Approximate String Matching using a Bidirectional Index

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Abstract

We study strategies of approximate pattern matching that exploit bidirectional text indexes, extending and generalizing ideas of [5]. We introduce a formalism, called search schemes, to specify search strategies of this type, then develop a probabilistic measure for the efficiency of a search scheme, prove several combinatorial results on efficient search schemes, and finally, provide experimental computations supporting the superiority of our strategies.

1 Introduction

Approximate string matching has numerous practical applications and long been a subject of extensive studies by algorithmic researchers. If errors are allowed in a match between a pattern string and a text string, most of the fundamental ideas behind exact string search algorithms become inapplicable. The Approximate string matching problem comes in different variants. In this paper, we are concerned with the indexing variant, when a static text is available for pre-processing and storing in a data structure, before any matching query is made.

The quest for efficient approximate string matching algorithms has been boosted by a new generation of DNA sequencing technologies, able to produce huge quantities of short DNA reads. Those reads can then be mapped to a given genomic sequence, which requires very fast and accurate approximate string matching algorithms. Many algorithms and associated software programs have been designed for this task, we refer to [10] for a survey, and many of them rely on full-text indexes.

The classical indexing paradigm consists in building a text index in order to quickly identify pattern occurrences, preferably within a worst-case time weakly dependent on the text length. In the context of approximate matching, even the case of one error turned out to be highly nontrivial and gave rise to a series of works (see [6] and references therein). In the case of k errors, existing solutions generally have time or space complexity that are exponential in k, see [15] for a survey.

Some of the existing algorithms use standard text indexes, such as suffix tree or suffix arrays. However, for large datasets occurring in modern applications, these

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indexes are known to take too much memory. Suffix arrays and suffix trees typically require at least 4 or 10 bytes per character respectively. The last years saw the emergence of succinct or compressed full-text indexes that occupy virtually as much memory as the sequence itself and yet provide very powerful functionalities [11]. For example, the FM-index [4], based on the Burrows-Wheeler Transform [2], may occupy 2–4 bits of memory per character for DNA texts. FM-index has now been used in many practical bioinformatics software programs, e.g. [8, 9, 14]. Even if succinct indexes are primarily designed for exact string search, using them for approximate matching naturally became an attractive opportunity. This direction has been taken in several papers, see [12], as well as in practical implementations [14].

Interestingly, succinct indexes can provide even more functionalities than classical ones. In particular, several succinct indexes can be made bidirectional, i.e. can perform pattern search in both directions [1, 5, 12, 13, 14]. Lam et al. [5] showed how a bidirectional FM-index can be used to efficiently search for strings up to a small number (one or two) errors. The idea is to partition the pattern into \( k + 1 \) equal parts, where \( k \) is the number of errors, and then perform multiple searches on the FM-index, where each search assumes a different distribution of mismatches among the pattern parts. Lam et al. implemented the proposed algorithm and reported that it outperforms in speed the best existing read alignment software [5]. Related algorithmic ideas appear also in [12].

In this paper, we extend the search strategy of [5] in two main directions. We consider the case of arbitrary \( k \) and propose to partition the pattern into more than \( k + 1 \) parts that can be of unequal size. To demonstrate the benefit of both ideas, we first introduce a general formal framework for this kind of algorithm, called search scheme, that allows us to easily specify them and to reason about them (Section 2). Then, in Section 3 we perform a probabilistic analysis that provides us with a quantitative measure of performance of a search scheme, and give an efficient algorithm for obtaining the optimal pattern partition for a given scheme. Furthermore, we prove several combinatorial results on the design of efficient search schemes (Section 4). Finally, Section 5 contains comparative analytical estimations, based on our probabilistic analysis, that demonstrate the superiority of our search strategies for many practical parameter ranges. We further report on large-scale experiments on genomic data supporting this analysis.

## 2 Bidirectional search

In the framework of text indexing, pattern search is usually done by scanning the pattern online and recomputing index points referring to the occurrences of the scanned part of the pattern. With classical text indexes, such as suffix trees or suffix arrays, the pattern is scanned left-to-right (forward search). However, some compact indexes such as FM-index provide a search algorithm that scans the pattern right-to-left (backward search).

Consider now approximate string matching, where \( k \) letter mismatches are allowed between a pattern \( P \) and a text \( T \). In this paper, we present our ideas for the case of Hamming distance. However, they also apply to the edit distance, see Conclusions. Both forward and backward search can be extended to approximate
search in a straightforward way, by exploring all possible mismatches along the
search, as long as their number does not exceed \( k \) and the current pattern still oc-
curs in the text. For the forward search, for example, the algorithm enumerates all
substrings of \( T \) with Hamming distance at most \( k \) to a prefix of \( P \). Starting with
the empty string, the enumeration is done by extending the current string with the
corresponding letter of \( P \), and with all other letters provided that the number of
accumulated mismatches has not yet reached \( k \). For each extension, its positions in
\( T \) are computed using the index. Note that the set of enumerated strings is closed
under prefixes and therefore can be represented by the nodes of a trie. Similarly
to forward search, backward search enumerates all substrings of \( T \) with Hamming
distance at most \( k \) to a suffix of \( P \).

Clearly, backward and forward search are symmetric and, once we have an im-
plementation of one, the other can be implemented similarly by constructing an
index for the reversed text. However, combining both forward and backward search
within one algorithm results in a more efficient search. To illustrate this, consider
the case \( k = 1 \). Partition \( P \) into two equal length parts \( P = P_1P_2 \). The idea is to
perform two complementary searches: forward search for occurrences of \( P \) with a
mismatch in \( P_2 \) and backward search for occurrences with a mismatch in \( P_1 \). In both
searches, branching is performed only after \( |P|/2 \) characters are matched. Then, the
number of strings enumerated by the two searches is much less than the number of
strings enumerated by a single standard forward search, even though two searches
are performed instead of one.

A bidirectional index of a text allows one to extend the current string \( S \) both left
and right, that is, compute the positions of both \( cS \) or \( Sc \) from the positions of \( S \).
Note that a bidirectional index allows forward and backward searches to alternate,
which will be crucial for our purposes. Lam et al. \[5\] showed how the FM-index can
be made bidirectional. Other succinct bidirectional indexes were given in \[1,12,13\].
Using a bidirectional index, such as FM-index, forward and backward searches can
be performed in time linear in the number of enumerated strings. Therefore, our
main goal is to organize the search so that the number of enumerated strings is
minimized.

Lam et al. \[5\] gave a new search algorithm, called bidirectional search, that
utilizes the bidirectional property of the index. Consider the case \( k = 2 \), studied
in \[5\]. In this case, the pattern is partitioned into three equal length parts, \( P = P_1P_2P_3 \).
There are now 6 cases to consider according to the placement of mismatches
within the parts: 011 (i.e. one mismatch in \( P_2 \) and one mismatch in \( P_3 \)), 101,
110, 002, 020, and 200. The algorithm of Lam et al. \[5\] performs three searches
(illustrated in Figure 1):

1. A forward search that allows no mismatches when processing characters of \( P_1 \),
   and 0 to 2 accumulated mismatches when processing characters of \( P_2 \) and \( P_3 \).
   This search handles the cases 011, 002, and 020 above.

2. A backward search that allows no mismatches when processing characters of \( P_3 \),
   0 to 1 accumulated mismatches when processing characters of \( P_2 \), and 0
   to 2 accumulated mismatches when processing characters of \( P_1 \). This search
   handles the cases 110 and 200 above.
Figure 1: The tries representing the searches of Lam et al. for binary alphabet \{0, 1\}, search string \(P = 011000\), and number of errors 2. Each trie represents one search and assumes that all the enumerated substrings exist in the text \(T\). In an actual search on a specific \(T\), each trie contains a subset of the nodes, depending on whether the strings of the nodes in the trie appear in \(T\). A vertical edge represents a match, and a diagonal edge represents a mismatch.

3. The remaining case is 101. This case is handled using a bidirectional search. It starts with a forward search on string \(P' = P_2P_3\) that allows no mismatches when processing characters of \(P_2\), and 0 to 1 accumulated mismatches when processing the characters of \(P_3\). For each string \(S\) of length \(|P'|\) enumerated by the forward search whose Hamming distance from \(P'\) is exactly 1, a backward search for \(P_1\) is performed by extending \(S\) to the left, allowing one additional mismatch. In other words, the search allows 1 to 2 accumulated mismatches when processing the characters of \(P_1\).

We now give a formal definition for the above. Suppose that pattern \(P\) is partitioned into \(p\) parts. A search is a triplet of strings \(S = (\pi, L, U)\) where \(\pi\) is a permutation string of length \(p\) over \(\{1, \ldots, p\}\), and \(L, U\) are strings of length \(p\) over \(\{0, \ldots, k\}\). String \(\pi\) indicates the order in which the parts of \(P\) are processed, and thus it must satisfy the following property: For every \(i > 1\), \(\pi(i)\) is either \((\min_{j<i} \pi(j)) - 1\) or \((\max_{j<i} \pi(j)) + 1\). Strings \(U\) and \(L\) give upper and lower bounds on the number of mismatches: When the \(j\)-th part is processed, the number of accumulated mismatches between the active strings and the corresponding substring of \(P\) must be between \(L[j]\) and \(U[j]\). Formally, for a string \(M\) over integers, the weight of \(M\) is \(\sum_{i} M[i]\). A search \(S = (\pi, L, U)\) covers a string \(M\) if \(L[i + 1] \leq \sum_{j=1}^{i} M[j] \leq U[i]\) for all \(i\) (assuming \(L[p+1] = 0\)). A \(k\)-mismatch search scheme \(\mathcal{S}\) is a collection of searches such that for every string \(M\) of weight \(k\), there is
a search in $S$ that covers $M$. For example, the 2-mismatch scheme of Lam et al. consists of searches $S_f = (123, 000, 022)$, $S_b = (321, 000, 012)$, and $S_{bd} = (231, 001, 012)$. We denote this scheme by $S_{LLTWWY}$.

In this work, we introduce two types of improvements over the search scheme of Lam et al.

**Uneven partition.** In $S_{LLTWWY}$, search $S_f$ enumerates more strings than the other two searches, as it allows 2 mismatches on the second processed part of $P$, while the other two searches allow only one mismatch. If we increase the length of $P_1$ in the partition of $P$, the number of strings enumerated by $S_f$ will decrease, while the number of strings enumerated by the two other searches will increase. We show that for some typical parameters of the problem, the decrease in the former number is larger than the increase of the latter number, leading to a more efficient search.

**More parts.** Another improvement can be achieved using partitions with $k + 2$ or more parts, rather than $k + 1$ parts. We explain in Section 3.2 why such partitions can reduce the number of enumerated strings.

### 3 Analysis of search schemes

In this section we show how to estimate the performance of a given search scheme $S$. Using this technique, we first explain why an uneven partition can lead to a better performance, and then present a dynamic programming algorithm for designing an optimal partition of a pattern.

#### 3.1 Estimating the efficiency of a search scheme

To measure the efficiency of a search scheme, we estimate the number of strings enumerated by all the searches of $S$. We assume that performing single steps of forward, backward, or bidirectional searches takes the same amount of time. It is fairly straightforward to extend the method of this section to the case when these times are not equal. Note that the bidirectional index of Lam et al. reportedly spends slightly more time (order of 10%) on forward search than on backward search.

For the analysis, we assume that characters of $T$ and $P$ are randomly chosen uniformly and independently from the alphabet. We note that it is possible to extend the method of this section to a non-uniform distribution. For more complex distributions, a Monte Carlo simulation can be applied which, however, requires much more time than the method of this section.

Let $\#str(S, X, \sigma, n)$ denote the expected number of strings enumerated when performing a search $S = (\pi, L, U)$ on a random text of length $n$ and random pattern of length $m$, where $X$ is a partition of the pattern and $\sigma$ is the size of the alphabet (note that $m$ is not a parameter for $\#str$ since the value of $m$ is implied from $X$). For a search scheme $S$, $\#str(S, X, \sigma, n) = \sum_{S \in S} \#str(S, X, \sigma, n)$.

Fix $S$, $X$, $\sigma$, and $n$. Let $A_l$ be the set of enumerated strings of length $l$ when performing the search $S$ on a random pattern of length $m$, partitioned by $X$, and a
text \( T \) containing all the strings of length at most \( m \) as substrings. Select a random order on the elements of \( A_i \), and let \( A_{li} \) be the \( i \)-th element of \( A_i \). By the linearity of the expectation,

\[
\#\text{str}(S, X, \sigma, n) = \sum_{l \geq 1} \sum_{i=1}^{n_l} \Pr_{T \in \Sigma^n}[A_{li} \text{ is a substring of } T],
\]

where \( n_l = |A_l| \). For any \( l \) and \( i \), the string \( A_{li} \) is a random string with uniform distribution over \( \Sigma^l \). Therefore, the probability that \( A_{li} \) is a substring of \( T \) can be approximated by \( 1 - e^{-n/\sigma^l} \) using the Chen-Stein method [3]. Therefore,

\[
\#\text{str}(S, X, \sigma, n) \approx \sum_{l=1}^{m} n_l (1 - e^{-n/\sigma^l}). \tag{1}
\]

In order to compute the values of \( n_l \), we give some definitions. Let \( n_{l,d} \) be the number of strings in \( A_l \) of length \( l \) with Hamming distance \( d \) to the prefix of \( P \) of length \( l \). Let \( U' \) be a string obtained from \( U \) by replacing each character \( U[i] \) of \( U \) by a run of \( U'[i] \) of length \( x_{\pi(i)} \), where \( x_j \) is the length of the \( j \)-th part in the partition \( X \). The string \( L' \) is defined analogously. In other words, the values \( L'[i], U'[i] \) give a lower and upper bounds on the number of allowed mismatches for an enumerated string of length \( i \). The values of \( n_l \) are given by the following recurrence.

\[
n_l = \sum_{d=L'[l]}^{U'[l]} n_{l,d}, \quad n_{l,d} = \begin{cases} n_{l-1,d} + (\sigma - 1)n_{l-1,d-1} & \text{if } l \geq 1 \text{ and } L'[l] \leq d \leq U'[l] \\ 1 & \text{if } l = 0 \text{ and } d = 0 \\ 0 & \text{otherwise} \end{cases}
\tag{2}
\]

For a specific search, a closed form formula can be given for \( n_l \).

Consider equation \((1)\). The value of the term \( 1 - e^{-n/\sigma^l} \) is very close to 1 for \( l \leq \log_{\sigma} n - O(1) \). When \( l \geq \log_{\sigma} n \), the value of this term decreases exponentially. Note that \( n_l \) increases exponentially, but the base of the exponent of \( n_l \) is \( \sigma - 1 \) whereas the base of \( 1 - e^{-n/\sigma^l} \) is \( 1/\sigma \). We can then approximate \( \#\text{str}(S, X, \sigma, n) \) with function \( \#\text{str}'(S, X, \sigma, n) \) defined by

\[
\#\text{str}'(S, X, \sigma, n) = \sum_{l=1}^{\lfloor \log_{\sigma} n \rfloor + c_\sigma} n_l (1 - e^{-n/\sigma^l}), \tag{3}
\]

where \( c_\sigma \) is a constant chosen so that \((\sigma - 1)/\sigma)^{c_\sigma} \) is sufficiently small.

If a search scheme \( S \) contains two or more searches with the same \( \pi \)-strings, these searches can be merged in order to eliminate the enumeration of the same string twice or more. It is straightforward to modify the computation of \( \#\text{str}(S, X, \sigma, n) \) to account for this optimization.

### 3.2 Uneven partitions

In this section we provide a formal explanation why an equal sized partition is not optimal for some parameters. For this, we replace \((3)\) by an even simpler estimator
of \(\#\text{str}(S,X,\sigma,n)\):

\[
\#\text{str}''(S,X,\sigma,n) = \sum_{i=1}^{[\log_\sigma n]} n_i. \quad (4)
\]

As an example, consider scheme \(S_{\text{LLTWWY}}\). Denote by \(x_1, x_2, x_3\) the lengths of the parts in a partition \(X\) of \(P\) into 3 parts. It is straightforward to give close formulas for \(\#\text{str}''(S,X,\sigma,n)\) for each search of \(S_{\text{LLTWWY}}\). For example,

\[
\#\text{str}''(S_f,X,\sigma,n) = \begin{cases} N & \text{if } N \leq x_1 \\ c_1(N-x_1)^3 + c_2(N-x_1)^2 + c_3(N-x_1) + N & \text{otherwise} \end{cases}
\]

where \(N = [\log_\sigma n]\), \(c_1 = (\sigma-1)^2/6\), \(c_2 = (\sigma-1)/2\), and \(c_3 = -(\sigma-1)^2/6+(\sigma-1)/2\). Similar formulas can be given for \(S_b\) and \(S_{bd}\). If \(x_1, x_2, x_3\) are “close” to \(m/3\) and \(N < m/3\) then \(\#\text{str}''(S_{\text{LLTWWY}},X,\sigma,n,m) = 3N\) and an equal sized partition is optimal in this case. However, if \(m/3 < N < 2m/3\), then

\[
\#\text{str}''(S_{\text{LLTWWY}},X,\sigma,n) = c_1(N-x_1)^3 + c_2(N-x_1)^2 + c_3(N-x_1)
\]

\[
+ c_1'(N-x_3)^2 + c_2'(N-x_3) + c_3'(N-x_2)^2 + c_2'(N-x_2) + 3N.
\]

It is now clear why the equal sized partition is not optimal in this case. The degree of \(N - x_1\) in the above polynomial is 3, while the degrees of \(N - x_2\) and \(N - x_3\) are 2. Thus, if \(x_1 = x_2 = x_3 = m/3\), decreasing \(x_2\) and \(x_3\) by, say 1, while increasing \(x_1\) by 2 reduces the value of the polynomial.

### 3.3 Computing an optimal partition

Let \(p\) be the number of parts. An optimal partition can be naively found by enumerating all \(\binom{m-1}{p-1}\) possible partitions, and for each partition \(X\), computing \(\#\text{str}'(S,X,\sigma,n)\). We now describe a more efficient dynamic programming algorithm that computes an optimal partition for a given search scheme \(S\).

The algorithm takes advantage of the fact that the value of \(\#\text{str}'(S,X,\sigma,n)\) does not depend on the entire partition \(X\), but only on the partition of a substring of \(P\) of length \(N = [\log_\sigma n] + c_\sigma\) induced by \(X\). We first give some definitions. Define \(S(i,j)\) to be the set containing every search \(S \in S\) such that \(i\) appears before \(j\) in the \(\pi\)-string of \(S\) (we assume \(S(i,p+1) = S\)). A partition of \(P\) is a partition of the set \{1, 2, ..., \(m\)\} into disjoint sets of the form \(\{i, i+1, \ldots, j\}\) which will be called intervals. A partition of a substring \(P[i..j]\) is a partition of \(\{i, i+1, \ldots, j\}\) into disjoint intervals.

The algorithm builds partial partitions of prefixes of \(P\), incrementally from left to right. That is, the partitions of \(P[1..m']\) are built from partitions of \(P[1..m']\) for \(m' < m''\) by extending them with interval \(\{m'+1, \ldots, m''\}\). Consider a partition \(X'\) of \(P[1..m']\), \(m' \geq N\), into \(p'\) parts, and let \(p'_2\) be the left-to-right rank of the interval in \(X'\) containing the position \(m' - N + 1\). For a search \(S \in S(p'_2, p'+1)\), the value of \(\#\text{str}'(S,X,\sigma,n)\) is the same for every extension of \(X'\) to a partition \(X\) of \(P\), since \(\#\text{str}'(S,X,\sigma,n)\) is determined by the partition of a substring of \(P\) of length \(N\) contained in \(P[1..m']\). Thus, for every partial partition \(X'\), the algorithm computes the value of \(\sum_{S \in S(p'_2, p'+1)} (S,X,\sigma,n)\) for some extension of \(X'\)
to a partition $X$. This value will be denoted $v(X')$. Note that for a partition $X$ of $P$, $v(X) = \#str'(S, X, \sigma, n)$. When the algorithm extends the partial partition $X'$ to a partial partition $X'' = X' \cup \{m' + 1, \ldots, m''\}$, it has to compute $v(X'')$. This is done by adding $v(X'') - v(X')$ to the already computed $v(X')$. By definition, $v(X'') - v(X') = \sum_{S \in S(p'_1, p''_1), \ldots, S(p'_p, p''_p)} \#str'(S, X, \sigma, n)$, where $p''_i = p'_i + 1$ and $p''_p$ is the left-to-right rank of the interval in $X'$ containing the position $m'' - N + 1$.

If $X'_1$ and $X'_2$ are partitions of $P[1..m']$ with the same number of parts and these partitions induce the same partition on $P[m' - N + 1..m']$, then for every partition $X''$ of $P[m' + 1..m'']$ we have $v(X'_1 \cup X'') - v(X'_2) = v(X'_2 \cup X'') - v(X'_2')$. Thus, for every $p' \leq p$ and every partition $X'$ of $P' = P[m' - N + 1..m']$, we need to store only one partition $X^*$ of $P[1..m']$ into $p'$ parts that induces the partition $X'$ on $P'$. The partition $X^*$ is chosen such that $v(X^*)$ is minimum among all partitions of $P[1..m']$ into $p'$ parts that induce the partition $X'$ on $P'$. This partition is called optimal partial partition. The number of optimal partial partitions is at most $mp \sum_{p'=1}^{p} \left( \frac{N-1}{p'-1} \right)$, which is much smaller than $\left( \frac{m-1}{p-1} \right)$ if $N$ is much smaller than $m$.

We obtain an algorithm whose time complexity is $O(m^2 + (|S|Nk + mp) \sum_{p'=1}^{p} \left( \frac{N-1}{p'-1} \right))$.

4 Properties of optimal search schemes

Designing an efficient search scheme for a given set of parameters consists of (1) choosing the number of parts, (2) choosing the searches, (3) choosing the partition of the pattern. While it is possible to enumerate all possible choices, and evaluate the efficiency of the resulting scheme using Section 3.1, this is generally infeasible due to a large number of possibilities. It is therefore desirable to have a combinatorial characterization of optimal search schemes.

The critical string of a search scheme $S$ is the lexicographically maximal $U$-string of a search in $S$. A search of $S$ is critical if its $U$-string is equal to the critical string of $S$. For example, the critical string of $S_{LUTWWY}$ is 022, and $S_f$ is the critical search. For typical parameters, critical searches of a search scheme constitute the bottleneck. Consider a search scheme $S$, and assume that the $L$-strings of all searches contain only zeros. Assume further that the pattern is partitioned into equal-size parts. Let $\ell$ be the maximum index such that for every search $S \in S$ and every $i \leq \ell$, $U[i]$ of $S$ is no larger than the number in position $i$ in the critical string of $S$. From Section 3, the number of strings enumerated by a search $S \in S$ depends mostly on the prefix of the $U$-string of $S$ of length $\lceil \log_n \ell \rceil / (m/p)$. Thus, if $\lceil \log_n \ell \rceil / (m/p) \leq \ell$, a critical search enumerates an equal or greater number of strings than a non-critical search.

We now consider the problem of designing a search scheme whose critical string is minimal. Let $\alpha(k, p)$ denote the lexicographically minimal critical string of a $k$-mismatch search scheme that partitions the pattern into $p$ parts. The next theorems give the values of $\alpha(k, k + 2)$ and $\alpha(k, k + 1)$. We need the following definition. A string over the alphabet of integers is called simple if it contains a substring of the form $01^j0$ for $j \geq 0$.

Lemma 1. (i) Every string $M$ of weight $k$ and length at least $k + 2$ is simple.
(ii) If \( M \) is a non-simple string of weight \( k \) and length \( k + 1 \) then \( M[1] \leq 1, M[k + 1] \leq 1, \) and \( M[i] \leq 2 \) for all \( 2 \leq i \leq k \). Moreover, there are no two consecutive 2’s in \( M \).

Proof. (i) The proof is by induction on \( k \). It is easy to verify that the lemma holds for \( k = 0 \). Suppose we proved the lemma for \( k' < k \). Let \( M \) be a string of weight \( k \) and length \( p \geq k + 2 \). If \( M[1] \geq 1 \) then by the induction hypothesis \( M[2..p] \) is simple, and therefore \( M \) is simple. Suppose that \( M[1] = 0 \). Let \( i > 1 \) be the minimum index such that \( M[i] \neq 1 \) (i must exist due to the assumption that \( p \geq k + 2 \)). If \( M[i] = 0 \) then we are done. Otherwise, we can use the induction hypothesis on \( M[i + 1..p] \) and obtain that \( M \) is simple.

(ii) Let \( M \) be a non-simple string of weight \( k \) and length \( k + 1 \). If \( M[1] \geq 2 \) then \( M' = M[2..k+1] \) has weight \( k - M[1] \leq k - 2 \) and length \( k \), and thus by (i) we obtain that \( M' \) is simple, contradicting the assumption that \( M \) is non-simple. Similarly, \( M[k+1] \) cannot be greater than 1. For \( 2 \leq i \leq k \), if \( M[i] \geq 3 \) then either \( M[1..i-1] \) or \( M[i+1..k+1] \) satisfies the condition of (i). Similarly, if \( M[i] = M[i + 1] = 2 \) then either \( M[1..i-1] \) or \( M[i+2..k+1] \) satisfies the condition of (i).

Theorem 2. \( \alpha(k, k + 1) = 013355 \cdots kk \) for every odd \( k \), and \( \alpha(k, k + 1) = 02244 \cdots kk \) for every even \( k \).

Proof. We first give an upper bound on \( \alpha(k, k + 1) \) for odd \( k \). We build a search scheme as follows. The scheme contains the searches \( S_{k,i,j} \) defined in the proof of Theorem 3 which cover all simple strings of weight \( k \) and length \( k + 1 \). In order to cover the non-simple strings, the scheme contains the following searches.

1. \( S_{k,i,j}^1 = ([i, k+1][i-1, 1], 0 \cdots 0, 013355 \cdots jj(j+1)k \cdots k) \) for every odd \( 3 \leq j \leq k \) (for \( j = k \), the \( U \)-string is 013355 \cdots kk).

2. \( S_{k,i,j}^2 = ([i, 1][i+1, k+1], 0 \cdots 0, 013355 \cdots jj(j+1)k \cdots k) \) for every odd \( 3 \leq j \leq k \) (for \( j = k \), the \( U \)-string is 013355 \cdots kk).

Let \( M \) be a non-simple string of weight \( k \) and length \( k + 1 \). By Lemma 1 \( M = X0M_10M_20 \cdots 0M_0Y \) where each of \( X \) and \( Y \) is either the string 1 or an empty string, and each \( M_i \) is either 2, 12, 21, or 121. A string \( M_i \) is called a block of type 1, 2, or 3 if \( M_i \) is equal to 12, 21, or 121, respectively. Let \( B_1, \ldots, B_{r'} \) be the blocks of type 1 and type 2, from left to right.

We consider several cases. The first case is when \( X \) and \( Y \) are empty strings, and \( B_1 \) is of type 1. Since the weight of \( M \) is odd, it follows that \( r' \) is odd. If \( M \) has no other blocks, \( M \) is covered by search \( S_{k,i,k}^1 \), where \( i + 1 \) is the index in \( M \) in which \( B_1 \) starts. Otherwise, if \( B_2 \) is of type 1, then \( M \) is covered by search \( S_{k,i,j}^2 \), where \( i + 1 \) is the index in \( M \) in which \( B_1 \) starts, and \( i + j + 1 \) is the index in which the first block to the right of \( B_1 \) starts (this block is either \( B_2 \), or a block of type 3). Now suppose that \( B_2 \) is of type 2. If \( B_3 \) is of type 2, then \( M \) is covered by search \( S_{k,i,j}^3 \), where \( i - 1 \) is the index in \( M \) in which \( B_3 \) ends, and \( i - j - 1 \) is the index in which the first block to the left of \( B_3 \) ends. By repeating these arguments, we obtain that \( M \) is covered unless the types of \( B_1, \ldots, B_{r'} \) alternate between type 1 and type 2. However, since \( r' \) is odd, \( B_{r'} \) is of type 1, and in this case \( M \) is covered
by $S^1_{k,i,j}$, where $i + 1$ is the index in $M$ in which $B_1$ starts, and $k - j$ is the index in which the first block to the left of $B_1$ ends.

Now, if $X$ is an empty string and $Y = 1$, define a string $M' = M20$. By the above, the string $M'$ is covered by some search $S'_{k+2,i,j}$. Then, $M$ is covered by either $S'_{k,i,j}$ or $S'_{k,i,j-2}$. The same argument holds for the case when $X = 1$. The proof for the case when $B_1$ is of type 2 is analogous and thus omitted.

The lower bound on $\alpha(k, k+1)$ for odd $k$ is obtained by considering the string $M = 012020\cdots 20$. The $U$-string of a search that covers $M$ must be at least $01355\cdots kk$.

We next give an upper bound on $\alpha(k, k+1)$ for even $k$. We define $k$-mismatch search schemes $S_k$ recursively. For $k = 0$, $S_0$ consists of a single search $S_{0,1} = (1,0,0)$. For $k \geq 2$, $S_k$ consists of the following searches.

1. For every search $S_{k-2,i} = (\pi,0\cdots 0,U)$ in $S_{k-2}$, $S_k$ contains a search $S_{k,i} = (\pi \cdot k(k+1),0\cdots 0,U \cdot kk)$.
2. A search $S_{k,k} = ([k+1,1],0\cdots 0,01kk\cdots k)$.
3. A search $S_{k,k+1} = (k(k+1)[k-1,1],0\cdots 0,01kk\cdots k)$.

Note that the critical string of $S_k$ is $02244\cdots kk$ corresponding to item 1 above. We now claim that all number strings of length $k + 1$ and weight at most $k$ are covered by the searches of $S_k$. The proof is by induction on $k$. The base $k = 0$ is trivial. Suppose the claim holds for $k - 2$. Let $M$ be a number string of length $k + 1$ and weight $k' \leq k$. If $M[k] + M[k+1] \leq 1$, then $M$ is covered by either $S_{k,k}$ or $S_{k,k+1}$. Otherwise, the weight of $M' = M[1..k-1]$ is at most $k' - 2$. By induction, $M'$ is covered by some search $S_{k-2,i}$. Then the search $S_{k,i}$ covers $M$.

To prove that $\alpha(k, k+1) \geq 02244\cdots kk$ for every $k$, consider the string $M = 0202\cdots 020$. It is easy to verify that the $U$-string of a search that covers $M$ must be at least $02244\cdots kk$.

**Theorem 3.** $\alpha(k, k+2) = 0123\cdots(k-1)kk$ for every $k \geq 1$.

**Proof.** We use the following notation. For two integers $i$ and $j$, $[i,j]$ denotes the string $i(i+1)(i+2)\cdots j$ if $i \leq j$, and the empty string if $i > j$. Moreover, $[i,j]$ denotes the string $i(i-1)(i-2)\cdots j$ if $i \geq j$, and the empty string if $i < j$.

We first give an upper bound on $\alpha(k,k+1)$. We build a $k$-mismatch search scheme $S$ that contains searches $S_{k,i,j} = ([i,k+2][i-1,1],0\cdots 0,[0,j]jk\cdots k)$ for all $i$ and $j$. Let $M$ be a string of weight $k$ and length $k + 2$. By Lemma 1 there are indices $i$ and $j$ such that $M[i..i+j+1] = 01'0$, and therefore $M$ is covered by $S_{k,i,j}$.

The lower bound is obtained from the string $M = 011\cdots 110$. It is easy to verify that the $U$-string of a search that covers $M$ must be at least $0123\cdots(k-1)kk$.

An important consequence of Theorems 2 and 3 is that for some typical cases, partitioning the pattern into $k + 2$ parts brings an advantage over $k + 1$ parts. For $k = 2$, for example, we have $\alpha(2,3) = 022$ while $\alpha(2,4) = 0122$. Since the second element of 0122 is smaller than that of 022, a 4-part search scheme potentially enumerates less strings than a 3-part scheme. On the other hand, the average length of a part is smaller when using 4 parts, and therefore the branching occurs
earlier in the searches of a 4-part scheme. The next section shows that for some parameters, \((k+2)\)-part schemes outperform \((k+1)\)-part schemes, while for other parameters the inverse occurs.

5 Case studies

5.1 Numerical comparison of search schemes

In this section, we examine the efficiency of several 2-mismatch and 3-mismatch search schemes. For 2 mismatches, we use the following schemes.

1. Slightly modified scheme \(S_{LLTWWY}\). The searches are: \(S_f = (123, 000, 022), \) \(S_b = (321, 000, 012), \) and \(S_{bd}' = (213, 001, 012). \) Note that the \(\pi\)-string of \(S_{bd}'\) is 213 and not 231 as in \(S_{bd}\). While \(S_{bd}\) and \(S_{bd}'\) have the same efficiency for equal-size partitions, this in not the case for unequally sized parts.

2. 4-part scheme whose searches are \((1234, 0000, 0112), (4321, 0000, 0122), \) \((2341, 0001, 0012), \) and \((1234, 0002, 0022). \)

3. 5-part scheme whose searches are \((12345, 00000, 01122), (54321, 00000, 00222), \) \((23451, 00000, 00112), \) and \((23451, 00000, 00112)\)

For 3 mismatches, the search scheme are

1. 4-part scheme whose searches are \((1234, 0000, 0133), (2134, 0011, 0133), \) \((3421, 0000, 0133), \) and \((4321, 0011, 0133). \)

2. 5-part scheme whose searches are \((12345, 00000, 01233), (23451, 00000, 01223), \) \((34521, 00001, 01133), \) and \((45321, 00012, 00333). \)

The search schemes above were generated by a greedy algorithm. At each step, the algorithm considers the uncovered string \(M\) of weight \(k\) such that the lexicographically minimal \(U\)-strings of searches that covers \(M\) is maximal. Among the searches that cover \(M\) with minimal \(U\)-string, a search that covers the maximum number of uncovered strings of weight \(k\) is chosen. The \(L\)-string of the search is chosen to be lexicographically maximal among all possible \(L\)-string that do not decrease the number of uncovered strings. For each search scheme and each choice of parameters, we obtained an optimal partition and computed the efficiency of the scheme according to Section 3.

Results for 2 mismatches are given in Table 1 and Table 2, for 4-letter and 30-letter alphabets respectively, and results for 3 mismatches are given in Table 3.

Our theoretical analysis indicates that an increased number of parts combined with uneven partitioning improves over a scheme with \(k+1\) equal sized parts when \(m/(k+1)\) is smaller than \(\log_2 n\) (see Section 3.2). This is confirmed by the numerical results in Tables 1, 2, and 3 which show significant improvement when \(m/(k+1)\) is small.

For big alphabets (Table 2), we observe a larger gain in efficiency. The is due to the fact that the values of \(n_l\) (see equation (2)) increase more rapidly when the
Table 1: Values of \(\text{#str}(S, X, 4, 4^{16})\) for 2-mismatch search schemes (recall that 4 is the size of the alphabet, and \(4^{16}\) is the length of the text). The second column gives \(\text{#str}\) values for the 3-part search scheme with equal-size parts. The other columns give \(\text{#str}\) values for different search schemes using an optimal partition of the pattern. For each search scheme, the optimal value of \(\text{#str}\) is shown in the first sub-column, and the optimal partition in the second sub-column.

| \(m\) | 3 equal | 3 unequal | 4 unequal | 5 unequal |
|------|---------|-----------|-----------|-----------|
| 24   | 1197    | 1077      | 9,7,8     | 959       | 7,4,4,9   | 939       | 7,1,6,1,9 |
| 36   | 241     | 165       | 15,10,11  | 140       | 12,5,7,12 | 165       | 11,1,9,1,14 |
| 48   | 53      | 53        | 16,16,16  | 51        | 16,7,9,16 | 53        | 16,1,15,1,15 |

Table 2: Values of \(\text{#str}(S, X, 30, 30^7)\) for 2-mismatch search schemes.

| \(m\) | 3 equal | 3 unequal | 4 unequal | 5 unequal |
|------|---------|-----------|-----------|-----------|
| 15   | 846     | 286       | 6,4,5     | 231       | 5,2,3,5   | 286       | 5,1,3,1,5 |
| 18   | 112     | 111       | 7,6,5     | 81        | 6,2,4,6   | 111       | 6,1,4,1,6 |
| 21   | 24      | 24        | 7,7,7     | 23        | 7,3,4,7   | 24        | 7,1,6,1,6 |

Table 3: Values of \(\text{#str}(S, X, 4, 4^{16})\) for 3-mismatch search schemes.

| \(m\) | 4 unequal | 5 unequal |
|------|-----------|-----------|
| 24   | 11222     | 6,6,6,6   | 8039      | 4,6,5,1,8 |
| 36   | 416       | 9,9,9,9   | 549       | 6,11,5,1,13 |
| 48   | 185       | 12,12,12,12 | 213     | 11,11,11,1,14 |

alphabet is large, and thus a change in the size of parts can have a bigger influence on these values.

For 3 mismatches (Table 3), we observe smaller gain. This is partly explained by Theorem 2, as with 3 mismatches and 4 parts, the critical string starts with 01 (compared to 02 for 2 mismatches and 3 parts), therefore 4 parts provide already a competitive search. Another interesting observation is that with 4 parts, the optimal partition is an even one, as the \(U\)-strings in all searches in the 4-part scheme are the same.

In conclusion, the ideas we proposed in this paper do bring a significant gain in efficiency for some parameter ranges, however the design of a search scheme should be done carefully for each specific set of parameters.

5.2 Experiments on genomic data

We implemented our method using the 2BWT library, provided by [5] (available at [http://i.cs.hku.hk/2bwt-tools/](http://i.cs.hku.hk/2bwt-tools/)) and experimentally compared different search schemes, both in terms of running time and average number of enumerated sub-strings.

The experiments were done on the sequence of human chromosome 14. The sequence is 88M long, with nucleotide distribution 29%, 21%, 21%, 29%. Searched patterns were obtained from Next-Generation Sequencing reads by cutting out
Table 4: Total time (in seconds) of searching for one million patterns in human chromosome 14, up to 2 mismatches. The 2nd column corresponds to the 3-equal-parts search scheme. The 3rd (respectively 4th and 5th) column shows the running time respectively for the 3-unequal-parts, 4-equal-parts and 4-unequal-parts searches, together with their ratio to the 3-equal-parts value.

| m  | 3 equal | 3 unequal | 4 equal | 4 unequal |
|----|---------|-----------|---------|-----------|
| 12 | 209     | 209 (100%)| 192 (92%)| 195 (93%) | 2,5,1,4 |
| 15 | 284     | 284 (100%)| 274 (96%)| 265 (93%) | 3,5,1,6 |
| 18 | 230     | 230 (100%)| 209 (91%)| 203 (88%) | 5,5,1,7 |
| 21 | 175     | 161 (92%) | 147 (84%)| 150 (86%) | 6,4,3,8 |
| 24 | 142     | 120 (85%) | 117 (82%)| 107 (75%) | 7,4,4,9 |
| 27 | 119     | 99 (83%)  | 96 (81%) | 82 (69%)  | 9,4,5,9 |
| 30 | 101     | 84 (83%)  | 76 (74%) | 68 (67%)  | 10,4,6,10 |
| 33 | 83      | 70 (84%)  | 63 (75%) | 58 (70%)  | 11,5,6,11 |
| 36 | 68      | 66 (97%)  | 62 (96%) | 50 (74%)  | 12,5,7,12 |
| 39 | 56      | 56 (100%) | 48 (86%) | 45 (80%)  | 13,6,7,13 |
| 42 | 45      | 45 (100%) | 44 (98%) | 38 (84%)  | 14,6,8,14 |
| 45 | 39      | 39 (100%) | 42 (108%)| 34 (87%)  | 15,7,8,15 |

Table 5: Average number of enumerated strings over one million searches in human chromosome 14, up to 2 mismatches.

| m  | 3 equal | 3 unequal | 4 equal | 4 unequal |
|----|---------|-----------|---------|-----------|
| 12 | 1230    | 1230 (100%)| 1221 (99%)| 1193 (97%) |
| 15 | 2048    | 2048 (100%)| 2136 (104%) | 1933 (94%)  |
| 18 | 1758    | 1758 (100%)| 1780 (101%)| 1632 (93%)  |
| 21 | 1300    | 1201 (92%) | 1161 (89%) | 1147 (88%)  |
| 24 | 1049    | 882 (84%)  | 927 (88%)  | 816 (78%)   |
| 27 | 904     | 749 (83%)  | 788 (87%)  | 679 (75%)   |
| 30 | 767     | 642 (84%)  | 523 (68%)  | 550 (71%)   |
| 33 | 637     | 556 (87%)  | 415 (65%)  | 476 (75%)   |
| 36 | 538     | 529 (98%)  | 415 (77%)  | 432 (80%)   |
| 39 | 428     | 428 (100%) | 398 (93%)  | 370 (86%)   |
| 42 | 349     | 349 (100%) | 359 (102%) | 319 (91%)   |
| 45 | 302     | 302 (100%) | 324 (107%) | 286 (95%)   |

strings of required length. Both the sequence and the reads were downloaded from http://gage.c.ncbi.nlm.nih.gov/data. For every pattern length and every search scheme, $10^6$ patterns were searched and the average number of enumerated strings was computed.

For the case of 2 mismatches, we implemented the 3-part and 4-part schemes from Section 5.1 as well as their equal part versions for comparison. For each pattern length, we computed an optimal partition, taking into account a non-identical distribution of nucleotides. Results are presented in Tables 4 and 5 showing respectively the total running time and the average number of enumerated substrings.

Comparing Tables 4 and 5, we observe, as expected, a strong correlation be-
Table 6: Total time (in seconds) of searching for one million patterns in human chromosome 14, up to 3 mismatches.

| m   | 4 equal | 5 equal | 5 unequal |
|-----|---------|---------|-----------|
| 6   | 43      | 41 (96%)| 43 (101%)| 1,1,2,1,1 |
| 9   | 441     | 409 (93%)| 439 (100%)| 1,2,3,1,2 |
| 12  | 1442    | 1328 (92%)| 1388 (96%)| 1,2,6,1,2 |
| 15  | 2208    | 2061 (93%)| 2095 (95%)| 2,2,6,1,4 |
| 18  | 1698    | 1587 (93%)| 1535 (90%)| 4,2,6,1,5 |
| 21  | 1131    | 1006 (89%)| 1033 (91%)| 3,6,4,1,7 |
| 24  | 678     | 596 (88%)| 635 (94%)| 2,9,3,1,9 |
| 27  | 396     | 405 (102%)| 363 (92%)| 3,10,3,1,10 |
| 30  | 214     | 293 (137%)| 239 (112%)| 4,10,4,1,11 |
| 33  | 151     | 218 (144%)| 188 (124%)| 6,9,6,1,11 |
| 36  | 135     | 163 (121%)| 171 (127%)| 8,8,8,1,11 |

between running time and the number of enumerated strings. Using unequal parts for 3-part schemes yields a notable time decrease (8–17%) for patterns of length between 21 and 33. Furthermore, using 4 parts leads to an even more important improvement, showing a significantly better results for all pattern length compared to the 3-equal-parts scheme of [5]. For pattern lengths from 21 to 42 we observe 16–36% improvement in running time and 12–35% improvement in the number of enumerated strings. For pattern lengths 24, 27, 39, 42, we observe that using unequal part lengths for 4-part schemes is beneficial. Overall, the experimental results are consistent with numerical estimations of Section 5.1. However, for pattern lengths 30–36, the 4-equal-parts scheme performs better than the 4-unequal-parts one, which illustrates that the optimal partition found for random texts may not be the best one for genomic sequences.

For the case of 3 mismatches, we implemented 4-part and 5-part schemes from Section 5.1, as well as their equal part versions for comparison. Results are presented in Tables 6 and 7 showing respectively the total running time and the average number of enumerated substrings. They show that compared to 4-equal-parts scheme, 5-equal-parts and 5-unequal-parts schemes yields a significant gain in time (4–12%) and the number of enumerated strings (1–37%) for pattern lengths 6–27. For some pattern lengths (12,15,21,24), we observe that 5-equal-parts scheme outperforms the 5-unequal-parts one.

6 Conclusions

This paper can be seen as the first step towards an automated design of efficient search schemes for approximate string matching, based on bidirectional indexes. More research has to be done in order to allow an automated design of optimal search schemes. It would be very interesting to study an approach when a search scheme is designed simultaneously with the partition, rather than independently as it was done in our work.

The results of this paper can be extended to approximate string matching under
edit distance. In this case, an elementary step of bidirectional search can be done with the algorithm of Landau et al. [7], as described in [12, Sect. 6]. The estimation of $n_l$ (Section 3) becomes more complicated though.

**Acknowledgements.** GK has been supported by the ABS2NGS grant of the French government (program *Investissement d’Avenir*) as well as by a EU Marie-Curie Intra-European Fellowship for Carrier Development. KS has been supported by the co-tutelle PhD fellowship of the French government. DT has been supported by ISF grant 981/11.

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