Information Processing Letters 116 (2016) 718–722

Contents lists available at ScienceDirect

Information Processing Letters

www.elsevier.com/locate/ipl

A tight upper bound on the number of cyclically adjacent transpositions to sort a permutation

Anke van Zuylen [a,*], James Bieron [a], Frans Schalekamp [b], Gexin Yu [a]

[a] Department of Mathematics, The College of William and Mary, Williamsburg, VA, 23185, United States
[b] School of Operations Research & Information Engineering, Cornell University, Ithaca, NY, 14853, United States

ARTICLE INFO

Article history:
Received 15 October 2015
Received in revised form 16 June 2016
Accepted 16 June 2016
Available online 17 June 2016
Communicated by M. Chrobak

Keywords:
Combinatorial problems
Permutations
Cayley graphs
Diameter
Sorting

ABSTRACT

We consider the problem of upper bounding the number of cyclically adjacent transpositions needed to sort a permutation. It is well known that any permutation can be sorted using at most $\frac{n(n-1)}{2}$ adjacent transpositions. We show that, if we allow all adjacent transpositions, as well as the transposition that interchanges the element in position 1 with the element in the last position, then the number of transpositions needed is at most $\lfloor \frac{n^2}{4} \rfloor$.

1. Introduction

In this note we show that the number of operations needed to sort a permutation of length n using "modified bubble sort", where, in addition to adjacent transpositions, we allow the transposition of the elements in the first and last position, is at most $\lfloor \frac{n^2}{4} \rfloor$. This answers an open question that has appeared in multiple contexts. One area where this question has been studied is in the design of interconnection networks, another area is the evolutionary history of the genome.

Interconnection networks are often modeled as undirected graphs, where the goal is to find a graph that has desirable features. The desirable features include the graph being symmetric, having a small diameter, being resistant to failure, etc. Motivated by these concerns, Akers and Krishnamurthy [1] initiate the study of using *Cayley graphs* in the design of interconnection networks. A Cayley graph is a directed graph that is associated with a group and a generating set S. Every element in the group is a node, and there is an arc (e_1, e_2) exactly when $e_2 = se_1$ for some $s \in S$ (where we use e_1 and e_2 to represent both elements in the group, and the nodes associated with these elements). Determining the diameter of this graph, for a given group and generating set, is important in assessing the quality of the network.

Another way of phrasing the result in this note (see below) is that the diameter of the Cayley graph associated with a permutation group of order $n!$, with generating set that consists of all *cyclically adjacent transpositions* is $\lfloor \frac{n^2}{4} \rfloor$. Recall that an adjacent transposition of a permutation is a transposition of two adjacent elements. By *cyclically adjacent transposition* we mean an adjacent transposition, or the transposition of the first and last element in the permutation. This particular Cayley graph is among the Cayley graphs studied in a survey on interconnection networks by Lakshmivarahan, Jwo and Dhrall [8], who refer to it as the modified bubble-sort graph. In their survey, the diameter of the modified bubble-sort graph is listed as being

* Corresponding author.
E-mail addresses: anke@wm.edu (A. van Zuylen), jcbieron@email.wm.edu (J. Bieron), fs@frans.us (F. Schalekamp), gyu@wm.com (G. Yu).

http://dx.doi.org/10.1016/j.ipl.2016.06.006
0020-0190/

unknown. See also Heydemann [6] for another survey of Cayley graphs as interconnection networks.

A second motivation for studying the diameter of this Cayley graph, is the problem of reconstructing the evolutionary history of the genome. Genetic material can be modeled as an element of a permutation group, and the modifications to genetic material can be modeled as generators (which are usually small changes, such as adjacent transpositions). Including the transposition of the first and last element in the permutation is a natural addition in case the genetic material belongs to certain bacteria and viruses, because the (physical) DNA of some bacteria and viruses has a circular structure. We refer the reader to the book [5] for a comprehensive survey on the combinatorial and algorithmic aspects of genome rearrangement.

Note that by symmetry, the diameter of the Cayley graph generated by (cyclically) adjacent transpositions is equal to the maximum over all permutations of the number of (cyclically) adjacent transpositions required to sort the permutation. When considering the Cayley graph generated by adjacent transpositions only, then the diameter is thus equal to the maximum number of operations it takes to bubble sort any permutation π. It is well known that this is equal to the number of inversions of π, and hence the diameter of this Cayley graph of a permutation group of order $n!$ is equal to $\frac{n(n-1)}{2}$.

When considering cyclically adjacent transpositions, the problem becomes remarkably more complex. Jerrum [7] gives a polynomial time algorithm for computing the length of a minimum length sequence of cyclically adjacent transpositions to sort any given permutation (and his method also implies an algorithm for computing a minimum length sequence). Jerrum's algorithm is quite sophisticated, and does not yield an easy expression for the maximum number of transpositions in the sequence. The result in this note relies crucially on the results by Jerrum [7]. Feng, Chitturi and Sudborough [4] prove that $\lfloor \frac{n^2}{4} \rfloor$ is a lower bound, and they conjecture that this bound is tight.

Chen and Skiena [3] consider a more general problem of sorting a permutation using reversals of (exactly) k consecutive elements. Note that a reversal for $k = 2$ is simply an adjacent transposition. Chen and Skiena give upper and lower bounds on the sorting distance for both the case of permutations and circular permutations, where the latter can be thought of as putting the permutation on a cycle, i.e. it identifies all n permutations that can be obtained by (repeatedly) moving every element one position to the right, and the last element to the first position. The upper bound obtained for circular permutations is $O(n^2/k + kn)$. Pevzner [9] and Bafna et al. [2] consider the same problem for the case when $k = 2$. We note that sorting circular permutations using adjacent transpositions is not the same as sorting a permutation using cyclically adjacent transpositions. For the first problem, the number of transpositions needed to sort $(n, 1, 2, 3, \dots, n-1)$ is 0, since the circular permutation $(n, 1, 2, 3, \dots, n-1)$ is equivalent to the identity. When considering the number of cyclically adjacent transpositions to sort the permutation $(n, 1, 2, 3, \dots, n-1)$, the answer is $n-1$.

To the best of our knowledge, the best known upper bound on the number of cyclically adjacent transpositions to sort a permutation was $\frac{n(n-1)}{2}$ prior to our work, i.e., no better upper bound was known than for the case when the transposition of the first and last element is excluded. In this paper, we prove that $\lfloor \frac{n^2}{4} \rfloor$ is an upper bound on the number of cyclically adjacent transpositions needed to sort any permutation of length n, thus resolving an open question of Feng, Chitturi and Sudborough [4]. This matches the lower bound given in [4].

2. Preliminaries

We now introduce the notation we will use. Let π be a permutation of $\{1, 2, \dots, n\}$. We will refer to $\pi(p)$ as the element that is in position p in π. If $\pi(p) = i$, we have $\pi^{-1}(i) = p$, i.e., $\pi^{-1}(i)$ gives the position of element i in π. We will sometimes write π as the ordered sequence $(\pi(1), \pi(2), \dots, \pi(n))$. In the following, we will use i, j, k when we want to refer to an element in $\{1, 2, \dots, n\}$ and p, q, r to refer to a position in $\{1, 2, \dots, n\}$.

Given a permutation π and $p, q \in \{1, 2, \dots, n\}$, applying the transposition (p, q) to π means that we "swap" the elements in positions p and q to obtain a new permutation $\tilde{\pi}$, where $\tilde{\pi}(p) = \pi(q)$, $\tilde{\pi}(q) = \pi(p)$, and $\tilde{\pi}(r) = \pi(r)$ for all $r \in \{1, 2, \dots, n\} \setminus \{p, q\}$.

We say a transposition (p, q) is *adjacent* if $q = p + 1$, and we say a transposition (p, q) is *cyclically adjacent* if $q \equiv p + 1 \pmod n$. From this point on, all transpositions will be cyclically adjacent transpositions, and we will therefore abbreviate cyclically adjacent transposition to *cat*.

It will be convenient to refer to a cat in terms of the elements that are involved in the cat. If $(\pi^{-1}(i), \pi^{-1}(j))$ is a cat, i.e., $\pi^{-1}(i) \equiv \pi^{-1}(j) - 1 \pmod n$, we may use the notion *swap* (i, j) to refer to this cat. We emphasize that a swap (i, j) in π is only defined if $(\pi^{-1}(i), \pi^{-1}(j))$ is a cat, and is denoted as an *ordered* pair, where the first element moves "in clockwise direction", i.e., from position $\pi^{-1}(i)$ to $\pi^{-1}(i) + 1 \equiv \pi^{-1}(j) \pmod n$ and the second element moves in "counterclockwise direction", i.e., from position $\pi^{-1}(j)$ to $\pi^{-1}(j) - 1 \equiv \pi^{-1}(i) \pmod n$.

We say a permutation π is *sorted by a sequence of cats*, if we obtain the identity after the sequence of cats is applied to π. It is well known that any permutation π can be sorted by at most $\frac{n(n-1)}{2}$ adjacent transpositions. We will show that any permutation π of $\{1, \dots, n\}$ can be sorted with a sequence of at most $\lfloor \frac{n^2}{4} \rfloor$ cats.

We now review and state results by Jerrum [7] that we will use in this note. Given a sequence of cats that sort π, we consider the corresponding sequence of swaps of elements. For this sequence of swaps, we let $c(i, j)$ be the number of times swap (i, j) occurs minus the number of times swap (j, i) occurs (we will refer to this quantity as the *net number of times swap* (i, j) occurs in the sequence). We define the net clockwise displacement for element i as $d(i) = \sum_{j \neq i} c(i, j)$. Then we have that

$$\sum_{i=1}^{n} d(i) = 0, \tag{1}$$

since