Longest Common Subsequence in $k$ Length Substrings

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Abstract. In this paper we define a new problem, motivated by computational biology, $LCS_k$ aiming at finding the maximal number of $k$ length substrings, matching in both input strings while preserving their order of appearance. The traditional LCS definition is a special case of our problem, where $k = 1$. We provide an algorithm, solving the general case in $O(n^2)$ time, where $n$ is the length of the input strings, equaling the time required for the special case of $k = 1$. The space requirement of the algorithm is $O(kn)$. We also define a complementary $ED_k$ distance measure and show that $ED_k(A, B)$ can be computed in $O(nm)$ time and $O(km)$ space, where $m, n$ are the lengths of the input sequences $A$ and $B$ respectively.

Keywords: Longest common subsequence, Similarity of strings, Edit distance, Dynamic programming.

1 Introduction

The Longest Common Subsequence problem, whose first famous dynamic programming solution appeared in 1974 [19], is one of the classical problems in computer science. The widely known string version appears in Definition 1.

Definition 1. The String Longest Common Subsequence ($LCS$) Problem:
Input: Two sequences $A = a_1a_2\ldots a_n$, $B = b_1b_2\ldots b_n$ over alphabet $\Sigma$.
Output: The length of the longest subsequence common of both strings, where a subsequence is a sequence that can be derived from another sequence by deleting some elements without changing the order of the remaining elements.

For example, for the sequences appearing in Figure 1, $LCS(A, B)$ is 5, where a possible such subsequence is $T T G T G$.

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Remark: We alternately use the terms string and sequence throughout the paper, since both terms are common as the input of the LCS problem. Nevertheless, a subsequence is obtained from a sequence by deleting symbols at any index we want, while a substring is a consecutive part of the string.

The LCS problem is motivated by the need to measure similarity of sequences and strings, and it has been very well studied (for a survey, see [6]). The well known dynamic programming solution [17] requires running time of $O(n^2)$, for two input strings of length $n$.

The LCS problem has also been investigated on more general structures such as trees and matrices [3], run-length encoded strings [4], weighted sequences [2], [7] and more. Many variants of the LCS problem were studied as well, among which LCS alignment [8], [15], [14], constrained LCS [18], [8], restricted LCS [10] and LCS approximation [12].

Motivation. The LCS has been also used as a measure of sequence similarity for biological sequence comparison. Its strength lies in its simplicity which has allowed development of an extremely fast, bit-parallel computation which uses the bits in a computer word to represent adjacent cells a row of the LCS scoring matrix and computer logic operations to calculate the scores from one row to the next [1], [9], [11]. For example, in a recent experiment, 25,000,000 bit-parallel LCS computations (sequence length = 63) took approximately 7 seconds on a typical desktop computer [5] or about 60 times faster than a standard algorithm. This speed makes the LCS attractive for sequence comparison performed on high-sequencing data. The disadvantage of the LCS is that it is a crude measure of similarity because consecutive matching letters in the LCS can have different spacings in the two sequences, i.e., there is no penalty for insertion and deletion. Indeed, as is well-known, there is a strong relation between the total number of insertions and deletions and the LCS. However, there are no limitations on the “distribution” of such insertions and deletions. Consider for example the following two sequences:

$$A = (GTG)^{n/3}$$

$$B = (TCC)^{n/3}$$

In these sequences the LCS is quite large, of size $n/3$, but no two matched symbols are consecutive in both sequences. Any common subsequence of this size “put together” separated elements implying a rather “artificial” similarity of the sequences.

What is proposed here is a definition of LCS that makes the measure of similarity more accurate because it enables forcing adjacent letters in the LCS to be adjacent in both sequences. In our problem, the common subsequence is required to consist of $k$ length substrings. A formal definition appears in Definition 2.
Definition 2. The Longest Common Subsequence in k Length Substrings Problem (LCSk):
Input: Two sequences \( A = a_1a_2\ldots a_n, B = b_1b_2\ldots b_n \) over alphabet \( \Sigma \).
Output: The maximal \( \ell \) s.t. there are \( \ell \) substrings,
\[ a_{i_1}...a_{i_1+k-1}...a_{i_\ell}...a_{i_\ell+k-1}, \]
identical to \( b_{j_1}b_{j_1+k-1}...b_{j_\ell}b_{j_\ell+k-1} \)
where \( \{a_{i_j}\} \) and \( \{b_{j_j}\} \) are in increasing order for \( 1 \leq f \leq \ell \) and
where two k length substrings in the same sequence, do not overlap.

We demonstrate LCSk considering the sequences appearing in Figure 1.

\[ A = \begin{array}{cccccccc}
1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 \\
T & G & C & G & T & G & T & G
\end{array}\]

\[ B = \begin{array}{cccccccc}
G & T & T & G & C & C
\end{array}\]

Fig. 1. An LCS2 example

A possible common subsequence in pairs \((k = 2)\) is \(G\ T\ T\ \ G\) obtained from \(a_4, a_5, a_7, a_8\) and \(b_1, b_2, b_5, b_6\). Though \(a_6 = b_4\), and such a match preserves the order of the common subsequence, it cannot be added to the common subsequence in pairs, since it is a match of a single symbol. For \(k = 3\), one of the possible solutions is \(T\ G\ C\) achieved by matching \(a_1, a_2, a_3\), with \(b_5, b_6, b_7\). For \(k = 4\) a possible solution is \(T\ G\ T\ G\) obtained from matching \(a_5, a_6, a_7, a_8\) and \(b_3, b_4, b_5, b_6\). Note that in the last two cases the solution contains a single triple and a single quadruplet.

The paper is organized as follows: Section 2 gives some preliminaries. The solution for the LCSk problem is detailed in Section 3. In Section 4 we refer to the complementary edit distance measure, EDk. Section 5 concludes the paper.

2 Preliminaries

The LCSk problem is a generalization of the LCS problem. We might consider using the solution of the latter in order to solve the former. If we perform the LCS algorithm on the input sequences, we can backtrack the dynamic programming table and mark the symbols participating in the common subsequence. We can then check whether those symbols appear in consecutive \(k\) length substrings in both input sequences, and delete them if not. Such a procedure guarantees a common subsequence in \(k\) length substrings but not necessarily the optimal length of the common subsequence. For example consider LCS2 of the sequences appearing on Figure 1. Applying the LCS algorithm on these strings may yield \(T\ T\ G\ T\ G\), containing a single non-overlapping pair matching while there exists LCS2 of \(T\ G\ T\ G\) having two pair matchings. Hence, a special algorithm designed for LCSk is required.

As the LCSk problem considers matchings of \(k\) consecutive symbols, throughout this paper we call such a matching a \(k\) matching. We will also need the term
predecessor. We use the following definitions for these terms:

**Definition 3.**

\[
\text{kMatch}(i, j) = \begin{cases} 
1 & \text{if } a_{i+f} = b_{j+f}, \text{ for every } 0 \leq f \leq k - 1 \\
0 & \text{Otherwise}
\end{cases}
\]

If \(k\text{Match}(i, j) = 1\), the matching substring is denoted \((i, j)\).

**Definition 4. Predecessors.** Let candidates\((i, j)\) be the set of all longest common subsequences, consisting of \(k\) matchings, of prefix \(A[1...i + k - 1]\) and prefix \(B[1...j + k - 1]\). Then let \(\text{pred}(i, j)\) be all the possible last \(k\) matchings in candidates\((i, j)\). That is, \(\text{pred}(i, j) = \{(s, t) | \exists c \in \text{candidates}(i, j), \text{where } (s, t) \text{ is the last } k \text{ matching in } c\}\).

We define the length of \(p \in \text{pred}(i, j)\) derived from candidate \(c\), to be the number of \(k\) matchings in \(c\) and denote it by \(|p|\).

**Example.** Consider LCS2 of the sequences of Figure 1. Let candidates\((5, 3)\) be the common subsequences in pairs of \(B[1...4] = \text{T G T G}\) and of \(A[1...6] = \text{T G C G T G}\), thus, candidates\((6, 4)\) contains\(\{\text{TG, GT}\}\). 

\(TG\) can be obtained in two ways: \(a_1a_2\) matched to \(b_3b_4\), or \(a_5a_6\) matched to \(b_3b_4\), and \(GT\) by \(a_4a_5\) matched to \(b_1b_2\) therefore, we have \(\text{pred}(i, j) = \{(1, 3), (5, 3), (4, 1)\}\).

In this example all predecessors are of length \(1\). Keeping the predecessors enables backtracking to reveal the longest common subsequence in \(k\) length substrings itself.

The following Lemma is necessary for the correctness of the solution.

**Lemma 1** Let \(p_1, p_2 \in \text{pred}(i, j)\), then if \(|p_1| + 1 = |p_2|\), then any maximal common subsequence of \(k\) length substrings using the \(k\) matching \(p_2\) has length greater or equal to that using the \(k\) matching \(p_1\).

**Proof.** Suppose \(p_1 = (s, t)\) and \(p_2 = (s', t')\). Several cases are possible for \(p_1, p_2\):

1. If \(s' < s\) and \(t' < t\), then the candidate whose last \(k\) matching is \(p_2\) might be further extended till \(A[s]\) and \(B[t]\), enlarging the difference between \(p_1\) and \(p_2\).
2. If \(s' = s\) and \(t' = t\) both predecessors have the same opportunities for extension.
3. If \(s + k - 1 < s'\) and \(t + k - 1 < t'\), the \(k\) matching \((s', t')\) can be added to the candidate whose last \(k\) matching is \((s, t)\), contradicting its maximality.
4. If there is an overlap between the \(k\) matchings represented by the predecessors, \(s < s' < s + k\) or \(t < t' < t + k\), starting from \(a_{s'+k}\), every \(k\) matching can be used to extend the common subsequence in \(k\) length substring, represented by both predecessors. However, the subsequence using \(p_1\) cannot have an additional \(k\) matching before \(a_{s'+k}\), as overlaps are forbidden. Consequently, the difference between the length of \(p_1\) and \(p_2\) is preserved in the extended maximal common subsequences.
3 Solving the LCSk Problem

As in other LCS variants, we solve the problem using a dynamic programming algorithm. We denote by $LCS_{ki,j}$ the longest common subsequence, consisting of $k$ matchings in the prefixes $A[1..i+k-1]$ and $B[1..j+k-1]$. Lemma 2 below, formally describes the computation of $LCS_{ki,j}$.

Lemma 2 The LCSk Recursive Rule.

$$LCSK_{i,j} = \max \begin{cases} LCS_{ki,j-1}, \\ LCS_{k-1,j}, \\ LCS_{k-i,j-k} + kMatch(i,j) \end{cases}$$

Proof. $LCS_{ki,j}$ contains the maximal number of common $k$ length substrings, preserving their order in the input sequences. A possible subsequence can be constructed by matching the substrings $a_{i}, \ldots, a_{i+k-1}$ with $b_{j}, \ldots, b_{j+k-1}$, in case all $a_{i+f}$ and all $b_{j+f}$, for $0 \leq f \leq k-1$, are not part of previous $k$ matchings. This is guaranteed when considering the prefixes $A[1..i-k]$ and $B[1..j-k]$ while trying to extend by one the common subsequence for cell $LCS_{ki,j}$. Another option of extending the subsequence is by using the $k$ matching $(s,j)$, for $s < i$. Similarly, we can use the $k$ matching $(i,t)$ for $t < j$. Note that the options of extending $LCS_{i-f,j-f}$, for $1 \leq f \leq k-1$ is included in both $LCS_{ki,j-1}$ and $LCS_{k-1,j}$. These claims can be easily proven using induction.

According to Lemma 2 we can solve the LCSk problem using a dynamic programming algorithm working on a two dimensional table of size $(n-k+1)^2$ where the rows represent the $A$ sequence and the columns stand for sequence $B$. Cell $LCS[i,j]$ contains the value $LCS_{ki,j}$ and the appropriate predecessors. Nevertheless, when we wish to attain the common subsequence itself, we encounter a complication.

In the original LCS algorithm, computing the common subsequence, requires maximizing three options of possible prefixes of the LCS. When some of these prefixes have the same length, there is no significance which of them is chosen, as a single common subsequence is sought and the selection has no effect on future matches. However, in the LCSk problem the situation is different. For example, consider $LCS_{2}$ for the strings of Figure 3. $LCS_{2}[3,3]$ equals 1 due to the $2Match$

$$A = \begin{array}{cccc} 1 & 2 & 3 & 4 & 5 \\ G & C & G & T & C \end{array}$$

$$B = \begin{array}{cccc} 1 & 2 & 3 & 4 & 5 \\ C & G & C & G & T \end{array}$$

Fig. 2. An LCS2 example

(1, 2) (matching $a_1a_2$ to $b_2, b_3$) $(G C)$, or by the $2Match$ of $(2, 1)$ $(C G)$. In spite of the fact that both common subsequences share the same length, the former
is part of the final solution as it enables a further 2Match at (3, 4) while the latter cannot be extended due to the overlap restriction. It, therefore, seems that all possibilities of common subsequence in \( k \) length substrings, that is, all predecessors should be saved at every calculation in order to enable a correct backtracking of the optimal solution. As the dynamic programming proceeds, this information can exponentially increase. Nevertheless, we prove in Lemma 3 that in the \( LCS_k \) problem only one maximal previously computed subsequence is required. The three options of forming \( LCS_k^{i,j} \), as appear in Lemma 2, compile candidates \((i, j)\), hence \( pred(i, j) \). Therefore, the \( pred(i, j) \) set should be updated after computing \( LCS_k^{i,j} \).

**Corollary 1** If \( LCS_k^{i,j-1} = LCS_k^{i-1,j} = LCS_k^{i-2,j-2+1}, \) and \( k \text{Match}(i,j)=1 \) then \( pred(i, j) = pred(i, j - 1) \cup pred(i - 1, j) \cup (i, j) \).

If \( LCS_k^{i,j-1} = LCS_k^{i-1,j} \) and \( k \text{Match}(i,j)=0 \) then \( pred(i, j) = pred(i, j - 1) \cup pred(i - 1, j) \).

In both cases, if one or more of the relevant \( LCS_k^{x,y}, x \leq i, y \leq j \) has shorter length, its corresponding pred is not included in \( pred(i, j) \).

**Proof.** Note, that the length of a predecessor \( p \in pred(i, j) \) equals the value of \( LCS_k^{i,j} \). Due to Lemma 1 there is no necessity to consider the shorter predecessors. Suppose all three sets contain predecessors representing common subsequences of the same length. Without further information, we cannot determine which common subsequence ending in \( pred(i, j - 1), \) \( pred(i - 1, j) \), or in \( k \text{ matching of } (i, j) \), will be in the maximal output, therefore, all predecessors must be considered.

### 3.1 The Backtrack Process

Using the recursive rule of Lemma 2, the value computed for \( LCS_k^{i-k+1,j-k+1} \) is the length of the common subsequence in \( k \) length substrings of sequences \( A \) and \( B \). In order to obtain the common subsequence itself we perform the following procedure. Consider the value saved in cell \( LCS_k[i,j] \), where \( i \) and \( j \) are initialized by \( n-k+1 \). We suppose that each cell contains a single predecessor, as will be proven hereafter in Lemma 3. Let the predecessor saved in the current cell be \((x, y)\). Two cases are regarded as long as \( i, j > 0 \).

1. If \( x = i \) and \( y = j \), then a \( k \) matching starts in these indices, therefore \( a_{i+f} \) for every \( 0 \leq f \leq k - 1 \) can be added to the constructed output, preserving the increase of the indices. In order to proceed we decrease both \( i, j \) by \( k \) to avoid previous \( k \) matchings overlapping \((i, j)\).

2. Otherwise, no \( k \) matching occurs in the current indices. The predecessor \((x, y)\) directs us to the cell containing a \( k \) matching which is part of an LCS with the value \( LCS_k^{i,j} \). Therefore, we decrease the indices \( i = x \) and \( j = y \).
3.2 Predecessors Elimination

We aim at minimizing the number of predecessors per $LCS_k[i, j]$ and therefore define a process of predecessors elimination. Eliminating a predecessor $p$, that is, deleting it from $\text{pred}(i, j)$ can be safely done if a maximal common subsequence in $k$ length substrings of the same length can be attained using another predecessor from $\text{pred}(i, j)$. Lemma 3 provides the elimination procedure and its correctness.

Lemma 3 Elimination Lemma. Let $p_1, p_2 \in \text{pred}(i, j)$ be $k$ matchings, where $|p_1| = |p_2|$, then one of $p_1, p_2$ can be arbitrarily eliminated.

Proof. Let $p_1 = (s, t)$, $p_2 = (s', t')$. In case $k\text{Match}(i, j) = 0$ then, if the backtracking pass through table cell $[i, j]$ it implies that the previously found $k$ matching is $(i + k, j + k)$ due to the second case of the backtracking procedure. Moreover, according to Corollary 1, both $\{s, s'\} \leq i$ and $\{t, t'\} \leq j$. As a consequence, there is no preference to one of the equal length predecessors as both cannot overlap the previous $k$ matching.

Suppose then that $k\text{Match}(i, j) = 1$ and $p_2 = (i, j)$. According to the backtracking procedure, we get to cell $[i, j]$ either by the first case of the procedure where there is a $k$ matching $(i + k, j + k)$ or by its second case where at cell $[i', j']$ there is no $k$ matching but it contains a predecessor $(i, j)$. The latter implies that the previously found $k$ matching is $(i + k + f, j + k + h)$ for $f, h > 0$.

There are two cases to consider.

1. If no optimal solution uses the $k$ matching $(i, j)$ it implies that the optimal solution includes $k$ matchings $(i', j')$ and $(i'', j'')$ where $i' < i < i' + k$ and $i'' - k < i < i''$ or $j' < j < j' + k$ and $j'' - k < j < j''$. If only one inequality holds for $i$ or $j$ then some optimal solution will include $(i, j)$, contradicting the case definition. According to the first case of the backtracking procedure, when backtracking from cell $[i', j']$, including the $k$ matching $(i'', j'')$, we decrease both indices by $k$. Since $i'' - k < i$ and $j'' - k < j$ cell $[i, j]$ will not be considered, therefore even if we saved $p_2$, that is we eliminated $p_1$, it has no consequence on the optimal solution.

2. If there exists an optimal solution including $p_2$ but we arbitrarily eliminated it. Since we proved that the previously found $k$ matching is $(i + k + f, j + k + h)$ for $f, h \geq 0$ there is no preference to $p_2$ over $p_1$ as they are both of the same length and both do not overlap the previously found $k$ matching according to Corollary 1. Apparently, $p_1$ is included in another optimal solution.

The $k\text{Match}$ function requires $k$ symbol matching for each table entry. Nevertheless, matches can be enlarged only on the diagonal of the table, from cell $[i, j]$ to cell $[i + 1, j + 1]$. We therefore suggest to save at every table cell $[i, j]$ a diagonal counter, named $d\text{count}$, counting the length of the longest match between the suffixes of $A[1 \ldots i]$ and $B[1 \ldots j]$. 
While filling the dynamic programming table, at cell \([i, j]\) we compare merely \(a_i\) with \(b_j\) and assign \(\text{dcount}[i, j]\) its value according to the following definition:

**Definition 5.**

\[
\text{dcount}[i, j] = \begin{cases} 
1 + \text{dcount}[i - 1, j - 1] & \text{if } a_i = b_j \\
0 & \text{if } a_i \neq b_j
\end{cases}
\]

Now, instead of using the \(\text{kMatch}\) function when computing the score of \(\text{LCS}_k[i, j]\), we need only compare \(\text{dcount}[i + k - 1, j + k - 1]\) with \(k\). The situation of \(\text{dcount}[i + k - 1, j + k - 1] > k\) occurs when there is an overlap between some matched substrings, but this is handled by the Elimination Lemma. Note that we need to proceed with the \(\text{dcount}\) computations \(k\) rows and columns ahead during the \(\text{LCS}_k\) computation.

**Example.** Figure 3 depicts an \(\text{LCS}_2\) table. We demonstrate the two cases in Lemma 3 where \(\text{kMatch}(i, j) = 1\). For the first case, consider cell \(\text{LCS}_2[5, 6]\) including \(\text{pred}_{5, 6} = \{(4, 5), (5, 6)\}\). Suppose we arbitrarily eliminate \((4, 5)\). The \(\text{LCS}_2\) may contain the 2 matching \((5, 6)\) that overlaps with \((4, 1), (4, 5)\) and on the same time overlaps also \((6, 7)\) what can decrease the length of the solution. Nevertheless, according to the backtracking procedure, after considering \(\text{LCS}_2[6, 7]\) we decrease the indices and go to \(\text{LCS}_2[4, 5]\) in which \((5, 6)\) cannot exist, due to Corollary 1.

For the second case consider cell \(\text{LCS}_2[2, 3]\) including \(\text{pred}_{2, 3} = \{(1, 1), (2, 3)\}\). \((2, 3)\) is included in one of the optimal solution. Suppose we eliminated it and retained \((1, 1)\). The backtracking path goes through cells \([7, 7]\) to \([6, 7]\) to \([4, 5]\) to \([2, 3]\) where it finds a non overlapping predecessor \((1, 1)\) with the same length as the deleted \((2, 3)\).

**Theorem 1** The \(\text{LCS}_k(A, B)\) problem can be solved in \(O(n^2)\) time and \(O(kn)\) space, where \(n\) is the length of the input sequences \(A, B\). Backtracking the solution requires time of \(O(\ell)\) where \(\ell\) is the number of \(k\) matchings in the solution, and \(O(n^2)\) space.

**Proof.** The algorithm fills a table of size \((n-k+1)^2\). Each entry is filled according to Lemma 2 by performing a constant number of comparisons in addition to applying \(\text{kMatch}(i, j)\). Thanks to the usage of \(\text{dcount}\), the \(\text{kMatch}\) is also reduced to a constant time operations as can be seen at Definition 5. In addition, unifying three \(\text{pred}\) sets of size one each does not increase the time requirements per entry. The Elimination procedure requires also constant time according to Lemma 3.

All in all, constant time operations are performed for each of the table entries, concluding in \(O(n^2)\) time requirement for computing the optimal length of the common subsequence in \(k\) length substrings.

During the backtracking process we go through the cells representing the \(k\) matchings of one optimal solution. If the difference between two such \(k\) matchings is more than \(k\), we go through an intermediate cell whose predecessor directs
Fig. 3. An LCS2 Table. The numbers represent the length of the common subsequence. The pairs in parenthesis stand for the predecessors. Each cell contains all possible predecessors according to Corollary 1. Due to the Elimination Lemma only one predecessor is retained. The diagonal counter \(d_{count}\) is denoted by \(dc\).

us to the next \(k\) matching. Hence finding the common subsequence in \(k\)-length substrings requires \(O(\ell)\) where \(\ell\) is the number of \(k\) matchings in the solution.

Regarding space: Each of the \(n^2\) entries contains, according to Corollary 1 three predecessors and the Eliminate function, due to Lemma 3 results in a single predecessor before considering further entries, implying \(O(n^2)\) space requirement. Nevertheless, due to Lemma 2 during the computation of \(LCSk[i, j]\) we need only row \(i - k\) and column \(j - k\) as well as cell \([i + k - 1, j - k + 1]\) for its \(d_{count}\) value. As a consequence, at each step we save \(O(k)\) rows and columns implying the space requirement is \(O(kn)\). In order to backtrack the solution, the whole table is needed, implying \(O(n^2)\) space requirement.
4 Edit Distance in k Length Substrings

The well-known edit distance suggested by Levenstein [16] is strongly related to the LCS similarity measure. The problem is formally defined as follows:

Definition 6. The Edit Distance (ED) Problem:
\textbf{Input:} Two sequences \( A = a_1 a_2 \ldots a_n \), \( B = b_1 b_2 \ldots b_m \) over alphabet \( \Sigma \).
\textbf{Output:} The minimal number of insertions, deletions and substitutions required to transform \( A \) into \( B \).

The Edit Distance problem is considered as a complement to the LCS problem in the following sense. When the allowed edit operations are insertions and deletions we have:

\[
ED(A, B) = |A| + |B| - 2 \text{LCS}(A, B).
\]

Having this relation to the LCS problem in mind, we would like to define an edit distance with regard to \( k \)-length substrings that will have a similar complementary nature to the LCS with \( k \)-length substrings. Definition 7 seems natural.

Definition 7. The Edit Distance in \( k \) Length Substrings Problem (ED\( k \)):
\textbf{Input:} Two sequences \( A = a_1 a_2 \ldots a_n \), \( B = b_1 b_2 \ldots b_m \) over alphabet \( \Sigma \).
\textbf{Output:} The minimal number of insertions, deletions and substitutions required to transform \( A \) into \( B \), while symbols between locations on which edit operations occur are \( k \)-length substrings forming LCS\( k \) of \( A \) and \( B \).

Note that according to Definition 7 it is possible that between two locations on which an edit operation occur there is a common substring of length greater than \( k \) but less than \( 2k \). Thus, this definition enables considering only \( k \) consecutive symbols as a common \( k \)-length substring. The rest of the common symbols are counted as substitution edit operations. This is due to the fact that in the edit distance problem there are matched symbols and unmatched symbols. However, the ED\( k \) distance of Definition 7 considers only not overlapping \( k \) matchings, therefore, any common substring shorter than \( k \) symbols cannot be considered matched.

In order to capture this difference, consider for example the sequences of Figure 1. For these sequences LCS\( 2(A, B) = 2 \) and a suggested common subsequence is \( G T T G \) given by \( 2\text{Match}(4,1) \) and \( 2\text{Match}(7,5) \). The prefix \( A[1..3] \) has 3 insertions that occur before the first \( 2\text{Match} \). Between both \( 2\text{Matches} \), sequence \( A \) has a single symbol \( G \) and sequence \( B \) has two symbols \( T \ G \). Although \( G \) appears in both sequences, it is considered as a substitution error due to the fact that \( k = 2 \), forcing a substitution and deletion errors. After the last \( 2\text{Match} \), \( B \) has additional two symbols, implying two insertion errors in \( A \). All in all, we have ED\( k(A, B) = 7 \).

Such a definition may be more accurate than the known edit distance when we do not allow changes to occur at every odd location for example. Instead, we
would like them to be distributed on the inputs, forcing some $k$-length substrings be identical allowing no edit operation in these substrings. The $ED_k$ is related to $LCS_k$ as the $ED$ is related to $LCS$. This is stated in the following observation.

**Observation 1** In case the allowed edit operations are insertions and deletions,

$$ED_k(A, B) = |A| + |B| - 2k \cdot LCS_k(A, B).$$

In spite of Observation 1, the $ED_k$ cannot be easily found based on finding an $LCS_k$ solution, because the substitution operation is usually used so different longest common subsequences in $k$-length substrings may define different number of required edit operations to transform one input into the other. To see this, consider the $LCS_2$ for the sequences appearing in Figure 1. The maximal number of 2 matchings between the inputs is two, however there are several options to select these 2 matchings, two of which appear in Figure 4. The upper option refers to 2 matchings $(5, 3)$ and $(7, 5)$ implying edit distance of 6, including 2 substitution operations. The lower option of considering $(1, 3)$ and $(7, 5)$ yielding 8 required edit operations. Consequently, finding a specific $LCS_k$ solution does not guarantee an optimal sequence of edit operations giving the optimal $ED_k$ distance and a separate dynamic programming for the $ED_k$ is in order.

![Fig. 4. 2 options for LCSk and the EDk derived](image)

### 4.1 Solving the $ED_k$ Problem

We suggest solving the $ED_k$ problem using dynamic programming, similarly to the original Edit Distance problem, with the required modifications. Entry $ED_k[i, j]$ contains the score of the edit distance in $k$ length substrings of the prefixes $A[1...i]$ and $B[1...j]$. The score of $ED_k[i, j]$ minimizes the number of edit operations required so far, taking into account all three edit operations. If we encounter $a_i$ not matching $b_j$, it means a required insertion or deletion of $a_i$ or a substitution operation. In the other case of $a_i = b_j$, we need to verify that a $k$ matching ends at $(i, j)$ in order to declare a $k$ length common substring requiring no edit operation. This can be easily ascertained by comparing $dcount[i, j]$ with $k$. 
According to Definition 7, unedited symbols should form a legal LCS\(_k\). Hence, it is necessary to verify that no two overlapping \( k \) matchings are left unedited. Naturally, \( EDk[i, 0] = i \) and \( EDk[0, j] = j \). Lemma 4 below formally describes the computation of \( EDk[i, j] \).

**Lemma 4** The ED\(_k\) Recursive Rule.

\[
EDk[i, j] = \min\left\{ \begin{array}{ll}
EDk[i - 1, j] + 1 & \text{if } dcount[i, j] \geq k \\
EDk[i, j - 1] + 1 & \text{if } dcount[i, j] < k \\
EDk[i - k, j - k] & \text{if } dcount[i, j] \geq k \\
EDk[i - 1, j - 1] + 1 & \text{if } dcount[i, j] < k
\end{array} \right.
\]

**Proof.** \( EDk[i, j] \) contains the minimal number of edit operations required in order to transform sequence \( A \) into sequence \( B \), with respect to \( k \) length sub-strings, preserving their order in the input sequences. The \( EDk[i, j] \) is obtained by minimizing the score due to all possible edit operations:

1. Considering \( a_i \) as a deleted symbol, implies increment of \( EDk[i - 1, j] \).
2. Considering \( b_j \) as a redundant symbol, hence an insertion in the \( A \) sequence is in order, implies increment of \( EDk[i, j - 1] \).
3. Considering \( a_i \) and \( b_j \) as the last matching symbols of a \( k \) matching or part of a substitution. Note that the same case holds for \( a_i \neq b_j \) and \( a_i = b_j \) if the equal symbols are part of a different \( k \) matching or a shorter matching due to the problem and the table entries definitions. We distinguish between these options by comparing \( dcount[i, j] \) with \( k \).
   
   (a) The case of \( a_i \) and \( b_j \) are the last matching symbols of a \( k \) matching implies \( dcount[i, j] \geq k \) as \( (i - k + 1, j - k + 1) \) is a common \( k \) length substring. Therefore, no increase to the previously computed score is required. Nevertheless, due to the necessity to avoid overlaps between \( k \) matchings, when \( (i - k + 1, j - k + 1) \) is a \( k \) matching, the \( EDk \) computation must verify that previous score does not take into account an overlapping \( k \) matching. Therefore, we consider \( EDk[i - k, j - k] \) referring to the minimal number of required edit operations when the last \( k \) matching can end by matching at most \( a_{i-k} \) with \( b_{j-k} \).
   
   (b) For the case of \( dcount[i, j] < k \), as there is no \( k \) matching ending at \( a_i \) and \( b_j \), we have a single substitution error. Consequently, there is no restriction on the ending of a previous \( k \) matching, as no overlap can occur at these indices, so we increment the score of \( EDk[i - 1, j - 1] \).

These claims can be easily proven by induction.

Note that as every symbol of the inputs is either part of a \( k \) matching or it represents an edit error, as a consequence, the minimization of the \( EDk \) scores avoiding overlaps between \( k \) matchings also maximizes the number of \( k \) length common substrings.

**Example.** Figure 4.1 depicts an ED2 table. We demonstrate all possible cases in the process of obtaining a minimal score.
1. Considering $ED2[6, 2]$, the minimal value that can be obtained is 4, by incrementing $ED2[5, 2]$

2. Considering $ED2[4, 7]$, the minimal value that can be obtained is 3, by incrementing $ED2[4, 6]$

3. (a) Considering $ED2[4, 5]$, we see $dcount[4, 5] = 3 > 2$ implying a 2 matching $(3, 4)$ (GC) ends by matching $a_4$ with $b_3$. In order to avoid overlaps, we use the score of $ED2[2, 3]$. This value is smaller than the other possible values in this entry.

(b) Considering $ED2[3, 3]$, we see $dcount[3, 3] = 0$ implying no 2 matching ends by matching $a_3$ with $b_3$. With no overlaps to avoid, we increment the score of $ED2[2, 2]$. The obtained value is smaller than the other possible values in this entry.

**Fig. 5.** An ED2 Table. The numbers represent the minimal number of required edit operations. The diagonal counter $dcount$ is denoted by $dc$.

**Theorem 2** The $EDk(A, B)$ problem can be solved in $O(nm)$ time and $O(km)$ space, where $m$, $n$ are the lengths of the input sequences $A$ and $B$ respectively. Backtracking the solution requires time of $O(EDk(A, B) + \ell)$ where $EDk(A, B)$ is the optimal score and $\ell$ is the number of $k$ matchings considered in the solution, and $O(nm)$ space.

**Proof.** Similarly to the proof of Theorem 1, we fill a table of size $nm$. Each entry is filled according to Lemma 4 by performing a constant number of comparisons.
The computation of the diagonal count $dcount[i, j]$ requires a constant time as well as appears in Definition 5. Hence, $O(nm)$ time is required for computing the optimal number of edit operations with respect to the longest common subsequence in $k$ length substrings.

In case we want to find selected edit operations and a common subsequence in $k$ length substrings suitable to the optimal $EDk$ score, we need to save at each table entry the indices of the entry from which the minimal score was deduced. Having this information, we start the backtracking from $EDk[n, m]$ and report an operation according to the indices saves there: $[n - 1, m]$ imply a deletion, $[n, m - 1]$ imply insertion, $[n - 1, m - 1]$ refer to substitution and $[n - k, m - k]$ stand for a $k$ matching. We repeat the process with the $EDk[f, g]$ where $[f, g]$ are the indices saved at the previous entry until $f = 0$ or $g = 0$. All in all, every edit operation and $k$ matching requires a constant time backtrack, yielding $O(EDk(A, B) + \ell)$ time requirement for the backtracking process. Note that this time is bounded by the maximal number of edit operation which is $\max\{n, m\}$.

Regarding space: Each of the $nm$ entries contains a constant number of values. Nevertheless, due to Lemma 4, during the computation of $EDk[i, j]$ we need only $k$ rows backwards. As a consequence, at each step we save $O(k)$ rows implying the space requirement is $O(km)$. In order to backtrack the solution, the whole table is needed, yielding $O(nm)$ space requirement.

5 Conclusion

In this paper we defined a generalization of the LCS problem, where each matching must consist of $k$ consecutive symbols, and by thoroughly understanding the traits of the problem proved an algorithm with the same time complexity as the special case of LCS can solve the generalized problem. We also considered an adequate complementary edit distance measure and showed similar results hold also for this distance measure. As we consider the LCS$^k$ as a more accurate sequence similarity measure, we believe this problem should also be studied for generalized sequences, such as weighted sequences [2]. Other ways for changing the traditional LCS definition to obtain more accurate similarity measures may also be suggested.

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