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Safety in *s-t* Paths, Trails and Walks

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Abstract
Given a directed graph G and a pair of nodes s and t, an *s-t bridge* of G is an edge whose removal breaks all s-t paths of G (and thus appears in all s-t paths). Computing all s-t bridges of G is a basic graph problem, solvable in linear time. In this paper, we consider a natural generalisation of this problem, with the notion of "safety" from bioinformatics. We say that a walk W is *safe* with respect to a set $\mathcal{W}$ of s-t walks, if W is a subwalk of all walks in $\mathcal{W}$. We start by considering the maximal safe walks when $\mathcal{W}$ consists of: all s-t paths, all s-t trails, or all s-t walks of G. We show that the solutions for the first two problems immediately follow from finding all s-t bridges after incorporating simple characterisations. However, solving the third problem requires non-trivial techniques for incorporating its characterisation. In particular, we show that there exists a compact representation computable in linear time, that allows outputting all maximal safe walks in time linear in their length. Our solutions also directly extend to multigraphs, except for the second problem, which requires a more involved approach. We further generalise these problems, by assuming that safety is defined only with respect to a subset of *visible* edges. Here we prove a dichotomy between the s-t paths and s-t trails cases, and the s-t walks case: the former two are NP-hard, while the latter is solvable with the same complexity as when all edges are visible. We also show that the same complexity results hold for the analogous generalisations of *s-t articulation points* (nodes appearing in all s-t paths). We thus obtain the best possible results for natural "safety"-generalisations of these

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two fundamental graph problems. Moreover, our algorithms are simple and do not employ any complex data structures, making them ideal for use in practice.

Keywords Directed graph · Connectivity problem · Graph algorithm · Strong bridge · Strong articulation point · Safety · Genome assembly

1 Introduction

Connectivity and reachability are fundamental graph-theoretical problems studied extensively in the literature [9,12,16,22]. A key notion underlying such algorithms is that of edges (or nodes) critical for connectivity or reachability. The most basic variant of these is a bridge (or articulation point), which is defined as follows. A *bridge* of an undirected graph, also referred to as a *cut edge*, is an edge whose removal increases the number of connected components. Similarly, a *strong bridge* in a (directed) graph is an edge whose removal increases the number of strongly connected components of the graph. (Strong) articulation points are defined in an analogous manner by replacing the edge with a node.

Special applications consider the notion of bridge to be parameterised by the nodes that become disconnected upon its removal [18,24]. Given a node s, we say that an edge is an *s bridge* (also referred to as *edge dominators* from source s [18]) if there exists a node t that is no longer reachable from s when the edge is removed. Moreover, given both nodes s and t, an *s-t bridge* is an edge whose removal makes t no longer reachable from s.

From this point onward we assume a fixed (directed) graph G without multiedges but possibly with loops, with n nodes and m edges, and two given nodes s and t of G. Since s-t bridges are exactly the edges (i.e., the paths of length one) appearing in all s-t paths, it is natural to generalise this notion by considering the *paths* (i.e., of length two or more) appearing in all s-t paths. An equivalent way of defining this problem is through the notion of *safety* [25,26]. Given a set of walks $\mathcal{W}$, we say that a walk (or any sequence of nodes or edges) W is *safe* with respect to $\mathcal{W}$ if W is a subwalk of all walks in $\mathcal{W}$. Our problem is obtained by taking $\mathcal{W}$ to be the set of all s-t paths.[1] We will also consider other natural generalisations for $\mathcal{W}$, e.g. all s-t trails and all s-t walks, as we will discuss in Sect. 1.1.

Safety is motivated by real-world problems whose computational formulation admits multiple solutions. For this reason, we will also refer to the set $\mathcal{W}$ as the *candidate set*. By looking at the parts common to all solutions—the safe parts—one can make more informed guesses on what can be correctly reported from the data. This approach is more feasible than e.g., the common approach of simply enumerating all solutions. The motivation for our work comes from the genome assembly problem in bioinformatics, which we review in Sect. 1.2.

Safety has several precursors, the closest being *persistence*: an individual node or edge is called *persistent* if it appears in all solutions to a problem on the given

[1] We will focus on *maximal* safe walks, namely those that cannot be extended left or right without losing safety.

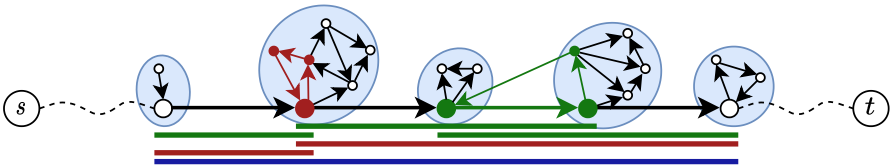


Fig. 1 Safe walks under different models for s-t-safety. The figure shows a sequence of s-t bridges as bold arrows and their bridge components as blue regions. Thick blue, red and green lines show the answers to the MaxSafe stPaths, stTrails and stWalks problems, respectively. Trail breakers and walk breakers have been highlighted in red and green, respectively (Color figure online)

graph. Persistent nodes and edges have been studied for maximum independent sets [17], maximum bipartite matchings [10], assignments and transportations [8]. Other previous notions include *d-transversals* [11] (sets of nodes or edges intersecting every solution to the problem in at least d elements), *d-blockers* [27] (sets of nodes or edges whose removal deteriorates the optimum solution to the problem by at least d), or *most vital nodes or edges* [2].

For undirected graphs, the classical algorithm by Tarjan [23] computes all bridges and articulation points in linear time. However, for directed graphs only recently Italiano et al. [18] presented an algorithm to compute all strong bridges and strong articulation points in linear time. They also showed that classical algorithms [15, 24] compute s bridges in linear time. The s articulation points (or *dominators*) are extensively studied resulting in several linear-time algorithms [1,3,4]. The s-t bridges were studied as minimum s-t cuts in network flow graphs, where an s-t bridge is a cut of *unit* size. These cuts can be discovered iteratively in the residual graph of the classic Ford Fulkerson algorithm [13] after pushing unit flow into the network. Contracting the first cut to s, the next s-t bridge can be discovered, and so on. Since only unit-sized flows are of interest, the algorithm completes in linear time. Recently, this algorithm was simplified for unit-sized cuts (s-t bridges) by Cairo et al. [5].

1.1 Problems Studied

Apart from the candidate set made up of all s-t *paths* (mentioned in the previous section), we will also consider two basic generalisations of it: the set of all s-t *trails* (i.e., walks from s to t which can repeat nodes, but not edges), and the set of all s-t *walks* (i.e., walks from s to t, which can repeat both nodes and edges). We denote the problems of computing the maximal safe walks (in terms of alternating sequences of nodes and edges) for each of these problems as MaxSafe followed by stPaths, stTrails, and stWalks, respectively.

In Fig. 1, we present examples for these problems. Neither of the coloured cycles can be used by an s-t path, therefore the whole thick bluetgm line is safe in stPaths. In stTrails, nodes can be reused and hence the red cycle (defined later as *trail breaker*), makes only the thick red lines as safe. In stWalks, s-t bridges can be reused as well and hence the green cycle (defined later as *walk breaker*), makes only the thick green lines as safe.

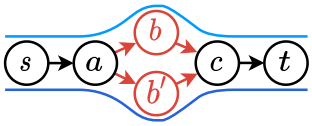


Fig. 2 Safety in the X-stWalks model where X is the black part of the graph. In both stWalks and X-stWalks the possible solution walks are (s, a, b, c, t) and (s, a, b', c, t), highlighted in blue and dark blue. Their X-subsequences are both $(s, a, |, c, t)$ which is therefore safe in the X-stWalks model. The invisible region is marked with a red | in the solution string (Color figure online)

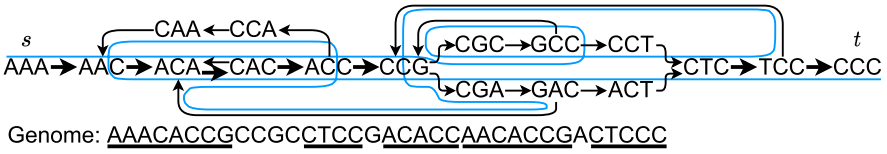
An alternative way to look at these problems is to define safety in terms of only nodes, instead of walks. We define the *node sequence* of a walk W as the sequence (i.e., string) corresponding to V obtained by reading the nodes of W in order. A sequence of nodes is *safe* if it is a substring of the node sequence of every walk in the candidate set. We denote the corresponding safety problems as MaxSafe followed by V-stPaths, V-stTrails, and V-stWalks, respectively. We alternatively refer to them as the V-*visible* problems, whereas the natural case is referred to as G-*visible*. The solutions to these V-visible problems can be obtained by simply leaving out the edges of maximal safe walks of G-visible problems. But when extending to multigraphs, the node-centric trails problem becomes more involved, since it allows the repetition of a node sequence in a trail if and only if the node sequence is connected by multiedges (see Sect. 7).

Another dimension for generalising the above models is to assume also a *visible* subset $X \subseteq V \cup E$ of nodes and edges and to define safety while looking only at the sequence of visible nodes and edges. We denote these problems as MaxSafe followed by X-stPaths, X-stTrails, and X-stWalks, respectively (or X-*visible* problems). For example, we say that a sequence of nodes and edges in X is *safe* for the X-stWalks problem if it is a substring of the X-*subsequence* (subsequence of elements in X) of each s-t walk. We also allow to mark the hidden parts in an X-subsequence with the special symbol | for easier processing in practice (see Fig. 2 for an example).

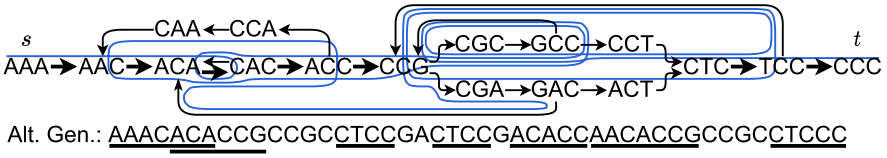
1.2 Bioinformatics Motivation

In this section we motivate our results from a bioinformatics perspective, and the rest of this paper can be read independently from this section.

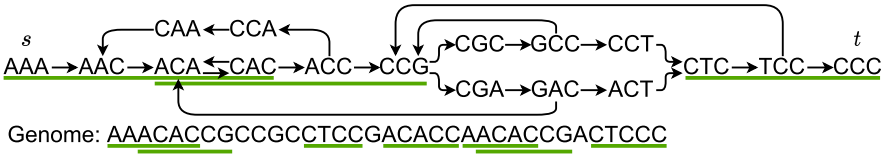
A notable example of a real-world problem admitting multiple solutions is the genome assembly problem from Bioinformatics: one is given a set S of short genomic fragments (or *reads*) and one needs to reconstruct the genome from which these were sequenced (see e.g. [19] for more details). A common approach is to build a graph from the reads, called the *genome graph*. For example, the *edge-centric de Bruijn graph of order* k for the set S of genomic sequences has a node for each distinct substring of length k appearing in some string of S. It further has an edge between two nodes a and b labeled with sequences $(a_1, \ldots, a_k)$ and $(b_1, \ldots, b_k)$, respectively, whenever $a_{i+1} = b_i$ for all i from 1 to $k - 1$ and $(a_1, \ldots, a_k, b_k)$ is a substring of some string in S. Each walk in the de Bruijn graph *spells* a sequence by concatenating the full sequence of its first node with only the last character of all following nodes. Practical



(a) The genome is spelled by the blue walk in the graph. Under the genome, the s-t bridges are highlighted in black. Note that even though in this example the highlighted sequences of consecutive s-t bridges are subwalks of the original genome walk, they are not necessarily subwalks of all possible s-t walks (see Figure 3b), and hence not necessarily safe in the stWalks model.



(b) An alternative genome that could be the ground truth of the graph. In this genome, the erroneous edge (CAC, ACA) is used. Under the genome, the s-t bridges are highlighted in black.

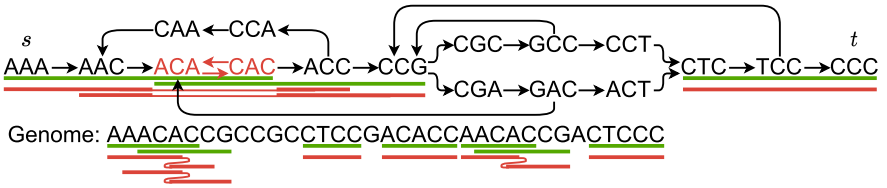


(c) The maximal safe walks in the stWalks model, and their occurrence in the genome are drawn in green. Note that the edge (CAC, ACA) prevents the two leftmost walks from being merged into a single safe walk, because the original genome could traverse this edge as in Figure 3b.

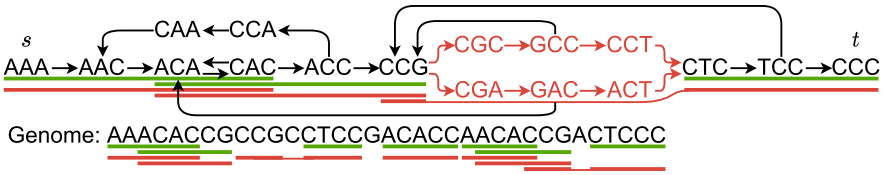
Fig. 3 A genome string, and the edge-centric de Bruijn graph G of order $k = 3$ built directly from the genome string, plus the additional edge (CAC, ACA). We call this additional edge *erroneous*, because its spelling $CACA$ is not a substring of the genome. We take $s = AAA$ and $t = CCC$

assemblers do not assemble full genomes, but instead efficiently output only shorter strings that are guaranteed to appear in the genome. Namely, they output the spellings of those walks that are common to all genome assembly solutions, where a solution is a certain type of walk of the graph. See Fig. 3 for an example of these notions.

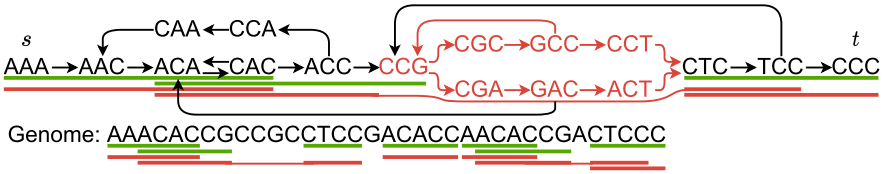
A natural notion of a genome assembly solution is that of a circular walk in the genome graph covering every edge or node at least once [25,26]. Finding all maximal safe walks for the edge-centric solution set can be solved optimally: an optimal quadratic-time algorithm was given in [6], and an optimal output-sensitive algorithm was given in [7]. In this paper we drop both the circularity and the covering requirements from this solution set. This yields more basic graph problems with more fundamental solution sets that can potentially be computed more efficiently in practice. In addition, we introduce a novel generalisation of the problems that makes a subset of nodes and edges *invisible* in the solution set. This models scenarios where we want to ignore some uncertain or complex parts of the graph, but still report if the walks



(a) The edge (CAC, ACA) was discovered to be erroneous due to low abundance. Because it is part of a short cycle which breaks safety, we make the whole short cycle invisible to allow safe solutions to skip the potentially erroneous part.



(b) A bubble was discovered and made invisible. Note that due to the edges outgoing from GCC and GAC, this bubble cannot be easily transformed into a single path.



(c) Suppose that the edge (GCC, CCG) was incorrectly classified as error at graph construction stage. By definition, marking it as invisible has no effect on correctness, and in fact marking also the bubble as invisible produces a longer safe sequence in the X-stWalks model as compared to Figure 4b. Note that simply deleting the edge (GCC, CCG) would result in potentially erroneous safe walks. Consider e.g. the sequence $(ACC, CCG, |, CTC)$, that would be safe if (GCC, CCG) was deleted and the bubble was invisible as in Figure 4b. This is incorrect, because an s-t walk can repeat CCG arbitrarily many times if (GCC, CCG) exists, like e.g. the alternative genome in Figure 3b.

Fig. 4 Example of the applications of the subset visibility model. Red parts of the graphs are invisible and black parts of the graphs are in X. The maximal safe walks in the stWalks model are drawn in green for comparison (they are as in Fig. 3c) and the maximal safe sequences in the X-stWalks model are drawn in red. Thin red lines mark invisible parts of the graph that are replaced with a special character | in the safe sequences. For example the rightmost safe sequence in Fig. 4b is $(CCG, |, CTC, TCC, CCC)$ and spells the string $CCG|CTCCC$ (Color figure online)

flanking this region always appear consecutive in all possible solutions. Moreover, keeping them in the graph still allows them to impact the safety of other walks.

In Fig. 4 we illustrate these positive aspects of the subset visibility model on the same example from Fig. 3. Recall that the edge (CAC, ACA) is erroneous. Figure 4a shows that if this error can be identified (e.g. in practical scenarios by keeping track of the *abundance* of each node or edge, that is in how many reads each node and edge is contained), then longer safe walks can be obtained in the subset visibility model, because we can connect the regions flanking this error.

Another type of graph structure breaking up safe walks are *bubbles*. These can be defined, for example, as a pair of short paths between two nodes of roughly equal

Table 1 Computational complexity of the problems studied in this paper for *multigraphs*. By $len(S)$ we denote the total length of the solution S in terms of number of edges (not required when the compact representation suffices). The complexity marked with (*) becomes $O(m+n)$ for simple graphs (without *multiedges*), while the others remain the same

Visibility	MaxSafe stPaths	MaxSafe stTrails	MaxSafe stWalks
G	$O(m+n)$	$O(m+n)$	$O(m+n+len(S))$
V	$O(m+n)$	$O(m+n+len(S))$*	$O(m+n+len(S))$
X	NP-hard	NP-hard	$O(m+n+len(S))$

length (there exist more advanced definitions such as e.g. superbubbles [21]). In Fig. 4b we mark a bubble of the graph as invisible and again show that longer safe walks can be obtained by connecting the two regions flanking the bubble. In fact, bubbles are common structures in de Bruijn graphs. In this example, the bubble arises from a string having two occurrences inside the genome, that differ by one character. Another common source of bubbles are sequencing errors. Furthermore, diploid genomes such as human contain a maternal and a paternal copy of the chromosomes, which are sequenced together. A position where the two copies differ analogously leads to a bubble.

In Fig. 4 we consider the case when during the graph construction stage an edge was falsely classified as error. If one were to simply delete it, this could lead to safe walks that may not be part of the original genome (and thus incorrect). However, if instead it is marked as invisible, this has no effect on correctness, and in fact it leads to longer safe walks.

1.3 Results and Overview of Our Approach

In this paper we characterise the complexity of all nine MaxSafe problems for graphs (possibly having loops), and later extend our results to multigraphs. We adapt our characterisations to optimal algorithms using the simple algorithm for computing all s-t bridges [5] at its core, where MaxSafe stWalks requires additional techniques.

All our results are also directly extendable to multigraphs, except for the V-visible stTrails which requires a more involved approach. See Table 1 for a summary of these results. The V-visible problems are an interesting special case of the X-visible problems, as they are solvable in linear time even though they restrict visibility. This is a useful observation, as genome assembly problems are often modelled with a node-centric graph [25,26]. In practice, the X-visible models are most likely to yield best results, as they have the best ability to extract long safe walks from a perturbed graph (recall Fig. 4). Moreover, in practice it might be hard to derive single-visit constraints for nodes or edges as in the paths and trails models. This makes X-stWalks likely the most practical variant. But to keep all options open and to allow for an incremental description of our results, we give a complete picture of the theoretical landscape and solve (or prove NP-hard) also the other problem variants.

We solve all the linearly solvable MaxSafe problems with a similar algorithmic approach. Observe that a non-empty walk is uniquely defined by a sequence of edges.

Therefore, we can simplify the G-visible and the V-visible problems to separately computing the maximal safe *edge sequences* (analogue to *node sequences*) and the maximal safe *empty* walks (i.e. that consist of a single node). To obtain the solutions of the G-visible problems, it then suffices to complete the edge sequences with their corresponding nodes. And to obtain the solutions of the V-visible problems, observe that a sequence of nodes is safe if and only if it spells out the nodes of a safe walk. Therefore we take the solution of the corresponding G-visible problem and remove the edges. This separation has the advantage that for the more complex graph structures that govern the safety of non-empty walks we only need to consider edges, and adding back the nodes in the end is trivial. Moreover, if we are only interested in safe sequences of edges, we simply skip adding the nodes. Using a simple graph transformation, the MaxSafe X-stWalks can also be solved by considering only edges.

Observe that for a sequence of edges to be safe in our models, each edge needs to be safe on its own. Therefore, a safe sequence can only contain visible s-t bridges, which we compute as the first step. This *bridge sequence* acts as the core of our solution, in the way that we can always describe the solution as a set of substrings of the bridge sequence, such that each s-t bridge is part of at least one maximal safe sequence. The bridge sequence (and similarly the articulation sequence) can be computed with the classical min-cut algorithm [13]. This algorithm was recently simplified for s-t bridges (or s-t articulation points) by Cairo et al. [5].

The second step of our algorithms is to compute certain *breaking structures* (as shown in Fig. 1) that determine which substrings of the bridge sequence are maximal safe. For stPaths and stTrails and their V-visible counterparts, the breaking structures do not cause solutions to overlap. Since the length of the bridge sequence is in $O(n)$ and the breaking structures that define non-overlapping solutions are simple, we obtain the following result.

Theorem 1 *Given a graph $G := (V, E)$ with n nodes, m edges and $s, t \in V$, there exist algorithms to compute* MaxSafe *G-visible (or V-visible)* stPaths *and* stTrails *in $O(m + n)$ time.*

When extending to stWalks, we get more complex breaking structures that both overlap themselves and cause the solutions to overlap. This poses two problems. First, there can be up to $O(n^2)$ of these breaking structures (see Fig. 8), and second, the total length of the solution can be up to $O(n^2)$ (see Fig. 9). To handle the high amount of breaking structures, we show that they can be reduced to a dominating set of size $O(n)$, which can be computed in $O(m + n)$ time without computing all breaking structures first. To handle the solution length, we make use of the bridge sequence B.

We show that there are at most $O(|B|)$ maximal safe sequences, which allows us to design a compact representation for the whole solution which can be unpacked in *output-sensitive* linear time (time linear in output size). This representation consists of the bridge sequence and the start and end indices of each maximal safe sequence. Its total size is $O(|B|)$, and since each bridge is safe it never exceeds the total length of the solution. We show that this data structure can be computed in $O(m + n)$ time.

In X-stWalks, we can also compute the respective breaking structures in linear time, and represent the solution as a set of subsequences of the sequence of visible bridges. In contrast to X-visible stPaths and stTrails, there are no restrictions on

visits to nodes or edges, so the question if a breaking structure is actually breaking can be decided independent of the global topology. This again results in an $O(m+n)$ algorithm.

Theorem 2 *Given a graph $G := (V, E)$ with n nodes, m edges and $s, t \in V$, the corresponding bridge sequence B and a subset $X \subseteq V \cup E$, there exist algorithms to compute a compact representation of the solution S of* MaxSafe *X-visible* stWalks *of size $O(|B|)$ in $O(m+n)$ time, which can report the complete solution in $O(len(S))$ time.*

Notice that Theorem 2 also works when considering *subset visibility* for stWalks. In contrast to this, when considering *subset visibility* for stPaths and stTrails, the respective safety problems are NP-hard. We prove that by reducing from the Detour problem of finding a u-v path passing through a third given node w (see Problem 1) which is known to be NP-hard. The reduction is possible since the problems forbid edge repetitions and with subset visibility we can focus on the nodes of the Detour instance. This reduction is not possible for stWalks since it allows to repeat nodes and edges arbitrarily.

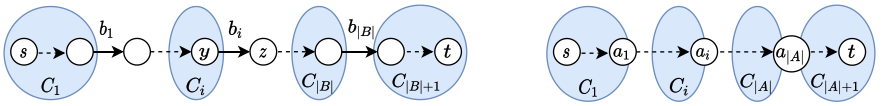
Theorem 3 *The* MaxSafe *X-visible* stPaths *and* stTrails *problems are NP-hard, even when deciding the safety of a sequence of just two elements of X and restricting X to contain only nodes or only edges.*

Organisation of the Paper. We describe the results in an incremental manner, gradually building upon the previous solution to solve harder problems. In Sect. 2 we define our notation and describe some preliminary results including the s-t bridge algorithm. In Sect. 3 we describe how the s-t bridge algorithm can be expanded to solve MaxSafe stPaths and MaxSafe stTrails. In Sect. 4 we characterise MaxSafe stWalks and in Sect. 5 we introduce an algorithm that can be used on top of the s-t bridge algorithm to solve MaxSafe stWalks. As stated above, solving these problems also solves all V-visible problems. In Sect. 6 we describe how that algorithm can be expanded to solve MaxSafe X-stWalks. In Sect. 7 we describe how to extend our results to multigraphs. In Sect. 8 we review our results.

2 Notation and Preliminaries

As defined above, we assume a fixed graph $G := (V, E)$, where V is a set of n nodes and E a set of m edges. Furthermore, we assume two nodes $s, t \in V$ are given. A *graph* is directed and may include loops, but not multiedges. A graph with multiedges is a *multigraph*. Given a set of nodes and edges $X \subseteq V \cup E$, or a single node or edge X, then $G[X]$ denotes its induced subgraph and $G - X$ is the result of removing all edges and nodes from X (together with their incident edges). If X contains only edges, we may also write $G \setminus X$.

Given an edge $e = (u, v)$, $\text{HEAD}(e) = v$ denotes its HEAD and $\text{TAIL}(e) = u$ denotes its TAIL. Given a sequence, a *subsequence* is obtained by removing arbitrary elements, while a *substring* is obtained by removing a prefix and a suffix (both possibly empty).



(a) Bridge sequence $B = \{b_1, \ldots, b_{|B|}\}$ and corresponding bridge components $\mathcal{C} = \{C_1, \ldots, C_{|B|+1}\}$.

(b) Articulation sequence $A = \{a_1, \ldots, a_{|A|}\}$ and its components $\mathcal{C} = \{C_1, \ldots, C_{|A|+1}\}$.

Fig. 5 Bridge and articulation sequences with their components along s-t path. Recall that C_i is the new part of G reachable from s in $G \setminus b_i$ (or $G - a_i$) in comparison to $G \setminus b_{i-1}$ (or $G - a_{i-1}$)

A sequence $W := (v_1, e_1, v_2, \ldots, v_{|W|}, e_{|W|}, v_{|W|+1})$ of nodes v_i and edges e_i is a v_1-$v_{|W|+1}$ *walk* (or simply *walk*) if $v_i = \text{TAIL}(e_i)$ and $v_{i+1} = \text{HEAD}(e_i)$ for all $i \in \{1, \ldots, |W|\}$. Its subsequence of only elements from a set X is called its X-*subsequence*; if $X = V$ it is called its *node sequence*, and if $X = E$ it is called its *edge sequence*. A walk W is a v_1-$v_{|W|+1}$ *trail* (or simply *trail*) if it repeats no edge, and it is a v_1-$v_{|W|+1}$ *path* (or simply *path*) if it additionally repeats no node, except that v_1 may equal $v_{|W|+1}$, in which case it is a *cycle*. A walk W is *empty* if it contains nothing or a single node and *non-empty* otherwise. A walk W *contains* a sequence of edges (or nodes), if that sequence is a substring of its edge sequence (or node sequence).

The *node expansion* of a node v is an operation that transforms G into a graph G' by adding a node v' and an edge e_v from v to v' and moving all out-edges from v to v'. We call e_v the *internal edge* of v.

Let $B = \{b_1, b_2, ..., b_{|B|}\}$ be the set of s-t bridges of G. By definition, for all $b_i \in B$ there exists no path from s to t in $G \setminus b_i$ (see Fig. 5a), and all s-t bridges in B appear on every s-t path in G. Further, the s-t bridges in B demonstrate the following interesting property.

Lemma 1 *The s-t bridges in B are visited in the same order by every s-t path in G.*

Proof It is sufficient to prove that for any $b_i \in B$, all $b_j \in B$ (where $j \neq i$) can be categorised into those which are always visited before b_i and those that are always visited after b_i irrespective of the s-t path chosen in G. Consider the graph $G \setminus b_i$, observe that every such b_j is either reachable from s, or can reach t. It cannot fall in both categories as it would result in an s-t path in $G \setminus b_i$, which violates b_i being an s-t bridge. Further, it has to be in at least one category by considering any s-t path of G, where b_i appears either between s and b_j or between b_j and t. Hence, those reachable from s in $G \setminus b_i$ are always visited before b_i, and those able to reach t in $G \setminus b_i$ are always visited after b_i, irrespective of the s-t path chosen in G. □

Thus, abusing the notation, we define B to be the *bridge sequence* containing the s-t bridges ordered by their visit time on any s-t path. Such a bridge sequence B implies an increasing part of the graph being reachable from s in $G \setminus b_i$, as i increases. We thus divide the graph reachable from s into *bridge components* $\mathcal{C} = \{C_1, C_2, ..., C_{|B|+1}\}$, where C_i (for $i \leq |B|$) denotes the part of the graph that is reachable from s in $G \setminus b_i$ but was not reachable in $G \setminus b_{i-1}$ (if any). Additionally, for notational convenience we assume $C_{|B|+1}$ to be the part of the graph reachable from s in G, but not in $G \setminus b_{|B|}$ (see Fig. 5a). Since bridge components are separated by s-t bridges, every s-t path enters

C_i at a unique node (HEAD(b_{i-1}) or s for C_1) referred to as its *entrance*. Similarly, it leaves C_i at a unique node (TAIL(b_i) or t for $C_{|B|+1}$) referred to as its *exit*.

Similarly, the *s-t articulation points* are defined as the set of nodes $A \subseteq V$, such that removal of any *s-t* articulation point in A disconnects all *s-t* paths in G. Thus, $A = \{a_1, a_2, ..., a_{|A|}\}$ is a set of nodes such that $\forall a_i \in A$ there exists no path from s to t in $G - a_i$. The *s-t* articulation points in A also follow a fixed order in every *s-t* path (like *s-t* bridges), so A can be treated as a sequence and it defines the corresponding components $\mathcal{C}$ (see Fig. 5b). Note that the *entrance* and *exit* of an articulation component C_i are the preceding and succeeding *s-t* articulation points (if any), else s and t respectively.

The *s-t* bridges and articulation points along with their component associations can be computed in linear time, using either flows as described above, or the referenced simplification.

Theorem 4 *([5,13]) Given a graph $G := (V, E)$ with n nodes, m edges and $s, t \in V$, there exists an algorithm to compute all s-t bridges and s-t articulation points, along with their component associations, in $O(m + n)$ time.*

3 Safety for stPaths and stTrails

The *s-t* bridge algorithm (Theorem 4) is the main building block for proving Theorem 1. Recall that we simplified the corresponding problems to only finding the maximal safe edge sequences. The solution to MaxSafe stPaths directly follows from the *s-t* bridge algorithm.

Observe that for two *s-t* bridges to form a safe sequence, they need to be adjacent. In the stPaths model, this is also sufficient, because visiting any other edge from the intermediate node would repeat the node to reach the latter edge (see the thick blue line in Fig. 1). Therefore, we get the following characterisation.

Theorem 5 *(Safety for stPaths) A substring of the bridge sequence is safe under the stPaths model, if and only if each consecutive pair of edges is adjacent.*

Proof ($\Rightarrow$) Let L be a substring of the bridge sequence that is safe under the stPaths model. Then L is a subpath of an arbitrary *s-t* path.

($\Leftarrow$) Let $L := (e_1, \ldots, e_{|L|})$ be a substring of the bridge sequence such that each consecutive pair of edges is adjacent. Let W be an *s-t* path and W_E its E-subsequence. We prove that L is a substring of W_E by induction. For the base case, note that W_E contains e_1 since L is made of strong *s-t* bridges. For the inductive step, assume that W_E contains $(e_1, \ldots, e_i)$ as substring. Since L is a substring of the bridge sequence, W contains e_{i+1} after e_i. And since HEAD(e_i) = TAIL(e_{i+1}) and W is a path, it contains e_{i+1} immediately after e_i. □

Since each *s-t* path is an *s-t* trail, adjacency is still necessary for safety of stTrails, but not sufficient. In Fig. 1, the *s-t* trail that uses the red cycle breaks the safe stPaths (thick blue line). Thus, such a red cycle or the non-adjacency of *s-t* bridges makes a *trail breaker*.

(a) A trail breaker between adjacent s-t bridges.

(b) A trail breaker between non-adjacent s-t bridges.

Fig. 6 Examples for trail breakers (red). The bold edges are s-t bridges and the blue regions mark bridge components. Note that in (**a**), the trail breaker could also be a loop (Color figure online)

Definition 1 (Trail Breaker) A *trail breaker* for two consecutive s-t bridges b_i and b_{i+1} is a non-empty path from $\text{HEAD}(b_i)$ to $\text{TAIL}(b_{i+1})$ that does not contain b_i or b_{i+1}.

Any path P which is a trail breaker for a sequence (b_i, b_{i+1}) lies completely within the bridge component C_{i+1}. Otherwise, P would also contain either b_i or b_{i+1}, which is not allowed. Note also that P is a cycle if $\text{HEAD}(b_i) = \text{TAIL}(b_{i+1})$. See Fig. 6a for an illustration of a circular trail breaker and Fig. 6b for a non-circular one. We get the following characterisation.

Theorem 6 *(Safety for* StTrails*) A substring of the bridge sequence is safe under the* StTrails *model, if and only if it has no trail breaker.*

Proof ($\Rightarrow$) Let L be a substring of the bridge sequence that is safe under the StTrails model. Assume for a contradiction that L contains a trail breaker P from $\text{HEAD}(e_i)$ to $\text{TAIL}(e_{i+1})$ for some $i \in \{1, \ldots, |L| - 1\}$. As such, P is completely inside a bridge component C (the one with exit $\text{TAIL}(e_{i+1})$). It holds that any s-t trail W (which contains L as substring, because L is safe) does not contain any edge from C. As a result, we can insert P in W between $\text{HEAD}(e_i)$ and $\text{TAIL}(e_{i+1})$ to obtain an s-t trail W' that does not contain L as a substring. This contradicts the safety of L.

($\Leftarrow$) Let $L := (e_1, \ldots, e_{|L|})$ be a substring of the bridge sequence that has no trail breaker. Let W be an s-t trail and let W_E be the E-subsequence of W. We prove that L is a substring of W_E by induction. Note that W_E contains e_1, by assumption. For the inductive step, suppose that W_E contains $(e_1, \ldots, e_i)$ as substring. Since L is a substring of the bridge sequence, W_E contains e_{i+1} after e_i. And since L has no trail breaker, each non-empty $\text{HEAD}(e_i)$-$\text{TAIL}(e_{i+1})$ path P contains e_i or e_{i+1}. But e_i is already used by W on the way to $\text{HEAD}(e_i)$, and e_{i+1} needs to be used to reach t from $\text{TAIL}(e_{i+1})$. So no such P can be a subwalk of W, and thus e_i is immediately followed by e_{i+1} in W_E. □

Using these characterisations, the s-t bridge algorithm can be directly used to solve the problems. After computing the s-t bridges and bridge components, the bridge sequence is split between non-adjacent pairs of consecutive s-t bridges, solving MaxSafe stPaths. For MaxSafe stTrails, the residual pairs of consecutive s-t bridges are checked for a trail breaker by checking if there is an incoming edge to $\text{TAIL}(b_i)$ from a node in C_i. Thus, both problems can be solved in $O(m + n)$ time, proving Theorem 1.

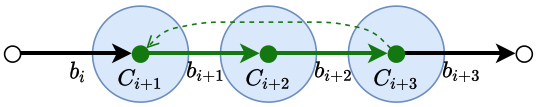


Fig. 7 An example for a walk breaker, highlighted in green. The bold edges are s-t bridges and the blue regions mark bridge components. In this example $L := (e_1 = b_i, \ldots, e_{|L|} = b_{i+3})$ and e_i, e_{i+1} can be chosen as any consecutive pair of edges in L (Color figure online)

4 Safety for StWalks

Unlike the previous problems, solving MaxSafe stWalks requires another algorithmic building block. Again, since each s-t trail is an s-t walk, the absence of trail breakers is necessary for safety for stWalks, but not sufficient. In Fig. 1, an s-t walk using the green cycle breaks the thick red line that is safe in stTrails. Thus, such a green cycle or a trail breaker makes a *walk breaker*.

Definition 2 (Walk Breaker) A *walk breaker* for a substring $L := (e_1, \ldots, e_{|L|})$ of the bridge sequence is a non-empty path from $\text{HEAD}(e_i)$ to $\text{TAIL}(e_{i+1})$ that does not contain the first or last edge from L. Its *bridge sequence* is L.

Walk breakers can stay within a single bridge component (like trail breakers, recall Fig. 6), but can also include multiple bridge components (see Fig. 7).

Characterisation for stWalks. Since a walk breaker P contains neither the first nor the last edge of its corresponding substring L of the bridge sequence, it contains no prefix or suffix of L. Therefore, if P is inserted into an s-t walk that contains L, then the result contains a prefix and a suffix of L that together spell L, but that are interrupted by a subwalk that neither completes a prefix or suffix nor contains L itself. Thus, P contradicts the safety of L. On the other hand, if it is possible to construct an s-t walk W that does not contain L, then W contains a last occurrence of e_1, the first s-t bridge of L. After this last occurrence of e_1, W contains a non-empty subwalk W' between a pair of consecutive s-t bridges e_i, e_{i+1} from L that does not contain e_1 or e_{i+1}, and hence neither $e_{|L|}$. Therefore, W' is a walk breaker for L. Resulting, we get the following characterisation.

Theorem 7 *(Safety for* stWalks*) A substring of the bridge sequence is safe under the* stWalks *model, if and only if it has no walk breaker.*

Proof ($\Rightarrow$) Let L be a substring of the bridge sequence that is safe under the stWalks model. If there is a walk breaker for L, then from an s-t walk W an s-t walk W' can be constructed by inserting the walk breaker into every occurrence of L. But then, L is not a substring of W'.

($\Leftarrow$) Let $L := (e_1, \ldots, e_{|L|})$ be a substring of the bridge sequence that has no walk breaker. Let W be an s-t walk and let W_E be its E-subsequence. Since L is a substring of the bridge sequence, W_E contains a substring W'_E that starts from the last occurrence of e_1 and ends in the first occurrence of $e_{|L|}$ after that, and L is a subsequence of W'_E. We prove that L is a prefix of W'_E by induction. By definition, W'_E starts with e_1. For the inductive step, suppose that $(e_1, \ldots, e_i)$ is a prefix of W'_E. By definition of W',

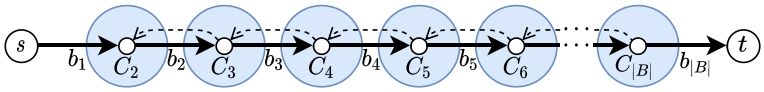


Fig. 8 A graph with $\Theta(n^2)$ walk breakers. The bold edges are s-t bridges and the blue regions mark bridge components (Color figure online)

none of its HEAD(e_i)-TAIL(e_{i+1})-subwalks contain e_1 or $e_{|L|}$. Therefore, since L does not have any walk breaker, e_{i+1} immediately follows e_i in W'_E. □

5 Computing Walk Breakers Efficiently

Since walk breakers can span over multiple bridge components, their structure is more complex than that of trail breakers. But as with trail breakers, the only edges of the walk breaker that are relevant are the s-t bridges. Moreover, since walk breakers cannot skip s-t bridges they always correspond to a *substring* of the bridge sequence, where walk breakers with same *substrings* are equivalent. We refer to this substring as the *bridge sequence* of the walk breaker, and call its first edge the *start* and its last edge the *end* of the walk breaker. If a walk breaker that connects b_i to b_{i+1}, $i \in \{1, \ldots, |B| - 1\}$ contains no s-t bridge (i.e. it is equivalent to a trail breaker), then we call b_{i+1} its start and b_i its end. We call the amount of s-t bridges in the bridge sequence of a walk breaker its *bridge length*.

Minimal Walk Breakers. Given s and t, in the worst case, a graph may contain up to $\Theta(n^2)$ different walk breakers; see Fig. 8 for an example. In this graph, there are $|B| - i - 1$ walk breakers of bridge length i, for each $i \in \{1, \ldots, |B| - 2\}$. However, if the bridge sequence of a walk breaker is a substring of the bridge sequence of another walk breaker, every walk proven unsafe by the *latter* is also proven unsafe by the *former*, i.e., the *former* dominates the *latter*. Hence, computing all walk breakers is wasteful and we only focus on inclusion-minimal walk breakers, referred to as *minimal walk breakers* which are only dominated by themselves.

With this notion of domination, it suffices to compute the set of minimal walk breakers in the graph to exclude all the unsafe walks. Note that at most one minimal walk breaker starts and ends at each s-t bridge, otherwise one would dominate the other. Therefore, there are at most $O(|B|)$ different minimal walk breakers for a bridge sequence B.

We now describe how to compute the minimal walk breakers (and hence the safe walks) in linear time.

Algorithm. Using s-t bridges and trail breakers (walk breakers of zero bridge length) computed earlier, we now compute the minimal walk breakers of non-zero bridge length in two stages. First, we compute the $O(|B|)$ walk breakers that are minimal with respect to their starts. Then we remove the dominated walk breakers to get the globally minimal walk breakers.

Algorithm 1: MINIMAL WALK BREAKERS

Input: Graph $G := (V, E)$, with s-t bridge sequence B and its components in $\mathcal{C}$.
Output: Set of walk breakers of non-zero bridge length that are minimal from their starts.

```
   /* Stage one                                                              */
1  forall the i ∈ {2, ..., |B|} do                  // initialise walk breakers
2      if there exists a trail breaker from b_{i-1} to b_i then end[i] ← i − 1 else end[i] ← |B|
       // signifies empty starting from i
3  forall the i ∈ {2, ..., |B| − 1} do  Mark nodes in C_i reverse reachable from TAIL(b_i)
4  forall the j ∈ {2, ..., |B| − 1} do
5      forall the u ∈ C_{j+1} do    // circular walk breakers ending with tail(b_j)
6          forall the (u, v) ∈ E : v ∈ C_i, 2 ≤ i ≤ j do
7              if v is marked then
8                  end[i] ← min{end[i], j}

   /* Stage two                                                              */
9  min ← |B|                                        // minimum end seen so far
10 forall the i ∈ {2, ..., |B|} in reverse do
11     if end[i] < min then                    // ignore dominated walk breakers
12         Add (i, end[i]) to SOL
13         min ← min{min, end[i]}            // walk breaker is new leftmost end
14     Return SOL
```

In the first stage, we start by performing backwards traversals from t and the tail of each s-t bridge that stay within the bridge component they started in. This way, we *mark* each node that is reverse reachable from the exit of its bridge component. Now, all the walk breakers minimal from their start correspond to *backward edges* e of the following form: an edge e from C_j to C_i $(i < j)$ where HEAD(e) is marked. Intuitively, a minimal walk breaker contains a single backward edge, because if it has multiple backward edges its minimality would be disproven by one of its backwards edges. Moreover, HEAD(e) needs to be marked to ensure that it reaches the bridge sequence to actually connect two s-t bridges (formally proved later).

Hence, we iterate over all such backward edges to compute the dominating walk breaker starting from each s-t bridge. In the second stage, we traverse the walk breakers in reverse order of their starts and remove those that do not end before their successor (in forward order), and hence are dominated by the successor.

All stages of Algorithm 1 run in linear time, and hence we get the following theorem (see Algorithm 1 for the pseudocode).

Theorem 8 *Given a graph $G := (V, E)$ with n nodes, m edges and $s, t \in V$, the set of minimal walk breakers for* STWALKS *can be computed in $O(m + n)$ time.*

Correctness. We now formally prove the following essential property of minimal walk breakers described above, which establishes the correctness of our algorithm.

Lemma 2 *A minimal walk breaker of non-zero bridge length with bridge sequence starting at b_i and ending at b_j $(i \leq j)$, satisfies the following conditions*

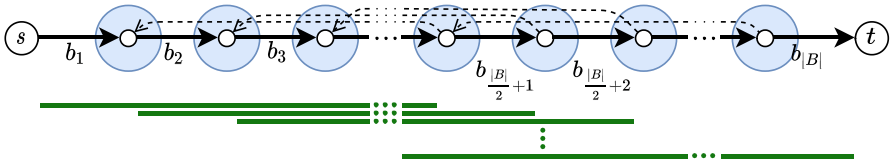


Fig. 9 A graph with maximal safe sequences for STWALKS of total length $\Theta(n^2)$ ($|B|$ is even)

(a) There exists a backward edge *e from* C_{j+1} *to* C_i.
(b) The exit of C_i *is reachable from* HEAD(e) *(i.e. marked).*

Proof We first prove that the minimal walk breaker contains a single backward edge by contradiction. Assume it contains multiple backward edges e_1, ..., e_k in order. Now consider a walk breaker using only the backward edge e_1, clearly its bridge sequence is a substring of the bridge sequence of the original walk breaker and hence dominates it.

Now, to complete the walk breaker we require TAIL(e) to be reachable from HEAD(b_j) and TAIL(b_i) to be reachable from HEAD(e). Since e originates from C_{j+1} with its entrance HEAD(b_j) we can reach TAIL(e). The latter case is ensured by the algorithm by marking only those nodes in C_i which can reach TAIL(b_i). Finally, if the edge e ends in C_i, it cannot start in a different bridge component C_k. If $k < i$ then the walk breaker would contain an s-t bridge before b_i; symmetrically also $k \not\geq j$ holds. If $k \in \{i+1, \ldots, j\}$, then there exists a walk breaker that starts in HEAD(b_i) and ends in TAIL(b_{k-1}), which contradicts the minimality of the walk breaker, ensuring that e starts in C_j. □

In contrast to the previous problems, solutions to MAXSAFE STWALKS might overlap. This allows the solutions' total length to be quadratic in the number of nodes (see Fig. 9). Therefore, instead of reporting the solution directly, the algorithm creates a *compact representation* from which the complete solution can be reported in time linear to its total length.

This representation consists of the bridge sequence, and the starts and ends of each maximal safe walk in the bridge sequence.

Now, each such maximal safe sequence begins with the start of previous walk breaker (or the first s-t bridge) and ends with the end of current walk breaker (or the last s-t bridge) (formally proved later). Note that the definition of the start and end for walk breakers of zero bridge length (trail breakers) perfectly fits this structure of the solution. Hence, the indices of the solution for the *compact representation* can be computed by simply iterating over all minimal walk breakers, requiring $O(|B|)$ time.

Resulting, the minimal walk breakers and the compact representation of the solution of size $O(|B|)$ can be computed in $O(m+n)$ time, which can be expanded to get the complete solution in time linear in the size of the solution. From this, the correctness of Theorem 2 follows for $X = V \cup E$, $X = V$ and $X = E$. Below we prove a property of safe walks central to the correctness of our description.

Lemma 3 *Given the ordered set of minimal walk breakers $\mathcal{P} = \{P_1, P_2, ..., P_k\}$ in the* stWalks*, a maximal safe sequence begins with b_1 and ends with $b_{|B|}$ if $\mathcal{P} = \emptyset$, and otherwise either:*

(a) starts with b_1 and ends with the end of P_1, or
(b) ends with $b_{|B|}$ and starts with the start of P_k, or
(c) starts with the start of P_i and ends with the end of P_{i+1} for some $i \in \{1, \ldots, k-1\}$.

Proof The case where $\mathcal{P} = \emptyset$ is trivial. Otherwise, let L be a maximal safe sequence. If L starts with an s-t bridge other than b_1 that is not the start of a minimal walk breaker, then it can be extended to the left without becoming unsafe, contradicting its maximality. By symmetry, L cannot end with an s-t bridge other than $b_{|B|}$ that is not the end of a minimal walk breaker. Therefore, the start and end s-t bridges considered in (a) –(c) are sufficient. It remains to prove that the pairings are correct.

(a) If L starts with b_1, then it needs to end no later than the end of P_1, since otherwise it would be proven unsafe by P_1. It can end no earlier, since no walk breaker ends before P_1.
(b) If L ends with $b_{|B|}$, then by symmetry with (a) it starts with P_k.
(c) If L starts with the start of P_i for some $i \in \{1, \ldots, k-1\}$, then it cannot end after the end of P_{i+1}, since otherwise it would be proven unsafe by P_{i+1}. Furthermore, if it ends in the end of P_{i+1}, then it is neither proven unsafe by P_i nor by P_{i+1}. And, since $\mathcal{P}$ is ordered, it is also not proven unsafe by another walk breaker. As such, L ends with the end of P_{i+1}.

□

6 Subset Visibility

In this section, we discuss X-visible variants of our problems. We prove that MaxSafe X-stPaths and MaxSafe X-stTrails are in fact NP-hard (Theorem 3). We then show how to solve MaxSafe X-stWalks as an extension of MaxSafe stWalks.

NP-hardness. We prove MaxSafe X-stPaths and MaxSafe X-stTrails to be NP-hard by reduction from the following problem, proven NP-complete in [14, Theorem 2].

Problem 1 *(*Detour*) Given a graph G and pairwise distinct nodes u, v, w of G, decide if there is a u-v path in G that contains w.*

Observe that with the following reduction, a certificate for the unsafety of a sequence is also a certificate for a detour. Therefore, as Detour is in NP, our NP-hard problems are in co-NP. Formally, we describe it as follows.

Theorem 3 *The* MaxSafe X*-visible* stPaths *and* stTrails *problems are NP-hard, even when deciding the safety of a sequence of just two elements of X and restricting X to contain only nodes or only edges.*

Proof Let G, u, v, w be an instance of DETOUR. In order to address the STTRAILS problem in the same way as the STPATHS problem, we transform G into the graph G' by expanding each node. For a node x we denote its internal edge as e_x.

For the rest of the proof we set $s = \text{HEAD}(e_u)$ and $t = \text{TAIL}(e_v)$. Every node of G' has either exactly one incoming edge or exactly one outgoing edge (i.e., some internal edge e_x). As such, any s-t walk visiting a node twice also visits some edge twice (i.e., some internal edge e_x incident to this repeated node of G'). Thus, all s-t trails of G' are s-t paths.

When we restrict $X \subseteq E$, we set $X = \{e_u, e_w, e_v\}$. We have that (e_u, e_v) is safe under the X-visible s-t paths model in G' if and only if G, u, v, w is a no-instance for DETOUR. Since all s-t trails of G' are s-t paths, the same holds also for the s-t trails model.

When we restrict $X \subseteq V$, we set $X = \{s, \text{TAIL}(e_w), t\}$, and analogously have that (s, t) is safe under the S-visible s-t paths model in G', or under the s-t trails model in G', respectively, if and only if G, u, v, w is a no-instance for DETOUR. □

When considering walks, both nodes and edges can be used without limits, and therefore the reduction from DETOUR does not work. Instead, our algorithm for MAXSAFE STWALKS can be extended to solve MAXSAFE X-STWALKS.

Characterisation for X-STWALKS.

In MAXSAFE X-STWALKS an additional subset $X \subseteq V \cup E$ of visible nodes and edges is given. By *expansion* of each visible node v and making its internal edge visible instead of v, we reduce the problem to $X \subseteq E$. Similar to previous problems, the solutions to MAXSAFE X-STWALKS are then substrings of the *X-bridge sequence*, which is the X-subsequence of the bridge sequence.

Such a substring is safe if it contains no *X-walk breaker*, which is a walk breaker with an X-edge. With these definitions we get the following characterisation.

Theorem 9 *(Safety for X-STWALKS) A substring of the X-bridge sequence is safe under the X-STWALKS model, if and only if it has no X-walk breaker.*

Proof ($\Rightarrow$) Let L be a substring of the X-bridge sequence that is safe under the X-STWALKS model where $X \subseteq E$. If L has an X-walk breaker, then from an s-t walk W an s-t walk W' can be constructed by inserting that X-walk breaker into every occurrence of L in the X-subsequence of W. But then L is not a substring of the X-subsequence of W'.

($\Leftarrow$) Let $L := (e_1, \ldots, e_{|L|})$ be a substring of the X-bridge sequence that has no X-walk breaker. Let W be an s-t walk and let W_X be its X-subsequence. Since L is a substring of the X-bridge sequence, W_X contains a substring W'_X that starts from the last occurrence of e_1 and ends in the first occurrence of $e_{|L|}$ after that, and L is a subsequence of W'_X. We prove that L is a prefix of W'_X by induction. By definition, W'_X starts with e_1. For the inductive step, suppose that $e_1, \ldots, e_i$ is a prefix of W'_X. By definition of W', none of its $\text{HEAD}(e_i)$-$\text{TAIL}(e_{i+1})$-subwalks contain e_1 or $e_{|L|}$. Therefore, since L does not have any X-walk breaker, no e_i-e_{i+1}-subwalk of W' contains an X-edge. Thus e_i is immediately followed by e_{i+1} in W'_X. □

From this we can derive an algorithm similar to that for MAXSAFE STWALKS. After computing the bridge sequence and components, we remove those s-t bridges that

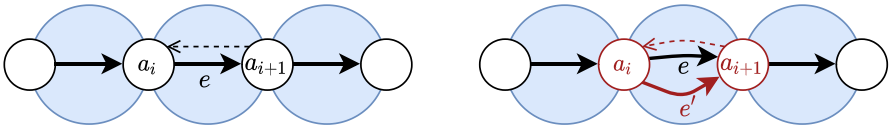


Fig. 10 Example for creating a trail breaker by adding a multiedge. Originally, the dashed edge cannot be used as a trail breaker without repeating the edge e. On adding the parallel edge e', the red cycle becomes a trail breaker repeating a_i and a_{i+1} without repeating an edge. The blue regions mark articulation components and each node is an s-t articulation point

are not in X and merge the corresponding bridge components. Then X-walk breakers of non-zero bridge length can be computed as before, since their s-t bridge is their X-edge. X-walk breakers of bridge length zero can be found by computing the reverse reachability from t as in Algorithm 1, and then iterating over each X-edge of a bridge component and checking whether its head is marked. When a consecutive pair of s-t bridges is not separated by an X-walk breaker of length zero, but is separated by a (G-)walk breaker of length zero, then we add a marker symbol between them in each safe sequence they are part of (see Fig. 2). The rest of the algorithm remains unchanged. This algorithm runs in the same time constraints as that for MaxSafe stWalks.

7 Extension to Multigraphs

Most of the results in this paper can be applied to graphs with multiedges without much change. The s-t bridge algorithm naturally extends to multiedges. Since including multiedges is a generalisation, the NP-hardness results remain valid. Even for the G-visible problems and the X-stWalks problem no change is required. In V-stPaths and V-stWalks, where the multiplicity of edges is not relevant, the parallel edges can simply be merged. Only in V-stTrails extending to multigraphs (denoted by V-stMTrails) is non-trivial, as merging parallel edges changes the set of candidate solutions. See for example Fig. 10, where adding a multiedge in a safe sequence of nodes creates a breaking structure.

To describe how to solve MaxSafe V-stMTrails, we now assume that $G' := (V, E)$ is a multigraph, G is G' with all parallel edges merged and $s, t \in V$ are given as before. First of all, observe that for a sequence of nodes to be safe in V-stMTrails, it needs to be a substring of the articulation sequence. Furthermore, we have a trivial necessary condition for safety, which is similar to the adjacency condition in the G-visible cases. A sequence of two nodes can only be safe if there is no path with more than one edge that connects the first to the second. This is equivalent to requiring that the two nodes are connected by an s-t bridge in G. From here on, we consider a sequence of nodes L that fulfills both of these conditions, where the second is fulfilled by each consecutive pair of nodes.

Let P be the path spelled by L, such that the edges of P are a substring of the bridge sequence. Such a P is safe in stPaths in G, and hence we can state that: for L to be safe also in V-stMTrails in G', it needs to spell out a path in G that is safe in stPaths. But we can make even more detailed relations to the G-visible cases.

For that, we denote the set of s-t trails in G as $\mathcal{T}$, the set of s-t trails in G' as $\mathcal{T}'$, and the set of s-t walks in G as $\mathcal{W}$. We furthermore denote with $V(\mathcal{T})$, $V(\mathcal{T}')$ and $V(\mathcal{W})$ the sets of node sequences associated with these sets of walks, respectively. That is, $V(\mathcal{T}')$ is the candidate set of V-stMTrails in G' and $V(\mathcal{T})$ and $V(\mathcal{W})$ are the candidate sets of V-stTrails and V-stWalks in G. Observe that we have the following relations:

$$V(\mathcal{T}) \subseteq V(\mathcal{T}') \subseteq V(\mathcal{W}) \tag{1}$$

Therefore, if L is safe for $V(\mathcal{T}')$, each element of $V(\mathcal{T}')$ contains L, and therefore each element of $V(\mathcal{T})$ contains L as well, which makes L safe for $V(\mathcal{T})$. The same argument makes L safe for $V(\mathcal{T}')$ if it is safe for $V(\mathcal{W})$. With these relations, we can detail our statement from above by stating that:

(a) For L to be safe in V-stMTrails in G', it needs to be safe in V-stTrails in G (because of the first inclusion in (1)). This is equivalent to L spelling out a path in G that is safe in stTrails.
(b) If L is safe in V-stWalks in G (which is equivalent to L spelling out a path in G that is safe in stWalks), then L is safe in V-stMTrails in G' (because of the second inclusion in (1)).

So, to compute the solutions of MaxSafe V-stMTrails that are not single nodes, we can start from the bridge sequence in G and proceed similarly to the G-visible cases. From statement (a), we know that trail breakers in G are breaking, while no other structure than a walk breaker in G can be breaking because of statement (b). Therefore, the question that remains is: what walk breakers in G of non-zero bridge length are actually breaking? To answer this question, observe that a walk breaker in G that contains an edge that is an s-t bridge in G' cannot be used by an s-t trail in G' without repeating that edge. All other walk breakers can be defined as follows.

Definition 3 Let G' be a multigraph and G be the graph obtained by merging the parallel edges of G'. We say that Q is a *trail multi-breaker* in G' if Q is a walk breaker in G that contains no s-t bridge of G'.

We can prove that these are exactly the breaking structures in V-stMTrails. Consider a trail multi-breaker Q that is a walk breaker of non-zero bridge length for P. Let P' be the set of all parallel edges of P in G' (in addition to the edges of P). Let R' be an s-t path in G'. It holds that Q and R' can only share edges in P', since otherwise Q would not be a walk breaker for P. And since Q contains no edge that is an s-t bridge in G', all shared edges are not s-t bridges. Therefore, since merging all parallel edges in P' produces the edges of P, which are s-t bridges, all edges that Q and R' can share have a parallel edge. Replacing the shared edges with the parallel edges in R' produces an s-t path in G' in which Q can be inserted. Therefore, Q can be used by an s-t trail in G'. Resulting, we get the following theorem.

Theorem 10 *A substring of the articulation sequence is safe under the V-stMTrails model if and only if it has no trail multi-breaker.*

Hence, MaxSafe V-stMTrails can be solved by computing walk breakers in G, and filtering to keep only those whose bridge sequence contains no edge that is an s-t bridge in G'. The solution can then be reported as for MaxSafe stWalks, and the whole algorithm runs in the same time constraints as MaxSafe stWalks.

8 Conclusions

On the theoretical side, we considered a natural generalisation of s-t bridges, with the notion of safety. We considered the standard solution sets of s-t paths, trails and walks, and natural extensions thereof. We fully characterised the complexity of all problems, obtaining a clear trichotomy between linearly solvable problems, problems that allow to compute a compact representation of the solution in linear time, and NP-hard problems.

On the practical side, our problems have potential applications in the genome assembly problem. Moreover in contrast to circular models considered so far with respect to the *safety* paradigm [6,7,20,25], our computational formulations can be applied to non-circular genomes, such as those of eukaryotes. Additionally, they can be applied to scenarios where more than one genome string (i.e. more chromosomes) has to be assembled from a single genome graph, such as when sequencing and assembling a human genome. Furthermore, since some parts of the graph may correspond to errors from the genome sequencing process, not all edges should be covered (i.e., explained) by the genome assembly solution, which motivates removing the edge-covering assumption. Moreover, uncertain or complex parts of the graph can be handled by the subset visibility models, which can lead to longer safe sequences skipping over invisible parts (recall Subsect. 1.2). Finally, all algorithms given here are much simpler than the ones of [6,7] (especially when using the simplified s-t bridge algorithm [5]), and thus potentially more suitable for practical applications.

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