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# Longest Common Substring with Approximately $k$ Mismatches

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## Abstract

In the longest common substring problem we are given two strings of length  $n$  and must find a substring of maximal length that occurs in both strings. It is well-known that the problem can be solved in linear time, but the solution is not robust and can vary greatly when the input strings are changed even by one letter. To circumvent this, Leimester and Morgenstern introduced the problem of the longest common substring with  $k$  mismatches. Lately, this problem has received a lot of attention in the literature, and several algorithms have been suggested. The running time of these algorithms is  $n^{2-o(1)}$ , and unfortunately, conditional lower bounds have been shown which imply that there is little hope to improve this bound.

In this paper we study a different but closely related problem of the longest common substring with approximately  $k$  mismatches and use computational geometry techniques to show that it admits a randomised solution with strongly subquadratic running time.

**1998 ACM Subject Classification** F.2.2. Nonnumerical Algorithms and Problems

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## 1 Introduction

Understanding how similar two strings are and what they share in common is a central task in stringology, the significance of which is witnessed for example by the 50,000+ citations of the paper introducing BLAST [3], a heuristic algorithmic tool for comparing biological sequences. This task can be formalised in many different ways, from the longest common substring problem to the edit distance problem. The longest common substring problem can be solved in optimal linear time and space, while the best known algorithms for the edit distance problem require  $n^{2-o(1)}$  time, which makes the longest common substring problem an attractive choice for many practical applications. On the other hand, the longest common substring problem is not robust and its solution can vary greatly when the input strings are changed even by one letter. To overcome this issue, recently there has been introduced a new problem called the longest common substring with  $k$  mismatches. In this paper we continue this line of research.

### 1.1 Related work

Let us start with a precise statement of the longest common substring problem.

► **Problem 1** (The longest common substring). Given two strings  $T_1, T_2$  of length  $n$ , find a substring of maximal length that occurs in  $T_1$  and  $T_2$  exactly.

The suffix tree of  $T_1$  and  $T_2$ , a data structure containing all suffixes of  $T_1$  and  $T_2$ , allows to solve this problem in linear time and space [32, 19, 21], which is optimal as any algorithm



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needs  $\Omega(n)$  time to read and  $\Omega(n)$  space to store the strings. However, if we only account for “additional” space, the space the algorithm uses apart from the space required to store the input, then the suffix tree-based solution is not optimal and has been improved in a series of publications [6, 25, 31].

The major disadvantage of the longest common substring problem is that its solution is not robust. Consider, for example, two pairs of strings:  $a^n$ ,  $a^{n-1}b$  and  $a^{(n-1)/2}ba^{(n-1)/2}$ ,  $a^{n-1}b$ . (Assume for simplicity that  $n - 1 \geq 2$  is even.) The longest common substring of the first pair of strings is twice as long as the longest common substring of the second pair of strings, although we changed only one letter. This makes the longest common substring unsuitable to be used as a measure of similarity of two strings: Intuitively, changing one letter must not change the measure of similarity much. To overcome this issue, it is natural to allow the substring to occur in  $T_1$  and  $T_2$  not exactly but with a small number of mismatches.

► **Problem 2** (The longest common substring with  $k$  mismatches). Given two strings  $T_1, T_2$  of length  $n$  and an integer  $k$ , find a substring of maximal length that occurs in  $T_1$  and  $T_2$  with at most  $k$  mismatches.

The problem can be solved in quadratic time and space by a dynamic programming algorithm, but there have been also shown more efficient solutions. The longest common substring with one mismatch problem was first considered in [7], where an  $\mathcal{O}(n^2)$ -time and  $\mathcal{O}(n)$ -space solution was given. This result was further improved by Flouri et al. who showed an  $\mathcal{O}(n \log n)$ -time and  $\mathcal{O}(n)$  space solution to the problem [16]. For a general value of  $k$ , the problem was first considered by Leimeister and Morgenstern [28] who presented a greedy heuristic algorithm for the problem. Later Flouri et al. showed that the longest common substring with  $k$  mismatches admits a quadratic time and constant (additional) space algorithm [16]. Apart from that, Grabowski presented two output-dependent algorithms with running times  $\mathcal{O}(n((k+1)(\ell_0+1))^k)$  and  $\mathcal{O}(n^2 \ell_k/k)$ , where  $\ell_0$  is the length of the longest common substring of  $T_1$  and  $T_2$  and  $\ell_k$  is the length of the longest common substring with  $k$  mismatches of  $T_1$  and  $T_2$  [18]. Finally, Aluru et al. gave an  $\mathcal{O}(2^k n)$ -space,  $\mathcal{O}(n(2 \log n)^{k+1})$ -time algorithm [4]. Yet, the worst-case running time of all these algorithms is still quadratic. Very recently, Abboud et al. [1] applied the polynomial method to develop a  $k^{1.5} n^2 / 2^{\Omega(\sqrt{\frac{\log n}{k}})}$ -time randomised solution to the problem.

The best algorithms for the edit distance problem and its variations (we do not give their precise statements here as it is not essential for the paper) also have  $n^{2-o(1)}$  running time [30, 12, 29], and these bounds are tight under the Strong Exponential Time Hypothesis (SETH) of Impagliazzo, Paturi and Zane: [8, 11]:

► **Hypothesis 1.** (SETH). For every  $\delta > 0$  there exists an integer  $m$  such that SAT on  $m$ -CNF formulas on  $n$  variables cannot be solved in  $m^{O(1)} 2^{(1-\delta)n}$  time.

## 1.2 Our contribution

In this paper we introduce a new problem called the longest common substring with approximately  $k$  mismatches, inspired by the work of Andoni and Indyk [5].

► **Problem 3** (The longest common substring with approximately  $k$  mismatches). Given two strings  $T_1, T_2$  of length  $n$ , an integer  $k$ , and a constant  $\varepsilon > 0$ . If  $\ell_k$  is the length of the longest common substring with  $k$  mismatches of  $T_1$  and  $T_2$ , return a substring of length at least  $\ell_k$  that occurs in  $T_1$  and  $T_2$  with at most  $(1 + \varepsilon) \cdot k$  mismatches.

In their work Andoni and Indyk used the technique of locality-sensitive hashing to develop a space-efficient randomised index for a variant of the approximate pattern matching problem.

We build up on their work with several new ideas in the construction and the analysis to develop a randomised subquadratic-time solution to Problem 3. Assume binary alphabet and let  $0 < \varepsilon < 2$  be an arbitrary constant.

► **Theorem 1.** *The longest common substring with approximately  $k$  mismatches can be solved in  $\mathcal{O}(n^{1+1/(1+\varepsilon)})$  space and  $\mathcal{O}(n^{1+1/(1+\varepsilon)} \log^2 n)$  time correctly with constant probability.*

If the alphabet is of constant size  $\sigma > 2$ , we can use a standard trick and encode  $T_1$  and  $T_2$  by replacing each letter  $a$  in them with a binary vector  $0^{a-1}10^{\sigma-a}$ . The Hamming distance (i.e. the number of mismatches) between any two substrings of  $T_1$  and  $T_2$  in the encoded form will be exactly twice as large as the Hamming distance between the original substrings, which allows to extend our solution naturally to this case as well at a cost of an additional constant factor.

We note that although the problem statement is not standard for stringology, it makes perfect sense from the practical point of view. Indeed, for most applications it is not important whether a returned substring occurs in  $T_1$  and  $T_2$  with for example 10 or  $(1 + \frac{1}{5}) \cdot 10 = 12$  mismatches. The result is also important from the theoretical point of view as it improves our understanding of the big picture of string comparison.

## 2 Overview

In this section we give an overview of the main ideas needed to prove Theorem 1. The classic solution to the longest common substring problem is based on two observations. The first observation is that the longest common substring of  $T_1$  and  $T_2$  is in fact the longest common prefix of some suffix of  $T_1$  and some suffix of  $T_2$ . The second observation is that the maximal length of the longest common prefix of a fixed suffix  $S$  of  $T_1$  and suffixes of  $T_2$  is reached on the two suffixes of  $T_2$  that are closest to  $S$  in the lexicographic order. This suggests the following algorithm: First, we build a suffix tree of  $T_1$  and  $T_2$ , which contains all suffixes of  $T_1$  and  $T_2$  and orders them lexicographically. Secondly, we compute the longest common prefix of each suffix of  $T_1$  and the two suffixes of  $T_2$  closest to  $S$  in the lexicographic order, one from the left and one from the right. The problem of computing the longest common prefix has been extensively studied in the literature and a number of very efficient deterministic and randomised solutions exist [9, 10, 14, 22, 20], for example, one can use a Lowest Common Ancestor (LCA) data structure, which can be constructed in linear time and space and maintains longest common prefix queries in  $\mathcal{O}(1)$  time [14, 20].

Our solution to the longest common substring with approximately  $k$  mismatches problem is somewhat similar. We will consider  $\theta(n^{1+1/(1+\varepsilon)} \log n)$  orderings on the suffixes of  $T_1$  and  $T_2$  and will show that with high probability the length of the longest common substring with approximately  $k$  mismatches is the answer to a longest common prefix with approximately  $k$  mismatches ( $\text{LCP}_{\bar{k}}$ ) query for some pair of suffixes that are close to each other in one of the orderings. In an  $\text{LCP}_{\bar{k}}$  query we are given two suffixes  $S_1, S_2$  of  $T_1$  and  $T_2$  and must output any integer in the interval  $[\ell_k, \ell_{(1+\varepsilon) \cdot k}]$ , where  $\ell_k$  and  $\ell_{(1+\varepsilon) \cdot k}$  are the lengths of the longest common prefixes of  $S_1$  and  $S_2$  with  $k$  and  $(1+\varepsilon) \cdot k$  mismatches respectively. Note that  $\text{LCP}_{\bar{k}}$  queries can be answered deterministically in  $\mathcal{O}(k)$  time using the kangaroo method [27, 17], but for the purposes of this paper we give a faster randomised solution.

► **Theorem 2.** *After  $\mathcal{O}(n \log^3 n)$  time and  $\mathcal{O}(n \log^2 n)$  space preprocessing of  $T_1$  and  $T_2$ , an  $\text{LCP}_{\bar{k}}$  query can be answered in  $\mathcal{O}(\log^2 n)$  time. The answer is correct with probability at least  $1 - \frac{1}{n^2}$ .*

## 21:4 Longest Common Substring with Approximately $k$ Mismatches

The key idea is to compute sketches for all power-of-two length substrings of  $T_1$  and  $T_2$ . The sketches will have logarithmic length (i.e., we will be able to compare them very fast) and the Hamming distance between them will be roughly equal to the Hamming distance between the original substrings. Once the sketches are computed, we can use a simple binary search to answer  $\text{LCP}_k$  queries in polylogarithmic time.

To define the orderings on suffixes of  $T_1$  and  $T_2$  we will use the locality-sensitive hashing technique, which was initially introduced for the needs of computational geometry [23]. In more detail, we will choose  $\theta(n^{1+1/(1+\varepsilon)} \log n)$  hash functions, where each function can be considered as a projection of a string of length  $n$  onto a random subset of its positions. By choosing the size of the subset appropriately, we will be able to guarantee that the hash function is locality-sensitive: For any two strings at the Hamming distance at most  $k$ , the values of the hash functions on them will be equal with high probability, while the values of the hash functions on any pair of strings at the Hamming distance bigger than  $(1 + \varepsilon) \cdot k$  will be different with high probability. For each hash function we will sort the suffixes of  $T_1$  and  $T_2$  by the lexicographic order on their hash values. As a corollary of the locality-sensitive property, if two suffixes of  $T_1$  and  $T_2$  have a long common prefix with at most  $k$  mismatches, with high probability they will be close to each other in the ordering.

### 3 Proof of Theorem 2

In this section we show Theorem 2. During the preprocessing stage, we compute sketches [26] of all substrings of the strings  $T_1$  and  $T_2$  of lengths  $\ell = 1, 2, \dots, 2^{\lfloor \log n \rfloor}$ , which can be defined in the following way. For a fixed  $\ell$  choose  $\lambda = 1.5 \ln n / \gamma^2$  binary vectors  $r_\ell^i$ , where  $\gamma$  is a constant to be defined later and let

$$r_\ell^i[j] = \begin{cases} 1 & \text{with probability } \frac{1}{4k} \\ 0 & \text{with probability } 1 - \frac{1}{4k} \end{cases} \text{ for all } i = 1, 2, \dots, \lambda \text{ and } j = 1, 2, \dots, \ell$$

For a string  $x$  of length  $\ell \in \{1, 2, \dots, 2^{\lfloor \log n \rfloor}\}$  we define a sketch  $\text{sk}(x)$  to be a vector of length  $\lambda$ , where  $\text{sk}(x)[i] = r_\ell^i \cdot x \pmod{2}$ . In other words, to obtain  $\text{sk}(x)$  we sample each position of  $x$  with probability  $\frac{1}{4k}$  and then sum the letters in the sampled positions modulo 2. All sketches can be computed in  $\mathcal{O}(n \log^3 n)$  time by independently running the Fast Fourier Transform (FFT) algorithm for each of the vectors  $r_\ell^i$ , and occupy  $\mathcal{O}(n \log^2 n)$  space [15]. Each substring  $S$  can be decomposed uniquely as  $x_1 x_2 \dots x_r$ , where  $r \in \mathcal{O}(\log n)$  and  $|x_1| > |x_2| > \dots > |x_r|$  are powers of two. We define a sketch  $\text{sk}(S) = \sum_q \text{sk}(x_q)$ . Let  $\delta_1 = \frac{1}{2}(1 - (1 - \frac{1}{4k})^k)$ ,  $\delta_2 = \frac{1}{2}(1 - (1 - \frac{1}{4k})^{(1+\varepsilon) \cdot k})$ , and  $\Delta = \frac{(\delta_1 + \delta_2)}{2} \cdot \lambda$ .

► **Lemma 3** ([26]). *For any  $i$  if the Hamming distance between  $S_1$  and  $S_2$  is at most  $k$ , then  $\text{sk}(S_1)[i] \neq \text{sk}(S_2)[i]$  with probability at most  $\delta_1$ . If the Hamming distance between  $S_1$  and  $S_2$  is at least  $(1 + \varepsilon) \cdot k$ , then  $\text{sk}(S_1)[i] \neq \text{sk}(S_2)[i]$  with probability at least  $\delta_2$ .*

**Proof.** Let  $m$  be the Hamming distance between  $S_1$  and  $S_2$  and let  $p_1, p_2, \dots, p_m$  be the positions of the mismatches between them. If none of the positions  $p_1, p_2, \dots, p_m$  are sampled, then  $\text{sk}(S_1)[i] = \text{sk}(S_2)[i]$ , and otherwise for each way of sampling  $p_1, p_2, \dots, p_{m-1}$  exactly one of the two choices for  $p_m$  will give  $\text{sk}(S_1)[i] = \text{sk}(S_2)[i]$ . (Recall that the alphabet is binary.) Hence, the probability that  $\text{sk}(S_1)[i] = \text{sk}(S_2)[i]$  is equal to  $\frac{1}{2}(1 - (1 - \frac{1}{4k})^m)$ , which is at most  $\delta_1$  if the Hamming distance between  $S_1$  and  $S_2$  is at most  $k$ , and at least  $\delta_2$  if the Hamming distance is greater than  $(1 + \varepsilon) \cdot k$ . ◀

► **Lemma 4.** *If the Hamming distance between sketches  $\text{sk}(S_1)$  and  $\text{sk}(S_2)$  is bigger than  $\Delta$ , then the Hamming distance between  $S_1$  and  $S_2$  is bigger than  $k$ . If the Hamming distance between sketches  $\text{sk}(S_1)$  and  $\text{sk}(S_2)$  is at most  $\Delta$ , then the Hamming distance between  $S_1$  and  $S_2$  is at most  $(1 + \varepsilon) \cdot k$ . Both claims are correct with probability at least  $1 - \frac{1}{n^3}$ .*

**Proof.** Let  $\chi_i$  be an indicator random variable that is equal to one if and only if  $\text{sk}(S_1)[i] = \text{sk}(S_2)[i]$ . The claim follows immediately from Lemma 3 and the following Chernoff bounds (see [2, Appendix A]). For  $\lambda$  independently and identically distributed binary variables  $\chi_1, \chi_2, \dots, \chi_\lambda$ ,  $\Pr[\sum_i \chi_i \geq (p + \gamma)] \leq e^{-2\lambda\gamma^2}$  and  $\Pr[\sum_i \chi_i < (p - \gamma)] \leq e^{-2\lambda\gamma^2}$ , where  $p = \Pr[\chi_i = 1]$ . We put  $\gamma = \frac{(\delta_2 - \delta_1)}{2}$  and obtain that the error probability is at most  $e^{-2\lambda\gamma^2} < \frac{1}{n^3}$ . (Note that  $\gamma = \Theta(1 - e^{\varepsilon/4})$  is a constant depending on  $\varepsilon$ .) ◀

Suppose we wish to answer an  $\text{LCP}_{\tilde{k}}$  query on two suffixes  $S_1, S_2$ . It suffices to find the longest prefixes of  $S_1, S_2$  such that the Hamming distance between their sketches is at most  $\Delta$ . As mentioned above, these prefixes can be represented uniquely as a concatenation of strings of power-of-two lengths  $\ell_1 > \ell_2 > \dots > \ell_r$ . To compute  $\ell_1$ , we initialise it with the biggest power of two not exceeding  $n$  and compute the Hamming distance between the sketches of corresponding substrings. If it is smaller than  $\Delta$ , we have found  $\ell_1$ , otherwise we divide  $\ell_1$  by two and continue. Suppose that we already know  $\ell_1, \ell_2, \dots, \ell_i$  and let  $h_i$  be the Hamming distance between the sketches of prefixes of  $S_1$  and  $S_2$  of lengths  $\ell_1 + \ell_2 + \dots + \ell_i$ . To compute  $\ell_{i+1}$ , we initialise it with  $\ell_i$  and then divide it by two until the Hamming distance between the corresponding substrings of length  $\ell_{i+1}$  is at most  $\Delta - h_i$ . From above it follows that the algorithm is correct with probability at least  $1 - \frac{1}{n^2}$  (we estimate error probability by the union bound) and that the query time is  $\mathcal{O}(\log^2 n)$ . This completes the proof of Theorem 2.

## 4 Proof of Theorem 1

Recall that we are given two strings  $T_1, T_2$  of length  $n$ , and if  $\ell_k$  is the length of the longest common substring with  $k$  mismatches of  $T_1$  and  $T_2$ , the objective is to return a substring of length at least  $\ell_k$  that occurs in  $T_1$  and  $T_2$  with at most  $(1 + \varepsilon) \cdot k$  mismatches.

### 4.1 Algorithm

We start by preprocessing  $T_1$  and  $T_2$  as described in Theorem 2. The main phase of the algorithm is defined by three parameters  $t, w$ , and  $m$  to be specified later, and consists of  $\theta(t! \log n)$  independent steps.

At each step we choose  $\binom{w}{t}$  hash functions, where each hash function can be considered as a  $t$ -tuple of projections of strings of length  $n$  onto subsets of their positions of size  $m$ . Let  $\mathcal{H}$  be a set of all projections of strings of length  $n$  onto a single position, i.e. the value of the  $i$ -th projection on a string of length  $n$  is simply its  $i$ -th letter. We start by choosing a set of  $w$  functions  $u_r \in \mathcal{H}^m$ ,  $r = 1, 2, \dots, w$ , uniformly at random. Each hash function  $h$  is defined to be a  $t$ -tuple of distinct functions  $u_r$ . More formally,  $h = (u_{r_1}, u_{r_2}, \dots, u_{r_t}) \in \mathcal{H}^{mt}$ , where  $1 \leq r_1 < r_2 < \dots < r_t \leq w$ . The fact that the hash functions are constructed from a small set of functions  $u_j$  will ensure faster running time for the algorithm.

Consider the set of all suffixes  $S_1, S_2, \dots, S_{2n}$  of  $T_1$  and  $T_2$ . We append each suffix in the set with an appropriate number of letters  $\$ \notin \Sigma$  so that all suffixes have length  $n$  and build a trie on strings  $h(S_1), h(S_2), \dots, h(S_{2n})$ .

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**Algorithm 1** Longest common substring with approximately  $k$  mismatches.
 

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1: Preprocess  $T_1, T_2$  for  $\text{LCP}_{\tilde{k}}$  queries
2: for  $i = 1, 2, \dots, \theta(t! \log n)$  do
3:   for  $r = 1, 2, \dots, w$  do
4:     Choose a function  $u_r \in \mathcal{H}^m$  uniformly at random
5:     Preprocess  $u_r$ 
6:   end for
7:   for all  $h = (u_{r_1}, u_{r_2}, \dots, u_{r_t})$  do
8:     Build a trie on  $h(S_1), h(S_2), \dots, h(S_{2n})$ 
9:     Augment the trie with an LCA data structure
10:  end for
11: for all suffixes  $S$  of  $T_1$  do
12:   Find the largest  $\ell$  s.t. the total size of the  $\ell$ -neighbourhoods of  $S$  is  $\geq 2\binom{w}{t}$ 
13:   Select a set  $\mathcal{S}$  of  $2\binom{w}{t}$  suffixes from the  $\ell$ -neighbourhoods of  $S$ 
14:   for all suffixes  $S' \in \mathcal{S}$  do
15:     Compute  $\text{LCP}_{\tilde{k}}(S, S')$ 
16:     Update the longest common substring with approximately  $k$  mismatches
17:   end for
18: end for
19: end for

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► **Theorem 5.** After  $\mathcal{O}(wn^{4/3} \log^{4/3} n)$ -time and  $\mathcal{O}(wn)$ -space preprocessing of functions  $u_r$ ,  $r = 1, 2, \dots, w$ , for any hash function  $h = (u_{r_1}, u_{r_2}, \dots, u_{r_t})$  a trie on  $h(S_1), h(S_2), \dots, h(S_{2n})$  can be built in  $\mathcal{O}(tn \log n)$  time and linear space.

Let us defer the proof of the theorem until we complete the description of the algorithm and show Theorem 1. The algorithm preprocesses  $u_1, u_2, \dots, u_w$ , and for each hash function  $h$  builds a trie on  $h(S_1), h(S_2), \dots, h(S_{2n})$ . It then augments the trie with an LCA data structure, which can be done in linear time and space [14, 20]. Given two strings  $h(S_i), h(S_j)$  the LCA data structure can find the length of their longest common prefix in constant time.

Consider a suffix  $S$  of  $T_1$  and let  $h$  be a hash function projecting a string of length  $n$  onto a subset  $\mathcal{P} \subseteq [1, n]$  of its positions. We define  $h|_{[\ell]}$  to be a projection onto a subset  $\mathcal{P} \cap [1, \ell]$  of positions. (In other words,  $h|_{[\ell]}$  is a function  $h$  applied to a prefix of a string of length  $\ell$ .) We further say that the  $\ell$ -neighbourhood of  $S$  is the set of all suffixes  $S'$  of  $T_2$  such that  $h|_{[\ell]}(S) = h|_{[\ell]}(S')$ . Note that for a fixed  $h$  and  $\ell$  the size of the  $\ell$ -neighbourhood of  $S$  is equal to the number of suffixes  $S'$  of  $T_2$  such that the length of the longest common prefix of  $h(S)$  and  $h(S')$  is at least  $|\mathcal{P} \cap [1, \ell]|$ . From the properties of the lexicographic order it follows that if  $S', S''$  are two suffixes of  $T_2$  and  $h(S'')$  is located between  $h(S')$  and  $h(S)$  in the trie for  $h$ , then the longest common prefix of  $h(S')$  and  $h(S)$  is no longer than the longest common prefix of  $h(S'')$  and  $h(S)$ . Therefore, the larger  $\ell$  is, the smaller the neighbourhood is. We use a simple binary search and the LCA data structures to find the largest  $\ell$  such that the total size of  $\ell$ -neighbourhoods for all hash functions is at least  $2\binom{w}{t}$  in  $\mathcal{O}\left(\binom{w}{t} \cdot \log^2 n\right)$  time. From the union of the  $\ell$ -neighbourhoods we select a multiset  $\mathcal{S}$  of  $2\binom{w}{t}$  suffixes ensuring that all suffixes  $S'$  such that the longest common prefix of  $h(S')$  and  $h(S)$  has length at least  $|\mathcal{P} \cap [1, \ell]| + 1$  are included. For each suffix  $S' \in \mathcal{S}$  we compute the longest common prefix with approximately  $k$  mismatches of  $S'$  and  $S$  by one  $\text{LCP}_{\tilde{k}}$  query (Theorem 2). The longest of all retrieved prefixes, over all suffixes  $S$  of  $T_1$ , is returned as an answer. The algorithm is summarised in the figure above. We will now proceed to its complexity and correctness.

## 4.2 Complexity and correctness

To ensure the complexity bounds and correctness of the algorithm, we must carefully choose the parameters  $t$ ,  $w$ , and  $m$ . Let  $p_1 = 1 - k/n$ , and  $p_2 = 1 - (1 + \varepsilon) \cdot k/n$ . The intuition behind  $p_1$  and  $p_2$  is that if  $S_1, S_2$  are two suffixes of length  $n$  and the Hamming distance between  $S_1$  and  $S_2$  is at most  $k$ , then  $p_1$  is a lower bound for the probability of two letters  $S_1[i], S_2[i]$  to be equal. On the other hand,  $p_2$  is an upper bound for the probability of two letters  $S_1[i], S_2[i]$  to be equal if the Hamming distance between  $S_1$  and  $S_2$  is at least  $(1 + \varepsilon) \cdot k$ . Let  $\rho = \log p_1 / \log p_2$ , and define

$$t = \left\lceil \sqrt{\frac{\rho \log n}{\ln \log n}} \right\rceil + 1, \quad w = \lceil n^{\rho/t} \rceil, \quad \text{and} \quad m = \left\lceil \frac{1}{t} \log_{p_2} \frac{1}{n^2} \right\rceil.$$

### 4.2.1 Complexity

To show the time complexity of the algorithm, we will start from the following simple observation.

► **Observation 6.**  $\rho \leq 1/(1 + \varepsilon)$  and  $2 \leq t \leq \sqrt{\log n}$ .

**Proof.** By Bernoulli's inequality  $(1 - k/n)^{1+\varepsilon} \geq 1 - (1 + \varepsilon) \cdot k/n$ . Hence, we obtain that  $\rho = \frac{\log(1-k/n)}{\log(1-(1+\varepsilon)k/n)} \leq \frac{1}{1+\varepsilon}$ . The second part of the lemma follows. ◀

► **Lemma 7.** *One step of the algorithm takes  $\mathcal{O}(wn^{4/3} \log^{4/3} n + \binom{w}{t} \cdot n \log^2 n)$  time.*

**Proof.** By Theorem 5, after  $\mathcal{O}(wn^{4/3} \log^{4/3} n)$ -time preprocessing we can build a trie and an LCA data structure on strings  $h(S_1), h(S_2), \dots, h(S_{2n})$  for a hash function  $h$  in  $\mathcal{O}(tn \log n) = \mathcal{O}(n \log^{3/2} n)$  time and there are  $\binom{w}{t}$  hash functions in total. For each suffix of  $T_1$  we then run  $2 \binom{w}{t}$  LCP $_{\tilde{k}}$  queries, which takes  $\mathcal{O}(\binom{w}{t} \cdot n \log^2 n)$  time. ◀

► **Corollary 8.** *The running time of the algorithm is  $\mathcal{O}(n^{1+1/(1+\varepsilon)} \log^2 n)$ .*

**Proof.** Preprocessing  $T_1, T_2$  for LCP $_{\tilde{k}}$  queries takes  $\mathcal{O}(n \log^3 n / \varepsilon^2)$  time (see Theorem 2). Each step of the algorithm takes  $\mathcal{O}(wn^{4/3} \log^{4/3} n + \binom{w}{t} \cdot n \log^2 n)$  time, and there are  $\theta(t! \log n)$  steps in total. To estimate the total running time of the algorithm we notice that  $wt! = \mathcal{O}(e^{\sqrt{\rho \log n \ln \log n}}) = \mathcal{O}(n^{o(1)})$  and  $\binom{w}{t} \cdot t! \leq \frac{w^t}{t!} t! = n^\rho \leq n^{1/(1+\varepsilon)}$ . Plugging these inequalities into the time bound for one step and recalling that  $0 < \varepsilon < 2$ , we obtain the claim. ◀

► **Lemma 9.** *The space complexity of the algorithm is  $\mathcal{O}(n^{1+1/(1+\varepsilon)})$ .*

**Proof.** The data structure for LCP $_{\tilde{k}}$  queries requires  $\mathcal{O}(n \log^3 n)$  space. At each step of the algorithm, preprocessing functions  $u_j$  requires  $\mathcal{O}(wn) = \mathcal{O}(n^{1+o(1)})$  space and the tries occupy  $\mathcal{O}(\binom{w}{t} \cdot n) = \mathcal{O}(n^{1+1/(1+\varepsilon)})$  space. ◀

### 4.2.2 Correctness

Let  $S$  be a suffix of  $T_1$ . Consider a set of the longest common prefixes with  $k$  mismatches of  $S$  and suffixes of  $T_2$  and let  $\ell_k$  be the maximal length of a prefix in this set achieved on some suffix  $S'$  of  $T_2$ .

► **Lemma 10.** *For each step with probability  $\geq \theta(1/t!)$  there exists a hash function  $h$  such that  $h|_{[\ell_k]}(S) = h|_{[\ell_k]}(S')$ .*



**Proof.** Consider strings  $S[1, \ell_k] \$^{n-\ell_k}$  and  $S'[1, \ell_k] \$^{n-\ell_k}$ . The Hamming distance between them is equal to the Hamming distance between  $S[1, \ell_k]$  and  $S'[1, \ell_k]$ , which is  $k$ . Moreover, for any hash function  $h$  we have that  $h(S[1, \ell_k] \$^{n-\ell_k}) = h(S'[1, \ell_k] \$^{n-\ell_k})$  if and only if  $h|_{[\ell_k]}(S) = h|_{[\ell_k]}(S')$ . Remember that each hash function is a  $t$ -tuple of functions  $u_j$ . Consequently, if  $h(S[1, \ell_k] \$^{n-\ell_k}) \neq h(S'[1, \ell_k] \$^{n-\ell_k})$  for all hash functions  $h$ , the strings collide on at most  $t - 1$  functions  $u_j$ . By [5, Lemma A.1] the probability of this event for two strings at the Hamming distance  $k$  is at most  $1 - \theta(1/t!)$ . ◀

As a corollary, we can choose the constant in the number of steps so that with probability  $\geq 1 - 1/n^2$  there will exist a step of algorithm such that for at least one hash function we will have  $h|_{[\ell_k]}(S) = h|_{[\ell_k]}(S')$ . The set  $\mathcal{S}$  of  $2^{\binom{w}{t}}$  suffixes that we sample from the  $\ell$ -neighbourhoods of  $S$  might or might not include the suffix  $S'$ . If it does, then the  $\text{LCP}_{\tilde{k}}$  query for  $S'$  and  $S$  will return a substring of length  $\geq \ell_k$  with high probability. If it does not, then by the definition of neighbourhoods for each suffix  $S'' \in \mathcal{S}$  belonging to the neighbourhood for a hash function  $g$  we have  $g|_{[\ell_k]}(S) = g|_{[\ell_k]}(S'')$ . We will show that only for a small number of such suffixes an  $\text{LCP}_{\tilde{k}}$  query can return a substring of length smaller than  $\ell_k$ .

► **Lemma 11.** *With probability  $\geq 1 - 2/n^2$  there are at most  $\binom{w}{t}$  suffixes  $S''$  such that  $g|_{[\ell_k]}(S) = g|_{[\ell_k]}(S'')$  but the  $\text{LCP}_{\tilde{k}}$  query returns a substring shorter than  $\ell_k$ .*

**Proof.** If the  $\text{LCP}_{\tilde{k}}$  query for  $S$  and  $S''$  returns a substring shorter than  $\ell_k$ , then with high probability the Hamming distance between  $S[1, \ell_k]$  and  $S''[1, \ell_k]$  is at least  $(1 + \varepsilon) \cdot k$ . Remember that a hash function  $g$  can be considered as a projection onto a random subset of positions of size  $mt$ , and therefore we obtain

$$\Pr[g|_{[\ell_k]}(S) = g|_{[\ell_k]}(S'')] = \Pr[g(S[1, \ell_k] \$^{n-\ell_k}) = g(S''[1, \ell_k] \$^{n-\ell_k})] \leq (p_2)^{mt} = \frac{1}{n^2}$$

We can consider an indicator random variable that is equal to one if for a suffix  $S''$  such that  $g|_{[\ell_k]}(S) = g|_{[\ell_k]}(S'')$  the  $\text{LCP}_{\tilde{k}}$  query returns a substring shorter than  $\ell_k$ , and to zero otherwise. By linearity, the expectation of their sum is at most  $\frac{2}{n^2} \cdot \binom{w}{t}$ . The claim follows from Markov's inequality. ◀

From Lemmas 10 and 11 and Theorem 2 it follows that the algorithm correctly finds the value of  $\ell$  for the suffix  $S$  of  $T_1$  with error probability  $\leq 3/n^2$ . Applying the union bound, we obtain that the error probability of the algorithm is constant.

### 4.3 Proof of Theorem 5

Recall that  $h$  is a  $t$ -tuple of functions  $u_r$ , i.e  $h = (u_{r_1}, u_{r_2}, \dots, u_{r_t})$ , where  $1 \leq r_1 < r_2 < \dots < r_t \leq w$ . Below we will show that after the preprocessing of functions  $u_r$  we will be able to compute the longest common prefix of any two strings  $u_r(S_i), u_r(S_j)$  in  $\mathcal{O}(1)$  time. As a result, we will be able to compute the longest common prefix of  $h(S_i), h(S_j)$  in  $\mathcal{O}(t)$  time. It also follows that we will be able to compare any two strings  $h(S_i), h(S_j)$  in  $\mathcal{O}(t)$  time as their order is defined by the letter following the longest common prefix. Therefore, we can sort strings  $h(S_1), h(S_2), \dots, h(S_{2n})$  in  $\mathcal{O}(tn \log n)$  time and  $\mathcal{O}(n)$  space and then compute the longest common prefix of each two adjacent strings in  $\mathcal{O}(tn)$  time. The trie on  $h(S_1), h(S_2), \dots, h(S_{2n})$  can then be built in  $\mathcal{O}(n)$  time by imitating its depth-first traverse.

It remains to explain how we preprocess functions  $u_r$ ,  $r = 1, 2, \dots, w$ . For each function  $u_r$  it suffices to build a trie on strings  $u_r(S_1), u_r(S_2), \dots, u_r(S_{2n})$  and to augment it with an

LCA data structure [14, 20]. We will consider two different methods for constructing the trie with time dependent on  $m$ . No matter what the value of  $m$  is, one of these methods will have  $\mathcal{O}(n^{4/3} \log^{1/3} n)$  running time. Let  $u_r$  be a projection along a subset  $\mathcal{P}$  of positions  $1 \leq p_1 \leq p_2 \leq \dots \leq p_m \leq n$  and denote  $T = T_1 \$^n T_2 \$^n$ .

► **Lemma 12.** *The trie can be built in  $\mathcal{O}(\sqrt{mn} \log n)$  time and  $\mathcal{O}(n)$  space correctly with error probability at most  $1/n^3$ .*

**Proof.** We partition  $\mathcal{P}$  into disjoint subsets  $B_1, B_2, \dots, B_{\sqrt{m}}$ , where

$$B_\ell = \{p_{\ell,1}, p_{\ell,2}, \dots, p_{\ell,\sqrt{m}}\} = \{p_{(\ell-1)\sqrt{m}+q} \mid q \in [1, \sqrt{m}]\}.$$

Now  $u_r$  can be represented as a  $\sqrt{m}$ -tuple of projections  $b_1, b_2, \dots, b_{\sqrt{m}}$  onto the subsets  $B_1, B_2, \dots, B_{\sqrt{m}}$  respectively. We will build the trie by layers to avoid space overhead. Suppose that we have built the trie for a function  $(b_1, b_2, \dots, b_{\ell-1})$  and we want to extend it to the trie for  $(b_1, b_2, \dots, b_{\ell-1}, b_\ell)$ .

Let  $p$  be a random prime of value at most  $n^{\mathcal{O}(1)}$ . We create a vector  $\chi$  of length  $n$ , where  $\chi[p_{\ell,q}] = 2^{\sqrt{m}-1-q}$  and zero for all positions not in  $B_\ell$ . We then run the FFT algorithm for  $\chi$  and  $T$  in the field  $\mathbb{Z}_p$  [15]. The output of the FFT algorithm will contain convolutions of  $\chi$  and all suffixes  $S_1, S_2, \dots, S_{2n}$ . The convolution of  $\chi$  and a suffix  $S_i$  is the Karp-Rabin fingerprint [24]  $\varphi_{\ell,i}$  of  $b_\ell(S_i)$ , where

$$\varphi_{\ell,i} = \sum_{q=1}^{\sqrt{m}} S_i[p_{\ell,q}] \cdot 2^{\sqrt{m}-1-q} \pmod{p}$$

If the fingerprints of  $b_\ell(S_i)$  and  $b_\ell(S_j)$  are equal, then  $b_\ell(S_i)$  and  $b_\ell(S_j)$  are equal with probability at least  $1 - \frac{1}{n^4}$ , and otherwise they differ. For a fixed leaf of the trie for  $(b_1, b_2, \dots, b_{\ell-1})$  we sort all suffixes that end in it by fingerprints  $\varphi_{\ell,i}$ , which takes  $\mathcal{O}(n \log n)$  time in total. For each two suffixes  $S_i, S_j$  that end in the same leaf, adjacent and have  $\varphi_{\ell,i} \neq \varphi_{\ell,j}$ , we compare  $b_\ell(S_i)$  and  $b_\ell(S_j)$  letter-by-letter in  $\mathcal{O}(\sqrt{m})$  time to find their longest common prefix. Note that this letter-by-letter comparison step will be executed at most  $n$  times, and therefore will take  $\mathcal{O}(\sqrt{mn})$  time in total. We then append each leaf with a trie on strings  $b_\ell(S_i)$  that can be built by imitating its depth-first traverse, which takes  $\mathcal{O}(n)$  time for a layer. ◀

The second method builds the trie in  $\mathcal{O}(n^2 \log^2 n/m)$  time by the algorithm described in the first paragraph of this section, and we only need to give a method for comparing the longest common prefix of  $u_r(S_i)$  and  $u_r(S_j)$  (or, equivalently, the first position where  $u_r(S_i)$  and  $u_r(S_j)$  differ.)

► **Lemma 13** ([5]). *After  $\mathcal{O}(n)$ -time and space preprocessing the first position where two strings  $u_r(S_i)$  and  $u_r(S_j)$  differ can be found in  $\mathcal{O}(n \log n/m)$  time correctly with error probability at most  $1/n^3$ .*

**Proof.** We start by building the suffix tree for the string  $T$ . The suffix tree can be built in  $\mathcal{O}(n)$  time and space [32, 13, 19]. Furthermore, we augment the suffix tree with an LCA data structure in  $\mathcal{O}(n)$  time [14, 20].

Let  $\ell = 3n \log n/m$ . We can find the first  $\ell$  positions  $q_1 < q_2 < \dots < q_\ell$  where  $S_i$  and  $S_j$  differ in  $\mathcal{O}(n \log n/m)$  time using the kangaroo method [27, 17]. The idea of the kangaroo method is as follows. We can find  $q_1$  by one query to the LCA data structure in  $\mathcal{O}(1)$  time. After removing the first  $q_1$  positions of  $S_i, S_j$ , we obtain suffixes  $S_{i+q_1}, S_{j+q_1}$  and find  $q_2$

by another query to the LCA data structure, and so on. If at least one of the positions  $q_1, q_2, \dots, q_\ell$  belongs to  $\mathcal{P}$ , then we return the first such position as an answer, and otherwise we say that  $u_r(S_i) = u_r(S_j)$ .

Let us show that if  $p$  is the first position where  $u_r(S_i)$  and  $u_r(S_j)$  differ, then  $p$  belongs to  $\{q_1, q_2, \dots, q_\ell\}$  with high probability. Because  $q_1 < q_2 < \dots < q_\ell$  are the first  $\ell$  positions where  $S_i$  and  $S_j$  differ, it suffices to show that at least one of these positions belongs to  $\mathcal{P}$ . We rely on the fact  $\mathcal{P}$  is a random subset of  $[1, n]$ . We have  $\Pr[q_1, q_2, \dots, q_\ell \notin \mathcal{P}] = (1 - \ell/n)^m = (1 - 3 \log n/m)^m \leq n^{-3}$ . ◀

As a corollary of Lemmas 12 and 13, the trie on strings  $u_r(S_1), u_r(S_2), \dots, u_r(S_{2n})$  can be built in  $\mathcal{O}(\min\{\sqrt{m}, n \log n/m\} \cdot n \log n) = \mathcal{O}(n^{4/3} \log^{4/3} n)$  time and  $\mathcal{O}(n)$  space correctly with high probability which implies Theorem 5 as explained in the beginning of this section.

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