

粗ソーティング:
逐次のおよび並列的アプローチ

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系列 $\alpha = (a_1, a_2, \dots, a_n)$ が、任意の $1 \leq i, j \leq n$ について $i - j > k$ ならば $a_j \leq a_i$ である時、その系列は k ソートであるという。我々はまず与えられた系列が k ソートであるかどうかを決定する実時間アルゴリズムと与えられた系列が k ソートであるような最小の k を求める線形時間のアルゴリズムを示す。次いで二つの k ソートである系列を併合して k ソートの一つの系列にするアルゴリズムと、 k ソートである系列を完全にソートするアルゴリズムを与える。これ等の計算時間はそれぞれ $O(n)$ と $O(n \log k)$ である。最後に、 k ソートである系列を完全にソートする並列アルゴリズムについて述べる。ここで述べる方法は多くの並列計算機アーキテクチャ上で適用できる。それ等の計算時間は $O(f(2k) \log k)$ である。ここで $f(t)$ は t 個の項の中間値を求めるために使用したアルゴリズムの並列計算時間である。

Roughly Sorting:
Sequential and Parallel Approach

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A sequence $\alpha = (a_1, a_2, \dots, a_n)$ is k -sorted if for all $1 \leq i, j \leq n$, $i - j > k$ implies $a_j \leq a_i$. We first show an online algorithm for determining if a given sequence is k -sorted and an $O(n)$ -time algorithm for finding the smallest k for a given sequence to be k -sorted. Next, we give two sequential algorithms that merge two k -sorted sequences to form a k -sorted sequence and completely sort a k -sorted sequence. Their running times are $O(n)$ and $O(n \log k)$, respectively. Finally, parallel versions of the complete-sorting algorithm are presented. They are adaptable for most parallel architectures. Their parallel running times are $O(f(2k) \log k)$, where $f(t)$ is the computing time of an algorithm used for finding the median among t elements.

1 Introduction

The concept of roughly sorting has appeared in the context of parallel sorting on a mesh-connected processor array. Igarashi and Sado have designed fast parallel sorting algorithms in which roughly sorted subfiles are merged [9,10]. Fundamental properties of roughly sorted sequences and some sequential algorithms have been studied in [4,5]. The notions of presortedness and nearly sorted lists [3,7,8] are related to the ideas presented in this paper, but are somewhat different from the roughly sorted lists we will study here.

A number of applications require only roughly or nearly sorted sequences[5]. For example, consider a sorted file in which the item values are occasionally updated. In many cases, the new item values may not differ greatly from the old ones. However, by replacing the old items with new ones, the sorted order may be disturbed. Since re-sorting the entire file is costly, it may be more efficient to leave it in a roughly sorted order. We may then use the algorithms described below to obtain a completely sorted file.

In this paper, we present algorithms, that create and manipulate roughly sorted sequences in both sequential and parallel environments. In Section 2, we formalize our notion of rough sortedness and k -sorted sequences. Algorithms that determine if a sequence is k -sorted and the k -sortedness of a sequence are given in Section 3. In Section 4, we present an algorithm that merges two k -sorted sequences into one k -sorted sequence. Finally, in Section 5, we design sequential and parallel algorithms that completely sort k -sorted sequences.

2 k -Sortedness

We begin by formalizing our notion of roughly sorted sequences. Let $\alpha = (a_1, a_2, \dots, a_n)$ be a sequence of n items and $\sigma = (a_{\sigma_1}, a_{\sigma_2}, \dots, a_{\sigma_n})$ the corresponding completely sorted sequence of elements.

Definition 2.1 A sequence α is k -sorted if and only if the following condition is satisfied:

$$\text{for all } i, j \ 1 \leq i \leq j \leq n, \ i - j \geq k \rightarrow a_j \leq a_i.$$

The above definition was introduced by Igarashi and Wood [5]. The **radius** of α is define to be the smallest k , such that α is k -sorted, and denoted by $ROUGH(\alpha)$. As shown by Estivill-Castro and Wood [4], the radius presortedness measure satisfies the axioms introduced by Mannila [7].

Observation 2.1 If a sequence α has no duplicate entries, then it is k -sorted if and only if for all i ,

$$|i - \sigma_i| \leq k.$$

Hence, for all i , a_i is no more than k places away from its proper position in a completely, or 0-sorted, sequence.

Observation 2.2 [5] α is k -sorted if and only if every $(2k+2)$ block, (i.e., a sequence of $(2k+2)$ consecutive elements of α), is k -sorted. This plays a key role in the design of our algorithms.

3 Determination of the Radius

Several interesting problems arise concerning k -sorted sequences. In particular, we might ask if a given sequence is k -sorted. Second, we might wish to compute the radius of a given sequence. We show that both of these questions can be answered efficiently.

Lemma 3.1 Given α , a sequence of n elements and a positive integer k , we can decide online(i.e., in n) whether α is k -sorted.

Proof: Imagine a bus with a passenger capacity of $k+1$. At each stop, one passenger gets off and another gets on (in a FIFO fashion). The driver always remembers max , the weight of the heaviest passenger that got off the bus so far. If the weight of the incoming passenger is less than max , the driver stops the bus and declares: *These people are not k -sorted*.

It is possible to implement the above with two pointers (always $k+1$ positions apart) to the sequence α and a variable max in which the value of the largest encountered element, outside the current $(k+1)$ is stored. Going left to right, the procedure will always identify the first occurrence of a violation of k -sortedness of α □

Below, we present an efficient algorithm $ROUGH(\alpha)$, i.e., the radius of α .

Definition 3.1 Let $\alpha = (a_1, a_2, \dots, a_n)$ be a sequence of n items. The **LR characteristic sequence** of α is defined to be (b_1, \dots, b_n) , where for each $i(1 \leq i \leq n)$ $b_i = \max\{a_1, \dots, a_i\}$. This sequence is denoted by $LR(\alpha)$. The **RL characteristic sequence** of α is defined to be (c_1, \dots, c_n) , where for each $i(1 \leq i \leq n)$ $c_i = \min\{a_i, \dots, a_n\}$. This sequence is denoted by $RL(\alpha)$.

Definition 3.2 Let $\alpha = (a_1, a_2, \dots, a_n)$ be a sequence of n items. Let $LR(\alpha) = (b_1, \dots, b_n)$ and $RL(\alpha) = (c_1, \dots, c_n)$. The **disorder measure sequence** of α is defined to be (d_1, \dots, d_n) , where for each $i(1 \leq i \leq n)$ $d_i = \max(\{i - j | c_i < b_j\} \cup \{0\})$. This sequence is denoted by $DM(\alpha)$.

Theorem 3.1 Let $\alpha = (a_1, a_2, \dots, a_n)$ be a sequence of n items. Then $ROUGH(\alpha) = \max\{d_i | d_i \text{ is an item of } DM(\alpha)\}$.

Proof: Suppose that $ROUGH(\alpha)=k$. If $k=0$, then α is completely sorted and $LR(\alpha)=RL(\alpha)$. Hence, in this case for any i ($1 \leq i \leq n$) $d_i = 0$, and the assertion of the theorem holds.

Suppose that $k \geq 1$. Then, there exists a pair of i and j such that $j - i = k$ and $a_i > a_j$. Hence, for such j , $d_i \geq j - i = k$. On the other hand, for any pair of i and j such that $j - i \leq k + 1$, $a_i \leq a_j$. Therefore, for any j ($1 \leq j \leq n$), $d_j < k + 1$ \square

Below, we present three procedures which construct the LR , RL , and the DM sequences of $\alpha = (a_1, a_2, \dots, a_n)$.

```

procedure  $LR(\alpha, B[1..n]);$ 
begin
   $B[1] := a_1;$ 
  for  $i := 2$  to  $n$ 
    if  $B[i - 1] < a_i$  then  $B[i] := a_i$ 
    else  $B[i] := B[i - 1]$ 
end.

procedure  $RL(\alpha, C[1..n]);$ 
begin
   $C[n] := a_n;$ 
  for  $i := n - 1$  downto  $1$ 
    if  $C[i + 1] > a_i$  then  $C[i] := a_i$ 
    else  $C[i] := C[i + 1]$ 
end.

procedure  $DM(B[1..n], C[1..n], D[1..n]);$ 
begin
  set queue  $Q$  empty;
  for  $i := n$  downto  $1$ 
    begin
      insert( $i, C[i]$ ) at the rear of  $Q$ ;
      while ( $Q$  not empty) and (the second
        component of  $Q(\text{first}) \leq B[i]$ )
        and (the second component of
           $Q(\text{first}) \geq B[i - 1]$  or  $i = 1$ ) do
        begin
          ( $t, C[t]$ ) := the first element of  $Q$ ;
           $D[t] := t - i$ ;
          remove the first element of  $Q$ 
        end
      end
    end
end.

```

Using procedure LR , RL , and DM , we can decide $\max\{d_i \mid d_i \text{ is an item in } DM(\alpha)\}$ in linear time to n . From Theorem 3.1, that value is equal to $ROUGH(\alpha)$.

An example of a 5-sorted sequence α , its LR and RL sequences, and the maximal element d_i , from the sequence DM , is shown in Figure 1.

4 Sequential k -Sorting

In this section, we present three algorithms that operate on k -sorted sequences. First, we describe procedure $HALVE$, which takes as input a $2k$ -sorted sequence γ and returns a $(k-1)$ -sorted sequence δ . Next, in procedure $MERGE$, we show how two k -sorted sequences, α and β , can be merged to produce a k -sorted sequence γ . Finally, procedure $QMSORT$ show how a k -sorted sequence α is sorted in time $O(n \log k)$.

```

procedure  $HALVE(\gamma, \delta, k);$ 
{Suppose  $\gamma = (a_1, a_2, \dots, a_n)$ . Assume  $n = 2kr$ . If  $n$ 
is not a multiple of  $2k$ , the procedure needs a minor
modification.}
begin
  1. for  $i := 1$  to  $r$ 
    begin
       $\alpha_i := a_{2k(i-1)+1} \dots a_{2ki};$ 
       $PARTITION(\alpha_i, \alpha_{i_1}, \alpha_{i_2})$ 
    end;

  2. for  $i := 1$  to  $r - 1$ 
    begin
       $\beta_i := \alpha_{i_2} \alpha_{(i+1)_1};$ 
       $PARTITION(\beta_i, \beta_{i_1}, \beta_{i_2})$ 
    end;

  3.  $\alpha_1 := \alpha_{1_1} \beta_{1_1}; \alpha_r := \beta_{(r-1)_2} \alpha_{r_2}$ 

  4. for  $i := 2$  to  $r - 1$ 
    begin
       $\alpha_i := \beta_{(i-1)_2} \beta_{i_1};$ 
       $PARTITION(\alpha_i, \alpha_{i_1}, \alpha_{i_2})$ 
    end;

  5.  $\delta := \alpha_{1_1} \alpha_{1_1} \dots \alpha_{r_1} \alpha_{r_2}$ 
end.

```

Here, $PARTITION(\alpha, \beta, \gamma)$ finds the median m of α and constructs a partition (β, γ) of α by m (i.e., any item in $\beta \leq m \leq$ any item in γ).

A computation process by $HALVE(\gamma, \delta, k)$ is depicted in Figure 2.

Theorem 4.1 Let γ be a $2k$ -sorted sequence of length n . Then $HALVE(\gamma, \delta, k)$ returns a $(k-1)$ -sorted sequence of γ in δ in $O(n)$ time.

Proof: We use the following notation: For x and y a pair of sequences, $x \leq y$ means that any item in x is not greater than any item in y . Since γ is initially $2k$ -sorted, after Step 1, for each odd i ,

$$\alpha_{1_1} \dots \alpha_{(i-2)_2} \leq \alpha_{i_1} \leq \alpha_{(i+1)_2} \dots \alpha_{r_2} \text{ and } \alpha_{i_1} \leq \alpha_{i_2}.$$

Hence, after Step 2, for each odd i ,

$$\alpha_{i_1} \dots \alpha_{(i-1)_2} \leq \alpha_{i_1} \leq \alpha_{(i+1)_i} \dots \alpha_{r_2}$$

Then, after Step 3, for each odd i ,

$$\alpha_{i_1} \dots \alpha_{(i-1)_2} \leq \alpha_{i_1} \leq \alpha_{i_2} \dots \alpha_{r_2}$$

Therefore, δ is a $(k-1)$ -sorted sequence of γ after Step 5. Since the median of n items can be found in $O(n)$ time (e.g., see [1]), the computing time of $HALVE(\gamma, \delta, k)$ is $O(n)$ \square

Procedure *MERGE* below takes as input two k -sorted sequences $\alpha = (a_1, a_2, \dots, a_n)$ and $\beta = (b_1, b_2, \dots, b_n)$, and returns (in γ) the resulting merged k -sorted sequence of length $2n$. For simplicity, we assume that k is even and $n = kr$. For n and k not satisfying these conditions, the procedure with a minor modification is still valid.

```

procedure MERGE( $\alpha, \beta, \gamma, k$ );
{ $\gamma$  is a queue and initially empty }
begin
  1. HALVE( $\alpha, \alpha', k/2$ ); HALVE( $\beta, \beta', k/2$ );
  { $\alpha' = a_1, \dots, a_n$  and  $\beta' = b_1, \dots, b_n$ }

  2. for  $i := 1$  to  $2r$ 
    begin
       $\alpha_i := a_{k(i-1)/2+1} \dots a_{ki/2}$ ;  $\beta_i := b_{k(i-1)/2+1} \dots b_{ki/2}$ ;
       $amax_i := \max(\alpha_i)$ ;  $bmax_i := \max(\beta_i)$ 
    end;

  3.  $p := q := 1$ ;

  4. while ( $p \leq 2r$  and  $q \leq 2r$ )
    begin
      if  $amax_p \leq bmax_q$  then
        begin
          add  $\alpha_p$  to  $\gamma$ ;
          all elements in  $\beta_q$  not greater than  $amax_p$ 
          are removed from  $\beta_q$  and added to  $\gamma$ ;
           $p := p + 1$ ; if  $\beta_q$  is empty then  $q := q + 1$ 
        end
      else
        begin
          add  $\beta_q$  to  $\gamma$ ;
          all elements from  $\alpha_p$  not greater than  $bmax_q$ 
          are removed from  $\alpha_p$  and added to  $\gamma$ ;
           $q := q + 1$ ; if  $\alpha_p$  is empty then  $p := p + 1$ 
        end
      end;

  5. if  $p \leq 2r$  then  $\alpha_p, \dots, \alpha_{2r}$  are added to  $\gamma$ ;

  6. if  $q \leq 2r$  then  $\beta_q, \dots, \beta_{2r}$  are added to  $\gamma$ 
end.

```

Theorem 4.2 Let α and β be two k -sorted sequences of length n . Then *MERGE*(α, β, γ, k) returns a k -sorted sequence of length $2n$ which is merged from α and β in $O(n)$ time.

proof: After Step 2, for any pair of i and j , such that $1 \leq i \leq j \leq 2r$, $\alpha_i \leq \alpha_j$ and $\beta_i \leq \beta_j$ (see Figure 2). For each t , at the beginning of t -th iteration of **while** statement of Step 4, any element in γ is not greater than any element in $\alpha_p, \dots, \alpha_{2r}, \beta_q, \dots, \beta_{2r}$. On the other hand, during the t -th iteration, the number of items transferred from α_p and β_p to γ is at most $2k$. Therefore, the sequence in γ is always k -sorted. Hence, at the end of computation, γ is a k -sorted sequence of length $2n$.

From Lemma 4.1, the computing time at Step 1 is $O(n)$. Step 2 obviously takes $O(n)$ time as well. For each iteration of the **while** statement, the computing time is $O(k)$. Since $r = O(n/k)$, the computing time at Step 4 is $O(n/k)O(k) = O(n)$. Therefore, the time for *MERGE*(α, β, γ, k) is $O(n)$. \square

Using procedure *HALVE*, we can design a very simple algorithm that completely sorts a k -sorted sequence in time $O(n \log k)$. It is a variation of the quicksort algorithm in which the partitioning element is chosen to be the median of a given subsequence. For this reason, we call the algorithm *QMSORT*. As shown in [4] and [5], the running time $O(n \log k)$ is optimal within a constant factor. The proof is based on the

decision tree argument. Algorithm *RHEAPSORT* [5] also completely sorts a k -sorted sequence in $O(n \log k)$ time. Its constant factor is smaller than the constant factor for *QMSORT*. However, as shown in the next section, *QMSORT* has a very natural and direct implementation for parallel environments, whereas the parallel implementation of *RHEAPSORT* seems to be impractical.

```

procedure QMSORT( $\alpha, k$ );
begin
  for  $I := \frac{k}{2}, \frac{k}{4}, \frac{k}{8}, \dots$  downto 1 HALVE( $\alpha, \alpha, I$ )
end.

```

Observe that the procedure *HALVE* reduces a $2k$ -sorted into a $(k-1)$ -sorted sequence. Hence it is pointless invoke *HALVE*($\alpha, \alpha, 0$). Moreover, to sort 1-sorted sequences, one may use algorithm *ONESORT* [5], which has been shown to be optimal in the worst case and to be close to the known lower bound in the average case.

The next theorem is an immediate consequence of Theorem 4.1.

Theorem 4.3 *QMSORT* sorts a k -sorted sequence in time $O(n \log k)$.

QMSORT may, of course, be used to sort an arbitrary sequence of n elements which by definition is at least $(n-1)$ -sorted, in time $O(n \log n)$.

5 Parallel k -sorting

In this section, our model of computation is the standard PRAM without concurrent reads or writes. First, let us examine the problem of transforming a $2k$ -sorted sequence of n elements into a $(k-1)$ -sorted sequence.

The procedure *PHALVE* takes as input a $2k$ -sorted sequence γ and returns a $(k-1)$ -sorted sequence δ .

```

procedure PHALVE( $\gamma, \delta, k$ );
{ Suppose  $\gamma = (a_1, a_2, \dots, a_n)$ . Assume  $n = 2kr$ . If  $n$ 
is not a multiple of  $2k$ , the procedure needs a minor
modification. }
begin
  1. for  $i := 1$  to  $r$  do in parallel
    begin
       $\alpha_i := a_{2k(i-1)+1} \dots a_{2ki}$ ;
      PPARTITION( $\alpha_i, \alpha_i, \alpha_{i_2}$ )
    end;

  2. for  $i := 1$  to  $r-1$  do in parallel
    begin
       $\beta_i := \alpha_{i_2} \alpha_{(i+1)_1}$ ;
      PPARTITION( $\beta_i, \beta_i, \beta_{i_2}$ )
    end;

  3.  $\alpha_1 := \alpha_{1_1} \beta_{1_1}$ ;  $\alpha_r := \beta_{(r-1)_2} \alpha_{r_2}$ ;

  4. for  $i := 2$  to  $r-1$  do in parallel
    begin
       $\alpha_i := \beta_{(i-1)_2} \beta_{i_1}$ ;
      PPARTITION( $\alpha_i, \alpha_{i_1}, \alpha_{i_2}$ )
    end;

  5.  $\delta := \alpha_{1_1} \alpha_{1_2} \dots \alpha_{r_1} \alpha_{r_2}$ 
end.

```

Let $f(t)$ denote the time for finding the median of t elements used in procedure *PPARTITION*.

Lemma 5.1 *The computing time for PHALVE(γ, δ, k) by the PRAM is $3f(2k) + O(1)$.*

We now present a parallel algorithm that sorts a k -sorted sequence α .

```

procedure PQMSORT( $\alpha, k$ );
begin
  for  $i := \frac{k}{2}, \frac{k}{4}, \frac{k}{8}, \dots$  downto 1 PHALVE( $\alpha, \alpha, i$ )
end.

```

Theorem 5.1 *PQMSORT sorts a k -sorted sequence of size n in time $O(f(2k) \log k)$, using $O(n)$ processors.*

Proof: The proof of correctness follows directly from Theorem 4.1. The overall running time for *PQMSORT* is $O(f(2k) \log k)$ by Lemma 5.1 \square

As stated in Theorem 5.1, the computing time of *PQMSORT* depends on the efficiency of the median finding algorithm used. For example, if we choose an $O(\log k)$ median algorithm, the time complexity of *PQMSORT* becomes $O(\log^2 k)$.

Corollary 5.1 *PQMSORT sorts a k -sorted sequence of size n in time $O(k \log k)$, using $(\frac{n}{k})$ processors.*

proof: The determination of the medians of each α_i and β_i can be performed by a single processor in $O(k)$ time \square

6 Concluding Remarks

We have designed a number of algorithms for roughly sorted sequences. These algorithms, with the exception of *PQMSORT*, are optimal to within constant factors. We do not yet know the optimal factors for the time complexities of these problems except for the algorithm given in the proof of Lemma 3.1. We are interested in accurate evaluations of these factors. It would also be of interest to redesign our algorithms using a simpler parallel model, e.g., the mesh-connected processor array, rather than the PRAM model of computation.

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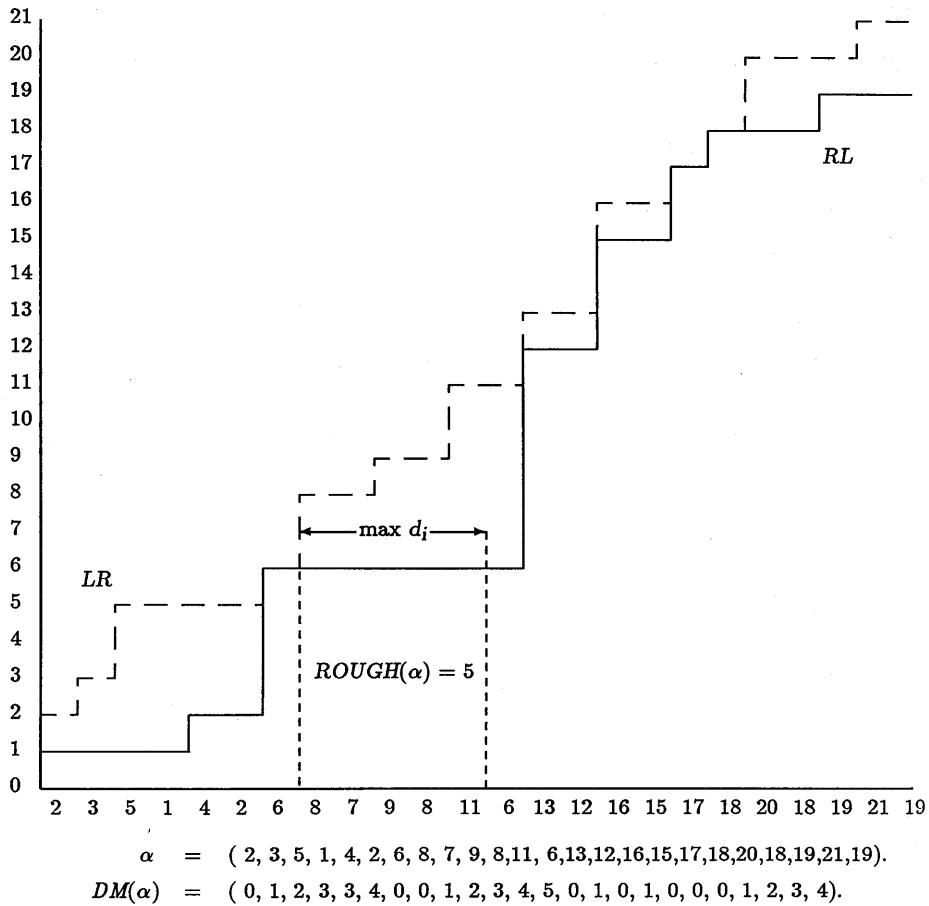


Figure 1. The LR and RL sequences, and the $\max d_i$ from DM , where

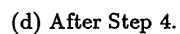
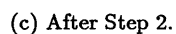
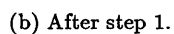
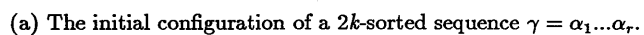


Figure 2. The order of α_{i_1} during the computation by

 $HALVE(\gamma, \delta, \kappa)$, where i is an odd integer.