Journal of Discrete Algorithms 49 (2018) 8–26

Contents lists available at ScienceDirect

Journal of Discrete Algorithms

www.elsevier.com/locate/jda

Common intervals and permutation reconstruction from *MinMax*-betweenness constraints

Léo Pelletier, Irena Rusu [*]

L.I.N.A., UMR 6241, Université de Nantes, 2 rue de la Houssinière, BP 92208, 44322 Nantes, France

ARTICLE INFO

Article history:
Received 30 August 2016
Received in revised form 26 March 2018
Accepted 4 May 2018
Available online xxxx

Keywords:
Betweenness
Permutation
Algorithm
Common intervals

ABSTRACT

The *MinMax*-BETWEENNESS problem is defined as follows. We are given a positive integer n and, for each $t = 0, 1, 2, \dots, n$, two integers m_t and M_t with $m_t \le t$ and $t + 1 \le M_t$ (this is called a *MinMax*-profile). The question is: Is there a permutation P on $\{0, 1, 2, \dots, n + 1\}$ such that m_t is the minimum and M_t is the maximum element of P located between t (included) and $t + 1$ (included), assuming 0 is the leftmost and $n + 1$ is the rightmost element of P?

We consider here the directed variant of the problem, where the left-to-right order of t and $t + 1$ on P is known for each $t = 0, 1, 2, \dots, n$. Whereas the complexity of the general directed or undirected problem is open, the particular case of the directed variant where the intervals $[m_t..M_t]$ ($t \ne 0, n + 1$), containing the integers between m_t (included) and M_t (included), are linearly ordered by inclusion is polynomially solvable. In this case, the *MinMax*-profile is called *linear*.

In this paper, we use separable *MinMax*-subprofiles, that are intimately related to common intervals, to deal with *MinMax*-profiles – that we name *L-reducible* – which are not linear, but present decomposition properties allowing us to handle them using linear *MinMax*-(sub)profiles. We show that for L-reducible *MinMax*-profiles the DIRECTED *MinMax*-BETWEENNESS problem is solvable in polynomial time. We also give a polynomial algorithm to recognize L-reducible *MinMax*-profiles, with running time of $O(n^2)$.

Moreover, we show that the DIRECTED *Min*-BETWEENNESS (resp. DIRECTED *Max*-BETWEENNESS) problem, where only m_t (resp. only M_t) is given for each $t = 0, 1, 2, \dots, n$, is polynomial.

1. Introduction

Let $[n] = \{1, 2, \dots, n\}$ and, for any pair of integers $a, b \in [n]$ with $a \le b$, denote by $[a..b]$ the set $\{a, a + 1, \dots, b\}$. We consider permutations on $[n]$, that are increased with elements 0 and $n + 1$, added respectively at the beginning (i.e. on the left side) and the end (i.e. on the right side) of each permutation. We define the *MinMax*-profile of a permutation as follows:

Definition 1. [10] The *MinMax-profile of a permutation* P on $[n] \cup \{0, n + 1\}$ is the set of so-called *MinMax-constraints*

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

---

[*] Corresponding author.
E-mail address: Irena.Rusu@univ-nantes.fr (I. Rusu).

https://doi.org/10.1016/j.jda.2018.05.001
1570-8667/© 2018 Elsevier B.V. All rights reserved.

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).

It is worth noticing here that the role of 0 and $n+1$ is to avoid a permutation and its mirror permutation to have the same *MinMax*-profile. When the permutation described by a *MinMax*-profile represents a genome, its *MinMax*-profile allows to solve a collection of problems issued from genome comparison applications.

The main notion involved in these applications is that of a common interval.

Definition 2. A *common interval* of K permutations $P_1, P_2, \ldots, P_K$ on $[n] \cup \{0, n+1\}$ is any set $S \subseteq [n]$ such that the elements in S appear on consecutive positions (but possibly with different orders) in each permutation P_k, $k = 1, 2, \ldots, K$.

When each permutation represents a genome, common intervals represent gene groups preserved during evolution. Identifying common intervals is therefore an interesting way to perform genomic analyses such as: compare genomes by computing distances between them, compute phylogenetic trees, find sets of genes that are involved in the same functional process. Finding the common intervals of two or more permutations has been done for instance in [12,3,8]. Practical applications of common intervals on genomes may be found in [1,2,5]. Subclasses of common intervals like conserved, nested, irreducible common, irreducible conserved and maximal nested intervals have also been defined and studied [4,6,7].

The first common framework for efficiently computing all these classes is the one we proposed in [10]. We defined *MinMax*-profiles together with a general algorithm that allows us to find common intervals in a simple way. More precisely, we generate and test interval candidates using only comparisons between their endpoints and the minimum and maximum values provided by the *MinMax*-profiles. This general algorithm can be successfully completed with filters allowing us to generate only subclasses of common intervals. In particular, all the abovementioned classes of common graphs are generated in this way in linear time. *MinMax*-profiles may be seen as a simple and powerful intermediate concept between a permutation and its set of common intervals. But the relationships between these three entities have to be studied before using *MinMax*-profiles instead of permutations, or instead of the common intervals, for further applications.

The question whether the *MinMax*-profile of a permutation is sufficient to deduce the permutation is therefore natural as it allows us to evaluate the quality of the information stored in a *MinMax*-profile. More generally, we ask whether an input data similar to the *MinMax*-profile of a permutation (and simply called a *MinMax*-profile) is really the *MinMax*-profile *of a permutation*. The *MinMax*-Betweenness problem has been proposed in [11], and has been investigated in the same paper in its directed form, where for each t the left-to-right order of t and $t+1$ on the sought permutation P is provided. The main result is that the Directed *MinMax*-Betweenness problem is polynomial for linear *MinMax*-profiles:

Definition 3. A *MinMax*-profile is called *linear* if the set of intervals $\{[m_t..M_t] \mid t = 1, 2, \ldots, n-1\}$ may be linearly ordered by inclusion.

The complexity of the problem in general is unknown. A similar problem is the Betweenness problem, where a set of *betweenness constraints* is given, and the goal is to find a permutation on $[n]$ satisfying a maximum number of betweenness constraints. A betweenness constraint is a triple (x, a, y) with distinct $x, a, y \in [n]$ which signifies that a is required to be between x and y on the sought permutation. The NP-completeness of Betweenness is shown in [9].

In this paper we investigate a new class of *MinMax*-profiles for which the Directed *MinMax*-Betweenness problem may be solved in polynomial time. The paper is organized as follows:

- In Section 2, we introduce *MinMax*-profiles in general (not only for permutations), we define the Directed *MinMax*-Betweenness problem and we identify the constraints that must satisfy any permutation corresponding to a given *MinMax*-profile, according to this problem. We show (Claim 1) that a small part of the constraints may be easily tested, and therefore we slightly simplify the problem.
- Section 3 is a large section in which we show that the problem may be solved in polynomial time for so-called L-reducible *MinMax*-profiles.
    - In Subsection 3.1, we recall the definition of non-trivial common intervals and define separable *MinMax*-subprofiles of a *MinMax*-profile. We identify (Claims 2 and 3) close relationships between separable *MinMax*-subprofiles and common intervals.
    - In Subsection 3.2, we give the algorithm for decomposing a *MinMax*-profile using a separable *MinMax*-subprofile (Algorithm 1). Then we prove the decomposition properties related to the solvability of *MinMax*-(sub)profiles (Theorem 1) and to the solvability of each particular conflict (Theorem 2). We characterize solvable conflicts (Corollary 1) and *MinMax*-profiles whose conflicts are all solvable (called L-reducible *MinMax*-profiles; Corollary 2). Then we prove the correctness and compute the running time of the permutation reconstruction algorithm (Algorithm 2) on L-reducible *MinMax*-profiles (Corollary 3).
- In Section 4 we give a quadratic algorithm (Algorithm 3) to recognize L-reducible *MinMax*-profiles. We show the correctness and the running time of particular steps of this algorithm (Claims 4, 5, 6) before concluding (Theorem 3).