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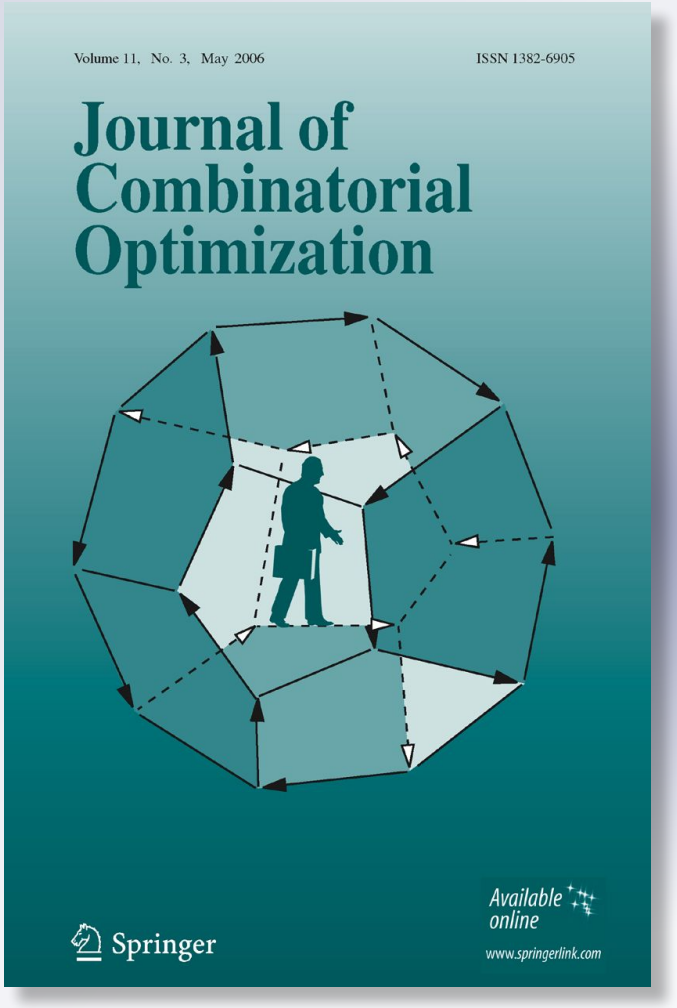


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# Exact and approximation algorithms for the complementary maximal strip recovery problem

**Haitao Jiang · Zhong Li · Guohui Lin · Lusheng Wang · Binhai Zhu**

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**Abstract** Given two genomic maps $G_1$ and $G_2$ each represented as a sequence of $n$ gene markers, the *maximal strip recovery* (MSR) problem is to retain the maximum number of markers in both $G_1$ and $G_2$ such that the resultant subsequences, denoted as $G_1^*$ and $G_2^*$, can be partitioned into the same set of maximal substrings of length greater than or equal to two. Such substrings can occur in the reversal and negated form. The *complementary* maximal strip recovery (CMSR) problem is to delete the minimum number of markers from both $G_1$ and $G_2$ for the same purpose, with its optimization goal exactly complementary to maximizing the total number of gene markers retained in the final maximal substrings. Both MSR and CMSR have been shown NP-hard and APX-hard. A 4-approximation algorithm is known for the MSR problem, but no constant ratio approximation algorithm for CMSR. In this paper, we present an $O(3^k n^2)$-time fixed-parameter tractable (FPT) algorithm, where $k$ is the size of the optimal solution, and a 3-approximation algorithm for the CMSR problem.

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## 1 Introduction

In comparative genomics, one of the first steps is to decompose two given genomes into synthetic blocks—segments of chromosomes that are deemed homologous in the two input genomes. Many decomposition methods have been proposed, but they are very vulnerable to ambiguities and errors. A few years back, the *maximal strip recovery* (MSR) problem was formulated for eliminating noise and ambiguities in genomic maps, which are isolated points that do not co-exist with other points (Choi et al. 2007; Zheng et al. 2007). In the more precise formulation, we are given two genomic maps $G_1$ and $G_2$ each represented as a sequence of $n$ distinct gene markers, and we want to retain the maximum number of markers in both $G_1$ and $G_2$ such that the resultant subsequences, denoted as $G_1^*$ and $G_2^*$, can be partitioned into the same set of maximal substrings of length greater than or equal to two. Each retained marker thus belongs to exactly one of these substrings, which can appear in the reversed and negated form and are taken as nontrivial chromosomal segments. The deleted markers are regarded as noise or errors.

The MSR problem, and its several close variants, have been shown NP-hard (Wang and Zhu 2010; Bulteau et al. 2009; Chen et al. 2009). More recently, it is shown to be APX-complete (Bulteau et al. 2009; Jiang 2009), admitting a 4-approximation algorithm (Chen et al. 2009). This approximation algorithm is a modification of an earlier heuristics for computing a maximum clique (and its complement, a maximum independent set) (Choi et al. 2007; Zheng et al. 2007), to convert the MSR problem to computing the maximum independent set in $t$-interval graphs, which admits a $2t$-approximation (Bar-Yehuda et al. 2006; Chen et al. 2009). In this paper, we investigate the complementary optimization goal to minimize the number of deleted markers—the *complementary MSR* problem, or CMSR for short. CMSR is certainly NP-hard, and was proven to be APX-hard recently (Jiang 2010). Nevertheless, there is no known constant ratio approximation algorithm. We present here an $O(3^k n^2)$-time exact bounded search tree algorithm for the problem, where $k$ is the size of the optimal solution, and a 3-approximation algorithm. We want to point out that, a short fixed-parameter tractable (FPT) algorithm was proposed in (Wang and Zhu 2010) based on an incorrect lemma, which is corrected in this paper as Lemma 1. This lemma is also useful in our FPT algorithm and the approximation algorithm.

In the sequel, we use a lower case letter to denote a gene marker. A negation sign together with the succeeding gene indicate that the gene is in its reversal and negated form. We reserve the dot symbol for connection use, for example, $a \cdot b$ means gene $b$ comes directly after gene $a$. When a common substring (also called *strip*, or *synthetic block*) of $G_1$ and $G_2$ is identified, we will (often) label it using a capital letter. We abuse this capital letter a bit to also denote the set of genes in the substring.

The rest of the paper is organized as follows. In Sect. 2, we present some structural properties of the optimal solutions to the CMSR problem, which will be used in the

design of the FPT algorithm, presented in Sect. 3, and the design and the worst-case performance analysis of the 3-approximation algorithm, presented in Sect. 4. We conclude the paper with a few open questions in Sect. 5.

## 2 Structural properties of the CMSR problem

We first look at an example instance of the CMSR problem (also an instance of the MSR problem), in which $G_1 = \langle a, b, c, d, e, f, g, h, i, j, k, \ell \rangle$ and $G_2 = \langle -i, -d, -g, -f, h, a, c, b, -\ell, -k, -j, -e \rangle$ (we use commas to separate the gene markers for easier reading). By deleting markers $c$, $d$, $e$, and $h$ from both $G_1$ and $G_2$, the resultant subsequences are $G_1^* = \langle a, b, f, g, i, j, k, \ell \rangle$ and $G_2^* = \langle -i, -g, -f, a, b, -\ell, -k, -j \rangle$. These two resultant subsequences can be decomposed into three maximal substrings $S_1 = a \cdot b$, $S_2 = f \cdot g \cdot i$ (appearing in the reversal and negated form in $G_2^*$), and $S_3 = j \cdot k \cdot \ell$ (appearing in the reversal and negated form in $G_2^*$). For this small instance, one can prove that the optimal solution to the MSR problem has size 8, and (consequently) the optimal solution to the CMSR problem has size 4.

Given any instance, in at most quadratic time, we can determine all maximal common substrings in $G_1$ and $G_2$. Note that the quadratic time could be improved to a linear time, with proper data structure such as suffix-tree. Note also that a substring and its reversed negated form are considered identical. Every letter in $G_1$ occurs in exactly one of these substrings. Some of these substrings have length greater than or equal to two, called *type-0* substrings; the others have length one, called *isolates*.

An optimal solution $OPT$ to the instance (of the CMSR problem) is a minimum-size subset of letters that, deleting them from $G_1$ and $G_2$ gives the remainder subsequences denoted $G_1^*$ and $G_2^*$, respectively, which can be partitioned into maximal substrings of length at least 2.

**Lemma 1** *There exists an optimal solution OPT to the instance, such that*

(1) *for each type-0 substring* $S$, *either* $S \subset OPT$ *or* $S \cap OPT = \emptyset$;
(2) *if* $|S| \geq 4$, *then* $S \cap OPT = \emptyset$.

*Proof* Let $OPT$ be an optimal solution. For a type-0 substring $S$, assume to the contrary that some but not all of its letters are in $OPT$. We know that the letters of $S - OPT$ appear consecutively in both $G_1^*$ and $G_2^*$, and they form or participate in a single maximal substring, denoted as $T$. We may put letters of $S \cap OPT$ back to $G_1^*$ and $G_2^*$ according to their positions in $G_1$ and $G_2$, respectively. These letters do not break but participate in the maximal substring $T$. This contradicts the optimality of $OPT$. Therefore, either $S \subset OPT$, or $S \cap OPT = \emptyset$.

If $S$ has length of 4 or greater and $S \subset OPT$, we again put the letters of $S$ back to $G_1^*$ and $G_2^*$ according to their positions in $G_1$ and $G_2$, respectively. This added $S$, as a consecutive segment, might break into maximal substrings of $G_1^*$ and $G_2^*$ to give rise to at most 4 distinct letters that no longer belong to any maximal substrings of length at least 2. Since $S$ becomes a (or part of a) maximal common substring, we can delete the (at least 4) letters of $S$ from $OPT$ while adding to $OPT$ the (at most 4) letters that

fall out of maximal substrings of length at least 2. The added letters certainly do not belong to any type-0 substrings. Therefore, this letter-swapping process gives another optimal solution that contains one less type-0 substring of length at least 4. Repeating the same argument if necessary, at the end we will achieve an optimal solution that do not contain any type-0 substring of length at least 4. □

Lemma 1 fixes an erroneous claim made in Wang and Zhu (2010), that *OPT* contains no type-0 substrings.

## 3 An exact bounded search tree algorithm

In this section, we consider solving CMSR with an FPT algorithm (Downey and Fellows 1999). Basically, an FPT algorithm for a decision problem $\Pi$ on whether or not there exists a solution of value (in our case, at most) $k$ is an algorithm that solves the problem in $O(f(k)n^c) = O^*(f(k))$ time, where $f(\cdot)$ is any function only on $k$, $n$ is the input size, and $c$ is some fixed constant not related to $k$.

Given any instance, in the FPT algorithm to be described, it first determines all type-0 substrings. By Lemma 1, it will never delete any letter of those type-0 substrings of length at least 4 (*i.e.*, they are all retained in $G_1^*$ and $G_2^*$). Some of these substrings, however, might get extended by appending other letters, or merge into longer final maximal common substrings of $G_1^*$ and $G_2^*$. Also by Lemma 1, in the sequel the algorithm considers maximal substrings of $G_1$ and $G_2$ as single units. For ease of presentation, all the type-0 substrings of length at least 4 are *marked*. The unmarked units are thus length-3 and length-2 type-0 substrings, and isolates. The FPT algorithm considers an isolate; it either deletes it from $G_1$ and $G_2$, or marks it as retained in (the final) $G_1^*$ and $G_2^*$ by deleting some other unmarked units from $G_1$ and $G_2$. In either case, a smaller instance is generated with the target solution value decreased by at least 1. The FPT algorithm recursively works on the smaller instances, with the terminating instances containing no isolates.

The FPT algorithm examines $G_1$ from head to tail (from left to right) to locate the first isolate, denoted as $u$. If there is none, then the algorithm terminates and it marks all unmarked units. Note that $u$ might not be the first unmarked unit in $G_1$, neither the first isolate in $G_2$. Note also that $u$ has to have an adjacent companion to stay together in a maximal common substring of $G_1^*$ and $G_2^*$. Let $P_1$ denote the rightmost marked unit to the left of $u$ in $G_1$, if exists; let $S_1$ denote the leftmost marked unit to the right of $u$ in $G_1$, if exists. By Lemma 1, this companion has to be the last letter of $P_1$, or the first letter of $S_1$, or some unmarked unit in between $P_1$ and $S_1$.

**Lemma 2** *If isolate $u$ is retained in the final $G_1^*$ and $G_2^*$, then at least one unmarked unit must be deleted.*

*Proof* Let $P_2$ denote the rightmost marked unit to the left of $u$ in $G_2$, if exists; let $S_2$ denote the leftmost marked unit to the right of $u$ in $G_2$, if exists (Fig. 1). We consider the following three cases.

In the first case, the adjacent companion of isolate $u$ to stay together in a maximal common substring of $G_1^*$ and $G_2^*$ is the last letter of $P_1$. It follows that $P_1$ and $P_2$

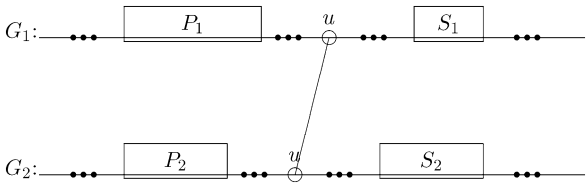


**Fig. 1** The local configuration at isolate $u$

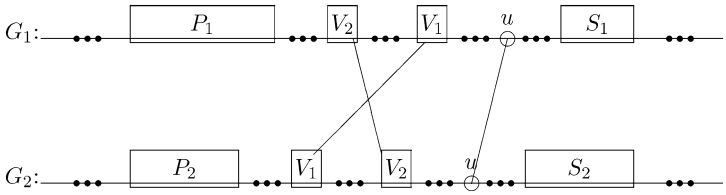


**Fig. 2** Searching for $V_1$ and $V_2$ to the left of isolate $u$

are identical. If there are letters in between $P_1$ and $u$ in $G_1$, the lemma is proved. Otherwise, $P_1 \cdot u$ is a substring of $G_1$. Similarly, if there are letters in between $P_2$ and $u$ in $G_2$, the lemma is proved. Otherwise, $P_2 \cdot u$ is a substring of $G_2$. This is a contradiction to the assumption that $u$ is an isolate.

In the second case, the adjacent companion of isolate $u$ to stay together in a maximal common substring of $G_1^*$ and $G_2^*$ is the first letter of $S_1$. This case can be similarly argued as in the first case.

In the last case, the adjacent companion of isolate $u$ to stay together in a maximal common substring of $G_1^*$ and $G_2^*$ is some unmarked unit, denoted as $V$, in between $P_1$ and $S_1$ in $G_1$. $V$ has to be in between $P_2$ and $S_2$ in $G_2$. Assume without loss of generality that $u$ appears to the left of $V$ in $G_1$. Then, $u$ also appears to the left of $V$ in $G_2$ (or $-u$ appears to the right of $-V$ in $G_2$). There must be some letters in between $u$ and $V$ in $G_1$ or in $G_2$, otherwise contradicting to the assumption $u$ is an isolate. These letters are not retained in $G_1^*$ and $G_2^*$. □

The key step in the FPT algorithm is to locate this adjacent companion of isolate $u$, if it is retained. The search process goes as follows. Compatible to the proof of Lemma 2, the algorithm scans from isolate $u$ to the left in $G_1$ to locate the first unit $V_1$ that also appears to the left of $u$ but not passing $P_2$ in $G_2$, if exists. This $V_1$ can be an unmarked unit, can also be $P_1$ (and thus $P_2$), but not to the left of $P_1$. The intention is that, if indeed the adjacent companion of isolate $u$ as described in Lemma 2 is to the left of $u$, then either it is $V_1$, or otherwise $V_1$ has to be deleted. Likewise, the algorithm scans from isolate $u$ to the left in $G_2$ to locate the first unit $V_2$ that also appears to the left of $u$ but not passing $P_1$ in $G_1$, if exists. Similarly, this $V_2$ can be an unmarked unit, can also be $P_2$ (and thus $P_1$), but not to the left of $P_2$.

Note that $V_1$ exists if and only if $V_2$ exists, since $V_1$ is a candidate when searching for $V_2$ and vice versus (Fig. 2). In Case L1, $V_1$ and $V_2$ are identical; thus firstly there must be some unmarked units in between $V_1$ and $u$ in either $G_1$ or $G_2$; and secondly the algorithm deletes these units to generate an instance of solution value $k' \leq k-1$, since at least a letter is deleted. In Case L2, $V_1$ and $V_2$ are different; thus they are

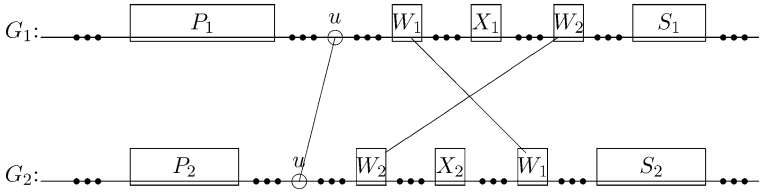


**Fig. 3** Searching for $W_1$, $W_2$, $X_1$, and $X_2$ to the right of isolate $u$

unmarked and they cannot co-exist in $G_1^*$ and $G_2^*$; let $A_1$ denote the set of letters in between $V_1$ and $u$ (including $V_1$) in $G_1$, and $A_2$ denote the set of letters in between $V_2$ and $u$ (including $V_2$) in $G_2$, then the algorithm deletes either all the letters of $A_1$ or all the letters of $A_2$ to generate two instances of solution value $k' \leq k-2$, since $|A_1|, |A_2| \geq 2$.

The algorithm also needs to explore to the right of isolate $u$ if the adjacent companion of isolate $u$ as described in Lemma 2 is to the right of $u$, and we use $W_1$ and $W_2$ to denote the counterparts (Fig. 3). First of all, if $V_1/V_2$ do not exist, then $W_1/W_2$ must exist for otherwise isolate $u$ has to be deleted. In Case R1, $W_1$ and $W_2$ are identical; then similarly there must be some unmarked units in between $u$ and $W_1$ in either $G_1$ or $G_2$; and the algorithm deletes these units to generate an instance of solution value $k' \leq k-1$. In the other case, $W_1$ and $W_2$ are different; let $B_1$ denote the set of letters in between $u$ and $W_1$ (including $W_1$) in $G_1$, and $B_2$ denote the set of letters in between $u$ and $W_2$ (including $W_2$) in $G_2$.

If $|B_1| = 1$, then $W_1$ is an isolate; the algorithm proceeds to scan from isolate $W_1$ further to the right in $G_1$ to locate the first unmarked unit $X_1$ that also appears to the right of $u$ in $G_2$. Since $W_2$ is a candidate for $X_1$, we conclude that such $X_1$ exists in between $W_1$ and $W_2$, or it is $W_2$. In Case R2, $X_1$ sits to the left of $W_1$ in $G_2$ and there are no units in between $W_1$ and $X_1$ in $G_1$; the algorithm deletes $W_1$ to generate an instance of solution value $k' = k-1$. The reason is that if $W_1$ is retained in $G_1^*$ and $G_2^*$, one can always delete it and add back $X_1$ to have another optimal solution. In the other case, if there are no units in between $W_1$ and $X_1$ in $G_1$, then $X_1$ must sit to the right of $W_1$ in $G_2$, and the algorithm adds the letters of $X_1$ to $B_1$; if $X_1$ sits to the left of $W_1$ in $G_2$, then there must be some units in between $W_1$ and $X_1$ in $G_1$, and the algorithm adds these units into $B_1$. By such an adding process, $B_1$ contains at least two letters.

If $|B_2| = 1$, the algorithm does exactly the same procedure, either falling into Case R2 to delete $W_2$ and generate an instance of solution value $k' = k-1$, or adding at least one extra letter to $B_2$.

Consequently, in the remaining case (Case R3), the algorithm faces with two sets $B_1$ and $B_2$, both of size at least 2. Due to the fact that none of the letters of $B_1$ can co-exist with any letter of $B_2$, the algorithm deletes either all the letters of $B_1$ or all the letters of $B_2$ to generate two instances of solution value $k' \leq k-2$, since $|B_1|, |B_2| \geq 2$.

Let $f(k)$ be the number of smaller instances that are solved for assembling an optimal solution to the instance of solution value $k$. The above analysis states that the

following recurrence holds.

$$f(k) \leq \begin{cases} f(k-1), & \text{if } u \text{ is deleted;} \\ +\max \begin{cases} O(1), & \text{if } u \text{ is kept and } V_1/V_2 \text{ do not exist;} \\ f(k-1), & \text{if } u \text{ is kept and falls into Case L1;} \\ 2f(k-2), & \text{if } u \text{ is kept and falls into Case L2;} \end{cases} \\ +\max \begin{cases} O(1), & \text{if } u \text{ is kept, } V_1/V_2 \text{ exist, but } W_1/W_2 \text{ do not exist;} \\ f(k-1), & \text{if } u \text{ is kept and falls into Case R1;} \\ f(k-1), & \text{if } u \text{ is kept and falls into Case R2;} \\ 2f(k-2), & \text{if } u \text{ is kept and falls into Case R3.} \end{cases} \end{cases}$$

Solving this recurrence gives us $f(k) \leq 3^k$. Since the preprocessing to determine all maximal common substrings of $G_1$ and $G_2$ needs at most quadratic time, so does the scanning process for isolate $u$, $V_1$, $V_2$, $W_1$, $W_2$, $X_1$ and $X_2$, if necessary and if they exist, the total running time of the FPT algorithm is $O(3^k n^2) = O^*(3^k)$. A high-level description of the algorithm is in Fig. 4. Therefore, we have proved the following theorem.

**Theorem 3** *The CMSR problem can be solved in $O(3^k n^2)$ time, where $n$ is the number of gene markers, $k$ is the minimum number of gene markers such that deleting them from the genomic maps partitions the remainder maps into a common set of synthetic blocks of size at least two.*

## 4 A 3-approximation algorithm

From Lemma 1, all type-0 substrings of length 4 and greater are retained in our approximation algorithm to be presented next. The output of our algorithm will be compared against an optimal solution *OPT* which also retains all these substrings. In the following, we only deal with length-3 and length-2 type-0 substrings, and isolates.

In the first step, our algorithm retains all length-3 and length-2 type-0 substrings. In the second step, our algorithm recursively removes one isolate; such a removed isolate has to satisfy the condition (C) listed in the following, with the goal that removing it from (the current) $G_1$ and $G_2$ gives rise to (at least) a new common substring of length 2. This new common substring is not a common substring to the original $G_1$ and $G_2$, and is called a type-1 substring for distinction purpose. Note that after such isolate removal, some units (type-0 and/or type-1 substrings, and/or isolates) might be able to be merged into longer maximal common substrings. For consistency purpose, we do not merge two existing substrings; but we will append isolates to existing substrings (type-0 or type-1) whenever possible, since our goal is to get rid of isolates. These appended isolates become no longer isolates, and the extended substrings keep their type (type-0 or type-1).

The isolate chosen to be removed by our algorithm has to satisfy the following condition (C). When none can be identified, the algorithm enters the last step to remove all the remaining isolates, if any. Denote this target isolate as $u$.

Input: two sequences (permutations) $G_1$ and $G_2$ on $n$ letters, parameter $k$.
Output: a set of $k$ letters or less, removing which from the two sequences results in a partition into maximal common substrings of length at least 2.

1. Determines all type-0 substrings, and marks those of length 4 and greater;
2. Scans $G_1$ from head to tail (left to right) for the first isolate $u$;
   2.1. if no such $u$ found, return;
   2.2. sets "`flag off`";
3. Deletes $u$, and recursively calls on the remainder sequences with parameter $k-1$;
4. Scans in $G_1$ from $u$ to its left for $V_1$;
   4.1. if no such $V_1$ found, sets `flag on`;
   4.2. else scans in $G_2$ from $u$ to its left for $V_2$;
      4.2.1. if $V_1 = V_2$, executes Case L1;
      4.2.2. else executes Case L2;
5. Scans in $G_1$ from $u$ to its right for $W_1$;
   5.1. if no such $W_1$ found and `flag on`, return `false`;
   5.2. else if no such $W_1$ found, return;
   5.3. else scans in $G_2$ from $u$ to its right for $W_2$;
      5.3.1. if $W_1 = W_2$, executes Case R1;
      5.3.2. else
         5.3.2.1. lets $B_1$ be the set of letters from $u$ up to $W_1$ in $G_1$, including $W_1$; lets $B_2$ be the set of letters from $u$ up to $W_2$ in $G_2$, including $W_2$;
         5.3.2.2. if $|B_1| = 1$, scans in $G_1$ from $W_1$ to its right for $X_1$;
            5.3.2.2.1. if no units in between $W_1$ and $X_1$ in $G_1$ and $X_1$ is to the left of $W_1$ in $G_2$, executes Case R2;
            5.3.2.2.2. else if no units in between $W_1$ and $X_1$ in $G_1$, then adds the letters of $X_1$ to $B_1$;
            5.3.2.2.3. else if $X_1$ is to the left of $W_1$ in $G_2$, then adds the letters in between $W_1$ and $X_1$ in $G_1$ to $B_1$;
         5.3.2.3. if $|B_2| = 1$, scans in $G_2$ from $W_2$ to its right for $X_2$;
            5.3.2.3.1. if no units in between $W_2$ and $X_2$ in $G_2$ and $X_2$ is to the left of $W_2$ in $G_1$, executes Case R2;
            5.3.2.3.2. else if no units in between $W_2$ and $X_2$ in $G_2$, then adds the letters of $X_2$ to $B_2$;
            5.3.2.3.3. else if $X_2$ is to the left of $W_2$ in $G_1$, then adds the letters in between $W_2$ and $X_2$ in $G_2$ to $B_2$;
         5.3.2.4. executes Case R3;

**Fig. 4** A high-level description of the FPT algorithm for the CMSR problem

(C) In either $G_1$ or $G_2$, two neighboring units of $u$ are also isolates; and after removing $u$, they form into a type-1 common substring of length 2.

It could be the case that in both $G_1$ and $G_2$, the two neighboring units of $u$ form into a type-1 common substring of length 2 after deleting $u$; our algorithm will identify the case and subsequently all these isolates become no longer isolates. There is another (disjoint) case in which, besides forming the type-1 common substring of length 2, another neighboring isolate of $u$ in different sequence can be appended to an existing, or the newly formed, substring; our algorithm will identify this case too

and subsequently the appended isolate becomes no longer an isolate. Intuitively, removing isolate $u$ saves (*i.e.*, retains) at least two other isolates, and can save one or two more isolates.

For ease of discussion, let $U = \{u_1, u_2, \ldots, u_m\}$ denote the set of isolates located in sequential order by our algorithm, which are all removed. Associated with each $u_j$, let $V_j$ denote the set of neighboring isolates of $u_j$ in the current $G_1$ and $G_2$ that become no longer isolates after removing $u_j$. We have $|V_j| \geq 2$, for $j = 1, 2, \ldots, m$. In particular, the two neighboring isolates of $u_j$ that form a type-1 substring after deleting $u_j$ are denoted as $a_j$ and $b_j$ (where there are two such pairs, $a_j$ and $b_j$ refer to an arbitrary one of them). Let $R$ denote the set of remaining isolates at the time the algorithm finds no isolates satisfying condition (C); that is, $R$ is the set of isolates deleted by our algorithm at the last step. The following two lemmas state some preliminary observations.

**Lemma 4** *The set of all isolates $I$ is the union of the disjoint sets $U, V_1, V_2, \ldots, V_m$, and $R$, that is, $I = U \cup \left(\bigcup_{j=1}^{m} V_j\right) \cup R$; moreover, the algorithm deletes all isolates of $U \cup R$, but no others.*

**Lemma 5** *In the original input sequences $G_1$ and $G_2$, the letters in between $a_j$ and $b_j$ all belong to $\{u_1, u_2, \ldots, u_{j-1}, u_j\}$; moreover, $u_j$ is in between $a_j$ and $b_j$ in exactly one of $G_1$ and $G_2$.*

Recall that we use in the discussion an optimal solution *OPT* which satisfies the two properties listed in Lemma 1. We partition *OPT* into a subset $O_3$ of length-3 type-0 substrings, a subset $O_2$ of length-2 type-0 substrings, and a subset $O_1$ of isolates: $OPT = O_3 \cup O_2 \cup O_1$. These substrings and isolates are referred to as units in the sequel. Consider the inverse process of deleting units of *OPT* from $G_1$ and $G_2$ to obtain the final sequences $G_1^*$ and $G_2^*$. In this inverse process, we add the units of *OPT* back to $G_1^*$ and $G_2^*$ using their original positions in $G_1$ and $G_2$ to re-construct $G_1$ and $G_2$. At the beginning of this process, there are no isolated letters in $G_1^*$ or $G_2^*$; all the isolates of $I$ are thus either units of $I \cap O_1$, or *generated* by inserting units of *OPT* back, which break the maximal common substrings into fragments of which some are single letters. At any time of the process, inserting one unit of *OPT* back to the current $G_1$ and $G_2$ can generate at most four fragments of single letters, since in the worst case two current length-2 substrings can be broken into four such fragments. Some of these single letters might not be the isolates of $U \cup R$; those that are in $U \cup R$, as well as the inserted unit when it belongs to $(U \cup R) \cap O_1$, are said to be associated with the inserted unit of *OPT*. We firstly insert units of $O_3$ and $O_2$, one by one; each of them is associated with at most four isolates of $U \cup R$ (Lemma 6); the resultant sequences are denoted as $G_1^0$ and $G_2^0$.

**Lemma 6** *The number of isolates of $U \cup R$ associated with each unit of $O_3 \cup O_2$ is at most four.*

Next, we insert isolates of $O_1 \cap (u_j \cup V_j)$ back into $G_1^0$ and $G_2^0$, for $j = 1, 2, \ldots, m$ sequentially. At the end of the inserting isolates of $O_1 \cap (u_j \cup V_j)$, the resultant

sequences are denoted as $G_1^j$ and $G_2^j$. We emphasize that this sequential order is very important, as we need it in the proof of Lemma 8, which counts the average number of isolates of $U \cup R$ associated with each isolate of $O_1 \cap (u_j \cup V_j)$.

**Lemma 7** *For any $j$, $u_j$ is an isolated letter in $G_1^j$ and $G_2^j$.*

*Proof* We prove this lemma by (finite) induction. Firstly, we notice that $a_1, b_1$, and $u_1$ cannot co-exist in $G_1^*$ and $G_2^*$, since otherwise $u_1$ would be the only letter in between $a_1$ and $b_1$ in exactly one of $G_1^*$ and $G_2^*$, and thus an isolated letter. Therefore, $O_1 \cap (u_1 \cup V_1) \neq \emptyset$. After inserting isolates of $O_1 \cap (u_1 \cup V_1)$ back, $a_1, b_1$, and $u_1$ are all present in $G_1^1$ and $G_2^1$. For the same reason that $u_1$ is the only letter in between $a_1$ and $b_1$ in exactly one of $G_1^1$ and $G_2^1$, $u_1$ is an isolated letter. That is, the lemma holds for $j = 1$.

Assume the lemma holds for all $i = 1, 2, \ldots, j-1$, that is, $u_1, u_2, \ldots, u_{j-1}$ are isolated letters in $G_1^{j-1}$ and $G_2^{j-1}$, and thus they are all isolated letters in $G_1^j$ and $G_2^j$. Due to the co-existence of $a_j, b_j$, and $u_j$ in $G_1^j$ and $G_2^j$, Lemma 5 tells that if $u_j$ is not an isolated letter, then it can only pair with some letter of $\{u_1, u_2, \ldots, u_{j-1}\}$ to sit together in a substring. This is a contradiction to the inductive assumption. Therefore, $u_j$ is an isolated letter in $G_1^j$ and $G_2^j$. □

**Lemma 8** *For any $j$, the average number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most* 2.5. *Moreover, by the end of this iteration of inserting process, $u_j$ is associated to some unit of OPT.*

*Proof* Recall that we insert isolates of $O_1 \cap (u_j \cup V_j)$ back into $G_1^0$ and $G_2^0$ in sequential order of $j$. When we start to insert isolates of $O_1 \cap (u_j \cup V_j)$, all isolates of $O_1 \cap \left(\bigcup_{i=1}^{j-1} u_i \cup V_i\right)$ have been inserted and the resultant sequences are $G_1^{j-1}$ and $G_2^{j-1}$.

Firstly, if $O_1 \cap (u_j \cup V_j) = \emptyset$, then the lemma is proved automatically. So we assume in the following that $O_1 \cap (u_j \cup V_j) \neq \emptyset$. Let $a_j$ and $b_j$ be the two neighboring isolates of $u_j$ when the approximation algorithm located $u_j$, as in Lemma 5, such that by removing $u_j$, $a_j \cdot b_j$ became a type-1 length-2 substring. We consider the following two disjoint cases: $u_j \in O_1$ and $u_j \notin O_1$.

In the first case, $u_j \in O_1$. When $a_j, b_j \in O_1$ and $a_j$ and $b_j$ are separated by certain letters of $\{u_1, u_2, \ldots, u_{j-1}\}$ in $G_1$ ($G_2$, respectively), inserting $a_j$ and $b_j$ into $G_1^{j-1}$ ($G_2^{j-1}$, respectively) does not generate any new isolates of $U \cup R$; when $a_j, b_j \in O_1$ and $a_j$ and $b_j$ are separated by no letters of $\{u_1, u_2, \ldots, u_{j-1}\}$ in $G_1$ ($G_2$, respectively), inserting $a_j$ and $b_j$ into $G_1^{j-1}$ ($G_2^{j-1}$, respectively) can generate at most two isolates of $U \cup R$. When one and only one of $a_j$ and $b_j$ is in $O_1$, then inserting it into $G_1^{j-1}$ and $G_2^{j-1}$ does not generate any new isolates of $U \cup R$.

If $|V_j| = 4$, then the other two letters, $c_j$ and $d_j$, have the same properties as $a_j$ and $b_j$. When $|V_j \cap O_1| = 4$, that is, $a_j, b_j, c_j, d_j \in OPT$, inserting $a_j, b_j$ and $c_j, d_j$ can generate at most 8 new isolates of $U \cup R$. When $|V_j \cap O_1| = 3$, and assuming $a_j, b_j, c_j \in OPT$, inserting $a_j, b_j$ can generate at most 4 new isolates of $U \cup R$, but

inserting $c_j$ generates no new isolates of $U \cup R$. When $|V_j \cap O_1| = 2$, and in the first scenario assuming $a_j, b_j \in OPT$, inserting $a_j, b_j$ can generate at most 4 new isolates of $U \cup R$; in the second scenario assuming $a_j, c_j \in OPT$, inserting $a_j, c_j$ generates no new isolates of $U \cup R$. When $|V_j \cap O_1| = 1$, and assuming $a_j \in OPT$, inserting $a_j$ generates no new isolates of $U \cup R$. After inserting isolates of $O_1 \cap V_j$, if any, inserting $u_j$ back into the current $G_1^{j-1}$ and $G_2^{j-1}$ does not generate any new isolates of $U \cup R$. In summary, for $|O_1 \cap V_j| = 4, 3, 2, 1$, and 0, respectively, the total number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most 8, 4, 4, 0, and 0, respectively. It follows that the average number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most $8/5$.

If $|V_j| = 3$, then the third letter, $c_j$, was appended to an existing (type-0 or type-1) substring $S$ when the approximation algorithm removed $u_j$. Similarly to the discussion on $a_j$ and $b_j$, $c_j$ and $S$ can only be separated by letters of $\{u_1, u_2, \ldots, u_{j-1}\}$, besides $u_j$, in $G_1$ and $G_2$. Moreover, $u_j$ is in between $c_j$ and $S$ in at most one of $G_1$ and $G_2$. Therefore, when $c_j \in O_1$, inserting it into $G_1^{j-1}$ and $G_2^{j-1}$ can generate at most one new isolate of $U \cup R$. After inserting isolates of $O_1 \cap V_j$, if any, inserting $u_j$ back into the current $G_1^{j-1}$ and $G_2^{j-1}$ does not generate any new isolates of $U \cup R$. Therefore, for $|O_1 \cap V_j| = 3, 2, 1$, and 0, respectively, the total number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most 5, 4, 1, and 0, respectively. It follows that the average number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most $4/3$.

If $|V_j| = 2$, after inserting isolates of $O_1 \cap V_j$, if any, inserting $u_j$ back into the current $G_1^{j-1}$ and $G_2^{j-1}$ can generate at most two isolates of $U \cup R$. Therefore, for $|O_1 \cap V_j| = 2, 1$, and 0, respectively, the total number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most 6, 2, and 0, respectively. It follows that the average number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most 2.

In the second case, $u_j \notin O_1$. Assume without loss of generality that $u_j$ is in between $a_j$ and $b_j$ in $G_1$ in Lemma 5. When $a_j \in O_1$ ($b_j \in O_1$, respectively) and $a_j$ ($b_j$, respectively) and $u_j$ are separated by certain letters of $\{u_1, u_2, \ldots, u_{j-1}\}$ in $G_1$, inserting $a_j$ ($b_j$, respectively) into $G_1^{j-1}$ does not generate any new isolates of $U \cup R$. When $a_j \in O_1$ ($b_j \in O_1$, respectively) and $a_j$ ($b_j$, respectively) and $u_j$ are separated by no letters of $\{u_1, u_2, \ldots, u_{j-1}\}$ in $G_1$, inserting $a_j$ ($b_j$, respectively) into $G_1^{j-1}$ can generate at most two isolates of $U \cup R$, including $u_j$. Nonetheless, when $a_j, b_j \in O_1$ and $a_j$ and $b_j$ are separated by no letters of $\{u_1, u_2, \ldots, u_{j-1}\}$ in $G_1$, inserting $a_j$ and $b_j$ into $G_1^{j-1}$ can generate at most three isolates of $U \cup R$, including $u_j$. Similarly, when $a_j, b_j \in O_1$ and $a_j$ and $b_j$ are separated by certain letters of $\{u_1, u_2, \ldots, u_{j-1}\}$ in $G_2$, inserting $a_j$ and $b_j$ into $G_2^{j-1}$ does not generate any new isolates of $U \cup R$; when $a_j, b_j \in O_1$ and $a_j$ and $b_j$ are separated by no letters of $\{u_1, u_2, \ldots, u_{j-1}\}$ in $G_2$, inserting $a_j$ and $b_j$ into $G_2^{j-1}$ can generate at most two isolates of $U \cup R$.

If $|V_j| = 4$, then the other two letters, $c_j$ and $d_j$, have the same properties as $a_j$ and $b_j$. Note that when inserting $a_j$ and $b_j$ into $G_1^{j-1}$ generates new isolates of $U \cup R$, these isolates will be seen again when inserting $c_j$ and $d_j$ into $G_2^{j-1}$. Therefore, for $|O_1 \cap V_j| = 4, 3, 2, 1$, and 0, respectively, the total number of isolates of $U \cup R$

associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most 7, 4, 2, 0, and 0, respectively. It follows that the average number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most $7/4$.

If $|V_j| = 3$, then the third letter, $c_j$, was appended to an existing (type-0 or type-1) substring $S$ when the approximation algorithm removed $u_j$. Similarly to the discussion on $a_j$ and $b_j$, $c_j$ and $S$ can only be separated by letters of $\{u_1, u_2, \ldots, u_{j-1}\}$ in $G_1$ and $G_2$, besides $u_j$ in $G_2$. Therefore, when $c_j \in O_1$, inserting $c_j$ into $G_2^{j-1}$ can generate at most one new isolate of $U \cup R$, which will be seen when inserting $b_j$ into $G_1^{j-1}$. Note that $S$ might start with $a_j$ or end with $b_j$. For $|O_1 \cap V_j| = 3, 2, 1$, and 0, respectively, the total number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most 4, 2, 0, and 0, respectively. It follows that the average number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most $4/3$.

If $|V_j| = 2$, for $|O_1 \cap V_j| = 2$, 1, and 0, respectively, the total number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most 5, 2, and 0, respectively. It follows that the average number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ is at most $5/2$.

From the above case analysis, we conclude that the average number of isolates of $U \cup R$ associated with isolates of $O_1 \cap (u_j \cup V_j)$ in the worst case is $5/2 = 2.5$. This finishes the proof. □

Lastly, we insert isolates of $O_1 \cap R$ back into $G_1^m$ and $G_2^m$. At the end of this last inserting process, we achieve the input sequences $G_1$ and $G_2$.

**Lemma 9** *The average number of isolates of $U \cup R$ associated with isolates of $O_1 \cap R$ is at most* 3.

*Proof* The key fact used in the proof is that after locating isolate $u_m$, removing it from the current sequences, and making letters in $V_m$ non-isolates, the approximation algorithm finds no more isolates to iterate the process. That is, for any two remaining isolates $r, s \in R$ that are not separated by any existing (type-0 or type-1) substring in both sequences (that is, $r$ and $s$ can potentially form into a substring, or participate together), there are at least two other isolates, duplications are separately counted, in between them, counting from both sequences.

In sequences $G_1^m$ and $G_2^m$ obtained after inserting units of $O_3 \cup O_2 \cup (O_1 \cap (U \cup \bigcup_{j=1}^m V_j))$ into $G_1^*$ and $G_2^*$, some units of $R$ are already isolates, while the other reside in substrings (of length at least two). These units residing in substrings are to be singled out by inserting units of $O_1 \cap R$ into $G_1^m$ and $G_2^m$; and it is these units that are associated with isolates of $O_1 \cap R$.

Let $S_1, S_2, \ldots, S_k$ denote the substrings in $G_1^m$ and $G_2^m$ that are made of isolates of $R$; and $T_1, T_2, \ldots, T_\ell$ denote the fragments of substrings in $G_1^m$ and $G_2^m$, where the substrings are not purely made of isolates of $R$, but the fragments are. Note that $|S_i| \geq 2$ for every $i$. To single out all letters of $\left(\bigcup_{i=1}^k S_i\right) \cup \left(\bigcup_{j=1}^\ell T_j\right)$, we first need at least one isolate of $O_1 \cap R$ to chop each $T_i$ off its host substring; afterwards, the above argument states that for every two adjacent letters in $S_i$ or $T_j$, there are at least two isolates of $O_1 \cap R$ in between them, counting from both sequences. This gives

a lower bound on the minimum number of isolates of $O_1 \cap R$. Since each isolate of $O_1 \cap R$ can appear in two places, we have

$$2|O_1 \cap R| \geq \ell + \sum_{i=1}^{k} 2(|S_i| - 1) + \sum_{j=1}^{\ell} 2(|T_j| - 1) \geq \sum_{i=1}^{k} |S_i| + \sum_{j=1}^{\ell} |T_j|.$$

Therefore, the total number of isolates of $U \cup R$ (in this case, $R$ only) that are associated with isolates of $O_1 \cap R$ is at most $\sum_{i=1}^{k} |S_i| + \sum_{j=1}^{\ell} |T_j| + |O_1 \cap R|$, which is less than or equal to $3|O_1 \cap R|$. This proves the lemma. □

**Theorem 10** *The CMSR problem admits a* 3*-approximation algorithm.*

*Proof* To summarize, all isolates of $U \cup R$ are associated with units of $OPT$. From Lemmas 6, 8, and 9, we have

$$|U \cup R| \leq 4|O_3 \cup O_2| + 2.5\left|O_1 \cap \left(U \cup \left(\bigcup_{j=1}^{m} V_j\right)\right)\right| + 3|O_1 \cap R|$$

$$\leq \frac{4}{3} \times 3|O_3| + 2 \times 2|O_2| + 3 \times |O_1| \leq 3|OPT|,$$

where $|OPT|$ denotes the number of letters in $OPT$ and thus $|OPT| = 3|O_3| + 2|O_2| + |O_1|$. Note that the algorithm deletes all isolates of $U \cup R$, but no others, and therefore it is a 3-approximation algorithm. □

## 5 Conclusions

In this paper, we presented a fixed-parameter tractable algorithm and a 3-approximation algorithm for the CMSR problem. The running time of the FPT algorithm is $O^*(3^k)$, where $k$ is the size of the optimal solutions. We believe that a more careful analysis on the local configuration of an isolate can lead to faster FPT algorithms. In the approximation algorithm, the key design technique is greedy, and the performance ratio is proven using an inverse amortized analysis. Better approximation algorithms are certainly our future work.

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