Filtration-Domination in Bifiltered Graphs

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Abstract

Bifiltered graphs are a versatile tool for modelling relations between data points across multiple grades of a two-dimensional scale. They are especially popular in topological data analysis, where the homological properties of the induced clique complexes are studied. To reduce the large size of these clique complexes, we identify filtration-dominated edges of the graph, whose removal preserves the relevant topological properties. We give two algorithms to detect filtration-dominated edges in a bifiltered graph and analyze their complexity. These two algorithms work directly on the bifiltered graph, without first extracting the clique complexes, which are generally much bigger. We present extensive experimental evaluation which shows that in most cases, more than 90% of the edges can be removed. In turn, we demonstrate that this often leads to a substantial speedup, and reduction in the memory usage, of the computational pipeline of multiparameter topological data analysis.

1 Introduction

Motivation and problem statement. A bifiltered graph is a finite simple graph $G = (V, E)$ together with a function $f$ that assigns to each grade $(s, t) \in \mathbb{R}^2$ a subgraph $G_{s,t}$ of $G$. Moreover, these subgraphs are nested, that is, whenever $s \leq s'$ and $t \leq t'$, we have $G_{s,t}$ is a subgraph of $G_{s',t'}$. Such bifiltered graphs appear naturally in the area of multiparameter persistence, a theme within topological data analysis that has received increasing attraction recently. The idea is that a bifiltered graph models the relations of data across various grades of a two-dimensional scale. See Figure 1 for an illustration of these concepts.

Having a bifiltered graph, the pipeline of multiparameter persistence usually proceeds by deriving a bifiltered simplicial complex (a higher-dimensional analogue of a graph) by considering the clique complexes of the subgraphs and to study their topological properties in terms of (persistent) homology. We postpone an explanation of these topological terms, which are not central to the results of the paper, to Section 3 the main problems in this pipeline are that the clique complexes derived from a graph can be much larger than the size of the graph, and computing its topological properties requires algorithms that, despite many ongoing efforts, scale not too favorably with respect to the complex size.

Therefore, we study the following problem: given a bifiltered graph $G$, our goal is to compute another, hopefully much smaller bifiltered graph $G'$ such that the clique complexes of $G$ and $G'$ are “equivalent under the lens of homology”. Formally, we require that the 2-parameter persistence modules (see Section 3) induced by $G$ and $G'$ are isomorphic.

Contribution. Even though the formal problem statement requires topological notation, our contribution can be in large parts understood in terms of elementary graph theory: Previous work \cite{9} defined the concept of dominated edges in a graph which can be expressed and checked combinatorially through the local neighborhood of the edge (see Section 2). We extend this concept to filtration-dominated edges which are edges dominated at all grades in a bifiltered graph. While filtration-domination is implicitly used in \cite{9,23}, our definition appears to be novel. It is not difficult to verify, using well-known algebraic machinery, that removing filtration-dominated edges from a bifiltered graph preserves its homological properties (Theorem 3.1). This suggests a greedy algorithm to decrease the size of a bifiltered graph: look for a filtration-dominated edge, remove it, and repeat with the smaller graph.

We design and analyze efficient algorithms to search for filtration-dominated edges (Section 4). We first give an algorithm for finding strongly filtration-dominated edges; such edges have an extra condition compared to the non-strong definition and can be detected efficiently in time proportional to the size of the local neighborhood of an edge. We use this algorithm as a subroutine to detect (non-strong) filtration-dominated edges using a simple point-location data structure in the plane. We analyze this algorithm and show that its runtime increases by a factor of $O(k \log k)$ compared to checking strong filtration-domination, where $k$ is the maximal degree in the graph.

Our final contribution is an extensive experimental
Figure 1: Illustration of a bifiltered graph. We sample points from a circle with noise and outliers. We estimate a density of each point, encoded by the color (darker means denser). Then, we define $G_{s,t}$ as the graph whose vertex set are points with density at least $s$ and whose edges have Euclidean length at most $t$. The figure shows six of these graphs with quite different topological configurations. The edges colored red are filtration-dominated during the run of our algorithm, and can be removed without changing the topology of the graph, in a sense made precise in Section 3.

Evaluation of our novel concepts and algorithms on a broad collection of artificial and real-world data. We show that in practice, only removing strongly filtration-dominated edges yields a slightly larger output graph than removing all filtration-dominated edges, but usually outperforms the general method in terms of computation time. Moreover, our greedy removal strategy can choose in what order to check edges for (strong) filtration-domination. We show that the more removals happen when checking edges that are added late in the bifiltered graph first. Finally, we demonstrate that our approach speeds up the pipeline of multiparameter persistence: the usual next step after constructing the clique complex is the computation of a minimal presentation which is a compact representation of the homological information of the complex. We demonstrate that patching our algorithm before the highly optimized minimal presentation algorithm mpfree yields speedups of more than an order of magnitude.

Related work. Our approach is inspired by, and generalizes the line of research by Pritam et al. [9, 23] who considered the same problem for unifiltered graphs (i.e., the scale is unidimensional and the grades are real values). The extension to bifiltered graphs is not entirely straightforward; most difficulties arise from the fact that $\mathbb{R}^2$ is only partially ordered. As an example, in a unifiltered graph, checking for domination of an edge reduces to examine the subgraphs of the grades where an edge is added; this is not true for bifiltered graphs, because two edges can appear at incomparable grades in $\mathbb{R}^2$. On the other hand, our solution yields an algorithm also for the unifiltered case by just ignoring a coordinate. Interestingly, our experiments show that our algorithm for bifiltered graphs sometimes yields a
 Persistent Homology has boosted the field of applied topology in the last 20 years. We refer to textbooks [15, 20, 31] and surveys [10, 12]. One of the most studied objects is the Victoris-Rips filtration, both in theory [11, 14, 30] and in practice [2, 6, 29]. From a finite metric space we construct a complete weighted graph where the weight is simply the distance of two points, resulting in a unifiltered graph depicted in the top row of Figure 1.

The introduction of a second parameter is often motivated by the fact that homological properties might change significantly in the presence of outliers [11, 14]. The natural idea is to combine the length parameter with some density measure on the points [8, 16, 33]. The clique complexes of the corresponding bifiltered graph, which is depicted in Figure 1, are called its density-Rips bifiltration. While we concentrate on this case in the experiments, there exist numerous alternative constructions; see [7, 10] for a comprehensive overview.

The restriction to exactly two parameters might appear rather specialized, as we can easily extend the concept of bifiltered graphs to multifiltered graphs, where the scale consists of grades in \( \mathbb{R}^d \), with \( d \) fixed. This choice is made partially for brevity and clarity of presentation; our approach can be generalized to more parameters with some extra care that we discuss in the conclusion. Moreover, on the computational side, the case of two parameters has been studied extensively recently [17, 25, 26, 27], and our approach contributes to establish a solid algorithmic layer for the case of bifiltered data sets.

As mentioned, the major obstacle in processing bifiltered simplicial complexes is their sheer size. A common practice is to construct the simplicial complex only up to a target dimension \( p \) and/or up to a maximal grade. This offers a trade-off between the size of the object to be processed and the information captured by it. A further line of research aims for removing simplices in bifiltered simplicial complexes in a topology-preserving way with techniques from Discrete Morse Theory [3, 4, 35]; see also [21]. In a similar spirit, minimal presentations [22, 23, 28] reduce a simplicial bifiltration to an algebraic description that captures the homological information (in a fixed dimension) in a minimal form. Common to these techniques is that the bifiltered complex has to be expanded before compression, that is, all its simplices have to be enumerated. Our approach, on the other hand, acts solely on the underlying graph and can thus be used as a preprocessing step for all mentioned approaches in the case of clique complexes.

2 Filtration-dominated edges

We use the following basic notions for a graph \( G = (V, E) \): Two vertices are adjacent if there is an edge between them. A subgraph \( G' = (V', E') \) of \( G \) is a graph with \( V' \subseteq V \) and \( E' \subseteq E \). The induced subgraph of \( V' \subseteq V \) is the subgraph \( G' = (V', E') \) with the largest possible \( E' \). We write \( G \setminus e \) for the subgraph of \( G \) with the same vertices and edges, except the edge \( e \). A \( k \)-clique in a graph is a complete subgraph with \( k \) vertices. Finally, we call a vertex \( v \) of \( G \) dominating if it is adjacent to all other vertices in the graph.

Fixing a graph \( G \) and an edge \( e \) of \( G \) with endpoints \( u \) and \( v \), we say that \( w \in G \) is an (edge) neighbor of \( e \) if \( w \) is both adjacent to \( u \) and to \( v \). We say that \( e \) is dominated in \( G \) by a vertex \( w \) if \( w \) is an edge neighbor of \( e \), and every other edge neighbor of \( e \) is adjacent to \( w \). Equivalently, writing \( N_G(e) \) for the set of all edge neighbors, \( e \) is dominated if \( w \) is a dominating vertex in the subgraph of \( G \) induced by \( N_G(e) \). Note that the vertex \( w \) need not to be dominating in the whole graph \( G \). Also, an edge might be dominated by more than one vertex. We say that \( e \) is dominated in \( G \) if it is dominated by some vertex in \( G \).

Recall the definition of a bifiltered graph from the beginning of the Introduction. In the following, when we talk about a bifiltered graph, we suppress the underlying function \( f \) from the notation and refer to the subgraph at a grade \( (s, t) \) as \( G_{s,t} \). Note that a subgraph \( G' \) of a bifiltered graph \( G \) is canonically bifiltered as well by defining \( G'_{s,t} := G_{s,t} \cap G' \) (where the intersection is taken vertex- and edge-wise).

The following simple definitions is the main concept of this work:

**Definition 2.1.** Let \( G \) be a bifiltered graph. An edge \( e \) is filtration-dominated in \( G \) if for every \( (s, t) \in \mathbb{R}^2 \) for which \( e \) is in \( G_{s,t} \), the edge \( e \) is also dominated in \( G_{s,t} \).

We say that \( e \) is strongly filtration-dominated by \( v \in G \), if for every \( (s, t) \in \mathbb{R}^2 \) for which \( e \) is in \( G_{s,t} \), the edge \( e \) is dominated by \( v \) in \( G_{s,t} \).

Note that if \( e \) is strongly filtration-dominated (by some vertex), it is filtration-dominated, but the converse might not hold.

The idea behind the definition is that filtration-dominated edges may be removed from the bifiltered graph without changing its relevant topological properties – we postpone the precise discussion to Section 3. Assuming this fact for now, we obtain a simple greedy framework to compress a bifiltered graph: we traverse the edges in arbitrary order, and, if an edge \( e \) is filtration-dominated, remove it from \( G \), and continue considering \( G \setminus e \).
Instead of deciding whether \( e \) is filtration-dominated in our framework, we can use any other predicate as long as we guarantee that only filtration-dominated edges are removed. In particular, we can check whether \( e \) is strongly filtration-dominated by some vertex of the graph. This change might result in keeping some filtration-dominated edges in the output; however, as we explain in Section 3, strong filtration-domination can be checked faster than filtration-domination, so there is a trade-off between compression rate and runtime.

The order in which the greedy algorithm traverses the edges has a significant effect on the runtime of the algorithm. As we show in Section 5, it is beneficial to check edges first that appear late in the bifiltered graph. As we show in Section 5, it is beneficial to check whether \( e \) is strongly filtration-dominated by some vertex of the graph. This change might result in keeping some filtration-dominated edges in the output; however, as we explain in Section 3, strong filtration-domination can be checked faster than filtration-domination, so there is a trade-off between compression rate and runtime.

3 Topological motivation

The purpose of this section is to justify the notion of filtration-domination from the previous section. We start with the main theorem of the section. Its proof is relatively short and follows straightforwardly from previous work; the bulk of this section is devoted to explain the terms used in the theorem. While these definitions are mostly self-contained, some machinery from (basic) algebraic topology is unavoidable.

**Theorem 3.1.** Let \( G \) be a bifiltered graph with a filtration-dominated edge \( e \), and let \( G' := G \setminus e \). Let \( \text{Clique}(G) \) denote the bifiltered clique complex induced by \( G \), and \( H_p(\text{Clique}(G)) \) denote the 2-parameter persistence module induced by that clique complex in dimension \( p \), where \( p \geq 0 \) is an arbitrary integer and homology is taken over any finite field. Define \( H_p(\text{Clique}(G')) \) in the same way. Then, the two defined persistence modules are isomorphic.

Simplicial complexes. A simplicial complex \( K \) is a collection of subsets of a non-empty finite set, \( V \), its vertex set, that is closed under taking subsets. That is, for every \( A \) in \( K \), all the subsets of \( A \) are in \( K \). An element of \( K \) of cardinality \( k+1 \) is called a \( k \)-simplex, and \( k \) is called the dimension of the simplex. A subcomplex \( L \) of \( K \) is a subcollection that is a simplicial complex itself. Note that a collection of \( 1 \)-simplices \( E \) over \( V \) simply defines a graph \( G = (V, E) \). Hence, simplicial complexes generalize graphs to higher dimensions.

The only type of simplicial complex that we consider in this work are **clique complexes** (also called “flag complexes”): given a graph \( G = (V, E) \), let \( \text{Clique}(G) \) be the simplicial complex whose \( k \)-simplices are the \( (k+1) \)-cliques of \( G \); this is a simplicial complex because subsets of cliques are cliques, and \( \text{Clique}(G) \) contains \( G \) because the 1- and 2-cliques of a graph are its vertices and edges, respectively. We point out that the clique complex is generally a very large object; in the extremal case of a complete graph \( K_n \) with \( n \) vertices, \( \text{Clique}(K_n) \) has \( \binom{n}{k+1} \) \( k \)-simplices and hence a total number of \( 2^n \) simplices.

A **bifiltered (simplicial) complex** is a simplicial complex \( K \) with a function that assigns to each grade \((s, t)\) in \( \mathbb{R}^2 \) a subcomplex \( K_{s,t} \), with the property that if \( s \leq s' \) and \( t \leq t' \), we have \( K_{s,t} \) is a subcomplex of \( K_{s', t'} \). This definition generalizes the notion of a bifiltered graph in the natural way. Given a bifiltered graph \( G \), its clique complex \( \text{Clique}(G) \) is naturally bifiltered by \( \text{Clique}(G)_{s,t} := \text{Clique}(G_{s,t}) \), and we call it its **clique bifiltration**.

**Persistence modules.** From now on, we write for two grades \( u = (u_1, u_2) \) and \( v = (v_1, v_2) \) in \( \mathbb{R}^2 \) that \( u \leq v \) if \( u_1 \leq v_1 \) and \( u_2 \leq v_2 \). Note that this is a partial order on \( \mathbb{R}^2 \).

A **bigraded (or 2-parameter) persistence module** \( M \) is a family of vector spaces \( \{M_u\}_{u \in \mathbb{R}^2} \) together with linear maps \( m_{u \rightarrow v} : M_u \rightarrow M_v \) whenever \( u \leq v \), such that \( m_{u \rightarrow v} \) is the identity function and \( m_{u \rightarrow w} \circ m_{v \rightarrow w} = m_{u \rightarrow w} \) whenever \( u \leq v \leq w \).

The natural way to obtain a bigraded persistence module is to apply (simplicial) homology over a fixed base field on a bifiltered simplicial complex. We omit a formal definition of homology and only describe the idea: A simplicial complex \( K \) can be interpreted as a topological space by embedding its vertex set in sufficiently high dimension and drawing its simplices as convex hulls of the embedded vertices such that no unwanted intersections happen; for a fixed integer \( p > 0 \), the \( p \)-th homology group \( H_p(K) \) is a vector space that captures, informally speaking, the \( p \)-dimensional hole structure of the embedding of \( K \). One can show that \( H_p(K) \) is independent of how \( K \) is embedded.

Crucially for us, homology is **functorial** which means in simplified terms that for complexes \( K \subseteq L \), we obtain an induced linear map \( i_{K \rightarrow L} : H_p(K) \rightarrow H_p(L) \) with the properties that \( i_{K \rightarrow K} = \text{id} \) and for complexes \( K \subseteq L \subseteq M \), we have \( i_{L \rightarrow M} \circ i_{K \rightarrow L} = i_{K \rightarrow M} \). It follows that applying \( p \)-dimensional homology (over a fixed base field) on a bifiltered simplicial complex \( K \) yields a bigraded persistence module which we denote by \( H_p(K) \). A persistence module captures the homological properties of a bifiltered simplicial complex and allows to rank the prominence of each hole in the dataset, depending on the range of grades on which each hole is present. That makes persistence modules (uni-, bi-, or multigraded) a central concept of topological data analysis.

Let \( M \) and \( N \) two persistence modules with linear maps \( m_{\rightarrow} \) and \( n_{\rightarrow} \), respectively. We say that \( M \) and
\( \mathcal{N} \) are isomorphic if there is a collection of vector space isomorphisms \( \phi_u : \mathcal{M}_u \to \mathcal{N}_u \) for each \( u \in \mathbb{R}^2 \), such that \( \phi_u \circ m_{u \to v} = n_{u \to v} \circ \phi_u \), for all \( u \leq v \). That means that we can switch back and forth between two isomorphic persistence modules freely: if the persistence modules are given by the homology of two bifiltered simplicial complexes, it means that these complexes are indistinguishable at all grades in terms of homology.

**Proof of Theorem 3.1.** We sketch the proof of the theorem. All involved techniques are elementary from combinatorial topology, but we cannot explain them in detail for the sake of brevity. The major tool is the following simple property that connects domination of edges in a graph with the homological properties of the clique complex:

**Lemma 3.1.** Let \( G \) be a graph in which \( e \) is a dominated edge. Then the inclusion \( \text{Clique}(G \setminus e) \subseteq \text{Clique}(G) \) induces an isomorphism \( H_p(\text{Clique}(G \setminus e)) \to H_p(\text{Clique}(G)) \) of the homology groups for every \( p \geq 0 \).

**Proof.** If \( e \) is dominated, it means that the subgraph induced by its edge neighbors has a dominating vertex \( v \). In topological language, the induced subgraph is the link of the edge in \( \text{Clique}(G) \), and this is a simplicial cone with apex \( v \). In this case, it is known that there is a sequence of elementary simple collapses that transforms \( \text{Clique}(G) \) into \( \text{Clique}(G \setminus e) \) [38, Lemma 2.7] [5, Lemma 8]. Since such simple collapses define a strong deformation retraction, the inclusion map induces an isomorphism in homology for every \( p \geq 0 \).

Now let \( G \) be a bifiltered graph and let \( e \) be filtration-dominated in \( G \). For every grade \( u \in \mathbb{R}^2 \), the inclusion \( (\text{Clique}(G \setminus e))_u \subseteq (\text{Clique}(G))_u \) induces an isomorphism in homology. If \( e \) is not in \( G \), this is trivial since \( G \setminus e = G \), and otherwise, it follows from the above lemma (Lemma 3.1) because \( e \) is dominated by definition. Hence we have an isomorphism \( \phi_u \) for every grade \( u \). Moreover, the fact that these isomorphisms are all induced by inclusion maps is enough to show that these isomorphisms commute with the linear maps of the persistence modules of \( \text{Clique}(G) \) and \( \text{Clique}(G \setminus e) \). This concludes the proof of Theorem 3.1.

**4 Algorithms**

We explain next how to decide (strong) filtration-domination of an edge in a bifiltered graph. Recall that we write \( (x_1, y_1) \leq (x_2, y_2) \) for points in \( \mathbb{R}^2 \) if \( x_1 \leq x_2 \) and \( y_1 \leq y_2 \). Moreover, for two arbitrary points \( (x_1, y_1) \) and \( (x_2, y_2) \), we define \( (x_1, y_1) \star (x_2, y_2) := (\max(x_1, x_2), \max(y_1, y_2)) \) as their join which is equivalently defined as the smallest element \((a, b)\) with respect to \( \leq \) such that \((x_1, y_1) \leq (a, b)\) and \((x_2, y_2) \leq (a, b)\). We also consider the join of more than 2 elements, which is defined analogously by the coordinate-wise maximum.

**1-critical bifiltered graphs.** We focus on bifiltered graphs \( G = (V, E) \) with the following property: for every edge \( e \), there is a unique critical grade, denoted by \( \text{crit}(e) \), in \( \mathbb{R}^2 \) such that \( e \in G_{t,s} \) if and only if \( \text{crit}(e) \leq (s, t) \). In other words, for every edge, there is a unique grade on which the edge “enters” the bifiltered graph, and hence, such bifiltered graphs are called 1-critical. This is a loss of generality since not all bifiltered graphs of interest are 1-critical. Nevertheless, the case of 1-critical bifiltrations has received attention in algorithmic contexts (e.g., [13, 19, 26]) because of its simplicity. Moreover, we restrict to the 1-critical case solely for the sake of brevity, and our approach extends to more general scenarios; we comment further on this in the conclusion.

Fix a total order on the vertex set \( V \) of the graph. Our input is a 1-critical bifiltered graph \( G = (V, E) \) in adjacency list representation, that is, we store an array of linked lists, one for each vertex \( v \). This list consists of pairs \((w, \alpha)\), where \( w \) is a vertex adjacent to \( v \), and \( \alpha = \text{crit}((v, w)) \). We assume the list is sorted by the first entry in the pair, with respect to the fixed total order on \( V \).

This data structure indeed determines a unique bifiltered graph: for instance, to compute \( G_{s,t} \), we can iterate through all adjacency lists and select exactly those edges \( e \) for which \( \text{crit}(e) \leq (s, t) \). Note that our representation does not specify critical grades for vertices, and we just assume that every vertex is present at all grades; this is not important since isolated vertices do not affect whether an edge is filtration-dominated.

**Strong filtration-domination.** Fix an edge \( e = (a, b) \) and a vertex \( v \) different from \( a \) and \( b \). How can we check whether \( v \) strongly filtration-dominates \( e \)? A necessary condition is that \( v \) is an edge neighbor of \( e \) at every grade where \( e \) is present; in particular, \( v \) must be an edge neighbor of \( e \) at \( \text{crit}(e) \). It is easy to verify that this is the case if and only if \( \text{crit}((a, v)) \leq \text{crit}(e) \) and \( \text{crit}((b, v)) \leq \text{crit}(e) \). We call \( v \) a potential strong dominator of \( e \) in this case.

Furthermore, whenever the edge \( e \) acquires an edge neighbor \( w \neq v \) in the bifiltered graph, the edge \((v, w)\) has to be present in the graph. This can also be checked efficiently, observing that \( w \) becomes edge neighbor of \( e \) at the unique grade \( \text{crit}((a, v)) \star \text{crit}((b, w)) \star \text{crit}(e) \), which we will denote by \( \text{crit}_w(v) \), and it only needs to be checked whether \( \text{crit}((v, w)) \leq \text{crit}_w(v) \).

The last condition is also sufficient for strong filtration-domination because it ensures that \( v \) is connected to all edge neighbors at every grade. This sug-
suggests the following algorithm for deciding whether \( e \) is strongly filtration-dominated by some vertex: first determine the potential strong dominators by iterating over the adjacency lists of \( a \) and \( b \) once, identifying the common neighbors, and checking the above criterion for potential strong domination. Then, we scan the adjacency lists of \( a, b \), and all potential strong dominators simultaneously in order, and check for every edge neighbor \( w \) of \( e \) and every potential strong dominator \( v \) the second condition from above. Because all adjacency lists are sorted according to the same total order, this algorithm requires only one scan through every adjacency list of a potential strong dominator. This implies a total running time to check for the strong filtration-domination of a fixed edge \( e \) of

\[
O(\deg(a) + \deg(b) + \sum_{v \in N_G(e)} \deg(v))
\]

which is both bounded by \( O(|E|) \) and \( O(k^2) \), where \( k \) is the maximal degree in the graph.

**Regions of non-domination.** In order to decide filtration-domination efficiently, we extend the above algorithm for strong filtration-domination in the following way: for a fixed edge \( e = \{a, b\} \) and a vertex \( v \), we compute a data structure that can answer the following query efficiently: Given a grade \((s, t)\), is \( e \) dominated by \( v \) in the graph \( G_{s,t} \)?

For notational convenience, define for two grades \( p, q \in \mathbb{R}^2 \)

\[
\Delta(p, q) := \{ r \in \mathbb{R}^2 : p \leq r \land q \not\subseteq r \}.
\]

The set \( \Delta(p, q) \) can be visualized as the difference between two upper-right quadrants in the plane, one anchored at \( p \) and one at \( q \). Note that if \( q \leq p \), \( \Delta(p, q) = \emptyset \). Generally, \( \Delta(p, q) \) is the union of two stripes, one horizontal and one vertical (where one or both stripes can be empty). See Figure 2 which illustrates this and the next paragraph.

Reviewing the algorithm for the strong case, there are two reasons why \( v \) does not dominate \( e \) in \( G_{s,t} \): Firstly, \( v \) might not be an edge neighbor of \( e \) in \( G_{s,t} \) which happens in the region \( \Delta(\text{crit}(e), \text{crit}(\{a, v\}) \ast \text{crit}(\{b, v\})) \). Secondly, we might have an edge neighbor \( w \) of \( e \) that is not adjacent to \( v \), which happens in the region \( \Delta(\text{crit}(w), \text{crit}(\{v, w\})) = \Delta(\text{crit}(e) \ast \text{crit}(\{a, w\}) \ast \text{crit}(\{b, w\}), \text{crit}(\{v, w\})) \). The union of all \( \Delta \)-regions is precisely the set of grades \((s, t)\) for which \( v \) does not dominate \( e \) in \( G_{s,t} \), and we call it the region of non-domination of \( v \).

Clearly, in the same running time as for checking strong filtration-domination, we can compute all \( \Delta \)-regions for all edge neighbors of \( e \). Let \( r \) denote the number of edge neighbors of \( e \). Then, \( r + 1 \) is an upper bound for the number of \( \Delta \)-regions for any \( v \). Given a query \((s, t) \in \mathbb{R}^2\), we could now answer whether \( v \) dominates \( e \) in \( G_{s,t} \) in \( O(r) \) time, just by checking whether \((s, t)\) is contained in any of the \( \Delta \)-regions.

We can reduce the query time to \( O(\log r) \) with \( O(r \log r) \) preprocessing and \( O(r) \) space, as we now briefly describe. Recall that every \( \Delta \)-region is the union of a vertical stripe and a horizontal stripe. Each vertical stripe is represented by a half-open interval determining its \( x \)-range, and the value of the \( y \)-coordinate of the segment that bounds it from below. Sweeping through all the interval endpoints from left to right, we can easily obtain in \( O(r \log r) \) time an ordered sequence of \( O(r) \) interior-disjoint vertical stripes whose union is precisely the union of the original vertical stripes. Given a query grade in \( \mathbb{R}^2 \), we can check if it is contained in this disjoint union of vertical stripes in \( O(\log r) \) time via binary search. An analogous procedure can be used for the horizontal stripes, yielding our desired bounds.

**Filtration-domination.** The idea to decide filtration-domination is to use the regions of non-domination described above to check whether at least one edge neighbor dominates \( e \) at every grade in \( \mathbb{R}^2 \). Naturally, as we cannot check all grades, we need to reduce the number of queries to a finite set. It is necessary, but not sufficient, to check for domination of \( e \) at the grade \( \text{crit}(w) \) only; however, it suffices to check at all joins of such critical grades.
Lemma 4.1. With the notation as before, define

\[ C := \{ \text{crit}(e) \} \cup \{ \text{crit}_e(w_1) \ast \text{crit}_e(w_2) \mid w_1, w_2 \in N_G(e) \} \]

(note that \( w_1 = w_2 \) is allowed). Then \( e \) is dominated for every grade in \( C \) if and only if it is filtration-dominated.

Proof. If \( e \) is filtration-dominated, it is dominated at every grade by definition. For the other direction, fix some grade \( q \). Let \( V_q \) denote the edge neighbors of \( e \) in \( G_q \); these are all edge neighbors \( w \) of \( e \) in \( G \) such that \( \text{crit}_e(w) \leq q \). The crucial property is now that there exists some grade \( c \in C \) with \( c \leq q \) and \( V_c = V_q \). To see that, note that we can move \( q \) horizontally to the left without changing \( V_q \) until we either hit the \( z \)-coordinate of some \( \text{crit}_e(w) \), or of \( \text{crit}(e) \). Then, we can move \( q \) vertically down until one of the same events happens. After these two transformations, we end up at a join of the critical grades of two edge neighbors, or at the critical grade of \( e \) itself.

With \( c \) as above, we define \( G_c^{(e)} \) as the subgraph of \( G_c \) induced by \( V_c \), and likewise \( G_c^{(e)} \) as the subgraph of \( G_q \) induced by \( V_q \). Since \( V_c = V_q \), both graphs have the same vertex set, and since \( G_c \) is a subgraph of \( G_q \), \( G_c^{(e)} \) is a subgraph of \( G_q^{(e)} \). By assumption, \( e \) is dominated in \( G_c \), meaning that \( G_c^{(e)} \) has a dominating vertex. Because a vertex in a graph remains dominating when adding edges to the graph, also \( G_q^{(e)} \) has a dominating vertex, so \( e \) is dominated in \( G_q \). \( \square \)

With that lemma, the algorithm for deciding filtration-domination of \( e \) is as follows: For every edge neighbor \( w \) of \( e \), prepare the data structure to check for domination of \( e \) by \( w \) at a query grade, as described in the previous paragraph. Then, compute the set \( C \) as in the lemma, and query each data structure for every point in \( C \). Return whether for all \( c \in C \), some edge neighbor dominates \( e \).

For the running time, let \( r \) again denote the number of edge neighbors of \( e \), and let \( m \) be the number of edges. We determine the \( \Delta \)-regions in \( O(m) \) time and construct the \( r \) data structures in total time \( O(r^2 \log r) \). The set \( C \) consists of \( O(r^2) \) elements, and for each of them, we need to query \( r \) data structures, incurring a total cost of \( O(r^3 \log r) \). Hence, in total, we arrive at a runtime of \( O(m + r^3 \log r) \) for deciding whether a fixed edge \( e \) is filtration-dominated.

5 Experimental Results

Experimental setup. We have implemented the algorithms in the Rust programming language, and compiled them with Rust 1.60 and the highest optimization levels. The code\footnote{https://github.com/aj-alonso/filtration_domination} which includes all code used to run the experiments and generate the tables, and all tested datasets are publicly available. We ran all the experiments in a workstation with an Intel Xeon E5-1650v3 CPU and 64 GB of RAM, running Ubuntu 20.04.4 LTS.

Datasets. We use real-world and synthetic datasets. The real-world datasets are netw-sc, senate, eleg, dragon, and hiv, as collected and described in [30]. The synthetic datasets are sphere, which is points sampled from the 2-sphere in \( \mathbb{R}^3 \) with outliers in the cube \([-2, 2]^3 \), as in [26], uniform, points sampled uniformly at random in \([0, 1]^2 \), circle, points sampled from a circle in the plane, torus, points sampled from a torus in \( \mathbb{R}^3 \), and swiss-roll, a two-dimensional plane rolled up into a spiral in \( \mathbb{R}^3 \) (see, for example, [34]).

In each dataset, we assign a density for every point using the Gaussian kernel density estimation function \[37\], with bandwidth parameter set to the 20th percentile of all distinct distances. Then, we consider the complete graph over the point cloud, bifiltered with respect to edge length and density, as depicted in Figure 1.

Comparing orders. We check every edge for (strong) filtration-domination once in the algorithm, but the order is arbitrary. We investigate the effect of choosing different orders. The grades are partially ordered by \( \leq \), and there are four natural ways to complete \( \leq \) to a total order: lexicographic, colexicographic, reverse lexicographic and reverse colexicographic. In addition, we also tested a random total order.

We run our algorithm once for each dataset and order. A comparison of the results is shown in Table 1. The reverse lexicographic and reverse colexicographic result in a greater number of removed edges in all cases, and successfully remove more than 90% of the edges in almost all cases. This can be explained by the fact that late edges (with respect to \( \leq \)) in the bifiltered graph tend to be filtration-dominated, and removing them decreases the number of edge neighbors of earlier edges, increasing their chances for being filtration-dominated. We also observe that more removals naturally implies faster runs. Note that for unfiltered graphs, recent work [23] also demonstrates the advantages of handling the edges in reverse order.

Among these two reverse orders, the reverse lexicographic order is usually a bit better, and so it is the one we use in the rest of the experiments.

Performance. We compare the filtration-domination and strong filtration-domination removal algorithms in Table 2. We observe that the number
Table 1: Comparison of the edges removed when using different orders. For each dataset and order, we show the percentage of removed edges after a single run of the filtration-domination removal algorithm. The cases where the algorithm took more than 2 hours are marked with an “—”.

| Order        | Datasets        |
|--------------|-----------------|
|              | senate | eleg  | netwsc | hiv   | dragon | sphere | uniform | circle | torus  | swiss roll |
| Random       | 48.2%  | 55.4% | 27.2%  | —     | —      | 23.0%  | 45.2%  | 9.6%   | 54.6%  | 60.0%    |
| Colexicographic | 59.8%  | 87.0% | 65.4%  | —     | —      | 21.2%  | 26.8%  | 17.4%  | 59.0%  | 50.8%    |
| Lexicographic | 61.2%  | 92.6% | 96.6%  | —     | —      | 21.2%  | 68.8%  | 17.4%  | 72.8%  | 65.6%    |
| Reverse colex.| 90.4%  | 97.4% | 99.4%  | 97.0% | 97.6%  | 25.2%  | 98.6%  | 27.4%  | 92.2%  | 89.8%    |
| Reverse lex. | 91.0%  | 97.6% | 99.4%  | 98.6% | 98.6%  | 25.0%  | 98.6%  | 24.2%  | 93.6%  | 94.2%    |

of remaining edges is smaller in the former variant as expected, but the ratio is never much more than a factor of 2, and sometimes close to 1. We also see that the performance of the latter variant is better (also expected), and the difference is sometimes more than an order of magnitude. We conclude that the strong version seems the better choice in general, although the non-strong version might be useful if subsequent computations scale very badly with the number of edges.

For comparison, we also run the state-of-the-art single-parameter algorithm\(^2\) of [23] on the single-parameter filtrations derived from our datasets (by dropping the density parameter). Interestingly, we observe that our algorithm often returns smaller output graphs, despite taking the density parameter into account and therefore being more selective for removing edges. This raises the question whether our methodology might also help to further improve the single-parameter case.

**Multiple iterations.** In the above experiments we have run our algorithm only once on each dataset. We can run the algorithm multiple times consecutively, by running the same algorithm on the output of the first run, and so on, possibly removing more edges each time. We test this assumption in this set of experiments. For each dataset we have run the strong filtration-domination removal algorithm 5 times, and the results are shown in Table 3. The bulk of the removals happens in the first iteration: the second and subsequent iterations remove less than 3% of the original edges, except in the senate dataset, where the second iteration removes 6% of the original edges. We note that subsequent iterations take a fraction of the running time of the first iteration, because they are run on smaller input.

**Different structure on the grades.** Filtration-domination of an edge in a bifiltered graph depends on both the structure of the underlying graph (the edge needs to be dominated), and the structure of the grades (it should be dominated at each grade it is present). We now test how the lack of structure on the grades affects the number of strongly filtration-dominated edges we remove. We modify the densities of the described datasets in two different ways: we zero out the density parameter (effectively making the graph unifiltered), and replace the densities by values sampled uniformly at random. We then run the strong filtration-domination removal algorithm, and show the results in Table 4. For each case, we also count the number of edges that are non-dominated in the subgraph of their respective critical grade: these edges cannot be removed right away, and we refer to them by being “free at birth” in Table 4. When we zero out the densities, in almost all datasets there are less than 10% of such edges. On the other hand, when using random density values there are more than 80% such edges in almost all datasets. In a way, this measures how the lack of structure on the grades affects the edges that can be removed, which is reflected upon the output: when using random density values we remove less than 2% of the edges in all cases.

**Speeding up multiparameter persistent homology.** We evaluate the impact of our algorithm as a preprocessing step for computing the minimal presentation of a persistence module in homology dimension 1 induced by a bifiltered graph. The standard approach is to first enumerate all triangles of the clique complexes and then computing the minimal presentation through manipulations of the boundary matrices of the simplicial complex; see [26, 28] for details. We suggest to first run our algorithm to obtain a smaller graph, and apply the two steps above on that smaller graph instead.

For the computation of the minimal presentation

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\(^2\)As implemented in GUDHI [24] version 3.6.0
Table 2: Performance evaluation. The first two columns describe the datasets. Each group of columns contains three subcolumns: “After”, the number of remaining edges after running the corresponding removal algorithm, “%”, the percentage of remaining edges, and “Time (s)”, the time taken in seconds.

| Datasets | Before | After | %  | Time (s) | After | %  | Time (s) | After | %  | Time (s) |
|----------|--------|-------|----|----------|-------|----|----------|-------|----|----------|
| senate   | 5253   | 476   | 9.1% | 0.23     | 1101  | 21.0% | 0.03     | 242   | 4.6% | 0.01     |
| eleg     | 43956  | 1026  | 2.3% | 0.48     | 1254  | 2.9%  | 0.25     | 1224  | 2.8% | 0.09     |
| netwsc   | 71631  | 424   | 0.6% | 0.42     | 426   | 0.6%  | 0.37     | 476   | 0.7% | 0.13     |
| hiv      | 591328 | 7820  | 1.3% | 269.00   | 18942 | 3.2%  | 35.79    | 18648 | 3.2% | 6.33     |
| dragon   | 1999000| 29893 | 1.5% | 225.22   | 45514 | 2.3%  | 66.79    | 53503 | 2.7% | 24.52    |
| sphere   | 4950   | 3710  | 74.9%| 4.25     | 3800  | 76.8% | 0.07     | 3752  | 75.8%| 0.02     |
| uniform  | 79800  | 1123  | 1.4% | 0.99     | 1143  | 1.4%  | 0.54     | 1138  | 1.4% | 0.21     |
| circle   | 4950   | 3710  | 74.9%| 4.25     | 4439  | 89.7% | 0.08     | 4169  | 84.2%| 0.03     |
| torus    | 199000 | 1135  | 5.7% | 0.37     | 1617  | 8.1%  | 0.09     | 1618  | 8.1% | 0.04     |
| swiss-roll| 19900 | 1135  | 5.7% | 0.37     | 1577  | 7.9%  | 0.09     | 2279  | 11.5%| 0.04     |

Table 3: Results after running the strong filtration-domination removal algorithm 5 consecutive times. There are 5 groups of columns, one for each iteration. The “Removed” column displays the percentage of the original edges removed in the corresponding iteration, and “Time (s)" displays the running time (in seconds) of the iteration.

| Dataset | Iteration 1 | | Iteration 2 | | Iteration 3 | | Iteration 4 | | Iteration 5 | |
|---------|------------|----------|------------|----------|------------|----------|------------|----------|
|         | Time (s)   | Removed  | Time (s)   | Removed  | Time (s)   | Removed  | Time (s)   | Removed  |
| senate  | 0.03       | 79.0%    | 0.00       | 6.0%     | 0.00       | 2.8%     | 0.00       | 0.8%     |
| eleg    | 0.26       | 97.2%    | 0.00       | 0.4%     | 0.01       | 0.0%     | 0.00       | 0.0%     |
| netwsc  | 0.37       | 99.4%    | 0.00       | 0.0%     | 0.00       | 0.0%     | 0.00       | 0.0%     |
| hiv     | 35.98      | 96.8%    | 0.30       | 1.4%     | 0.12       | 0.6%     | 0.07       | 0.2%     |
| dragon  | 67.12      | 97.8%    | 0.24       | 0.6%     | 0.14       | 0.2%     | 0.11       | 0.0%     |
| sphere  | 0.06       | 23.2%    | 0.06       | 0.4%     | 0.05       | 0.0%     | 0.05       | 0.0%     |
| uniform | 0.55       | 98.6%    | 0.00       | 0.0%     | 0.00       | 0.0%     | 0.00       | 0.0%     |
| circle  | 0.07       | 10.4%    | 0.04       | 2.4%     | 0.04       | 1.2%     | 0.04       | 1.0%     |
| torus   | 0.09       | 91.8%    | 0.00       | 1.6%     | 0.01       | 0.4%     | 0.00       | 0.0%     |
| swiss-roll | 0.10 | 92.0%    | 0.00       | 2.6%     | 0.00       | 0.8%     | 0.00       | 0.2%     |

we use mpfree⁴ (in parallel mode) which is currently the fastest software available for this task. As we see in Table 5, our preprocessing speeds up the computations significantly in most examples.

Perhaps even more importantly, our approach also reduces the memory consumption of the minimal presentation pipeline, which is the limiting factor for large inputs, as can be seen in the case of the dragon and hiv datasets, where the pipeline ran out of memory without first doing preprocessing. In the datasets where the algorithm does not remove many edges—sphere and circle in this case—the memory savings are limited. However, in most cases the memory savings are high. The most extreme case is the uniform dataset, where memory consumption goes from 5.58 GB to 11.33 MB. This difference can be explained by looking at the size of the input fed into mpfree: for first dimensional homology, the input consists of all triangles and all edges of the clique bifiltration. The number of edges is reduced from 79800 to 1143, as shown in Table 2, and the number of triangles is reduced from 10586800 to 875.

6 Conclusion

We have shown that with the right design choices, the concept of filtration-domination can lead to fast computation of the topological properties of bifiltered clique complexes. The presented results already demonstrate this for a natural and important class of datasets. However, our approach can also be adapted in several directions, and we plan to investigate them in the full version
Table 4: Analysis of the removed edges under changes to the structure of the grades. There are three groups of columns: the first one represents the original dataset with no modification to the densities, in the second one we artificially zero out all the density values, and in the third one we replace the densities by random values sampled uniformly. “Free at birth” shows the percentage of edges that are not dominated when they appear (at their critical grade), and “Removed” is the percentage of edges removed after running our strong filtration-domination removal algorithm.

| Dataset | Original densities | Zeroed densities | Random densities |
|---------|--------------------|------------------|------------------|
|        | Free at birth | Removed | Free at birth | Removed | Free at birth | Removed |
| senate | 3.4%   | 79.0% | 2.8%   | 95.0% | 71.2% | 1.6% |
| eleg  | 1.2%   | 97.2% | 1.6%   | 97.0% | 82.4% | 1.4% |
| netwsc | 0.2%   | 99.4% | 0.2%   | 99.4% | 84.0% | 1.2% |
| hiv   | 0.6%   | 96.8% | 1.4%   | 96.2% | 92.0% | 0.4% |
| dragon | 0.4%   | 97.8% | 0.6%   | 97.2% | 94.6% | 0.2% |
| sphere | 7.8%   | 23.2% | 16.4%  | 23.8% | 74.4% | 0.6% |
| uniform | 0.8%   | 98.6% | 0.8%   | 98.6% | 86.0% | 0.8% |
| circle | 6.4%   | 10.4% | 10.0%  | 18.4% | 67.8% | 0.2% |
| torus | 2.6%   | 91.8% | 3.0%   | 91.6% | 78.4% | 1.2% |
| swiss-roll | 2.6% | 92.0% | 4.0%   | 88.0% | 79.4% | 1.2% |

Table 5: Impact of our algorithm as a preprocessing step for minimal presentations. Inside each group of columns, the “Build (s)” column displays the time taken in seconds to build the clique bifiltration, “mpfree (s)” the time taken to run mpfree, and “Memory” the maximum amount of memory used by the pipeline, over all the steps (including the preprocessing if applied). In addition, the “Removal (s)” column displays the time taken to run our algorithm, and “Speedup” is the speedup compared to not doing preprocessing. The ∞ symbol means that the pipeline ran out of memory, and in that case both the timing and speedup values are marked with an “—”.

| Dataset | No preprocessing | With preprocessing |
|---------|------------------|--------------------|
|        | Memory | Build (s) | mpfree (s) | Memory | Removal (s) | Build (s) | mpfree (s) | Speedup |
| senate | 87.98 MB | 0.05 | 0.49 | 8.2 MB | 0.03 | 0.00 | 0.10 | 4.15 |
| eleg | 2.17 GB | 1.32 | 11.52 | 8.36 MB | 0.29 | 0.00 | 0.03 | 40.13 |
| netwsc | 4.25 GB | 3.03 | 21.05 | 11.42 MB | 0.37 | 0.00 | 0.01 | 63.37 |
| hiv | ∞ | — | — | 366.25 MB | 35.74 | 0.16 | 2.25 | — |
| dragon | ∞ | — | — | 382.55 MB | 67.10 | 0.22 | 4.57 | — |
| sphere | 90.33 MB | 0.05 | 0.50 | 64.07 MB | 0.07 | 0.03 | 0.37 | 1.17 |
| uniform | 5.58 GB | 3.67 | 36.99 | 11.33 MB | 0.56 | 0.00 | 0.02 | 70.10 |
| circle | 95.19 MB | 0.05 | 0.50 | 83.31 MB | 0.08 | 0.04 | 0.42 | 1.02 |
| torus | 725.54 MB | 0.41 | 4.35 | 7.81 MB | 0.10 | 0.00 | 0.03 | 36.62 |
| swiss-roll | 703.13 MB | 0.40 | 4.23 | 7.98 MB | 0.09 | 0.00 | 0.04 | 35.62 |

of the paper:
First of all, we can lift the restriction to 1-critical bifiltered graphs, and allow to associate an arbitrary (finite) number of critical values to every edge. Algorithmically, we can either try to adapt our algorithms to handle such multicritical edges, or we just pretend that there are multiple copies of the same edge coming in at different grades, and we can remove them independently. The question is which of the option is more efficient. Such a generalization would allow us to extend our experimental evaluation to other natural types of bifiltrations, for instance degree-Rips bifiltrations [7, 27, 32].

The concepts of filtration-domination and strongly filtration-domination extend to any number of parameters. This is also true for the ideas behind our al-
algorithms. In particular, it is straightforward to adapt the algorithm to check for strong filtration-domination to such more general cases. The extension to an efficient filtration-domination test requires some care, as the data structure for the domination check gets more involved in this case.

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