Efficiently Approximating Edit Distance Between Pseudorandom Strings

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Abstract
We present an algorithm for approximating the edit distance ed(x, y) between two strings x and y in time parameterized by the degree to which one of the strings x satisfies a natural pseudorandomness property. The pseudorandomness model is asymmetric in that no requirements are placed on the second string y, which may be constructed by an adversary with full knowledge of x.

We say that x is (p, B)-pseudorandom if all pairs a and b of disjoint B-letter substrings of x satisfy ed(a, b) ≥ pB. Given parameters p and B, our algorithm computes the edit distance between a (p, B)-pseudorandom string x and an arbitrary string y within a factor of O(1/p) in time ˜O(nB), with high probability. If x is generated at random, then with high probability it will be ˜Ω(1, O(log n))-pseudorandom, allowing us to compute ed(x, y) within a constant factor in near linear time. For strings x of varying degrees of pseudorandomness, our algorithm offers a continuum of runtimes.

Our algorithm is robust in the sense that it can handle a small portion of x being adversarial (i.e., not satisfying the pseudorandomness property). In this case, the algorithm incurs an additive approximation error proportional to the fraction of x which behaves maliciously.

The asymmetry of our pseudorandomness model has particular appeal for the case where x is a source string, meaning that ed(x, y) will be computed for many strings y. Suppose that one wishes to achieve an O(α)-approximation for each ed(x, y) computation, and that B is the smallest block-size for which the string x is (1/α, B)-pseudorandom. We show that without knowing B beforehand, x may be preprocessed in time ˜O(n1.5B), so that all future computations of the form ed(x, y) may be O(α)-approximated in time ˜O(nB). Furthermore, for the special case where only a single ed(x, y) computation will be performed, we show how to achieve an O(α)-approximation in time ˜O(n4/3B2/3).

1 Introduction
The edit distance ed(x, y) between two strings x and y over an alphabet Σ is the minimum number of insertions, deletions, and substitutions of characters needed to transform x to y. The textbook dynamic-programming algorithm for edit distance runs in time O(n^2) [23], and conditional lower bounds suggest that no algorithm can do more than a sub-polynomial factor better [5] (unless the Strong Exponential Time Hypothesis fails).

The difficulty of computing edit distance poses a significant challenge for applications involving large strings. In computational biology, for example, edit distance is an important tool for comparing differences between genetic sequences [19] [1] [20]. Rather than relying on the quadratic-time algorithm, such applications have often resorted to the use of fast heuristics [12] [19] [10] [17].

On the theoretical side, extensive work has been done towards algorithms that circumvent the quadratic lower bound, either by approximating edit distance, or by making assumptions on the input [3] [4] [7] [21] [14] [15] [2] [8] [11] [13].

One of the most notable successes in this direction is the algorithm of Landau and Myers [15] with runtime parameterized by the edit distance, computing ed(x, y) in time O(n + ed(x, y)^2). The algorithm runs in linear time when the edit distance is small (say, less than \sqrt{n}), and offers a continuum of runtimes for larger edit distances. Another celebrated result is the approximation algorithm of Andoni et al. [3], which approximates edit distance within a factor of (log n)^{O(1/ε)} in time O(n^{1+ε}). A recent breakthrough by Chakraborty et al. [7] gives the first approximation algorithm to achieve a sub-logarithmic approximation ratio in strongly subquadratic time. Their algorithm computes a constant approximation for edit distance in time O(n^{12/14}). It remains unknown whether a sub-logarithmic approximation for edit distance can be computed in close to linear time.

It was recently shown by Andoni and Krauthgamer [2] that better tradeoffs could be achieved if certain randomness assumptions are placed on x and y. In particular, they introduce the smoothed complexity model, in which x and y are binary strings which are assumed to be partly determined by a random process: Given two initial strings x^ε and y^ε with longest common subsequence A, x and y are defined by perturbing each letter of x^ε and y^ε with probability p, except that A is perturbed in the same way inside each of the two strings. Given two strings x and y which are constructed in this manner, the algorithm of [2] can be used to compute an O \left( \frac{1}{cp} \log \frac{1}{εp} \right) -approximation for ed(x, y) in time O \left( n^{1+ε}/\sqrt{ed(x, y)} \right). For constant p and small ε < 1, this gives a constant approximation in close to linear (or potentially sublinear) time.

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Our Contribution We consider an asymmetric randomness model for edit distance, in which one of the strings $x$ is presumed to satisfy natural randomness properties, but in which the string $y$ may be constructed by an adversary (with full knowledge of $x$). We show for a random string $x \in \Sigma^n$ and an arbitrary string $y \in \Sigma^\alpha$ there is an approximation algorithm that computes $\text{ed}(x, y)$ up to a constant factor in near linear time, with high probability.

Rather than requiring that the string $x$ is truly random, our algorithm also works for any string $x$ satisfying the following property: There is some constant $c > 1$ such that for any two disjoint substrings $a$ and $b$ in $x$ of length $c \log n$, the edit distance between $a$ and $b$ is at least $\log n$.

By relaxing the above property, one can define a natural notion of pseudorandomness for a string $x$. Specifically, we say that $x$ is $(p, B)$-pseudorandom if all pairs $a$ and $b$ of disjoint $B$-letter substrings of $x$ satisfies $\text{ed}(a, b) \geq pB$.

Given parameters $p$ and $B$, our main result is an algorithm that computes the edit distance between a $(p, B)$-pseudorandom string $x$ and an arbitrary string $y$ within a factor of $O(1/p)$ in time $O(nB)$, with high probability (Section 3).

An interesting feature of our algorithm is that it allows for substantial speedups over the quadratic-time algorithm (as well as the low for substantial speedups over the quadratic-time probability (Section 3).)

$\text{(p, B)}$-pseudorandom, and then use our algorithm with approximation algorithm on a string $x, y \in \Sigma^\alpha$ computes $\text{ed}(x, y)$ in time $O(n^{1.5}B+\alpha)$-time preprocessing step on $x$, so that any edit distance computation $\text{ed}(x, y)$ can later be $O(\alpha)$-approximated in time $O(nB)$. We also consider the special case where we wish to perform only a single computation $\text{ed}(x, y)$, but we do not know beforehand the minimum (power-of-two) block size $B$ for which $x$ is $(1/\alpha, B)$-pseudorandom; for this case we present an algorithm which runs in time $\tilde{O}(n^{1.5}B^{2/3})$.

Our approximation algorithm is robust to a small portion of $x$ being determined by an adversary, rather than satisfying the pseudorandomness property, and the algorithm does not require us to know which portions of $x$ have been affected by the adversary. In this case, the algorithm incurs an additive approximation error proportional to the fraction of $x$ which has been constructed adversarially.

Relationship to the Smoothed Complexity Model Interestingly, the smoothed complexity model [2] can be viewed as a special case of our pseudorandomness model. In particular, the string $x$ in the smoothed complexity model will be $(p, O(1/p) \log n)$-pseudorandom with high probability (see Lemma 2.2 of [2]). Our algorithm can therefore be used in the smoothed complexity model to obtain an $\tilde{O}(n/p)$-time algorithm with approximation ratio $O(1/p)$.

Both our algorithm and the algorithm of [2] use substring matching between $x$ and $y$ as an important algorithmic component, where two substrings are said to match if their edit distance is relatively small. Substring matching also plays an important role in a number of the practical heuristics for computing edit distance, including the widely used PatternHunter tool [17]. The prominent role of the technique within both our algorithm and the algorithm of [2] helps provide theoretical motivation for why the technique has had such empirical success in practice. The empirical success of the technique may also be an indicator that real-world inputs satisfy some variant of $(p, B)$-pseudorandomness. Evaluating to what degree this is the case would be an important direction of future work.

Beyond the use of substring matching, the techniques used in [2] largely differ from ours. In particular, it seems difficult to extend the techniques used in [2] to our pseudorandomness model without using space (and time) exponential in $p \cdot B$.

Related Work on Average-Case Analysis for Approximate String Matching In the Approximate String Matching Problem, we are given a string $x \in \Sigma^n$, a pattern $p$ of length at most $n$, and a threshold $k$. The goal is to output all positions $i$ in $x$ such that there exists some $j > i$ for which $\text{ed}(x_i \cdots x_j, p) < k$. It was shown by Landau et al. [14] that the Approximate String Matching Problem can be solved in time $O(nk)$ using space $O(n)$.

Additional space improvements have been presented for the case where $x$ is selected at random from $\Sigma^n$. Notably, an algorithm due to Myers [18] achieves space $O(k)$ for random $x$. Improvements in runtime have also been presented. In particular, an al-
algorithm due to Chang and Lampe [9] achieves runtime $O(nk/\sqrt{|\Sigma|})$.

For strings $x$ and $y$ of length $n$, selected from a constant-size alphabet $\Sigma$, no known algorithm for Approximate String Matching achieves a strongly subquadratic running time, even for $x$ selected at random. Consequently, there is relatively little overlap between the setting considered in this paper and past work on Approximate String Matching.

2 Technical Overview

In this section, we present a brief technical overview of our approximation algorithm and of our algorithms for parameter detection.

Approximation Algorithm for $x$ a $(p,B)$-Pseudorandom String In Section 3 we present our approximation algorithm for computing the edit distance between a $(p,B)$-pseudorandom string $x$ and an arbitrary string $y$. A rough summary of our approximation algorithm is as follows: We break the strings $x$ and $y$ into blocks of size $\Theta(B)$, and define a notion of a block $x^i$ from $x$ edit matching with a block $y^j$ from $y$. In order to find a sequence of edits from $x$ to $y$, we perform the following tasks recursively. We select a random pivot block $x^i$ from the blocks in the middle half of $x$. If the pivot either edit matches with no blocks in $y$, or edit matches with more than one block in $y$, then we consider it to be invalid, and we sample another random pivot until we find a valid one, giving up after $100\log n$ consecutive failures. If, on the other hand, the pivot edit matches with exactly one block $y^j$ in $y$, then we break the strings at $x^i$ and $y^j$, respectively, and recursively try to align the two strings in each of the two halves. The base case for our algorithm occurs when either the strings $x$ and $y$ differ in size from each other by exactly $100\log n$; or when $|x| = 0$. Our algorithm outputs a non-crossing matching between the blocks of $x$ and the blocks of $y$, where two blocks are only permitted to be matched if they edit match. By considering only sequences of edits which roughly respect the matchings between blocks, we are then able to efficiently find a sequence of edits from $x$ to $y$.

In analyzing the algorithm, we consider an optimal alignment $T$ between $x$ and $y$, and based on $T$ we define two types of subproblems: live subproblems and dead subproblems. Dead subproblems are those which are either between vastly differently sized substrings $u$ and $v$, or which are between substrings $u$ and $v$ which are far apart and not aligned with one-another by $T$. These subproblems prove simple to analyze because any mistakes the algorithm makes on a dead subproblem can be easily accounted for by the inherent misalignment in the subproblem.

The remaining subproblems are known as live subproblems, and require a more sophisticated analysis. For each block $x^i$ in $x$, we denote by $\phi(i)$ the index of the block in $y$ closest to where the optimal alignment $T$ maps $x^i$. (i.e., the alignment $T$ maps the block $x^i$ to roughly where $y^j$ sits in $y$.) One of the key insights is that each live subproblem $A$ must satisfy the following property:

- **The Pivot Pairing Property:** If the algorithm selects a block $x^i$ as block pivot, then the block $y^\phi(i)$ must appear in the substring of $y$ considered by the subproblem.

If a pivot block $x^i$ edit matches with its counterpart $y^\phi(i)$, then any live subproblem which selects $x^i$ will be guaranteed to perform well. Using the $(p,B)$-pseudorandomness property of $x$, we are able to show that at most $O(\frac{1}{p}\text{ed}(x,y))$ of the letters in $x$ reside in blocks $x^i$ that do not edit match with their counterpart $y^\phi(i)$. The blocks containing these letters, which we will call dirty blocks, are the blocks which place our algorithm at risk of exhibiting a large approximation ratio.

The Pivot Pairing Property has the following important consequence for dirty blocks: For each dirty block $x^i$, any live subproblem $A$ which uses $x^i$ as a pivot block, must pair $x^i$ with one of at most two blocks $y^{j_1}$ and $y^{j_2}$, where $j_1$ is the largest value of $x^i$ edit matches with $y^j$, and $j_2$ is the smallest value of $x^i$ edit matches with $y^j$. Since each dirty block has only two potential partners for it to pair with inside any live subproblem, there are, in total, only $O(\frac{1}{p}\text{ed}(x,y))$ pairs $(x^i,y^j)$ for which the algorithm is at risk of at some point selecting $x^i$ as a pivot and erroneously matching it with $y^j$. Call such a pair a dirty pair.

In order to analyze the distortion of our algorithm, we consider each dirty pair $(x^i,y^j)$, and bound the expected damage to the algorithm’s output incurred by the pair. For a given live subproblem $A$ that is at risk of pairing $x^i$ as a pivot with $y^j$, let $r$ denote the number of blocks in the substring of $x$ considered by $A$. We show that because $A$ is a live subproblem, it must contain $\Omega(r)$ valid pivot block options, meaning that $x^i$ has a probability of at most $\Omega(1/r)$ of being selected. If the block $x^i$ is selected as a pivot and is matched with the block $y^j$, then we are able to bound the damage incurred to the algorithm (in terms of number of edits added to the final alignment) by $O(B\cdot|\phi(i) - j|)$, the number of letters which lie between where the optimal alignment $T$ maps $x^i$ and where our algorithm places $x^i$ within $y$. It follows that the expected damage incurred by the
pair \((x^i, y^j)\) to our subproblem \(A\) is at most

\[
O \left( \frac{1}{r} \cdot B \cdot |\phi(i) - j| \right).
\]

Using the Pivot Pairing Property, we can show that the size \(r\) must be at least \(\sigma = \Omega(|\phi(i) - j|)\), since the subproblem must involve both \(y^i\) and \(y^{\phi(i)}\). Moreover, for each range of the form \(R_l = [2^l \sigma, 2^{l+1} \sigma]\), there can be at most a constant number of subproblems \(A\) that contain \(x^i\) and have a size \(r\) lying in the range. For each range \(R_l\), it follows that the expected damage incurred by the pair \((x^i, y^j)\) to live subproblems for which \(r \in R_l\) is at most

\[
O \left( \frac{1}{2^l} \cdot B \cdot |\phi(i) - j| \right) = O \left( \frac{1}{2^l} B \right).
\]

Summing over \(l\), we find that the total expected damage incurred by \((x^i, y^j)\) is at most

\[
O \left( \sum_{l \geq 0} \frac{1}{2^l} B \right) = O(B).
\]

Summing over the \(O\left(\frac{1}{pB} \text{ed}(x, y)\right)\) dirty pairs \((x^i, y^j)\), the total expected error in our algorithm’s estimate for edit distance can be bounded by

\[
O \left( \frac{1}{pB} \text{ed}(x, y) \cdot B \right) = O \left( \frac{1}{p} \text{ed}(x, y) \right),
\]

as desired.

We break the full presentation and analysis of the algorithm into two parts:

- The first part is an approximation algorithm for a combinatorial matching problem in which the blocks in the strings \(x\) and \(y\) have been replaced with abstract objects (essentially characters), and in which a comparison function \(f(i, j)\) determines whether the blocks \(x^i\) and \(y^j\) may be matched with one another. The algorithm and analysis for this problem essentially follow the outline above.

- The second part is a reduction from approximating \(\text{ed}(x, y)\) between two strings (one of which is \((p, B)\)-pseudorandom) to the combinatorial matching problem. The reduction breaks the string \(x\) into parts \(x^1, x^2, \ldots\) of size \(6B\) and breaks the string \(y\) into parts \(y^1, y^2, \ldots\) of size \(3B\). Roughly speaking, we say that \(x^i\) edit matches with \(y^j\) if there is a \(6B\)-letter substring \(a\) containing \(y^j\) for which \(\text{ed}(x^i, a) \leq O\left(\frac{1}{p} B\right)\), and if the same is not true for \(y^{j-1}\).

The reduction encounters two technical subtleties. The first is that, although the strings \(x\) and \(y\) are the same length initially, they are mapped by the reduction to strings of length \(\frac{n}{6B}\) and \(\frac{n}{3B}\), respectively. As a result, every alignment in the resulting matching problem must leave at least half of the blocks in \(y\) unmatched. This is resolved by defining an asymmetric cost model for alignments in the problem which we reduce to; in particular, a block \(y^i\) only pays for being unmatched if the three blocks to each of its immediate left and right are also unmatched. The second subtlety is the handling of the case where some fraction of the blocks in \(x\) have been modified by an adversary, rather than satisfying the \((p, B)\)-pseudorandomness property within \(x\). The reduction is designed to hide this aspect of the problem from the combinatorial matching problem which we reduce to, by ensuring that the optimal cost for the matching problem is given by \(O \left( \frac{1}{p} \text{ed}(x, y) + M(x) \right)\), where \(M(x)\) is the number of letters in \(x\) which lie in adversarially designed blocks.

**Parameter Detection** In Section 4 we turn our attention to parameter detection. In particular, consider a source string \(x\) and suppose we wish to compute an \(O(\alpha)\)-approximation for \(\text{ed}(x, y)\) for a large number of strings \(y\). Define \(B\) to be the smallest power-of-two block-size for which \(x\) is \((1/\alpha, B)\)-pseudorandom. Without knowing \(B\) beforehand, we show how to preprocess \(x\) in time \(O(n^{1.5}(\sqrt{B} + \alpha))\) in order so that all future computations of \(\text{ed}(x, y)\) can be \(O(\alpha)\)-approximated in time \(O(nB)\). One way to do this would be to find the first \(B_i = 2^i\alpha\) for which \(x\) is \((1/\alpha, B_i)\)-pseudorandom, which would take roughly quadratic time per \(B_i\). The key observation to improve upon this is that, since we are willing to spend time \(O(nB)\) to approximate each value \(\text{ed}(x, y)\), if it turns out that \(\text{ed}(x, y) \leq \sqrt{nB}\), then we may use the \(O(n + \text{ed}(x, y)^2)\)-time algorithm of [15] in order to exactly compute \(\text{ed}(x, y)\) in the desired time bound. By exploiting this trick, we can tolerate our approximation algorithm for \(\text{ed}(x, y)\) having additive error of \(\sqrt{nB}\). Consequently, rather than finding the first \(B_i\) for which \(x\) is \((1/\alpha, B_i)\)-pseudorandom, we can instead check for the weaker condition that \(x\) is \((1/\alpha, B_i)\)-pseudorandom with the exception of blocks containing at most \(O(\sqrt{nB})\) letters in \(x\). Using random sampling, this can be done in time \(O(n^{1.5}(\sqrt{B} + \alpha))\), as desired. In a similar manner, for the case where only a single computation \(\text{ed}(x, y)\) is to be performed, we obtain an \(O(\alpha)\)-approximation in time \(O(n^{4/3}B^{2/3})\).
3 Edit Distance Between Pseudorandom Strings

Let \( 0 < p < 1 \) and \( B \in \mathbb{N} \) be parameters. Throughout the section, we will use \( \Sigma \) to denote the alphabet over which strings are taken. We will present a randomized algorithm that computes the edit distance between a \((p, B)\)-pseudorandom string \( x \in \Sigma^n \) and an arbitrary string \( y \in \Sigma^n \) within a factor of \( O(1/p) \) in time \( \tilde{O}(nB) \).

Additionally, our algorithm will be able to handle a small portion of \( x \) behaving maliciously. In the following definition, we define a quantity \( M(x) \) which captures the degree to which \( x \) is not \((p, B)\)-pseudorandom.

**Definition 3.1.** Consider \( x \in \Sigma^n \), and break it into blocks \( x^1, x^2, \ldots, x^{\lfloor n/6B \rfloor} \) of size \( 6B \). If \( n \) is not a multiple of \( 6B \), then pad the final block with null characters so that it is length \( 6B \). We say a block \( x^i \) in \( x \) is \( p \)-unique if each \( B \)-letter substring of \( x^i \) has edit distance at least \( pB \) from each \( B \)-letter substring in \( x \) that does not intersect \( x^i \). Define the quantity \( M(x) \) (which will often be abbreviated by \( M \)) to be the number of letters in \( x \) (including null characters padded on the end) that are not in \( p \)-unique blocks.

The goal of the section is to prove the following theorem:

**Theorem 3.1.** Let \( n \in \mathbb{N} \) be a string-length parameter, \( p \in (0, 1) \) be a parameter such that \( 1/p \in \mathbb{N} \), and \( B \in \mathbb{N} \) be a block-size parameter.

Consider as inputs a string \( x \in \Sigma^n \) and an arbitrary string \( y \in \Sigma^n \). Then there exists a randomized algorithm which in time \( \tilde{O}(n \cdot B) \) finds a sequence of \( t \) edits between \( x \) and \( y \), where \( t \) is no greater than

\[
O \left( \frac{1}{p} \text{ed}(x, y) + M(x) \right),
\]

in expectation.

Notice that by repeatedly applying Theorem 3.1 \( O(\log n) \) times, and taking the smallest returned sequence of edits, one can further ensure that Equation (3.1) will hold with high probability.

An important corollary of Theorem 3.1 is for the case where \( x \) is fully random.

**Corollary 3.2.** There is an algorithm which, given a random string \( x \in \Sigma^n \), and an arbitrary string \( y \in \Sigma^n \), finds a sequence of \( O(\text{ed}(x, y)) \) edits between \( x \) and \( y \) in time \( O(n) \), with high probability.

**Proof.** This follows from Theorem 3.1 and the fact that \( x \) will be \((\Omega(1), O(\log n))\)-pseudorandom with high probability (See 2.2 of [2]). \( \square \)

For the rest of the section, we will assume without loss of generality that \( n \) is a multiple of \( 6B \). Notice that by padding \( x \) with null characters, one can ensure that the last block is of length \( 6B \) without increasing \( M(x) \), and furthermore, if one places the same padding on \( y \), then the edit distance between the padded strings will be the same as between the original strings.

For the rest of the section, let \( n, p, B, x, y \) be as defined in Theorem 3.1 and assume that \( 6B \parallel n \). In order to prove Theorem 3.1, we will reduce it to a combinatorial problem which we call the Clean Alignment Problem. Formally, Theorem 3.1 can be viewed as presenting a \( \tilde{O}(nB) \)-time solution to the Pseudorandom Edit Distance Problem, defined as follows.

- **The Pseudorandom Edit Distance Problem (PEDP):** Given \( x \in \Sigma^n \) and an arbitrary \( y \in \Sigma^n \), recover a sequence of \( t \) edits from \( x \) to \( y \) for \( t \) satisfying \( \mathbb{E}[t] \leq O(1/p \cdot \text{ed}(x, y) + M(x)) \).

We will reduce PEDP to the Clean Alignment Problem, defined below. Specifically, any algorithm for the Clean Alignment Problem which runs in time \( T(n) \) will imply an algorithm for PEDP which runs in time \( \tilde{O}(T(n) \cdot B) \).

- **The Clean Alignment Problem:** Consider strings \( x \) and \( y \) of possibly different lengths. Let \( f : [|x|] \times [|y|] \to \{0, 1\} \) be a comparison function for \( x \) and \( y \). If \( f(i, j) = 1 \), we say that \( x_i \) edit matches with \( y_j \).

An alignment \( A \) (i.e., a non-crossing matching) between the letters of \( x \) and the letters of \( y \) is said to be an *edit-matching alignment* if every edge \((x_i, y_j) \in A\) satisfies \( f(i, j) = 1 \). The cost of an alignment is defined asymmetrically: The \( x \)-portion cost of \( A \) is the number of letters in \( x \) to be unmatched by \( A \); the \( y \)-portion cost is the number of \( i \) for which \( y_i, y_{i+1}, \ldots, y_{i+6} \) are all unmatched by \( A \). The cost of \( A \) is the sum of the \( x \)-portion and \( y \)-portion costs.

An edit-matching alignment is said to be clean if for all \((x_i, y_j) \in A\), \( x_i \) is the only letter in \( x \) which \( y \)-edit matches with \( y_j \), and \( y_j \) is the only letter in \( y \) which \( x \)-edit matches with \( x_i \).

Given \( x, y, \) and \( f \), the goal of the Clean Alignment Problem is to recover a (not necessarily clean) edit-matching alignment between \( x \) and \( y \) whose expected cost is within a constant factor of the optimal cost of a clean edit-matching alignment.

We remark that the difficulty of the Clean Alignment Problem comes from the fact that the function \( f \) in
the Clean Alignment Problem needs not satisfy any natural properties (such as e.g., some form of transitivity). Thus the only way to determine whether \( f(i, j) = 1 \) for two letters \( x_i \) and \( y_j \), is to explicitly evaluate \( f(i, j) \). In order for an algorithm to run in time \( \tilde{O}(n) \), as desired, it must very selectively determine for which values of \( i \) and \( j \) to query \( f(i, j) \).

The reader may notice that the Clean Alignment Problem is completely determined by \( f \), \( |x| \), and \( |y| \). That is, the actual contents of \( x \) and \( y \) are irrelevant. Nonetheless, for ease of presentation, we include \( x \) and \( y \) as inputs. For examples of a comparison function \( f \), and of clean edit-matching alignments, see Figure 1.

The remainder of the section is outlined as follows. In Subsection 3.1 we present an algorithm for the Clean Alignment Problem which runs in near linear time. In Subsection 3.2 we then present a reduction from PDEP to the Clean Alignment Problem, completing the proof of Theorem 3.1.

### 3.1 The Clean Alignment Problem

In this section we present an approximation algorithm for the Clean Alignment Problem. The algorithm is given by Algorithm 1 and the key properties of the algorithm are stated in Theorem 3.3.

For this section, consider \( u, v \in \Sigma^{\leq n} \) (meaning they are of length at most \( n \) over the alphabet \( \Sigma \)), and let \( \Pi(u, v) \) denote the edit-matching alignment given by the output of Algorithm 1 on \( u \) and \( v \). Moreover, let \( T \) be an optimal clean edit-matching alignment between \( u \) and \( v \).

**Theorem 3.3.** Algorithm 1 can be evaluated in time \( \tilde{O}(n) \). Moreover, if \( t \) is the cost of \( T \), then the expected number of edges in \( T \setminus \Pi(u, v) \) is at most \( O(t) \), in expectation.

Note that removing an edge from an edit-matching alignment can increase each of the \( u \)-portion and the \( v \)-portions of the cost by at most 1 each. Thus Theorem 3.3 implies that Algorithm 1 achieves constant multiplicative error, in expectation, for the Clean Alignment Problem.

**Corollary 3.4.** Algorithm 1 solves the Clean Alignment Problem in time \( \tilde{O}(n) \).

**Remark 3.5.** Algorithm 1 is motivated in part by our previous work on efficiently embedding Ulam distance (edit distance over permutations) into Hamming space with (optimal) expected distortion \( O(\log n) \) \( \frac{1}{2} \). In particular, a similar analysis to that of Ulam could be employed in order to prove that Algorithm 1 has approximation ratio \( O(\log n) \), in expectation. The key difference between Algorithm 1 and the embedding of Ulam is that Algorithm 1 is permitted to try \( O(\log n) \) options for pivots in order to find a “good” one, while the embedding of Ulam (by virtue of being oblivious to \( y \)) is forced to blindly select a pivot. Surprisingly, this minor difference allows for the more sophisticated analysis of Algorithm 1 below, resulting in a constant expected approximation ratio.

Before analyzing Algorithm 1, we first introduce several conventions for talking about the algorithm's subproblems.

**Definition 3.6.** Consider a subproblem \( A \) which involves a substring \( u_i \cdots u_j \) of \( u \) and a substring \( v_k \cdots v_l \) of \( v \). We call \( u_i \cdots u_j \) the \( u \)-chunk of \( A \) and \( v_k \cdots v_l \) the \( v \)-chunk of \( A \).

**Definition 3.7.** For any subproblem \( A \) which has a substring \( u_i \cdots u_j \) of \( u \) and a substring \( v_k \cdots v_l \) of \( v \) we call \( u_i \cdots u_j \) the \( u \)-chunk of \( A \) and \( v_k \cdots v_l \) the \( v \)-chunk of \( A \).

We classify subproblems into two types, live subproblems and dead subproblems. Dead subproblems will act essentially as base cases in the analysis of the algorithm. Live subproblems, on the other hand, will prove far more interesting to analyze.

**Definition 3.8.** For any subproblem \( A \), we define \( T \cap A \) to be the set of edges in \( T \) which go between the \( u \)-chunk and \( v \)-chunk of \( A \). That is, \( T \cap A \) is formally \( T \cap \{(u_i, v_j) \mid u_i \in a, v_j \in b\} \), where \( a \) is the \( u \)-chunk and \( b \) is the \( v \)-chunk of \( A \).

One important property of live subproblems is that they have many valid options for the algorithm to select as a pivot.

**Lemma 3.10.** For a live subproblem \( A \), at least \( 4/5 \) of \( A \)'s pivot options are valid pivots.
Proof. Let \( a \) be the \( u \)-chunk and \( b \) be the \( v \)-chunk of \( A \). By the definition of a live subproblem, fewer than \( 1/10 \) of the elements in \( a \) fail to be matched by \( T \) to an element of \( b \). Since at least \( 1/2 \) of the elements of \( a \) are pivot options, at least \( .8 \) of the pivot options must be matched by \( T \) to an element of \( b \). Because \( T \) is a clean edit-matching alignment, any pivot-option which is matched by \( T \) to an element of \( b \) must be a valid pivot. \( \square \)

When the algorithm decides on a pivot on which to split a subproblem \( A \), the quality of that pivot can be captured by what we refer to as the cost increase of \( A \):

**Definition 3.11.** For a live subproblem \( A \) with subproblems \( B \) and \( C \), we define the cost increase \( c(A) \) of \( A \) as follows. If the algorithm fails to select a pivot, or selects a pivot \( u_i \) in \( A \) and matches it with some \( v_j \) for which \((u_i, v_j) \in T\), then the cost increase is \( c(A) = 0 \). Otherwise the cost increase is \( c(A) = |T \cap A| - |T \cap B| - |T \cap C| \). That is, \( c(A) \) is the number of edges in \( T \) that are cut by the selection of the subproblems \( B \) and \( C \).

The key technical challenge in the section will be to bound the cost increases summed over all live subproblems. We begin by presenting three properties of live subproblems which will be useful in the analysis. These properties rely on the notion of a position map, defined as follows.

**Definition 3.12.** The position map \( \phi : [u] \to [v] \) maps positions in \( u \) to the position in \( v \) to which they are assigned by the alignment \( T \). Formally, if \( u_l \) is edit matched to some \( v_k \) by \( T \), we define \( \phi(l) = k \), and otherwise we recursively define \( \phi(l) = \phi(l - 1) \) (or \( \phi(l) = 1 \) if \( l = 1 \)).

**Lemma 3.13.** Suppose a live subproblem \( A \) selects some \( u_i \) as a pivot and matches \( u_i \) to some \( v_j \). Then the following three properties hold:

1. The cost increase of \( A \) will be at most \( |\phi(i) - j| + 1 \).
2. The letter \( v_{\phi(j)} \) is contained in \( A \)'s \( v \)-chunk.
3. The size of \( A \)'s \( u \)-chunk is at least

\[ \max \left( 1, \frac{|\phi(u_i) - j| - 11}{8} \right) \]

**Proof.** We begin by proving the first property. Since every edge \((u_r, v_s) \in T \cap A \) either satisfies \( r \geq i \) and
Algorithm 1 Approximation Algorithm for The Clean Alignment Problem

Input: Strings $u, v \in \Sigma^{\leq n}$, comparison function $f$.
Output: An edit-matching alignment between $u$ and $v$.

1. If $|v| \geq 8|u| + 12$ or $|u| \geq 2|v|$, return $\emptyset$.
2. If $|u| = 0$, return $\emptyset$.
3. For $100 \log n$ attempts:
   (a) Randomly sample a letter $u_i$ satisfying $\frac{1}{4}|u| \leq i \leq \left\lceil \frac{3}{4}|u| \right\rceil$.
   (b) In time $O(|v|)$, construct the set $S = \{j \mid f(i, j) = 1\}$.
   (c) If $|S|$ is of size one, containing a single element $j$, then:
      i. Initialize an output set $O$ containing the single edge $(u_i, v_j)$
      ii. Recurse on $u_1 \cdots u_{i-1}$ and $v_1 \cdots v_{j-1}$, and add the resulting edges to $O$.
      iii. Recurse on $u_{i+1} \cdots u_{|u|}$ and $v_{j+1} \cdots v_{|v|}$, and add the resulting edges to $O$.
   iv. Return $O$.
4. Return $\emptyset$.

$s \geq \phi(i)$ or $r < i$ and $s < \phi(i)$, all edges $(u_r, v_s)$ in the set
   $$(T \cap A) \setminus ((T \cap B) \cup (T \cap C))$$
must satisfy the property that $s$ is between $j$ and $\phi(i)$ inclusive. The number $c(A)$ of such edges can therefore be at most
   $$|\phi(i) - j| + 1.$$  

To prove the second property, suppose for contradiction that $v_{\phi(i)}$ is not contained in $A$’s $v$-chunk. Then because $\phi$ is weakly increasing, it must be that $v_{\phi(k)}$ is not in $A$’s $v$-chunk for at least $1/4$ of the $u_k$’s in $A$’s $u$-chunk. But this would mean that the subproblem $A$ is dead, a contradiction.

Finally, to prove the third property, notice that the second property forces the size of $A$’s $v$-chunk to be at least $|\phi(u_i) - j| + 1$. By the definition of a live subproblem, it follows that the size of $A$’s $u$-chunk must be at least
   $$\max\left(1, \frac{|\phi(u_i) - j| - 11}{8}\right),$$
as desired.

Next we present the key technical lemma of the section, in which we bound the sum of the cost increases of all live subproblems.

Lemma 3.14. Let $t$ be the cost of the optimal clean edit-matching $T$. Let $S$ be the sum of the cost increases over all live subproblems. Then $\mathbb{E}[S] \leq O(t)$.

Proof. Rather than attributing the cost increase $c(A)$ to the subproblem $A$, we will instead attribute the cost to $u_i$, where $u_i$ is the pivot selected within the subproblem. If a letter $u_i$ is edit matched by $T$, then no non-zero cost increase will ever be attributed to it, since the only way $u_i$ can be selected as a pivot is if it is to be correctly matched with $v_{\phi(i)}$. (Recall, in particular, that $T$ is a clean edit-matching alignment.) If, on the other hand, $u_i$ is unmatched by $T$, then we will prove that the expected sum of cost increases attributed to it is $O(1)$. Since there are $O(t)$ such $u_i$’s (recall $t$ is the cost of $T$), this will complete the proof.

For the rest of the proof, consider some $u_i$ not matched by $T$. By the second part of Lemma 3.13, in order for a subproblem $A$ to attribute its cost increase to $u_i$, it must be that $u_i$ is in $A$’s $u$-chunk and $v_{\phi(i)}$ is in $A$’s $v$-chunk. Moreover, because $v_{\phi(i)}$ is in $A$’s $v$-chunk, there are at most two options for the letter $v_j$ which the algorithm pairs $u_i$ with – namely, $v_j$ must either the first letter $v_{j_1}$ to $v_{\phi(i)}$’s left for which $f(i, j_1) = 1$, or it must be the first such letter $v_{j_2}$ to $v_{\phi(i)}$’s right. We say that the cost increase of $A$ is attributed to the $(u_i, v_{j_1})$ pair if $j = j_1$, and is attributed to the $(u_i, v_{j_2})$ pair if $j = j_2$. For the rest of the proof, we will consider $j_q$ for some $q \in \{1, 2\}$, and show that the total cost increases attributed to the pair $(u_i, v_{j_q})$ is at most $O(1)$, in expectation.

Define $R_i$ to be the range $[(10/9)^l \sigma, (10/9)^{l+1} \sigma]$, for $l \geq 0$ and for
   $$\sigma = \max\left(1, \frac{|\phi(i) - j_q| - 11}{8}\right).$$
Definition 3.15. The induced cost of a subproblem $A$ with $u$-chunk $a$ and $v$-chunk $b$ is the cost of the clean edit-matching alignment between $a$ and $b$ obtained by restricting $T$ to the two substrings (i.e., the alignment with edges $T \cap A$).

The surplus cost of the subproblem is the number of edges in $T$ between $a$ and $b$ that do not appear in the algorithm’s output (i.e., $|T \cap A| - |\Pi(u,v)|$).

The ratio of a subproblem’s induced cost to its surplus cost is a natural measure of how well $\Pi$ performs on the subproblem. The next lemma shows that, in this regard, Algorithm $1$ behaves well on dead subproblems.

Lemma 3.16. The surplus cost of the return value of a dead subproblem is at most $O(c)$, where $c$ is the induced cost of the subproblem.

Proof. Let $a$ be the $u$-chunk and $b$ be the $v$-chunk of a dead subproblem.

If $|a| = 0$, then the surplus cost of the subproblem is $0$, and is thus trivially at most $O(c)$.

In the remaining cases, we will show that the induced cost $c$ is at least $\Omega(|a|)$, making the surplus cost $O(c)$ trivially.

If at least $1/10$ of the elements of $a$ are not matched by $T$ to an element of $b$, then the induced cost $c$ is at least $|a|/10$, as desired. Similarly, if $|a| \geq 2|b|$, then at least half of the elements of $a$ will not be matched by an $T$, implying that the induced cost $c$ is at least $|a|/2$.

If $|b| \geq 8|a| + 12$, then the $b$-portion cost of any edit-matching alignment between $a$ and $b$ must be at least $|a|$. In particular, the number of edges in such an alignment can be at most $|a|$, and each edge can be contained in at most 7 contiguous substrings of length 7 in $b$. As a result, at most $7|a|$ of the contiguous substrings of length 7 in $b$ can contain a letter incident to an edge. Since $b$ contains at least $8|a|$ contiguous substrings of length 7, the $b$-portion cost of any edit matching alignment must be at least $|a|$. □

Combining Lemmas 3.14 and 3.16, we are now prepared to prove Theorem 3.3.

Proof. [Proof of Theorem 3.3] It is straightforward to prove that Algorithm $1$ runs in time $\tilde{O}(n)$. For the rest of the proof we focus on the cost of the edit-matching alignment $\Pi$ given by the algorithm. Specifically, we wish to show that the number of edges in $T \setminus \Pi$ is at most $O(t)$ in expectation.

Consider a live subproblem $A$. By Lemma 3.10, each of the $100 \log n$ attempts at selecting a pivot will succeed with probability at least $0.8$, and with probability greater than $1 - \frac{1}{100 \log n}$, a pivot will end up being selected. Since there are $O(n)$ subproblems in the entire algorithm, with probability at least $1 - O\left(\frac{1}{\log n}\right)$, every live subproblem will succeed in one of its $100 \log n$ attempts to spawn recursive children. Noting that the number of edges in $T \setminus \Pi(u, v)$ is at most $O(n)$, it follows that the cases where some live subproblem fails to spawn children have negligible impact on $\mathbb{E}[|T \setminus \Pi(u, v)|]$. For the rest of the proof, we will condition on all live subproblems succeeding at spawning children.

Recall that $c(A)$ denotes the cost increase of a live subproblem $A$. For a live subproblem $A$ with children subproblems $B$ and $C$, we also define the induced cost increase $c'(A)$ to be the induced cost of $B$ plus the induced cost of $C$ minus the induced cost of $A$. Note that $c'(A) \leq 2c(A)$, since the increases in induced cost between $A$ and its subproblems $B$ and $C$ can be attributed to the removals of edges. (Recall that the removal of an edge from an edit-matching alignment increases each of the $u$-portion cost and $v$-portion cost by at most one.)

Let $I$ be the sum of the cost increases over all live subproblems, and $I'$ be the sum of the induced cost increases over all live subproblems. Note that the induced cost of the root subproblem is precisely the cost $t$ of the optimal clean edit-matching alignment $T$. Call a dead subproblem fresh if its parent subproblem is live. Then the sum of the induced costs of all fresh dead subproblems is exactly $t + I'$. By Lemma 3.10 it
follows that the sum $S$ of the surplus costs of all fresh dead subproblems is at most $O(t + I')$. Since $I' \leq 2I$, we have that $S \leq O(t + I)$.

Observe that $|T \setminus \Pi(u,v)|$ is precisely $I$, the sum of the cost increases over all live subproblems, plus $S$, the sum of the surplus costs over all fresh dead subproblems. Thus

$$|T \setminus \Pi(u,v)| \leq O(I + S) \leq O(t + I).$$

By Lemma 3.14 $E[I] \leq O(t)$, completing the proof.

\[ \square \]

### 3.2 Reduction to The Clean Alignment Problem

In this section, we prove the following theorem:

**Theorem 3.17.** Suppose there is an algorithm for the Clean Alignment Problem that runs in time $O(n)$. Then there is an algorithm for the Pseudorandom Edit Distance Problem which runs in time $O(nB)$.

Before proving Theorem 3.17, we combine it with Corollary 3.4 in order to complete the proof of Theorem 3.1 establishing an efficient solution to the Pseudorandom Edit Distance Problem.

**Proof.** [Proof of Theorem 3.1] By Theorem 3.17, it suffices to present a solution to the Clean Alignment Problem which runs in time $O(n)$. Corollary 3.4 gives such a solution.

The reduction which we will use to prove Theorem 3.17 can be easily stated: Recall that $x^1, x^2, \ldots, x^{n/6B}$ breaks $x$ into blocks of length $6B$. Let $y^1, \ldots, y^{n/3B}$ be $y$ broken into blocks of size $3B$.

Let $r$ be the starting index $r = (j - 1) \cdot 3B + 1$ of the block $y^j$. We say that $x^i$ partially edit matches with $y^j$ if there is some $s = r + t \cdot pB/100$ with $t \in \{0, \ldots, 300/p - 1\}$ such that $y_s \cdots y_{s + 6B - 1}$ has edit distance no greater than $pB/8$ from $x^i$. That is, $x^i$ partially edit matches $y^j$ if there is a $6B$-letter substring $a$ of $y$ such that (1) $a$’s start position appears in $y^{j-1}$; (2) $a$’s zero-indexed start position is a multiple of $pB/100$; and (3) $\text{ed}(a, x^i) \leq pB/8$. Note that $x^i$ can only partially edit match with $y^j$ for values of $j \geq 2$.

We say that $x^i$ (fully) edit matches with $y^j$ if $x^i$ partially matches with $y^j$ but does not partially match with $y^{j-1}$.

In order to prove Theorem 3.17, we will show that in order to solve the Pseudorandom Edit Distance Problem on $x$ and $y$, it suffices to solve the Clean Alignment Problem on $(x^1, \ldots, x^{n/6B})$ and $(y^1, \ldots, y^{n/3B})$, with $f(i,j)$ defined to indicate whether $x^i$ and $y^j$ edit match.

We begin by deriving several important properties of this definition of edit matching. Recall that a block $x^i$ is $p$-unique if its $B$-letter substrings are all of edit distance at least $pB$ from the $B$-letter substrings not intersecting $x^i$.

**Lemma 3.18.** Suppose $x^i$ and $x^j$ both partially edit match with $y^k$. Then neither $x^i$ nor $x^j$ are $p$-unique.

**Proof.** Since $x^i$ partially edit matches with $y^k$, there is a substring $a$ of $x^i$ which is within $pB/8$ edits of $y^k$ (because $x^i$ must be within $pB/8$ edits of a string containing $y^k$). Similarly, there is a substring $b$ of $x^j$ which is within $pB/8$ edits of $y^k$. By the triangle inequality, $\text{ed}(a, b) \leq pB/4$. It follows that the first $B$ letters of $a$ are within $pB/2$ edits of the first $B$ letters of $b$. (Indeed, if we consider an optimal sequence of edits from $a$ to $b$ restricted to the first $B$ letters of $a$, then that sequence of edits must result in a string of length no more than $\text{ed}(a, b) \leq pB/4$ away from $B$.) Therefore, neither $x^i$ nor $x^j$ are $p$-unique.

For the rest of the subsection, fix an optimal substitution-free sequence of edits $A$ between $x$ and $y$. (That is, $A$ consists only of insertions and deletions.) We will sometimes view $A$ as a sequence of edits, and other times consider it as a non-crossing matching between the letters in $x$ and those in $y$ such that each edge must be between two letters of the same value; the insertions and deletions correspond with letters which are left unmatched. As such, we will often refer to $A$ as an alignment, rather than a sequence of edits.

Assign each edit in $A$ to a block $x^i$ in which it occurs (deciding boundary cases arbitrarily), and define $c_i$ to be the number of edits attributed to each block $x^i$. Notice, in particular, that $\sum_i c_i = \text{ed}(x, y)$, that each $x^i$ is transformed by $A$ into some substring of $y$ via $c_i$ edits, and that the concatenation of the resulting substrings of $y$ forms all of $y$. Similarly, attribute to the blocks of $y$ costs $d_i$ such that $\sum_i d_i = \text{ed}(x, y)$ and such that each $y^j$ is transformed by $d_i$ edits into some substring of $x$. We will use these values $c_i$ and $d_i$ to aid us in our analysis for the rest of the section.

We continue by stating another important property of edit matching blocks. We call $x^j$ *polygamous* if it partially edit matches with some $y^k$ and $y^j$ for which $k$ and $l$ differ by more than one. Otherwise, $x^j$ is said to be *monogamous*, even if it fails to partially edit match with any $y^k$. The next lemma bounds the number of polygamous $x^j$’s.

**Lemma 3.19.** The number of letters in polygamous $x^j$’s is at most $O\left( \frac{1}{p} \text{ed}(x, y) + M(x) \right)$.

**Proof.** Since only $M(x)$ letters in $x$ reside in non-$p$-unique blocks, it suffices to show that the num-
Lemma 3.20. Let $E$ be a set of disjoint edges between $\{x^i\}$ and $\{y^j\}$ such that for all $e = (x^i, y^j) \in E$, $x^i$ edit matches with $y^j$. Let $t$ be the number of letters in $x$ which reside in a block unmatched by $E$. Then in time $O(Bn \log n)$, one can recover from $E$ a sequence of $O\left(\frac{1}{p}\text{ed}(x, y) + M + t\right)$ edits from $x$ to $y$.

Proof. Because $\sum c_i = \text{ed}(x, y)$, all but $O\left(\frac{1}{p}\text{ed}(x, y)\right)$ of the letters in $x$ are contained in $x^i$'s satisfying $c_i \leq pB/100$. Moreover, by Lemma 3.19 at most $O\left(\frac{1}{p}\text{ed}(x, y) + M\right)$ letters are contained in polygamous $x^i$'s.

Now consider a monogamous $x^i$ for which $c_i \leq pB/100$. We claim that $x^i$ must partially edit match to a $y^j$ which is within fewer than $6B$ positions of where $x^i$ is mapped to by $A$ (meaning each letter in $x^i$ that is matched by $A$ is matched to a letter within fewer than $6B$ positions of $y^j$). In particular, if $A$ transforms $x^i$ into a substring of $y$ beginning at some $y_k$, then because $c_i \leq pB/100$, it must be that $\text{ed}(x^i, y_k \cdots y_{k+6B-1}) \leq pB/50$. If we define $k'$ to be $k$ rounded down to the nearest position whose zero-indexed position is a multiple of $pB/100$, then it follows that $\text{ed}(x^i, y_{k'} \cdots y_{k'+6B-1}) \leq pB/25$. If we define $k''$ to be $k'$ rounded up to the next multiple of $3B$, then $x^i$ partially edit matches with $y_{k''/3B}$. By construction of $y_{k''/3B}$, each letter in $x^i$ that is matched by $A$ is matched to a letter within fewer than $6B$ positions of $y_{k''/3B}$.

Define $j$ to be $k''/3B$. Since $x^i$ partially edit matches with $y^j$ and $x^i$ is monogamous, the unique $y^j$ to which $x^i$ edit matches must satisfy $j' \in \{j - 1, j\}$. This, in turn, means that every letter in $x^i$ which is matched by $A$ to a letter in $y$ is matched to a letter in $y$ within fewer than $9B$ positions of $y^j$.

Recall that all but at most $O\left(\frac{1}{p}\text{ed}(x, y) + M\right)$ of the letters in $x$ reside in blocks $x^i$ which are monogamous and satisfy $c_i \leq pB/100$. Moreover, of these letters, all but at most $t$ of them reside in a block $x^i$ which is edit matched by $E$. Hence, with the exception of $x^i$'s containing a total of at most $O\left(\frac{1}{p}\text{ed}(x, y) + M + t\right)$ letters, every $x^i$ is edit matched by $E$ to a single $y^j$, and any edges in the alignment $A$ between a letter in $x^i$ and a letter in $y$ have to concern a letter in $y$ within fewer than $9B$ positions of $y^j$.

Consider the set $T$ of edges between letters in $x$ and $y$, where an edge $(x_r, y_s)$ is included if $x_r$ is in some $x^i$ which is matched by $E$ to some $y^j$ within fewer than $9B$ positions of $y_s$. Note that $T$ contains at most $O(nB)$ edges. We have shown that the intersection between $T$ and the edges in the alignment $A$ yields an alignment which matches all but at most $O(\text{ed}(x, y) + M + t)$ letters of $x$ (and thus also of $y$ since $|y| = |x|$). Applying...
Lemma 3.1 of [2], which finds the optimal alignment restricted to a set \( T \) of edges in time \( O(|T| \log n) \), it follows that we can recover a sequence of \( O(\text{ed}(x, y) + M + t) \) edits from \( x \) to \( y \) in time \( O(Bn \log n) \). □

To complete the proof of Theorem 5.17 using Lemma 3.21, it suffices to show that any optimal clean edit-matching alignment between \((x^1, \ldots, x^{n/6B})\) and \((y^1, \ldots, y^{n/3B})\) leaves no more than \( O(\text{ed}(x, y) + M) \) letters unmatched.

We begin by analyzing the cost of an optimal (possibly crossing) edit matching. An edit matching between \((x^1, \ldots, x^{n/6B})\) and \((y^1, \ldots, y^{n/3B})\) is a matching whose edges are between edit-matched \( x^i \)'s and \( y^j \)'s. The cost of an edit matching is defined in the same asymmetric manner as the cost of an edit-matching alignment.

**LEMMA 3.21.** Let \( T \) be a minimum-cost edit matching between \((x^1, \ldots, x^{n/6B})\) and \((y^1, \ldots, y^{n/3B})\). Then the cost of \( T \) is at most

\[
O\left(\frac{1}{p^B} \text{ed}(x, y) + M\right).
\]

**Proof.** Recall that any block \( x^i \) with \( c_i \leq pB/100 \) partially edit matches to some \( y^j \), and thus also edit matches to some \( y^j \). (See the proof of Lemma 3.20.) It follows that all but \( O\left(\frac{1}{p^B} \text{ed}(x, y) \right) \) of the blocks \( x^i \) edit match with some \( y^j \).

By Lemma 3.18, all but \( O\left(\frac{1}{p^B} \text{ed}(x, y) + M/B\right) \) of the \( x^i \)'s edit match with some \( y^j \)'s that don’t edit match with any other \( x^i \)'s. It follows that there is an edit matching between \((x^1, \ldots, x^{n/6B})\) and \((y^1, \ldots, y^{n/3B})\) in which all but \( O\left(\frac{1}{p^B} \text{ed}(x, y) + M/B\right) \) of the \( x^i \)'s are matched.

The \( x \)-portion cost of such an edit matching \( T \) is at most \( O\left(\frac{1}{p^B} \text{ed}(x, y) + M/B\right) \). Lemma 3.20 can be applied to \( T \) to recover a sequence of \( O\left(\frac{1}{p^B} \text{ed}(x, y) + M\right) \) edits from \( x \) to \( y \). Recall that the sequence of edits recovered by Lemma 3.20 removes any letters in \( y \) which are not within fewer than 9B positions of some \( y^j \) that is matched by \( T \). Hence, given any seven adjacent \( y^j \)'s left unmatched by \( T \) (corresponding with \( 21B \) unmatched letters), the middle \( y^j \)' of the seven must incur \( 3B \) edits in the process described by Lemma 3.20. Since only \( O\left(\frac{1}{p^B} \text{ed}(x, y) + M\right) \) edits can be incurred in total, the \( y \)-portion cost of \( T \) cannot exceed

\[
O\left(\frac{1}{p^B} \text{ed}(x, y) + M\right).
\]

This completes the proof of the lemma. □

The preceding lemma bounds the cost of a minimum-cost edit matching. The next lemma will allow us to bound the cost of a minimum-cost edit-matching alignment. In particular, the lemma shows that in any edit matching, the crossings can be eliminated by removing only edges that are incident to an \( x^i \) with one of three properties: \( x^i \) is either polygamous, non-p-unique, or satisfies \( c_i \geq pB/100 \). Since one can bound the number of such \( x^i \)'s, it follows that we can transform any edit matching into an edit-matching alignment by removing only a small number of edges.

**LEMMA 3.22.** Suppose that for \( i < j \) and \( k \leq l \), \( x^i \) edit matches with \( x^j \) and \( x^j \) edit matches with \( x^k \). Then either \( \max(c_i, c_j) \geq pB/100 \), or at least one of \( x^i \) or \( x^j \) are either polygamous or non-p-unique.

**Proof.** If both \( c_i \) and \( c_j \) are smaller than \( pB/100 \), then the alignment \( A \) tells us how to partially edit match \( x^i \) and \( x^j \) each to some \( y^q \) and \( y^r \) with \( q \leq r \) (as done in the proof of Lemma 3.20). If \( q = r \), then by Lemma 3.18 neither \( x^i \) nor \( x^j \) are p-unique. If \( q < r \) and both \( x^i \) and \( x^j \) are monogamous, then since \( k \leq l \), it follows that \( k = l \). But by Lemma 3.18 this prevents either \( x^i \) or \( x^j \) from being p-unique.

Therefore, if both \( c_i \) and \( c_j \) are less than \( pB/100 \), then at least one of \( x^i \) or \( x^j \) are either polygamous or non-p-unique. □

Finally, we can now bound the cost of an optimal clean edit-matching alignment.

**LEMMA 3.23.** Let \( T \) be a minimum-cost clean edit-matching alignment between \((x^1, \ldots, x^{n/6B})\) and \((y^1, \ldots, y^{n/3B})\). Then the cost of \( T \) is at most

\[
O\left(\frac{1}{p^B} \text{ed}(x, y) + M\right).
\]

**Proof.** Consider an optimal edit-matching \( T_0 \). By Lemma 3.21, the cost of \( T_0 \) is no greater than \( O\left(\frac{1}{p^B} \text{ed}(x, y) + M\right) \).

To obtain \( T \), remove from \( T_0 \) any edges involving some \( x^i \) such that either \( c_i < pB/100 \), \( x^i \) is polygamous, or \( x^i \) is non-p-unique. This removes at most \( O\left(\frac{\text{ed}(x, y)}{p^B}\right) \) \( x^i \)'s with \( c_i < pB/100 \), at most \( O\left(\frac{1}{p^B} \text{ed}(x, y) + M/B\right) \) \( x^i \)'s which are polygamous (Lemma 3.19), and at most \( M/B \) \( x^i \)'s which are not p-unique. Since each edge-removal can increase the \( x \)-portion and \( y \)-portion
costs each by at most one, the cost of $T$ is at most $O\left(\frac{1}{B} \text{ed}(x, y) + M\right)$.

By Lemma \ref{lem:3.22}, $T$ has no crossings. Moreover, because $T$ does not match any polygamous $x^i$'s, and because by Lemma \ref{lem:3.18} $T$ does not match any $y^j$'s that edit match to more than one $x^i$, $T$ is a clean edit-matching alignment. □

Theorem \ref{thm:3.17} follows easily from the preceding lemmas.

**Proof.** [Proof of Theorem \ref{thm:3.17}] We will assume without loss of generality that $p \geq 1/B$, since otherwise we may replace $p$ with $1/B$ without changing the definition of $p$-unique blocks.

Suppose there is an algorithm for the Clean Alignment Problem that runs in time $\tilde{O}(n)$ and returns a clean edit-matching alignment whose cost is within a factor of $O(1)$ of optimal, in expectation.

For a given $i$ and $j$, determining whether $x^i$ edit matches $y^j$ can be done in time $O(B^2)$. In particular, we need only compute the edit distances between $x^i$ and $O(1/p)$ substrings of $y$. Denote these substrings by $a_1, \ldots, a_q$. For each $a_s$, we wish to determine whether $\text{ed}(x^i, a_s) \leq pB/8$. Using the exact algorithm of \cite{15}, which computes $\text{ed}(u, v)$ in time $O(|u| + |v| + \text{ed}(u, v)^2)$, determining whether $\text{ed}(x^i, a_s) \leq pB/8$ can be done in time $O\left(B^2 + (pB)^2\right) \leq O(pB^3)$. Performing $O(1/p)$ such computations in order to determine whether $x^i$ edit matches with $y^j$ therefore takes time $O(B^3)$.

Thus the algorithm for the Clean Alignment Problem can be employed to find a clean edit-matching alignment between $(x^1, \ldots, x^{n/6B})$ and $(y^1, \ldots, y^{n/3B})$ in time $\tilde{O}\left((n/B)B^2\right) = \tilde{O}(nB)$.

The cost $t$ of this alignment will have expected value at most

$$O\left(\frac{1}{p} \text{ed}(x, y) + M\right),$$

by Lemma \ref{lem:3.20}.

By Lemma \ref{lem:3.20}, one can then recover in time $O(Bn \log n)$ a sequence of $t'$ edits from $x$ to $y$ satisfying

$$\mathbb{E}[t'] \leq O\left(\frac{1}{p} \text{ed}(x, y) + M\right),$$

as desired. □

**Remark 3.24.** When $p^2 \geq \frac{1}{B}$, we can use the bound $O(B + (pB^2)) \leq O(p^2 B^2)$ (rather than bounding the quantity by $pB^2$) in order to prove a slightly better runtime of $O(p \cdot nB)$.

## 4 Determining parameters $p$ and $B$

In this section, we consider the situation where the parameters $p$ and $B$ are not known beforehand. Throughout the section, for a string $x$, and parameters $p$ and $B$, we define $M_{p,B}(x)$ (often abbreviated by $M_{p,B}$) to be the quantity $M(x)$ defined in Section 3 (in which the parameters $p$ and $B$ were implicit).

We consider two settings. In the first setting, we are given two strings $x$ and $y$ and wish to compute $\text{ed}(x, y)$ within a factor of $O(\alpha)$ as fast as possible. Theorem 4.1 gives an algorithm for this problem which runs in time $O(n^{4/3}B^{2/3})$, where $B$ is the smallest block size for which the string $x$ is $(\alpha, B)$-pseudorandom.

**Theorem 4.1.** Let $x$ and $y$ be strings in $\Sigma^n$. Let $\alpha > 1$ be an approximation threshold, and suppose there is a power-of-two block-size $B$ for which the string $x$ is $(1/\alpha, B)$-pseudorandom. Then without knowing $B$ beforehand, one can still (with high probability) approximate $\text{ed}(x, y)$ within a factor of $O(\alpha)$ in time $O(n^{4/3}B^{1/3})$.

Moreover, rather than $x$ being $(1/\alpha, B)$-pseudorandom, it suffices that $M_{1/\alpha, B}(x) < n^{2/3}B^{1/3}$.

In the second setting we consider, one is given a source string $x$ which one intends to compare with many other strings $y$. Defining $\alpha$ and $B$ as before, we present an $O(n^{1.5}(\sqrt{B} + \alpha))$-time algorithm for preprocessing $x$, so that any edit distance computation $\text{ed}(x, y)$ can later be $\alpha$-approximated in time $O(nB)$.

**Theorem 4.2.** Let $x$ be a string in $\Sigma^n$. Let $\alpha > 1$ be an approximation threshold, and suppose there is a power-of-two block-size $B$ for which the string $x$ is $(1/\alpha, B)$-pseudorandom. Then without knowing $B$ beforehand, one can (with high probability) construct an algorithm $S$ in time $O(n^{1.5}(\sqrt{B} + \alpha))$ so that $S$ is an $O(nB)$-time algorithm for approximating $\text{ed}(x, y)$ within a factor of $O(\alpha)$ (with high probability) for arbitrary strings $y \in \Sigma^n$.

Moreover, rather than $x$ being $(1/\alpha, B)$-pseudorandom, it suffices that $M_{1/\alpha, B}(x) < n^{1/2}B^{1/2}$.

The proofs of Theorems 4.1 and 4.2 will rely on the following lemma:

**Lemma 4.3.** Consider a string $x$ of length $n$, and a parameter $B \in \mathbb{N}$ such that $B$ is a power of two. Then for any threshold $n'$ and value $p = \frac{1}{2^{n'}}$, there is an algorithm which runs in time $O(n^{2-\epsilon}(B + 1/p^2))$, and which with high probability returns true if $M_{p, 2B} \leq n'/2$, and false if $M_{p, B} > 2n'$. (Otherwise, the algorithm may return true or false arbitrarily.)
Proof. We will assume without loss of generality that $n$ is a multiple of $6B$, since otherwise $x$ can be padded with null characters to be a length divisible $6B$, without changing $M_{p,B}$. Let $x^1 \ldots x^n/6B$ be the $6B$-letter blocks that make up $x$.

Let $c$ be a sufficiently large constant. The algorithm uses a simple random sampling approach. We randomly sample $s = cn^1-c \log n$ blocks $x^1, \ldots, x^s$ from $x$. For each of these blocks $x^i$, we will perform a test on $x^i$ which returns true if $x^i$ is $(p/2)$-unique, returns false if $x^i$ is not $p$-unique, and may return either true or false otherwise. (We will describe how this test, which we call the uniqueness test, works at the end of the proof.) Let $r$ be the number of $x^i$’s for which the uniqueness test returns false. Because the uniqueness test returns true whenever $x^i$ is $(p/2)$-unique,

$$
E[r] \leq s \cdot \frac{M_{p,B}/n}{n} = \frac{M_{p,B} \cdot c \log n}{n^2}.
$$

Thus if $M_{p,B} \leq n^2/2$, then $E[r] \leq \frac{c}{2} \log n$, which by a Chernoff bound means that (for $c$ large enough) with high probability $r < c \log n$. On the other hand, because the uniqueness test returns false whenever $x^i$ is not $p$-unique,

$$
E[r] \geq s \cdot \frac{M_{p,B}/n}{n} = \frac{M_{p,B} \cdot c \log n}{n^2}.
$$

Thus if $M_{p,B} \geq 2n^2$, then $E[r] \geq 2c \log n$, which by a Chernoff bound means that (for $c$ large enough) $r > c \log n$ with high probability. It follows that by returning whether $r \leq c \log n$, our algorithm will with high probability return true if $M_{p,B} \leq n^2/2$, and return false if $M_{p,B} > 2n^2$.

In the remainder of the proof, we describe the uniqueness test for a given block $x^i$, and evaluate the runtime of the algorithm. The uniqueness test for $x^i$ examines every $B$-letter substring $a$ in $x$ such that $a$ does not intersect $x^i$ and such that $a$ ends in a position divisible by $\frac{pB}{n}$, and also examines each $B$-letter substring $b$ in $x$ that is contained entirely in $x^i$ and ends in a position divisible by $\frac{pB}{n}$. For each such pair $a$ and $b$, the algorithm uses the low-distance regime algorithm of [13] to determine in time $O(B + n^2B^2)$ whether $ed(a,b) \leq B/2$. The uniqueness test returns true if and only if $ed(a,b) \leq B/2$ for all such $a$ and $b$. Notice that if $x^i$ is $(p/2)$-unique, then the uniqueness test will necessarily return true. Moreover, if the uniqueness test returns true, then for every $B$-letter substring $a'$ in $x$ not intersecting $x^i$, and every $B$-letter substring $b'$ in $x^i$, it must be that $ed(a,b) \leq B/2 + \frac{4M_p}{n^2} \leq B$, meaning that $x^i$ is $p$-unique. Hence the uniqueness test satisfies both properties required from it.

Finally, we evaluate the runtime of our algorithm. Since there are $O(n/(pB))$ options for $a$ and $O(1/p)$ options for $b$ in each uniqueness test, each uniqueness test runs in time

$$
O \left( \frac{n}{pB} \cdot \frac{1}{p} \cdot (B + p^2B^2) \right) \leq O(nB + n/p^2).
$$

Since our algorithm runs $\tilde{O}(n^{1-\epsilon})$ uniqueness tests, the full runtime is $\tilde{O}(n^{2-\epsilon} + (B/1/p^2))$. □

Using Lemma [13] we now prove Theorem 4.1

Proof. [Proof of Theorem 4.1] Assume without loss of generality that $\alpha$ is a power of two. To accomplish the desired time bound, we run two algorithms in parallel. The first algorithm is the low-distance regime algorithm of [13] which runs in time $O(n + ed(x,y)^2)$. The second algorithm considers values $B_i = \alpha \cdot 2^i$ for $i = 0, 1, 2, \ldots$, and applies Lemma [13] to each $B_i$ with $p = \frac{2}{\alpha}$ and $n^2 = 2n^{2/3} \cdot \alpha^{2/3} \cdot (B_j + \alpha^2)^{1/3}$, upon finding a $B_j$ for which Lemma [13] returns true, the algorithm approximates $ed(x,y)$ in time $\tilde{O}(n \cdot B_j)$ by treating $x$ as $(2/\alpha, B_j)$-pseudorandom.

If the low-distance regime algorithm finishes first, then we can return $ed(x,y)$ exactly. If the second algorithm terminates first, then we continue to run the low-distance regime algorithm until it has run for time $\Theta(n^{4/3} \cdot \alpha^2 \cdot (B_j + \alpha^2)^{2/3})$, and only if the low-distance regime algorithm does not terminate in that time window do we use the output of the second algorithm.

Because $p = \frac{2}{\alpha}$ and $n^2 = 2n^{2/3} \cdot \alpha^{2/3} \cdot (B_j + \alpha^2)^{1/3}$, the second algorithm’s runtime will be

$$
\tilde{O}(n^{2-\epsilon}B_j + 1/p^2) = \tilde{O}(n^{4/3}(B_j + \alpha^2)^{2/3}/\alpha^{2/3}) \\
\leq \tilde{O}(n^{4/3}(B_j/\alpha^2)^{2/3} + \alpha^{2/3}) \\
\leq \tilde{O}(n^{4/3}B_j^{2/3}).
$$

Notice that Lemma [13] guarantees with high probability that $B_j \leq B$ (because $M_{1/\alpha,B} < n^{2/3} \cdot B^{1/3}$), meaning that with high probability our algorithm achieves runtime $\tilde{O}(n^{4/3}B^{2/3})$, as desired.

To prove the accuracy of our algorithm, consider the case where the output is determined by the second algorithm. By Lemma [13] with high probability, $M_{2/\alpha,B_j} \leq 2n^2 = 4n^{2/3} \cdot \alpha^{2/3} \cdot (B_j + \alpha^2)^{1/3}$. By (the high-probability version of) Theorem 4.1 it follows that the second algorithm will find a sequence of $t$ edits for some $t$ satisfying

$$
t \leq O(\alpha ed(x,y) + n^{2/3} \cdot \alpha^{2/3} \cdot (B_j + \alpha^2)^{1/3}),
$$
with high probability. Moreover, because the low-distance regime algorithm did not finish in the time $O(n^{4/3}(B_j + \alpha^2)^{2/3}/\alpha^{2/3})$, it must be that $\text{ed}(x, y) \geq n^{2/3} \cdot (B_j + \alpha^2)^{1/3}/\alpha^{1/3}$. Plugging this into Equation 4.3, we get that $t \leq O(\alpha \text{ed}(x, y))$, as desired. \hfill \Box

Finally, we prove Theorem 4.2.

Proof. [Proof of Theorem 4.2] We assume without loss of generality that $\alpha$ is a power of two. Our preprocessing step goes as follows. We consider values $B_i = \alpha 2^i$ for $i = 0, 1, 2, \ldots$, and apply Lemma 4.3 to each $B_i$ with $p = \frac{\alpha}{2}$ and $n^e = 2n^{1/2} \cdot (B_j + \alpha^2)^{1/2}$; upon finding a $B_j$ for which Lemma 4.3 returns true, we have completed the preprocessing step. Note that the preprocessing step takes time

$$\tilde{O}(n^{2-e}(B_j + \alpha^2))$$

$$= \tilde{O}(n^{1.5} \sqrt{B_j + \alpha^2}),$$

and since with high probability $B_j$ will be at most $B$ (by Lemma 4.3) and because of the fact that $M_{1/\alpha, B} < n^{1/2} \cdot B^{1/2}$, it follows that with high probability the runtime of the preprocessing step is at most $\tilde{O}(n^{1.5} \sqrt{B + \alpha^2})$, as desired.

Given a string $y$, we can then approximate $\text{ed}(x, y)$ as follows. We first run the low-distance regime algorithm of 15 for time $\Theta(n \cdot B_j)$, and if it completes then we return its output. Otherwise, we may conclude that

$$\text{ed}(x, y) \geq \sqrt{nB_j}.$$  

In the latter case, we treat $x$ as $(2/\alpha, B_j)$-pseudorandom and generate an estimate for $\text{ed}(x, y)$ in time $\tilde{O}(n \cdot B_j)$ (using the high-probability version of Theorem 3.1). By Lemma 4.3 we know that with high probability $M_{2/\alpha, B_j} \leq 2n^e = 4n^{1/2} \cdot (B_j + \alpha^2)^{1/2}$. By Theorem 3.1 it follows that with high probability the number of edits $t$ which we find between the strings $x$ and $y$ will satisfy

$$t \leq O \left( \alpha \text{ed}(x, y) + n^{1/2} \cdot (B_j + \alpha^2)^{1/2} \right)$$

$$\leq O \left( \alpha \text{ed}(x, y) + \alpha \cdot n^{1/2} \cdot B_j^{1/2} \right).$$

By (4.4), we get $t \leq O(\alpha \text{ed}(x, y))$, as desired. \hfill \Box

5 Conclusion

In this paper, we have proposed a natural model of pseudorandomness for strings which allows for edit distance to be efficiently approximated. We conclude by presenting two directions for future work.

- One important direction for future work is to investigate the degree to which the algorithm presented is practical for real-world inputs. In particular, for what parameters $p$ and $B$ do real-world inputs tend to be (almost) $(p, B)$-pseudorandom?

- On the theoretical side, it is interesting to note that in the smoothed complexity model the algorithm of 2 achieves sublinear runtime for strings $x$ and $y$ of sufficiently large edit distance apart. Can such a result be replicated in our pseudorandomness model?

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