Parallel Algorithms for Butterfly Computations

Jessica Shi
MIT CSAIL
jeshi@mit.edu

Julian Shun
MIT CSAIL
jshun@mit.edu

Abstract

Butterflies are the smallest non-trivial subgraph in bipartite graphs, and therefore having efficient computations for analyzing them is crucial to improving the quality of certain applications on bipartite graphs. In this paper, we design a framework called ParButterfly that produces new parallel algorithms for the following problems on processing butterflies: global counting, per-vertex counting, per-edge counting, tip decomposition (vertex peeling), and wing decomposition (edge peeling). The main component of these algorithms is combining wedges incident on subsets of vertices, and our framework allows us to use different methods for wedge aggregation, including combining via sorting, hashing, histogramming, and batching. Moreover, ranking the vertices can speed up butterfly counting, as we only need to consider wedges formed by a particular ordering of the vertices. ParButterfly supports different ways to rank the vertices, including side ordering, approximate and exact degree ordering, and approximate and exact complement coreness ordering. For counting, ParButterfly also supports both exact computation as well as approximate computation via graph sparsification. We prove strong theoretical guarantees on the work and give parallel running times of the algorithms as obtained in our framework.

We perform a comprehensive evaluation of all of the algorithms obtained from ParButterfly on a collection of real-world bipartite graphs using a 48-core machine. Our algorithms obtain significant parallel speedup, outperforming the fastest sequential algorithms by up to 13.6x with a self-relative speedup of up to 38.5x. Compared to general subgraph counting solutions, we are orders of magnitude faster.

1 Introduction

A fundamental problem in large-scale network analysis is finding and enumerating basic graph motifs. Graph motifs that represent the building blocks of certain networks can reveal the underlying structures of these networks. Importantly, triangles are core substructures in unipartite graphs, and indeed, triangle counting is a key metric that is widely applicable in areas including social network analysis [43], spam and fraud detection [8], and link classification and recommendation [59].

However, many real-world graphs are bipartite and model the affiliations and connections between two groups. For example, bipartite graphs are used to represent peer-to-peer exchange networks (linking peers to the data that they request), group membership networks (e.g., linking actors to movies that they acted in), recommendation systems (linking users to items that they rated), factor graphs for error-correcting codes, and hypergraphs [12, 37]. However, bipartite graphs contain no triangles. The smallest non-trivial subgraph is a butterfly (also known as rectangles), which is a (2,2)-biclique (containing two vertices on each side and all four possible edges among them), and therefore having efficient algorithms for counting butterflies is crucial for applications on bipartite graphs [61, 5, 51]. Moreover, butterfly counting naturally lends itself to finding dense subgraph structures in bipartite networks. In particular, Sariyuce and Pinar [52] developed a
peeling algorithm to hierarchically discover dense subgraphs, similar to the $k$-core decomposition for unipartite graphs [53, 41]. An example bipartite graph along with its butterflies is shown in Figure 1.

There has been recent work on designing efficient sequential algorithms for butterfly counting and peeling [14, 61, 66, 51, 52]. However, given the high computational requirements of butterfly computations, it is natural to study whether we can obtain performance improves by taking advantage of parallel machines. This paper presents a framework for butterfly computations, called PARBUTTERFLY, that enables us to obtain the first parallel algorithms for butterfly counting and peeling. PARBUTTERFLY is a modular framework that enables us to easily experiment with many variations of our algorithms. We not only show that our algorithms are efficient in practice but also prove strong theoretical bounds on their work and span. Given that all real-world bipartite graphs fit on a multicore machine, we design parallel algorithms for this setting in the paper.

For butterfly counting, the main procedure consists of finding wedges (2-paths) in the graph and combining them to count butterflies. See Figure 1 for an example of wedges in a graph. In particular, we want to find all wedges originating from each vertex, and then aggregating the counts of wedges incident to every distinct pair of vertices forming the endpoints of the wedge. With the wedge counts, we can obtain global butterfly counts, per-vertex butterfly counts, as well as per-edge butterfly counts. Our PARBUTTERFLY framework provides different methods for aggregating wedges in parallel, including using sorting, hashing, histogramming, and batching. Moreover, we can speed up butterfly counting by first ranking the vertices and only considering wedges formed by a particular ordering of the vertices. PARBUTTERFLY supports different parallel methods to rank the vertices, including side-ordering, approximate and exact degree-ordering, and approximate and exact complement-coreness ordering. These orderings can be used in conjunction with any of the aggregation methods. To further speed up computations on large graphs, PARBUTTERFLY also supports parallel approximate butterfly counting via graph sparsification based on ideas by Sanei-Mehri et al. [51] for the sequential setting.

PARBUTTERFLY also provides parallel algorithms for peeling bipartite networks based on sequential algorithms developed by Sariyuce and Pinar for dense subgraph discovery [52]. Our peeling algorithms iteratively remove the vertices (tip decomposition) or edges (wing decomposition) with the lowest butterfly count until the graph becomes empty. Each iteration removes vertices (edges) from the graph in parallel and updates the butterfly counts of neighboring vertices (edges) using
any of the parallel wedge aggregation techniques that we developed for counting. We make use of a parallel bucketing data structure by Dhulipala et al. [IS] to efficiently maintain the butterfly counts of the vertices or edges in the graph.

We prove theoretical bounds showing that our algorithms are highly parallel and that their asymptotic work does not increase over the corresponding sequential algorithms. Several variants of our counting and peeling algorithms are work-efficient, matching the work of the best sequential algorithm. In particular, for a graph $G(V,E)$ with $m$ edges and arboricity $\alpha^2$ PARButterfly can give a counting algorithm that takes $O(\alpha m)$ work and $O(\log m)$ span. PARButterfly also gives a vertex-peeling algorithm that takes $O(\rho_v \log n + \sum_{v \in V} \deg(v)^2)$ work and $O(\rho_v \log^2 m)$ span and an edge-peeling algorithm that takes $O(\rho_e \log n + \sum_{(u,v) \in E} \sum_{u' \in N(v)} \min(\deg(u), \deg(u'))$ work and $O(\rho_e \log^2 m)$ span, where $\rho_v$ and $\rho_e$ are the number of vertex and edge peeling iterations required to remove the entire graph.

We present a comprehensive experimental evaluation of all of the different variants of counting and peeling algorithms provided by the PARButterfly framework. On a 48-core machine, our counting algorithms achieve self-relative speedups of up to 38.5x and outperform the fastest sequential baseline by up to 13.6x. Our peeling algorithms achieve self-relative speedups of up to 10.7x and outperform the fastest sequential baseline by up to 2082.3x. We believe our speedups over the best sequential baseline is notable given that the baseline is challenging to outperform due to its low overheads. Compared to PGD, the state-of-the-art parallel subgraph counting solution that can be used for butterfly counting as a special case, we are 49.6–564.8x faster. We find that although the sorting, hashing, and histogramming aggregation approaches achieve better theoretical complexity, batching usually performs the best in practice due to lower overheads.

In summary, the contributions of this paper are as follows.

1. The first parallel algorithms for butterfly counting and peeling.
2. A framework PARButterfly with different ranking and wedge aggregation schemes that can be used for parallel butterfly counting and peeling.
3. Strong theoretical bounds on the PARButterfly algorithms.
4. A comprehensive experimental evaluation on a 48-core machine demonstrating high parallel scalability and low running times compared to the best sequential baselines, as well as significant speedups over the state-of-the-art parallel subgraph counting solution.

## 2 Preliminaries

**Graph Notation.** For the purposes of this paper, every bipartite graph $G = (U, V, E)$ is simple and undirected. For any vertex $v \in U \cup V$, let $N(v)$ denote the neighborhood of $v$ and let $N_2(v)$ denote the 2-hop neighborhood of $v$ (that is, the set of all vertices reachable from $v$ by a path of length 2). For added clarity, let $N^G(v)$ denote the neighborhood of $v$ in graph $G$ and let $N^G_2(v)$ denote the 2-hop neighborhood of $v$ in graph $G$. Let $\deg(v)$ denote the degree of $v$. Also, let $n = |U| + |V|$ denote the number of vertices in $G$, and let $m = |E|$ denote the number of edges in $G$.

A **butterfly** is a set of four vertices $u_1, u_2 \in U$ and $v_1, v_2 \in V$ with edges $(u_1, v_1), (u_1, v_2), (u_2, v_1), (u_2, v_2) \in E$. A **wedge** is a set of three vertices $u_1, u_2 \in U$ and $v \in V$, with edges $(u_1, v), (u_2, v) \in E$. We call the vertices $u_1, u_2$ **endpoints** and the vertex $v$ the **center**. Symmetrically, a wedge can also consist of vertices $v_1, v_2 \in V$ and $u \in U$, with edges $(v_1, u), (v_2, u) \in E$.

The arboricity of a graph is defined to be the minimum number of disjoint forests that a graph can be partitioned into.
We call the vertices $v_1, v_2$ endpoints and the vertex $u$ the center. Note that we can decompose a butterfly into two wedges that share the same endpoints but have distinct centers.

The **arboricity** $\alpha$ of a graph is the minimum number of spanning forests needed to cover the graph. In general, $\alpha$ is upper bounded by $O(\sqrt{m})$ and lower bounded by $O(1)$ [14]. Importantly, $\sum_{(u,v) \in E} \min(\text{deg}(u), \text{deg}(v)) = O(\alpha m)$.

We store our graphs in compressed sparse row (CSR) format, which requires $O(m + n)$ space. We initially maintain separate offset and edge arrays for each vertex partition $U$ and $V$, and we assume that all arrays are stored consecutively in memory.

**Model of Computation.** In this paper, we use the work-span model of parallel computation to analyze our algorithms. The **work** of an algorithm is defined to be the total number of instructions, and the **span** is defined to be the longest dependency path [33, 16]. Importantly, we aim for algorithms to be **work-efficient**, that is, a work complexity that matches the best-known sequential time complexity. We assume concurrent reads and writes as well as fetch-and-adds are supported. The work-span model is a widely-used model for parallel algorithms, and allows one to design algorithms using dynamic multithreading in a theoretically and practically efficient manner [11]. Notable languages that support dynamic multithreading including Cilk and OpenMP.

**Parallel primitives.** We use certain parallel primitives, including prefix sum (scan) and filter. **Prefix sum** takes as input a sequence $A$ of length $n$, an identity element $\varepsilon$, and an associative binary operator $\oplus$, and returns the sequence $B$ of length $n$ where $B[i] = \bigoplus_{j<i} A[j] \oplus \varepsilon$. **Filter** takes as input a sequence $A$ of length $n$ and a predicate function $f$, and returns the sequence $B$ containing elements $a \in A$ such that $f(a)$ is true, in the same order that these elements appeared in $A$. Note that filter can be implemented using prefix sum. Both of these algorithms take $O(n)$ work and $O(\log n)$ span [33].

We also use several parallel primitives in our algorithms for aggregating equal keys together. **Semisort** groups together equal keys but makes no guarantee on total order. For a sequence of length $n$, parallel semisort takes $O(n)$ expected work and $O(\log n)$ span with high probability [27]. Aggregation can be done on the output of semisort using prefix sums in the same bounds. Additionally, we use parallel hash tables and histograms for aggregation, which have the same bounds as semisort [18, 19, 54].

3 ParButterfly Framework

In this section, we describe the PARBUTTERFLY framework and its components. Section 3.1 describes the procedures for counting butterflies and Section 3.2 describes the butterfly peeling procedures. Section 4 goes into more detail on the parallel algorithms that can be plugged into the framework, as well as their analysis.

3.1 Counting Framework

Figure 2 shows the high-level structure of the PARBUTTERFLY framework. Step 1 assigns a global ordering to the vertices, which helps reduce the overall work of the algorithm. Step 2 retrieves all the wedges in the graph, but only where the second and third vertices of the wedge have higher rank than the first vertex.

Step 3 counts for every pair of vertices the number of wedges that share those two vertices as endpoints. Step 4 uses the wedge counts to obtain global butterfly counts, per-vertex butterfly

---

3 By “with high probability” (w.h.p.), we mean that the probability is at least $1 - 1/n^c$ for any constant $c > 0$ for an input of size $n$. 

ParButterfly Framework for Counting

1. Rank vertices: Assign a global ordering, rank, to the vertices.
2. Retrieve wedges: Retrieve a list \( W \) of wedges \( (x, y, z) \) where \( \text{rank}(y) > \text{rank}(x) \) and \( \text{rank}(x) > \text{rank}(z) \).
3. Count wedges: For every pair of vertices \( (x_1, x_2) \), how many distinct wedges share \( x_1 \) and \( x_2 \) as endpoints.
4. Count butterflies: Use the wedge counts to obtain the global butterfly count, per-vertex butterfly counts, or per-edge butterfly counts.

Figure 2: ParButterfly Framework for Counting

| Step 1 | Step 2 | Step 3 | Step 4 |
|--------|--------|--------|--------|
| 1. \( v_3 \) | \( v_3 \) | \( (v_3, v_1, u_1) \) | \( + \left( \binom{2}{1} \right) \) butterflies on \( v_1, v_3 \) |
| 2. \( u_1 \) | \( (v_3, v_1, u_1) \) | \( (v_3, v_1, u_2) \) | \( + (2 - 1) \) butterflies on \( u_1, u_2 \) |
| 3. \( u_2 \) | \( (v_3, v_2, u_1) \) | \( (v_3, v_2, u_2) \) | \( + \left( \binom{2}{1} \right) \) butterflies on \( v_2, v_3 \) |
| 4. \( v_1 \) | \( (u_1, u_2, v_1) \) | \( (u_1, u_2, v_2) \) | \( + (2 - 1) \) butterflies on \( u_1, u_2 \) |
| 5. \( v_2 \) | \( (u_1, u_2, v_1) \) | \( (u_1, u_2, v_2) \) | \( + \left( \binom{2}{1} \right) \) butterflies on \( v_1, v_2 \) |
| 6. \( u_3 \) | \( (u_1, u_2, v_1) \) | \( (u_1, u_2, v_2) \) | \( + \left( \binom{2}{1} \right) \) butterflies on \( v_1, v_2 \) |

Figure 3: We execute butterfly counting per vertex on the graph in Figure 1. In Step 1, we order vertices in decreasing order of degree. Then, in Step 2, we retrieve wedges in the order given by Step 1. For each vertex \( v \) in order, we retrieve all wedges where \( v \) is an endpoint and where the other two vertices have higher rank. In this example, only \( v_3 \) and \( u_1 \) produce wedges, as listed. In Step 3, we aggregate edges by endpoint, and this produces the butterfly counts for Step 4. Note that if we have \( w \) wedges that share the same endpoint, this produces \( \binom{w}{2} \) butterflies for each of the two endpoints and \( w - 1 \) butterflies for each of the centers of the \( w \) wedges.

Counts, or per-edge butterfly counts. For each step, there are several options with respect to implementation, each of which can be independently chosen and used together within ParButterfly. These options offer tradeoffs between work-efficiency and performance.

Figure 3 shows an example of executing each of the four steps on an example graph.

All of the options within our counting framework (which we describe in more detail below) are as follows:

- **Ranking**: side order, degree order, approximate degree order, complement degeneracy order, approximate complement degeneracy order
- **Wedge aggregation**: sorting, hashing, histogramming, simple batching, wedge-aware batching
  - **Max wedges in memory** (for sorting, hashing, histogramming)
- Max array size in memory (for batching)
- **Butterfly aggregation**: atomic fetch-and-add, wedge aggregation
- **Count format**: global, per-vertex, per-edge
- **Approximate counts**: precise, edge sparsification, colorful sparsification

### 3.1.1 Ranking

The ordering of vertices when we retrieve wedges is significant in the sense that it affects the number of wedges that we must process. As we discuss in Section 4.1, Sanei-Mehri et al. \[51\] order all vertices from one bipartition of the graph first, depending on which bipartition produced the least number of wedges, giving them practical improvements in their serial implementation. We refer to this ordering as *side order*. Chiba and Nishizeki \[14\] achieve a lower work complexity for counting by ordering vertices in decreasing order of degree, which we refer to as *degree order*.

For practical speedups, we also introduce *approximate degree order*, which orders vertices in decreasing order of the logarithm of their degree (*log-degree*). Since the ordering of vertices in many real-world graphs have good locality, approximate degree order preserves the locality among vertices with equal log-degree. We show in Section 4.4 that the work of butterfly counting using approximate degree order is the same as that of using degree order.

Furthermore, we show in Section 5 that empirically, the same number or fewer wedges must be processed (compared to both side and degree order) if we consider vertices in complement degeneracy order. Note that *degeneracy order*, also known as the ordering given by vertex coreness, is a well-studied ordering of vertices given by repeatedly finding and removing vertices of smallest degree \[53, 41\]. This ordering can be obtained serially in linear time using a k-core decomposition algorithm \[41\], and can be obtained in parallel in linear work by repeatedly removing (peeling) all vertices with the smallest degree from the graph in parallel \[18\]. The span of peeling is proportional to the number of peeling rounds needed to reduce the graph to an empty graph.

We define *complement degeneracy order* to be the ordering of vertices given by repeatedly finding and removing vertices of largest degree. This mirrors the idea of using decreasing order of degree, but encapsulates more structural information about the graph.

However, using complement degeneracy order is not practically efficient. In the same way that the span of k-core is limited by the peeling complexity of the graph, the span of finding complement degeneracy order is limited by the number of rounds needed to reduce a graph to an empty graph where each round deletes all maximum degree vertices of the graph. As such, we define *approximate complement degeneracy order*, which repeatedly finds and removes vertices of largest log-degree. Not only does this reduce the number of rounds needed, but it also closely approximates the number of wedges that must be processed using complement degeneracy order. We further show in Section 4.5 that using complement degeneracy order and approximate complement degeneracy order give the same work-efficient bounds as using degree order.

In total, the options for ranking are side order, degree order, approximate degree order, complement degeneracy order, and approximate complement degeneracy order.

### 3.1.2 Wedge counting

We obtain wedge counts by aggregating wedges by endpoints; importantly, there are many aggregation algorithms that offer tradeoffs between work-efficiency and practical performance. PAR-Butterfly implements fully-parallel methods for combining including sorting, hashing, and histogramming, as well as a partially-parallel batching method.
We can aggregate the wedges by endpoints by semisorting key-value pairs where the key is the two endpoints and the value is the center vertex. This ensures that all elements with the same key are grouped together, after which we can compute the size of each group to get the number of wedges shared by the two endpoints. We implemented this approach using the implementation of parallel sample sort from PBBS \[10, 55\] due to its better cache-efficiency over parallel semisort.

Alternatively, we can use a parallel hash table which stores key-value pairs where the key is two endpoints and the pair is a count. We then insert the endpoints of all wedges into the hash table, with a value of 1, and sum the values when duplicate keys are inserted. In the end, the value associated with each key represents the number of wedges that the two endpoints share. We use a parallel hash table based on linear probing \[54\].

Another option is to insert all the key-value pairs into a parallel histogramming data structure which will automatically count the number of occurrences of each distinct key. The parallel histogramming data structure that we use is implemented using a combination of semisorting and hashing \[18\].

Finally, our partially-parallel batching method involves processing a certain number of vertices in parallel, and finds the wedges these vertices. Each vertex aggregates its wedges serially, using an array large enough to contain all possible second endpoints. The simple setting in our framework fixes the number of vertices as a constant based on the space available to hold the arrays for aggregation, while the wedge-aware setting determines the number of vertices dynamically based on the number of wedges that each vertex processes.

In total, the options for combining wedges are sorting, hashing, histogramming, simple batching, and wedge-aware batching.

3.1.3 Butterfly counting

There are two main methods to translate wedge counts into butterfly counts, either per-vertex or per-edge; see Step 4 from Figure 3 for an example of computing butterfly counts per vertex, which must then be aggregated and appropriately stored.\[4\] One method is to make use of atomic fetch-and-add operations, and simply add the obtained butterfly count for the given vertex/edge directly into a final array. This allows us to obtain butterfly counts without explicitly re-aggregating.

The second method is to reuse the aggregation method chosen for the wedge counting step and use sorting, hashing, or histogramming to combine the butterfly counts per-vertex or per-edge.\[5\]

3.1.4 Other options

There are a few miscellaneous options with regards to butterfly counting in PARButterfly. First, butterfly counts can be given per vertex, per edge, or in total.

Also, for wedge aggregation methods apart from batching, since the number of wedges can be quadratic in the size of the original graph, it may not be possible to fit all wedges in memory at once; as such, a parameter in our framework takes into account the number of wedges that can be handled in memory and batches wedges appropriately. Similarly, for wedge aggregation by batching, a parameter takes into account the available space and appropriately determines the number of rounds to be batched.

Finally, PARButterfly implements both edge sparsification and colorful sparsification as described by Sanei-Mehri \textit{et al.} \[51\] to obtain approximate total butterfly counts. For approximate

\[4\]For total counts, butterfly counts can simply be computed and summed in parallel directly.

\[5\]Note that this is not feasible for partially-parallel batching, so in that case, the only option is to use atomic fetch-and-add operations.
ParButterfly Framework for Peeling

1. Obtain butterfly counts: Obtain per-vertex or per-edge butterfly counts from the counting framework.
2. Peel: Iteratively remove vertices or edges with the lowest butterfly count from the graph until an empty graph is reached.

Figure 4: ParButterfly Framework for Peeling

counting, the sub-sampled graph is simply passed to the framework shown in Figure 2, and the final result scaled appropriately. Note that these can only be used for total counts, and as such cannot be combined with the peeling framework described in Section 3.2.

3.2 Peeling Framework

Butterfly peeling involves classifying induced subgraphs by the number of butterflies that they contain. More formally, a vertex induced subgraph is a $k$-tip if it is a maximal induced subgraph such that considering a bipartition, every vertex in that bipartition is contained within at least $k$ butterflies and every pair of vertices in that bipartition is connected by some sequence of butterflies. Similarly, an edge induced subgraph is a $k$-wing if it is a maximal induced subgraph such that every edge is contained within at least $k$ butterflies and every pair of edges is connected by some sequence of butterflies.

The tip number of a vertex $v$ is the maximum $k$ such that there exists a $k$-tip containing $v$, and the wing number of an edge $(u,v)$ is the maximum $k$ such that there exists a $k$-wing containing $(u,v)$. Vertex peeling, or tip decomposition, involves finding all tip numbers of the vertices in a bipartition $U$, and edge peeling, or wing decomposition, involves finding all wing numbers of the edges.

The sequential algorithms for vertex peeling and edge peeling involve finding butterfly counts and in every round, removing the vertex or edge contained within the fewest number of butterflies respectively. In parallel, instead of removing a single vertex or edge per round, we remove all vertices or edges that are contained within the minimum number of butterflies.

For example, using the graph in Figure 1 and the counting algorithm in Figure 3, we see that $u_3$ is contained within 0 butterflies, and $u_1$ and $u_2$ are each contained within 3 butterflies. If we peel on the bipartition $U$, we would peel $u_3$ in our first round, and no butterfly counts would be updated. Then, we peel $u_1$ and $u_2$ simultaneously in the second round, since both have butterfly count 3. Note that the tip number of $u_3$ is 0, while the tip numbers of $u_1$ and $u_2$ are 3.

The peeling framework is shown in Figure 4 and supports vertex peeling (tip decomposition) and edge peeling (wing decomposition). Because it also involves iterating over wedges and aggregating wedges by endpoint, it contains similar parameters to those in the counting framework. However, there are a few key differences between counting and peeling.

First, ranking is irrelevant, because all wedges associated with a peeled vertex must be accounted for regardless of vertex order. Also, using atomic fetch-and-add operations to update butterfly counts after obtaining wedge counts is no longer feasible, because the updated vertices must still be aggregated and stored in some way in order to update the number of wedges on vertices or edges in the 2-hop neighborhoods of the peeled vertices or edges. In this sense, obtaining butterfly counts from wedge counts can only be achieved using a re-aggregation algorithm. Finally, vertex or edge
peeling can only be performed if the counting framework produced per-vertex or per-edge butterfly counts, respectively.

Thus, the main parameter for the peeling framework is the choice of method for wedge aggregation:

- **Wedge aggregation**: sorting, hashing, histogramming, simple batching, wedge-aware batching

These are precisely the same options described in Section 3.1.2. Note that the peeling framework is based on the parallel implementation of k-core using bucketing from Julienne [18].

4 ParButterfly Algorithms

We describe here our parallel algorithms for butterfly counting and peeling in more detail. Our theoretically-efficient parallel algorithms are based on the work-efficient sequential butterfly counting algorithm, introduced by Chiba and Nishizeki [14]. We use ideas from Wang et al. [61] and Sanei-Mehri et al. [51] to efficiently store butterfly counts per vertex.

4.1 Preprocessing

The main subroutine in butterfly counting involves processing a subset of wedges of the graph; previous work differ in the way in which they choose wedges to process.

As mentioned in Section 3.1.1, Chiba and Nishizeki [14] choose wedges by first ordering vertices by decreasing order of degree and then for each vertex in order, extracting all wedges with said vertex as an endpoint and deleting the processed vertex from the graph. Note that the ordering of vertices does not affect the correctness of the algorithm – in fact, Sanei-Mehri et al. [51] use this precise algorithm but with all vertices from one bipartition of the graph ordered before all vertices from the other bipartition. Importantly, Chiba and Nishizeki’s [14] original decreasing degree ordering gives the work-efficient bounds $O(\alpha m)$ on butterfly counting.

Throughout this section, we use decreasing degree ordering to obtain the same work-efficient bounds in our parallel algorithms. However, note that using approximate degree ordering, complement degeneracy ordering, and approximate complement degeneracy ordering also gives us these work-efficient bounds; we prove the work-efficiency of these orderings in Sections 4.4 and 4.5. Furthermore, the exact and approximate counting algorithms described in Sections 4.2 and 4.3 work for any ordering; only the theoretical analysis depends on the ordering.

We use $\text{rank}$ to denote the index of a vertex in some ordering, in cases where the ordering that we are using is clear or need not be specified. We define a modified degree, $\text{deg}_v(u)$, to be the number of neighbors $u' \in N(u)$ such that $\text{rank}(u') > \text{rank}(v)$. We also define a modified neighborhood, $N_v(u)$, to be the set of neighbors $u' \in N(u)$ such that $\text{rank}(u') > \text{rank}(v)$.

We give a preprocessing algorithm, PREPROCESS (Algorithm 1), which takes as input a bipartite graph and a ranking function $f$, and renames vertices by their rank in the ordering.

The output is a general graph (we discard bipartite information in our renaming). PREPROCESS also sorts neighbors by decreasing order of rank.

PREPROCESS begins by sorting vertices in increasing order of rank. Assuming that $f$ returns an integer in the range $[0, n]$, which is true in all of the orderings provided in PARBUTTERFLY, this can be done in $O(n)$ expected work and $O(\log n)$ span w.h.p. with parallel integer sort [49]. Renaming our graph based on vertex rank takes $O(m)$ work and $O(1)$ span (to retrieve the relevant ranks). Finally, sorting the neighbors of our renamed graph and the modified degrees takes $O(m)$ expected
In this section, we describe and analyze our parallel algorithms for butterfly counting.

4.2 Counting algorithms

Importantly, the following equations describe the number of butterflies per vertex and per edge. Sanei-Mehri et al. \[51\] derived and proved the per-vertex equation, as based on Wang et al.’s equation for the total number of butterflies. We give a short proof of the per-edge equation.

**Lemma 4.2.** For a bipartite graph \( G = (U, V, E) \), the number of butterflies containing a vertex \( u \) is given by

\[
\sum_{u' \in N_2(u)} \binom{|N(u) \cap N(u')} 2.
\]  

The number of butterflies containing an edge \((u, v) \in E\) is given by

\[
\sum_{u' \in N(v) \setminus \{u\}} (|N(u) \cap N(u')| - 1).
\]  

**Proof.** The proof for the number of butterflies per vertex is given by Sanei-Mehri et al. \[51\]. For the number of butterflies per edge, we note that given an edge \((u, v) \in E\), each butterfly that \((u, v)\) is contained within has additional vertices \(u' \in U, v' \in V\) and additional edges \((u', v'), (u, v'), (u', v') \in E\). Thus, iterating over all \(u' \in N(v)\) (where \(u' \neq u\)), it suffices to count the number of vertices \(v' \neq v\) such that \(v'\) is adjacent to \(u\) and to \(u'\). In other words, it suffices to count \(v' \in N(u) \cap N(u') \setminus \{v\}\). This gives us precisely \(\sum_{u' \in N(v) \setminus \{u\}} (|N(u) \cap N(u')| - 1)\) as the number of butterflies containing \((u, v)\), as desired. \(\square\)
Algorithm 2 Parallel wedge retrieval

1: procedure GET-WEDGES($G = (V, E)$)
2: Use prefix-sum to compute a function $I$ that maps wedges to indices in order
3: Initialize $W$ to be an array of wedges
4: parfor $u_1 \in V$ do
5: \hspace{1em} parfor $i \leftarrow 0$ to $\deg_{u_1}(u_1)$ do
6: \hspace{2em} $v \leftarrow N(u_1)[i]$ \hspace{1em} $\triangleright v$ is the $i$th neighbor of $u_1$
7: \hspace{1em} parfor $j \leftarrow 0$ to $\deg_{u_1}(v)$ do
8: \hspace{2em} $u_2 \leftarrow N(v)[j]$ \hspace{1em} $\triangleright u_2$ is the $j$th neighbor of $v$
9: \hspace{1em} $W[I(i, j)] \leftarrow ((u_1, u_2), 1, v)$ \hspace{1em} $(u_1, u_2)$ is the key, 1 is the frequency
10: end parfor
11: return $W$

Note that in both equations given by Lemma 4.2, we iterate over wedges with endpoints $u$ and $u'$ to obtain our desired counts (Step 4 of Figure 2). We now describe how to retrieve the list of wedges (Step 2 of Figure 2).

4.2.1 Wedge retrieval

There is a subtle point to make in retrieving all wedges. Once we have retrieved all wedges with endpoint $u$, Equation (1) dictates the number of butterflies that $u$ contributes to the second endpoints of these wedges, and Equation (2) dictates the number of butterflies that $u$ contributes to the centers of these wedges. In this sense, given the wedges with endpoint $u$, we can count not only the number of butterflies on $u$, but also the number of butterflies that $u$ contributes to other vertices of our graph. Thus, after processing these wedges, we can safely remove $u$ from our graph and there is no need to reconsider wedges containing $u$. (importantly, there is no need to consider wedges with center $u$).

From Chiba and Nishizeki’s [12] work, to minimize the total number of wedges that we process, we must retrieve all wedges considering endpoints $u$ in decreasing order of degree, and then delete said vertex from the graph (i.e., do not consider any other wedge containing $u$).

We introduce here a parallel wedge retrieval algorithm, GET-WEDGES (Algorithm 2), that takes $O(\alpha m)$ work and $O(\log m)$ span. We assume that GET-WEDGES takes as input a preprocessed (ranked) graph. The algorithm first constructs an index function $I$ that indicates which wedges correspond to which indices in our final wedges array (Line 2). The algorithm then iterates through all vertices $u$ and retrieves all wedges with endpoint $u$ such that the center and second endpoint both have rank greater than $u$ (Lines 4–9). This is equivalent to Chiba and Nishizeki’s algorithm which deletes vertices from the graph, but the advantage is that since we do not modify the graph, all wedges can be processed in parallel. We process exactly the set of wedges that Chiba and Nishizeki process, and they prove that there are $O(\alpha m)$ such wedges.

Constructing the index function uses multiple prefix sums, which takes $O(n + m)$ work and $O(\log m)$ span. Since the adjacency lists are sorted in decreasing order of rank, we can obtain the end index of the loops on Line 7 using an exponential search in $O(\deg_{u_1}(v))$ work and $O(\log(\deg_{u_1}(v)))$ span. Then, iterating over all wedges takes $O(\alpha m)$ work and $O(1)$ span. In total, we have $O(\alpha m)$ work and $O(\log m)$ span, as desired.

Finally, note that as discussed in Section 2 since we have $O(\alpha m)$ wedges, GET-FREQ takes $O(\alpha m)$ expected work and $O(\log m)$ span w.h.p.

The following lemma summarizes the complexity of the first three steps.
Algorithm 3 Parallel work-efficient butterfly counting per vertex

1: procedure COUNT-V-WEDGES(G = (U, V, E), W)
2: \((R, F) \leftarrow \text{GET-FREQ}(W)\) \hspace{1cm} \triangleright \text{Aggregate } W \text{ and retrieve wedge frequencies}
3: Initialize \(B\) to store butterfly counts per vertex
4: \textbf{parfor} \(i \leftarrow 0\ \text{to } |F| - 1\ \text{do}
5: \((u_1, u_2, d) \leftarrow R[i]\)
6: Store \((u_1, (d_1^i))\) and \((u_2, (d_2^i))\) in \(B\) \hspace{1cm} \triangleright \text{Store butterfly counts per endpoint}
7: \textbf{parfor} \(j \leftarrow F[i]\ \text{to } F[i + 1]\ \text{do}
8: \((v, d) \leftarrow F[j]\)
9: Store \((v, d - 1)\) in \(B\) \hspace{1cm} \triangleright \text{Store butterfly counts per center}
10: \((B, \_ ) \leftarrow \text{GET-FREQ}(B)\) \hspace{1cm} \triangleright \text{Aggregate } B \text{ and retrieve butterfly counts}
11: \textbf{return} \(B\)

12: procedure COUNT-V(G = (U, V, E))
13: \(G' = (V', E') \leftarrow \text{PREPROCESS}(G)\)
14: \(W \leftarrow \text{GET-WEDGES}(G')\) \hspace{1cm} \triangleright \text{Array of wedges}
15: \textbf{return} \(\text{COUNT-V-WEDGES}(G, W)\)

Lemma 4.3. Retrieving a list of all wedges and counting the number of wedges that share the same endpoints can be implemented in \(O(\alpha m)\) expected work and \(O(\log m)\) span w.h.p.

Note that this is a better worst-case work bound than the work bound of \(O(\sum_{v \in V} \deg(v)^2)\) using side order. In the worst-case \(O(\alpha m) = O(m^{1.5})\) while \(O(\sum_{v \in V} \deg(v)^2) = O(mn)\). We have that \(mn = \Omega(m^{1.5})\), since \(n = \Omega(m^{0.5})\).

4.2.2 Per vertex

We now describe the full butterfly counting per vertex algorithm, which is given as COUNT-V in Algorithm 3. We implement preprocessing and wedge retrieval as described previously, in Line 13 and Line 14, respectively.

We note that following Line 2, by counting the frequency of wedges by endpoints, for each fixed vertex \(u_1\) we have obtained in \(R\) a list of all possible endpoints \((u_1, u_2) \in V' \times V'\) with the size of their intersection \(|N(u_1) \cap N(u_2)|\). Thus, by Lemma 4.2 for each endpoint \(u_2, u_1\) contributes \((|N(u) \cap N(u')|)\) butterflies, and for each center \(v\) (as given in \(W\)), \(u_1\) contributes \(|N(u_1) \cap N(u_2)| - 1\) butterflies.

For instance, using the example from Figure 3, \(W\) would be in the sorted order as displayed in Step 3, \(R\) would contain the frequencies per pair of endpoints \{((v_3, v_1), 2), ((v_3, v_2), 2), ((u_1, u_2), 2)\}, and \(F\) would contain the indices \{0, 2, 4\} marking where each set of wedges as grouped by endpoints appear in \(W\).

As such, we compute the per-vertex counts by iterating through \(R\) to add the requisite count to each endpoint (Line 6) and iterating through \(W\) to add the requisite count to each center (Line 9).

Extracting the butterfly counts from our wedges takes \(O(\alpha m)\) work (since we are iterating through \(W\)) and \(O(1)\) span, and as discussed in Section 2 GET-FREQ takes \(O(\alpha m)\) expected work and \(O(\log m)\) span w.h.p. The total complexity of butterfly counting per vertex is given as follows.

Theorem 4.4. Butterfly counting per vertex can be performed in \(O(\alpha m)\) expected work and \(O(\log m)\) span w.h.p.
AlGORITHM 4 Parallel work-efficient butterfly counting per edge

1: procedure COUNT-E-WEDGES\( (G = (U, V, E), W) \)  
2: \( (R, F) \leftarrow \text{get-freq}(W) \) \hspace{1cm} \text{\triangleright Aggregate } W \text{ and retrieve wedge frequencies}  
3: Initialize \( B \) to store butterfly counts per edge  
4: parfor \( i \leftarrow 0 \) to \(|F| - 1\) do  
5: \( ((u_1, u_2), d) \leftarrow R[i] \)  
6: parfor \( j \leftarrow F[i] \) to \( F[i + 1] \) do  
7: \( (u_1, v) \leftarrow W[j] \)  
8: Store \( ((u_1, v), d - 1) \) and \( ((u_2, v), d - 1) \) in \( B \)  
9: \( (B, \_ \_ ) \leftarrow \text{get-freq}(B) \) \hspace{1cm} \text{\triangleright Aggregate } B \text{ and retrieve butterfly counts}  
10: return \( B \)  

11: procedure COUNT-E\( (G = (U, V, E)) \)  
12: \( G' = (V', E') \leftarrow \text{preprocess}(G) \)  
13: \( W \leftarrow \text{get-wedges}(G') \) \hspace{1cm} \text{\triangleright Array of wedges}  
14: return \( \text{COUNT-E-WEDGES}(G, W) \)

4.2.3 Per edge

We now describe the full butterfly counting per edge algorithm, which is given as COUNT-E in Algorithm 4. We implement preprocessing and wedge retrieval as described previously, in Line 12 and Line 13, respectively.

As we discussed in Section 4.2.2, following Step 3 for each fixed vertex \( u_1 \) we have in \( R \) a list of all possible endpoints \((u_1, u_2) \in V' \times V'\) with the size of their intersection \(|N(u_1) \cap N(u_2)|\). Thus, by Lemma 4.2, we compute per-edge counts by iterating through all of our wedge counts and adding \(|N(u_1) \cap N(u_2)| - 1\) to our butterfly counts for the edges contained in the wedges with endpoints \( u_1 \) and \( u_2 \). We note that \( W \) has already been aggregated, and \( F \) gives us the sections of \( W \) that hold wedges corresponding with the endpoints described in \( R \). As such, we can iterate through \( R \) to obtain our count \(|N(u_1) \cap N(u_2)| - 1\), and use \( F \) to iterate through \( W \) to obtain the edges contained in the corresponding wedges. Then, as in Section 4.2.2, we use get-freq to obtain the total sums.

Extracting the butterfly counts from our wedges takes \( O(\alpha m) \) work (since we are essentially iterating through \( W \)), \( O(1) \) span. As discussed in Section 2, get-freq takes \( O(\alpha m) \) expected work and \( O(\log m) \) span w.h.p. The total complexity of butterfly counting per edge is given as follows.

\textbf{Theorem 4.5.} Butterfly counting per edge can be performed in \( O(\alpha m) \) expected work and \( O(\log m) \) span w.h.p.

4.3 Approximate counting

Sanei-Mehri \textit{et al.} [51] describe for computing approximate total butterfly counts based on sampling and graph sparsification. Their sparsification methods are shown to have better performance, and so we focus on parallelizing these methods. The methods are based on creating a sparsified graph, running an exact counting algorithm on the sparsified graph, and scaling up the count returned to obtain an unbiased estimate of the total butterfly count.

The \textit{edge sparsification} method sparsifies the graph by keeping each edge independently with probability \( p \). The butterfly count of the sparsified graph is divided by \( p^4 \) so obtain an
unbiased estimate (since each butterfly remains in the sparsified graph with probability \( p^4 \). Our parallel algorithm simply applies a filter over the adjacency lists of the graph, keeping an edge with probability \( p \). This takes \( O(m) \) work and \( O(O(\log m)) \) span.

The **colorful sparsification** method sparsifies the graph by assigning a random color in \([1, \ldots, \lceil 1/p \rceil]\) to each vertex and keeping an edge if the colors of its two endpoints match. Sanei-Mehri et al. [51] show that each butterfly is kept with probability \( p^3 \), and so the butterfly count on the sparsified graph is divided by \( p^3 \) to obtain an unbiased estimate. Our parallel algorithm uses a hash function to map each vertex to a color, and then applies a filter over the adjacency lists of the graph, keeping an edge if its two endpoints have the same color. This takes \( O(m) \) work and \( O(O(\log m)) \) span.

The variance bounds of our estimates are the same as shown by Sanei-Mehri et al. [51], and we refer the reader to their paper for details. The expected number of edges in both methods is \( pm \), and by plugging this into the bounds for exact butterfly counting, and including the cost of sparsification, we obtain the following theorem.

**Theorem 4.6.** Approximate butterfly counting with sampling rate \( p \) can be performed in \( O((1 + \alpha'p)m) \) expected work and \( O(O(\log m)) \) span w.h.p., where \( \alpha' \) is the arboricity of the sparsified graph.

### 4.4 Approximate degree ordering

We show now that using approximate degree ordering in our preprocessing step also gives work-efficient bounds for butterfly counting. The proof for this closely follows Chiba and Nishizeki’s [14] proof for degree ordering; notably, Chiba and Nishizeki prove that \( O(\sum_{(u,v) \in E} \min(\deg(u), \deg(v))) = O(\alpha m) \).

**Theorem 4.7.** Butterfly counting per vertex and per edge using approximate degree ordering is work-efficient.

**Proof.** The total work of our counting algorithms, as discussed in Sections 4.2.2 and 4.2.3, is given precisely by the number of wedges that we must process, or for a preprocessed graph \( G' = (V', E') \),

\[
O(\sum_{u \in V'} \sum_{v \in N_u(u)} \deg_{u}(v)).
\]

We must have that \( \deg_{u}(v) \leq \deg(v) \leq 2 \cdot \deg(u) \); otherwise, \( v \) would appear before \( u \) in approximate degree order. Moreover, in our double summation, each edge appears precisely once by virtue of our ordering; thus, our bound becomes \( O(\sum_{(u,v) \in E} (2 \cdot \min(\deg(u), \deg(v)))) = O(\alpha m) \), as desired.

### 4.5 Complement degeneracy ordering

We also show that using complement degeneracy ordering and approximate complement degeneracy ordering in our preprocessing step similarly gives work-efficient bounds for butterfly counting. As before, the proof for this closely follows from Chiba and Nishizeki’s [14] proof for degree ordering.

**Theorem 4.8.** Butterfly counting per vertex and per edge using complement degeneracy ordering is work-efficient.

**Proof.** The total work of our counting algorithms, as discussed in Sections 4.2.2 and 4.2.3, is given precisely by the number of wedges that we must process, or for a preprocessed graph \( G' = (V', E') \),

\[
O(\sum_{v \in V'} \sum_{u \in N_v(u)} \deg_{v}(u)).
\]

It is clear that \( \deg_{v}(u) \leq \deg(v) \) by construction. We would like to show that \( \deg_{u}(v) \leq \deg(u) \) as well.
Consider the sequential complement $k$-cores algorithm. For every round $r$, let $\deg^r(u)$ denote the degree of $u$ considering only the induced subgraph on unpeeled vertices. When we peel a vertex $u$ in round $r$, we have for all neighbors $v$ of $u$, $\deg^r(v) \leq \deg^r(u)$. By our ordering construction, we have $\deg_u(v) = \deg^r(v)$, and trivially, $\deg^r(v) \leq \deg(u)$. Thus, $\deg_u(v) \leq \deg(u)$, as desired.

Thus, the number of wedges that we must process is bounded by $O(\sum_{u \in V} \sum_{v \in N_u(u)} \min(\deg(u), \deg(v)))$. Each edge appears precisely once in this double summation by virtue of our ordering. Therefore, our bound becomes $O(\sum_{(u,v) \in E} \min(\deg(u), \deg(v))) = O(\alpha m)$, as desired.

\begin{theorem}
Butterfly counting per vertex and per edge using approximate complement degeneracy ordering is work-efficient.
\end{theorem}

\begin{proof}
This directly follows from the proof of Theorem 4.5, except in each round $r$, when we peel a vertex $u$, we have for all neighbors $v$ of $u$, $\deg^r(v) \leq 2 \cdot \deg^r(u)$. Thus, $\deg_u(v) \leq 2 \cdot \deg(u)$, so the number of wedges that we must process is bounded by $O(\sum_{(u,v) \in E} (2 \cdot \min(\deg(u), \deg(v)))) = O(\alpha m)$.
\end{proof}

### 4.6 Peeling algorithms

We now describe and analyze our parallel algorithms for butterfly peeling. Note that the sequential algorithm for butterfly peeling [52] is precisely the sequential algorithm for $k$-core [53, 41], except that instead of computing and updating the number of neighbors removed from each vertex per round, we compute and update the number of butterflies removed from each vertex or edge per round. As such, we base our parallel butterfly peeling algorithm on the parallel bucketing-based algorithm for $k$-core in Julienne [18]. In parallel, our butterfly peeling algorithm removes (peels) all vertices or edges with the minimum butterfly count in each round, and repeats until the entire graph has been peeled.

Sariy"uce and Pinar [52] state that their sequential butterfly peeling algorithms per vertex and per edge take $O(\sum_{v \in V} \deg(v)^2)$ work and $O(\sum_{n \in U} \sum_{\{v_1, v_2 \in N(u)\}} \max(\deg(v_1), \deg(v_2)))$ work, respectively. They account for the time needed to update butterfly counts, but do not discuss how to extract the vertex or edge with the minimum butterfly count in every round. In their implementation, their bucketing data structure is an array of size on the order of the number of butterflies, and they perform a sequential scan through this array to find vertices to peel. Importantly, they scan through empty buckets in their algorithm, and as such their total time complexity for their implementations of both butterfly peeling algorithms is on the order of the number of butterflies.

We consider here a more efficient bucketing structure, which stores the non-empty buckets in a Fibonacci heap [22], keyed by the number of butterflies. Then, we have an added $O(\log n)$ factor to extract the bucket containing vertices with the minimum butterfly count. Note that insertion and updating keys in Fibonacci heaps take $O(1)$ amortized time per key, which does not contribute more to our work. To use this in our parallel peeling algorithms we need to ensure that batch insertions, decrease-keys, and deletions in the Fibonacci are work-efficient and have low span. We present a parallel Fibonacci heap and prove its bounds in Appendix [A]. We show that a batch of $k$ insertions takes $O(k)$ expected work and $O(\log n)$ span w.h.p., a batch of $k$ decrease-key operations takes amortized $O(k)$ work and $O(\log^2 n)$ span, and a parallel delete-min operation takes amortized $O(\log n)$ work and $O(\log n)$ span. Note that we had to parallelize the delete-min operation in order to prove that the worst-case span was $O(\log n)$. The work of our parallel algorithms improve over the sequential algorithms of Sariy"uce and Pinar [52].
4.6.1 Per vertex

The parallel vertex peeling (tip decomposition) algorithm is given in coreness-v (Algorithm [5]). Note that it is sufficient to peel vertices considering only one bipartition of the graph. We peel on the bipartition that produces the fewest number of wedges (considering the vertices in that bipartition as endpoints), which mirrors Sariyüce and Pinar’s [52] sequential algorithm and gives us work-efficient bounds for peeling; more concretely, we consider the bipartition $X$ such that $\sum_{v \in X} \left( \frac{\text{deg}(v)}{2} \right)$ is minimized. Without loss of generality, let $U$ be this bipartition.

Vertex peeling takes as input the per-vertex butterfly counts from the PARBUTTERFLY counting framework. We create a bucketing structure mapping vertices in $U$ to buckets based on their butterfly count (Line 11). While not all vertices have been peeled, we retrieve the bucket containing vertices with the lowest butterfly count (Line 16), peel them from the graph and compute the wedges that were removed due to peeling (Line 16). Finally, we update the buckets of the remaining vertices whose butterfly count was affected due to the peeling (Line 17).

The main subroutine in coreness-v is update-v (Lines 1–9), which returns a subset of vertices whose butterfly counts have changed after peeling a given set of vertices. In order to compute updated butterfly counts, the equations in Lemma 4.2 apply and we use precisely the same overall steps in our counting algorithms: wedge retrieval, wedge counting, and butterfly counting. Importantly, for wedge retrieval, for every peeled vertex $v_1$, we must gather all wedges with an endpoint $v_1$ in order to account for all butterflies containing $v_1$ (from Equation (1)). We process all peeled vertices $v_1$ in parallel (Line 3), and for each one we find all vertices $v_2$ in its 2-hop neighborhood, each of which contributes a wedge (Lines 4–6). Finally, we aggregate the number of deleted butterflies per vertex (Line 7), and subtract them from the previous butterfly counts (Line 8). Similar to Algorithm 2, we also need to compute a mapping from wedges to indices in $W$ using prefix sums, but we omit this from the pseudocode for simplicity.

The latter two steps, wedge counting and butterfly counting, are precisely as given in our vertex counting algorithm; specifically, these are encapsulated by count-v-wedges in Algorithm 3.

Note that the work of coreness-v is dominated by the total work spent in the update-v subroutine. Since update-v will eventually process in the subsets $A$ all vertices in $U$, the total work in wedge retrieval is precisely the number of wedges with endpoints in $U$, or $O(\sum_{v \in V} \text{deg}(v))$. The work analysis for count-v-wedges then follows from a similar analysis as in Section 4.2.2. Extracting the next bucket on Line 14 and updating the buckets on Line 17 take logarithmic work and polylogarithmic span per round, as previously discussed.

To analyze the span of coreness-v, we define $\rho_v$ to be the vertex peeling complexity of the graph, or the number of rounds needed to completely peel the graph where in each round, all vertices with the minimum butterfly count are peeled. Then, since the span of each call of update-v is bounded by $O(\log m)$ w.h.p. as discussed in Section 4.2.2, and since the span of updating buckets is bounded by $O(\rho_v \log^2 m)$, the span of coreness-v overall is given by $O(\rho_v \log^2 m)$ w.h.p.

In total, the complexity of butterfly peeling by vertex is as follows.

**Theorem 4.10.** Butterfly peeling by vertex can be performed in $O(\rho_v \log n + \sum_{v \in V} \text{deg}(v)^2)$ expected work and $O(\rho_v \log^2 m)$ span w.h.p., where $\rho_v$ is the vertex peeling complexity.

If the maximum number of butterflies per-vertex is $\Omega(\rho_v \log n + \sum_{v \in V} \text{deg}(v)^2)$, which is very likely true in practice, then the work of our algorithm is faster than the sequential algorithm by Sariyüce and Pinar’s [52], which takes $O(\text{max-butterflies} + \sum_{v \in V} \text{deg}(v)^2)$ work, where max-butterflies is the maximum number of butterflies per-vertex.

We must now handle the case where the number of butterflies is $O(\rho_v \log n)$. Since we do not know $\rho_v$ at the beginning of the algorithm, we do know that $\rho_v \leq n$. Thus, we will check if the
Algorithm 5 Parallel vertex peeling (tip decomposition)

1: procedure UPDATE-V(G = (U, V, E), B, A)
2: Initialize W to be an array of wedges
3: parfor u₁ ∈ A do
4: parfor v ∈ N(u₁) do
5: parfor u₂ ∈ N(v) where u₂ ≠ u₁ do
6: Store ((u₁, u₂), 1, v) in W ⊿ (u₁, u₂) is the key, 1 is the frequency
7: B′ ← COUNT-V-WEDGES(G, W)
8: Subtract corresponding counts B′ from B
9: return B

10: procedure CORENESS-V(G = (U, V, E), B) ⊿ B is an array of butterfly counts per vertex
11: Let K be a bucketing structure mapping U to buckets based on # of butterflies
12: f ← 0
13: while f < |U| do
14: A ← all vertices in next bucket (to be peeled)
15: f ← f + |A|
16: B ← UPDATE-V(G, B, A) ⊿ Update # butterflies
17: Update the buckets of changed vertices in B
18: return K

maximum number of butterflies per-vertex is $O(n \log n + \sum_{v \in V} \deg(v)^2)$ at the beginning of the algorithm, and if so, we can use the original bucketing structure of Dhulipala et al. [19], which will give an algorithm with $O(\max$-butterflies + $\sum_{v \in V} \deg(v)^2)$ expected work and $O(\rho_v \log m)$ span w.h.p., matching the work bound of Sariyüce and Pinar. Therefore, our algorithm is work-efficient.

4.6.2 Per edge

While the basic bucketing structure for butterfly peeling by edge follows that for butterfly peeling by vertex (and parallel $k$-core [18]), the algorithm to update butterfly counts within each round represents a significant departure from our previous counting algorithms.

In particular, based on Lemma 4.2 in order to obtain all butterflies containing some edge $(u₁, v₁)$, we must consider all neighbors $u₂ ∈ N(v₁) \setminus \{u₁\}$ and then find the intersection $N(u₁) \cap N(u₂)$. Each vertex $v₂$ in this intersection where $v₂ ≠ v₁$ produces a butterfly $(u₁, v₁, u₂, v₂)$. Importantly, there is no simple aggregation method using wedges in this scenario; we must necessarily find each butterfly individually in order to count contributions from each edge. Note that this is precisely the serial update algorithm that Sariyüce and Pinar [52] use for edge peeling.

The full algorithm for parallel edge peeling is given in CORENESS-E (Algorithm 6). Edge peeling takes as input the per-edge butterfly counts from the PARBUTTERFLY counting framework. Line 14 initializes a bucketing structure mapping each edge to a bucket based on its butterfly count. While not all edges have been peeled, we retrieve the bucket containing vertices with the lowest butterfly count (Line 17), peel them from the graph and compute the wedges that were removed due to peeling (Line 19). Finally, we update the buckets of the remaining vertices whose butterfly count was affected due to the peeling (Line 20).

The main subroutine is UPDATE-E (Lines 1–12), which returns a subset of edges whose butterfly counts have changed after peeling a given set of edges. For each peeled edge $(u₁, v₁)$ in parallel (Line 3), we find all neighbors $u₂$ of $v₁$ where $u₂ ≠ u₁$ and compute the intersection of the neighborhoods
of $u_1$ and $u_2$ (Lines 4–5). All vertices $v_2 \neq v_1$ in their intersection contribute a deleted wedge, and we indicate the number of deleted wedges on the remaining edges of the butterfly $(u_2, v_1), (u_1, v_2)$, and $(u_2, v_2)$ in an array $B'$ (Lines 6–9). Finally, we aggregate the number of deleted butterflies per edge (Line 10), and subtract them from the previous butterfly counts (Line 11). A mapping from edges to indices in $B'$ is needed (computed using prefix sums), and is omitted for simplicity.

The work of \textsc{coreness-e} is again dominated by the total work spent in the \textsc{update-e} subroutine. We can optimize the intersection on Line 5 by using hash tables to store the adjacency lists of the vertices so that we only perform $O\left(\min(\deg(u), \deg(u'))\right)$ work when intersecting $N(u)$ and $N(u')$ (by scanning through the smaller list in parallel and performing lookups in the larger list). This gives us $O\left(\sum_{(u,v)\in E} \sum_{u'\in N(v)} \min(\deg(u), \deg(u'))\right)$ expected work. As in vertex peeling, to analyze the span of \textsc{coreness-e}, we define $\rho_e$ to be the edge peeling complexity of the graph, or the number of rounds needed to completely peel the graph where in each round, all edges with the minimum butterfly count are peeled. Note that the span of \textsc{update-e} is bounded by the span of \textsc{get-freq} and of updating buckets, giving us $O\left(\log^2 m\right)$ span w.h.p. Thus, the span of \textsc{coreness-e} overall is $O\left(\rho_e \log^2 m\right)$ w.h.p.

In total, the complexity of butterfly peeling by edge is as follows.

**Theorem 4.11.** Butterfly peeling by edge can be performed in $O\left(\rho_e \log m + \sum_{(u,v)\in E} \sum_{u'\in N(v)} \min(\deg(u), \deg(u'))\right)$ expected work and $O\left(\rho_e \log^2 m\right)$ span w.h.p., where $\rho_e$ is the edge peeling complexity.

Similar to vertex peeling, if the maximum number of butterflies per-edge is $\Omega\left(\rho_e \log m + \sum_{(u,v)\in E} \sum_{u'\in N(v)} \min(\deg(u), \deg(u'))\right)$, again very likely true in practice, then the work of our algorithm is faster than the sequential algorithm by Sariyuce and Pinar’s [52], which takes $O\left(\max\text{-butterflies} + \sum_{(u,v)\in E} \sum_{u'\in N(v)} \min(\deg(u), \deg(u'))\right)$ work, where max-butterflies is the maximum number of butterflies per-edge, and assuming that their intersection is optimized.

To deal with the case where the maximum number of butterflies per-edge is small, we will check if the maximum number of butterflies per-vertex is $O\left(\rho_e \log m + \sum_{(u,v)\in E} \sum_{u'\in N(v)} \min(\deg(u), \deg(u'))\right)$ at the beginning of the algorithm (we know that $\rho_e \leq m$), and if so, we can use the original bucketing structure of Dhulipala et al [19], which will give an algorithm with $O\left(\max\text{-butterflies} + \sum_{(u,v)\in E} \sum_{u'\in N(v)} \min(\deg(u), \deg(u'))\right)$ expected work and $O\left(\rho_e \log m\right)$ span w.h.p., matching the work bound of Sariyuce and Pinar. Therefore, our algorithm is work-efficient.

## 5 Experiments

We evaluate our butterfly counting algorithms in practice, in terms of scalability and performance compared to previous algorithms.

### 5.1 Environment

We run our experiments on the m5d.24xlarge AWS EC2 instance, which consists of 48 cores (with two-way hyper-threading), with 3.1 GHz Intel Xeon Platinum 8175 processors and 384 GiB of main memory. We use Cilk Plus’s work-stealing scheduler [11] [38] and we compile our programs with g++ (version 7.3.1) using the -O3 flag.

We test our algorithms on a variety of real-world bipartite graphs from the Koblenz Network Collection (KONECT) [38] [4]. We preprocess the graphs to remove self-loops and multiple edges.

We took our datasets from \url{http://konect.uni-koblenz.de/} which is no longer up. There is a new website hosting the KONECT database at \url{http://konect.cc/} but the dblp, itwiki, and enwiki datasets are different on this new website. All other datasets are consistent between the two websites.
Algorithm 6 Parallel edge peeling (wing decomposition)

1: procedure UPDATE-E(G = (U, V, E), B, A)  
2: Initialize B’ to store updated butterfly counts  
3: parfor (u₁, v₁) ∈ A do  
4: parfor u₂ ∈ N(v₁) where u₂ ≠ u₁ do  
5: N ← INTERSECT(N(u₁), N(u₂))  
6: Store (u₂, v₁, |N| - 1, _) in B’  
7: parfor v₂ ∈ N where v₂ ≠ v₁ do  
8: Store (u₁, v₂, 1, _) in B’  
9: Store (u₂, v₂, 1, _) in B’  
10: (B″, _) ← GET-FREQ(B’)  
11: Subtract corresponding counts in B″ from B  
12: return B  

13: procedure CORENESS-E(G = (U, V, E), B) ⊿ B is an array of butterfly counts per edge  
14: Let K be a bucketing structure mapping E to buckets based on # of butterflies  
15: f ← 0  
16: while f < m do  
17: A ← all edges in next bucket (to be peeled)  
18: f ← f + |A|  
19: B ← UPDATE-E(G, B, A)  
20: Update the buckets of changed edges in B  
21: return K  

Table 1 describes the properties of these graphs, including sizes, number of butterflies, and peeling complexities.

Notationally, when discussing wedge and butterfly aggregation methods, we use the prefix “A” to refer to using atomic fetch-and-add for butterfly aggregation, and we take a lack of prefix to mean that the wedge aggregation method was used for butterfly aggregation. “BatchWA” is the wedge-aware version of batching that dynamically assigns tasks to workers that have a roughly equal number of wedges to process. For the sorting, hashing, and histogramming aggregation methods, we fix the maximum number of wedges in memory at any time to be 257,750,000. For wedge aggregation using batching, we fix the the maximum array size to be 23,009,996,160.

5.2 Results

5.2.1 Butterfly counting

Figures 5, 6, and 7 show the runtimes over different aggregation methods for counting per vertex, per edge, and in total, respectively, for the seven datasets in Table 1 with sequential counting times exceeding 1 second. The times are normalized to the fastest combination of aggregation and ranking methods for each dataset. Considering different wedge and butterfly aggregation methods, we find that simple batching and wedge-aware batching give the best runtimes for butterfly counting in general. Of the work-efficient aggregation methods, hashing and histogramming with atomic fetch-and-add are often faster than sorting, particularly for larger graphs due to increased parallelism and locality respectively.

Table 2 shows our runtimes for sequential butterfly counting, as well as runtimes from algorithms and implementations from previous works, all of which we set up and tested in the same
Table 1: These are relevant statistics for the KONECT graphs that we experimented on. Note that we only tested peeling algorithms on graphs for which Sariyüce and Pinar’s serial peeling algorithms completed in less than 5.5 hours. As such, there are certain graphs for which we have no available $\rho_v$ and $\rho_e$ data, and these entries are represented by a dash.

Figure 5: These are the runtimes for butterfly counting per vertex, considering different wedge aggregation and butterfly aggregation methods. We consider the ranking that produces the fastest runtime for each graph; * refers to side ranking, # refers to approximate co degeneracy ranking, and ◦ refers to approximate degree ranking. All times are scaled by the fastest runtime, as indicated in parentheses.

**Figure 6**: Visualizing the multiplicative slowdowns for various methods and datasets.

**Figure 7**: The runtimes for butterfly counting per vertex for different rankings using the simple batching method. The times are normalized to the time for the fastest ranking for each dataset. Side ordering outperforms the other rankings for itwiki, livejournal, and orkut, while

5.2.2 Ranking

Figure 10 shows the runtimes for butterfly counting per vertex for different rankings using the simple batching method. The times are normalized to the time for the fastest ranking for each dataset. Side ordering outperforms the other rankings for itwiki, livejournal, and orkut, while

By “large enough,” we mean graphs for which the sequential counting algorithms take more than 2 seconds to complete.
Figure 6: These are the runtimes for butterfly counting per edge, considering different wedge aggregation and butterfly aggregation methods. We consider the ranking that produces the fastest runtime for each graph; * refers to side ranking, # refers to approximate co degeneracy ranking, and ◦ refers to approximate degree ranking. All times are scaled by the fastest runtime, as indicated in parentheses.

Figure 7: These are the runtimes for butterfly counting in total, considering different wedge aggregation methods (butterfly aggregation does not apply). We consider the ranking that produces the fastest runtime for each graph; * refers to side ranking, # refers to approximate co degeneracy ranking, and ◦ refers to approximate degree ranking. All times are scaled by the fastest runtime, as parentheses.

Table 2: These are runtimes in seconds for sequential butterfly counting from our framework, as well as runtimes from previous work. Note that PGD [2] is parallel, while the rest of the implementations are serial. Also, for the runtimes from our framework, we have noted the ranking used; * refers to side ranking, # refers to approximate co degeneracy ranking, and ◦ refers to approximate degree ranking.

approximate complement degeneracy, approximate degree, and degree orderings outperform side
Figure 8: These are the runtimes for butterfly counting per vertex on livejournal using side ranking, over different numbers of threads. The self-relative speedups are between 13.7–28.3x.

Figure 9: These are the runtimes for butterfly counting per edge on livejournal using approximate degree ranking, over different numbers of threads. The self-relative speedups are between 15.9–38.0x.

Figure 10: These are the runtimes for butterfly counting per vertex, considering different rankings. We use simple batching as our wedge aggregation method. All times are scaled by the fastest runtime, as indicated in parentheses. Moreover, the time taken to rank each graph is included in the runtimes.

ordering for discogs, enwiki, delicious, and web.

Note that different rankings change the number of wedges that we must process; in particular, we found that complement degeneracy minimizes the number of wedges that we process across all of the real-world graphs considered. However, complement degeneracy is not a feasible ordering in practice, since the runtime of ranking is limited by peeling complexity and often exceeds the runtime of the actual counting. Moreover, side ordering often outperforms the other rankings due to better locality, especially if the number of wedges processed by the other rankings does not greatly exceed the number of wedges given by side ordering. We found that the approximate complete degeneracy, degree, and approximate degree orders perform similarly, and these orderings are all...
Table 3: These are the fractional values \( f = (w_s - w_r)/w_s \), where \( w_s \) is the number of wedges that must be processed using side ordering and \( w_r \) is the number of wedges that must be processed using the labeled ordering. Note that for itwiki, the number of wedges produced by degree ordering is precisely equal to the number of wedges produced by side ordering.

Figure 11: These are the runtimes for colorful sparsification and edge sparsification over different probabilities \( p \). We considered both the runtimes on 48 cores hyperthreaded and on a single thread. We ran these algorithms on orkut, using simple batch aggregation and side ranking.

As such, we devise a fractional metric \( f \) that in general determines whether side ordering outperforms other rankings. If we let \( w_s \) be the number of wedges processed by using side ordering and \( w_r \) be the number of wedges processed by using another ranking, our metric is \((w_s - w_r)/w_s\). If this metric is below 0.1, then side ordering outperforms or performs just as well as other rankings. Table 3 shows this metric across all of the rankings implemented in ParButterfly. Note that this metric is fairly similar across these other rankings, and is particularly high for web, explaining the significant speedup obtained by using approximate degree ordering over side ordering for web.

5.2.3 Approximate counting

Figure 11 shows runtimes for both colorful sparsification and edge sparsification on orkut, as well as the corresponding single-threaded times. We see that for sparsification, over a variety of probabilities \( p \) we achieve self-relative speedups between 4.9–21.4x. Furthermore, we observe that colorful sparsification is faster than edge sparsification for a given value of \( p \).
Figure 12: These are the runtimes for butterfly vertex peeling with different wedge aggregation methods (these runtimes do not include the time taken to count butterflies). All times are scaled by the fastest runtime, as indicated in parentheses. Also, note that the runtimes for discogs_style represent single-threaded runtimes; this is because we did not see any parallel speedups for discogs_style, due to the small number of vertices that were peeled.

Figure 13: These are the runtimes for butterfly edge peeling with different wedge aggregation methods (these runtimes do not include the time taken to count butterflies). All times are scaled by the fastest runtime, as indicated in parentheses.

Table 4: These are runtimes in seconds for serial butterfly peeling from Sariyüce and Pinar [52]. Note that these runtimes do not include the time taken to count butterflies.
5.2.4 Butterfly peeling

Figures 12 and 13 show the runtimes over different wedge aggregation methods for vertex peeling and edge peeling, respectively (the runtimes do not include the time for counting butterflies). We only report times for the datasets for which finished within 5.5 hours. We find that for vertex peeling, aggregation by histogramming largely gives the best runtimes, while for edge peeling, all of our aggregation methods give similar results.

We compare our parallel peeling times to serial peeling times from Sariyüz and Pinar’s [52] implementation, which we ran in our environment and which are shown in Table 4. Compared to Sariyüz and Pinar [52], we achieve speedups between 1.3–2082.3x for vertex peeling and between 3.4–7.0x for edge peeling. Our speedups are highly variable because they depend heavily on the peeling complexities; they are in general smaller for graphs with high peeling complexities compared to the size of the graph, while our largest speedup of 2082.3x occurs for vertex peeling on discogs style.

Moreover, comparing our parallel peeling times to their corresponding single-threaded times, we achieve speedups between 1.0–10.7x for vertex peeling and between 2.3–10.4x for edge peeling. Note that these speedups were obtained using discogs and discogs style for vertex peeling and using dblp and github for edge peeling. We did not see self-relative parallel speedups for vertex peeling on discogs style, because the number of vertices peeled (383) was too small.

6 Related Work

There have been several sequential algorithms designed for butterfly counting and peeling. Wang et al. [61] propose the first algorithm for butterfly counting over vertices in $O\left( \sum_{v \in V} \deg(v)^2 \right)$ work, and Sanei-Mehri et al. [51] introduce a practical speedup by choosing the vertex partition with fewer edges to iterate over. Sanei-Mehri et al. [51] also introduce approximate counting algorithms based on sampling and graph sparsification. Later, Zhu et al. [66] present a sequential algorithm for counting over vertices based on ordering vertices (although they do not specify which order) in $O\left( \sum_{v \in V} \deg(v)^2 \right)$ work. They extend their algorithm to the external-memory setting and also design sampling algorithms. Unfortunately, their source code is unavailable so we could not use it as one of the sequential baselines. Sariyüz and Pinar [52] introduce algorithms for butterfly counting over edges, which similarly takes $O\left( \sum_{v \in V} \deg(v)^2 \right)$ work, and for butterfly peeling over vertices and over edges, which take $O\left( \rho_v \log n + \sum_{v \in V} \deg(v)^2 \right)$ work and $O\left( \rho_e \log n + \sum_{u \in U} \sum_{v_1,v_2 \in N(u)} \max(\deg(v_1), \deg(v_2)) \right)$ work, respectively.

Surprisingly, Chiba and Nishizeki’s [14] original work on counting 4-cycles in general graphs applies directly to bipartite graphs and has a better time complexity than these other works. Chiba and Nishizeki [14] use a ranking algorithm that counts the total number of 4-cycles in a graph in $O(\alpha m)$ time, where $\alpha$ is the arboricity of the graph. While they only give a total count in their work, their algorithm can easily be extended to obtain counts per-vertex and per-edge in the same time complexity.

In terms of prior work on parallelizing these algorithms, Wang et al. [61] implement a distributed algorithm using MPI that partitions the vertices across processors, and each processor sequentially counts the number of butterflies for vertices in its partition. They also implement a MapReduce algorithm, but show that it is less efficient than their MPI-based algorithm. The largest graph they report parallel times for is the deli graph with 140 million edges and $1.8 \times 10^{10}$ butterflies; this is

---

8 Note that these are corrections to Sariyüz and Pinar’s [52] butterfly peeling bounds, which we discuss in Section 4.6.

9 Notably, Chiba and Nishizeki [14] count 4-cycles as subgraphs, not as induced subgraphs.
the delicious tag-item graph in KONECT [36]. On this graph, they take 110 seconds on 16 nodes, whereas on the same graph we take 5.17 seconds on 16 cores.

Very recently, and independently of our work, Wang et al. [62] describe an algorithm for butterfly counting using degree ordering, as done in Chiba and Nishizeki [14], and also propose a cache optimization for wedge retrieval. Their parallel algorithm is similar to our simple parallelization except they manually schedule the threads, whereas we use the Cilk scheduler. They use their algorithm to speed up approximate butterfly counting, and also propose an external-memory variant. It would be interesting future work to combine our theoretically-efficient parallel counting algorithms with their cache optimization, and also use them in our parallel peeling algorithms.

There has been recent work on algorithms for finding subgraphs of size 4 or 5 [29, 21, 48, 2, 17], which can be used for butterfly counting as a special case. Marcus and Shavitt [40] design a sequential algorithm for finding subgraphs of up to size 4. Hocevar and Demsar [29] present a sequential algorithm for counting subgraphs of up to size 5. Pinar et al. [48] also present an algorithm for counting subgraphs of up to size 5 based on degree ordering as done in Chiba and Nishizeki [14]. For the special case of butterfly counting, their algorithm is the fastest among sequential solutions, and we compare with it in Section 5. The same algorithm for butterfly counting was also described by Xia [64]. Elenberg et al. [21] present a distributed algorithm for counting subgraphs of size 4. Ahmed et al. [2] present the PGD shared-memory framework for counting subgraphs of up to size 4, which we compare with in Section 5. The work of their algorithm for counting 4-cycles is $O(\sum_{(u,v) \in E}(\deg(v) + \sum_{u' \in N(v)} \deg(u')))$, which is higher our algorithms. Aberger et al. [1] design the EmptyHeaded framework for parallel subgraph finding based on worst-case optimal join algorithms [44]. For butterfly counting, their approach takes quadratic work. We were unable to obtain runtimes for EmptyHeaded because it ran out of memory in our environment. Dave et al. [17] present a parallel method for counting subgraphs of up to size 5 local to each edge. For counting 4-cycles, their algorithm is the same as PGD, which we compare with. There have also been various methods for approximating subgraph counts via sampling [34, 3, 4, 63, 32, 13, 50, 42]. Finally, there has also been significant work for the past decade on parallel triangle counting algorithms (e.g., [56, 7, 57, 6, 46, 47, 45, 58, 60, 39, 35, 26, 25, 30, 19, 28, 65] and papers from the annual GraphChallenge [24], among many others).

7 Conclusion

We have designed a framework PARBUTTERFLY that provides efficient parallel algorithms for butterfly counting (global, per-vertex, and per-edge) and peeling (by vertex and by edge). We have also shown strong theoretical bounds in terms of work and span for these algorithms. The PARBUTTERFLY framework is built with modular components that can be easily adjusted for practical efficiency. PARBUTTERFLY outperforms the best existing parallel butterfly counting implementations, and we outperform the fastest sequential baseline by up to 13.6x for butterfly counting and 2082.3x for butterfly peeling.

Acknowledgements

We thank Laxman Dhulipala for helpful discussions about bucketing.
References

[1] C. R. Aberger, A. Lamb, S. Tu, A. Nötzli, K. Olukotun, and C. Ré. EmptyHeaded: A relational engine for graph processing. *ACM Trans. Database Syst.*, 42(4):20:1–20:44, 2017.

[2] N. K. Ahmed, J. Neville, R. A. Rossi, N. G. Duffield, and T. L. Willke. Graphlet decomposition: framework, algorithms, and applications. *Knowl. Inf. Syst.*, 50(3):689–722, 2017.

[3] N. K. Ahmed, T. L. Willke, and R. A. Rossi. Estimation of local subgraph counts. In *IEEE International Conference on Big Data*, pages 586–595, 2016.

[4] N. K. Ahmed, T. L. Willke, and R. A. Rossi. Exact and estimation of local edge-centric graphlet counts. In *International Workshop on Big Data, Streams and Heterogeneous Source Mining: Algorithms, Systems, Programming Models and Applications*, pages 1–17, 2016.

[5] S. G. Aksoy, T. G. Kolda, and A. Pinar. Measuring and modeling bipartite graphs with community structure. *J. Complex Networks*, 5:581–603, 2017.

[6] S. Arifuzzaman, M. Khan, and M. Marathe. PATRIC: A parallel algorithm for counting triangles in massive networks. In *ACM Conference on Information and Knowledge Management (CIKM)*, pages 529–538, 2013.

[7] A. Azad, A. Bulu, and J. Gilbert. Parallel triangle counting and enumeration using matrix algebra. In *IEEE International Parallel and Distributed Processing Symposium Workshop*, pages 804–811, 2015.

[8] L. Becchetti, P. Boldi, C. Castillo, and A. Gionis. Efficient semi-streaming algorithms for local triangle counting in massive graphs. In *ACM SIGKDD International Conference on Knowledge Discovery and Data Mining*, pages 16–24, 2008.

[9] D. Bhattarai. Towards scalable parallel fibonacci heap implementation. Master’s thesis, St. Cloud State University, 2018.

[10] G. E. Blelloch, P. B. Gibbons, and H. V. Simhadri. Low depth cache-oblivious algorithms. In *ACM Symposium on Parallelism in Algorithms and Architectures (SPAA)*, pages 189–199, 2010.

[11] R. D. Blumofe and C. E. Leiserson. Scheduling multithreaded computations by work stealing. *J. ACM*, 46(5):720–748, Sept. 1999.

[12] S. P. Borgatti and M. G. Everett. Network analysis of 2-mode data. *Social Networks*, 19(3):243–269, 1997.

[13] M. Bressan, F. Chierichetti, R. Kumar, S. Leucci, and A. Panconesi. Motif counting beyond five nodes. *TKDD*, 12(4):48:1–48:25, 2018.

[14] N. Chiba and T. Nishizeki. Arboricity and subgraph listing algorithms. *SIAM J. Comput.*, 14(1):210–223, Feb. 1985.

[15] J. Cohen. Graph twiddling in a MapReduce world. *Computing in Science and Eng.*, 11(4):29–41, July 2009.

[16] T. H. Cormen, C. E. Leiserson, R. L. Rivest, and C. Stein. *Introduction to Algorithms (3. ed.)*. MIT Press, 2009.
[17] V. S. Dave, N. K. Ahmed, and M. Hasan. PE-CLoG: Counting edge-centric local graphlets. In IEEE International Conference on Big Data, pages 586–595, 2017.

[18] L. Dhulipala, G. Blelloch, and J. Shun. Julienne: A framework for parallel graph algorithms using work-efficient bucketing. In ACM Symposium on Parallelism in Algorithms and Architectures (SPAA), pages 293–304, 2017.

[19] L. Dhulipala, G. E. Blelloch, and J. Shun. Theoretically efficient parallel graph algorithms can be fast and scalable. In ACM Symposium on Parallelism in Algorithms and Architectures (SPAA), pages 393–404, 2018.

[20] J. R. Driscoll, H. N. Gabow, R. Shrairman, and R. E. Tarjan. Relaxed heaps: An alternative to fibonacci heaps with applications to parallel computation. Commun. ACM, 31(11):1343–1354, Nov. 1988.

[21] E. R. Elenberg, K. Shanmugam, M. Borokhovich, and A. G. Dimakis. Distributed estimation of graph 4-profiles. In International Conference on World Wide Web (WWW), pages 483–493, 2016.

[22] M. L. Fredman and R. E. Tarjan. Fibonacci heaps and their uses in improved network optimization algorithms. In Proceedings of the 25th Annual Symposium on Foundations of Computer Science, 1984, SFCS ’84, pages 338–346, Washington, DC, USA, 1984. IEEE Computer Society.

[23] J. Gil, Y. Matias, and U. Vishkin. Towards a theory of nearly constant time parallel algorithms. In IEEE Symposium on Foundations of Computer Science (FOCS), pages 698–710, 1991.

[24] GraphChallenge. http://graphchallenge.mit.edu/.

[25] O. Green, L. M. Munguia, and D. A. Bader. Load balanced clustering coefficients. In Workshop on Parallel Programming for Analytics Applications, pages 3–10, 2014.

[26] O. Green, P. Yalamanchili, and L. M. Munguia. Fast triangle counting on the GPU. In Workshop on Irregular Applications: Architectures and Algorithms, pages 1–8, 2015.

[27] Y. Gu, J. Shun, Y. Sun, and G. E. Blelloch. A top-down parallel semisort. In ACM Symposium on Parallelism in Algorithms and Architectures (SPAA), pages 24–34, 2015.

[28] S. Han, L. Zou, and J. X. Yu. Speeding up set intersections in graph algorithms using simd instructions. In ACM SIGMOD International Conference on Management of Data, pages 1587–1602, 2018.

[29] T. Hocevar and J. Demsar. A combinatorial approach to graphlet counting. Bioinformatics, pages 559–65, 2014.

[30] Y. Hu, H. Liu, and H. H. Huang. TriCore: Parallel triangle counting on gpus. In International Conference for High Performance Computing, Networking, Storage, and Analysis (SC), pages 14:1–14:12, 2018.

[31] Q. Huang and W. E. Weihl. An evaluation of concurrent priority queue algorithms. In IEEE Symposium on Parallel and Distributed Processing, pages 518–525, 1991.
[32] S. Jain and C. Seshadhri. A fast and provable method for estimating clique counts using Turán’s theorem. In *International Conference on World Wide Web (WWW)*, pages 441–449, 2017.

[33] J. Jaja. *Introduction to Parallel Algorithms*. Addison-Wesley Professional, 1992.

[34] M. Jha, C. Seshadhri, and A. Pinar. Path sampling: A fast and provable method for estimating 4-vertex subgraph counts. In *International Conference on World Wide Web (WWW)*, pages 495–505, 2015.

[35] T. G. Kolda, A. Pinar, T. Plantenga, C. Seshadhri, and C. Task. Counting triangles in massive graphs with MapReduce. *SIAM Journal on Scientific Computing*, 36(5):S48–S77, 2014.

[36] J. Kunegis. KONECT: the Koblenz network collection. pages 1343–1350, 05 2013.

[37] M. Latapy, C. Magnien, and N. D. Vecchio. Basic notions for the analysis of large two-mode networks. *Social Networks*, 30(1):31 – 48, 2008.

[38] C. E. Leiserson. The Cilk++ concurrency platform. *The Journal of Supercomputing*, 51(3), 2010.

[39] D. Makkar, D. A. Bader, and O. Green. Exact and parallel triangle counting in dynamic graphs. In *IEEE International Conference on High Performance Computing (HiPC)*, pages 2–12, 2017.

[40] D. Marcus and Y. Shavitt. Efficient counting of network motifs. In *IEEE International Conference on Distributed Computing Systems Workshops*, pages 92–98, 2010.

[41] D. W. Matula and L. L. Beck. Smallest-last ordering and clustering and graph coloring algorithms. *J. ACM*, 30(3):417–427, July 1983.

[42] D. Mawhirter, B. Wu, D. Mehta, and C. Ai. ApproxG: Fast approximate parallel graphlet counting through accuracy control. In *IEEE/ACM International Symposium on Cluster, Cloud and Grid Computing (CCGRID)*, pages 533–542, 2018.

[43] M. E. J. Newman. The structure and function of complex networks. *SIAM Review*, 45:167–256, 2003.

[44] H. Q. Ngo, E. Porat, C. Ré, and A. Rudra. Worst-case optimal join algorithms. *J. ACM*, 65(3):16:1–16:40, Mar. 2018.

[45] R. Pagh and C. E. Tsourakakis. Colorful triangle counting and a MapReduce implementation. *Inf. Process. Lett.*, 112(7):277–281, Mar. 2012.

[46] H.-M. Park and C.-W. Chung. An efficient MapReduce algorithm for counting triangles in a very large graph. In *ACM Conference on Information and Knowledge Management (CIKM)*, pages 539–548, 2013.

[47] H.-M. Park, F. Silvestri, U. Kang, and R. Pagh. MapReduce triangle enumeration with guarantees. In *ACM Conference on Information and Knowledge Management (CIKM)*, pages 1739–1748, 2014.

[48] A. Pinar, C. Seshadhri, and V. Vishal. ESCAPE: Efficiently counting all 5-vertex subgraphs. In *International Conference on World Wide Web (WWW)*, pages 1431–1440, 2017.
[49] S. Rajasekaran and J. H. Reif. Optimal and sublogarithmic time randomized parallel sorting algorithms. *SIAM J. Comput.*, 18(3):594–607, June 1989.

[50] R. A. Rossi, R. Zhou, and N. K. Ahmed. Estimation of graphlet counts in massive networks. *IEEE Trans. Neural Netw. Learning Syst.*, 30(1):44–57, 2019.

[51] S.-V. Sanei-Mehri, A. E. Sariyuce, and S. Tirthapura. Butterfly counting in bipartite networks. In *ACM SIGKDD International Conference on Knowledge Discovery and Data Mining*, pages 2150–2159, 2018.

[52] A. E. Sariyuce and A. Pinar. Peeling bipartite networks for dense subgraph discovery. In *ACM International Conference on Web Search and Data Mining (WSDM)*, pages 504–512, 2018.

[53] S. B. Seidman. Network structure and minimum degree. *Social Networks*, 5(3):269 – 287, 1983.

[54] J. Shun and G. E. Blelloch. Phase-concurrent hash tables for determinism. In *ACM Symposium on Parallelism in Algorithms and Architectures (SPAA)*, pages 96–107, 2014.

[55] J. Shun, G. E. Blelloch, J. T. Fineman, P. B. Gibbons, A. Kyrola, H. V. Simhadri, and K. Tangwongsan. Brief announcement: The Problem Based Benchmark Suite. In *ACM Symposium on Parallelism in Algorithms and Architectures (SPAA)*, pages 68–70, 2012.

[56] J. Shun and K. Tangwongsan. Multicore triangle computations without tuning. In *IEEE International Conference on Data Engineering (ICDE)*, pages 149–160, 2015.

[57] S. Suri and S. Vassilvitskii. Counting triangles and the curse of the last reducer. In *International World Wide Web Conference (WWW)*, pages 607–614, 2011.

[58] K. Tangwongsan, A. Pavan, and S. Tirthapura. Parallel triangle counting in massive streaming graphs. In *ACM Conference on Information and Knowledge Management (CIKM)*, pages 781–786, 2013.

[59] C. E. Tsourakakis, P. Drineas, E. Michelakis, I. Koutis, and C. Faloutsos. Spectral counting of triangles via element-wise sparsification and triangle-based link recommendation. *Social Network Analysis and Mining*, 1(2):75–81, Apr 2011.

[60] C. E. Tsourakakis, U. Kang, G. L. Miller, and C. Faloutsos. DOULION: Counting triangles in massive graphs with a coin. In *ACM SIGKDD Conference on Knowledge Discovery and Data Mining*, pages 837–846, 2009.

[61] J. Wang, A. W.-C. Fu, and J. Cheng. Rectangle counting in large bipartite graphs. In *IEEE International Congress on Big Data*, pages 17–24, 2014.

[62] K. Wang, X. Lin, L. Qin, W. Zhang, and Y. Zhang. Vertex priority based butterfly counting for large-scale bipartite networks. *PVLDB*, 12(10), June 2019.

[63] P. Wang, J. Zhao, X. Zhang, Z. Li, J. Cheng, J. C. S. Lui, D. Towsley, J. Tao, and X. Guan. MOSS-5: A fast method of approximating counts of 5-node graphlets in large graphs. *IEEE Transactions on Knowledge and Data Engineering*, 30(1):73–86, Jan 2018.

[64] X. Xia. Efficient and scalable listing of four-vertex subgraphs. Master’s thesis, Texas A&M University, 2016.
[65] Y. Zhang, H. Jiang, F. Wang, Y. Hua, D. Feng, and X. Xu. LiteTE: Lightweight, communication-efficient distributed-memory triangle enumerating. *IEEE Access*, 7:26294–26306, 2019.

[66] R. Zhu, Z. Zou, and J. Li. Fast rectangle counting on massive networks. In *IEEE International Conference on Data Mining (ICDM)*, pages 847–856, 2018.
A Parallel Fibonacci heap

Fibonacci heaps were first introduced by Fredman and Tarjan [22]. In this section, we show that we can parallelize batches of insertion and decrease-key operations work-efficiently, with logarithmic span. Also, we show that a single work-efficient parallel delete-min can be performed with logarithmic span, which is sufficient for our purposes.

Previous work has also explored parallelism in Fibonacci heaps. Driscoll et al. [20] present relaxed heaps, which achieve the same bounds as Fibonacci heaps, but can be used to obtain a parallel implementation of Dijkstra’s algorithm; however their data structures do not support batch-parallel insertions or decrease-key operations. Huang and Weihl [31] and Bhattarai [9] present implementations of parallel Fibonacci heaps by relaxing the semantics of delete-min, although no theoretical bounds are given.

A Fibonacci heap $H$ consists of heap-ordered trees (maintained using a root list), with certain nodes marked and a pointer to the minimum element. Since we use $H$ to bucket values with the same key, each node consists of a key and an associated bucket, which holds a list of the values. Let $n$ denote the number of elements in our Fibonacci heap. The rank of a node $x$ is the number of children that $x$ contains, and the rank of a heap is the maximum rank of any node in the heap. Note that the rank of a Fibonacci heap is bounded by $O(\log n)$. We also define $t(H)$ to be the number of trees in $H$, and we define $m(H)$ to be the number of marked nodes in $H$.

We begin by giving a brief overview of the sequential Fibonacci heap operations:

- **Insert** ($O(1)$ work): To insert node $x$, we add $x$ to the root list as a new singleton tree and update the minimum pointer if needed.

- **Delete-min** ($O(\log n)$ amortized work): We delete the minimum node as given by the minimum pointer, and add all of its children to the root list. We update the minimum pointer if needed. We then merge trees until no two trees have the same rank; a merge occurs by taking two trees of the same rank, and assigning the larger root as a child of the smaller root.

- **Decrease-key** ($O(1)$ amortized work): To decrease the key of a node $x$, we first check if decreasing the key would violate heap order. If not, we simply decrease the key and update the minimum pointer if needed. Otherwise, we cut the node $x$ and its subtree from its parent, and add it to the root list. If the parent of $x$ was unmarked, we mark the parent. Otherwise, we cut the parent, add it to the root list, and unmark it; we recurse in the same manner on its parent.

Note that for our amortized analysis, our potential function is $\Phi(H) = t(H) + 2 \cdot m(H)$.

We also make a few key modifications for our purposes. Instead of keeping marks on nodes as a boolean value, each node stores a number of marks which it accumulates. Moreover, we keep a parallel hash table that stores pointers to nodes, keyed by the keys of the nodes; we use here a parallel hash table based on linear probing [54]. The added hash table is necessary to ensure that all nodes with the same key are aggregated into a single node.

A.1 Batch insertion

For parallel batch insertion, let $K$ denote the set of key value pairs that we are adding to our heap. First, we semisort the keys in $K$. For each distinct key, we then check if it appears in our hash table; if so, then we simply add the corresponding set of values to the existing bucket in the heap as a batch. Otherwise, we add the new key to the hash table, and create a singleton tree where the
Algorithm 7 Parallel delete-min

1: **procedure** PAR-DELETE-MIN(H)
2: Delete the minimum node and add all children to root list
3: Initialize B such that B[i] contains all roots with rank i
4: **while** 3 a bucket in B with > 1 root **do**
5: Initialize B’ to hold updated trees
6: **parfor** i ← 0 to |B| **do**
7: Partition the roots in B[i] into pairs
8: If a root is leftover, insert it into B'[i]
9: Merge the trees in every pair and insert the new roots into B'[i + 1]
10: B ← B'
11: Use **scan** among the root nodes to update the minimum pointer
12: **return** H

bucket consists of all new values corresponding to that key. We add all new singleton trees to the root list, and update the minimum pointer.

Note that we can perform the semisort and the find operations in our hash table in parallel, in expected $O(k)$ work and $O(\log n)$ span w.h.p. Creating new singleton trees takes $O(k)$ work and constant span, and to update the minimum pointer, we use a parallel scan between the newly added nodes and the previous minimum of the heap, which takes $O(k)$ work and $O(\log k)$ span.

The total complexity of batch insertion is given as follows.

**Lemma A.1.** Parallel batch insertion of $k$ elements into a Fibonacci heap takes $O(k)$ expected work and $O(\log n)$ span w.h.p.

A.2 Delete-min

The amortized work of delete-min is $O(\log n)$, but we describe how to parallelize delete-min in order to get worst-case bounds for the span. The parallel delete-min operation is given in PAR-DELETE-MIN (Algorithm 7). We first delete the minimum node and add all of its children to the root list, in parallel (Line 2). Then, the main component of our parallel delete-min operation involves consolidating trees such that no two trees share the same rank (Lines 3–10).

In more detail, we place each tree into a bucket based on its rank (Line 3), and then merge pairs of trees with the same rank in every round (Lines 7–9). After $O(\log n)$ rounds, each bucket will necessarily contain at most one tree; we can show this inductively.

If we assume that after round i, all buckets $\leq i$ each contain at most one tree, we see that when we process round $i + 1$, no merged tree can be added to an bucket $\leq i + 1$ (since the rank of merged trees can only increase). Moreover, bucket $i + 1$ contains at most one leftover root, and all other roots have been merged and inserted into bucket $i + 2$. Thus, the number of rounds needed to complete our consolidation step is bounded above by the rank of $H$, which is $O(\log n)$.

The final step in our algorithm is updating the minimum pointer (Line 11).

The amortized work of our parallel delete-min operation is precisely the amortized work of the sequential delete-min operation. This is because the actual cost of our parallel delete-min operation is precisely the actual cost of the sequential delete-min operation, and the amortized analysis follows directly. Our actual cost is given by $O(t(H) + \log n)$, where $t(H)$ accounts for merging trees and $\log n$ accounts for adding the children of the minimum node to the root list and updating the minimum pointer. Moreover, if we let $H'$ represent our heap after performing PAR-DELETE-MIN,
the change in potential is \( \Delta \Phi \leq t(H') - t(H) \leq \text{rank}(H') + 1 - t(H) = O(\log n - t(H)) \), because no two trees have the same rank after performing our consolidations. Thus, in total, the amortized work is \( O(\log n) \), as desired.

The span of our algorithm is dominated by the span of the while loop. In particular, note that every iteration of our while loop has \( O(1) \) span, because we can perform the pairwise merges fully in parallel. As we previously discussed, we have at most \( O(\log n) \) iterations of our while loop, and so the span of parallel delete-min is \( O(\log n) \). The total complexity of parallel delete-min is as follows.

**Lemma A.2.** Parallel delete-min for a Fibonacci heap takes \( O(\log n) \) amortized work and \( O(\log n) \) worst-case span.

### A.3 Batch decrease-key

The parallel batch decrease-key operation is given in \textsc{batch-decrease-key} (Algorithm 8). We first ascertain if a node needs to be decreased. If not all values in the bucket need to be updated, then those values can simply be removed and reinserted with the updated key; the bucket holding the rest of the values can remain with the original key. Otherwise, if all values in the bucket need to be updated, we keep only the first element in the bucket and decrease the key for that element, and we reinsert the other values with the updated key (Lines 3–10). Note that for all key-value pairs that must be reinserted, we perform all insertions in batch on Line 26, using the algorithm in Section A.1.

Note that we can determine if all values in a bucket need to be updated by using a parallel hash table to aggregate counts on the number of times each key appears in \( K \). This takes \( O(k) \) work and \( O(\log k) \) span. Moreover, as discussed in Section A.1 our batch insertions take \( O(k) \) work and \( O(\log n) \) span w.h.p.

We consider for the rest of this section the nodes whose keys must actually be decreased. We check if these decreases violate heap order (Line 13). If not, we can directly decrease the key (Line 17). Otherwise, we cut these nodes from their trees and mark their parents (Lines 14–15). Then, we recursively cut all parents that have been marked more than once, mark their parents, and repeat (Lines 18–25).

Note that on Lines 15 and 24, we increment the number of marks of nodes in parallel, which could cause conflicts if the same parent node must be marked multiple times. Instead, to obtain our complexity bounds, we can record in an array when we would like to mark a parent. Then, we can semisort the array and use \texttt{reduce} to obtain the number of marks to be added to each parent. This maintains our work bounds, but note that the span of the semisort is \( O(\log n) \) w.h.p.

We now focus on the amortized work analysis. Let \( k \) denote the number of keys in \( K \) and let \( c \) be the total number of cuts that we perform in this algorithm. Note that decreasing our keys takes \( O(k) \) total work, and the rest of the work is given by the total number of cuts, or \( O(c) \).

Recall that our potential function is \( \Phi(H) = t(H) + 2 \cdot m(H) \). Let \( H' \) represent our heap after performing \textsc{batch-decrease-key}. The change in the number of trees is given by \( t(H') - t(H) = c \), since every new cut produces a new tree.

The change in the number of marks is \( m(H') - m(H) \leq k - (c - k) = 2k - c \). The argument for this is similar to the sequential argument.

For each cut parent node \( p \), we arbitrarily set a key in \( K \) as having propagated the cut as follows. Let \( c(p) \) denote the key that propagated the cut parent \( p \), and let \( M(p) \) denote the set of all nodes that marked \( p \) in the round immediately before \( p \) was cut. Then, we set \( c(x) = x \) for each key \( x \) in \( K \), and we set \( c(p) \) to be an arbitrary key in \( C(p) = \{ c(p') \mid p' \in M(p) \} \); in other words, \( c(p) \) is one of the keys that propagated a node that marked \( p \) in the round immediately before \( p \) was cut.
Algorithm 8 Parallel batch decrease-key

1: procedure BATCH-DECREASE-KEY$(H, K)$
2:    $\triangleright K$ is an array of triples, holding the key-value pair to be decreased and the updated key
3:    Let $n_k$ be $\#$ times $k$ appears in a key-value pair in $K$
4:    Initialize $I$ to be an array of key-value pairs that must be re-inserted
5:    Initialize $K'$ to be an updated $K$
6:    $\parfor (k, v, k') \in K$ do
7:        if $n_k = \text{size of } k$'s bucket and $v$ is the first element in the bucket then
8:            Add $(k, v, k')$ to $K'$
9:        else
10:            Add $(k', v)$ to $I$ and remove $v$ from the bucket
11:    $\parfor (k, \_, k') \in K'$ do
12:        if changing the key to $k'$ violates heap order then
13:            Cut $k$ and add to root list with key $k'$
14:            Add a mark to the original parent of $k$ and add the parent to $M$
15:        else
16:            Change the key to $k'$
17:        $M \leftarrow$ nodes in $M$ with $>1$ marks
18:    while $M$ is nonempty do
19:        Initialize $M'$ to be an array of marked nodes
20:        $\parfor p \in M$ do
21:            Cut $p$ and add to root list
22:            Set $\#$ marks on $p$ to $0$ if $\#$ marks on $p$ is even, and $1$ otherwise
23:            Add a mark to $p$'s original parent and add the parent to $M'$
24:        $M \leftarrow$ nodes in $M'$ with $>1$ marks
25:    $H \leftarrow$ \textsc{batch-insert}$(I)$
26: return $H$

Each key $x$ then has a well-defined propagation path, which is the maximal path of nodes that $x$ has propagated. The last node $\ell$ of the propagation path must either be a root node or a node whose parent $x$ has not propagated. Note that $x$ may mark $\ell$'s parent without cutting this parent from its tree; we call this mark an allowance. In this sense, each key $x$ in $K$ has one mark in its allowance. We have $k$ marks in the total allowance of our heap.

It remains, then, to count the change in the number of marks on each propagation path. We claim that if we have already counted the $k$ allowances in the change in the number of marks $(m(H') - m(H))$, we can now subtract a mark for each cut parent on a propagation path. There are two cases.

If a cut parent $p$ at the start of our algorithm already contained a mark, then the node that propagated the cut added a mark, canceling out the previous mark. Thus, $c(p)$ has effectively subtracted a mark from $p$.

If a cut parent $p$ had no marks at the start of our algorithm, a child node $p'$ such that $c(p') \neq c(p)$ must have marked $p$ within our algorithm. Necessarily, $c(p')$ must have ended its propagation path at $p'$, so it charged its mark allowance to $p$. Then, when the node that propagated the cut, $c(p)$, added a mark, this cancels out the mark that $p'$ made. Since we have already counted the mark that $p'$ made in its allowance, we can subtract a mark to account for the cancellation.
In total, we see that we can subtract a mark for each cut parent on a propagation path. The number of cut parents is at least \( c - k \), so we have \( m(H') - m(H) \leq k - (c - k) = 2k - c \), as desired.

As such, the change in potential is \( \Phi(H') - \Phi(H) \leq c + 2(2k - c) = 4k - c \). The actual work of \textsc{batch-decrease-key} is \( O(k + c) \), and the amortized work of is \( O(k + c) + 4k - c = O(k) \) by scaling up the units of potential appropriately.

The span of our algorithm is again dominated by the span of the while loop. We have at most \( O(\log n) \) iterations of the while loop, since it is bounded by the maximum tree height of our heap, which is bounded by the rank of the heap. Each iteration of the while loop has span \( O(\log n) \), due to the semisort needed to accumulate marks. Thus, the span of our algorithm is \( O(\log^2 n) \).

The total complexity of parallel batch decrease-key is as follows.

**Lemma A.3.** Parallel batch decrease-key of \( k \) elements into a Fibonacci heap takes \( O(k) \) amortized work and \( O(\log^2 n) \) span.