Algorithms for Longest Common Abelian Factors

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Abstract

In this paper we consider the problem of computing the longest common abelian factor (LCAF) between two given strings. We present a simple $O(\sigma n^2)$ time algorithm, where $n$ is the length of the strings and $\sigma$ is the alphabet size, and a sub-quadratic running time solution for the binary string case, both having linear space requirement. Furthermore, we present a modified algorithm applying some interesting tricks and experimentally show that the resulting algorithm runs faster.

1. Introduction

Abelian properties concerning words have been investigated since the very beginning of the study of Formal Languages and Combinatorics on Words. Abelian powers were first considered in 1961 by Erdős \cite{Erd61} as a natural generalization of usual powers. In 1966, Parikh \cite{Par66} defined a vector having length equal to the alphabet cardinality, which reports the number of occurrences of each alphabet symbol inside a given string. Later on, the scientific community started referring to such a vector as the \textit{Parikh vector}. Clearly, two strings having the same Parikh vector are permutations of one another and there is an \textit{abelian match} between them.

Abelian properties of strings have recently grown tremendous interest among the Stringology researchers and have become an involving topic of discussion in the recent issues of the StringMasters meetings. Despite the fact that there are not so many real life applications where comparing commutative sequence of objects is relevant, abelian combinatorics has a potential role in filtering the data in order to find potential occurrences of some approximate matches. For instance, when one is looking for typing errors in a natural language, it can be useful to select the abelian matches first and then look for swap of adjacent or even near appearing letters. The swap errors and the inversion errors are also very common in the evolutionary process of the genetic code of a living organism and hence is often interesting from Bioinformatics perspective. Similar applications can also be found in the context of network communications.

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In this paper, we focus on the problem of finding the Longest Common Abelian Factor of two given strings. The problem is combinatorially interesting and analogous to the Longest Common Substring (LCStr) problem for the usual strings. The LCStr problem is a Historical problem and Dan Gusfield reported the following in his book [Gus97, Sec. 7.4] regarding the belief of Don Knuth about the complexity of the problem:

...in 1970 Don Knuth conjectured a linear time algorithm for this problem would be impossible.

However, contrary to the above conjecture, decades later, a linear time solution for the LCStr problem was in fact obtained by using the linear construction of the suffix tree. For Stringology researchers this alone could be the motivation for considering LCAF from both algorithmic and combinatorics point of view. However, despite a number of works on abelian matching, to the best of our knowledge, this problem has never been considered until very recently when it was posed in the latest issue of the StringMasters, i.e., StringMasters 2013. To this end, this research work can be seen as a first attempt to solve this problem with the hope of many more to follow.

In this paper, we first present a simple solution to the problem running in $O(\sigma n^2)$ time, where $\sigma$ is the alphabet size (Section 3). Then we present a sub-quadratic algorithm for the binary string case (Section 4). Both the algorithms have linear space requirement. Furthermore, we present a modified algorithm applying some interesting tricks (Section 5) and experimentally show that the resulting algorithm runs in $O(n \log n)$ time (Section 6).

2. Preliminaries

An alphabet $\Sigma$ of size $\sigma > 0$ is a finite set whose elements are called letters. A string on an alphabet $\Sigma$ is a finite, possibly empty, sequence of elements of $\Sigma$. The zero-letter sequence is called the empty string, and is denoted by $\varepsilon$. The length of a string $S$ is defined as the length of the sequence associated with the string $S$, and is denoted by $|S|$. We denote by $S[i]$ the $i$-th letter of $S$, for all $1 \leq i \leq |S|$ and $S = S[1..|S|]$. A string $w$ is a factor of a string $S$ if there exist two strings $u$ and $v$, possibly empty, such that $S = uvw$. A factor $w$ of a string $S$ is proper if $w \neq S$. If $u = \varepsilon$ ($v = \varepsilon$), then $w$ is a prefix (suffix) of $S$.

Given a string $S$ over the alphabet $\Sigma = \{a_1, \ldots, a_\sigma\}$, we denote by $|S|_{a_j}$ the number of $a_j$’s in $S$, for $1 \leq j \leq \sigma$. We define the Parikh vector of $S$ as $P_S = (|S|_{a_1}, \ldots, |S|_{a_\sigma})$.

In the binary case, we denote $\Sigma = \{0, 1\}$, the number of 0’s in $S$ by $|S|_0$, the number of 1’s in $S$ by $|S|_1$ and the Parikh vector of $S$ as $P_S = (|S|_0, |S|_1)$. We now focus on binary strings. The general alphabet case will be considered later.

For a given binary string $S$ of length $n$, we define an $n \times n$ matrix $M_S$ as follows. Each row of $M_S$ is dedicated to a particular length of factors of $S$. So, Row $\ell$ of $M_S$ is dedicated to $\ell$-length factors of $S$. Each column of $M_S$ is dedicated to a particular starting position of factors of $S$. So, Column $i$ of
Given a binary string $S$ of length $n$, $M_S$ is an $n \times n$ matrix such that $M_S[i][j]$ is dedicated to the position $i$ of $S$. Hence, $M_S[i][j]$ is dedicated to the $\ell$-length factor that starts at position $i$ of $S$ and it reports the number of 1’s of that factor. Now, $M_S[i][j] = m$ if and only if the $\ell$-length factor that starts at position $i$ of $S$ has a total of $m$ 1’s, that is, $|S[i..i+\ell-1]|_1 = m$. We formally define the matrix $M_S$ as follows.

**Definition 1.** Given a binary string $S$ of length $n$, $M_S$ is an $n \times n$ matrix such that $M_S[i][j] = |S[i..i+\ell-1]|_1$, for $1 \leq \ell \leq n$ and $1 \leq i \leq (n - \ell + 1)$, and $M_S[i][j] = 0$, otherwise.

In what follows, we will use $M_S[\ell]$ to refer to Row $\ell$ of $M_S$. Assume that we are given two strings $A$ and $B$ on an alphabet $\Sigma$. For the sake of ease, we assume that $|A| = |B| = n$. We want to find the length of a longest common abelian factor between $A$ and $B$.

**Definition 2.** Given two strings $A$ and $B$ over the alphabet $\Sigma$, we say that $w$ is a common abelian factor for $A$ and $B$ if there exist a factor (or substring) $u$ in $A$ and a factor $v$ in $B$ such that $P_u = P_v$. A common abelian factor of the highest length is called the Longest Common Abelian Factor (LCAF) between $A$ and $B$. The length of LCAF is referred to as the LCAF length.

In this paper we study the following problem.

**Problem 1 (LCAF Problem).** Given two strings $A$ and $B$ over the alphabet $\Sigma$, compute the length of an LCAF and identify some occurrences of an LCAF between $A$ and $B$.

Assume that the strings $A$ and $B$ of length $n$ are given. Now, suppose that the matrices $M_A$ and $M_B$ for the binary strings $A$ and $B$ have been computed. Now we have the following easy lemma that will be useful for us later.

**Lemma 2.** There is a common abelian factor of length $\ell$ between $A$ and $B$ if and only if there exists $p, q$ such that $1 \leq p, q \leq n - \ell + 1$ and $M_A[\ell][p] = M_B[\ell][q]$.

**Proof.** Suppose there exists $p, q$ such that $1 \leq p, q \leq n - \ell + 1$ and $M_A[\ell][p] = M_B[\ell][q]$. By definition this means $|A[p..p+\ell-1]|_1 = |B[q..q+\ell-1]|_1$. So there is a common abelian factor of length $\ell$ between $A$ and $B$. The other way is also obvious by definition.

Clearly, if we have $M_A$ and $M_B$ we can compute the LCAF by identifying the highest $\ell$ such that there exists $p, q$ having $1 \leq p, q \leq n - \ell + 1$ and $M_A[\ell][p] = M_B[\ell][q]$. Then we can say that the LCAF between $A$ and $B$ is either $A[p..p+\ell-1]$ or $B[q..q+\ell-1]$ having length $\ell$.

We now generalize the definition of the matrix $M_S$ for strings over a fixed size alphabet $\Sigma = \{\sigma_1, \ldots, \sigma_\sigma\}$ by defining an $n \times n$ matrix $M_S$ of $(\sigma - 1)$-length vectors. $M_S[\ell][i] = V_{\ell,i}$, where $V_{\ell,i}[j] = |S[i..i+\ell-1]|_{a_j}$, for $1 \leq \ell \leq n$, $1 \leq i \leq (n - \ell + 1)$ and $1 \leq j \leq \sigma$, and $V_{\ell,i}[j] = 0$, otherwise. We will refer to the $j$-th element of the array $V_{\ell,i}$ of the matrix $M_S$ by using the notation $M_S[\ell][i][j]$. 

\[ M_S[i][j] = |S[i..i+\ell-1]|_{a_j}, \]
Notice that the last component of a Parikh vector is determined by using the length of the string and all the other components of the Parikh vector. Now, \( M_S[\ell][i][j] = m \) if and only if the \( \ell \)-length factor that starts at position \( i \) of \( S \) has a total of \( m \) \( a_j \)'s, that is \( |S[i \ldots i + \ell - 1]|_{a_j} = m \). Clearly, we can compute \( M_S[\ell] \) using the following steps. Similar to the binary case, the above computation runs in linear time because we can compute \( |S[i + 1 \ldots i + 1 + \ell - 1]|_{a_j} \) from \( |S[i \ldots i + \ell - 1]|_{a_j} \) in constant time by simply decrementing the \( S[i] \) component and incrementing the \( S[i + \ell] \) one.

3. A Quadratic Algorithm

A simple approach for finding the LCAF length considers computing, for \( 1 \leq \ell \leq n \), the Parikh vectors of all the factors of length \( \ell \) in both \( A \) and \( B \), i.e., \( M_A[\ell] \) and \( M_B[\ell] \). Then, we check whether \( M_A[\ell] \) and \( M_B[\ell] \) have non-empty intersection. If yes, then \( \ell \) could be the LCAF length. So, we return the highest of such \( \ell \). Moreover, if one knows a Parikh vector having the LCAF length belonging to such intersection, a linear scan of \( A \) and \( B \) produces one occurrence of such a factor. The asymptotic time complexity of this approach is \( O(\sigma n^2) \) and it requires \( O(\sigma n \log n) \) bits of extra space. The basic steps are outlined as follows.

1. For \( \ell = 1 \) to \( n \) do the following
2. For \( i = 1 \) to \( n - \ell + 1 \) do the following
3. \hspace{1cm} compute \( M_A[\ell][i] \) and \( M_B[\ell][i] \)
4. \hspace{1cm} If \( M_A[\ell] \cap M_B[\ell] \neq \emptyset \) then
5. \hspace{1cm} \hspace{1cm} LCAF = \( \ell \)

It is well known that, for fixed length \( \ell \), one can compute all the Parikh vectors in linear time and store them in \( O(\sigma n \log n) \) bits. Now once \( M_A \) and \( M_B \) are computed, we simply need to apply the idea of Lemma \( 2 \). The idea is to check for all values of \( \ell \) whether there exists a pair \( p,q \) such that \( 1 \leq p,q \leq n - \ell + 1 \) and \( M_A[\ell][p] = M_B[\ell][q] \). Then return the highest value of \( \ell \) and corresponding values of \( p,q \).

In the binary case, a Parikh vector is fully represented by just one arbitrary chosen component. Hence, the set of Parikh vectors of binary factors is just a one dimension list of integers that can be stored in \( O(n \log n) \) bits, since we have \( n \) values in the range \([0 \ldots n]\). The intersection can be accomplished in two steps. First, we sort the \( M_A[\ell] \) and \( M_B[\ell] \) rows in \( O(n) \) time by putting them in two lists and using the classic Counting Sort algorithm [CLRS01, Section 8.2]. Then, we check for a non empty intersection with a simple linear scan of the two lists in linear time by starting in parallel from the beginning of the two lists and moving forward element by element on the list having the smallest value among the two examined elements. A further linear scan of \( M_A[\ell] \) and \( M_B[\ell] \)
will find the indexes $p, q$ of an element of the not empty intersection. This gives us an $O(n^2)$ time algorithm requiring $O(n \log n)$ bits of space for computing an LCAF of two given binary strings.

In the more general case of alphabet greater than two, comparing two Parikh vectors is no more a constant time operation and checking for empty intersections is not a trivial task. In fact, sorting the set of vectors requires a full order to be defined. We can define an order component by component giving more value to the first component, then to the second one and so on. More formally, we define $x < y$, with $x, y \in \mathbb{N}^\sigma$, if there exist $1 \leq k \geq \sigma$ such that $x[k] < y[k]$ and, for any $i$ with $1 \leq i < k$, $x[i] = y[i]$. Notice that comparing two vectors will take $O(\sigma)$ time.

Now, one can sort two list of $n$ vectors of dimension $\sigma - 1$, i.e., $M_A[\ell]$ and $M_B[\ell]$, in $O(\sigma n)$ by using $n$ comparisons taking $O(\sigma)$ each. Therefore, now the algorithm runs in $O(\sigma n^2)$ time using $O(\sigma n \log \sigma)$ bits of extra space.

4. A Sub-quadratic Algorithm for the Binary Case

In Section 3, we have presented an $O(n^2)$ algorithm to compute the LCAF between two binary strings and two occurrences of common abelian factors, one in each string, having LCAF length. In this section, we show how we can achieve a better running time for the LCAF problem. We will make use of the recent data structure of Moosa and Rahman [MR10] for indexing an abelian pattern. The results of Moosa and Rahman [MR10] is presented in the form of following lemmas with appropriate rephrasing to facilitate our description.

**Lemma 3.** (Interpolation lemma). If $S_1$ and $S_2$ are two substrings of a string $S$ on a binary alphabet such that $\ell = |S_1| = |S_2|$, $i = |S_1|_1$, $j = |S_2|_1$, $j > i + 1$, then, there exists another substring $S_3$ such that $\ell = |S_3|$ and $i < |S_3|_1 < j$.

**Lemma 4.** Suppose we are given a string $S$ of length $n$ on a binary alphabet. Suppose that $\maxOne(S, \ell)$ and $\minOne(S, \ell)$ denote, respectively, the maximum and minimum number of 1’s in any substring of $S$ having length $\ell$. Then, for all $1 \leq \ell \leq n$, $\maxOne(S, \ell)$ and $\minOne(S, \ell)$ can be computed in $O(n^2 / \log n)$ time and linear space.

A result similar to Lemma 3 is contained in the paper of Cicales et al. [CFL09, Lemma 4], while the result of Lemma 4 has been discovered simultaneously and independently by Moosa and Rahman [MR10] and by Burcsi et al. [BCFL10]. In addition to the above results we further use the following lemma.

**Lemma 5.** Suppose we are given two binary strings $A, B$ of length $n$ each. There is a common abelian factor of $A$ and $B$ having length $\ell$ if and only if $\maxOne(B, \ell) \geq \minOne(A, \ell)$ and $\maxOne(A, \ell) \geq \minOne(B, \ell)$.

**Proof.** Assume that $\min_A = \minOne(A, \ell)$, $\max_A = \maxOne(A, \ell)$, $\min_B = \minOne(B, \ell)$, $\max_B = \maxOne(B, \ell)$. Now by Lemma 3 for all $\min_A \leq k_A \leq \max_A$, $\min_B \leq k_B \leq \max_B$, we have $\min_A \leq k_A \leq \max_A$ and $\min_B \leq k_B \leq \max_B$. Thus, $\minOne(A, \ell)$ and $\minOne(B, \ell)$ are both greater than or equal to $\min_A$ and $\min_B$, respectively. Similarly, $\maxOne(A, \ell)$ and $\maxOne(B, \ell)$ are both less than or equal to $\max_A$ and $\max_B$, respectively. Therefore, $\maxOne(A, \ell) \geq \minOne(A, \ell)$ and $\maxOne(B, \ell) \geq \minOne(B, \ell)$, which is the desired result.
max_A, we have some ℓ-length substrings A(k_A) of A such that |A(k_A)|_1 = k_A.
Similarly, for all min_B ≤ k_B ≤ max_B, we have some ℓ-length factors B(k) of B such that |B(k_B)|_1 = k_B. Now, consider the range [min_A..max_A] and [min_B..max_B]. Clearly, these two ranges overlap if and only if max_B ≤ min_A and max_A ≤ min_B. If these two ranges overlap then there exists some k such that min_A ≤ k ≤ max_A and min_B ≤ k ≤ max_B. Then we must have some substring ℓ-length factors A(k) and B(k). Hence the result follows.

Let us now focus on devising an algorithm for computing the LCAF given two binary strings A and B of length n. For all 1 ≤ ℓ ≤ n, we compute maxOne(A,ℓ), minOne(A,ℓ), maxOne(B,ℓ) and minOne(B,ℓ) in \(O(n^2 / \log n)\) time (Lemma 4). Now we try to check the necessary and sufficient condition of Lemma 5 for all 1 ≤ ℓ ≤ n starting from n down to 1. We compute the highest ℓ such that

\[[\text{minOne}(A,ℓ)..\text{maxOne}(A,ℓ)] \text{ and } [\text{minOne}(B,ℓ)..\text{maxOne}(B,ℓ)] \text{ overlap.}\]

Suppose that \(K\) is the set of values that is contained in the above overlap, that is \(K = \{ k \mid k \in [\text{minOne}(A,ℓ)..\text{maxOne}(A,ℓ)] \text{ and } k \in [\text{minOne}(B,ℓ)..\text{maxOne}(B,ℓ)] \}\). Then by Lemma 5, we must have a set \(S\) of common abelian factors of A, B such that for all \(S \in S\), |S| = ℓ. Since we identify the highest ℓ, the length of a longest common factor must be ℓ, i.e., LCAF length is ℓ. Additionally, we have further identified the number of 1’s in such longest factors in the form of the set \(K\). Also, note that for a \(k \in K\) we must have a factor \(S \in S\) such that |S|_1 = k.

Now let us focus on identifying an occurrence of the LCAF. There are a number of ways to do that. But a straightforward and conceptually easy way is to run the folklore ℓ-window based algorithm in [MR10] on the strings A and B to find the ℓ-length factor with number of 1’s equal to a particular value \(k \in K\).

The overall running time of the algorithm is deduced as follows. By Lemma 4, the computation of maxOne(A,ℓ), minOne(A,ℓ), maxOne(B,ℓ) and minOne(B,ℓ) can be done in \(O(n^2 / \log n)\) time and linear space. The checking of the condition of Lemma 5 can be done in constant time for a particular value of ℓ. Therefore, in total, it can be done in \(O(n)\) time. Finally, the folklore algorithm requires \(O(n)\) time to identify an occurrence (or all of them) of the factors. In total the running time is \(O(n^2 / \log n)\) and linear space.

5. Towards a Better Time Complexity

In this section we discuss a simple variant of the quadratic algorithm presented in [3]. We recall that the main idea of the quadratic solution is to find the greatest ℓ with \(M_A[\ell] \cap M_B[\ell] \neq \emptyset\). The variant we present here is based on the following two simple observations:

1. One can start considering sets of factors of decreasing lengths;

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2. When an empty intersection is found between \( M_A[\ell] \) and \( M_B[\ell] \), some rows can possibly be skipped based on the evaluation of the gap between \( M_A[\ell] \) and \( M_B[\ell] \).

The first observation is trivial. The second observation is what we call the skip trick. Assume that \( M_A[\ell] \) and \( M_B[\ell] \) have been computed and \( M_A[\ell] \cap M_B[\ell] = \emptyset \) have been found. It is easy to see that, for any starting position \( i \) and for any component \( j \) (i.e., a letter \( a_j \)), we have

\[
M_A[\ell][i][j] - 1 \leq M_A[\ell - 1][i][j] \leq M_A[\ell][i][j] + 1
\]

Exploiting this property, we keep track, along the computation of \( M_A[\ell] \) and \( M_B[\ell] \), of the minimum and maximum values that appear in Parikh vectors of factors of length \( \ell \). We use four arrays indexed by \( \sigma \), namely \( \min_A, \max_A, \min_B, \max_B \). Notice that such arrays do not represent Parikh vectors as they just contain min and max values component by component. Formally, \( \min_A[j] = \min\{M_A[\ell][i][j]\} \), for any \( i = 1, \ldots, \ell + 1 \). The others have similar definitions.

We compare, component by component, the range of \( a_j \) in \( A \) and \( B \) and we skip as many Rows as \( \max_{j=1}^{\ell - 1} (\min_B[j] - \max_A[j]) \), assuming \( \min_B[j] \geq \max_A[j] \) (swap \( A \) and \( B \), otherwise). The modified algorithm is reported in Algorithm 1.

Note that the tricks employed in our skip trick algorithm are motivated by the fact that the expected value of the LCAF length of an independent and identically distributed (i.i.d.) source is exponentially close to \( n \) according to classic Large Deviation results [Ell85]. The same result is classically extended to an ergodic source and it is meant to be a good approximation for real life data when the two strings follow the same probability distribution. Based on this, we have the following conjecture.

**Conjecture 6.** The expected length of LCAF between two strings \( A, B \) drawn from an i.i.d. source is \( \text{LCAF}_\text{avg} = n - O(\log n) \), where \( |A| = |B| = n \), and the number of computed Rows in Algorithm 1 is \( O(\log n) \) in average.

Finally, we will make use of one more trick, that is, computing the first vector of the current row in constant time from the first vector of the previous row, when we skip some rows, instead of computing the new row from scratch, we can use the first vector of the row below to compute the first vector of the new row. When we compute the rows we need, we will just populate the required two lists and save a copy of the first vector of the computed row as we will need it along the next iterative steps as shown in Algorithm 2.

For instance, if we know \( \mathcal{M}[\ell] \) and we jump to \( \mathcal{M}[\ell - 3] \), i.e., we skip \( \mathcal{M}[\ell - 1] \) and \( \mathcal{M}[\ell - 2] \), we take \( \mathcal{M}[\ell][1] \) and compute in constant time \( \mathcal{M}[\ell - 1][1], \mathcal{M}[\ell - 2][1] \), then again compute \( \mathcal{M}[\ell - 3][1] \). From \( \mathcal{M}[\ell][1] \), to compute \( \mathcal{M}[\ell - 1][1] \), we have to subtract 1 from the vector \( \mathcal{M}[\ell][1] \) at index \( s[\ell] \), that is the last character of the factor of length \( \ell \) starting at position 1 (i.e., \( \mathcal{M}[\ell][1] \)). For example, consider \( s = aacgctaatcgy \), we have \( \mathcal{M}[12][1] = (4a, 4c, 1g, 2t) \) and \( \mathcal{M}[11][1] = (4a, 4c, 1g, 2t) \), i.e., \( (4a, 4c, 2g, 2t) \) minus \( 1g \).
Algorithm 1 Compute LCAF of $x$ and $y$ using the skip trick.

1: function COMPUTE_LCAF($x, y$)
2:     set $\ell = n = |x|$
3:     set found = False
4:     compute $\max_x = \text{MAX}(x, \ell)$, $\max_y = \text{MAX}(y, \ell)$
5:     compute $\min_x = \text{MIN}(x, \ell)$, $\min_y = \text{MIN}(y, \ell)$
6:     if $\max_x == \max_y$ then
7:         found = True
8:     else
9:         $\ell = \ell - \text{SKIP}(\min_x, \max_x, \min_y, \max_y)$
10:    end if
11:    while (found == False) AND ($\ell \geq 0$) do
12:        compute $\max_x = \text{MAX}(x, \ell)$, $\min_x = \text{MIN}(x, \ell)$
13:        compute $\max_y = \text{MAX}(y, \ell)$, $\min_y = \text{MIN}(y, \ell)$
14:        compute $\text{list}_x = M_x[\ell]$, $\text{list}_y = M_y[\ell]$
15:        sort $\text{list}_x$, $\text{list}_y$
16:        compute $\text{list}_x \cap \text{list}_y$
17:        if $\text{list}_x \cap \text{list}_y \neq \emptyset$ then
18:            found = True
19:            break
20:        end if
21:        $\ell = \ell - \text{SKIP}(\min_x, \max_x, \min_y, \max_y)$
22:    end while
23:    return $\ell$
24: end function

25: function MAX($s, \ell$)
26:     int count[$\sigma$, $\max[\sigma]$
27:     for ($i = 1; i \leq \ell; i++$) do
28:         count[$s[i]]++$
29:     end for
30:     max = count
31:     for ($i = \ell; i < |s| - \ell; i++$) do
32:         count[$s[i-1]]- -$
33:         count[$s[i+\ell-1]]++$
34:         if count[$s[i+\ell-1]] \geq \max[s[i+\ell-1]]$ then
35:             $\max[s[i+\ell-1]] = \text{count}[s[i+\ell-1]]$
36:         end if
37:     end for
38:     return max
39: end function

40: function SKIP($\min_x, \max_x, \min_y, \max_y$)
41:     int gap[$\sigma - 1$
42:     for ($j = 1; j < \sigma; j++$) do
43:         if $\max_x[j] >= \min_y[j]$ then
44:             gap[$j] = |\min_x[j] - \max_y[j]|$
45:         else
46:             gap[$j] = |\min_y[j] - \max_x[j]|$
47:         end if
48:     end for
49:     return $\max$(gap)
50: end function
6. Experiments

We have conducted some experiments to analyze the behaviour and running time of our skip trick algorithm in practice. The experiments have been run on a Windows Server 2008 R2 64-bit Operating System, with Intel(R) Core(TM) i7 2600 processor @ 3.40GHz having an installed memory (RAM) of 8.00 GB. Codes were implemented in C# language using Visual Studio 2010.

![Figure 1](image1.png)

Figure 1: Plot of the average number of rows computed executing Algorithm 1 on all the strings of length 2, 3, ..., 16 over the binary alphabet.

Our first experiment have been carried out principally to verify our rationale behind using the skip trick. We experimentally evaluated the expected number of rows computed in average by using the skip trick of Algorithm 1.

![Figure 2](image2.png)

Figure 2: Plot of the average number of rows computed executing Algorithm 1 on both genomic and random datasets over the DNA alphabet.

Figure 1 shows the average number of rows computed executing Algorithm 1 on all the strings of length 2, 3, ..., 16 over the binary alphabet. Naive method line refers to the number of rows used without the skip trick, but starting from
\( \ell = n \) and decreasing \( \ell \) by one at each step. Notice that the skip trick line is always below the \( \log n \) line.

To this end we have conducted an experiment to evaluate the expected number of rows computed by our skip trick algorithm. In particular, we have implemented the skip trick algorithm as well as the naive algorithm and have counted the average number of rows computed by the algorithms on all the strings of length 2, 3, \ldots 16 on binary alphabet. The results are reported in Figure 1. It shows that the computed rows of \( x, y \), starting from \( \ell = n \) to \( \ell = n - \log n \), sum up to \( O(\log n) \).

On the other hand, to reach a conclusion in this aspect we would have to increase the value of \( n \) in our experiment to substantially more than 64; for \( n = 64 \), \( \sqrt{n} \) is just above \( \log n \). Regrettably, limitation of computing power prevents us from doing such an experiment. So, we resort to two more (non-comprehensive) experimental setup as follows to check the practical running time of the skip trick algorithm.

\[ \begin{array}{c|cccccccccccccccc}
\hline
\text{Length} & 10 & 20 & 30 & 40 & 50 & 60 & 70 & 80 & 90 & 100 & 110 & 120 & 130 & 140 & 150 & 160 & 170 & 180 & 190 & 200 \\
\hline
\text{Genomic Data} & 4 & 8 & 12 & 16 & 20 & 24 & 28 & 32 & 36 & 40 & 44 & 48 & 52 & 56 & 60 & 64 & 68 & 72 & 76 & 80 \\
\text{First Vector} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\text{Computed Rows} & 4 & 8 & 12 & 16 & 20 & 24 & 28 & 32 & 36 & 40 & 44 & 48 & 52 & 56 & 60 & 64 & 68 & 72 & 76 & 80 \\
\text{Total} & 4 & 8 & 12 & 16 & 20 & 24 & 28 & 32 & 36 & 40 & 44 & 48 & 52 & 56 & 60 & 64 & 68 & 72 & 76 & 80 \\
\text{\( n \log(n) \)} & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
\hline
\end{array} \]

![Figure 3: Plot of the average number of rows computed executing Algorithm 1 on sequences taken from the Homo sapiens genome.](image)

Furthermore, we conduct our experiments on two datasets, real genomic data and random data. We have taken a sequence \( S \) from the Homo sapiens genome (250MB) for the former dataset. The latter dataset is generated randomly on the DNA alphabet (i.e., \( \Sigma = \{a, c, g, t\} \)). In particular, Here we have run the skip trick algorithm on 2 sets of pairs of strings of lengths 10, 20, \ldots, 1000. For the genomic dataset, these pairs of strings have been created as follows. For each length \( \ell \), \( \ell \in \{10, 20, \ldots, 1000\} \) two indexes \( i, j \in [1, |x| - \ell] \) have been randomly selected to get a pair of strings \( S[i:i + \ell - 1], S[j:j + \ell - 1] \), each of length \( \ell \). A total of 1000 pairs of strings have been generated in this way for each length \( \ell \) and the skip trick algorithm has been run on these pairs to get the average results. On the other hand for random dataset, we simply generate the same number of strings pairs randomly and run the skip trick algorithm on each pair of strings and get the average results for each length group. In both cases, we basically count the numbers of computed rows.
Figure 4: Plot of the average number of rows computed executing Algorithm 1 on randomly generated sequences over the alphabet $\Sigma = \{a, c, g, t\}$.

Figure 2 shows the average number of rows computed executing Algorithm 1 on both genomic and random datasets over the DNA alphabet (i.e., $\Sigma = \{a, c, g, t\}$). Notice that the skip trick line is always below the $\log n$ line. Figure 2 shows that the computed rows of $x, y$, starting from $\ell = n$ to $\ell = n - \log n$, sum up to $O(\log n)$.

We experimentally evaluated the computing of the first vector and the expected number of rows computed in average by employing the first vector trick (Algorithm 2). We have used the same experiment configuration as the above. The average number of rows and of the first vector computed executing Algorithm 2 on both genomic and random datasets over the DNA alphabet (i.e., $\Sigma = \{a, c, g, t\}$). In both cases, we basically count the numbers of computed rows and the first vector. The results are illustrated in Figures 3 and 4.

In both cases, The figures report the average count of computed rows (Number of Rows), the average count of the first vector (First Vector) and the summation of these two counts (Total). It also shows the $n \log n$ curve. Both of the figures show that the algorithm computed the first vector of the visited rows in $O(n)$ and the total running time for Algorithm 2 would be $O(n \log n)$ in practice.

Since any row computation takes $O(\sigma n)$, this suggests an average time complexity of $O(\sigma n \log n)$, i.e., $O(n \log n)$ for a constant alphabet.

7. Conclusion

In this paper we present a simple quadratic running time algorithm for the LCAF problem and a sub-quadratic running time solution for the binary string case, both having linear space requirement. Furthermore, we present a variant of the quadratic solution that is experimentally shown to achieve a better time complexity of $O(n \log n)$. 
Algorithm 2 Compute LCAF of $x$ and $y$ using the first vector trick.

1: function FIRST($s, \ell$)
2:    int first[\sigma]
3:    for ($i = 1; i < \ell; i++)$ do
4:        first[$s[i]]++
5:    end for
6:    return first
7: end function

8: function ROW($s, \ell, $ first)
9:    int row[\sigma]
10:   row = first
11:   for ($i = 1; i < |s| - \ell; i++)$ do
12:       row[$s[i - 1]]--
13:       row[$s[i + \ell - 1]]++
14:    end for
15:    return row
16: end function

17: function COMPUTELCAF($x, y$)
18:    set \ell = n = |x|
19:    set found = False
20:    compute first$_x = FIRST(x, \ell$
21:    compute first$_y = FIRST(y, \ell$
22:    while (found == False) AND (\ell \geq 0) do
23:        compute row$_x = ROW(x, \ell, $ first$_x$
24:        compute row$_y = ROW(y, \ell, $ first$_y$
25:        compute list$_x = M_x[\ell], list_y = M_y[\ell$
26:        sort list$_x, list_B$
27:        compute list$_x \cap list_y$
28:        if list$_x \cap list_y \neq \emptyset$ then
29:            found = True
30:            break
31:        end if
32:        compute max$_x = MAX(x, \ell), min$_x = MIN(x, \ell$
33:        compute max$_y = MAX(y, \ell), min$_y = MIN(y, \ell$
34:        \ell = \ell - SKIP(min$_x, max$_x, min$_y, max$_y$
35:    end while
36:    return \ell
37: end function

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