

# Complexity of determining the maximum infection time in the geodetic convexity

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## Abstract

In the geodetic convexity of a graph  $G$ , we define the interval of a set  $S \subseteq V(G)$  as the set formed by  $S$  and all vertices in all shortest paths with endpoints in  $S$ . We say  $S$  is convex if it is equal to its interval. The convex hull of  $S$  can be obtained by repeatedly applying the interval function until obtaining a convex set. Here we consider the problem of determining the maximum  $k$  such that there is a set of vertices  $S$ , whose convex hull is  $V(G)$ , such that it is necessary at least  $k$  applications of the interval function to obtain  $V(G)$ . We show that this problem is NP-complete for bipartite graphs and give a polynomial time algorithm for distance-hereditary graphs.

*Keywords:* Geodetic Convexity, maximum infection time, NP-completeness.

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## 1 Introduction

A family  $\mathcal{C}$  of subsets of a finite set  $V$  is a *convexity on  $V$*  if  $\emptyset, V \in \mathcal{C}$  and  $\mathcal{C}$  is closed under intersections. A set  $S$  of  $\mathcal{C}$  is called a  *$\mathcal{C}$ -convex set*. When  $V$  is the vertex set of a (simple and undirected) graph  $G$ , it is standard to define  $\mathcal{C}$  using a family  $\mathcal{P}$  of paths of  $G$  in such a way that a set  $S \subseteq V(G)$  is a

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$\mathcal{C}$ -convex set if and only if for every path  $P$  in  $\mathcal{P}$  whose extremities belong to  $S$ , all vertices of  $P$  also belong to  $S$ . In that case we have a *graph convexity*.

The most studied graph convexities are the *geodetic convexity* [10,11], the *monophonic convexity* [7,9] and the  *$P_3$  convexity* [1], where  $\mathcal{P}$  is, respectively, the family of all shortest paths, of all induced paths, and of all paths of order three of the graph. A rich source on general convexities is [13].

The  $\mathcal{C}$ -convex hull of  $S$  is the smallest  $\mathcal{C}$ -convex set  $H_{\mathcal{C}}(S)$  containing  $S$ . We say that  $S$  is a  $\mathcal{C}$ -hull set of  $G$  if  $H_{\mathcal{C}}(S) = V(G)$ . The  $\mathcal{C}$ -interval of  $S$ ,  $I_{\mathcal{C}}(S)$ , consists of  $S$  and all vertices lying in some path of  $\mathcal{P}$  that has endpoints in  $S$ . Observe that, since  $\mathcal{P}$  is finite, the  $\mathcal{C}$ -convex hull of  $S$  can be obtained by iteratively applying the  $\mathcal{C}$ -interval function until obtaining a  $\mathcal{C}$ -convex set.

We may also see the above process as an infection that starts at the set  $S$  and spreads to other vertices through the paths (of  $\mathcal{P}$ ) that connect two infected vertices. Here, we are interested in the maximum amount of time needed to infect all vertices starting with a  $\mathcal{C}$ -hull set. More precisely, let  $I_{\mathcal{C}}^0(S) = S$  and  $I_{\mathcal{C}}^k(S) = I_{\mathcal{C}}(I_{\mathcal{C}}^{k-1}(S))$  for  $k \geq 1$ . We say that a hull set  $S$  takes time  $k$  to infect  $G$  if  $I_{\mathcal{C}}^k(S) = V(G)$  but  $I_{\mathcal{C}}^{k-1}(S) \neq V(G)$  (when  $S = V(G)$  we say it takes time 0 to infect  $G$ ). The *infection time of  $G$  relative to  $\mathcal{C}$* , called  $t_{\mathcal{C}}(G)$ , is the maximum  $k$  such that there is a  $\mathcal{C}$ -hull set  $S$  which takes time  $k$  to infect  $G$ . We considered the decision version of this problem.

MAX INFECTION TIME ON CONVEXITY  $\mathcal{C}$

*Input:* A graph  $G$  and an integer  $k$ .

*Question:* Is  $t_{\mathcal{C}}(G) \geq k$ ?

There is vast literature about “infection problems”, also studied under the names “dissemination”, “diffusion” or “conversion”. However, the way such infections spread varies considerably. For example, another common model is  $r$ -neighbour bootstrap percolation in which a vertex becomes infected if it has at least  $r$  infected neighbours, a model introduced by Chalupa, Leath and Reich [5] that found many applications in physics and computer science [8].

The question about the maximum infection time was originally posed by Bollobás for the 2-neighbour bootstrap percolation in the square grid, and solved by Benevides and Przykucki [4]. Note that the 2-neighbour bootstrap percolation model coincides with the infection problem for the  $P_3$  convexity. The MAX INFECTION TIME ON THE  $P_3$  CONVEXITY was considered in [3] where it was shown that it is NP-complete for general graphs and any fixed  $k \geq 4$ , and for bipartite graphs and any fixed  $k \geq 7$ . It was also given polynomial algorithms for planar graphs, trees, and chordal graphs.

In this work we consider the MAX INFECTION TIME problem on the geodetic

convexity. This problem is, therefore, at the intersection of two large branches: “convexity problems” and “infection problems”. In Section 2, we prove that the INFECTION TIME ON GEODETIC CONVEXITY is NP-complete even if the input graph is bipartite and  $k \geq 2$  is fixed. In Section 3, we give a polynomial time algorithm for computing the infection time of a distance-hereditary graph.

We will use the following notation. For any positive integer  $n$ , we define  $[n] = \{k : k \text{ is integer and } 1 \leq k \leq n\}$ . For two vertices  $u, v$  in a graph, the distance from  $u$  to  $v$ ,  $d(u, v)$ , is given by the number of edges in a shortest path between  $u$  and  $v$ . When there is no ambiguity about the convexity that we are using, we drop the symbol  $(\mathcal{C})$  of the convexity.

## 2 Bipartite graphs

In this section we give a sketch of the proof of the following theorem.

**Theorem 2.1** MAX INFECTION TIME ON GEODETIC CONVEXITY, for fixed  $k \geq 2$ , is NP-complete even if the input graph is known to be bipartite.

**Proof** [Sketch] We do a reduction from 3SAT. Consider a boolean formula  $\mathcal{F}$  with  $m$  clauses on a set with  $n$  variables. We construct a bipartite graph  $G$  in the following way. For each clause  $C_i$  of  $\mathcal{F}$  we build the clause gadget depicted in Figure 1 which, for every  $l \in [3]$ , has vertices  $u_i, t_i, v_{i,l}, w_{i,l}, x_{i,l}, y_{i,l}$  along with the edges  $u_i t_i, u_i v_{i,l}, t_i w_{i,l}, v_{i,l} w_{i,l}, w_{i,l} x_{i,l}, x_{i,l} y_{i,l}$ .

We construct a graph  $G$  as follows. Add each clause gadget to  $G$  and further add vertices  $q, r$  and  $s$  along with the edges  $r x_{i,l}, s t_i$  for every  $i \in [m]$  and  $l \in [3]$ . Finally, for every pair of literals  $\ell_{i,a} \in C_i$  and  $\ell_{j,b} \in C_j$ , for  $i \neq j$  and  $a, b \in [3]$ , such that  $\ell_{i,a}$  and  $\ell_{j,b}$  are not the negation of each other, add vertices  $o_{i,a,j,b}, p_{i,a,j,b}$  along with the edges  $o_{i,a,j,b} p_{i,a,j,b}, o_{i,a,j,b} q, o_{i,a,j,b} w_{i,a}, o_{i,a,j,b} w_{j,b}$ , completing the construction of  $G$ . See Figure 2 for a partial construction of the graph  $G$  and note that the gray and white vertices define a bipartition.

We denote  $W = \{w_{i,l} : \text{for } i \in [m] \text{ and } l \in [3]\}$ ,  $T = \{t_i : \text{for } i \in [m]\}$  and similarly  $O = \{o_{i,a,j,b}\}$ , for all values of  $i, a, j, b$  for which  $o_{i,a,j,b}$  is defined. Define  $X, Y, V, U$  and  $P$  in an analogous way. Finally for every  $i \in [m]$ , let  $D_i = \{u_i, v_{i,1}, v_{i,2}, v_{i,3}\}$ .

For  $k = 2$ , the proof of Theorem 2.1 follows from the fact that there exists a truth assignment to the variables  $\{x_1, \dots, x_n\}$  satisfying all clauses of  $\mathcal{F}$  if and only if the infection time of  $G$  is at least 2.

Now suppose that  $k > 2$ . We construct a graph  $H_N$ , such that  $|V(H_N)| = N + 3$  and  $t(H_N) = N$  as follows: start with a 4-cycle  $H_1 = v_1 v_2 v_3 v_4$  and build

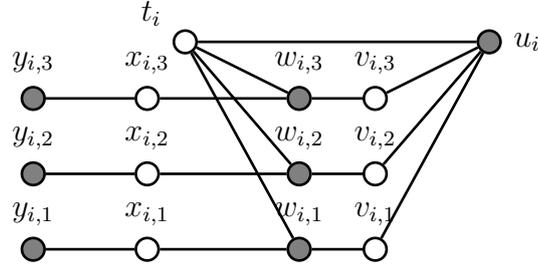


Figure 1. Clause gadget.

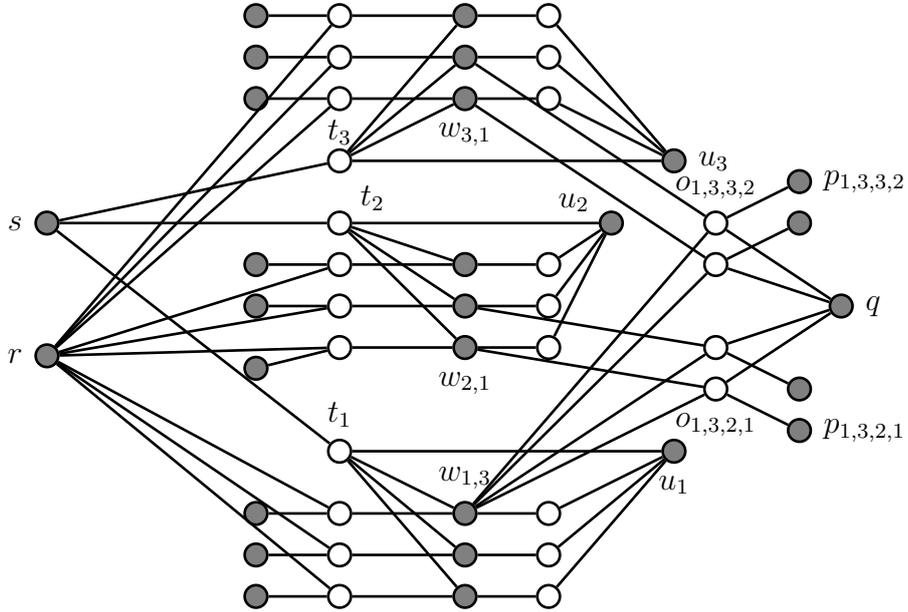


Figure 2. Partial construction of  $G$  for  $\mathcal{F} = \{C_1, C_2, C_3\}$  where  $C_1 = \{x_1, x_2, x_4\}$ ,  $C_2 = \{\bar{x}_2, x_3, \bar{x}_4\}$ ,  $C_3 = \{\bar{x}_1, x_2, \bar{x}_4\}$ .

$H_N$  from  $H_{N-1}$  by adding a vertex  $v_N$  adjacent to  $v_{N-1}$  and  $v_{N-3}$ . (Figure 2).

To finish the proof, it suffices to add to the construction of  $G$  a vertex  $s'$  twin to  $s$  and a copy of the graph  $H_{k-2}$ , such that  $s'$  and  $s$  are identified to the vertices  $v_1$  and  $v_3$  of the copy of  $H_{k-2}$ , respectively. This new graph  $G$  has infection time  $k$  if and only if  $\mathcal{F}$  is satisfiable.  $\square$

### 3 Distance-hereditary graphs

Now, we give the main idea on how to compute  $t(G)$  (in the geodetic convexity) in polynomial time for a distance-hereditary graph  $G$ . A connected graph  $G$

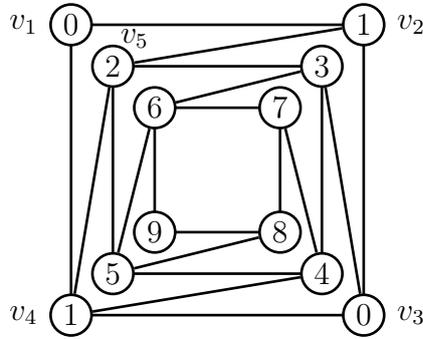


Figure 3. The Graph  $H_9$ . A value inside the vertex is the time which the vertex becomes infected starting from the hull set  $v_1, v_3$ .

is *distance-hereditary* if every pair of vertices has the same distance in every connected induced subgraph of  $G$  (which contains both). This graph class admits a characterization by induced forbidden subgraphs and polynomial time algorithm of recognition [2]. Notice that the graphs  $H_N$ , defined at the end of the proof of Theorem 2.1 (Figure 2) are distance-hereditary. So, there are distance-hereditary graphs with large infection time (compared to  $|V(G)|$ ).

Observe that geodetic and monophonic convexities coincide for distance-hereditary graphs, since for this class of graphs every shortest path is an induced path and vice-versa. Dourado, Protti, Szwarcfiter [7] have recently proved that, although even computing the interval function of a given set in the monophonic convexity is an NP-hard problem, it is possible to compute the size of the smallest (monophonic)-hull set of an arbitrary graph using the so called minimal clique decomposition tree. Our algorithm will start by constructing a minimal clique decomposition tree  $T$  of  $G$ , which can be done in  $O(n^3m)$  steps [7].

We remark that in order to compute  $t(G)$ , (surprisingly) it is not enough to look only at the minimum hull sets [4]. But it clearly suffices to look only to the minimal ones, as every hull set contains a minimal hull set.

We can prove that it is possible to characterize, for general graphs in the *monophonic convexity*, all minimal hull sets. This is a direct consequence of some results in [7], by looking to the atoms of  $G$  (i.e., certain subgraphs which have no clique separator). For this we use a classification of the leaves of a minimal clique decomposition tree  $T$  of  $G$  (see [7]). Then, we can proceed with a finer analysis which further restricts our search space to a polynomial number of sets in a way that it is possible to determine  $t(G)$  by computing the infection time of only such sets. The later can be done applying the interval function (which takes polynomial time for the geodetic convexity [6]).

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