

# Parallel Local Graph Clustering

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## ABSTRACT

Graph clustering has many important applications in computing, but due to growing sizes of graph, even traditionally fast clustering methods such as spectral partitioning can be computationally expensive for real-world graphs of interest. Motivated partly by this, so-called local algorithms for graph clustering have received significant interest due to the fact that they can find good clusters in a graph with work proportional to the size of the cluster rather than that of the entire graph. This feature has proven to be crucial in making such graph clustering and many of its downstream applications efficient in practice. While local clustering algorithms are already faster than traditional algorithms that touch the entire graph, they are sequential and there is an opportunity to make them even more efficient via parallelization. In this paper, we show how to parallelize many of these algorithms in the shared-memory multicore setting, and we analyze the parallel complexity of these algorithms. We present comprehensive experiments on large-scale graphs showing that our parallel algorithms achieve good parallel speedups on a modern multicore machine, thus significantly speeding up the analysis of local graph clusters in the very large-scale setting.

## 1 Introduction

Given a graph, the task of graph clustering is often described as that of finding a set (or sets) of vertices that are more related, in some sense, to each other than to other vertices in the graph. Applications of graph clustering arise in many areas of computing, including in community detection in social networks [20], load balancing parallel computations [13], unsupervised learning [36], and optimizing digital map databases [21].

There are a large number of algorithms for graph clustering, each with different computational costs and producing clusters with different properties (see [40] for a survey of graph clustering algorithms). However, most traditional algorithms for graph clustering require touching the entire graph at least once, and often many more times. With the massive graphs that are available today, e.g., extremely large graphs arising in social media, scientific, and intelligence applications, these traditionally-fast algorithms can be very computationally expensive. A standard example of this can be found in the large-scale empirical analysis of Leskovec et al. [29, 30] and Jeub et al. [23]. Therefore, there has been a surge of interest in *local graph*

*clustering algorithms*, or algorithms whose running time depends only on the size of the cluster found and is independent of or depends at most polylogarithmically on the size of the entire graph (we refer to this as a *local running time*).

Local graph clustering was first used by Spielman and Teng [44] to develop nearly linear-time algorithms for computing approximately-balanced graph partitions and solving sparse linear systems. Since then, there have been many improved local graph clustering algorithms developed [2, 7, 15, 27], which we review in Section 5. Local graph clustering algorithms have been used in many real-world applications. For example, Andersen and Lang [5] use a variant of the algorithm of Spielman and Teng [44] to identify communities in networks. Leskovec et al. [29, 30] and Jeub et al. [23] use the algorithm of Andersen et al. [2] as well as other graph clustering algorithms to study the properties of clusters of different sizes in social and Web graphs. A major conclusion of [29, 30, 23] was that large social and information networks typically have good small clusters as opposed to large clusters, thus indicating that local algorithms are useful not only for computational efficiency, but also for identifying clusters that are more meaningful or useful in practice. Mahoney et al. [32] and Maji et al. [33] use local algorithms to obtain cuts for image segmentation and community detection. These algorithms have also been applied to find communities in protein networks [47, 31]. There have been many other papers applying local algorithms to community detection, e.g., [4, 49, 24, 25, 48, 50, 18].

Existing clustering algorithms with local running times are described for the sequential setting, which is not surprising since meaningful local clusters in the small to medium-sized graphs studied in the past tend to be very small [29, 23], and hence algorithms to find these local clusters terminate very quickly. Even for these small to medium-sized graphs, these local algorithms have proven to be very useful; and currently the applicability of these methods to extremely large graphs, e.g., those with one billion or more vertices or edges, is limited by large-scale implementations. Moreover, with the massive graphs that are available today, one would like to test the hypothesis that meaningful local clusters can be larger, and this will lead to increased running times of local clustering algorithms. The efficiency of these algorithms can be improved via parallelization.

A straightforward way to use parallelism is to run many local graph computations independently in parallel, and this can be useful for certain applications. However, since all of the local algorithms have many input parameters that affect both the cluster quality and computation time, it may be hard to know a priori how to set the input parameters for the multiple independent computations. We believe that these local algorithms are more useful in an *interactive setting*, where a data analyst wants to quickly explore the properties of local clusters found in a graph. In such a setting, an analyst would run a computation, study the result, and based on that determine

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what computation to run next. Furthermore, the analyst may want to repeatedly remove local clusters from a graph for his or her application. To keep response times low, it is important that a single local computation be made efficient. If each run of the algorithm returns nearly instantaneously rather than in tens of seconds to minutes, this drastically improves user experience as well as productivity. The goal of this paper is to achieve this via parallelism.

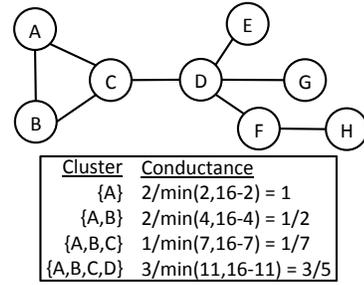
This paper develops parallel versions of several local graph clustering algorithms—the Nibble algorithm of Spielman and Teng [44, 45], the PageRank-Nibble algorithm of Andersen et al. [2], the deterministic heat kernel PageRank algorithm of Kloster and Gleich [24], and the randomized heat kernel PageRank algorithm of Chung and Simpson [10]. These algorithms all diffuse probability mass from a seed vertex, and return an approximate PageRank (probability) vector. The vector returned at the end is then processed by a sweep cut procedure to generate a graph partition (the sweep cut sorts the vertices in non-increasing order of degree-weighted probability and returns the best partition among all prefixes of the ordering). The approach that we take to parallelizing the diffusion process of these algorithms is to iteratively process subsets of vertices and their edges until a termination criteria is met. Each iteration processes a possibly different subset of vertices/edges (determined from the previous iteration) in parallel. We develop an efficient parallel algorithm for performing the sweep cut as well. All of our parallel algorithms return clusters with the same quality guarantees as their sequential counterparts. In addition, we prove theoretical bounds on the computational complexity of the parallel algorithms, showing that their asymptotic work matches those of the corresponding sequential algorithms (and thus have local running times) and that most of them have good parallelism. The only other work on parallelizing local graph clustering algorithms that we are aware of is a parallelization of the PageRank-Nibble algorithm of Andersen et al. [2] in the distributed setting by Perozzi et al. [38]. However, their algorithm does not have a local running time since it does work proportional to at least the number of vertices in the graph.

We implement all of our parallel algorithms in the Ligra graph processing framework for shared-memory [41]. Ligra is well-suited for these applications because it only does work proportional to the number of active vertices (and their edges) in each iteration, which enables local implementations of the algorithms. In contrast, many other systems (e.g., GraphLab [19] and Pregel [34]) require touching all of the vertices in the graph on each iteration, which would lead to inefficient implementations of local algorithms. Our implementations are all lock-free, and use only basic parallel primitives such as prefix sums, filter, and sorting, as well as data-parallel functions in Ligra that map computations over subsets of vertices or edges.

We present a comprehensive experimental evaluation of our parallel algorithms, and compare them to their sequential counterparts. Our experiments on a modern 40-core machine show that our parallel implementations of the four diffusion methods achieve good speedups with increasing core count. For PageRank-Nibble, we describe an optimization that speeds up both the sequential and the parallel algorithms. Our parallel sweep cut procedure also performs very well in practice, achieving 23–28x speedup on 40 cores. Due to the efficiency of our algorithms, we are able to generate network community profile plots (a concept introduced in [29] and used in [23] that quantifies the best cluster as a function of cluster size) for some of the largest publicly-available real-world graphs.

## 2 Preliminaries

**Graph Notation.** We denote a graph by  $G(V, E)$ , where  $V$  is the set of vertices and  $E$  is the set of edges in the graph. All of the graphs that we study in this paper are *undirected* and *unweighted*.



**Figure 1:** An example graph with  $n = 8$  and  $m = 8$ . The conductance of several clusters are shown.

The number of vertices in a graph is  $n = |V|$ , and the number of undirected edges is  $m = |E|$ . The vertices are assumed to be indexed from 0 to  $n - 1$ . We define  $d(v)$  to be the degree of a vertex  $v$  (i.e., the number of edges incident on  $v$ ). We define the **volume** of a set of vertices  $S$  to be  $\text{vol}(S) = \sum_{v \in S} d(v)$ , and the **boundary** of  $S$  to be  $\partial(S) = \{(x, y) \in E \mid x \in S, y \notin S\}$  (the number of edges leaving a set). The **conductance** of a cluster  $S$  in a graph is defined to be  $\phi(S) = |\partial(S)| / \min(\text{vol}(S), 2m - \text{vol}(S))$ . This is a widely-used metric to measure cluster quality. Intuitively, low-conductance vertex sets tend to correspond to higher-quality clusters because these sets are larger and have fewer edges to vertices outside of the set. Figure 1 shows an example graph and the conductance of several clusters in the graph.

**Local Algorithms.** *Local graph clustering algorithms* have the guarantee that if there exists a cluster  $S$  with conductance  $\phi$ , and one picks a starting vertex in  $S$  then the algorithm returns a cluster of conductance  $f(\phi, n)$  with constant probability.<sup>1</sup> They also have a work bound (number of operations) that depends linearly on the size of the cluster and at most polylogarithmically on the graph size. Local algorithms have been used in theory as subroutines to obtain nearly linear time graph partitioning algorithms [2, 1, 7, 45], which in turn have applications in solving sparse linear systems [44].

**Atomic Operations.** A *compare-and-swap* is an atomic instruction supported on modern multicore machines that takes three arguments—a memory location, an expected value, and a new value; if the value stored at the location is equal to the expected value then it atomically updates the location with the new value and returns true, and otherwise returns false. A *fetch-and-add (fetchAdd)* takes two arguments, a location  $x$  and a value  $y$ , and atomically adds  $y$  to the value at location  $x$ . It can be implemented using a loop with a compare-and-swap until the update is successful. In the paper, we use the notation  $\&x$  to denote the memory location of variable  $x$ .

**Parallel Model.** Algorithms in this paper are analyzed in the work-depth model [22, 12], where **work** is equal to the number of operations required (equivalent to sequential running time) and **depth** is equal to the number of time steps required (the longest chain of sequential dependencies). The work-depth model is a natural shared-memory parallel extension of the commonly-used sequential RAM model [12] and has been used for decades to develop parallel algorithms (see, e.g., [22, 12]).

By Brent’s theorem [8], an algorithm with work  $W$  and depth  $D$  has overall running time  $W/P + D$ , where  $P$  is the number of processors available. Concurrent reads and writes are allowed in the model, with which a compare-and-swap can be simulated. A fetch-and-add can be simulated in linear work and logarithmic depth in the number of updates. A **work-efficient** parallel algorithm is one whose work asymptotically matches that of the sequential algorithm, which is important since in practice the  $W/P$  term in the running time often dominates.

<sup>1</sup>  $f(\phi, n)$  is a function of  $\phi$  and  $n$  that determines the approximation guarantee of the algorithm. We will plug in specific values when we discuss the individual algorithms.

**Parallel Primitives.** We will use the basic parallel primitives, prefix sum and filter [22]. *Prefix sum* takes an array  $X$  of length  $N$ , an associative binary operator  $\oplus$  (e.g., the addition operator or the minimum operator), and returns the array  $(X[0], X[0] \oplus X[1], \dots, X[0] \oplus X[1] \oplus \dots \oplus X[N-1])$ .<sup>2</sup> *Filter* takes an array  $X$  of length  $N$  and a predicate function  $f$ , and returns an array  $X'$  of length  $N' \leq N$  containing the elements in  $x \in X$  such that  $f(a)$  is true, in the same order that they appear in  $X$ . Filter can be implemented using prefix sum, and both require  $O(N)$  work and  $O(\log N)$  depth [22]. We also use parallel comparison sorting, which for  $N$  elements can be done in  $O(N \log N)$  work and  $O(\log N)$  depth [22], and parallel integer sorting, which can be done in  $O(N)$  work and  $O(\log N)$  depth with probability  $1 - 1/N^{O(1)}$  (we refer to this as a *high probability bound*) for  $N$  integers in the range  $[1, \dots, O(N \log^{O(1)} N)]$  [39].

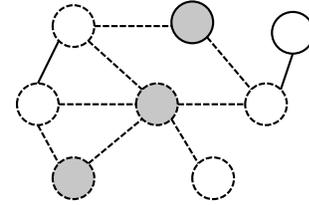
**Sparse Sets.** Our implementations use hash tables to represent a sparse set to store data associated with the vertices touched in the graph. This is because we can only afford to do work proportional to those vertices (and their edges), and cannot initialize an array of size  $|V|$  at the beginning. For sequential implementations we use the `unordered_map` data structure in STL. For parallel implementations, we use the non-deterministic concurrent hash table described in [42], which allows for insertions and searches in parallel. The hash table is a lock-free table based on linear probing, and makes heavy use of compare-and-swap and fetch-and-add. For a batch of  $N$  inserts and/or searches, parallel hashing takes  $O(N)$  work and  $O(\log N)$  depth with high probability [16]. We set the size of the hash tables to be proportional to the number of the elements  $N$  that we need to store, so that it can be initialized in  $O(N)$  work and  $O(1)$  depth. All of the parallel algorithms that we present use sparse sets, and so their complexity bounds will be high probability bounds.

In our pseudocode, we use sparse sets to store key-value pairs where the key is the vertex ID and the value is the associated data. We use the notation  $\mathbf{p}[k]$  to denote the value in the sparse set  $\mathbf{p}$  associated with the key  $k$ . If we attempt to update data for a non-existent key  $k$  in the sparse set, we assume that prior to updating, a pair  $(k, \perp)$  will be created in the set, where  $\perp$  is a zero element defined when creating the set. Both STL's `unordered_map` and the concurrent hash table that we use support this functionality. For all of our implementations,  $\perp = 0$ .

**Ligra Framework.** Our parallel implementations are written using Ligra, a graph processing framework for shared-memory machines [41]. Ligra is very well-suited for implementing local algorithms since it only does work proportional to the vertices and edges touched, whereas many other graph processing systems (e.g., GraphLab [19] and Pregel [34]) do work proportional to at least the number of vertices in the graph on every iteration. This feature of Ligra is crucial in obtaining running times proportional to just the number of vertices and edges explored. Implementations in Ligra have been shown to be simple and concise, with performance close to hand-optimized implementations of the algorithms. We chose to implement the graph algorithms in shared-memory because the largest publicly-available real-world graphs can fit in the memory of a single machine, and shared-memory graph processing has been shown to be much more efficient than their distributed-memory counterparts [41, 35].

Ligra provides a *vertexSubset* data structure used for representing a subset of the vertices, and two simple functions, one for mapping over vertices and one for mapping over edges. We describe simplified versions of these functions, which suffices for implementing

<sup>2</sup>This definition is for the inclusive version of prefix sum, in contrast to the exclusive version of prefix sum, commonly used in parallel algorithms.



**Figure 2:** An example graph where the shaded vertices are in the vertexSubset  $U$ . A VERTEXMAP applied to  $U$  applies a function to data associated with the shaded vertices. An EDGEMAP applied to  $U$  applies a function to all of the edges incident to  $U$  (indicated by dashed lines), and can modify the neighbors of  $U$  (indicated by dashed circles).

the algorithms in this paper (see [41] for the more general versions). VERTEXMAP takes as input a vertexSubset  $U$  and a boolean function  $F$ , and applies  $F$  to all vertices in  $U$ .  $F$  can side-effect data structures associated with the vertices. EDGEMAP takes as input a graph  $G(V, E)$ , vertexSubset  $U$ , and boolean update function  $F$ , and applies  $F$  to all edges  $(u, v) \in E$  where  $u \in U$ . Again,  $F$  can side-effect data structures associated with the vertices. The programmer ensures the parallel correctness of the functions passed to VERTEXMAP and EDGEMAP by using atomic operations where necessary. An example graph is shown in Figure 2, where the shaded vertices are in a vertexSubset; VERTEXMAP applies a function to data associated with the shaded vertices in parallel, and EDGEMAP applies a function to the incident edges (dashed lines) and neighbors (dashed circles) of the shaded vertices in parallel. Note that in some cases multiple shaded vertices have edges to the same neighbor, so the function must be correct when run in parallel.

EDGEMAP is implemented by doing work proportional to the number of vertices in its input vertexSubset and the sum of their outgoing degrees, and processes the vertices and all of their edges in parallel. VERTEXMAP is implemented by doing work proportional to the number of vertices in its input vertexSubset, and processes all of the vertices in parallel. Doing work proportional to only the size of the input vertexSubset and its edges makes Ligra efficient for implementing local graph algorithms that only need to touch part of the graph. The Ligra code compiles with either Cilk Plus or OpenMP for parallelism. We refer the reader to [41] for more implementation details.

### 3 Parallel Algorithms

In this section, we review sequential local clustering algorithms and show how to parallelize them. We describe our parallel algorithms without any specific setting of parameters, which in prior literature are often set to specific values for theoretical purposes. Additionally, we assume the seed set contains just a single vertex, although all of the algorithms extend to seed sets with multiple vertices.

At a high-level, our clustering algorithms are based on iteratively processing subsets of vertices and their edges in parallel until a termination criteria is met. For most of the algorithms, we use the data-parallel VERTEXMAP and EDGEMAP functions in Ligra to process each subset. One challenge in parallelizing the algorithms is in guaranteeing a local running time. To address this challenge, we ensure that each iteration only does work proportional to the size of the subset of vertices and their edges through a careful representation of sparse sets as well as formulating the algorithms to use Ligra's functions, which are local when used appropriately. The second challenge is in identifying which sets of vertices can be processed in parallel while guaranteeing work-efficiency and convergence. This requires additional effort for some of the algorithms.

All of our clustering algorithms compute a vector  $\mathbf{p}$ , which is passed to a sweep cut rounding procedure to generate a cluster. Thus, we first describe the sweep cut procedure and how to parallelize it

in Section 3.1, and then describe our main clustering routines in Sections 3.2–3.5.

### 3.1 Sweep Cut

Often the solution vector  $\mathbf{p}$  obtained by spectral partitioning algorithms contains real numbers instead of being a binary vector that represents a partition of the graph. Therefore, spectral algorithms are combined with a rounding procedure which produces a partition from  $\mathbf{p}$  that guarantees a good worst-case approximation to the combinatorial minimum conductance problem.

The sweep cut procedure is commonly used, and takes as input a graph  $G$  and a vector  $\mathbf{p}$  (represented as a sparse set in a local implementation). It first takes the vertices  $v$  with non-zero values in  $\mathbf{p}$  and sorts them in non-increasing order of  $\mathbf{p}[v]/d(v)$ . This gives an ordered set  $\{v_1, \dots, v_N\}$ , where  $N$  is the number of non-zeros in  $\mathbf{p}$ ,  $\mathbf{p}[v_i] > 0$ , and  $\mathbf{p}[v_i]/d(v_i) \geq \mathbf{p}[v_{i+1}]/d(v_{i+1})$  for all  $i$ . It then computes the conductance of clusters defined by  $S_j = \{v_1, \dots, v_j\}$  for  $1 \leq j \leq N$  and returns the set with smallest conductance. For example, in the graph in Figure 1 if the ordered set is  $\{A, B, C, D\}$ , then the output set of the sweep cut procedure would be  $\{A, B, C\}$  since it has the lowest conductance among the four sets considered.

The sequential algorithm for the sweep cut first sorts the vertices, and then iterates through the vertices  $v_i$  in increasing order of  $i$ , inserts  $v_i$  into a set  $S$ , maintaining the volume  $\text{vol}(S)$  and the number of outgoing edges  $\partial(S)$  in each iteration. This also allows the conductance to be computed in each iteration. The lowest conductance as well as the iteration number  $i^*$  that leads to the lowest conductance is stored, and the final set returned is  $S_{i^*}$ . If  $S$  is represented as a sparse set, we can check in constant work if an endpoint of an edge is in  $S$ . Thus,  $\partial(S)$  can be easily updated in each iteration as follows: for each edge  $(v_i, w) \in E$ , if  $w \in S$  then decrement  $\partial(S)$ , and otherwise increment  $\partial(S)$ .  $\text{vol}(S)$  is easily updated by incrementing it by  $d(v_i)$ . The sorting costs  $O(N \log N)$  work, and the subsequent iterations costs  $O(\text{vol}(S_N))$  work, giving an overall work of  $O(N \log N + \text{vol}(S_N))$ .

We now show that the sweep cut procedure can be parallelized work-efficiently. The challenging part is in computing the conductance of all of the sets  $S_i$  in parallel without increasing the asymptotic work. A naive approach would be to form all sets  $S_i$  for  $1 \leq i \leq N$ , and compute  $\partial(S_i)$  and  $\text{vol}(S_i)$  for each one independently. However, this leads to  $O(N \log N + \sum_{i=1}^N \text{vol}(S_i)) = O(N \log N + N \text{vol}(S_N))$  work. The following theorem describes a work-efficient solution, and we illustrate the algorithm with an example afterward.

**Theorem 1.** *A sweep cut can be implemented in  $O(N \log N + \text{vol}(S_N))$  work and  $O(\log \text{vol}(S_N))$  depth with high probability.*

*Proof.* The initial sort can be parallelized in  $O(N \log N)$  work and  $O(\log N)$  depth [22]. We then create a sparse set, called rank, indexed by the vertex identifiers, storing their rank in the sorted set  $S_N = \{v_1, \dots, v_N\}$ . We create an array  $Z$  of size  $2\text{vol}(S_N)$ , and for each vertex  $v \in S_N$ , we look at all edges  $(v, w) \in E$  and if  $\text{rank}[w] > \text{rank}[v]$  (case (a)) we create two pairs  $(1, \text{rank}[v])$  and  $(-1, \text{rank}[w])$  in the two positions corresponding to  $(v, w)$  in  $Z$ , and otherwise (case (b)) we create two pairs  $(0, \text{rank}[v])$  and  $(0, \text{rank}[w])$ . In either case, ranks can be looked up in  $O(1)$  work and if  $w \notin S_N$ , we give it a default rank of  $N + 1$ . The offsets into  $Z$  can be obtained via a prefix sums computation over the degrees of vertices in  $S_N$  in sorted order. This also allows us to obtain  $\text{vol}(S_i)$  for each  $i$ . We then sort  $Z$  by increasing order of the second value of the pairs (the order among pairs with equal second value does not matter). Next, we apply a prefix sums over the sorted  $Z$  with the addition operator on the first value of the pairs.

Since  $Z$  is sorted in increasing order of rank, the final prefix sums give the number of crossing edges for each possible cut.  $\partial(S_i)$  for each possible  $S_i$  can be obtained by looking at entries  $Z[j]$  where the second value of the pair  $Z[j]$  is  $i$  and the second value of the pair  $Z[j + 1]$  is  $i + 1$ . The first value of  $Z[j]$  stores the number of crossing edges for the set  $S_i$ . This is because case (a) corresponds to the fact that  $v$  is before  $w$  in the ordering—so if they are not on the same side of the cut, the edge  $(v, w)$  will contribute 1 to the prefix sums of the cut at any  $u$  where  $\text{rank}(v) < \text{rank}(u) < \text{rank}(w)$ ; and if they are on the same side of the cut, both the 1 and the  $-1$  entries of the edge will cancel out in the prefix sum, leading to an overall contribution of 0 for that edge. Case (b) corresponds to a duplicate edge, and so does not contribute to the number of crossing edges.

Since we have the volume of all possible sets  $S_i$ , we can compute the conductance of each possible cut. A prefix sums using the minimum operator over the  $N$  conductance values gives the cut with the lowest conductance.

The prefix sums used in the computation contribute  $O(\text{vol}(S_N))$  to the work, and  $O(\log \text{vol}(S_N))$  to the depth. Sorting  $Z$  by the rank of vertices using a parallel integer sort takes  $O(\text{vol}(S_N))$  work and  $O(\log \text{vol}(S_N))$  depth with high probability since the maximum rank is  $N + 1 = O(\text{vol}(S_N))$ . Creating the sparse set rank takes  $O(N)$  work and  $O(\log N)$  depth using a hash table. Including the cost of the initial sort gives the bounds of the theorem.  $\square$

**Example.** We now illustrate the parallel sweep cut algorithm described in Theorem 1 with an example. Again, let us consider the example graph in Figure 1, and the set  $\{A, B, C, D\}$ , which we assume has already been sorted in non-increasing order of  $\mathbf{p}[v]/d(v)$ . The sparse set rank stores the following mapping:  $\text{rank} = [A \rightarrow 1, B \rightarrow 2, C \rightarrow 3, D \rightarrow 4]$ . To obtain the volume of each of the four possible sets, we first create an array with the degree of the vertices ordered by rank, and then apply a prefix sums over it. In the example, the array of degrees is  $[2, 2, 3, 4]$ , and the result of the prefix sums is  $[2, 4, 7, 11]$ . The array  $Z$  is of size twice the volume of the set  $\{A, B, C, D\}$ , which is 22. The entries of  $Z$  are shown below:

$$Z = [(1, 1), (-1, 2), (1, 1), (-1, 3), (0, 2), (0, 1), (1, 2), (-1, 3), (0, 3), (0, 1), (0, 3), (0, 2), (1, 3), (-1, 4), (0, 4), (0, 3), (1, 4), (-1, 5), (1, 4), (-1, 5), (1, 4), (-1, 5)]$$

For clarity, we have placed the pairs for each vertex on separate rows. As an example, let us consider the entries for vertex  $B$ , which are on the second row. The first edge of  $B$  is to  $A$ , and the ranks of  $B$  and  $A$  are 2 and 1, respectively. Since  $\text{rank}(A) < \text{rank}(B)$ , we are in case (b) and create the pairs  $(0, 2)$  and  $(0, 1)$ . The second edge of  $B$  is to  $C$ , whose rank is 3. Since  $\text{rank}(C) > \text{rank}(B)$ , we are in case (a) and create the pairs  $(1, 2)$  and  $(-1, 3)$ . The pairs for the other vertices are constructed in a similar fashion (note that the rank of vertices not in the input set is 5).

Next, we sort  $Z$  by increasing order of the second value of the pairs. The sorted array  $Z_{\text{sorted}}$  is shown below, where pairs with the same rank (second entry) are on the same row:

$$Z_{\text{sorted}} = [(1, 1), (1, 1), (0, 1), (0, 1), (-1, 2), (0, 2), (1, 2), (0, 2), (-1, 3), (-1, 3), (0, 3), (0, 3), (1, 3), (0, 3), (-1, 4), (0, 4), (1, 4), (1, 4), (1, 4), (-1, 5), (-1, 5), (-1, 5)]$$

Next we apply a prefix sum over the first value of the pairs in  $Z_{\text{sorted}}$ . The resulting array  $Z_{\text{sorted, summed}}$  is shown below:

$$Z_{\text{sorted, summed}} = [(1, 1), (2, 1), (2, 1), (2, 1), (1, 2), (1, 2), (2, 2), (2, 2), (1, 3), (0, 3), (0, 3), (0, 3), (1, 3), (1, 3), (0, 4), (0, 4), (1, 4), (2, 4), (3, 4), (2, 5), (1, 5), (0, 5)]$$

With  $Z_{\text{sorted, summed}}$ , we can obtain the number of crossing edges for each of the sets. The number of crossing edges for the set  $\{A\}$  is found by looking at the pair in  $Z_{\text{sorted, summed}}$  whose second value is  $\text{rank}[A] = 1$  and whose next pair's second value is  $\text{rank}[A] + 1 = 2$ . This is the 4'th entry of the array, (2, 1), and the first entry of the pair is the number of crossing edges, which is 2. In general the relevant pair containing the number of crossing edges is the last pair with a given second value, and these pairs all appear as the last pair of a row of  $Z_{\text{sorted, summed}}$  shown above. We find the number of crossing edges for the set  $\{A, B\}$  to be 2,  $\{A, B, C\}$  to be 1, and  $\{A, B, C, D\}$  to be 3.

With the number of crossing edges and the volume of each possible set, we can compute the conductance of each possible set, and take the one with the lowest conductance using prefix sums. In the example, the conductance of each set is shown in Figure 1, and the set with the lowest conductance is  $\{A, B, C\}$ .

### 3.2 Nibble

Spielman and Teng [44] present the first local algorithm for graph clustering, called *Nibble*, which gives an approximation guarantee of  $f(\phi, n) = O(\phi^{1/3} \log^{2/3} n)$  and requires  $O(|S| \text{polylog}(n) / \phi^{5/3})$  work.<sup>3</sup> It was later improved to  $f(\phi, n) = O(\sqrt{\phi} \log^3 n)$  with  $O(|S| \text{polylog}(n) / \phi^2)$  work [45]. Their algorithm is based on computing the distribution of a random walk starting at the seed vertex, but at each step truncating small probabilities to zero. The sweep cut procedure is then applied on the distribution to give a partition.

The Nibble algorithm [45] takes as input the maximum number of iterations  $T$ , an error parameter  $\epsilon$ , a target conductance  $\phi$ , and a seed vertex  $x$ . On each iteration (for up to  $T$  iterations) Nibble computes a weight vector, computes a sweep cut on the vector, and either returns the cluster if its conductance is below  $\phi$  or continues running. Let  $\mathbf{p}_0$  be the initial weight vector, and  $\mathbf{p}_i$  denote the vector on iteration  $i$ .  $\mathbf{p}_0$  is initialized with weight 1 on the seed vertex and 0 everywhere else.  $\mathbf{p}_i$  represents the weights generated by a lazy random walk with truncation from the seed vertex after  $i$  steps, where on each step  $\mathbf{p}_i(v)$  is truncated to 0 if  $\mathbf{p}_i(v) < d(v)\epsilon$ . Computing  $\mathbf{p}_{i+1}$  from  $\mathbf{p}_i$  simply requires truncating all  $p_i(v) < d(v)\epsilon$  to 0 and for each remaining non-zero entry  $\mathbf{p}_i(v)$ , sending half of its mass to  $\mathbf{p}_{i+1}(v)$  and the remaining to its neighbors, evenly distributed among them.

In practice, computing the sweep cut on each iteration of the algorithm is unnecessary if one does not know what target conductance is desirable for the particular graph. As such, we modify the Nibble algorithm so that it runs for  $T$  iterations, returning  $\mathbf{p}_T$ , unless there are no vertices on some iteration  $i$  such that  $\mathbf{p}_i(v) \geq d(v)\epsilon$ , in which case we return  $\mathbf{p}_{i-1}$ .

Our implementations use sparse sets to represent the  $\mathbf{p}$  vector of the current and previous iteration (vectors from prior iterations can be safely discarded), so that the work is local. For the sequential implementation, the update procedure simply follows the description above. Our parallel implementation uses a VERTEXMAP and EDGEMAP on each iteration to update the  $\mathbf{p}$  vector of the next iteration. The pseudocode is shown in Figure 3. As discussed in Section 2, we assume that the size of a sparse set is proportional to the number of elements it represents, and furthermore when accessing a non-existing element  $v$ , the entry  $(v, 0)$  will be automatically created in the set. Initially, the seed vertex is placed on the frontier and in the weight vector  $\mathbf{p}$  (Lines 8–9). On each iteration the algorithm clears  $\mathbf{p}'$ , used to store the next weight vector, applies a VERTEXMAP to send half of the mass of each vertex to itself (Line 12), and then an EDGEMAP to send the remaining half of the mass evenly among all neighbors (Line 13). In Line 14, the frontier is updated to contain just the vertices that have enough mass (equivalent

```

1: sparseSet  $\mathbf{p} = \{\}$ 
2: sparseSet  $\mathbf{p}' = \{\}$ 
3: procedure UPDATENGH( $s, d$ ) ▷ passed to EDGEMAP
4:   fetchAdd(& $\mathbf{p}'[d], \mathbf{p}[s] / (2d(s))$ )
5: procedure UPDATESELF( $v$ ) ▷ passed to VERTEXMAP
6:    $\mathbf{p}'[v] = \mathbf{p}[v] / 2$ 
7: procedure NIBBLE( $G, x, \epsilon, T$ )
8:    $\mathbf{p} = \{(x, 1)\}$ 
9:   vertexSubset Frontier =  $\{x\}$  ▷ seed vertex
10:  for  $t = 1$  to  $T$  do
11:     $\mathbf{p}' = \{\}$ 
12:    VERTEXMAP(Frontier, UPDATESELF)
13:    EDGEMAP( $G, \text{Frontier}, \text{UPDATENGH}$ )
14:    Frontier =  $\{v \mid \mathbf{p}'[v] \geq d(v)\epsilon\}$  ▷ using filter
15:    if (size(Frontier) == 0) then break
16:    else  $\mathbf{p} = \mathbf{p}'$ 
17:  return  $\mathbf{p}$ 

```

Figure 3: Pseudocode for parallel Nibble.

to the thresholding operation described in [45]), and only needs to check the vertices in the frontier at the beginning of the iteration and their neighbors. The algorithm breaks on Line 15 if the frontier is empty, and otherwise updates  $\mathbf{p}$  to be the new vector  $\mathbf{p}'$  on Line 16.

For concreteness, if the input graph is the graph from Figure 2, and the shaded vertices represent the frontier, then the VERTEXMAP on Line 12 would apply the function UPDATESELF to the  $\mathbf{p}$  and  $\mathbf{p}'$  entries of the shaded vertices, and the EDGEMAP on Line 13 would apply the function UPDATENGH to the dashed edges, reading from the  $\mathbf{p}$  entries of the shaded vertices and writing to the  $\mathbf{p}'$  entries of the dashed vertices. Line 14 would find a new set of shaded vertices (vertexSubset) to represent the next frontier.

Spielman and Teng [45] show that each iteration of the algorithm processes  $O(1/\epsilon)$  vertices and edges, and so takes  $O(1/\epsilon)$  work ( $O((1/\epsilon) \log(1/\epsilon))$  work if including the per-iteration sweep cut). We can parallelize the updates across all vertices and edges in each iteration, and for  $N$  updates, the fetch-and-adds together take  $O(\log N)$  depth and  $O(N)$  work. The filter performs  $O(1/\epsilon)$  work since we only check the vertices on the frontier and their neighbors. This gives a work-efficient parallelization of each iteration in  $O(\log(1/\epsilon))$  depth, and gives an overall depth of  $O(T \log(1/\epsilon))$ . Including the sweep cut on each round, as done in [45], does not increase the depth as it can be parallelized in logarithmic depth as shown in Theorem 1.

**Theorem 2.** *The parallel algorithm for Nibble requires  $O(T/\epsilon)$  work ( $O((T/\epsilon) \log(1/\epsilon))$  work if performing a sweep cut per iteration) and  $O(T \log(1/\epsilon))$  depth with high probability.*

### 3.3 PR-Nibble

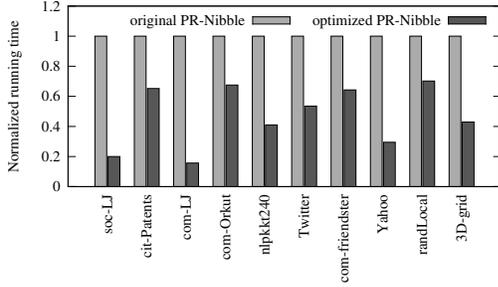
Andersen, Chung, and Lang [2] give an improved local clustering algorithm, *PageRank-Nibble (PR-Nibble)*, with  $f(\phi, n) = O(\sqrt{\phi} \log n)$  and work  $O(|S| \text{polylog}(n) / \phi)$ . Their algorithm generates an approximate PageRank vector based on repeatedly pushing mass from vertices that have enough residual. Again a sweep cut is applied to the resulting vector to give a partition.

The PR-Nibble algorithm [2] takes as input an error parameter  $\epsilon$ , a teleportation parameter  $0 < \alpha < 1$ , and a seed vertex  $x$ . The algorithm maintains two vectors,  $\mathbf{p}$  (the PageRank vector) and  $\mathbf{r}$  (the residual vector). At the end of the algorithm,  $\mathbf{p}$  is returned to be used in the sweep cut procedure. Initially,  $\mathbf{p}$  is set to 0 everywhere (i.e., the sparse set representing it is empty), and  $\mathbf{r}$  is set to store a mass of 1 on  $x$  and 0 everywhere else (i.e., the sparse set contains just the entry  $(x, 1)$ ).

On each iteration, a vertex  $v$  with  $\mathbf{r}(v) \geq d(v)\epsilon$  is chosen to perform a *push* operation. Following the description in [2], a push operation on vertex  $v$  will perform the following three steps:

1.  $\mathbf{p}[v] = \mathbf{p}[v] + \alpha \mathbf{r}[v]$

<sup>3</sup>We use the notation  $\text{polylog}(n)$  to mean  $\log^{O(1)} n$ .



**Figure 4:** Running times of the original version of sequential PR-Nibble versus the optimized version with  $\alpha = 0.01$  and  $\epsilon = 10^{-7}$ . The running times are normalized to that of original PR-Nibble. See Section 4 for more information about the graphs and machine specifications.

- For each  $w$  such that  $(v, w) \in E$ :

$$\mathbf{r}[w] = \mathbf{r}[w] + (1 - \alpha)\mathbf{r}[v]/(2d(v))$$

- $\mathbf{r}[v] = (1 - \alpha)\mathbf{r}[v]/2$

The PR-Nibble simply repeatedly applies the push operation on a vertex until no vertices satisfy the criterion  $\mathbf{r}(v) \geq d(v)\epsilon$ , at which point it returns  $\mathbf{p}$  and terminates. The work of the algorithm has been shown to be  $O(1/(\alpha\epsilon))$  in [2].

Again, our sequential implementation simply follows the above procedure, and uses sparse sets to represent  $\mathbf{p}$  and  $\mathbf{r}$  to obtain the local work bound. As described in [2], we use a queue to store the vertices with  $\mathbf{r}(v) \geq d(v)\epsilon$ , and whenever we apply a push on  $v$ , we check if any of its neighbors satisfy the criterion, and if so we add it to the back of the queue. We repeatedly push from  $v$  until it is below the threshold.

**An Optimization.** We implement an optimization to speed up the code in practice. In particular, we use a more aggressive implementation of the push procedure as follows:

- $\mathbf{p}[v] = \mathbf{p}[v] + (2\alpha/(1 + \alpha))\mathbf{r}[v]$
- For each  $w$  such that  $(v, w) \in E$ :

$$\mathbf{r}[w] = \mathbf{r}[w] + ((1 - \alpha)/(1 + \alpha))\mathbf{r}[v]/d(v)$$

- $\mathbf{r}[v] = 0$

This rule can be shown to approximate the same linear system as the original rule [2], and the solution generated can be shown to have the same asymptotic conductance guarantees as the original PR-Nibble algorithm. The work of this modified algorithm can be shown to also be  $O(1/(\alpha\epsilon))$  by using the same proof as in Lemma 2 of [2] and observing that at least  $(2\alpha\epsilon/(1 + \alpha))d(v) \geq \alpha\epsilon d(v)$  mass is pushed from  $\mathbf{r}$  per iteration.

Figure 4 shows the normalized running times of the original PR-Nibble algorithm versus our modified version with the optimized update rule for  $\alpha = 0.01$  and  $\epsilon = 10^{-7}$  on various input graphs. In the experiment, both versions return clusters with the same conductance for the same input graph. We see that the optimized version always improves the running time, and by a factor of 1.4–6.4x for the graphs that we experimented with.

We also tried using a priority queue instead of a regular queue to store the vertices, where the priority of a vertex  $v$  is the value of  $\mathbf{r}(v)/d(v)$  when it is first inserted into the queue (with a higher value corresponding to a higher priority). We did not find this to help much in practice, and sometimes performance was worse due to the overheads of priority queue operations.

**Parallel Implementation.** The PR-Nibble algorithm as described above is sequential because each iteration performs a push on only one vertex. To add parallelism, instead of selecting a single vertex in an iteration, we select *all* vertices  $v$  where  $\mathbf{r}(v) \geq d(v)\epsilon$ , and perform pushes on them in parallel. This idea was described by Perozzi et al. [38], who implemented it for the distributed setting.

```

1: sparseSet  $\mathbf{p} = \{\}$ 
2: sparseSet  $\mathbf{r} = \{\}$ 
3: sparseSet  $\mathbf{r}' = \{\}$ 
4: procedure UPDATENGH( $s, d$ ) ▷ passed to EDGEMAP
5:   fetchAdd(& $\mathbf{r}'[d], (1 - \alpha)\mathbf{r}[s]/(2d(s))$ )
6: procedure UPDATESSELF( $v$ ) ▷ passed to VERTEXMAP
7:    $\mathbf{p}[v] = \mathbf{p}[v] + \alpha\mathbf{r}[v]$ 
8:    $\mathbf{r}'[v] = (1 - \alpha)\mathbf{r}[v]/2$ 
9: procedure PR-NIBBLE( $G, x, \epsilon, \alpha$ )
10:   $\mathbf{r} = \{(x, 1)\}$ 
11:  vertexSubset Frontier =  $\{x\}$  ▷ seed vertex
12:  while (size(Frontier) > 0) do
13:     $\mathbf{r}' = \{\}$ 
14:    VERTEXMAP(Frontier, UPDATESSELF)
15:    EDGEMAP( $G$ , Frontier, UPDATENGH)
16:     $\mathbf{r} = \mathbf{r}'$ 
17:    Frontier =  $\{v \mid \mathbf{r}[v] \geq d(v)\epsilon\}$  ▷ using filter
18:  return  $\mathbf{p}$ 

```

**Figure 5:** Pseudocode for parallel PR-Nibble with the original update rule.

```

1: procedure UPDATENGH( $s, d$ ) ▷ passed to EDGEMAP
2:   fetchAdd(& $\mathbf{r}'[d], ((1 - \alpha)/(1 + \alpha))\mathbf{r}[s]/d(s)$ )
3: procedure UPDATESSELF( $v$ ) ▷ passed to VERTEXMAP
4:    $\mathbf{p}[v] = \mathbf{p}[v] + (2\alpha/(1 + \alpha))\mathbf{r}[v]$ 
5:    $\mathbf{r}'[v] = 0$ 

```

**Figure 6:** Update functions for the optimized version of parallel PR-Nibble. The rest of the code is the same as in Figure 5.

Unfortunately their algorithm does not have a local running time since it does work proportional to at least the number of vertices in the graph. Here we develop a work-efficient parallel algorithm (and thus with local running time) in the shared-memory setting based on this idea.

In our parallel algorithm, we maintain an additional vector  $\mathbf{r}'$ , which is set to  $\mathbf{r}$  at the beginning of an iteration, and during the iteration vertices read values from  $\mathbf{r}$  and write values to  $\mathbf{r}'$ . At the end of the iteration,  $\mathbf{r}$  is set to  $\mathbf{r}'$ . Thus, the pushes use information in the  $\mathbf{r}$  vector computed from previous iterations, and do not take into account updates that occur within the current iteration. We also tried an asynchronous version which only maintains a single  $\mathbf{r}$  vector, with updates always going to that vector, but found that mass would leak when running in parallel due to race conditions, and it was unclear what the meaning of the solution at the end was. Developing an asynchronous version that preserves mass and works well in practice is a direction for future work.

We implement a parallel version of PR-Nibble with the original update rule (Figure 5) as well as a version with the optimized update rule, which requires changing only the update functions passed to EDGEMAP (Figure 6). The implementations are very similar to that of Nibble—the main differences are in the update rules and the fact that PR-Nibble runs until the size of the frontier becomes empty whereas Nibble will stop after at most  $T$  iterations.

Unlike Nibble, the amount of work performed in the parallel versions of PR-Nibble can differ from the sequential version as the parallel version pushes from all vertices above the threshold with their residual at the *start of an iteration*. In particular, the sequential version selects and pushes a single vertex based on the most recent value of  $\mathbf{r}$  whereas the parallel version selects and pushes vertices based on the value of  $\mathbf{r}$  before any of the vertices in the same iteration have been processed. The residual of the vertex when it is pushed in the parallel version can be lower than when it is pushed in the sequential version, causing less progress to be made towards termination, and leading to more pushes overall. However, the following theorem shows that the asymptotic work complexity of the parallel versions match that of the sequential versions.

**Theorem 3.** *The work of the parallel implementations of PR-Nibble using either update rule is  $O(1/(\alpha\epsilon))$  with high probability.*

*Proof.* The proof is very similar to how the work is bounded in the sequential algorithm [2] and involves showing that the  $l_1$  norm (sum

Input Graph	Num. Pushes (sequential)	Num. Pushes (parallel)	Num. Iterations (parallel)
soc-LJ	475,815	535,418	66
cit-Patents	4,154,752	5,323,710	139
com-LJ	763,213	917,798	77
com-Orkut	516,787	803,038	166
Twitter	125,478	127,625	44
com-friendster	1,731,670	2,086,491	65
Yahoo	740,410	830,457	96

**Table 1:** Number of pushes and number of iterations for PR-Nibble on several graphs using  $\alpha = 0.01$  and  $\epsilon = 10^{-7}$ . More information about the graphs can be found in Table 2 of Section 4.

of entries) of the residual vector  $\mathbf{r}$  sufficiently decreases in each iteration. This idea is also used in [38].

Our proof will be for PR-Nibble using the optimized update rule, but the proof is similar when using the original rule. Denote the residual vector  $\mathbf{r}$  at the beginning of iteration  $i$  by  $\mathbf{r}_i$ . In the pseudocode, each iteration will generate  $\mathbf{r}_{i+1}$  by moving mass from  $\mathbf{r}_i$  into  $\mathbf{r}'$ . Denote the set of active vertices in iteration  $i$  by  $A_i$ . Any vertex  $v$  processed in the iteration will have  $\mathbf{r}_i(v) \geq \epsilon d(v)$  (as the frontier is defined by vertices that satisfy this property) and do  $O(d(v))$  work to perform the push. It will also contribute  $O(d(v))$  work towards the filter on Line 17. The work of an iteration is thus  $\sum_{v \in A_i} O(d(v))$ , and the total work of the algorithm is  $\sum_{i=1}^T \sum_{v \in A_i} O(d(v))$  if it runs for  $T$  iterations.

A push from vertex  $v$  will first set  $\mathbf{r}'[v]$  to 0, and then add a total of  $((1 - \alpha)/(1 + \alpha))\mathbf{r}_i(v)$  mass to its neighbors' entries in the  $\mathbf{r}'[v]$  vector. Thus the total contribution to  $|\mathbf{r}_i|_1 - |\mathbf{r}_{i+1}|_1$  of vertex  $v$  is  $(1 - (1 - \alpha)/(1 + \alpha))\mathbf{r}_i[v] = (2\alpha/(1 + \alpha))\mathbf{r}_i[v] \geq (2\alpha/(1 + \alpha))\epsilon d(v) \geq \alpha \epsilon d(v)$ . Parallel updates to  $\mathbf{r}'$  will be correctly reflected due to the use of the atomic fetch-and-add function, and so all vertices  $v$  that are on the frontier in iteration  $i$  will contribute at least  $\alpha \epsilon d(v)$  to the difference  $|\mathbf{r}_i|_1 - |\mathbf{r}_{i+1}|_1$ .

We know that  $|\mathbf{r}_1|_1 = 1$  and  $|\mathbf{r}_T|_1 \leq 1$ , and so  $1 \geq |\mathbf{r}_1|_1 - |\mathbf{r}_T|_1 = \sum_{i=1}^T (|\mathbf{r}_i|_1 - |\mathbf{r}_{i+1}|_1) \geq \sum_{i=1}^T \sum_{v \in A_i} \alpha \epsilon d(v)$ . Rearranging, we have  $\sum_{i=1}^T \sum_{v \in A_i} d(v) \leq 1/(\alpha \epsilon)$ . Thus, the total work of the algorithm is  $\sum_{i=1}^T \sum_{v \in A_i} O(d(v)) \leq O(1/(\alpha \epsilon))$ . Note that this bound is independent of  $T$ .  $\square$

We also note that both versions of parallel PR-Nibble can be shown to satisfy the same asymptotic conductance guarantees as the sequential algorithm of [2].

In practice we found that the parallel versions do more work than the corresponding sequential versions, but benefit from a fewer number of iterations, each of which can be parallelized. Table 1 shows the number of pushes for both the sequential and parallel versions of PR-Nibble with the optimized update rule on several real-world graphs. The table also shows the number of iterations required for parallel PR-Nibble (the number of iterations for sequential PR-Nibble is equal to the number of pushes). We see that the number of pushes of the parallel version is higher by at most a factor of 1.6x and usually much less. The number of iterations is significantly lower than the number of pushes, indicating that on average there are many pushes to do in an iteration, so parallelism is abundant.

We also implemented a parallel version which in each iteration processes the top  $\beta$ -fraction ( $0 < \beta \leq 1$ ) of the vertices in the set  $\{v \mid \mathbf{r}[v] \geq d(v)\epsilon\}$  with the highest  $\mathbf{r}[v]/d(v)$  values. The  $\beta$  parameter trades off between additional work and parallelism. We found that this optimization helped in practice for certain graphs, but not by much. Furthermore the best value of  $\beta$  varies among graphs. We do not report the details of the performance of this variant in this paper due to space constraints.

### 3.4 Deterministic Heat Kernel PageRank

Kloster and Gleich [24] present an algorithm for approximating the heat kernel PageRank distribution of a graph, a concept that was first introduced in [9]. For a seed vector  $\mathbf{s}$ , random walk matrix  $\mathbf{P} = \mathbf{A}\mathbf{D}^{-1}$  ( $\mathbf{A}$  is the adjacency matrix corresponding to the graph, and  $\mathbf{D}$  is the diagonal matrix with  $\mathbf{D}[i, i]$  containing  $d(i)$ ) and parameters  $k$  and  $t$ , the heat kernel PageRank vector is defined to be  $\mathbf{h} = e^{-t}(\sum_{k=0}^{\infty} \frac{t^k}{k!}(\mathbf{P})^k)\mathbf{s}$ .

The algorithm of Kloster and Gleich, which we refer to as **HK-PR**, takes as input parameters  $N$ ,  $\epsilon$ ,  $t$ , and a seed vertex  $x$ . It approximates  $\mathbf{h}$  by approximating  $\sum_{k=0}^{\infty} \frac{t^k}{k!}(\mathbf{P})^k$  with its degree- $N$  Taylor polynomial  $\sum_{k=0}^N \frac{t^k}{k!}(\mathbf{P})^k$ , which can be cast as a linear system. Their algorithm first computes values  $\psi_k = \sum_{m=0}^{N-k} \frac{k!}{(m+k)!} t^m$  for  $k = 0, \dots, N$ . It uses a vector  $\mathbf{r}$ , indexed by integer pairs and initialized with  $\mathbf{r}[(s, 0)] = 1$ , a vector  $\mathbf{p}$  initialized to contain all 0's, and a queue initialized to contain just  $(s, 0)$ . Both  $\mathbf{r}$  and  $\mathbf{p}$  are represented using sparse sets. Each iteration removes an entry  $(v, j)$  from the front of the queue, and performs the following update:

1.  $\mathbf{p}[v] = \mathbf{p}[v] + \mathbf{r}[(v, j)]$
2.  $M = t \cdot \mathbf{r}[(v, j)] / ((j + 1)d(v))$
3. for each  $w$  such that  $(v, w) \in E$ :
  - if  $j + 1 == N$ : then  $\mathbf{p}[w] = \mathbf{p}[w] + \mathbf{r}[(v, j)]/d(v)$
  - else:
    - if  $\mathbf{r}[(w, j + 1)] < \frac{e^{-t}\epsilon d(w)}{2^N \psi_{j+1}}$  and  $\mathbf{r}[(w, j + 1)] + M \geq \frac{e^{-t}\epsilon d(w)}{2^N \psi_{j+1}}$ : then add  $(w, j + 1)$  to the queue
    - $\mathbf{r}[(w, j + 1)] = \mathbf{r}[(w, j + 1)] + M$

The vector  $\mathbf{p}$  is output when the queue becomes empty, and a sweep cut is applied on it to obtain a cluster. The algorithm is deterministic in that it will generate the same  $\mathbf{p}$  every time given the same inputs.

Our sequential implementation follows the procedure above. We observe that this algorithm can be parallelized by applying the above procedure on all queue entries  $(v, j)$  with the same  $j$  value in order of increasing  $j$  because processing these entries only causes updates to entries  $(w, j + 1)$  in  $\mathbf{r}$ , and can only possibly add entries with the same form to the queue. Conflicting updates can be resolved with fetch-and-add. Except for when  $j = N - 1$ , the queue entries  $(v, j)$  only update  $\mathbf{p}[v]$ , so there will be no conflicting updates to the  $\mathbf{p}$  vector among different vertices  $v$ . For  $j = N - 1$ , we can use a fetch-and-add to correctly update the  $\mathbf{p}$  vector.

The pseudocode for our parallel implementation is shown in Figure 7. We no longer need to index  $\mathbf{r}$  with the second integer  $j$ , since this is now implicitly captured by the iteration number of the algorithm. We use  $\mathbf{r}$  to store the values for the current iteration and  $\mathbf{r}'$  to store the values for the next iteration. We initialize  $\mathbf{r}$  and the frontier to contain just the seed vertex (Lines 12–13). On each iteration we apply a VERTEXMAP to update the  $\mathbf{p}$  values of the frontier vertices (Line 16). If it is not the last round ( $j + 1 < N$ ), we apply an EDGEMAP to update the  $\mathbf{r}'$  values of the neighbors of the frontier using the update rule with fetch-and-add (Line 19), and generate a new frontier for the next round based on the threshold specified in the sequential algorithm using a filter (Line 21). For the last round, we apply an EDGEMAP to update the  $\mathbf{p}$  values of the neighbors of the frontier (Line 24). This parallel algorithm applies the same updates as the sequential algorithm and thus the vector returned is the same.

As shown in [24], the sequential algorithm explores  $O(Ne^t/\epsilon)$  edges, leading to an overall work of  $O(Ne^t/\epsilon)$ . Our parallel algorithm only does a constant factor more work (the work of the

```

1: sparseSet  $\mathbf{p} = \{\}$ 
2: sparseSet  $\mathbf{r} = \{\}$ 
3: sparseSet  $\mathbf{r}' = \{\}$ 
4: procedure UPDATENGH( $s, d$ )  $\triangleright$  passed to EDGEMAP on all rounds but the last
5:   fetchAdd(& $\mathbf{r}'[d], t \cdot \mathbf{r}[s] / ((j + 1)d(s))$ )
6: procedure UPDATENGHLAST( $s, d$ )  $\triangleright$  passed to EDGEMAP on the last round
7:   fetchAdd(& $\mathbf{p}[d], \mathbf{r}[s] / d(s)$ )
8: procedure UPDATESELF( $v$ )  $\triangleright$  passed to VERTEXMAP
9:    $\mathbf{p}[v] = \mathbf{p}[v] + \mathbf{r}[v]$ 
10: procedure HK-PR( $G, x, N, \epsilon, t$ )
11:   precompute  $\psi_k = \sum_{m=0}^{N-k} \frac{k!}{(m+k)!} t^m$  for  $k = 0, \dots, N$ 
12:    $\mathbf{r} = \{(x, 1)\}$ 
13:   vertexSubset Frontier =  $\{x\}$   $\triangleright$  seed vertex
14:    $j = 0$ 
15:   while (size(Frontier) > 0) do
16:     VERTEXMAP(Frontier, UPDATESELF)
17:     if  $j + 1 == N$  then
18:        $\mathbf{r}' = \{\}$ 
19:       EDGEMAP( $G, \text{Frontier}, \text{UPDATENGH}$ )
20:        $\mathbf{r} = \mathbf{r}'$ 
21:       Frontier =  $\{v \mid \mathbf{r}[v] \geq \frac{e^t \epsilon d(v)}{2N \psi_{j+1}(t)}\}$   $\triangleright$  using filter
22:        $j = j + 1$ 
23:     else  $\triangleright$  last round
24:       EDGEMAP( $G, \text{Frontier}, \text{UPDATENGHLAST}$ )
25:       break
26:   return  $\mathbf{p}$ 

```

Figure 7: Pseudocode for parallel HK-PR.

filter is proportional to the number of edges processed in the iteration), and so also has a work bound of  $O(Ne^t/\epsilon)$ . The depth for iteration  $j$  is  $O(\log U_j)$  for the fetch-and-adds and filter, where  $U_j$  is the number of vertices and edges processed in the iteration, and  $\sum_{j=0}^N U_j = O(Ne^t/\epsilon)$ . This gives an overall depth of  $\sum_{j=0}^N O(\log U_j) = O(Nt \log(1/\epsilon))$ , where we use the fact that the logarithm is a concave function and the sum is maximized when all  $U_j$ 's are equal. The initialization on Line 11 can be done in  $O(N^2)$  work and  $O(\log N)$  depth using prefix sums, which is work-efficient. This gives the following theorem.

**Theorem 4.** *The parallel algorithm for HK-PR requires  $O(N^2 + Ne^t/\epsilon)$  work and  $O(Nt \log(1/\epsilon))$  depth with high probability.*

As noted in [24], in practice  $N$  is set to at most  $2t \log(1/\epsilon)$ , so the  $O(N^2)$  term in the work is a lower-order term.

### 3.5 Randomized Heat Kernel PageRank

Chung and Simpson [10] describe a randomized algorithm for approximating the heat kernel PageRank based on running a sample of random walks and computing the distribution of the last vertices visited in the random walks. We refer to this algorithm as *rand-HK-PR*. The algorithm takes as input parameters  $x, N, K$ , and  $t$ , where  $x$  is the seed vertex,  $N$  is the number of random walks to perform,  $K$  is the maximum length of a random walk, and  $t$  is a parameter to the heat kernel PageRank equation, as defined in Section 3.4. Rand-HK-PR runs  $N$  random walks starting from  $x$ , where each step of the walk visits a neighbor of the current vertex with equal probability, and the walk length is  $k$  with probability  $e^{-t} t^k / k!$ . The maximum walk length is set to  $K$ . It maintains a vector  $\mathbf{p}$ , where  $\mathbf{p}[v]$  stores the number of random walks that ended on vertex  $v$ . The sequential algorithm stores  $\mathbf{p}$  as a sparse set, initialized to be empty, and executes one random walk at a time for  $N$  times, each time incrementing  $\mathbf{p}[v]$  by 1 where  $v$  is the last vertex visited in the random walk. The vector returned and passed to the sweep cut procedure is  $(1/N)\mathbf{p}$ .

The algorithm is easily parallelizable by running all of the random walks in parallel and incrementing  $\mathbf{p}$  using a fetch-and-add. However, we found that naively implementing this approach led to poor speed up since many random walks end up on the same vertex causing high memory contention when using fetch-and-adds to update that location. Instead, we keep an array  $A$  of length  $N$

Input Graph	Num. Vertices	Num. Edges <sup>†</sup>
soc-LJ	4,847,571	42,851,237
cit-Patents	6,009,555	16,518,947
com-LJ	4,036,538	34,681,189
com-Orkut	3,072,627	117,185,083
nlpkkt240	27,993,601	373,239,376
Twitter	41,652,231	1,202,513,046
com-friendster	124,836,180	1,806,607,135
Yahoo	1,413,511,391	6,434,561,035
randLocal (synthetic)	10,000,000	49,100,524
3D-grid (synthetic)	9,938,375	29,815,125

Table 2: Graph inputs used in experiments. <sup>†</sup>Number of unique undirected edges.

and have the  $i$ 'th random walk store its destination vertex into  $A[i]$ . Afterward we sort  $A$ , and compute the number of random walks ending on each vertex using prefix sums and filter. In particular, we create an auxiliary array  $B$ , and for all locations  $i$  in the sorted  $A$  array such that  $A[i] \neq A[i-1]$ ,  $B[i] = i$ , and otherwise  $B[i] = -1$ . Filtering out all  $-1$  entries in  $B$  gives the offsets where the entries in  $A$  differ, and the difference between consecutive offsets gives the number of random walks ending at a particular value, which allows us to compute  $\mathbf{p}$ . The prefix sums and filter take  $O(N)$  work and  $O(\log N)$  depth. To perform the sorting in  $O(N)$  work and  $O(\log N)$  depth, we compute a mapping from each last-visited vertex to an integer in  $[0, \dots, N]$  using a parallel hash table, so that the maximum value is bounded by  $N$ , and then use a parallel integer sort [39] on the mapped values.

The sequential algorithm takes  $O(NK)$  work since  $N$  random walks of length  $O(K)$  are executed. The parallel algorithm takes  $O(NK)$  work and  $O(K + \log N)$  depth, as all random walks are run in parallel and each takes  $O(K)$  steps. This gives a work-efficient parallel algorithm, and we have the following theorem:

**Theorem 5.** *The parallel algorithm for rand-HK-PR takes  $O(NK)$  work and  $O(K + \log N)$  depth with high probability.*

In contrast to the previous three algorithms, we do not need to use the Ligra functions for this algorithm since the random walks are independent and only process a single vertex in each iteration.

We note that Chung and Simpson describe a distributed version of their algorithm [11]. This work differs from ours in that it assumes the input graph is the network of processors and studies how to compute local clusters with limited communication. In contrast, we study the setting where the input graph is independent of the number of processors or their layout, and our goal is to speed up the computation by taking advantage of parallel resources.

## 4 Experiments

We present an experimental study of both parallel and sequential implementations of the local clustering algorithms described in Section 3 on large-scale undirected graphs. All of our implementations are available at <https://github.com/jshun/ligra/>.

**Input Graphs.** We use a set of unweighted undirected real-world and synthetic graphs, whose sizes are shown in Table 2. We obtained the *soc-LJ*, *cit-Patents*, *com-LJ*, *com-Orkut*, and *com-friendster* real-world graphs from <http://snap.stanford.edu/>. *nlpkkt240* is a graph derived from a matrix of a constrained optimization problem from <http://www.cise.ufl.edu/research/sparse/matrices/>. *Twitter* is a symmetrized version of a snapshot of the Twitter network [26]. *Yahoo* is a symmetrized version of a Web graph from <http://webscope.sandbox.yahoo.com>. *randLocal* is a random graph where every vertex has five edges to neighbors chosen with probability proportional to the difference in the neighbor's ID value from the vertex's ID. *3D-grid* is a synthetic grid graph in 3-dimensional space where every vertex has six edges, each connecting it to its 2 neighbors in each dimension. We remove all self and duplicate edges from the graphs.

Algorithm	soc-LJ		cit-Patents		com-LJ		com-Orkut		nlpkt240		Twitter		com-friendster		Yahoo		randLocal		3D-grid	
	$T_1$	$T_{40}$	$T_1$	$T_{40}$	$T_1$	$T_{40}$	$T_1$	$T_{40}$	$T_1$	$T_{40}$	$T_1$	$T_{40}$	$T_1$	$T_{40}$	$T_1$	$T_{40}$	$T_1$	$T_{40}$	$T_1$	$T_{40}$
Parallel Nibble	19.20	0.664	3.06	0.195	15.30	0.566	3.83	0.290	0.02	0.047	1.60	0.167	4.53	0.297	1.88	0.214	2.47	0.196	0.01	0.040
Sequential Nibble	24.90	–	4.16	–	17.80	–	8.26	–	0.02	–	7.93	–	8.40	–	1.97	–	5.88	–	0.01	–
Parallel PR-Nibble	6.08	0.350	21.50	0.978	7.59	0.436	9.86	0.572	1.82	0.530	2.50	0.177	8.62	0.492	6.16	0.623	28.90	1.250	1.90	0.502
Sequential PR-Nibble	2.17	–	8.92	–	2.74	–	1.94	–	2.21	–	0.70	–	7.97	–	3.56	–	9.46	–	1.41	–
Parallel HK-PR	56.60	1.710	11.00	0.430	39.70	1.230	28.80	0.918	0.02	0.049	7.55	0.434	20.40	0.866	6.40	0.377	11.90	0.479	0.01	0.049
Sequential HK-PR	241.00	–	24.20	–	156.00	–	93.40	–	0.03	–	28.60	–	68.30	–	11.30	–	32.00	–	0.02	–
Parallel rand-HK-PR	129.00	2.080	23.10	0.634	117.00	1.610	83.90	1.390	23.70	0.568	75.70	1.390	45.30	0.825	42.40	0.901	33.90	0.744	21.20	0.496
Sequential rand-HK-PR	195.00	–	43.20	–	154.00	–	121.00	–	18.90	–	160.00	–	85.60	–	67.10	–	51.70	–	19.10	–
Parallel Sweep	4.37	0.189	1.98	0.075	5.10	0.217	6.73	0.285	0.01	0.003	75.00	3.180	5.00	0.221	43.10	1.550	2.24	0.083	0.01	0.01
Sequential Sweep	2.57	–	1.51	–	3.20	–	3.40	–	0.01	–	40.10	–	3.66	–	6.43	–	1.72	–	0.01	–

**Table 3:** Running times (seconds) of sequential and parallel local graph clustering algorithms and the sweep cut procedure.  $T_1$  is the single-thread time and  $T_{40}$  is the parallel time using 40 cores with hyper-threading. The parameters are set as follows:  $T = 20$  and  $\epsilon = 10^{-8}$  for Nibble;  $\alpha = 0.01$  and  $\epsilon = 10^{-7}$  for PR-Nibble;  $t = 10$ ,  $N = 20$ , and  $\epsilon = 10^{-7}$  for HK-PR; and  $t = 10$ ,  $K = 10$ , and  $N = 10^8$  for rand-HK-PR. The running times for the sweep cut are based on using the output of Nibble.

**Experimental Setup.** We run our experiments on a 40-core Intel machine (with two-way hyper-threading<sup>4</sup>) with  $4 \times 2.4$ GHz Intel 10-core E7-8870 Xeon processors (with a 1066MHz bus and 30MB L3 cache) and 256GB of main memory. The parallel programs are compiled with Cilk Plus from the g++ compiler (version 4.8.0) with the `-O3` flag (they can also be compiled with OpenMP with similar performance). Our parallel implementations are all written in Ligra [41], with the exception of rand-HK-PR, which does not need Ligra’s functionality. The parallel implementations of prefix sum, filter, comparison sort, and integer sort that we use are from the Problem Based Benchmark Suite [43]. The concurrent hash table for representing sparse sets is from [42]. For both sequential and parallel PR-Nibble, we report performance of the versions using the optimized update rule as described in Section 3.3.

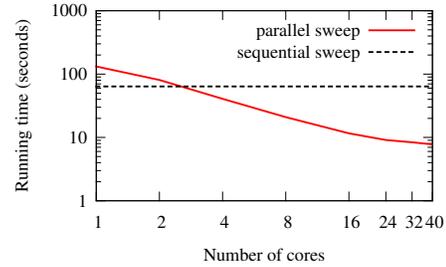
**Parameter setting versus algorithm performance.** We first study how the setting of the various parameters in Nibble, PR-Nibble, HK-PR, and rand-HK-PR affect their running time and the conductance of the cluster generated. Figure 8 shows the results of this study on the Yahoo graph, the largest graph in this paper. All experiments start from the same seed vertex, which was chosen by sampling  $10^4$  vertices and picking the one that gave the lowest-conductance clusters. The trends are the same for both sequential and parallel implementations, and the reported results are for the sequential implementations.

As expected, for Nibble (Figures 8(a) and 8(b)), we see that increasing  $T$  and/or decreasing  $\epsilon$  leads to higher running time and improved conductance. The same thing happens for HK-PR (Figures 8(e) and 8(f)) when increasing  $N$  and/or decreasing  $\epsilon$ . For PR-Nibble, we see that decreasing  $\epsilon$  leads to higher running time and lower conductance (Figures 8(c) and 8(d)). Finally, for rand-HK-PR, we see that increasing  $K$  and/or increasing  $N$  leads to higher running time and lower conductance (Figures 8(g) and 8(h)).

**Parallel Performance of Local Clustering.** Here we study the parallel scalability of our implementations of Nibble, PR-Nibble, HK-PR, and Rand-HK-PR. Table 3 shows the parallel ( $T_{40}$ ) and single-thread ( $T_1$ ) running times of our parallel implementations, as well as the running time of the sequential implementation, for a setting of the parameters described in the table caption. All of the experiments start from a single arbitrary vertex in the largest component.<sup>5</sup> The parameters were set so that for most graphs at least tens of thousands of vertices were touched; otherwise the algorithms finish in milliseconds, and there is not enough work to benefit from parallelism. For all graphs except for nlpkt240 and 3D-grid, we see reasonable parallel speedup over the single-thread times. For nlpkt240 and 3D-grid, not many vertices are touched as the graphs are not well-connected, and so the experiments terminated quickly.

<sup>4</sup>A form of simultaneous multithreading developed by Intel in which there are two logical processors per physical core.

<sup>5</sup>Our codes can easily be modified to take as input a seed set with multiple vertices. This would increase the frontier sizes at each iteration, leading to more parallelism.



**Figure 10:** Running time (seconds) versus core count in log-log scale of sweep cut on a cluster with 1.3 million vertices and 566 million edges. On 40 cores, 80 hyper-threads are used.

For these types of graphs, there are no good local clusters, and so it may not be useful to run a local clustering algorithm. We note that the running times of the algorithms depend highly on the seed vertex and parameter settings, but we believe that our parallel algorithms are useful in cases where at least tens of thousands of vertices are touched (which is a small number for massive graphs). For Nibble, HK-PR, and rand-HK-PR we see that the parallel version on a single thread actually outperforms the sequential version in most cases. For Nibble and HK-PR, we believe this is because our concurrent hash table (used to represent the sparse sets) is more efficient than STL’s `unordered_map`, even on one thread. For rand-HK-PR, the parallel method uses sorting to obtain the vector rather than maintaining it in a sparse set as in the sequential case, and this seems to be more efficient even on a single thread in most cases.

Figure 9 shows the self-relative speedups (relative to the algorithm’s single-thread time  $T_1$ ) of the four algorithms versus thread count on several input graphs. Nibble, PR-Nibble, and HK-PR get reasonable parallel speedup (9–35x on 40 cores), although the speedup is not perfect due to memory contention when running in parallel and also due to some frontiers being too small to benefit from parallelism. rand-HK-PR gets even better speedup as most of the algorithm is embarrassingly parallel (over 40x on 40 cores due to two-way hyper-threading).

**Sweep Cut Performance.** Here we study the performance of our parallel sweep cut algorithm. Table 3 shows the running time of our parallel sweep cut implementation and the standard sequential implementation on the output of Nibble. The performance trends for sweep cut were similar when applied to outputs of the other clustering algorithms. Except for nlpkt240 and 3D-grid, where the input cluster was too small to benefit from parallelism, the self-relative speedup of parallel sweep ranges from 23 to 28 on 40 cores with hyper-threading. On a single thread, parallel sweep is slower than sequential sweep due to overheads of the parallel algorithm (e.g., scanning over the edges several times instead of just once).

Figure 10 shows the running time of sweep cut as a function of thread count (log-log scale). The input cluster was generated by running Nibble on the Yahoo graph with  $T = 20$  and  $\epsilon = 10^{-9}$ . The number of vertices in the cluster is 1.3 million and its volume is 566 million. We see that the the parallel implementation scales well

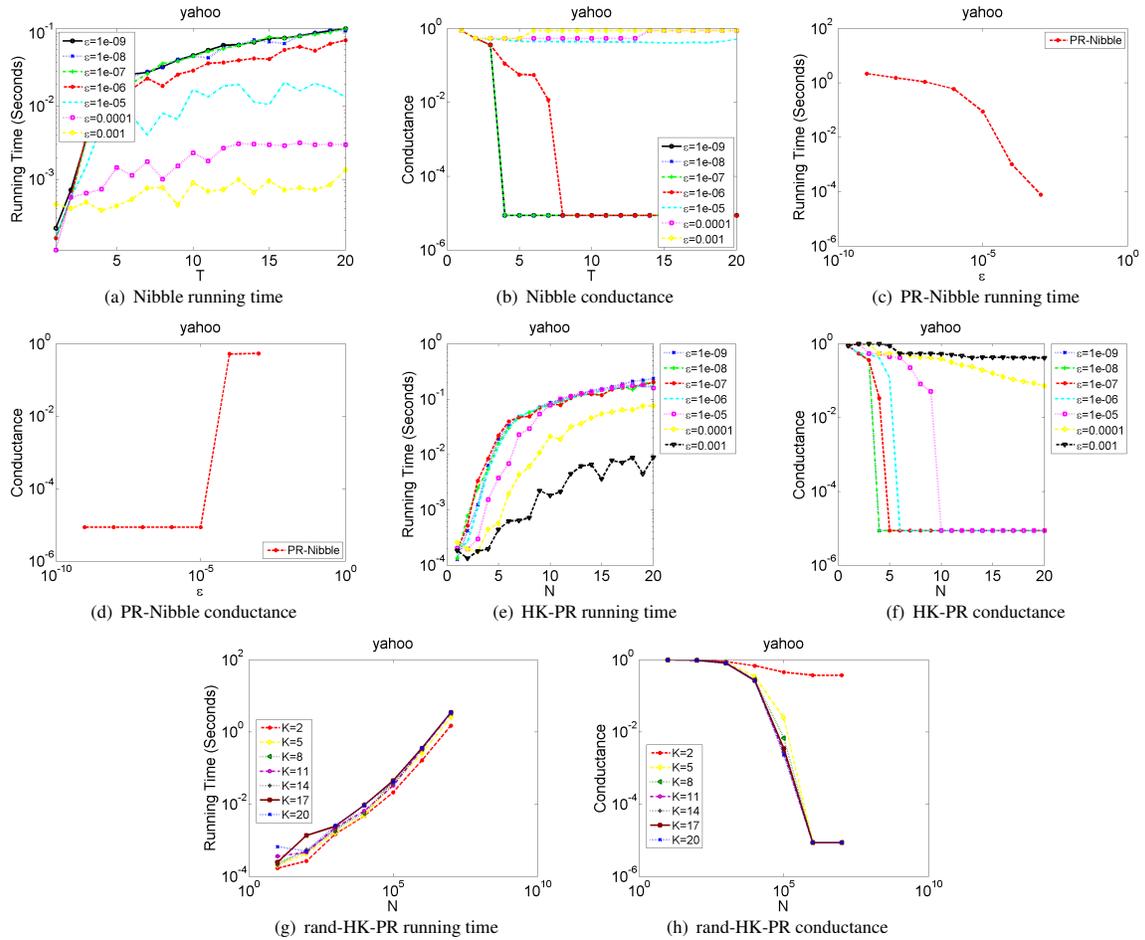


Figure 8: Running time (seconds) and conductance of algorithms as a function of parameter settings on the Yahoo graph. (Best viewed in color.)

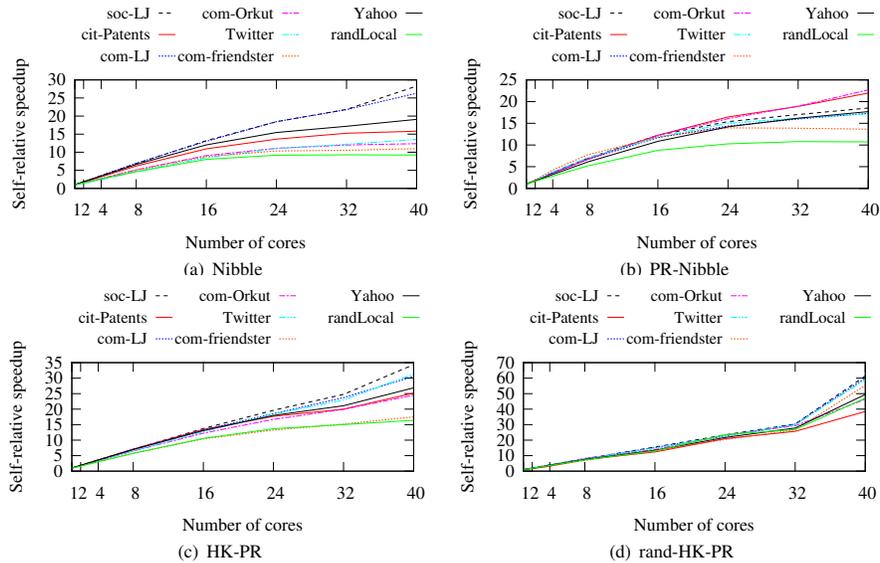


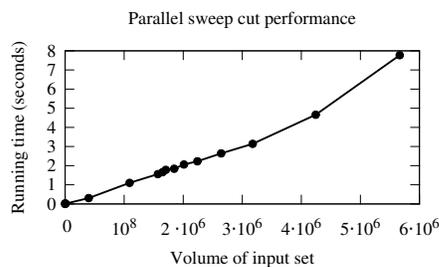
Figure 9: Parallel self-relative speedup versus cores count for the four parallel algorithms on several input graphs. On 40 cores, 80 hyper-threads are used. (Best viewed in color.)

(almost linearly) with the number of threads, and outperforms the sequential implementation with 4 or more threads.

Figure 11 shows the running time of the parallel sweep cut on 40 cores versus the volume of the input set, generated by running Nibble with different parameter settings on the Yahoo graph. We see that the running time scales nearly linearly, which is expected since the time is dominated by linear-work operations (the only part that

scales super-linearly is the initial sort, which takes a small fraction of the total time).

From Table 3, we can see that the sweep cut takes a significant fraction of (in some cases dominating) the overall time of running Nibble followed by a sweep cut procedure. This was also true for the other local clustering algorithms. Thus parallelizing the sweep cut procedure is important in achieving good overall performance.



**Figure 11:** Running time (seconds) versus cluster volume for parallel sweep cut on 40 cores with hyper-threading.

**Network Community Profiles.** Due to the efficiency of our parallel algorithms we are able to quickly generate network community profile (NCP) plots for large graphs, which show the (approximate) best conductance for clusters of a given size in the graph versus the cluster size [29]. Figure 12 shows the NCPs for several graphs with at least a billion edges, larger than any of the graphs whose NCP has been studied before [29, 23]. The data was collected by running PR-Nibble from  $10^5$  random seed vertices and by varying  $\alpha$  and  $\epsilon$ . For Twitter and com-friendster, the curves are downwards sloping with increasing cluster size until around 10–100 vertices, and then upwards sloping, which is consistent with the observation by Leskovec et al. [29], that good communities are relatively small. For Yahoo, although there are low-conductance clusters with small size, there also seems to be many low-conductance clusters at larger sizes (tens of thousands of vertices).

## 5 Other Related Work

Andersen and Lang [5] developed a variant of the Nibble algorithm with multiple starting vertices for finding communities in graphs. The PR-Nibble algorithm has been extended to directed graphs [3]. A variant of PR-Nibble has also been used to obtain clusters with better guarantees when the cluster is internally well-connected [51]. Finally, statistical/optimization perspectives on the PR-Nibble algorithm have been proposed [17, 14].

Andersen and Peres [7] present an algorithm called *evolving sets*, where  $f(\phi, n) = O(\sqrt{\phi} \log n)$  and that has a work bound of  $O(|S| \text{polylog}(n)/\sqrt{\phi})$ . The algorithm maintains the position of a random walk starting at the seed vertex. Starting with a single vertex in a set  $S$ , each iteration of the algorithm adds or deletes vertices from  $S$  based on whether the probability of transitioning to a given vertex from the current set is above some randomly chosen threshold. If in any iteration the conductance of  $S$  is at most  $f(\phi, n)$ , then the algorithm returns  $S$ . We implemented this algorithm but found the behavior of the algorithm to vary widely as the random choices in each iteration can lead to very different sets. We note that the algorithm can be parallelized work-efficiently by using data-parallel operations but we omit the discussion in this paper due to space constraints. Subsequent to the work of Andersen and Peres, there have been other local clustering algorithms developed with stronger guarantees [15, 27, 28].

Mahoney et al. [32] describe a spectral algorithm for finding clusters that are locally-biased towards a seed set in terms of satisfying an additional “locality” constraint in the spectral optimization program. However, the algorithm itself is not local as it requires work at least linear in the graph size.

Finally, there have been algorithms developed that take as input a local cluster and return a nearby local cluster with better conductance [6, 32, 37, 46].

## 6 Conclusion

We have presented work-efficient parallel algorithms for local graph clustering and our experiments demonstrated that the algorithms achieve good performance and scalability, significantly improving

the efficiency of the exploration of local graph clusters in massive graphs. We have performed experiments studying the output cluster conductance versus running time of the four local algorithms but did not find any one algorithm that always dominated the others. Since all of our parallel algorithms are efficient, data analysts can use any of them for graph cluster exploration, or even use all of them to find slightly different clusters of similar size from the same seed set.

We believe that our algorithms are extremely useful in the interactive setting where a graph is loaded once into memory and many local cluster computations are executed on it. In the setting where one only wants to run a few queries, our algorithms are still very efficient but the cost of loading the graph will not be amortized across the queries. To improve the performance in this setting, we are interested in developing efficient methods for traversing graphs locally from disk. We are also interested in parallelizing local flow-based algorithms [37, 46] for improving cluster quality.

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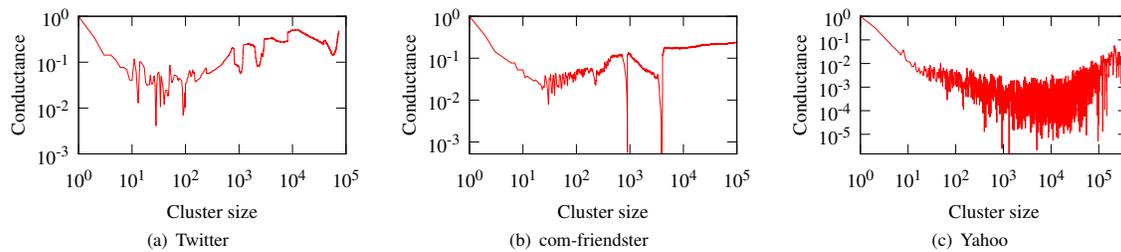


Figure 12: Network community profile (NCP) plots for billion-edge graphs.

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