



Permutation reconstruction from *MinMax*-Betweenness constraints



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ABSTRACT

In this paper, we investigate the reconstruction of permutations on $\{1, 2, \dots, n\}$ from betweenness constraints involving the minimum and the maximum element located between t and $t + 1$, for all $t = 1, 2, \dots, n - 1$. We propose two variants of the problem (directed and undirected), and focus first on the directed version, for which we draw up general features and design a polynomial algorithm in a particular case. Then, we investigate necessary and sufficient conditions for the uniqueness of the reconstruction in both directed and undirected versions, using a parameter k whose variation controls the stringency of the betweenness constraints. We finally point out open problems.

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1. Introduction

The BETWEENNESS problem is motivated by physical mapping in molecular biology and the design of circuits [2]. In this problem, we are given the set $[n] := \{1, 2, \dots, n\}$, for some positive integer n , and a set of m betweenness constraints ($m > 0$), each represented as a triple (x, a, y) with distinct $x, a, y \in [n]$ and signifying that a is required to be between x and y , that is, either x precedes a which precedes y in the left-to-right order, or y precedes a which precedes x in the left-to-right order. The goal is to find a permutation on $[n]$ satisfying a maximum number of betweenness constraints. In [2], it is shown that the BETWEENNESS problem is NP-complete even in the particular case where all the constraints have to be satisfied.

In this paper we are interested in a problem related to the BETWEENNESS problem, which also finds its motivations in molecular biology. Given K ($K \geq 2$) permutations on the same set $[n]$, representing K genomes given by the sequences of their genes, a *common interval* of these permutations is a subset of $[n]$ whose elements are consecutive (*i.e.* they form an interval) on each of the K permutations. Common intervals thus represent regions of the genomes which have identical gene content, but possibly different gene order. Computing common intervals or specific subclasses of them in linear time (up to the number of output intervals) has been done by case-by-case approaches until recently, when we proposed [3] a common linear framework, whose basis is the notion of *MinMax*-profile. The *MinMax*-profile of a permutation P forgets the order of the elements in a permutation, and keeps only essential betweenness information, defined as, for each $t \in [n - 1]$, the minimum and maximum value in the interval delimited by the elements t (included) and $t + 1$ (included) on P (with no restriction on the relative positions of t and $t + 1$ on P). When K permutations are available, their *MinMax*-profile is defined similarly, by considering for every $t \in [n - 1]$ the global minimum and the global maximum of the K intervals delimited by t and $t + 1$ on the K permutations. We show in [3] that, assuming the permutations have been renumbered such that one of them is the identity permutation, the *MinMax*-profile of K permutations is all we need to find common intervals, as well as all the specific subclasses of common intervals defined in the literature, in linear time (up to the number of output intervals).

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Hence, the *MinMax*-profile is a simplified representation of a (set of) permutation(s), which is sufficient to efficiently solve a number of problems related to finding common intervals in permutations. Moreover, it may be computed in linear time [3]. However, it can be easily seen that distinct (sets of) permutations may have the same *MinMax*-profile, implying that the *MinMax*-profile captures a part, but not all, of the information in the (set of) permutation(s).

In this paper, we study the reconstruction of a permutation from a given *MinMax*-profile, and discuss possible generalizations.

2. Definitions and problems

In the remainder of the paper, permutations are defined on $[n]$ and are increased with elements 0 and $n + 1$, added respectively at the beginning and the end of each permutation (and assumed to be fixed). This is due to the need to make the distinction between a permutation and its reverse order permutation.

Definition 1. [3] The *MinMax*-profile of a permutation P on $[n] \cup \{0, n + 1\}$ is the set of *MinMax*-constraints

$$\text{MinMax}(P) = \left\{ t \xrightarrow{[\min_t, \max_t]} t + 1 \mid 0 \leq t \leq n \right\}$$

where \min_t (\max_t , respectively) is the minimum (maximum respectively) element in the interval delimited on P by the element t (included) and the element $t + 1$ (included).

Note that the relative positions on P (i.e. which one is on the left of the other) of $t, t + 1$ on the one hand, and of \min_t, \max_t on the other hand are not indicated by a *MinMax*-profile. In the case where the relative positions of t and $t + 1$ are known for all t , we use the term of *directed MinMax-profile* and the notations $t \xrightarrow{[\min_t, \max_t]} t + 1$ when t is on the left of $t + 1$, respectively $t \xleftarrow{[\min_t, \max_t]} t + 1$ when $t + 1$ is on the left of t .

Example 1. Let $P = (064729185310)$ be a permutation on $[9] \cup \{0, 10\}$. Then its *MinMax*-profile is (note that the *MinMax*-constraints sharing an element are concatenated):

$$0 \xrightarrow{[0, 9]} 1 \xrightarrow{[1, 9]} 2 \xrightarrow{[1, 9]} 3 \xrightarrow{[1, 9]} 4 \xrightarrow{[1, 9]} 5 \xrightarrow{[1, 9]} 6 \xrightarrow{[4, 7]} 7 \xrightarrow{[1, 9]} 8 \xrightarrow{[1, 9]} 9 \xrightarrow{[1, 10]} 10$$

whereas its directed *MinMax*-profile is:

$$0 \xrightarrow{[0, 9]} 1 \xleftarrow{[1, 9]} 2 \xrightarrow{[1, 9]} 3 \xleftarrow{[1, 9]} 4 \xrightarrow{[1, 9]} 5 \xleftarrow{[1, 9]} 6 \xrightarrow{[4, 7]} 7 \xrightarrow{[1, 9]} 8 \xleftarrow{[1, 9]} 9 \xrightarrow{[1, 10]} 10.$$

Notice that the *MinMax*-profile and the directed *MinMax*-profile of any permutation obtained by arbitrarily permuting the elements $\{3, 5, 8\}$ are the same, illustrating that a (directed or not) *MinMax*-profile may correspond to several distinct permutations.

The *MinMax-profile* of a set \mathcal{P} of permutations is defined similarly [3], by requiring that \min_t and \max_t be defined over the union of the intervals delimited by t (included) and $t + 1$ (included) on the K permutations in \mathcal{P} . This definition is given here for the sake of completeness, but is little used in the paper.

We distinguish between the *MinMax*-profile of a (set of) permutation(s) and a *MinMax-profile*:

Definition 2. A *MinMax-profile* on $[n] \cup \{0, n + 1\}$ is a set of *MinMax*-constraints

$$F = \left\{ t \xrightarrow{[m_t, M_t]} t + 1 \mid 0 \leq t \leq n \right\}$$

with $0 \leq m_t \leq t < t + 1 \leq M_t \leq n + 1$.

Again, a *MinMax-profile* is *directed* when for all $t, 0 \leq t \leq n$, the relative position of t with respect to $t + 1$ is given. A *MinMax-profile* may be the *MinMax-profile* of some permutation, or of a set of permutations, but may also be the profile of no (set of) permutation(s). We limit this study to one permutation, and therefore formulate the following problem:

MinMax-BETWEENNESS

Input: A positive integer n , a *MinMax-profile* F on $[n] \cup \{0, n + 1\}$.

Question: Is there a permutation P on $[n] \cup \{0, n + 1\}$ whose *MinMax-profile* is F ?

Looking for a permutation P with *MinMax*-constraints defined by F means satisfying a number of betweenness constraints, as well as a number of non-betweenness constraints. We use the notation $x \xleftrightarrow{a} y$, with $x, y, a \in [n]$ and

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