Approximate Parameterized Matching

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Abstract. Two equal length strings s and s', over alphabets Σ_s and $\Sigma_{s'}$, *parameterize match* if there exists a bijection $\pi : \Sigma_s \rightarrow \Sigma_{s'}$ such that $\pi(s) = s'$, where $\pi(s)$ is the renaming of each character of s via π. *Parameterized matching* is the problem of finding all parameterized matches of a pattern string p in a text t, and *approximate parameterized matching* is the problem of finding at each location a bijection π that maximizes the number of characters that are mapped from p to the appropriate $|p|$-length substring of t.

Parameterized matching was introduced as a model for software duplication detection in software maintenance systems and also has applications in image processing and computational biology. For example, approximate parameterized matching models image searching with variable color maps in the presence of errors.

We consider the problem for which an error threshold, k, is given, and the goal is to find all locations in t for which there exists a bijection π which maps p into the appropriate $|p|$-length substring of t with at most k mismatched mapped elements. Our main result is an algorithm for this problem with $O(nk^{1.5} + mk \log m)$ time complexity, where $m = |p|$ and $n = |t|$. We also show that when $|p| = |t| = m$, the problem is equivalent to the maximum matching problem on graphs, yielding a $O(m + k^{1.5})$ solution.

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1. *Introduction*

In the traditional pattern matching model [Boyer and Moore 1977; Knuth et al. 1977], one seeks exact occurrences of a given pattern p in a text t, that is, text locations where every text symbol is equal to its corresponding pattern symbol. For two equal length strings s and s', we say that s is a *parameterized match* of s' if there exists a bijection π from the alphabet of s to the alphabet of s' such that every symbol of s' is equal to the image under π of the corresponding symbol of s. In the parameterized matching problem, introduced by Baker [1993, 1997], one seeks all text locations for which the pattern p parameterize matches the substring of length $|p|$ beginning at that location.

Baker [1993, 1997] introduced parameterized matching for applications that arise in software tools for analyzing source code. Specifically, the application is to identify duplicate code in large software systems for reuse. Here it is desirable to find not only exact matches between program fragments but also parameterized matches, namely, where the two program fragments are equal but possibly use interchangeable identifiers (representing variable, constant, or function names).

When program fragments that repeat are discovered, other files of the program are searched to find repetitions of the program fragment in other locations. (It is often the case that repeating fragments have many appearances.) This application is exactly captured by the notion of the parameterized matching problem. It turns out that the parameterized matching problem arises in other applications such as in image processing and computational biology, see Amir et al. [2003].

In Baker [1993, 1997], an optimal, linear time algorithm was given for parameterized matching. However, it was assumed that the alphabet was of constant size. Amir et al. [1994] presented tight bounds for parameterized matching in the presence of an unbounded size alphabet.

In Baker [1996], a novel method was presented for parameterized matching by constructing *parameterized suffix trees*, which also allows for online parameterized matching. The parameterized suffix trees are constructed by converting the pattern string into a *predecessor string*. A *predecessor string* of a string s has at each location i the distance between i and the location containing the previous appearance of the symbol. The first appearance of each symbol is replaced with a 0. For example, the predecessor string of *aabbaba* is 0, 1, 0, 1, 3, 2, 2. A simple and well-known fact is that:

OBSERVATION 1. *s and s' parameterize match if and only if they have the same predecessor string.*

The parameterized suffix tree is constructed in a manner that every path corresponds to a suffix, in the standard sense, but is labeled with the predecessor string of the appropriate suffix. Branching in the parameterized suffix tree occurs according to the labels of the predecessor strings. The parameterized suffix tree was further explored by Kosaraju [1995] and faster constructions were given by Cole and Hariharan [2000].

One of the interesting problems in Web searching is searching for color images, see Amir et al. [2002]; Babu et al. [1995]; Swain and Ballard [1991]. The simplest possible case is searching for an icon in a screen, a task that the Human-Computer Interaction Lab at the University of Maryland was confronted with. If the colors are fixed, this is exact 2-dimensional pattern matching [Amir et al. 1994]. However, if the color maps in pattern and text differ, the exact matching algorithm would not find the pattern. Parameterized 2-dimensional search is precisely what is needed. A nearly optimal algorithm to solve the 2-dimensional parameterized matching problem was given in Amir et al. [2003].

In reality, when searching for an image, one needs to take into account the occurrence of errors that distort the image. Errors occur in various forms, depending upon the application. Several distance metrics have been defined to account for such errors. Two of the most classical distance metrics are the Hamming distance and the edit distance [Levenshtein 1966]. The *Hamming distance* between two equal-length strings is the number of mismatching characters when the strings are aligned. The *edit distance* is the minimal number of character replacements, insertions, and deletions needed to convert one string into another [Levenshtein 1966].

In Baker [1999], the parameterized match problem was considered in conjunction with the edit distance. Here the definition of edit distance was slightly modified so that the edit operations are defined to be insertion, deletion, and parameterized replacements, that is, the replacement of a substring with a string that parameterize matches it. An algorithm was devised for finding the parameterized edit distance of two strings whose efficiency is close to the efficiency of the algorithms for computing the classical edit distance. Also an algorithm was suggested for the decision variant of the problem where a parameter k is given, and it is necessary to decide whether the strings are within (parameterized edit) distance k.

However, it turns out that the operation of parameterized replacement relaxes the problem to an easier problem. The reason that the problem becomes easier is that two substrings that participate in two parameterized replacements are independent of each other (in the parameterized sense).

A more rigid, but more realistic, definition for the Hamming distance variant was given in Apostolico et al. [2007]. For a pair of equal length strings s and s' and a bijection π defined on the alphabet of s, the π-mismatch is the Hamming distance between the image under π of s and s'. The minimal π-mismatch over all bijections π is the approximate parameterized match. The problem considered in Apostolico et al. [2007] is to find for each location i of a text t the approximate parameterized match of a pattern p with the substring beginning at location i. In Apostolico et al. [2007], the problem was defined, and linear time algorithms were given for the case were the pattern is binary or the text is binary. However, this solution does not carry over to larger alphabets.

Unfortunately, under this definition the methods for classical string matching with errors for Hamming distance, for example, Galil and Giancarlo [1986] and Landau and Vishkin [1988], also known as pattern matching with mismatches, seem to fail. Following is an outline of the method [Galil and Giancarlo 1986] for pattern matching with mismatches.

The pattern is compared separately to each suffix of the text, beginning at locations $1 \leq i \leq n$. Using a suffix tree of the text and precomputed longest common ancestor (LCA) information (which can be computed once in linear time, see Harel and Tarjan [1984], and Schieber and Vishkin [1988]), one can find the longest common prefix of the pattern and the corresponding suffix (in constant time). There must be a mismatch immediately following. The algorithm jumps over the mismatch and repeats the process taking into consideration the offsets of the pattern and suffix.

When attempting to apply this technique to a parameterized suffix tree, it fails. To illustrate this, consider the first matching substring (up until the first error) and the next matching substring (after the error). Both of these substrings parameterize match the substring of the text that they are aligned with. However, it is possible that combined they do not form a parameterized match. (See Example 1.) In Example 1, *abab* parameterize matches *cdcd*, followed by a mismatch and subsequently followed by *abaa* parameterized matching *efee*. However, different π's are required for the local parameterized matches. This example also emphasizes why the definition of Baker [1999] is a simplification. Specifically, each local parameterized matching substring is one replacement, that is, *abab* with *cdcd* is one replacement, and *abaa* with *efee* is one more replacement. However, a more precise definition would capture the globality of the parameterized matching not allowing, in this case, *abab* to parameterize match to two different substrings.

Example 1.

$$p = a\ b\ a\ b\ a\ a\ b\ a\ a\ \ldots$$
$$t = \ldots\ c\ d\ c\ d\ d\ e\ f\ e\ e\ \ldots$$

In this article we consider the problem of parameterized matching with k mismatches. The parameterized matching problem with k mismatches seeks all parameterized matches of a pattern p in a text t, with at most k mismatches.

For the case where $|p| = |t| = m$, which we call the string comparison problem, we show an $O(m^{1.5})$ algorithm for the problem by using maximum matching algorithms. For the string comparison problem with threshold k, we show an $O(m+k^{1.5})$ time algorithm. We also show that improving on either of these will lead to better maximum matching algorithms for sparse graphs, a long open question.

The main result of the article is an algorithm that solves the parameterized matching with k mismatches problem, given a pattern of length m and a text of length n, in $O(nk^{1.5} + mk \log m)$ time. This immediately yields a 2-dimensional algorithm of time complexity $O(n^2mk^{1.5} + m^2k \log m)$, where $|p| = m^2$ and $|t| = n^2$.

Roadmap. In Section 2, we give preliminaries and definitions of the problem. In Section 3, we present an algorithm that compares two equal length strings for a parameterized match with k mismatches. A reduction from maximum matching in graphs to the string comparison problem is also given in Section 3. The algorithmic techniques introduced in Section 3 are used in the following section, Section 4, where we present the algorithm for the general problem of parameterized string matching with k mismatches. In Section 5, we discuss the pattern preprocessing stage of the algorithm. In Section 6, we show an extension of our algorithm for images, and finally, in Section 7, we discuss future directions for research.

2. *Preliminaries and Definitions*

Given a *string* $s = s_1 s_2 \cdots s_n$ of *length* $|s| = n$ over an alphabet Σ_s, and a bijection π from Σ_s to some other alphabet $\Sigma_{s'}$, the *image* of s under π is the string $s' = \pi(s) = \pi(s_1) \cdot \ldots \cdot \pi(s_n)$, that is obtained by applying π to all characters of s.

Given two equal-length strings w and u over alphabets Σ_w and Σ_u and a bijection π from Σ_w to Σ_u, the π-mismatch between w and u is $Ham(\pi(w), u)$, where $Ham(s, t)$ is the Hamming distance between s and t. We say that *w parameterized k-matches u* if there exists a π such that the π-mismatch $\leq k$. The *approximate parameterized match* between w and u is the minimum π-mismatch (over all bijections π).

For given input text x, $|x| = n$, and pattern y, $|y| = m$, the problem of *approximate parameterized matching* for y in x consists of computing the *approximate parameterized match* between y and every (consecutive) substring of length m of x. Hence, approximate parameterized searching requires computing the π yielding minimum π-mismatch for y at each position of x. Of course, the best π is not necessarily the same at every position. The problem of *parameterized matching with k mismatches* consists of computing for each location i of x whether y parameterized k-matches the (consecutive) substring of length m beginning at location i. Sometimes π itself is also desired (however, any π with π-mismatch of no more than k will be satisfactory).

3. *String Comparison Problem*

We begin by evaluating two equal-length strings for a parameterized k-match as follows.

Input: Two strings, $s = s_1, s_2, \ldots, s_m$ and $s' = s'_1, s'_2, \ldots, s'_m$, and an integer k.

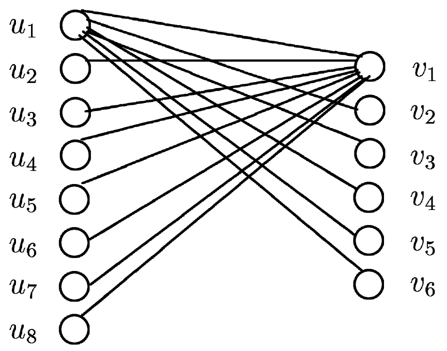
Output: True, if there exists π such that the π-mismatch of s and t is no more than k.
False, otherwise.

In standard string comparison, we simply compare the characters and count the number of mismatches in $O(m)$ time. In approximate parameterized matching the naive method of solving the problem is to check the π-mismatch for every possible π. However, this takes exponential time.

One way to solve the problem is to reduce the problem to a maximal bipartite weighted matching in a graph. We construct a bipartite graph $B = (U \cup V, E)$ in the following way. $U = \Sigma_s$ and $V = \Sigma_{s'}$. There is an edge between $a \in \Sigma_s$ and $b \in \Sigma_{s'}$ if and only if there is at least one a in s that is aligned with a b in s'. The weight of this edge is the number of a's in s that are aligned to b's in s'. It is easy to see the following.

OBSERVATION 2. *A maximum weighted matching in B corresponds to a minimal π-mismatch where π is defined by the edges of the matching.*

The problem of maximum bipartite matching has been widely studied and efficient algorithms have been devised, for example, Fredman and Tarjan [1987], Gabow [1985], Gabow and Tarjan [1989], and Kao et al. [2001]. For integer weights where the largest weight is bounded by $|V|$, the fastest algorithm runs in time $O(E\sqrt{V})$ [Kao et al. 2001]. This solution yields an $O(m^{1.5})$ time algorithm for the problem of parameterized string comparison with mismatches. The advantage of the algorithm is that it views the whole string at once and efficiently finds the best function. In the case where we have a general text (i.e., of length longer than m), which is the parameterized pattern matching problem with inputs t of length n, and p of length m, the bipartite matching solution yields an $O(nm^{1.5})$ time algorithm.



$E = \{(u_1,v_1),(u_1,v_2),(u_1,v_3),(u_1,v_4),(u_1,v_5),(u_1,v_6),(u_2,v_1),(u_3,v_1),(u_4,v_1),(u_5,v_1),(u_6,v_1),$ $(u_7,v_1),(u_8,v_1)\}$ and
$s_U = u_1u_1u_1u_1u_1u_1u_2u_3u_4u_5u_6u_7u_8$ and $s_V = v_1v_2v_3v_4v_5v_6v_1v_1v_1v_1v_1v_1v_1$.

FIG. 1. An example of a bipartite graph and its corresponding strings. The maximum matching and bijection is of size 2.

3.1. REDUCING MAXIMUM MATCHING TO THE STRING COMPARISON PROBLEM.

While we have seen that the maximum matching problem can be used to solve the string comparison problem, we will now see the reverse.

LEMMA 3.1. *Let $B = (U \cup V, E)$ be a bipartite graph. If the string comparison problem can be solved in $O(f(m))$ time then a maximum matching in B can be found in $O(f(|E|)$ time.*

PROOF. Let $U = \{u_1, u_2, \ldots, u_{|U|}\}$, $V = \{v_1, v_2, \ldots, v_{|V|}\}$, and $E = \{e_1, \ldots, e_{|E|}\}$. Create two strings s_U and s_V of length $|E|$, where for edge $e_i = \{u_j, v_l\}$ we set the ith location of s_U to be u_j and the ith location of s_V to be v_l. See Figure 1 for an example.

We let s_U and s_V be the input of the string comparison problem and note that by construction the alphabet of s_U is U, and the alphabet of s_V is V. Hence a bijection in the string comparison problem is a bijection from U to V which is a matching in B. In the string comparison problem, we want to minimize the mismatches, which are those edges that are not in the bijection, and, in the matching problem, we want to maximize the number of edges in the bijection. Since these two objective functions are equivalent, the result follows. □

Since it is always true that $|E| < |V|^2$, it follows that $|E|^{1/4} < \sqrt{|V|}$. Hence, it would be surprising to solve the string comparison problem in $o(m^{1.25})$. In fact, even for graphs with a linear number of edges, the best known algorithm is $O(E\sqrt{V})$, and hence an algorithm for the string comparison problem in $o(m^{1.5})$ would have implications on the maximum matching problem as well.

Note that for the string comparison problem one can reduce the approximate parameterized matching version to the parameterized matching with k mismatches version. This is done by binary searching on k to find the optimal solution for the string comparison problem in the approximate parameterized matching version. Hence an algorithm for detecting whether the string comparison problem has a bijection with fewer than k mismatches with time $o(\frac{k^{1.5}}{\log k} + m)$ would imply a faster maximum matching algorithm.

3.2. MISMATCH PAIRS AND PARAMETERIZED PROPERTIES. Obviously, one may use the solution of approximate parameterized string comparison to solve the problem of parameterized matching with k, mismatches. However, it is desirable to construct an algorithm with running time dependent on k rather than m. The bipartite matching method does not seem to give insight into how to achieve this goal. In order to give an algorithm dependent on k, we introduce a new method for detecting whether two equal-length strings have a parameterized k-match. The ideas used in this new comparison algorithm will be used in the following section to yield an efficient solution for the problem of parameterized matching with k mismatches.

When faced with the problem of parameterized matching with mismatches, the initial difficulty is to decide for a given location whether it is a match or a mismatch. Simple comparisons do not suffice since any symbol can match (or mismatch) every other symbol. In the bipartite solution, this difficulty is overcome by viewing the entire string at once. A bijection is found over all characters, excluding at most k locations. Thus, it is obvious that the locations that are excluded from the matching are mismatched locations. For our purposes, we would like to be able to decide locally, that is, before π is ascertained, whether a given location is good or bad.

Definition 3.2. Let s and s' be two equal-length strings. A *mismatch pair* between s and s' is a pair of locations (i,j) such that one of the following holds,

$$1.\ s_i = s_j \text{ and } s'_i \neq s'_j \qquad 2.\ s_i \neq s_j \text{ and } s'_i = s'_j.$$

It immediately follows from the definition Lemma 3.3

LEMMA 3.3. *Given two equal-length strings, s and s', if (i, j) is a mismatch pair between s and s', then for every bijection $\Pi : \Sigma_s \rightarrow \Sigma_{s'}$ either location i or location j, or both locations i and j are mismatches, that is, $\pi(s_i) \neq s'_i$ or $\pi(s_j) \neq s'_j$ or both are unequal.*

Conversely,

LEMMA 3.4. *Let s and s' be two equal-length strings, and let $S \subseteq \{1, \ldots, m\}$ be a set of locations which does not contain any mismatch pair. Then there exists a bijection $\pi : \Sigma_s \rightarrow \Sigma_{s'}$ that is parameterized on S, that is, for every $i \in S$, $\pi(s_i) = s'_i$.*

PROOF. S does not contain any mismatch pair. Hence, for any two locations i and j in S, if $s_i = s_j$, then $s'_i = s'_j$, and if $s_i \neq s_j$, then $s'_i \neq s'_j$. Hence there is a bijection $\pi : \Sigma_s \rightarrow \Sigma_{s'}$ that is a parameterized match on the set of locations S. □

The idea of our algorithm is to count the mismatch pairs between s and s'. Since each pair contributes at least one error to the parameterized match between s and s', it follows immediately from Lemma 3.3 that if there are more than k mismatch pairs, then s does not parameterize k-match s'. We claim that if there are fewer than $k/2 + 1$ mismatch pairs, then s parameterize k-matches s'.

Definition 3.5. Given two equal-length strings, s and s', a collection L of mismatch pairs is said to be a *maximal disjoint collection* if (1) all mismatch pairs in L are disjoint, that is, do not share a common location, and (2) there is no mismatch pair that can be added to L without violating disjointness.

COROLLARY 3.6. *Let s and s' be two strings, and let L be a maximal disjoint collection of mismatch pairs of s and s'. If $|L| > k$, then for every $\Pi : \Sigma_s \rightarrow \Sigma'_s$,* *the Π-mismatch is greater than k. If $|L| \leq k/2$, then there exists $\Pi : \Sigma_s \rightarrow \Sigma'_s$ such that the Π-mismatch counter is less than or equal to k.*

PROOF. Combining Lemma 3.3 and Lemma 3.4 yields the proof. □

3.3. PARAMETERIZED COMPARISON OF TWO EQUAL LENGTH STRINGS. The method uses Corollary 3.6. First the mismatch pairs need to be found. In fact, by Corollary 3.6 only $k+1$ of them need to be found since $k+1$ mismatch pairs implies that there is no parameterized k-match. After the mismatch pairs are found, if the number of mismatch pairs mp is less than $k/2$ or more than k, we can immediately announce a match or mismatch according to Corollary 3.6. The difficult case to detect is whether there indeed is a parameterized k-match for $k/2 < mp \leq k$. This is done with the bipartite matching algorithm. However, here the bipartite graph needs to be constructed somewhat differently. While the case where $mp \leq k/2$ implies an immediate match, for simplicity of presentation, we will not differentiate between the case of $mp \leq k/2$ and $k/2 < mp \leq k$. Thus from here on, we will only bother with the cases $mp \leq k$ and $mp > k$.

3.3.1. *Find Mismatch Pairs.* In order to find the mismatch pairs of equal-length strings s and s', we use a simple stack scheme, one stack for each character in the alphabet. We do the search in two phases. First mismatch pairs are searched according to the first rule of Definition 3.2, that is, $s_i = s_j$, but $s'_i \neq s'_j$. This is done by scanning the strings from left-to-right, and, for each character $s_i = \sigma$ of the first string s, we go to the stack designated for σ and do the following. If it is empty, we push the character s'_i of the second string s' onto the stack along with the location i. If it is not empty, we check the top of the stack designated for σ and compare the character at the top of the stack with s'_i. If they are the same, we push s'_i and i onto the stack. If they are not the same, we pop from the stack the <character, location> pair $< \tau, j >$ and (i, j) is declared a mismatch pair.

In the second phase, we consider the locations that have not been declared as mismatch pairs and look for mismatch pairs that satisfy the second rule of Definition 3.2, that is, $s_i \neq s_j$, but $s'_i = s'_j$. This is done as in phase one with the roles of s and s' reversed (and disregarding locations that have already been declared as part of mismatch pairs).

Time Complexity. The algorithm makes two simple scans of the strings and each character in the string is pushed/popped onto at most one stack. Hence the running time and space is $O(m)$, where m is the length of the strings.

3.3.2. *Verification.* The verification is performed only when the number of mismatch pairs that were found, mp, satisfies $mp \leq k$. Verification consists of a procedure that finds the minimal π-mismatch over all bijections π. The technique used is similar to the bipartite matching algorithm discussed in the beginning of the section. It is easier to comprehend the algorithm if it is assumed that the alphabets Σ_s and $\Sigma_{s'}$ do not have characters in common, even though this assumption is not necessary at all.

Let $\hat{L} \subset \{1, \ldots, m\}$ be the locations that appear in a mismatch pair. We say that a symbol $a \in \Sigma_s$ is *mismatched* if there is a location $i \in \hat{L}$ such that $s_i = a$. Likewise, $b \in \Sigma_{s'}$ is *mismatched* if there is a location $i \in \hat{L}$ such that $s'_i = b$. A symbol $a \in \Sigma_s$, or $b \in \Sigma_{s'}$, is *free* if it is not mismatched.

Construct a bipartite graph $B = (U \cup V, E)$ defined as follows. U contains all mismatched symbols $a \in \Sigma_s$ and V contains all mismatched symbols $b \in \Sigma_{s'}$. Moreover, U contains all free symbols $a \in \Sigma_s$ for which there is a location $i \in \{1, \dots, m\} - \hat{L}$ such that $s_i = a$, and s'_i is a mismatched symbol. Likewise, V contains all free symbols $b \in \Sigma_{s'}$ for which there is a location $i \in \{1, \dots, m\} - \hat{L}$ such that $s'_i = b$ and s_i is a mismatched symbol. The edges as before have weights that correspond to the number of locations where they are aligned with each other.

LEMMA 3.7. *The bipartite graph B is of size $O(k)$. Moreover, given the mismatch pairs it can be constructed in $O(k)$ time.*

PROOF. This lemma follows by observing that, for any $a \in \Sigma_s$, all appearances of a in locations of $\{1, \dots, m\} - \hat{L}$ are aligned with a given symbol $b \in \Sigma_{s'}$ by definition of mismatch pairs. Symmetrically, the same is true for any $b \in \Sigma_{s'}$. On the other hand, $\hat{L}$ is of size $O(k)$. □

While Lemma 3.7 states that the bipartite graph is of size $O(k)$, it still may be the case that the edge weights may be substantially larger. However, if there exists an edge $e = (a, b)$ with weight $> k$, then it must be that $\pi(a) = b$ for otherwise we immediately have $> k$ mismatches. Thus, we may remove every edge with weight $> k$, along with their vertices. Note that we will need to account for the other edges that were removed and connected to one of these vertices. What remains is a bipartite graph with edge weights between 1 and k.

THEOREM 3.8. *Given two equal-length strings s and s' with $mp \leq k$ mismatch pairs, it is possible to verify whether there is a parameterized k-match between s and s' in $O(k^{1.5})$ time.*

PROOF. A bijection $\pi : \Sigma_s \to \Sigma'_s$ is equivalent to a matching in the constructed graph B as each is a one-one mapping of the same vertex/alphabet set. In a maximum matching, we desire to maximize the sum of the weights of the edges chosen and in a bijection to minimize the number of edges that are not selected that is, the mismatches. These objective functions are equivalent.

Since the size of the bipartite graph B is $O(k)$ by Lemma 3.7, it follows that the maximum weighted bipartite matching can be solved in $O(k^{1.5})$ time [Kao et al. 2001]. □

Time Complexity. Given two equal-length strings s and s', it is possible to determine whether s parameterized k-matches s' in $O(m + k^{1.5})$ time, $O(m)$ to find the mismatch pairs and $O(k^{1.5})$ to check these pairs with the appropriate bipartite matching.

4. *An Algorithm for Parameterized Matching with k Mismatches*

We are now ready to introduce our algorithm for the problem of parameterized matching with k mismatches:

Input: Two strings, $t = t_1, t_2, \dots, t_n$ and $p = p_1, p_2, \dots, p_m$, and an integer k.
Output: All locations i in t where p parameterized k-matches $t_i, \dots, t_{i+m-1}$.

Our algorithm has two phases, the *pattern preprocessing phase* and the *text scanning phase*. In this section, we present the text scanning phase and will assume

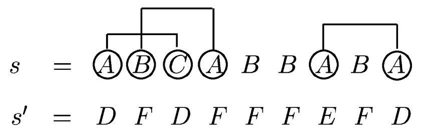


FIG. 2. An example of a maximal set of 3 mismatch pairs. This is a 3-good witness and a 2-bad witness.

that the pattern preprocessing phase is given. The output of the preprocessing phase is described in Section 4.1. In the following section, we describe an efficient method to preprocess the pattern for the needs of the text scanning phase.

Definition 4.1. Let s and s' be two-equal length strings. Let L be a collection of disjoint mismatch pairs between s and s'. If L is maximal and $|L| \leq k$, then L is said to be a *k-good witness* for s and s'. If $|L| > k$, then L is said to be a *k-bad witness* for s and s'.

See Figure 2 for an example of a 3-good witness and a 2-bad witness.

The text scanning phase has two stages the (a) *filter stage* and the (b) *verification stage*. In the filter stage, for each text location i, we find either a k-good witness or a k-bad witness for p and $t_i \ldots t_{i+m-1}$. Obviously, by Corollary 3.6, if there is a k-bad witness, then p cannot parameterize k-match $t_i \ldots t_{i+m-1}$. Hence, after the filter stage, it remains to verify for those locations i which have a k-good witness whether p parameterize k-matches $t_i \ldots t_{i+m-1}$. The verification stage is identical to the verification procedure in Section 3.3.2, and hence we will not dwell on this stage.

4.1. THE FILTER STAGE.

The underlying idea of the filter stage is similar to Landau and Vishkin [1986]. Like the KMP algorithm [Knuth et al. 1977], one location after another is evaluated utilizing the knowledge accumulated at the previous locations combined with the information gathered in the pattern preprocessing stage. The information of the pattern preprocessing stage is the following.

Output of Pattern Preprocessing. For each location i of p, a maximal disjoint collection of mismatch pairs L for some pattern prefix $p_1, \ldots, p_{j-i+1}$ and $p_i, \ldots, p_j$ such that either $|L| = 3k+3$ or $j = m$ and $|L| \leq 3k+3$.

As the first step of the algorithm, we consider the first text location, that is, when text $t_1 \ldots t_m$ is aligned with $p_1 \ldots p_m$. Using the method in Section 3.3.1, we can find all the mismatch pairs in $O(m)$ time, and hence find a k-good or k-bad witness for the first text location. When evaluating subsequent locations i, we maintain the following invariant: For all locations $l < i$, we have either a k-good or k-bad witness for location l.

It is important to observe that, when evaluating location i of the text, if we discover a maximal disjoint collection of mismatch pairs of size $k+1$, that is, a k-bad witness, between a prefix $p_1, \ldots, p_j$ of the pattern and $t_i, \ldots, t_{i+j-1}$, we will stop our search since this immediately implies that $p_1, \ldots, p_m$ and $t_i, \ldots, t_{i+m-1}$ have a k-bad witness. We say that $i+j$ is a *stop location* for i. If we have a k-good witness at location i then $i+m$ is its *stop location*. When evaluating location i of the text, each of the previous locations has a stop location. The location ℓ that has a maximal stop location over all locations $l < i$, is called a *maximal stopper at i*.

The reason for working with the maximal stopper at i is that the text beyond the stop location of the maximal stopper has not yet been scanned. If we can show that

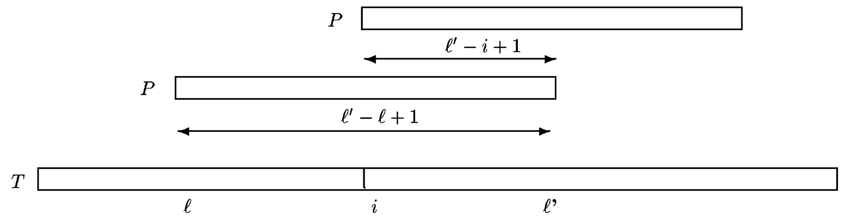


FIG. 3. The maximal stopper and the current location.

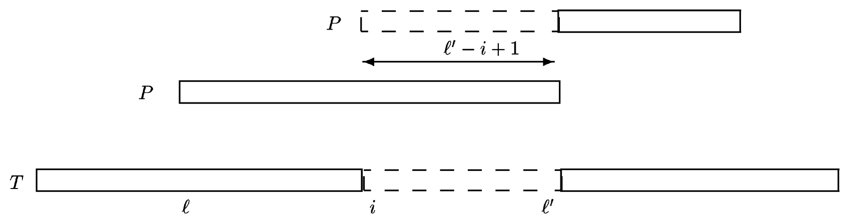


FIG. 4. The overlap to be computed.

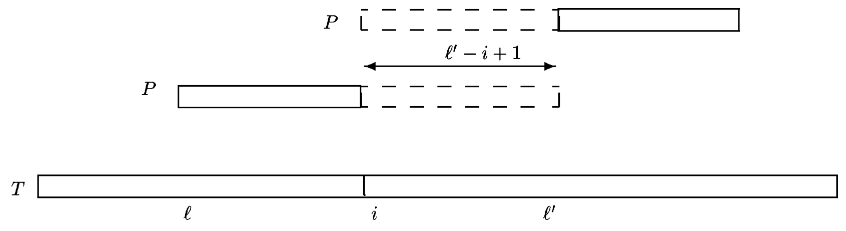


FIG. 5. The two cases hinge on the pattern preprocessing of this overlap.

the time to compute a k-bad witness or find a maximal disjoint collection of mismatch pairs for location i up until the maximal stopper, that is, for $p_1, \ldots, p_{\ell'-i+1}$ with $t_i, \ldots, t_{\ell'}$ where ℓ' is the stop location of ℓ, is $O(k)$, then we will spend overall $O(n + nk)$ time for computing, $O(nk)$ to compute up until the maximal stopper for each location, and $O(n)$ for the scanning and updating the current maximal collection of mismatch pairs.

4.1.1. *Computing Up Until the Maximal Stopper.* The situation now is that we are evaluating a location i of t. Let ℓ be the maximal stopper at i. We utilize two pieces of precomputed information; (1) the pattern preprocessing for location $i - \ell + 1$ of p and (2) the k-good witness or k-bad witness (of size $k + 1$) for location ℓ of t. Let ℓ' be the stop location of ℓ. See Figure 3. We would like to evaluate the overlap of $p_1, \ldots, p_{\ell'-i+1}$ with $t_i, \ldots, t_{\ell'}$ and to find a maximal disjoint collection L of mismatch pairs on this overlap or, if it exists, a maximal disjoint collection L of mismatch pairs of size $k + 1$ on a prefix of the overlap. See Figure 4.

There are two possible cases. One possibility is that the pattern preprocessing returns $3k + 3$ mismatch pairs for a prefix $p_1, \ldots, p_j$ and $p_{i-\ell+1}, \ldots, p_{i-\ell+j+1}$ where $j \leq \ell' - i + 1$. See Figure 5. Yet, there are $\leq k + 1$ mismatch pairs between $p_1, \ldots, p_{\ell'-\ell+1}$ and $t_\ell, \ldots, t_{\ell'}$, as shown in Figure 6.

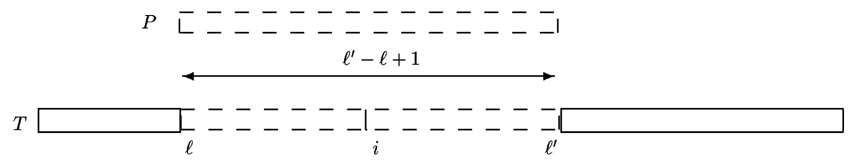


FIG. 6. The maximal stopper location has at most $k + 1$ mismatches until its stop location.

LEMMA 4.2. *Let s, s' and s'' be three equal-length strings such that there is a maximal collection of mismatch pairs, $L_{s,s'}$, between s and s' of size $\leq M$, and a maximal collection of mismatch pairs $L_{s',s''}$ between s' and s'' of size $\geq 3M$. Then there must be a maximal collection of mismatch pairs $L_{s,s''}$ between s and s'' of size $\geq M$.*

PROOF. Since each mismatch pair is composed of 2 locations, there must be at least M mismatch pairs between s' and s'' which do not participate in mismatch pairs between s and s'. It follows from the definition of mismatch pairs that these M mismatch pairs are also mismatch pairs between s and s''. $\square$

Set M to be $k + 1$ and one can use Lemma 4.2 for the case at hand, namely, there must be at least $k + 1$ mismatch pairs between $p_1, \ldots, p_{\ell'-i+1}$ and $t_i, \ldots, t_{\ell'}$, which defines a k-bad witness.

The second case is where the pattern preprocessing returns fewer than $3k + 3$ mismatch pairs or it returns $3k + 3$ mismatch pairs but it does so for a prefix $p_1, \ldots, p_j$ and $p_{\ell-i+1}, \ldots, p_{\ell-i+j+1}$ where $j > \ell' - i + 1$. See Figure 5. However, since ℓ's stop location is ℓ', we still have an upper bound of $k + 1$ mismatch pairs between $p_1, \ldots, p_{\ell'-\ell+1}$ and $t_\ell, \ldots, t_{\ell'}$. So, we can utilize this fact.

LEMMA 4.3. *Given three strings, s, s', s'', such that there are maximal disjoint collections of mismatch pairs, $L_{s,s'}$ and $L_{s',s''}$, of sizes $O(k)$, $O(k)$ time, one can find a k-good or k-bad witness for s and s''.*

PROOF. Let $\bar{L}_{s,s'}$ be the indices that are not in any mismatch pair between s and s'. By Lemma 3.4, there exists a bijection $\pi : \Sigma_s \rightarrow \Sigma_{s'}$ such that π defines a parameterized match on $\bar{L}_{s,s'}$. Likewise, if $\bar{L}_{s',s''}$ are the indices that are not in any mismatch pair between s' and s'', then there is a bijection $\pi' : \Sigma_{s'} \rightarrow \Sigma_{s''}$ that defines a parameterized match on $\bar{L}_{s',s''}$.

The set of indices that participates in no mismatch pair in either of the pairs is $\bar{L}_{s,s'} \cap \bar{L}_{s',s''}$. On this set, $\pi' \cdot \pi$ defines a parameterized match. However, the number of locations participating in the mismatch pairs is bounded by k. Using linked lists for each character, one can now construct the, at most, $O(k)$ mismatch pairs in $O(k)$ time. $\square$

4.1.2. *Putting it All Together.* The filter stage takes $O(nk)$ time and the verification stage takes $O(nk^{1.5})$.

THEOREM 4.4. *Given the preprocessing stage, we can announce for each location i of t whether p parameterized k-matches $t_i, \ldots, t_{i+m-1}$ in $O(nk^{1.5})$ time.*

5. *Pattern Preprocessing*

In this section, we solve the pattern preprocessing necessary for the general algorithm.

Input: A pattern $p = p_1, \dots, p_m$ and an integer k.

Output: For each location i, $1 \leq i \leq m$ a maximal disjoint collection of mismatch pairs L for the minimal pattern prefix $p_1, \dots, p_{j-i+1}$ and $p_i, \dots, p_j$ such that either $|L| = 3k + 3$ or $j = m$ and $|L| \leq 3k + 3$.

The naive method takes $O(m^2)$ by applying the method from Section 3.3.1. However, this does not exploit any previous information for a new iteration. Since every alignment combines two previous alignments, we can get a better result. Assume, without loss of generality, that m is a power of 3. We divide the set of alignments into $\log_3 m + 1$ sequences as follows;

$R_1 = [2, 3], R_3 = [4, 5, 6, 7, 8, 9], \dots, R_i = [3^{i-1} + 1, \dots, 3^i], \dots, R_{\log_3 m} = [3^{\log_3 m-1} + 1, \dots, 3^{\log_3 m}]$ $1 \leq i \leq \log_3 m$.

At each step, we compute the desired mismatches for each set of alignments R_i. Step i uses the information computed in steps $1 \cdots i - 1$. We further divide each set into two halves and compute the first half followed by the second half. This is possible since each R_i contains an even number of elements as $3^i - 3^{i-1} = 2 * 3^{i-1}$. We split each sequence R_i into two equal-length sequences $R_i^1[3^{i-1}+1, \dots, 2*3^{i-1}]$ and $R_i^2 = [2 * 3^{i-1} + 1, \dots, 3^i]$. For each of the new sequences, we have the following.

LEMMA 5.1. *If $r_1, r_2 \in R_i^1$ (the first half of set R_i) or $r_1, r_2 \in R_i^2$ (the second half of R_i) such that $r_1 < r_2$ then $r_2 - r_1 \in R_j$ for $j < i$.*

PROOF. We assume that $r_1, r_2 \in R_i^1$ (the proof for the other case is symmetric). Obviously $r_2 \leq 2 * 3^{i-1}$ and $r_1 \geq 3^{i-1} + 1$, then $r_2 - r_1 \leq 2 * 3^{i-1} - 3^{i-1} - 1 = 3^{i-1} - 1$. □

This gives a handle on how to compute our desired output. Denote $f_i = min\{j \in R_i^1\}$ and $m_i = min\{j \in R_i^2\}$ the representatives of their sequences. We compute the following two stages for each group R_i, in order $R_1, \dots, R_{\log_3 m}$.

(1) Compute a maximal disjoint collection of mismatch pairs L for some pattern prefix $p_1, \dots, p_{j+1}$ and $p_{f_i}, \dots, p_{f_i+j}$ such that $|L| = (3k + 3)3^{\log_3 m-i}$ or $f_i + j = m$ and $|L| \leq (3k + 3)3^{\log_3 m-i}$. Do the same with $p_{m_i}, \dots, p_{m_i+j}$.

(2) Now for each $j \in R_i^1$ apply the algorithm for the text described in the previous section on the pattern p, the pattern shifted by f_i (R_i^1's representative) and the pattern shifted by j. Do the same with m_i for R_i^2.

The central idea and importance behind the choice of the number of mismatch pairs that we seek is to satisfy Lemma 4.2. It can be verified that indeed our choice of sizes always satisfies that there are 3 times as many mismatch pairs as in the previous iteration.

THEOREM 5.2. *Given a pattern p of length m, it is possible to precompute its $3k + 3$ mismatch pairs at each alignment in $O(km \log_3 m)$ time.*

PROOF. The time complexity for each group R_i with $O(3^{i-1})$ members is $3^{\log_3 m-i+1}(3k + 3)$ for finding the mismatches, multiply by $O(3^{i-1})$ members, which is $O(mk)$ for a group, plus $O(m)$ for the first and the middle elements. All together it is $O(km \log_3 m)$. □

COROLLARY 5.3. *Given a pattern p and text t, we can solve the parameterized matching with k mismatches problem in $O(nk^{1.5} + km \log m)$ time.*

6. *2-D Parameterized Matching with k Mismatches*

Two-dimensional parameterized matching has applications in image search with variable colors and errors. In this section, we present an extension of our algorithm for 2-dimensional approximate parameterized matching.

Input: Two images, text $T[1 \cdots n][1 \cdots n]$, and pattern $P[1 \cdots m][1 \cdots m]$, and an integer k.

Output: All locations (i, j) in T such that P parameterized k-matches the $m \times m$ image whose upper left corner is $T[i, j]$.

We begin with the assumption that the text has exactly m rows and then multiply the resulting time complexity by n. Both the text and the pattern are linearized column-by-column. Our string matching algorithm of Section 4 can be applied to the linear pattern and text. Care must be taken that only those locations whose index is divisible by m will be considered. This can clearly be accomplished in $O(n)$ time. Thus, the time complexity for each m rows of the text is $O(nmk^{1.5})$.

THEOREM 6.1. *Given an $m \times m$ image P and an $n \times n$ image T, we can solve the parameterized matching with k mismatches problem in $O(n^2mk^{1.5} + m^2k \log m)$ time.*

7. *Future Work*

The first obvious question to be asked is whether faster solutions for the problem exist. For the one-dimensional case, the reduction to bipartite matchings seem to make this a somewhat challenging problem to answer. However, the 2-dimensional case leaves room for improvement.

Another interesting question suggested by an anonymous referee is to consider the problem of enumerating all the bijections of the solution. Recall that the solution is approximate and hence the bijection that maximizes matches need not be unique. In this case, would the time complexity still be independent of the size of the alphabets? This can be further explored asking for all bijections matching within threshold k, that is, all bijections that are within k mismatches of the maximal approximate match.

Naturally, one may ask what happens if you consider the edit distance. Recall the discussion in the introduction which pointed to the work of Baker [1999]. However, as alluded to in the introduction, the correct way for defining the edit distance problem in our opinion is to allow the operations and then apply the edit distance. This gives a global definition which presents another interesting problem.

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