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ABSTRACT

Space saving techniques in computations of longest common subsequences are useful in many applications. This paper presents two linear space algorithms for this problem, one taking time O(n(m-l)) and the other taking time $O(mlog(\min[s,m,2n/l]))$, where m and $n (m \le n)$ are the lengths of the two input strings, l is the length of the longest common subsequences and s is the size of the alphabet. Along the way, a very simple O(m(m-l)) algorithm is also proposed for the case of strings of equal length.

Key Words and Phrases: Longest Common Subsequence, Linear Space, Finger Trees, Design and Analysis of Algorithms.

1. INTRODUCTION

Given a string α over an alphabet $\Sigma = (\sigma_1, \sigma_2, \dots, \sigma_s)$, a subsequence of α is any string γ that can be obtained from α by deleting zero or more (not necessarily consecutive) symbols. The longest common subsequence (LCS) problem for input strings $\alpha = a_1 a_2 \dots a_m$ and $\beta = b_1 b_2 \dots b_n$ ($m \le n$) consists of finding a third string $\gamma = c_1 c_2 \dots c_l$ such that γ is a subsequence of α and also a subsequence of β , and γ is of maximum possible length. In general, string γ is not unique.

The LCS problem arises in a number of applications spanning from text editing to molecular sequence comparisons, and it has been studied extensively over the past. General lower bounds for the problem are time $\Omega(n\log n)$ or linear time, according to whether the size s of Σ is unbounded or bounded. For unbounded alphabets, any algorithm using only "equal-unequal" comparisons takes $\Omega(nm)$ time in the worst case [AH]. The asymptotically fastest general solution takes time $O(n^2 \log \log n / \log n)$ [MP]. Time $\Theta(mn)$ is achieved by the following dynamic programming algorithm [HC, WF]. Let L[0...m, 0...n] be an integer matrix initially filled with zeroes. Now execute:

for i=1 to m do for j=1 to n do if $a_i=b_j$ then L[i,j] = L[i-1,j-1] + 1else $L[i,j] = Max\{L[i,j-1], L[i-1,j]\}.$

The above code transforms L in such a way that L[i,j] $(1 \le i \le m, 1 \le j \le n)$ contains the length of an LCS between $\alpha_i = a_1 a_2 ... a_i$ and $\beta_j = b_1 b_2 ... b_j$. If only the length of γ is desired, then this code is easily adapted to run in linear space. If an LCS is wanted, it becomes necessary to keep a record of the decision made at every step, so that γ can be retrieved at the end through backtracking. The early $\Theta(nm)$ time algorithm in [HC] achieves both a linear space bound and the production of an LCS at the outset, through a combination of dynamic programming and divide-and-conquer. Subsequent linear space algorithms such as in [AG, MY] follow the same basic divide-and-conquer scheme as in [HC] but require less than time $\Theta(nm)$ for

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favorable inputs.

Efficient algorithmic design for the LCS problem has experienced a new wave of interest in recent years, especially due to the need to process increasingly numerous and long inputs that arises in molecular sequence comparisons (see, e.g., [MA, SK]). The resulting constructions improve on the time performance in cases of special interest, or use only linear space, or do both. For instance, the algorithms in [AG1] improve on an early algorithm in [HI] for the case of strings that differ in length considerably, and improve on the worst case performance of the strategy in [HS]. Another line of research has focused on the efficient handling of the cases where the length of an LCS is expectedly close to the length of the shorter input string. One of the early constructions in [HI] achieves time $O((m-l)l\log n)$ for this case. (An additional $\Theta(n\log s)$ term is to be added to all time bounds reported here. Usually, this term is charged by a preprocessing phase.) More recently, an alternate construction requiring O((m-l)n) was proposed in [NY], along with another $O((m-l)l\log n)$ algorithm (it is relatively easy to check that the second bound can be reduced to $O(m(m-l)\min\{\log l, \log l, \log 2n/l\})$ by the techniques developed in [AG1]). Linear space implementation of the O((m-l)n) algorithm in [NY] was subsequently achieved in [KR], through a divide and conquer scheme that is reminiscent of, but not identical to that of [HC]. An algorithm taking time O(ne) in terms of the quantity e=m+n-2l was proposed in [MY]. This algorithm has expected time $O(n+e^2)$ and a nice, though admittedly unpractical, $O(n\log n + e^2)$ variation. Also these strategies can be implemented in linear space. Since $l \leq m$, however, then $e^2 = \Theta(n^2)$ for $n \geq 2m$. In other words, the bound in [MY] is comparable to those in [HI, NY, KR] only in the case of strings of nearly equal length.

In this paper, we propose additional linear space algorithms suitable for the case where l is close to m, or m is much smaller than n, or both conditions are met. We start by showing that, for m=n, an O(n(n-l)) algorithm of great conceptual simplicity results from introducing some kind of dualization in the classic strategy of [HS]. Equally simple extensions enable to handle

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the case $m \le n$, in time O(n(m-l)) and linear space. Finally, we present a linear space implementation of one of the algorithms in [AG1], preserving the $O(ml\log(min[s,m, 2n/m]))$ time bound of that algorithm. Ş,

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2. PRELIMINARIES

The ordered pair of positions i and j of L, denoted [i, j], is a match iff $a_i=b_j=\sigma_i$ for some $i, 1 \le t \le s$. If [i, j] is a match, and an LCS $\gamma_{i,j}$ of α_i and β_j has length k, then k is the rank of [i, j]. The match [i, j] is k-dominant if it has rank k and for any other pair [i', j'] of rank k either i' > i and $j' \le j$ or $i' \le i$ and j' > j. Computing the k-dominant matches (k=1,2,...,l) is all is needed to solve the LCS problem (see, e.g., [AG1, HI]).

It is useful to define, on the set of matches in L, the following partial order relation: match [i,j] precedes match [i',j'] if $i \le i'$ and $j \le j'$. Then, the LCS problem translates into the problem of finding a longest chain in the poset of matches. Most known approaches to the LCS problem compute a minimal antichain decomposition (refer, e.g., to [BO]) for this poset. A set of matches having equal rank is an antichain in this decomposition. For general posets, a minimal antichain decomposition is computed by flow techniques [BO], although not in time linear in the number of elements of the poset. The main algorithms discussed in this paper have their natural predecessors in [HS] and [HI]. In terms of antichain decompositions, the approach of [HI] consists of computing the antichains one at a time, while that of [HS] extends partial antichains relative to all ranks already discovered, one step at a time. The interested reader shall find that also the approach in [NY], which yields bounds of O(n(m-l)) or $O(m(m-l)\log n)$ may fall into this second category.

Our algorithms achieve linear space through a divide-and-conquer scheme similar to that of [KR]. The recurrent step of this scheme takes as input: (1) two strings ε and δ such that ε is always a substring, say, of β and δ is always a substring of the other string; (2) the length *l* of an LCS of ε and δ . The task of the step is to produce an LCS of ε and δ . This is achieved by first computing a suitable *cut* for an LCS of ε and δ and then by applying the same scheme on the two subdomains of the problem induced by the cut. A cut is any pair [u, v] such that an LCS of ε and δ can be formed by concatenating an LCS of the prefixes ε_u and δ_v with an LCS of the corresponding suffixes of the two strings. A more detailed description of the scheme is as follows.

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Procedure lcs (\varepsilon, \delta, i1, i2, j1, j2, l, LCS)

begin

if l=c or min[|\varepsilon|, |\delta|] – l = c for some constant c then

determine an LCS in time O (|\varepsilon| |\delta|) and space O (min[|\varepsilon|, |\delta|])

else

begin (split the problem into subproblems)

choose a cut [u, v], 1 \le u \le |\varepsilon|, 1 \le v \le |\delta|

lcs (\varepsilon, \delta, i1, i1+u-1, j1, j1+v-1, l_1, LCS 1);

lcs (\varepsilon, \delta, i1+u, i2, j1+v, j2, l_2, LCS 2);

LCS = LCS 1 || LCS 2;

end
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end.

The major difference between the above scheme and that in [HC] is in the fact that here l has to be computed prior to running *lcs*. In the following sections, we present various ways of computing l and correspondingly choose and compute a suitable cut inside *lcs*. Obviously, the overall time performance of the scheme depends crucially on the way that cuts are chosen and computed. As in the algorithm of [KR], we want to choose the cuts so as to achieve the best balance, in the sense that the total time required to solve both induced subproblems is about one half of the time required to solve the original problem.

3. THE O(n(n-l)) PROCEDURE LENGTH1 FOR THE CASE n = m

In this section, we assume n=m and present a simple O(n(n-l)) time strategy which is complementary to that used in Hunt and Szymanski [HS] (to keep our presentation short, some familiarity with [HS] is assumed). The case n=m arises in the row-wise comparison of digitized pictures and thus has special interest. The Hunt-Szymanski approach consists of detecting the dominant matches of all available ranks by processing the matches in the L matrix row by row. For this purpose, a list of thresholds we will call *row-THRESH* is used. After the processing of a row, the k-th entry in *row-THRESH* contains the column of the leftmost k-dominant match found so far. For example, for $\alpha = abcdbb$ and $\beta = cbacba$, the L-matrix would be as shown in Figure 1. After processing the sixth row, the final set of row thresholds would be $\{1,2,5\}$. The approach of [HS] consists of updating *row-THRESH* row after row, based on the new matches introduced by each row. Note that m-l = 3 positions are missing from the final set of thresholds, namely positions 3, 4, and 6. We call each such missing position a gap, and we call the sorted list of gaps *row-COTHRESH*.

		С	b	а	¢	b	а	
		1	2	3	4	5	б	
					_			
а	1	0	0	1	1	1	1	
b	2	0	1	1	1	2	[2	
С	3	1	1	1	2	2	2	
d	4	1	1	1	2	2	2	
ь	5	1	2	2	2	13]3	
ь	6	1	2	2	2	3	3	

Figure 1

The trace of row-THRESH on an L-matrix

Similarly, we can define the list *colu-THRESH* such that the k-th entry contains the row number of the rightmost k-dominant match found so far. For the example in Figure 1, the final set of column thresholds would be $\{1,2,5\}$. The corresponding set *colu-COTHRESH* of gaps would be $\{3,4,6\}$. Clearly, the *COTHRESH* lists can be deduced from the *THRESH* lists, and vice versa. If m-l < l, then the *COTHRESH* lists give a more compact encoding of the final set

of thresholds. Unfortunately, this is not always true at any stage of the row-by-row computation, since *THRESH* can be initially more sparse and *COTHRESH* correspondingly denser. However, if we consider only the upper-left square submatrices of the *L*-matrix, then we can obtain a suitable bound on the size of the *COTHRESH* lists.

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Lemma 1. The total number of gaps falling within the first *i* positions of either the *i*-th row or the *i*-th column of the *L*-matrix cannot be larger than m-l.

Proof. There must be an equal number of gaps, say q, in the *i*-th row and in the *i*-th column. If q > m-l, then the number of matches contributed to any LCS by the upper left *i*-*i* submatrix of the *L*-matrix cannot exceed i-q. Since the remaining portion of the *L*-matrix cannot contribute more than m-i matches, it must be the case that $l \le (m-i) + (i-q) < m - (m-l) = l$, which is a contradiction. \Box

Lemma 1 suggests that the length of an LCS of α and β with $|\alpha| = |\beta|$ can be found by extending, one row and one column at a time, submatrices of the *L*-matrix. This is done by the procedure *length1* which we now describe. At the *i*-th iteration, the procedure scans from left to right the O(m-l) cells of the two *COTHRESH* lists. If in the *row-COTHRESH* list we find a cell containing position p < i such that $a_i = b_p$, then [i,p] is a dominant match. Continuing the scan, the first cell (if any) is located with an entry larger than 1+p', where p' is the value stored in the immediately preceding cell. This jump in the list of gaps represents a threshold, namely, the first threshold to the right of p. If such a cell is found, then for some i' < i, [i',p'+1] is a dominant match having the same rank as [i,p]. Hence, gap p'+1 is inserted into *row-COTHRESH*. If no such cell is found, then [i,p] is the first dominant match found of its rank, and the cell containing i is removed from *col-COTHRESH*. The processing of the *col-COTHRESH* list is similar. Note that we can easily determine the rank of any newly detected dominant match, as follows. Call a position in which a gap does not occur a *line*. Upon beginning the scan of a *COTHRESH* list, initialize r to 1. During the scan, increment r by the number (zero or greater) of lines that are skipped over at each step. Then, when a dominant match is found, it will be of rank r. The highest rank detected is the length of an LCS for the two input strings. Some extra bookkeeping can be added to the process to enable the retrieval of an LCS γ at the end. This would, however, havoc the linearity of space. At this stage, we are interested mainly in the computation of $|\gamma|$, and the tedious details involved in such a bookkeeping are omitted. We summarize the preceding discussion in the following claim.

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Claim 1. Given two strings α and β with $|\alpha| = |\beta| = n$, the procedure *length1* computes the length of an LCS of α and β in time O(n(n-l)) and linear space.

3. COMPUTING THE LENGTH WHEN n > m

When n > m the condition of Lemma 1 is no longer met. We shall see, however, that the basic technique of the preceding section can still be applied, with small changes. The main tool needed is a procedure that tests, for any integer p in the range [0,m], whether α and β have an LCS of length m-p. We describe first such a procedure, which we call *length2*. Later, we show that a procedure *length3* for computing the length of an LCS of α and β in O(n(m-l)) time descends naturally from *length2*.

Procedure *length2* uses the following simple observation. Suppose strings α and β have LCS length of *l*. Then there is at least one such LCS, say, γ , that uses only dominant matches. Let [i, j] be one such match. Then, [i, j] appears in the *j*-th *colu-THRESH* list and, implicitly, in the *j*-th *colu-COTHRESH* list. Let *f* be the number of gaps preceding [i, j] in column *j* of the L matrix. Then the prefix of γ that is an LCS for α_i and β_j uses precisely i-f rows among the first *i* rows of the L matrix. By an argument similar to that of Lemma 1, it must be that $f \le m-l$, since the remaining m-i rows cannot contribute more than m-i matches to γ . In other words, no dominant match in an LCS can be preceded by more than m-l gaps in the cothresh list relative to the column where that match occurs.

In conclusion, to test whether there is a solution of length m-p, it is sufficient to produce the *n* successive updates of the first *p* entries of *colu-COTHRESH*. By our preceding discussion, this takes time O(np) and linear space. At the end, either we will obtain a match of rank m-por higher in this list, or we will know that no LCS of length at least m-p exists. We are now ready to present procedure *length3*, which simply consists of running the O(pn) procedure *length2* with p=0,1,2,4,8,... until it succeeds. Procedure *length2* will succeed when *p* is at most 2(m-l). Thus the total time spent by *length3* is proportional to $2n(m-l) + n(m-l) + 1/2n(m-l) + \cdots + 2n + n + n = 4n(m-l) + n$, which is O(n(m-l)). This establishes the following claim.

Claim 2. Procedure length3 computes the length l of γ in O(n(m-l)) time and linear space.

4. THE LINEAR SPACE, O(n(m-l)) TIME ALGORITHM LCS1

In this section, we show that length 2 and length 3 (length 1 if m=n) can be easily combined with *lcs* to produce an LCS of the two input strings α and β . We call the resulting algorithm *lcs* 1. In what follows, we describe the structure of *lcs* 1 and maintain the following bounds.

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The two issues to be addressed are the computation of *l* that has to precede the execution of *lcs* and the choice and computation of a cut inside the body of *lcs*. We use *length* 1 or *length* 3, depending on whether m=n or m < n, to compute *l*. From this, we know p=m-l. This takes time O(np) and linear space. We now call *lcs* on $\varepsilon = \beta$ and $\delta = \alpha$. Inside *lcs*, we will maintain that the value $w = |\delta| - l$ (i.e., the value of *p* relative to the current subdomain of the problem) is always known. More precisely, we maintain that at the *k*-th level of recursion, $w \le \lceil p/2^k \rceil$. This is achieved by computing cuts that always divide *w* in two halves. We call these cuts *balanced cuts*. We will show how the computation of all balanced cuts needed at the *k*-th level of recursion can be carried out in time $O(np/2^k)$ and linear space. Before describing how this is done, we observe that this condition establishes, for the time bound T(n,p) of *lcs*, a recurrence of the form: $T(n,p) = cnp + T(n_1,np/2) + T(n_2,np/2)$, with $n_1 + n_2 = n$ and *c* a constant. With initial conditions of the type $T(h, 0) \le bph$, where *b* is another constant, this recurrence has solution O(np).

Let n and $m \le n$ be the lengths of ε and δ , respectively, and let l = m-p be the length of an LCS for the two strings. The following lemma will be used to find a balanced cut for ε and δ (see Fig. 2).

Lemma 2 Assume $m > p \ge 2$ and let $p = p_1 + p_2 + p_3$ with $p_1 \ne 0$, $p_2 = 0$, and $p_3 \ne 0$. Then, there is an LCS $\gamma = \gamma^1 \gamma^2 \gamma^3$ of ε and δ for which it is possible to write $\varepsilon = \varepsilon^1 \varepsilon^2 \varepsilon^3$ and $\delta = \delta^1 d\delta^2 d'\delta^3$ with d and d' symbols of Σ , in such a way that: (1) γ consists only of dominant matches; (2) for i = 1, 2, 3, γ^i is an LCS of ε^i and δ^i and $|\delta^i| - |\gamma^i| = p_i$; (3) let e and e' be, respectively, the last symbol of ε^1 and the first symbol of ε^3 , then e and d do not form a dominant match in L and $e' \ne d'$. Proof. In the *L*-matrix, consider in succession the columns relative to the positions of δ . We start with a counter initialized to zero and update it according to the following. Consider column 1. As is easy to check, if there is any match in column 1, then the one such match occupying the row of lowest index is also the unique dominant match in column 1. If there is a solution γ that uses a match in this column, then we pick the only dominant match in this column and initialize with it a string γ' . If this is not the case, we increment the counter by one. Assume we have handled all columns up to h-1 updating the counter or extending the prefix γ' of an optimal solution γ , according to the cases met. Considering column h, we increment the counter if and only if no match in that column could be used to extend the length of γ' by one unit in such a way that the extended string would still be the prefix of an optimal solution. If some such matches exist, we append to γ' the one such match contained in the row of smallest possible index (observe that the match thus selected is a dominant match). In conclusion, each column at which the counter is not incremented extends the subsequence γ' by one new dominant match, while the fact that the counter is incremented at some column h signals that γ' could not have been continued into an optimal solution γ had we picked a match in column h.

Let now j be the leftmost column at which the counter reaches the value p_1 , and let i be the row containing the last one among the matches appended to γ' . We claim that entry [i, j]cannot be a dominant match. In fact, if [i, j] is a match, then clearly its rank is at least $|\gamma'|$. Assuming the rank of [i, j] higher than $|\gamma'|$ leads to a contradiction. In fact, in this case we can find a string η such that $\eta\gamma''$ is an LCS of ε and δ , $\gamma = \gamma'\gamma''$ is also an LCS of ε and δ and yet $|\eta\gamma| > |\gamma|$. Thus, either [i, j] is not a match or it is a non dominant match of rank equal to the last match of γ' used so far. We set δ^1 equal to the prefix of δ of length j-1, ε^1 equal to the prefix of ε of length i, $\gamma^1 = \gamma'$, $e = \varepsilon[i]$ and $d = \delta[j]$. These choices are consistent with the properties listed in the Lemma for the objects involved.

To continue with the columns of L that fall past column j, we distinguish two cases, according to whether or not γ' can be extended with a match in column j+1. If γ' can be ÷,

extended with a match in column j+1, let j+1, j+2,..., j+g be the longest run of consecutive columns such that each column contributes a new match to γ' . By the hypothesis $p_1 < p$, we have j+g < m (i.e., we must be forced to skip at least one more column). Let i' be the row such that [i', j+g] is a match of γ' . Then, by our choice of g the entry [i'+1, j+g+1] cannot be a match. We set ε^2 equal to the substring of ε that starts at position i+1 and ends at position i', δ^2 equal to the substring of δ that starts at j+1 and ends at j+g, and $e' = \varepsilon[i'+1]$ and $d' = \delta[j+g+1]$. Finally, we take the suffix of length g of γ' as γ^2 . Clearly, these assignments satisfy the conditions in the claim. The choices performed so far induce a unique choice of ε^3 , δ^3 , and γ^3 . By our construction of γ' , there is an optimal solution γ which has $\gamma' = \gamma^1 \gamma^2$ as a prefix. In any such solution, γ' must be followed by an LCS of ε^3 and δ^3 of length $|\delta^3| - (p-p_1-p_2)$, i.e., of length $|\delta^3| - p_3$. Thus the remaining conditions of the claim are also met. If γ' cannot be extended with a match in column j+1, then the claim still holds by simply taking δ_2 and γ_2 both empty. \Box

With $p_1 = \lceil p/2 \rceil$ Lemma 2 can be used in the computation of a balanced cut for ε and δ , as follows. We treat the case where p is even, the case of odd p being quite similar. Let j and j'=j+g+1 be the positions in δ of d and d', respectively, and let i be the position in ε of the last symbol of ε^1 . Clearly, [i', j'-1] is a balanced cut. Observe that this cut coincides with [i, j] if γ^2 is empty.

We now run length 2 on the ordered pair (δ , ε) and with parameter p/2+1. We use this run to prepare an array *REACH* with the property that *REACH* [*i*] contains the column index relative to the p/2+1-st gap in the *COTHRESH* list at row *i*. Observe that, by condition 3 of the lemma, if *i'*+1 is the position in ε of the first symbol of ε_3 , then *REACH* [*i'*+1] equals precisely the position *j'* of *d'* in δ .



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Illustrating Lemma 2

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Next, we run a copy of *length* 2 on the ordered pair (δ^R , ε^R) of the *reverse* strings of the two input strings, this time with parameter p/2. An array *REVREACH* similar to *REACH* is built in this way. Since [i'+1,j'] is not a match and we know that $|\delta_3| - |\gamma_3| = p/2$, then *REVREACH* [i'+1] = j'.

Clearly, any index i^* for which $REACH[i^*] = REVREACH[i^*]$ yields a corresponding balanced cut $[i^*-1, REACH[i^*] - 1]$. By Lemma 2 and the above discussion, at least one such index is guaranteed to exist. In conclusion, we only need to scan the two arrays REACH and REVREACH looking for the first index k such that REACH[k] = REVREACH[k]. Having found such an index, we can set, for our balanced cut [u,v], u = k-1 and v = REACH[k]-1 = REVREACH[k]-1.

As mentioned, the case of odd p is dealt with similarly. At the top level of the recursion, this process takes O(np) time and linear space. Since the parameter p is halved at each level, the overall time taken by the computation of cuts is still O(np). The recursion can stop whenever the current partition of L has an associated value of either the l or p not larger than some preassigned constant. For any such partition, an LCS can be found by known methods in linear space.

5. THE PROCEDURE LENGTH4

In this section, we present a procedure length 4 that computes the length of an LCS of α and β in time $O(lm \log(\min[s,m, 2n/m]))$. Since symbols not appearing in α cannot contribute to an LCS, we can eliminate such symbols from β and assume henceforth $s \leq m$, which eliminates the logm from the bound. The procedure length 4 is a direct derivation of an algorithm in [AG1]. For the subsequent developments, we need to describe it in some detail. The procedure consists of lsub stages which identify the lsub antichains of L in succession. It exploits the same criterion as in [HI] to trace an antichain: if [i, j] is a k-dominant match then [i', j'] with i' > i is a k-dominant match iff j' < j. At stage k only the leftmost k-dominant match is recorded in the array RANK. The procedure uses the following auxiliary structures:

- For each symbol of the alphabet σ , a list σ -OCC of all the occurrences of σ in β ;

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- An array *PEBBLE* such that *PEBBLE*[*i*] (*i*=1,...,*m*) contains a pointer to an entry of a_i -OCC. At the beginning, *PEBBLE*[*i*] (*i*=*i*₁,...,*i*₂) points to the the entry *j* of a_i -OCC, which corresponds to the leftmost occurrence of a_i in the interval [*j*₁,...,*j*₂], if any. *PEBBLE*[*i*] is then said to be *active*. The procedure advances an active pebble until it becomes *inactive*, i.e. reaches an entry larger than *j*2, or the last entry of a_i -OCC. By the end of the execution of *length* 4 each pebble is set to point to the rightmost position that it can occupy in the interval [*j*1...*j*2].

The algorithm uses also the function $closest(\sigma, b_t)$ which for any given character σ returns the pointer to the entry in the σ -OCC list corresponding to leftmost occurrence of σ in β which falls past b_t .

```
Procedure length4 (i1, i2, j1, j2, RANK, lsub)
0 RANK[k] = 0, k=1,2,...,(i2-i1);
1 \ k = 0
2 while there are active pebbles do (start stage k+1)
3 begin T=j2+1; k=k+1;
4
       for i = i 1 - 1 + k to i 2 do (advance pebbles)
        begin
5
           t = T;
6
           if PEBBLE [i] is active and a_i - OCC [PEBBLE [i]] < T then
            (update threshold, update leftmost k-dominant match )
7
                 begin T = a_i - OCC [PEBBLE[i]]; RANK[k] = Tend;
            (advance pebble, or make it inactive)
8
           PEBBLE[i] = closest[a_i, t];
9
           if PEBBLE [i] is active and a_i - OCC [PEBBLE [i]] > j2 then
                begin PEBBLE [i]=PEBBLE [i]-1; make PEBBLE [i] inactive end;
10
        end;
```

end (lsub = k).

The procedure length 4 detects all dominant matches [AG1]. Unlike the algorithm presented in [AG1], however, it records only the leftmost dominant match incurred for each k. This achieves the linear space bound.

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All the elementary steps of length 4, with the exception of the executions of closest, take constant time. On an input of size n + m the procedure handles at most m pebbles during each of the lsub stages. Thus the total time spent by length is O(mlsub + total time required byclosest). The second term is obviously implementation dependent. One efficient implementation of closest is discussed in [AG1]. It rests on two auxiliary structures which we now proceed to describe. First, we prepare, in time $\Theta(n)$, the table CLOSE[1...n+1] which is subdivided into consecutive blocks of size s and defined as follows. Letting $p = j \mod s$ (j=1,...,n), CLOSE[j]contains the leftmost position not smaller than j where σ_p occurs in β . The use of such table allows to implement closest in time O(logs). Next, we assume that each σ -OCC list is assigned a finger tree [AG1, AP, BT, ME]. Roughly, a finger-tree is a balanced search tree which can be traversed in any direction. The finger is a pointer to any leaf in the tree. The main advantage conveyed by finger-trees is that, in such a tree, the search for an item displaced d positions (leaves) away from the current position of the finger can be carried out in $O(\log d)$ time. If the finger is updated to point to the last searched item at all times, then searching for m consecutive items in a tree which stores n keys is afforded in $O(\sum_{k=1}^{m} \log d_k)$, where the intervals

 d_k 's are subject to the constraint that $\sum_{k=1}^m d_k \le 2n$. As is well known, this yields the overall time bound of $O(m\log(2n/m))$.

In order to keep track of the fingers we institute a new global variable, namely, the array of integers FINGER[1...m]. At its inception, the procedure *length* 4 moves all the fingers FINGER[i1], FINGER[i1+1],..., FINGER[i2], originally coincident with the pebbles, onto the rightmost position in the interval [j1...j2] that they can occupy on their corresponding σ -OCC lists. This positioning of each finger is accomplished in O(min[logs,log(j2-j1)]) time through an application of *closest*. Fingers set from different rows on the same σ -OCC list merge into one single *representative* finger.

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During the execution of each stage of *length* 4, the (representative) finger associated with each symbol in [i 1...i 2] is reconsidered immediately following a *closest* query and the possible consequent update of the pebble (cfr. lines 8-10 of *length* 4). At that point, we simply set: *FINGER* [i] = PEBBLE[i]. Thus through each individual stage, the finger associated with each symbol moves from right to left. Each of the manipulations just described takes constant time. Finally, both fingers and pebbles are taken back to their initial (leftmost) position soon after the last stage of *length* 4 has been completed. Overall, this takes time O(i2-i1). We summarize some results in [AG1] in the form of the following:

Claim 4. By the combined use of *FINGER* and *CLOSE*, the procedure length 4 computes the length *lsub* of an LCS of $\alpha_{i1} \cdots \alpha_{i2}$ and $\beta_{j1} \dots \beta_{j2}$ in time $O(lsub \cdot (i2-i1) \cdot min[logs, log(2n/(i2-i1))])$ and linear space.

6. THE LINEAR SPACE ALGORITHM LCS2

We now show that the procedure length 4 can be cast in the divide-and-conquer scheme of Section 2 to produce an algorithm lcs 2 that has time bound $O(ml\log(min[s, 2n/l]))$ and space $\Theta(n)$. For $l = \Theta(m)$ (i.e., in applications that use this algorithm fruitfully), this time bound is equal to that of the algorithm in [AG1].

We remove the previous assumption according to which, upon calling length 4 with jparameters j1, j2, the procedure always finds pebbles and fingers pointing to the leftmost positions in the interval [j1...j2]. We replace it with the new assumption that either all pebbles and fingers occupy the rightmost positions in the interval [j1...j2], or else they all occupy the leftmost one. Procedure *length* 4 checks at its inception which case applies, and brings all pebbles to their leftmost positions, if necessary. This does not affect the time bound of the procedure. Algorithm lcs 1 uses length 4 both to compute l prior to executing lcs and to compute cuts inside the body of lcs. For this latter task we use a scheme similar to that of lcs 1. We outline the method for the case of even l, the case of odd l being handled similarly. We run two copies of length 4, on the two mirror images of the problem, with the proviso that computation in each row is stopped as soon as a dominant match of rank l/2 is detected. All matches of rank l/2 so detected by each version of the procedure are stored in one of two associated lists. Observe that the number of such matches cannot exceed the total number of dominant matches detected, and this latter number cannot be larger than ml, the number of matches handled at most by the procedure. At the end, we scan the two lists looking for the first pair of matches, one from one list and one from the other, that form a chain. From the positions in L of these two matches, we can infer a balanced cut. In the present context, a cut is balanced if it identifies two submatrices L' and L'' of L with the property that an optimal solution γ can be formed by concatenating two optimal solutions γ' and γ' entirely contained, respectively, in L' and L'' and both of length l/2. Leaving the details for an exercise, we concentrate on the following claim.

Claim 5. The procedure lcs 2 finds an LCS in time O(mlog(min[s, 2n/l])) and space $\Theta(n)$.

Proof. Each execution of length 4 at the k-th level of the recursion can be bounded in terms of $m_f l/2^k \log(\min[s, 2n/m_f])$, where m_f denotes the number of rows assigned to the f-th subproblem. By the preceding discussion, the time needed to scan each pair of antichains of maximum rank in order to find a balanced cut for that pair can be absorbed in this bound. There are 2^k calls at level k, yielding a total time:

$$\sum_{f=1}^{2^{k}} m_{f} \frac{l}{2^{k}} \log(\min[s, \frac{2n}{m_{f}}]),$$

up to a multiplicative constant. Now it is

$$\sum_{f=1}^{2^{*}} m_{f} = m.$$

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Since $m_f \ge l/2^k$, we have that the total work at this level of recursion can be bounded in terms of the quantity:

$$m \cdot \frac{l}{2^k} \cdot \log(\min[s, \frac{2n}{l} 2^k]) \leq m \cdot \frac{l}{2^k} \cdot \log(\min[s 2^k, \frac{2n}{l} 2^k]).$$

The right term can be rewritten as:

$$m \cdot \frac{l}{2^k} \log(2^k \cdot \min[s, \frac{2n}{l}]) = m \cdot k \cdot \frac{l}{2^k} + m \cdot \frac{l}{2^k} \log(\min[s, \frac{2n}{l}]).$$

Adding up through $k = 1, 2, ..., \log l$ yields:

$$ml\sum_{k=1}^{\log l} \frac{k}{2^{k}} + ml \, \log(min[s, \frac{2n}{l}]) \sum_{k=1}^{\log l} \frac{1}{2^{k}}.$$

from which we obtain the O(mlog(min[s, 2n/l])) time bound.

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