a positive score. This conversion standardizes the range of values for all scoring functions to between -1 and 1. The th_s threshold ensures that pairs with a z-score less than th_s receive a negative similarity score, indicating a possible lack of relatedness. This aligns with the requirements proposed by Dayhoff et al. (1978) for PAM matrices, one of the most widely used similarity metrics for protein sequence alignments which require the expected similarity score of two random unrelated components be negative so only related components get a positive similarity score.

The threshold value th_s is crucial in distinguishing between similarity scores of semantically similar text pair from random text pair. We hypothesize similarity scores between unrelated text units follow a normal distribution. To determine th_s, we computed cosine similarities for 100M random paragraph pairs using SBERT embeddings. We use the fitted normal distribution ($\mu = 0.097, \sigma = 0.099$) presented in Figure 5 in the appendix to estimate the probability of chance similarity score X. We set a default minimum threshold of +3 z-score for SW alignment, resulting in a ∼0.0015% probability of positive score for unrelated paragraphs following the three-sigma rule (Pukelsheim, 1994).

4 Statistical Significance of Alignments

Determining the significance of a semantic text alignment is a critical aspect that is dependent on both the domain and the user's definition of significance. For instance, two essays on the same topic are expected to have more semantically similar text segments than two fictional books by different authors. We discuss how SW can produce weak noise alignments between unrelated texts in Appendix C. Significance testing can distinguish between real and noise alignments that occur by chance.

4.1 Computing Statistical Significance

We propose a sampling-based method for computing the statistical significance of alignment scores that can aid in computing thresholds for significance. Altschul and Gish (1996) hypothesizes that the gapped alignment scores of unrelated protein sequences follow an extreme value distribution of type I, specifically the Gumbel distribution. We argue that the same hypothesis holds for unrelated narrative texts sequences too and evaluate it here. Altschul and Gish (1996) defines the alignment score as the maximum value in the DP matrix computed by SW alignment. They estimate the probability of getting an alignment score $S \geq x$ as:

$$P(S \geq x) = 1 - \exp(-Kmne^{-\lambda x}) \qquad (4)$$

Here m and n are lengths of the two random sequences, while λ and K are parameters that define the Gumbel distribution. The probability density function of the Gumbel distribution is:

$$f_{\text{gumbel}}(x) = \frac{1}{\beta} \times e^{-(z+e^{-z})} \qquad (5)$$

where, $z = \frac{x-\mu}{\beta}$, $\mu = \log(K*m*n)/\lambda$ and $\beta = \frac{1}{\lambda}$. To estimate distribution parameters for the literary domain, we pair 1000 unrelated books by unique authors and align all possible pairs using SW with SBERT similarity at the paragraph level. After excluding the pairs having no alignment we get a distribution of size $\sim 2.5 \times 10^5$.

To simplify the estimation, we set m and n to be the mean length of books in the dataset and do maximum likelihood estimation to find the two unknown parameters K and λ for fitting the Gumbel distribution. We present the distribution of alignment scores and the associated Gumbel distribution in Figure 2. We observe that the fitted Gumbel distribution closely follows the original distribution. We present p-values of some example alignments using the Gumbel distribution in Appendix B.

5 Experiments and Applications

5.1 Datasets

We created four different datasets for experiments on narrative alignment tasks over different scales and applications. The properties of these datasets, discussed below, are summarized in Table 2:

RelBook Dataset: Project Gutenberg (Gutenberg, n.d.)hosts tens of thousands of books that have been used in previous research in NLP (Rae et al., 2019). We manually selected a set of 36 non-English books that have multiple English translations in Project Gutenberg. We pair these translations to create a set of 36 pairs of related books.

Classics Stories Dataset: We extracted 14 story pairs from two books: *Tales From Dickens* by Hallie Erminie Rives, containing shorter adaptations of Dickens' classics for young readers, and *The World's Greatest Books — Volume 03*, containing selected abridged excerpts from Dickens' classics. Alignment of two abridged versions of *Oliver Twist* are shown in Table 1.

SummaryBook Dataset: We use summaries of over 2,000 classic novels from *Masterplots* (Magill, 1989). We intersected the *Masterplots* summaries with the set of books from Project Gutenberg, using titles, authors, and other metadata, to obtain a set of 464 pairs of books and summaries.

Fables Dataset: We curated seven different compilations of *Aesop's Fables* from Project Gutenberg, each containing independent 5-to-15 sentence versions of the classic fables. From this we created a set of 150 story pairs, each comprising of two different versions of the same fable. Two human annotators also manually aligned corresponding sentence pairs for each fable-pair, where many-to-many mapping is allowed. We found a 80.42% agreement and a Cohen's Kappa score of 0.746, indicating a substantial agreement (Landis and Koch, 1977) between the two annotators. Appendix D details the annotation process.

5.2 Comparison of Similarity Functions

In this experiment, we explore the effectiveness of different similarity metrics in distinguishing between related and unrelated book pairs. We hypothesize that related pairs (*RelBooks*) should yield higher alignment scores than unrelated book pairs. We compute SW alignment for each related and unrelated book pair using the similarity metrics discussed in Section 3.2, and plot an ROC curve in Figure 3 to evaluate SW alignment performance for classifying relatedness.

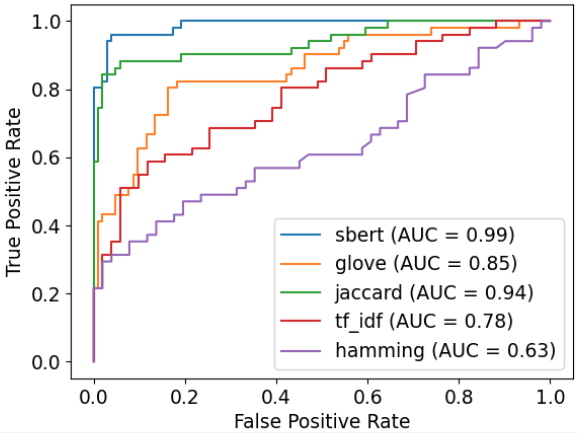

Figure 3: ROC curves distinguishing related and unrelated pairs of books from alignment order correlation, for different similarity metrics. SBERT is the best at identifying pairs of related books.

We observe that the SBERT embeddings have the highest AUC score of 0.99, with Jaccard coming close second with 0.94. The weaker performance of widely-used metrics such as TF-IDF with $AUC = 0.78$ shows the non-triviality of the task as well as the strengths of the SBERT embeddings. We discuss how we create the unrelated book pairs and present an additional experiment using this data in Appendix C.

5.3 Plagiarism Detection for PAN13 Dataset

The PAN13 plagiarism detection dataset (Potthast et al., 2013) contains 10,000 pairs of documents from the ClueWeb 2009 corpus evenly split as training and test set. In each pair, text segments from the source document are inserted into the target document using automated obfuscation strategies, creating what are referred to as plagiarized cases. These cases can be identified through high-scoring local alignments of the two documents.

We use our alignment system at the sentence and paragraph level for this dataset and report the results in Table 3. We identify the optimal z-threshold th_s for positive matches as discussed in the Section 3.3 using the training set and run the system against the test set. We do no optimization of our system, except for the z-threshold search. Our out-of-the-box system demonstrated competitive

	No Obfuscation			Random Obfuscation			Translation Obfuscation			Summary Obfuscation			Entire Corpus		
	precision	recall	F-1	precision	recall	F-1	precision	recall	F-1	precision	recall	F-1	precision	recall	F-1
Torrejón and Ramos (2013)	.90	.95	**.92**	.91	.63	.74	**.90**	.81	.85	.91	.22	.35	**.89**	.76	.82
Leilei et al. (2013)	.76	.91	.83	.86	.79	.82	.86	.85	.85	.96	.30	.46	.83	.81	.82
Suchomel et al. (2013)	.69	**.99**	.81	.83	.69	.75	.68	.67	.67	.67	.56	.61	.73	.77	.75
Sanchez-Perez et al. (2014)	.83	.98	.90	.91	**.86**	**.88**	.88	**.89**	**.88**	**.99**	.41	.58	.88	**.88**	**.88**
Altheneyan and Menai (2020)	-	-	-	**.92**	.85	**.88**	-	-	-	-	-	-	.89	.85	.87
Jaccard+SW	.70	.97	.81	.82	.74	.78	.74	.80	.77	.39	.68	.50	.73	.82	.77
SBERT+SW	**.91**	.79	.84	.89	.43	.58	.86	.66	.75	.93	**.78**	**.85**	.84	.67	.75

Table 3: We report the performance of the top-3 teams in the plagiarism detection contest and recent state-of-the-art results, along with our text alignment tool on different subsets of the PAN-13 dataset (Potthast et al., 2013). The subsets are created based on how the plagiarism was inserted in the query documents. We present a subset of the results for Altheneyan and Menai (2020), as they did not provide results for all subsets of the dataset individually. SBERT+SW performs remarkably better than other methods on the Summary Obfuscation subset.

Method	Unit Size	Percent Fidelity	Mean Rank	MRR	Worst Rank
Jaccard + SW	Sentence	78.2	1.84	0.85	26
	Paragraph	77.7	2.36	0.84	41
	Chunk	21.4	6.36	0.35	**18**
SBERT + SW	Sentence	85.8	1.42	0.91	29
	Paragraph	88.4	1.36	0.93	36
	Chunk	**90.6**	**1.31**	**0.94**	34

Table 4: Performance of SBERT+SW and Jaccard+SW for different segmentation unit sizes for the BookSummary dataset. SBERT outperforms Jaccard for all unit sizes. SBERT shows better performance as summary sentences are aligned with larger units of the book. Percent fidelity denotes the fraction of cases where the related pair was ranked 1.

performance against carefully-tuned approaches discussed by Potthast et al. (2013). Notably, our alignment method using SBERT embeddings outperformed other methods for detecting summary obfuscations, where the entire source document is summarized and placed at a random position in the target document. This superior performance can be attributed to SBERT capturing semantic similarities between text chunks of varying lengths.

5.4 Book/Summary Alignment

Here we evaluate the importance of segmentation size and the strength of different similarity metrics in aligning texts of different lengths. For each summary in the book-summary dataset, we pick 49 unrelated books of similar length creating 49 unrelated and 1 related pairs for each summary. We then compute the alignments, and rank the 50 pairs based on the maximum alignment score. We segment the summaries into sentences and repeat the experiment for different choices of segmentation sizes for the book: sentences, paragraphs, book chunks. For book chunks, we segment the book into m equal chunks for a summary of length m. Table 4 reports the Mean Reciprocal Ranks (MRR) and other results showing that SBERT is more effective in representing texts of different length for alignment than Jaccard.

Method	Precision	Recall	F1
Random	0.17	0.27	0.21
Seq. Baseline	0.31	0.54	0.40
ChatGPT	0.42	0.51	0.46
SW+Jaccard	0.62	0.69	0.65
SW+SBERT	**0.63**	**0.71**	**0.67**

Table 5: Performance of GNAT vs. ChatGPT for the Fables dataset. The test dataset consists of 2175 sentences for 120 fable pairs. Each sentence of the first fable of the pair is aligned with a sentence of the second fable or marked as unaligned.

5.5 Generative One-shot Learner Comparison

Generative models have shown promising results for many in-context learning tasks, where the model generates outputs based on one or more input-output examples. To evaluate performance of ChatGPT, based on GPT 3.5 architecture, (OpenAI, 2023) for text alignment, we provide the model with one example alignment prompt using the Fables dataset and then query it. The details of the prompts is discussed in Appendix Table 8. The limitation on the text size that can be passed as prompt to a generative model prevents longer texts from being used for this experiment.

We then compare the performance of ChatGPT and our tool in Table 5 against human annotation for the *Fables* dataset. Although ChatGPT outperformed our twin baselines of random and equally-spaced sequential alignment, our alignment method incorporating Jaccard and SBERT embeddings performed significantly better.

6 Conclusion

We have developed a tool for narrative text alignment using the Smith-Waterman algorithm with different similarity metrics, including a methodology to measure the statistical significance of aligned text segments. GNAT can be applied to the pairwise comparison of texts from any domain with varying unit sizes for text segmentation. While our evaluations were confined to English documents, the applicability of GNAT extends to languages supported by embedding models akin to SBERT. For languages with limited resources, embedding models can be trained following Reimers and Gurevych (2020), subsequently enabling the deployment of GNAT.

The next important direction here involves exploring how sequence database search tools like BLAST (Altschul et al., 1990) can be adapted for text search. One possible approach uses nearest neighbor search over embeddings in the database using parts of a query document to find seed positions for alignment, and then extends the alignments bidirectionally for faster heuristic searches. Another research direction is analyzing how the sampling based statistical significance testing method performs for different granularity levels, especially for alignment at the word or sentence level.

Limitations

This paper documents the design and performance of a general narrative alignment tool, *GNAT*. Although we have presented experimental results to validate its utility in four different domains involving texts with varying absolute and relative lengths, every tool has practical performance limits.

As implemented, the Smith-Waterman algorithm uses running time and space (memory) which grows quadratically, as the product of the two text sizes. The recursive algorithmic approach of (Hirschberg, 1975) can reduce the memory requirements to linear in the lengths of the texts, at the cost of a constant-factor overhead in running time. Such methods would be preferred when aligning pairs of very long texts, although we have successfully aligned all attempted pairs of books over the course of this study.

The primary motivation of this project originates from a goal to create a general purpose alignment tool that anyone can use out-of-the-box with minimal effort. Almost all of our experiments showed SBERT embeddings to be superior to the other metrics. However creating SBERT embeddings is a computationally heavy task, especially when the text sequences are long and GPUs are unavailable. This restricts users with limited computational power from utilizing the full power of our tool. In such scenarios, using Jaccard as the choice of similarity metric will be ideal as Jaccard is the second strongest similarity metric supported by our tool and, it does not demand substantial computational resources. To address this limitation, we plan to include smaller versions of embedding models in the tool in the future that would require less resources.

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