Approximate Similarity Search Under Edit Distance Using Locality-Sensitive Hashing

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Abstract

Edit distance similarity search, also called approximate pattern matching, is a fundamental problem with widespread applications. The goal of the problem is to preprocess $n$ strings of length $d$, to quickly answer queries $q$ of the form: if there is a database string within edit distance $r$ of $q$, return a database string within edit distance $cr$ of $q$. A data structure solving this problem is analyzed using two criteria: the amount of extra space used in preprocessing, and the expected time to answer a query.

Previous approaches to this problem have either used trie-based methods, which give exact solutions at the cost of expensive queries, or embeddings, which only work for large (superconstant) values of $c$.

In this work we achieve the first bounds for any approximation factor $c$, via a simple and easy-to-implement hash function. This gives a running time of $\tilde{O}(d3^r n^{1/c})$, with space $\tilde{O}(3^r n^{1+1/c} + dn)$. We show how to apply these ideas to the closely-related Approximate Nearest Neighbor problem for edit distance, obtaining similar time bounds.
1 Introduction

For a large database of items, a similarity search query asks which database item is most similar to the query. This leads to a basic algorithmic question: how can we preprocess the database to answer these queries as quickly as possible?

Similarity search is used frequently in a wide variety of applications. Unfortunately, for databases containing high-dimensional items, algorithm designers have had trouble obtaining bounds that are significantly faster than a linear scan of the entire database. This has often been referred to as the “curse of dimensionality.” Recent work in fine-grained complexity has begun to explain this difficulty: achieving significantly better than linear search time would violate the strong exponential time hypothesis. [4, 29, 57]

However, these queries can be relaxed to approximate similarity search queries. For an approximation factor $c$, we want to find a database item that is at most a $c$ factor less similar than the most similar item.

Approximate similarity search is fairly well-understood for many metrics; see [6] for a survey. For example, in Euclidean space we have theoretical upper bounds [7, 27], fast implementations [13, 32, 38, 48, 59], and lower bounds for a broad class of algorithms [7]. Many of these results are based on locality-sensitive hashing (LSH), originally described in [37]. A hash is locality-sensitive if similar items are more likely to share the same hash value.

When a database contains text items, a natural notion of similarity is edit distance: how many character inserts, deletes, and replacements are required to get from the query string to a database string? In fact, edit distance similarity search is frequently used in computational biology [40, 45, 55], spellcheckers [19, 60], computer security (in the context of finding similarity to weak passwords) [49], and many more applications, see e.g. [16].

Surprisingly, finding an efficient algorithm for approximate similarity search under edit distance remains essentially open. Known results focus on methods for exact similarity search (with $c = 1$), which incur expensive query times, and on embeddings, which require very large—in fact superconstant—approximation factors $c$.

In this paper we give the first bounds for edit distance similarity search that apply for any approximation factor $c$. These bounds are based on a simple locality-sensitive hash function.

1.1 Results

The main result of our paper is the first locality-sensitive hash for edit distance. We analyze the performance of this hash when applied to the problems of approximate similarity search and approximate nearest neighbor search, obtaining the first non-trivial bounds that apply to any approximation factors $c$.

Let $n$ be the number of strings stored in the database. We assume that all query strings and all database strings have length at most $d$. We assume $d = O(n)$ and the size of the alphabet is $O(n)$.

We begin with a result for queries with a fixed radius $r$: for each query, if there exists a database point within distance $r$, we aim to return a database point within distance $cr$. The parameter $r$ is known ahead of time when building the data structure. We refer to these as Approximate Similarity Search queries.

**Theorem 1.** There exists a data structure answering Approximate Similarity Search queries under Edit Distance in $\tilde{O}(d^3n^{1/c})$ time per query and $\tilde{O}(3^c n^{1+1/c} + dn)$ space.

We also give a data structure that answers queries where the distance $r$ to the closest neighbor is not known during preprocessing. We refer to these as Approximate Nearest Neighbor queries.
**Theorem 2.** There exists a data structure answering Approximate Nearest Neighbor Search queries under Edit Distance in $\tilde{O}(d^3 n^{1/c})$ time per query and $\tilde{O}(dn^2)$ space.

**Implications for Related Problems.** Our results lead to immediate bounds for similarity join, where all close pairs in a database are computed; see e.g. [56].

Much of the previous work on approximate similarity search under edit distance considered a variant of this problem: there is a long text $T$, and we want to find all locations in $T$ that have low edit distance to the query $q$. Our results immediately apply to this problem by treating all $d$-length substrings of $T$ as the database of items; this leads to an extra factor of $d$ in time and space.

Frequently, practical situations may require that we find all of the neighbors with distance at most $r$, or (similarly) the $k$ closest neighbors. See e.g. [2] for a discussion of this problem in the context of LSH. Our analysis immediately applies to these problems. However, if there are $k$ desired points, the running time increases by a factor $k$.

**1.2 Related Work**

The most similar related work is an independent construction of an LSH for edit distance by Marçais et al. [50]. Their work uses a fundamentally different approach, based on an ordered min-hash of $k$-mers. Their results include bounds proving that the hash is locality-sensitive; however, these bounds do not place any closed-form guarantees on the gap between $p_1$ (the probability that similar items collide) and $p_2$ (the probability that dissimilar items collide), and therefore do not lead to similarity search bounds.

**Exact Similarity Search Under Edit Distance.** Exact similarity search under edit distance (i.e. with $c = 1$) has been studied for many years. This problem was generally referred to as “approximate pattern matching.” For a survey of past results, see [16, 47, 53].

A breakthrough paper of Cole, Gottlieb, and Lewenstein achieved a data structure with space $O(n(\log n)^r)$ and query time $O(d + (\log n)^r)$ for constant $r$ [30]. This stood in contrast to previous work, which generally had to assume that the length of the strings $d$ or the size of the alphabet $|\Sigma|$ was a constant to achieve similar bounds. Later work improved on this result [23, 33]. However, these results all have essentially $(\log n)^r$ query time.

Ignoring constant terms (and assuming constant $r$), we can compare our running time against the exact method as $n^{1/c}$ vs $(\log n)^r$. The polynomial term is better if $rc > \log n / \log \log n$. For reasonable values of $n$ this inequality is satisfied even if $r$ and $c$ are small constants—for example, for $n = 2^{32}$ and $c \to 1$, this implies better asymptotics for $r \geq 6$.

**Approximate Similarity Search Under Edit Distance.** Previous results for approximate similarity search with worst-case bounds used either product metrics, or embeddings into $L_1$.

In techniques based on *product metrics*, each point is mapped into several separate metrics. The distance between two points is defined as their maximum distance in any of these metrics. Using this concept, Indyk provided an extremely fast (but large) nearest-neighbor data structure requiring $O(d)$ query time and $n^{d/(1+\log c)}$ space for any $c \geq 3$ [36].

A different line of work focused on embeddings into $L_1$ space. Because there are approximate nearest neighbor data structures for $L_1$ space that require $n^{1/c}$ time and $n^{1+1/c}$ space, an embedding with stretch $\alpha$ leads to an efficient approximate nearest neighbor data structure for

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1 This sweeps significant time issues under the rug, such as the relative cost of performing an entire edit distance computation vs a series of trie operations. This calculation is only intended to compare asymptotics; we leave experimental analysis to future work.

2 This can be improved to $n^{1/(2c-1)}$ and $n^{1+1/(2c-1)}$ time and space respectively using data-dependent techniques, and can be further generalized to other time-space tradeoffs; see [7].
A long line of work on improving the stretch of these embeddings ultimately resulted in a deterministic embedding with stretch

\[ \exp\left(\sqrt{\log d / \log \log d}\right) \] 

[54]. Even better bounds can be obtained with randomized embeddings. Jowhari gave a randomized embedding with stretch

\[ O((\log d)^2 \log^* d / \log^* d) \] 

[39]. More recently, the CGK embedding parameterized by \( r \) instead of \( d \), giving an embedding into \( L_1 \) with stretch \( O(r) \) [22]. The CGK embedding implies an approximate similarity search algorithm with running time \( n^{O(r/c)} \), nontrivial for \( c \gg r \).

However, the constants proven in the CGK result are not very favorable—the upper limit on overall stretch given in the paper is 2592\( r \) (though this may be improvable with tighter random walk analysis). Nonetheless, this approach has already been shown to have great practical potential. In [61], this approach was adapted to perform edit distance similarity joins orders of magnitude faster than the previous state of the art, with a negligible impact on correctness. Interestingly, the authors report very little stretch in the embeddings (essentially constant rather than \( O(r) \)). It would be interesting to see if this implies that a practical implementation of our algorithm would outperform our worst-case bounds as well.

There is a lower bound of \( \Omega(\log d) \) for the stretch of any embedding of edit distance into \( L_1 \) [41]. This implies that embedding into \( L_1 \) is a hopeless strategy for \( c < \log d \), whereas we obtain nontrivial bounds even for constant \( c \). Thus, for this parameter range, using a locality-sensitive hash is fundamentally more powerful than embedding into \( L_1 \).

**Lower Bounds.** There are conditional lower bounds for approximate similarity search under edit distance based on the strong exponential hypothesis (SETH). In short, as the approximation factor \( c \to 1 \), the strong exponential time hypothesis implies that any approximate similarity search algorithm with polynomial preprocessing time must approach linear search time [29, 57].

**Other Work on Edit Distance.** The goal of sketching edit distance is to map strings at a given edit distance \( r \) to much smaller strings, while being able to recover the approximate edit distance between them [15]. Closely-related problems include error correcting codes for deletions [17] and the edit distance document exchange problem [25]. These problems share some high-level similarity with ours: the goal is to process the strings into easier-to-digest variants while retaining the important edit distance information. Indeed, both the sketching results of Belazzougui and Zhang [15] and our LSH are derived in part from the CGK embedding [22].

Approximating the edit distance (between a single pair of strings) is a classic algorithmic problem. Andoni et al. give an algorithm with approximation ratio \( (\log d)^{O(1/\epsilon)} \) running in \( O(d^{1+\epsilon}) \) time; this is the best known near-linear-time algorithm. Recently, Chakraborty et al. gave a truly subquadratic algorithm that approximates the edit distance to within a constant factor [21]. These approximation algorithms are not immediately useful for our parameter ranges (they essentially only have the potential to improve \( \text{poly}(r) \) terms in our running time). However, these algorithms work in large part by ruling out large portions of the edit distance dynamic programming table. There seems to be potential to interface these ideas with our hash, which performs a random walk through the table.

Further work has resulted in near-linear algorithms to approximate the edit distance for several special cases [14, 18, 31, 32, 43].

**Locality-Sensitive Hashing.** Locality-Sensitive Hashing was introduced by Indyk and Motwani to avoid the “curse of dimensionality,” in which high-dimensional similarity search problems generally have exponential dependence on \( d \) [35, 37].

LSH has led to efficient approximate similarity search algorithms for Hamming distance [12, 35, 37], \( L_1 \) and \( L_2 \) [7, 11], cosine similarity [5, 24], inner product similarity [3], and Jaccard similarity [20, 28]. Further work has extended LSH to Las Vegas guarantees [1] and examined its performance on non-worst-case datasets [44, 51].
Recently, a line of work has focused on LSH on arbitrary normed metrics \[8–10\]. Unfortunately, edit distance is not a normed space, so these techniques do not immediately apply.

## 2 Model and Preliminaries

In this section, we define our model and give notation that will be used in the paper.

We denote the alphabet used in our problem instance as \(\Sigma\). We assume that \(\perp\) and \($\) are not in \(\Sigma\).

We call a string \($\)-terminal if its last character is \($\), and it does not contain \($\) in any other position. The hash appends \($\) to each string being hashed, so that we can assume each input string is \($\)-terminal.

We index into strings using 0-indexed subscripts; \(x_0\) is the first character of \(x\) and \(x_i\) is the \(i+1\)st character. We use \(x[i]\) to denote the prefix of \(x\) of length \(i\); thus \(x[i] = x_0 \ldots x_{i-1}\). Finally, we use \(x \circ y\) to denote the concatenation of two strings \(x\) and \(y\), and \(|x|\) to denote the length of a string \(x\).

### 2.1 Edit Distance

Edit distance is defined using three operations: inserts, deletes, and replacements. Given a string \(x = x_1x_2 \ldots x_d\), inserting a character \(\sigma\) at position \(i\) results in a string \(x' = x_1 \ldots x_{i-1}\sigma x_i \ldots x_d\). Replacing the character at position \(i\) with \(\sigma\) results in \(x' = x_1 \ldots x_{i-1}\sigma x_{i+1} \ldots x_d\). Finally, deletion of the character at position \(i\) results in \(x' = x_1 \ldots x_{i-1}x_{i+1} \ldots x_d\). We refer to these three operations as edits.

The edit distance from \(x\) to \(y\) is defined as the smallest number of edits that must be applied to \(x\) to obtain \(y\). We denote this as \(\text{ED}(x, y)\).

### 2.2 Model and Problem Definition

In this paper we solve the approximate similarity search problem under edit distance, which can be defined as follows.

**Definition 3** (Approximate Similarity Search Under Edit Distance). *Given a set of \(n\) strings \(S\) and constants \(c\) and \(r\), preprocess \(S\) to quickly answer queries of the form, “if there exists a \(y \in S\) with \(\text{ED}(q, y) \leq r\), return a \(y' \in S\) with \(\text{ED}(q, y') \leq cr\) with probability > \(1/10\).”*

The above is sometimes called the approximate near neighbor problem. The constant \(1/10\) is arbitrary and can be increased to any desired constant without affecting our final bounds.

**Nearest Neighbor Search.** Oftentimes, we want to find the nearest database item to each query rather than parameterizing explicitly by \(r\).

**Definition 4** (Approximate Nearest Neighbor Search Under Edit Distance). *Given a set of \(n\) strings \(S\) and a constant \(c\), preprocess \(S\) to quickly answer queries of the form, “for the smallest \(r\) such that there exists a \(y \in S\) with \(\text{ED}(q, y) \leq r\), return a \(y' \in S\) with \(\text{ED}(q, y') \leq cr\) with probability > \(1/10\).”*

For most previous LSH-based approaches, efficient Nearest Neighbor Search algorithms follow immediately from Approximate Similarity Search algorithms using the black box reduction of Har-Peled, Indyk, and Motwani \[35\]. However, the exponential dependence on \(r\) in our bounds appears to cause significant difficulties with this approach. Fortunately, the discrete nature of edit distance means that we can use a different technique, iterating through the possible values of \(r\). We describe this in detail in Section 4.4.
2.3 Locality-Sensitive Hashing

A hash family is locality sensitive if close elements are more likely to hash together than far elements.

Definition 5 (Locality-Sensitive Hash). A hash family \( \mathcal{H} \) is \((r, cr, p_1, p_2)\)-sensitive under a distance function \(d(x, y)\) if

- for all \(x_1, y_1\) such that \(d(x_1, y_1) \leq r\), \(Pr_{h \in \mathcal{H}}(h(x_1) = h(y_1)) \geq p_1\), and
- for all \(x_2, y_2\) such that \(d(x_2, y_2) \geq cr\), \(Pr_{h \in \mathcal{H}}(h(x_1) = h(y_1)) \leq p_2\).

This paper gives the first direct\(^3\) locality-sensitive hash under edit distance with closed forms for \(p_1\) and \(p_2\), and the first to achieve Approximate Similarity Search guarantees for all \(c > 1\). We bound \(p_1\) and \(p_2\) for any \(r\) and \(cr\) in Lemma 14 and Lemma 15 respectively.

Some previous work (i.e. [26, 31]) has a stricter definition of locality sensitive hash: it requires that there exists a function \(f\) such that \(Pr(h(x) = h(y)) = f(d(x, y))\). Our hash function does not satisfy this definition; the exact value of \(x\) and \(y\) is necessary to determine their collision probability (see Lemma 16 for example).

A Note on Concatenating Hashes. Most previous approaches to nearest neighbor search begin with an LSH family that has \(p_1, p_2 = \Omega(1)\). A logarithmic number of independent hashes are concatenated together so that the concatenated function has collision probability \(1/n\). This technique was originally developed in [37], and has been used extensively since; e.g. in [2, 7, 28].

However, in this paper, we use a single function each time we hash. We directly set the hash parameters to achieve a desirable \(p_1\) and \(p_2\) (in particular, we want \(p_2 \approx 1/n\)). This is due to the stray constant term in Lemma 15. While our hash could work via concatenating several copies of a relatively large-probability\(^4\) LSH, this would result in a data structure with larger space and slower running time. One interesting implication is that, unlike many previous LSH results, our running time is not best stated with a parameter \(\rho = \log p_1 / \log p_2\)—rather, we choose our hashing parameters to obtain the \(p_1\) and \(p_2\) that give the best bounds for a given \(r\), \(c\), and \(n\).

3 The Locality-Sensitive Hash

Each hash function from our family maps a string \(x\) of length \(d\) with alphabet \(\Sigma\) to a string \(h(x)\) with alphabet \(\Sigma \cup \{\perp\}\) of length \(O(d + \log n)\). The function scans over \(x\) one character at a time, adding characters to \(h(x)\) based on the current character of \(x\) and the current length of \(h(x)\). Once the function has finished scanning \(x\), it stops writing and outputs \(h(x)\).

At a high level, for two strings \(x\) and \(y\), our hash function can be viewed as randomly guessing a sequence of edits \(T\), where \(h(x) = h(y)\) if and only if applying the edits in \(T\) to \(x\) obtains \(y\). Equivalently, one can view the hash as a random walk through the dynamic programming table for edit distance, where matching edges are traversed with probability 1, and non-matching edges are traversed with a tunable probability \(p \leq 1/3\). We discuss and prove these relationships in Section 4.1.

Parameters of the Hash Function. We parameterize our algorithm using a parameter \(p \leq 1/3\). By selecting \(p\) we can control the values of \(p_1\) and \(p_2\) attained by our hash (see Lemmas 14 and 15). We will specify \(p\) to optimize nearest neighbor search performance for a given \(r\), \(c\), and \(n\) in Section 4.3. We split \(p\) into two separate parameters \(p_a\) and \(p_r\) defined as

\[
p_a = \sqrt{\frac{p}{1 + p}} \quad \text{and} \quad p_r = \frac{\sqrt{p}}{\sqrt{1 + p} - \sqrt{p}}.
\]

\(^3\)By direct, we mean that this hash does not embed into \(L_1\) or use product metrics as an intermediary.

\(^4\)Although less than constant—Lemma 13 and the assumption that \(p \leq 1/3\) implies \(p_1 \leq (1/3)^c\).
Since $p \leq 1/3$, $p_a \leq 1/2$ and $p_r \leq 1$. For the remainder of this section, we will describe how the algorithm behaves using $p_a$ and $p_r$. The rationale behind these values for $p_a$ and $p_r$ will become clear in the proof of Lemma 13.

Underlying Function. Each hash function in our hash family has an underlying function that maps each \textit{(character, hash position)} pair to a pair of uniform random real numbers: $\rho : (\Sigma \cup \{$\} $\times \{1, \ldots , 8d/(1-p_a) + 6 \log n\} \rightarrow (0,1) \times (0,1)$\footnote{Adding $\$$ to the alphabet allows us to hash past the end of a string—this helps with edits that append characters.}\[^5\] We discuss how to store these functions and relax the assumption that these are real numbers in Section 4.5.

A hash function is completely determined by its underlying function $\rho$—in particular, two hash functions $h_1$ and $h_2$ have identical outputs on all strings if their underlying functions $\rho_1$ and $\rho_2$ are identical. Thus, we pick a random function from our hash family by sampling a random underlying function. We use $h_\rho(x)$ to denote the hash of $x$ using underlying function $\rho$.

The key idea behind the underlying function is that the random choices made by the hash depend only on the current character seen in the input string, and the current length of the output string. This means that if two strings are aligned—in particular, if the “current” character of $y$ matches the “current” character of $y$—the hash of each will make the same random choices, so the hashes will stay the same until there is a mismatch. This is the “oblivious synchronization mechanism” described in \[^{22}\].

3.1 How to Hash

A hash function $h$ is selected from the family $H$ by sampling a random underlying function $\rho$. We denote the hash of a string $x$ using $\rho$ as $h_\rho(x)$. The remainder of this section describes how to determine $h_\rho(x)$ for a given $x$ and $\rho$.

To hash $x$, the first step is to append $\$$ to the end of $x$ to obtain $x \circ \$$. We will treat $x \leftarrow x \circ \$\$ as the input string from now on—in other words, we assume that $x$ is $\$$-terminal.

The hash consists of a scan from left to right across $x$, adding characters one by one to an output string $s$. When this process finishes, $s$ is returned as the final hash value.

Let $i$ be the current index of $x$ being scanned by the hash function. Begin by setting $i = 0$, and $s$ to the empty string.

The hash function repeats the following process while $i < |x|$ and $|s| < 8d/(1-p_a) + 6 \log n$\footnote{The requirement $|s| < 8d/(1-p_a) + 6 \log n$ is useful to bound the size of the underlying function in Section 4.5.}.

Let $(r_1, r_2)$ be the current value of the underlying function based on $x_i$ and $|s|$; in other words, $(r_1, r_2) \leftarrow \rho(x_i, |s|)$. The hash performs one of three actions based on $r_1$ and $r_2$. Each action appends one character to the string $s$. We name these cases \textit{hash-insert}, \textit{hash-replace}, and \textit{hash-match}.

- If $r_1 \leq p_a$, \textbf{hash-insert}: the hash appends $\perp$ to $s$.
- If $r_1 > p_a$ and $r_2 \leq p_r$, \textbf{hash-replace}: the hash appends $\perp$ to $s$ and increments $i$.
- If $r_1 > p_a$ and $r_2 > p_r$, \textbf{hash-match}: the hash appends $x_i$ to $s$ and increments $i$.

When $i \geq |x|$ or $|s| \geq 8d/(1-p_a) + 6 \log n$, the hash stops and returns $s$ as $h_\rho(x)$.

We give pseudocode for this hash function and give an example hash in Appendix A.

Similarities with the CGK embedding. Our hash function follows some of the same high-level structure as the CGK embedding \[^{22}\]. In fact, our hash reduces to their embedding by omitting the appended character $\$$, and setting $p_a = 1/2$ and $p_r = 0$. Our performance speedup comes from the following changes:
choosing $p_a$ to optimize for similarity search rather than embedding guarantees;
• using repeated “embeddings,” to find a particularly effective sequence of alignments; and
• combining a bit-sampling-like approach\(^7\) with the embedding itself. In particular, we gain
performance because a hash-insert always writes $\bot$—once the hash “guesses” the insert, it
does not need to worry about sampling that character. This is how the value of $p_r$ is used in
our approach.

4 Analysis

We begin in Section 4.1 with some structure that relates hash collisions between two strings $x$ and
$y$ with sequences of edits that transform $x$ into $y$. We use this to bound the probability that $x$ and
$y$ collide in Section 4.2. With this we can prove our main results in Sections 4.3 and 4.4. Finally
we discuss how to store the underlying functions in Section 4.5.

4.1 Interpreting the Hash

In this section, we discuss when two strings $x$ and $y$ hash (with an underlying function $\rho$) to the
same string $h_\rho(x) = h_\rho(y)$.

We define three sequences to help us analyze the hash. In short, the transcript of $x$ and $\rho$ lists
the decisions made by the hash function as it scans $x$ using the underlying function $\rho$. The grid
walk of $x$, $y$, and $\rho$ is a sequence based on the transcripts (under $\rho$) of $x$ and $y$—it consists of
some edits, and some extra operations that help keep track of how the hashes of $x$ and $y$ interact.
Finally, the transformation of $x$, $y$, and $\rho$ is a sequence of edits based on the grid walk of $x$, $y$, and
$\rho$.

Using these three concepts we can set up the basic structure to bound the probability that $x$
and $y$ hash together using their edit distance. We use these definitions to analyze the probability
of collision in Section 4.2.

**Transcripts.** A transcript is a sequence of hash operations: each element of the sequence is a
hash-insert, hash-replace, or hash-match. Essentially, the transcript of $x$ and $\rho$, denoted $\tau(x, \rho)$, is
a log of the actions taken by the hash on string $x$ using underlying function $\rho$.

We define an index function $i(x, k, \rho)$. The idea is that $i(x, k, \rho)$ is the value of $i$ when the
$k + 1$st hash character is written, when hashing $x$ using underlying function $\rho$.

We set $\tau(x, 0, \rho) = 0$ for all $x$ and $\rho$. Let $(r_{1,k}, r_{2,k}) = \rho(i(x, k, \rho), k)$. We can now recursively
define both $\tau(x, \rho)$ and $i(x, k, \rho)$. We denote the $k + 1$st character of $\tau(x, \rho)$ using $\tau_k(x, \rho)$.

- If $r_{1,k} \leq p_a$, then $i(x, k + 1, \rho) = i(x, k, \rho)$, and $\tau_k(x, \rho) = \text{hash-insert}$.
- If $r_{1,k} > p_a$ and $r_{2,k} \leq p_r$, then $i(x, k + 1, \rho) = i(x, k, \rho) + 1$, and $\tau_k(x, \rho) = \text{hash-replace}$.
- If $r_{1,k} > p_a$ and $r_{2,k} > p_r$, then $i(x, k + 1, \rho) = i(x, k, \rho) + 1$, and $\tau_k(x, \rho) = \text{hash-match}$.

A transcript $\tau(x, \rho)$ is complete if $|\tau(x, \rho)| < 8d/(1 - p_a) + 6 \log n$.

**Lemma 6.** For any string $x$ of length at most $d$,

$$\Pr_{\rho}[\text{$\tau(x, \rho)$ is complete}] \geq 1 - 1/n^2$$

**Proof.** If $\tau(x, \rho)$ has $\ell$ hash-insert operations, then $|\tau(x, \rho)| \leq d + \ell + 1$. We bound the probability
that $\ell > 7d/(1 - p_a) + 6 \log n$.

\(^7\)After embedding into Hamming space, one often uses bit sampling [37] to find the most similar vectors. The
“sampled” bits in our hash are those that were written out explicitly, i.e. that were not replaced with $\bot$. 7
For each character in $x$, we can model the length of $\tau(x, \rho)$ as a series of independent coin flips. On heads (with probability $p_a$), $\ell$ increases. After $|x|$ tails, the process stops. Thus we expect $1/(1-p_a)$ hash-insert operations for each character of $x$, and at most $d/(1-p_a)$ hash-insert operations overall; in other words $\mathbb{E}[\ell] \leq d/(1-p_a)$.

Using standard Chernoff bounds (i.e. \cite{52} Exercise 4.7), the probability that $\ell > 7d/(1-p_a) + 6 \log n$ is at most $\exp(-(6d/(1-p_a) + 6 \log n)/3) < 1/n^2$. \hfill $\square$

**Grid Walks.** A grid walk $g(x, y, \rho)$ for two strings $x$ and $y$ and underlying function $\rho$ is a sequence that helps us examine how $h_\rho(x)$ and $h_\rho(y)$ interact—it is a bridge between the transcript of $x$, $y$, and $\rho$, and the transformation induced by $x$, $y$, and $\rho$ (which is a sequence of edits). We formally define the grid walk, and discuss how it corresponds to a random walk in a graph. This graph is closely based on the dynamic programming table for $x$ and $y$.

The grid walk is a sequence of length $\max(\tau(x, \rho), \tau(y, \rho))$. The grid walk has an alphabet of size 6: each character is one of $\{$insert, delete, replace, loop, match, stop$\}$. We define a directed graph $G(x, y)$ to help explain how to construct the walk. Graph $G(x, y)$ is a directed graph with $|x||y| + 1$ nodes. We label one node as the stop node. We label the other $|x||y|$ nodes using two-dimensional coordinates $(i, j)$ with $0 \leq i < |x|$, and $0 \leq j < |y|$. We visualize node $(0, 0)$ as being in the upper-left corner, with $i$ increasing while moving right.

We now list all arcs between nodes. We label each with a grid walk character; this will be useful for analyzing $g(x, y, \rho)$. Consider an $(i, j)$ with $0 \leq i < |x| - 1$ and $0 \leq j < |y| - 1$. For any $(i, j)$ with $x_i \neq y_j$, we place five arcs:

- a delete arc from $(i, j)$ to $(i + 1, j)$,
- a replace arc from $(i, j)$ to $(i + 1, j + 1)$,
- an insert arc from $(i, j)$ to $(i, j + 1)$,
- a loop arc from $(i, j)$ to $(i, j)$, and
- a stop arc from $(i, j)$ to the stop node.

These arcs are shown in Figure 1a. For any $(i, j)$ with $x_i = y_j$, we place two edges: a match arc from $(i, j)$ to $(i + 1, j + 1)$, and a loop arc from $(i, j)$ to $(i, j)$; see Figure 1b.

The rightmost and bottommost nodes of the grid are largely defined likewise, but arcs that lead to nonexistent nodes instead lead to the stop node.\footnote{Since $x$ and $y$ are $S$-terminal, these nodes never satisfy $x_i = y_j$ except at $(|x| - 1, |y| - 1)$.} For $0 \leq j < |y| - 1$ there is an insert arc.

![Figure 1: The edges for a single node $(i, j)$ with $i < |x| - 1$ and $j < |y| - 1$. (a) represents the edges if $x_i \neq y_j$; (b) represents the edges if $x_i = y_j$.](image)
Figure 2: This figure shows $G(x, y)$ for $x = abc\$ and $y = cab\$. For clarity, all edge labels are omitted and stop edges are partially transparent.

The stop node has six self loops with labels match, insert, replace, delete, loop, and stop.

We now define the grid walk $g(x, y, \rho)$. We will use $G(x, y)$ to relate $g(x, y, \rho)$ to $h_\rho(x)$ and $h_\rho(y)$ in Lemmas 7 and 8.

We determine the $k$th character of $g(x, y, \rho)$, denoted $g_k(x, y, \rho)$, using $\tau_k(x, \rho)$ and $\tau_k(y, \rho)$, as well as $x_{i(x,k,\rho)}$ and $y_{i(y,k,\rho)}$. For $k > \min\{|\tau(x, \rho)|, |\tau(y, \rho)|\}$, $g_k(x, y, \rho) = \text{stop}$.

If $x_{i(x,k,\rho)} \neq y_{i(y,k,\rho)}$, we define $g_k(x, y, \rho)$ using Table 1.

If $x_{i(x,k,\rho)} = y_{i(y,k,\rho)}$, then $\tau_k(x, \rho) = \tau_k(y, \rho)$. If $\tau_k(x, \rho) = \tau_k(y, \rho)$ is a hash-insert, then $g_k(x, y, \rho) = \text{loop}$; otherwise, $g_k(x, y, \rho) = \text{match}$.

We say that a grid walk is complete if both $\tau(x, \rho)$ and $\tau(y, \rho)$ are complete. We say that a grid walk is alive if it is complete and it does not contain stop.

The next lemma motivates this definition: the grid walk defines a path through the grid corresponding to the hashes of $x$ and $y$.

**Lemma 7.** Consider a walk through $G(x, y)$ which at step $i$ takes the edge with label corresponding to $g_i(x, y, \rho)$. Assume $k$ is such that the prefix $g(x, y, \rho)[k]$ of length $k$ is alive. Then after $k$ steps, the walk arrives at node $(i(x, k, \rho), i(y, k, \rho))$.

**Proof.** We prove this by induction on $k$. We prove both that the walk arrives at node $(i(x, k, \rho), i(y, k, \rho))$, and that the walk is well-defined: the next character in $g(x, y, \rho)$ always corresponds to an outgoing edge of the current node.

For the base case $k = 0$ the proof is immediate, since $(i(x, 0, \rho), i(y, 0, \rho)) = (0, 0)$. Furthermore, node $(0, 0)$ has an outgoing match edge if and only if $x_0 = y_0$ (otherwise it has an outgoing insert, delete, and replace edge); similarly, $g_0(x, y, \rho) = \text{match}$ only if $x_0 = y_0$ (the rest of the cases follow likewise).

| $\tau_k(x, \rho)$ | $\tau_k(y, \rho)$ | $g_k(x, y, \rho)$ |
|-------------------|-------------------|-------------------|
| hash-replace      | hash-replace      | replace           |
| hash-replace      | hash-insert       | delete            |
| hash-insert       | hash-replace      | insert            |
| hash-insert       | hash-insert       | loop              |
| hash-match        | -                 | stop              |
| -                 | hash-match        | stop              |

Table 1: This table defines a grid walk for non-matching characters in strings $x$ and $y$, given the corresponding transcripts.
Assume that after $k-1$ steps, the walk using $g(x,y,\rho)[k-1]$ arrives at node $(i(x, k-1, \rho), i(y, k-1, \rho))$. We begin by proving that the walk remains well-defined. We have $g_{k-1}(x,y,\rho) = \text{match}$ only if $x_i(x,k-1,\rho) = y_i(y,k-1,\rho)$; in this case $(i(x, k-1, \rho), i(y, k-1, \rho))$ has an outgoing $\text{match}$ edge. We have $g_{k-1}(x,y,\rho) = \text{insert}$ (or $\text{delete}$ or $\text{replace}$) only if $x_i(x,k-1,\rho) \neq y_i(y,k-1,\rho)$; again node $(i(x, k-1, \rho), i(y, k-1, \rho))$ has the corresponding outgoing edge. All nodes have outgoing $\text{loop}$ and $\text{stop}$ edges.

Now we show that after $k$ steps, the walk using $g(x,y,\rho)[k]$ arrives at node $(i(x,k), i(y,k))$.

We split into five cases based on $g_{k-1}(x,y,\rho)$ (if $g_{k-1}(x,y,\rho) = \text{stop}$ the lemma no longer holds).

**replace** We have $\tau_k(x,\rho) = \text{hash-replace}$, and $\tau_k(y,\rho) = \text{hash-replace}$. Thus, $i(x,k,\rho) = i(x,k-1,\rho) + 1$ and $i(y,k,\rho) = i(y,k-1,\rho) + 1$. In $G(x,y)$, the edge labelled $\text{replace}$ leads to node $(i(x,k-1,\rho) + 1, i(y,k-1,\rho) + 1)$.

**match** We have $\tau_k(x,\rho) = \text{hash-replace}$, and $\tau_k(y,\rho) = \text{hash-replace}$. Thus, $i(x,k,\rho) = i(x,k-1,\rho) + 1$ and $i(y,k,\rho) = i(y,k-1,\rho) + 1$. In $G(x,y)$, the edge labelled $\text{match}$ leads to node $(i(x,k-1,\rho) + 1, i(y,k-1,\rho) + 1)$.

**delete** We have $\tau_k(x,\rho) = \text{hash-replace}$, and $\tau_k(y,\rho) = \text{hash-insert}$. Thus, $i(x,k,\rho) = i(x,k-1,\rho) + 1$ and $i(y,k,\rho) = i(y,k-1,\rho)$. In $G(x,y)$, the edge labelled $\text{insert}$ leads to node $(i(x,k-1,\rho) + 1, i(y,k-1,\rho))$.

**insert** We have $\tau_k(x,\rho) = \text{hash-insert}$, and $\tau_k(y,\rho) = \text{hash-replace}$. Thus, $i(x,k,\rho) = i(x,k-1,\rho)$ and $i(y,k,\rho) = i(y,k-1,\rho) + 1$. In $G(x,y)$, the edge labelled $\text{insert}$ leads to node $(i(x,k-1,\rho), i(y,k-1,\rho) + 1)$.

**loop** We have $\tau_k(x,\rho) = \text{hash-insert}$, and $\tau_k(y,\rho) = \text{hash-insert}$. Thus, $i(x,k,\rho) = i(x,k-1,\rho)$ and $i(y,k,\rho) = i(y,k-1,\rho)$. In $G(x,y)$, the edge labelled $\text{loop}$ leads to node $(i(x,k-1,\rho), i(y,k-1,\rho))$.

With this in mind, we can relate grid walks to hash collisions.

**Lemma 8.** Let $x$ and $y$ be any two strings, and $\rho$ be any underlying function where both $\tau(x,\rho)$ and $\tau(y,\rho)$ are complete.

Then $h_\rho(x) = h_\rho(y)$ if and only if $g(x,y,\rho)$ is alive. Furthermore, if $h_\rho(x) = h_\rho(y)$ then the path defined by $g(x,y,\rho)$ reaches node $(|x|, |y|)$.

**Proof.** If direction: Assume that $h_\rho(x) = h_\rho(y)$; we show that the path defined by $g(x,y,\rho)$ is alive and reaches $(|x|, |y|)$.

First, $g(x,y,\rho)$ must be alive: $g_k(x,y,\rho) = \text{stop}$ only when $x_i(x,k,\rho) \neq y_i(y,k,\rho)$ and either $\tau_k(x,\rho) = \text{hash-match}$ or $\tau_k(y,\rho) = \text{hash-match}$, or when $k > \min\{|\tau(x,\rho)|, |\tau(y,\rho)|\}$. Since $x_i(x,k,\rho)$ (resp. $y_i(y,k,\rho)$) is appended to the hash on a hash-match, this contradicts $h_\rho(x) = h_\rho(y)$. Furthermore, we must have $|\tau(x,\rho)| = |\tau(y,\rho)|$ because $|\tau(x,\rho)| = |h_\rho(x)| = |h_\rho(y)| = |\tau(y,\rho)|$.

Since $\tau(x,\rho)$ and $\tau(y,\rho)$ are complete, $i(x,|\tau(x,\rho)| - 1, \rho) = |x|$ and $i(y,|\tau(y,\rho)| - 1, \rho) = |y|$. Thus, by Lemma 7 the walk reaches $(|x|, |y|)$.

Only If direction: We show that if $h_\rho(x) \neq h_\rho(y)$ then $g(x,y,\rho)$ is not alive. Let $k$ be the smallest index such that the $k$th character of $h_\rho(x)$ is not equal to the $k$th character of $h_\rho(y)$. At least one of these characters cannot be $\perp$; thus either $\tau_k(x,\rho) = \text{hash-match}$, or $\tau_k(y,\rho) = \text{hash-match}$. If $x_i(x,k,\rho) \neq y_i(y,k,\rho)$, then $g_k(x,y,\rho) = \text{stop}$ and we are done. Otherwise, $x_i(x,k,\rho) = y_i(y,k,\rho)$; thus $\tau_k(x,\rho) = \tau_k(y,\rho)$, and the $k$th character of both $h_\rho(x)$ and $h_\rho(y)$ is $x_i(x,k,\rho) = y_i(y,k,\rho)$. But this contradicts the definition of $k$. 

\[\square\]
We now bound the probability that the grid walk traverses each edge in $G(x, y)$.

**Lemma 9.** Let $x$ and $y$ be any two strings, and for any $k < 8d/(1 - p_a) + 6 \log n$ let $E_k$ be the event that $i(x, k, \rho) < |x|$, $i(y, k, \rho) < |y|$, and $x_{i(x,k,\rho)} \neq y_{i(y,k,\rho)}$.

Then if $P_{\rho}[E_k] > 0$, the following four conditional bounds hold:
- $P_{\rho}[g_k(x, y, \rho) = \text{loop} \mid E_k] = p_a^2$.
- $P_{\rho}[g_k(x, y, \rho) = \text{delete} \mid E_k] = p_a(1 - p_a)p_r$.
- $P_{\rho}[g_k(x, y, \rho) = \text{insert} \mid E_k] = p_a(1 - p_a)p_r$.
- $P_{\rho}[g_k(x, y, \rho) = \text{replace} \mid E_k] = (1 - p_a)^2p_r$.

**Proof.** We have $|\tau(x, \rho)| > k$ and $|\tau(y, \rho)| > k$ from $E_k$. Thus:
- $P_{\rho}[\tau_k(x, \rho) = \text{hash-insert} \mid E_k] = p_a$
- $P_{\rho}[\tau_k(x, \rho) = \text{hash-replace} \mid E_k] = (1 - p_a)p_r$
- $P_{\rho}[\tau_k(x, \rho) = \text{hash-match} \mid E_k] = (1 - p_a)(1 - p_r)$.

The respective probabilities for $\tau_k(y, \rho)$ hold as well. Combining these probabilities with Table 1 gives the lemma.

**Transformations.** We call a sequence of edits for a pair of strings $x$ and $y$ greedy if they can be applied to $x$ in order from left to right, and all operations are performed on non-matching positions. We formally define this in Definition [10]. With this in mind, we can simplify a sequence of edits for a given $x$ and $y$, with the understanding that they will be applied greedily.

A transformation is a sequence of edits with position and character information removed: it is a sequence consisting only of insert, delete, and replace. We let $T(x, y)$ be the string that results from greedily applying the edits in $T$ to $x$ when $x$ does not match $y$. We say that a transformation is valid for strings $x$ and $y$ if the total number of delete or replace operations in $T$ is at most $|x|$, and the total number of insert or replace operations in $T$ is at most $|y|$. The following definition formally defines how to apply these edits.

**Definition 10.** Let $x$ and $y$ be two $\$-$terminal strings, and let $T$ be a transformation that is valid for $x$ and $y$.

If $T$ is empty, $T(x, y) = x$. Otherwise we define $T(x, y)$ inductively. Let $T' = T[|T| - 1]$ be $T$ with the last operation removed, let $\sigma = T[|T| - 1]$ be the last operation in $T$, and let $i$ be the smallest index such that the $i$th character of $T'(x, y)$ is not equal to $y_i$. Position $i$ always exists if $T'(x, y) \neq y$ because $x$ and $y$ are $\$-$terminal; otherwise $i = 0$.

We split into three cases depending on $\sigma$. If $\sigma = \text{insert}$, we obtain $T(x, y)$ by inserting $y_i$ at position $i$ in $T'(x, y)$. If $\sigma = \text{delete}$, we obtain $T(x, y)$ by deleting the $i$th character of $T'(x, y)$. Finally, if $\sigma = \text{replace}$, we obtain $T(x, y)$ by replacing the $i$th character of $T'(x, y)$ with $y_i$.

We say that a transformation $T$ solves $x$ and $y$ if $T$ is valid for $x$ and $y$, $T(x, y) = y$, and for any $i < |T|$, the prefix $T'[i]$ satisfies $T'(x, y) \neq y$.

A classic observation is that edit distance operations can be applied from left to right, greedily skipping all matches. The following lemma shows that this intuition applies to transformations. Since Definition [10] does not allow characters to be appended onto the end of $x$, we use the appended character $\$ to ensure that there is an optimal transformation between any pair of strings.

**Lemma 11.** Let $x$ and $y$ be two strings that do not contain $\$$. Then if $\ED(x, y) = r$,
- there exists a transformation $T$ of length $r$ that solves $x \circ \$ and $y \circ \$,$ and
- there does not exist any transformation $T'$ of length $< r$ that solves $x \circ \$ and $y \circ \$.

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9The case where $i$ is reset to 0 is included for completeness and will not be used in the rest of the paper.
Proof. We prove a single statement implying the lemma: if $\hat{T}$ is the shortest transformation that solves $x \circ \$ \Leftrightarrow y \circ \$ \Leftrightarrow$, then $|\hat{T}| = ED(x, y)$.

Let $\sigma_1, \ldots, \sigma_r$ be the sequence of edits applied to $x \circ \$ \Leftrightarrow y \circ \$ \Leftrightarrow$ in Definition 10. These operations apply to increasing indices $i$ because $\hat{T}$ is the shortest transformation satisfying $\hat{T}(x \circ \$, $y \circ \$ \Leftrightarrow$. Let $\sigma_i$ be the last operation that applies to an index $i < |x|$. Let $\hat{y} = \hat{T}[i+1](x \circ \$, $y \circ \$ \Leftrightarrow$ be the string obtained after applying the operations of $\hat{T}$ through $\sigma_i$. Clearly, $x$ is a prefix of $\hat{y}$. We claim that because $\hat{T}$ is the shortest transformation, the operations in $\hat{T}$ after $\sigma_i$ must be $|\hat{y}| - |x| - 1 \text{ insert}$ operations. Clearly there must be at least $|\hat{y}| - |x| - 1 \text{ operations}$ after $\sigma_i$ because $i$ is increasing and only one character in $\hat{y}$ matches the final character $\$ \Leftrightarrow$ of $x$. By the same argument, if $\hat{T}$ has any $\text{ delete}$ or $\text{ replace}$ operations it cannot meet this bound.

With this we have $ED(x, y) \leq |\hat{T}|$ because we can apply $\sigma_1, \ldots, \sigma_r$, followed by $|\hat{y}| - |x| - 1 \text{ insert}$ operations to $x$ to obtain $y$. This totals to $|\hat{T}|$ operations overall.

We also have $ED(x, y) \geq |\hat{T}|$ by minimality of $\hat{T}$ because any sequence of edits applied to $x$ that obtains $y$ will obtain $y \circ \$ \Leftrightarrow$ when applied to $x \circ \$ \Leftrightarrow$. $\square$

For a given $x$, $y$, and $\rho$, we obtain the transformation induced by $x$, $y$, and $\rho$, denoted $\mathcal{T}(x, y, \rho)$, by removing $\text{ loop}$ and $\text{ match}$ from $g(x, y, \rho)$ if $g(x, y, \rho)$ is alive. Otherwise, $\mathcal{T}(x, y, \rho)$ is the empty string.

In Lemma 12 we show that strings $x$ and $y$ collide exactly when their induced transformation $T$ solves $x$ and $y$. This can be seen intuitively in Figure 2—the grid walk is essentially a random walk through the dynamic programming table.

**Lemma 12.** Let $x$ and $y$ be two strings with $x \neq y$, and let $T = \mathcal{T}(x, y, \rho)$. Then $h_\rho(x) = h_\rho(y)$ if and only if $T$ solves $x$ and $y$.

**Proof.** If direction: Assume $T$ solves $x$ and $y$. Since $x \neq y$, $T$ must be nonempty; thus $g(x, y, \rho)$ is alive. By Lemma 8 $h_\rho(x) = h_\rho(y)$.

Only If direction: Assume $h_\rho(x) = h_\rho(y)$; by Lemma 8 $g(x, y, \rho)$ is alive.

Let $g(x, y, \rho)[k]$ be the prefix of $g(x, y, \rho)$ of length $k$, and let $T^k$ be $g(x, y, \rho)[k]$ with $\text{ loop}$ and $\text{ match}$ removed. We prove by induction that $T^k(x[i(x, k, \rho)], y[i(y, k, \rho)]) = y[i(y, k, \rho)]$. This is trivially satisfied for $k = 0$.

Assume that $T^{k-1}(x[i(x, k-1, \rho)], y[i(y, k-1, \rho)]) = y[i(y, k-1, \rho)]$. We split into five cases based on the $k^{th}$ operation in $g(x, y, \rho)$.

**match** We must have $x[i(x, k-1, \rho)] = y[i(y, k-1, \rho)]$ and $T^k = T^{k-1}$. Furthermore, $i(x, k, \rho) = i(x, k-1, \rho) + 1$ and $i(y, k, \rho) = i(y, k-1, \rho) + 1$. Thus $T^k(x[i(x, k, \rho)], y[i(y, k, \rho)]) = T^{k-1}(x[i(x, k-1, \rho)], y[i(y, k-1, \rho)]) = y[i(y, k, \rho)]$.

**insert** We have $i(x, k, \rho) = i(x, k-1, \rho)$ and $i(y, k, \rho) = i(y, k-1, \rho) + 1$. Thus, $T^{k-1}(x[i(x, k, \rho)], y[i(y, k, \rho)]) = y[i(y, k-1, \rho)] + 1$ and $y[i(y, k, \rho)]$ differ only in the last character. Then $T^k(x[i(x, k, \rho)], y[i(y, k, \rho)]) = T^{k-1}(x[i(x, k-1, \rho)], y[i(y, k-1, \rho)]) \circ y[i(y, k, \rho)] = y[i(y, k, \rho)]$.

**replace** We have $i(x, k, \rho) = i(x, k-1, \rho) + 1$ and $i(y, k, \rho) = i(y, k-1, \rho) + 1$. Thus, $T^{k-1}(x[i(x, k, \rho)], y[i(y, k, \rho)]) = y[i(y, k-1, \rho)] \circ x[i(x, k, \rho)] = y[i(y, k, \rho)]$. By definition, the final character of $T^{k-1}(x[i(x, k, \rho)], y[i(y, k, \rho)])$ is replaced with $y[i(y, k, \rho)]$. Obtaining $T^k(x[i(x, k, \rho)], y[i(y, k, \rho)]) = y[i(y, k-1, \rho)] \circ y[i(y, k, \rho)] = y[i(y, k, \rho)]$.

**delete** We have $i(x, k, \rho) = i(x, k-1, \rho) + 1$ and $i(y, k, \rho) = i(y, k-1, \rho)$. Thus, $T^{k-1}(x[i(x, k, \rho)], y[i(y, k, \rho)]) = y[i(y, k-1, \rho)] \circ x[i(x, k, \rho)] = y[i(y, k, \rho)]$. Then $T^k(x[i(x, k, \rho)], y[i(y, k, \rho)]) = T^{k-1}(x[i(x, k-1, \rho)], y[i(y, k-1, \rho)]) = y[i(y, k, \rho)]$. 12
We have $i(x,k,\rho)=i(x,k-1,\rho)$, $i(y,k,\rho)=i(y,k-1,\rho)$, and $T^k=T^{k-1}$. We immediately obtain $T^k[x[i(x,k,\rho)],y[i(y,k,\rho)]]=y[i(y,k,\rho)]$.

By Lemma 8, $g(x,y,\rho)$ reaches node $(|x|,|y|)$, so the above shows that with $k=|g(x,y,\rho)|, T(x,y)=y$.

We are finally ready to prove Lemma 13, which forms the basis of our performance analysis.

**Lemma 13.** For any $\$-terminal strings $x$ and $y$, let $T$ be a transformation of length $t$ that is valid for $x$ and $y$. Then

$$p^t - 2/n^2 \leq \Pr(T \text{ is a prefix of } T(x,y,\rho)) \leq p^t.$$  

**Proof.** Let $G_T$ be the set of all grid walks $g$ (i.e. the set of all sequences consisting of grid walk operations) such that $g$ does not contain stop, and deleting loop and match from $g$ results in $T_g$ such that $T$ is a prefix of $T_g$. Then by definition, if $T$ is a prefix of $T(x,y,\rho)$ then $g(x,y,\rho) \in G_T$; furthermore, if $g(x,y,\rho) \in G_T$ and $g(x,y,\rho)$ is complete, then $T$ is a prefix of $T(x,y,\rho)$.

We begin by proving that $\Pr(\sigma(x,y,\rho) \in G_T) = p^t$. We prove this by induction on $t$; $t=0$ is trivially satisfied. We assume that $\Pr(\sigma(x,y,\rho) \in G_T) = p^{t-1}$ for any $G_T$ with $|T'|=t-1$, and prove that it holds for any $T$ with $|T|=t$.

Let $\sigma$ be the last operation in $T$, and let $T'=T[|T|−1]$ be $T$ with $\sigma$ removed. Thus, $g(x,y,\rho) \in G_T$ only if there exist grid walks $g'$ and $g''$ satisfying

- $g' \in G_T'$,
- $g''$ consists of loop and match operations concatenated onto the end of $g' \circ \sigma$, ending with a match operation, and
- $g(x,y,\rho)$ consists of zero or more loop operations concatenated onto $g''$.

By definition of conditional probability,

$$\Pr(g(x,y,\rho) \in G_T) = \sum_{g'} \Pr(g' \in G_T') \sum_{g''} \Pr(g'' \in G_T \mid g' \in G_T') \Pr(g(x,y,\rho) \in G_T \mid g'' \in G_T).$$

We bound these terms one at a time.

Clearly there is only one $g'$ satisfying the conditions, which can be obtained by taking the prefix of $g(x,y,\rho)$ before the final insert, delete, or replace operation. By the inductive hypothesis, $\sum_{g'} \Pr(g' \in G_T') = p^{t-1}$.

We now bound $\Pr(g'' \in G_T \mid g' \in G_T')$. The conditional means that we can invoke Lemma 9 (as $\Pr(E_k) = p^{t-1} > 0$).

We have $\Pr(g'' \in G_T \mid g' \in G_T') = \Pr(g'' \in G_T \mid g' \circ \sigma \in G_T) \Pr(g' \circ \sigma \in G_T \mid g' \in G_T')$.

We split into two cases depending on $\sigma$. Recall that $p_r = p_a/(1-p_a)$. Since $T$ is valid, if $\sigma = \text{delete}$ or $\sigma = \text{replace}$ we cannot have $i(x,k,\rho) = |x| - 1$; similarly if $\sigma = \text{insert}$ or $\sigma = \text{replace}$ we cannot have $i(y,k,\rho) = |y| - 1$. Then by Lemma 9 if $\sigma = \text{delete}$ or $\sigma = \text{insert},$

$$\Pr(g' \circ \sigma \in G_T \mid g' \in G_T') = p_a(1-p_a)p_r = p_a^2.$$  

Similarly, if $\sigma = \text{replace},$

$$\Pr(g' \circ \sigma \in G_T \mid g' \in G_T') = (1-p_a)^2p_r = p_a^2.$$  

For any $k$ such that $i(x,k,\rho) = i(y,k,\rho)$, $g_k(x,y,\rho) \neq \text{stop}$ by definition; meanwhile, if $i(x,k,\rho) \neq i(y,k,\rho)$ then $g_k(x,y,\rho) \neq \text{match}$. Thus, $\sum_{g''} \Pr(g'' \in G_T \mid g' \circ \sigma \in G_T) = 1.$
Finally we bound \( \Pr[g(x, y, \rho) \in G_T | g'' \in G_T] \). Let \( \ell \) be the number of operations concatenated onto \( g'' \) to obtain \( g(x, y, \rho) \). Then by Lemma 9

\[
\Pr[g(x, y, \rho) \in G_T | g'' \in G_T] = \sum_{\ell} p^{2\ell}_a = 1/(1 - p^2_a).
\]

Multiplying the above bounds, we have \( \Pr[g(x, y, \rho) \in G_T] = p^{\ell - 1}p^2_a/(1 - p^2_a) \). Noting that \( p = p^2_a/(1 - p^2_a) \), we obtain \( \Pr[g(x, y, \rho) \in G_T] = p^r \).

We have that if \( T \) is a prefix of \( T(x, y, \rho) \) then \( g(x, y, \rho) \in G_T \); thus \( \Pr_T[T \text{ is a prefix of } T(x, y, \rho)] \leq p_T \).

Meanwhile, \( T \) is a prefix of \( T(x, y, \rho) \) if \( g(x, y, \rho) \in G_T \) and \( g(x, y, \rho) \) is complete. By the inclusion-exclusion principle,

\[
\Pr[T \text{ is a prefix of } T(x, y, \rho)] = \Pr[g(x, y, \rho) \in G_T] + \Pr[g(x, y, \rho) \text{ is complete}] - \Pr[g(x, y, \rho) \in G_T \text{ or } g(x, y, \rho) \text{ is complete}] \\
\quad \geq p^r + \Pr[g(x, y, \rho) \text{ is complete}] - 1
\]

We have that \( \Pr[g(x, y, \rho) \text{ is complete}] = 1 - \Pr[\tau(x, \rho) \text{ or } \tau(y, \rho) \text{ is not complete}] \). By union bound and Lemma 6, \( \Pr[g(x, y, \rho) \text{ is complete}] \geq 1 - 2/n^2 \). Substituting, \( \Pr[T \text{ is a prefix of } T(x, y, \rho)] \geq p^r - 2/n^2 \).

### 4.2 Bounds on Collision Probabilities

**Lemma 14.** If \( x \) and \( y \) satisfy \( \text{ED}(x, y) \leq r \), then

\[
\Pr_{\rho} h_{\rho}(x) = h_{\rho}(y) \geq p^r - 2/n^2.
\]

*Proof.* Because \( \text{ED}(x, y) \leq r \), by Lemma 11 there exists a transformation \( T \) of length \( r \) that solves \( x \) and \( y \). By Lemma 13, \( h \) induces \( T \) on \( x \) and \( y \) (which is sufficient for \( h(x) = h(y) \) by Lemma 12) with probability \( p^r - 2/n^2 \).

**Lemma 15.** If \( x \) and \( y \) satisfy \( \text{ED}(x, y) \geq cr \), then

\[
\Pr_{\rho} h_{\rho}(x) = h_{\rho}(y) \leq (3p)^{cr}
\]

*Proof.* Let \( \mathcal{T} \) be the set of all transformations that solve \( x \) and \( y \). By Lemma 12 and Lemma 13

\[
\Pr_{h \in \mathcal{H}} (h(x) = h(y)) \leq \sum_{T \in \mathcal{T}} p^{||T||}.
\]

Since all pairs \( T_1, T_2 \in \mathcal{T} \) solve \( x \) and \( y \), there is no pair \( T_1, T_2 \in \mathcal{T} \) such that \( T_1 \) is a prefix of \( T_2 \). Thus, \( \mathcal{T} \) can be viewed as the leaves of a trie of branching factor at most 3, where each leaf has depth at least \( cr \).

We show that without loss of generality all leaves are at depth \( cr \). Assume (for a contradiction) that the maximum depth of the tree is \( i > cr \). Consider a leaf \( T_1 \) at the maximum depth of the trie \( i \), and its siblings \( T_2 \) and \( T_3 \) if they exist. Collapse this leaf and its siblings, replacing them instead with a leaf \( T'_p \) corresponding to their parent in the trie; call the resulting set \( \mathcal{T}' \). Since we have added a transformation of length \( i - 1 \) and removed at most three of length \( i \), this changes the total cost of \( \mathcal{T} \) by at least \( p^{i - 1} - 3p^i \); this is positive since \( p \leq 1/3 \). Repeating this process...
results in a set $\mathcal{T}_M$ with all nodes at depth $cr$, where $\mathcal{T}_M$ gives larger collision probability than the original set $\mathcal{T}$, contradicting the definition of $\mathcal{T}$.

There are at most $3^{cr}$ transformations in $\mathcal{T}_M$, each of length $cr$. Thus

$$\Pr_{h \in H}(h(x) = h(y)) \leq 3^{cr}p^{cr}. \quad \square$$

The following special case is not used in our similarity search bounds, but may be useful in understanding performance on some datasets.

**Lemma 16.** Let $x$ and $y$ be two $\$-terminal strings with $\text{ED}(x, y) \geq cr$ such that for all $i < |x| - 1$ and $j < |y| - 1, x_i \neq y_j$. Then

$$\Pr_{\rho}(h_{\rho}(x) = h_{\rho}(y)) \leq \left(\frac{2p}{1-p}\right)^{cr}.$$  

**Proof.** Let $GR(i, j)$ be the set of all grid walks reaching node $(i, j)$ in $G(x, y)$. Let $W(i, j) = \Pr[g(x, y, \rho) \in GR(i, j)]$. We have $W(0, 0) = 1$.

Clearly, $GR(i, j)$ is a subset of $GR(i - 1, j) \cup GR(i - 1, j - 1) \cup GR(i, j - 1)$. In fact, using a case-by-case analysis essentially identical to that of Lemma 13,

$$W(i, j) \leq p \cdot W(i - 1, j) + p \cdot W(i - 1, j - 1) + p \cdot W(i, j - 1).$$

We take $W(i^*, -1) = W(-1, j^*) = 0$ for all $i^*$ and $j^*$ so that we can state this recursion without border cases.

We show by induction that if $\max\{i, j\} = \ell$, then $W(i, j) \leq (2p/(1 - p))^\ell$. This is already satisfied for $\ell = 0$.

Assume that the induction is satisfied for all $W(i^*, j^*)$ with $\max\{i^*, j^*\} = \ell - 1$. For all $(i, j)$ such that $\max\{i, j\} = \ell$, at most two of $(i - 1, j - 1), (i - 1, j), (i, j - 1)$ have max $\ell - 1$; all remaining pairs have max $\ell$. Thus

$$W(i, j) \leq p \left(\frac{2p}{1-p}\right)^{\ell-1} + p \left(\frac{2p}{1-p}\right)^{\ell-1} + p \left(\frac{2p}{1-p}\right)^{\ell} \leq \left(\frac{2p}{1-p}\right)^{\ell}$$

All grid walks in $G(x, y)$ that go through $(|x| - 1, |y| - 1)$ must be in $GR(|x| - 1, |y| - 1)$. Since we must have $\max\{|x|, |y|\} \geq cr + 1$, the proof is complete. \quad \square

### 4.3 Final Running Time for Approximate Similarity Search

In this section, we describe how to get from our LSH to an algorithm satisfying Definition 3, proving Theorem 4.

**Space and Preprocessing.** To preprocess, we first pick $k = \Theta(1/p_1)$ underlying hash functions $\rho_1, \rho_2, \ldots, \rho_k$. For each string $x$ stored in the database, we calculate $h_{\rho_1}(x), \ldots, h_{\rho_k}(x)$, and store them in a dictionary data structure for fast lookups (for example, these can be stored in a hash table, where each $h_{\rho}(x)$ has a back pointer to $x$).

We can further decrease the space by storing a random log $n$-bit hash of $h_{\rho}(x)$ for all $\rho$, rather than the full hash string of length $\Theta(d)$. This does not affect the expected query time. We set $1/p_1 = 3^n n^{1/c}$ (see the discussion below), leading to space $\tilde{O}(3^n n^{1+1/c} + dn)$.

We store the underlying functions $\rho_1, \rho_2, \ldots, \rho_k$ so they can be used during queries. We discuss how this can be achieved in $O(|\Sigma| (\log n)(d + \log n)) = \tilde{O}(dn)$ space in Section 4.5.
Queries. For a given query $q$, we calculate $h_{p_1}(q), h_{p_2}(q), \ldots, h_{p_k}(q)$. For each database string $x$ that collides with $q$ (i.e. for each $x$ such that there exists an $i$ with $h_{p_i}(q) = h_{p_i}(x)$), we calculate $\text{ED}(x, q)$. We return $x$ if the distance is at most $c r$. After repeating this for all $k$ underlying functions, we return that there is no close point.

Correctness of the data structure follows from the definition of $p_1$: if $\text{ED}(q, x) \leq r$, then after $k = 1/p_1$ independent hash functions, $q$ and $x$ collide on at least one hash function with probability at least 1/10. Increasing $k$ by constant factors can improve this bound to any constant.

The cost of each repetition is the cost to hash, plus the number of database elements at distance $> c r$ that collide with $q$. The cost to hash is $O(d/(1 - p_a) + \log n)$, and the cost to test if two strings have distance at most $c r$ is $O(d c r)$ by \[58\] \[10\]. The number of elements with distance $> c r$ that collide with $q$ is at most $n p_2$ in expectation. Thus our total expected cost can be written

$$O \left( \frac{1}{p_1} \left( \frac{d}{1 - p_a} + \log n + (d c r) n p_2 \right) \right).$$

This can be minimized (up to a factor $O(\log n)$) by setting $p_2 = 1/ncr$ (recall that $p_a \leq 1/2$).

Thus, we set $p_2 = 1/ncr$, which occurs at $p = 1/(3(ncr)^{1/cr})$. Using this value of $p$, we get $p_1 \geq \rho^r = \Omega(1/(r^3 n^{1/c}))$.

Putting this all together, the expected query time is $\widetilde{O}(d^3 n^{1/c})$.

4.4 Approximate Nearest Neighbor

In this section we generalize Section 4.3 to prove Theorem 2.

Let $R = \{i \in \{1, \ldots, d\} \mid 3^n r^{1/c} \leq n\}$. We build $O(\log n)$ copies of the data structure described in Section 4.3 for each $r^* \in R$.

Queries. We iterate through each $r^* \in R$ in increasing order, querying the data structure as described above. If we find a string at distance at most $c r^*$ we stop and return it. Once we have iterated through all of $R$ we return failure.

Assume the actual nearest neighbor is at distance $r$. By Chernoff bounds, we succeed with high probability when $r^* = r$; that is, we return a string at distance at most $c r$. Thus, the cost is at most $\sum r^* = 1 \widetilde{O}(d^3 r^{n^{1/c}}) = \widetilde{O}(d^3 r^{n^{1/c}})$ with high probability.

Space. We build $O(\log n)$ copies of each data structure; thus the total space is $\sum_{r=1}^{r^*} \widetilde{O}(3^r n^{1+1/c} + dn) = \widetilde{O}(n^2 + dn)$ by definition of $r^*$. We obtain preprocessing time $\widetilde{O}(dn^2)$ immediately.

4.5 Storing Underlying Functions

Our algorithm uses a large number of fully-random, real-number hashes; this causes issues with the space bounds since we need to store each hash. In this section we relax this assumption.

We modify $\rho$ to hash to a uniformly random element of the set $\{0, \epsilon, 2\epsilon, \ldots, 1\}$. Since the domain of each $\rho$ has size $O(|\Sigma| (d + \log n))$, this means that each $\rho$ can be stored in $O(|\Sigma| \log(1/\epsilon)(d + \log n)) = O(\log n)$ bits of space.

Intuitively, setting $\epsilon = 1/n^2$ should not affect our query bounds, while still retaining the space bounds of Theorems 1 and 2. We prove this formally in Lemma 17.

**Lemma 17.** For any hash $h_{\rho}$, let $\hat{h}_{\rho}$ be the hash function obtained by modifying Section 3.7 to use thresholds $\hat{p}_a$ and $\hat{p}_r$, with $p_a \leq \hat{p}_a \leq p_a + \epsilon$, $p_r \leq \hat{p}_r \leq p_r + \epsilon$, and $\epsilon = 1/n^2$.

Then if $x$ and $y$ satisfy $\text{ED}(x, y) \leq r$, then $\Pr(\hat{h}(x) = \hat{h}(y)) \geq \Omega(p^r - 2/n^2)$. If $x'$ and $y'$ satisfy $\text{ED}(x', y') \geq c r$ then $\Pr(\hat{h}(x) = \hat{h}(y)) \leq O((3p)^{cr})$.

\[10\] This can be improved to $O(d \text{polylog }d)$ using \[34\]; this does not affect the final running time.
Proof. Since \( p_1 = \Omega(1/(r^3 n^{1/c})) \), we have (omitting constants for simplicity) \( p = 1/(3n^{1/rc}) \).
Therefore, \( p_a = \sqrt{1/(1 + 3n^{1/rc})} > 1/n \), and thus \( p_r = p_a/(1 - p_a) \gg 1/n \). Thus, \( p_a < \hat{p}_a < p_a(1 + 1/n) \) and \( p_r < \hat{p}_r < p_r(1 + 1/n) \).

Let \( \epsilon' \) satisfy

\[
\frac{p(1 - \epsilon')}{(1 - \hat{p}_a^2)} \leq p(1 + \epsilon') \quad \text{and} \quad \frac{p(1 - \epsilon')}{(1 - \hat{p}_a^2)} \leq \frac{(1 - \hat{p}_a^2)\hat{p}_r^2}{(1 - \hat{p}_a^2)} \leq p(1 + \epsilon').
\]

Then the proof of Lemma 13 gives that for any $\$-$terminal strings \( x \) and \( y \), and any transformation \( T \) of length \( t \),

\[
(p(1 - \epsilon'))^t - 1/n^2 \leq \Pr_x[T \text{ is a prefix of } T(x, y, \rho)] \leq (p(1 + \epsilon'))^t.
\]

So long as \((1 \pm \epsilon')^t = \Theta(1)\) we are done. Clearly this is the case for \( \epsilon' = O(1/n) \) since \( t \leq 2d = O(n) \).

We prove each bound in Equation (1) one term at a time for \( \epsilon' = O(1/n) \).

First inequality (recall that \( p_a \leq 1/2 \)):

\[
\frac{\hat{p}_a(1 - \hat{p}_a)p_r}{(1 - \hat{p}_a^2)} \geq \frac{p_a(1 - p_a)(1 + 1/n)p_r}{1 - p_a^2} = \frac{p_a(1 - p_a)p_r}{1 - p_a^2} - \frac{pp_a}{n(1 - p_a)} = p(1 - O(n)).
\]

Second inequality:

\[
\frac{\hat{p}_a(1 - \hat{p}_a)p_r}{(1 - \hat{p}_a^2)} < \frac{p_a(1 + 1/n)^2(1 - p_a)p_r}{1 - (p_a(1 + 1/n))^2} = \frac{p_a(1 - p_a)p_r}{(1 + 1/n)^2 - p_a^2} < \frac{p_a(1 - p_a)p_r}{1 - O(1/n^2) - p_a^2} < \frac{p_a(1 - p_a)p_r}{(1 - p_a^2)(1 - O(1/n^2))} = p(1 + O(1/n^2)).
\]

Third inequality:

\[
\frac{(1 - \hat{p}_a^2)p_r^2}{(1 - \hat{p}_a^2)} \geq \frac{(1 - p_a(1 + 1/n))^2p_r^2}{(1 - p_a^2)} \geq \frac{((1 - p_a)^2 - 2p_a/n + p_a^2(2/n + 1/n^2))p_r^2}{(1 - p_a^2)} = \frac{((1 - p_a)^2 - 2p_a/n)p_r^2}{(1 - p_a^2)} - \frac{2p_ap_r^2}{n(1 - p_a^2)} \geq p(1 - O(1/n)).
\]

Fourth inequality (this is largely the same as the second inequality):

\[
\frac{(1 - \hat{p}_a^2)p_r^2}{(1 - \hat{p}_a^2)} \leq \frac{(1 - p_a)^2p_r(1 + 1/n)^2}{1 - (p_a(1 + 1/n))^2} = p(1 + O(1/n^2)).
\]

\[\square\]

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A Pseudocode and Example Hash

Algorithm 1 Calculating $h_\rho(x)$

1: $i \leftarrow 0$
2: Create an empty string $s$
3: while $i < |x|$ and $|s| < 8d/(1 - p_a) + 6 \log n$ do
4: \hspace{1em} $(r_1, r_2) \leftarrow \rho(x_i, |s|)$
5: \hspace{1em} if $r_1 \leq p_a$ then
6: \hspace{2em} Append ⊥ to $s$
7: \hspace{1em} else if $r_2 \leq p_r$ then
8: \hspace{2em} Append ⊥ to $s$
9: \hspace{1em} else
10: \hspace{2em} Append $x_i$ to $s$
11: i $\leftarrow$ i + 1
12: return $s$

Below we give an example of how three strings $x$, $y$, and $z$ are hashed using an underlying function $\rho_1$. We use $\Sigma = \{a, b, c\}$ and $p = 1/8$, so $p_a = 1/3$ and $p_r = 1/2$. For simplicity, we round the values of $\rho_1$ to the first decimal place, and truncate the domain of $\rho_1$ to only show values of $|s|$ up to 5.
Figure 3: This figure shows $G(x, y)$. For clarity, all edge labels are omitted and \texttt{stop} edges are partially transparent. The edges traversed by $g(x, y, \rho_1)$ are bold and colored blue.