

# Mining Maximal Cliques from a Large Graph using MapReduce: Tackling Highly Uneven Subproblem Sizes

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## Abstract

We consider Maximal Clique Enumeration (MCE) from a large graph. A maximal clique is perhaps the most fundamental dense substructure in a graph, and MCE is an important tool to discover densely connected subgraphs, with numerous applications to data mining on web graphs, social networks, and biological networks. While effective sequential methods for MCE are known, scalable parallel methods for MCE are still lacking.

We present a new parallel algorithm for MCE, Parallel Enumeration of Cliques using Ordering (*PECO*), designed for the MapReduce framework. Unlike previous works, which required a post-processing step to remove duplicate and non-maximal cliques, *PECO* enumerates only maximal cliques with no duplicates. The key technical ingredient is a total ordering of the vertices of the graph which is used in a novel way to achieve a load balanced distribution of work, and to eliminate redundant work among processors. We implemented *PECO* on Hadoop MapReduce, and our experiments on a cluster show that the algorithm can effectively process a variety of large real-world graphs with millions of vertices and tens of millions of maximal cliques, and scales well with the degree of available parallelism.

*Keywords:* Graph mining, Maximal Clique Enumeration, Enumeration algorithm, MapReduce, Hadoop, Parallel algorithm, Clique, Load Balancing

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## 1. Introduction

We consider the enumeration of dense substructures in a large graph. Large Graphs of the order of millions or billions of nodes and edges arise during the analysis of the web [1], social networks [2], and scientific applications [3]. These graphs typically do not fit in the memory of a single machine and even if they do, the computational demands of analyzing such graphs is so high that it is necessary to process them in parallel to achieve a reasonable turnaround time.

Perhaps the most elementary dense substructure in a graph, also probably the most commonly used, is a maximal clique. Enumerating all maximal cliques in a graph is known as the maximal clique enumeration problem (MCE). MCE is a fundamental problem in graph analysis, and has been used widely, for instance, in clustering and community detection in social and biological networks [3], in the study of the co-expression of genes under stress [4], in integrating different types of genome mapping data [5], and other applications in bioinformatics and data mining [6, 7, 8, 9, 10, 11, 12].

We consider parallel methods for enumerating all maximal cliques in a graph. While our algorithm maybe more broadly applicable, in this work we focus our implementation on the widely used *MapReduce* [13, 14, 15] framework for cluster computing. While MCE is widely studied in the sequential setting [16, 17, 18, 19, 20, 21, 22, 23, 24, 25], there is relatively less work on parallel methods [26, 27, 28, 29, 30].

In processing a large graph, it is natural to try breaking up the graph into subgraphs and process the subgraphs by parallel tasks. This approach presents some challenges in the context of MCE. First, it is necessary to avoid overlap among different coordinating tasks. The difficulty is that in almost any method of dividing a graph for parallel processing for MCE, subgraphs assigned to different tasks will overlap. However, the algorithm should be careful in not repeating the same work among different tasks, at the same time enumerating all maximal cliques. The second challenge is that the distribution of work among different processors (reducers) should be *load balanced*. In the absence of load balancing, the time taken by different processors could be widely different, so that the parallel resources

are not used efficiently, leading to a poor parallel runtime. The above challenges arise in parallelizing any computation using MapReduce, but are especially acute in parallel MCE, since straightforward methods of task division can lead to workloads that are extremely imbalanced.

### *Our Contributions*

We present a novel parallel MCE algorithm called *PECO* (**P**arallel **E**numeration of **C**liques using **O**rdering). To our knowledge, this is currently the fastest parallel algorithm for MCE using MapReduce, and improves on prior work in the following ways.

Prior algorithms using MapReduce [29] follow the strategy of first enumerating a set of cliques that are not necessarily maximal, but include all maximal cliques in the graph. This is then followed by a post-processing step that removes non-maximal cliques and duplicates. This post-processing step can be expensive, since the presence of non-maximal cliques and duplicates can make the intermediate output much larger than the final output size. In contrast, *PECO* outputs only maximal cliques without duplicates, and does not need an additional post-processing step.

Second, *PECO* provides the first effective solution to *load balance* among parallel tasks, in the MapReduce framework. This is a challenging problem in case of parallel MCE, due to non-uniform subproblem sizes, and the unbalanced lengths of search paths in different subproblems [28]. In our experiments, we found load balance to be one of the most important factors contributing to total runtime of enumeration. The technical ingredient in our algorithm is a carefully chosen ordering among all vertices in the graph, and the use of this ordering in load balancing and eliminating overlapping work among subproblems.

*Experimental Results.* We implemented *PECO* on a Hadoop MapReduce cluster, and our experiments with a variety of large real world graphs showed that *PECO* can enumerate maximal cliques within large graphs of millions of vertices and tens of millions of maximal cliques, and that it scales well with an increasing number of reducers. Our experiments revealed that *PECO* outperforms previous solutions [29] by orders of magnitude, especially for large graphs.

## 2. Preliminaries

Let  $G = (V, E)$  be an undirected unweighted graph where  $V$  is the set of vertices and  $E$  the set of edges. We assume every vertex in  $V$  has a unique identifier, chosen from a totally ordered set. This is not a restrictive assumption in practice. For example, if each vertex represented a webpage, then the vertices can be ordered using the lexicographic ordering among the respective URLs. For  $v \in V$ , let  $\Gamma(v)$  denote the set of all vertices that are adjacent to  $v$  in  $G$ ; we refer to this as the neighborhood of  $v$ . A subset  $C \subseteq V$  is a *clique* in  $G$  if for every pair of vertices  $u, w \in C$  the edge  $(u, w)$  exists in  $E$ . A clique  $C$  is *maximal* in  $G$  if no vertex  $u \in V - C$  can be added to  $C$  to form a larger clique. In the remainder of this paper, any reference to a clique refers to a maximal clique, unless otherwise specified. The MCE problem is: *Given an undirected graph  $G$ , enumerate all maximal cliques in  $G$ .*

*MapReduce.* MapReduce [13] is a popular framework designed for processing large data sets on a cluster of computers. A MapReduce program is written through specifying map and reduce functions. The map function takes as input a key-value pair  $(k, v)$  and emits zero, one, or more new key-value pairs  $(k', v')$ . All tuples with the same key are grouped together and passed to a reduce function, which processes a particular key  $k$  and all values that are associated with  $k$ , and outputs a final list of key-value pairs. The outputs of one MapReduce round can be the input to the next round. The Mapreduce system takes care of scheduling the map and reduce tasks in parallel. Further details on the framework are available in [13, 31].

The rest of this paper is organized as follows. We present related work in Section 3, describe our algorithm and analysis in Section 4, and results from Experiments in Section 5.

## 3. Related Work

We first discuss related work on sequential MCE and then on parallel MCE.

*Sequential MCE.* An early work due to Bron and Kerbosch [16] is an algorithm based on depth-first-search with good experimental performance on typical inputs, but whose worst case behavior is poor. Other algorithms stemming from this work include [21, 24, 17, 20].

Some of these algorithms, especially [24, 20], have asymptotically near-optimal worst case performance, and also run fast on typical inputs. The number of maximal cliques in a graph can be exponential in the number of vertices [32], although this is not true in the typical case.

Another branch of enumeration algorithms provide output sensitive runtime guarantees, i.e. the runtime is proportional to the size of the output. These algorithms stem from the Tsukiyama *et al.* [25] algorithm, which has a running time of  $O(|V||E|\mu)$ , where  $\mu$  is the number of maximal cliques. Other output sensitive algorithms include [18, 19, 22, 23], with [23] providing one of the best theoretical guarantees. However, these output sensitive algorithms tend not to perform as well as the worst case optimal algorithms in practice [24, 20]. Other works on sequential MCE include Kose *et al.* [33], who take a breadth first search approach, an external memory algorithm due to Cheng *et al.* [34], and pruning strategies for enumerating large cliques, due to Modani and Dey [35].

*Parallel MCE.* Early works in the area of parallel MCE include Zhang *et al.* [26] and Du *et al.* [27]. Zhang *et al.* developed an algorithm based on the Kose *et al.* [33] algorithm. Since these algorithms are based on breadth first search, they are able to enumerate maximal cliques in increasing order of size, but this makes the memory requirements very large. Du *et al.* [27], present a parallel algorithm based on the output-sensitive class of algorithms. However, as also noted by Schmidt *et al.* [28], this algorithm suffers from poor load balance; the graphs addressed by these experiments are quite small, they have about 150,000 maximal cliques and a million edges.

Schmidt *et al.* [28] identify load balancing as a significant issue in parallel MCE and present a parallel algorithm that uses “work stealing” to dynamically distribute load among processors. Their algorithm is designed for use with MPI, where the user can control the actions of a process and the manner of parallelism to a high degree of detail, when compared with MapReduce. In their algorithm, processes explore tasks in parallel until they run out of work, at which point idle processes request for more work from busy processes (work stealing). This continues until all processes are idle. Such types of work stealing and dynamic

load balancing are expensive to implement in the MapReduce model, since the processes are synchronized at each stage of Map and Reduce – for instance, all mappers need to complete before reducers start processing data. Our algorithm also implements effective load balancing, but in a more pre-determined and static manner.

Wu *et al.* [29] present an MCE algorithm designed for MapReduce. The algorithm splits the input graph into many subgraphs, which are then independently processed to enumerate cliques. However this work does not address load balancing, and in addition, their algorithm may enumerate non-maximal cliques, so that an additional post-processing step is needed to only emit maximal cliques. We compared our algorithm with the algorithm of Wu *et al.* (which we call as the WYZW algorithm), and present the results in Section 5.

dMaximalCliques [30] is another parallel MCE algorithm, based on the sequential algorithm of Tsukiyama *et al.* [25]. This algorithm works in two phases. The first phase enumerates maximal, duplicate, and non-maximal cliques, and the second post-processing phase removes duplicate and non-maximal cliques from the output. However, this post-processing phase can be very expensive since the output prior to filtering can become much larger than the final output; for instance, on the wikipedia-3 graph the first enumeration phase takes 7 minutes (on 20 processors), and the second post-processing phase takes 228 minutes (on 80 processors). The algorithm is implemented for the Sector/Sphere [36] framework.

*Problems Related to MCE.* Angel *et al.* [37] study the problem of dense subgraph maintenance on a dynamic graph defined by an update stream of edges, but their focus is on maintaining cliques, without the constraint that they be maximal. Agarwal *et al.* [38] also consider dynamic maintenance of dense substructures, but their focus is on subgraphs that are near-cliques (also known as quasi-cliques). Bahmani *et al.* [39] present multi-pass streaming algorithms for maintaining the densest subgraph in a large graph, and also a MapReduce implementation. Their notion of densest subgraph is a subgraph whose ratio of number of edges to number of vertices is as large as possible, subject to the subgraph having a minimum number of vertices. This problem is different from MCE, since the densest subgraph does not have to be (and is typically not) a clique, let alone a maximal clique.

## 4. Algorithm

We first discuss a straightforward approach to parallel MCE using MapReduce. For  $v \in V$ , let  $\Gamma(v)$  denote the neighbors of  $v$  in  $G$ , and let  $G_v$  denote the subgraph of  $G$  induced by  $v \cup \Gamma(v)$ . The following observation is easy to verify: each maximal clique  $C \subseteq V$  is also a maximal clique in  $G_v$  for any vertex  $v \in C$ , and vice versa. A parallel algorithm works as follows: first construct (in parallel) the different subgraphs  $\{G_v | v \in V\}$  and then separately enumerate maximal cliques in each of them using a sequential MCE algorithm, such as the ones in [16, 24, 20]. The details are as follows.

The algorithm takes as input an undirected graph stored as an adjacency list. The adjacency list consists for each vertex  $u \in V$ , the set of all vertices adjacent to  $u$ . During the **map** phase (described in Algorithm 2), when processing the entry for vertex  $v$ , the map task will send the tuple  $\langle v, \Gamma(v) \rangle$  to each neighbor of  $v$ ; i.e. the key is a neighbor of the vertex identifier  $v$ , and the value is the neighborhood  $\Gamma(v)$ . The **reduce** task handling vertex  $v$  (Algorithm 3) will receive  $\Gamma(u)$  from each neighbor  $u$  of  $v$ , and will construct the subgraph  $G_v$ . The reduce task then runs a sequential MCE algorithm to enumerate all cliques containing  $v$  in  $G_v$ . Note that if the input is a list of edges, then the adjacency list can be constructed using a single round of MapReduce.

There are three main problems with the straightforward approach.

- I. The first is *duplication of cliques* in the results. A clique  $C$  with  $k$  vertices will be enumerated  $k$  times, once for each vertex  $v \in C$ . In earlier approaches [29, 30], this was handled using a post-processing step that eliminated duplicates. But a post-processing step has two problems; one is that it requires another communication-intensive round of MapReduce. The other is that size of intermediate output, with duplicate cliques, can be much larger than the size of the final output.
- II. The second is *redundant work* in computing cliques. The different subgraphs  $G_v$  are explored by independent reduce tasks without communication among them, and the work done to enumerate a clique of size  $k$  is repeated  $k$ -fold. This is a major source of inefficiency in parallelization. Note that even if communication were allowed between

different tasks exploring the subgraphs  $G_v$ , it is non-trivial to eliminate this redundant work in clique enumeration.

- III. The third is *load balancing*. This problem arises since the subproblems for different vertices may vastly vary in size. For example, a vertex that is a part of many maximal cliques, or a part of maximal cliques of a relatively large size, will give rise to a more computationally intensive subproblem than a vertex that is part of only a few maximal cliques. Consequently, the distribution of work across subproblems is non-uniform, sometimes to an extreme degree.

To better understand load balance, we implemented the above straightforward algorithm (modified to suppress duplicate maximal cliques) and ran it on several graphs, recording the completion time of each reduce task in each execution. We found that in a typical execution, most reduce tasks finish quickly, while only a few are left running for a long period of time. Figures 1 show the completion time of the reduce tasks when the algorithm is run on two different graphs (the wiki-talk and the as-skitter graphs; we refer the reader to Section 5 for a description of these input graphs). In each case, it can be seen that a single reduce task or a small number of reduce tasks dominate the runtime, so that the load is heavily skewed towards only a few reducers, and the total runtime is not very different from the runtime of a sequential algorithm on a single processor.

The above issues seriously limit the performance of the naive algorithm. We now discuss our approach and how it overcomes these issues.

#### 4.1. Intuition

The key to our approach is an appropriately chosen *total order* among all vertices in  $V$ . Let **rank** define a function whose domain is  $V$  and which assigns an element from some totally ordered universe to each vertex in  $V$ . For  $u, v \in V$  and  $u \neq v$ , either  $\mathbf{rank}(u) > \mathbf{rank}(v)$  or  $\mathbf{rank}(v) > \mathbf{rank}(u)$ . The function **rank** implicitly defines a total order among all vertices in  $V$ .

*Eliminating Duplicate Cliques.* Given the **rank** function, Problem I (duplicate cliques) is handled as follows. When a clique  $C$  is found by the reduce task for vertex  $v$ ,  $C$  is output

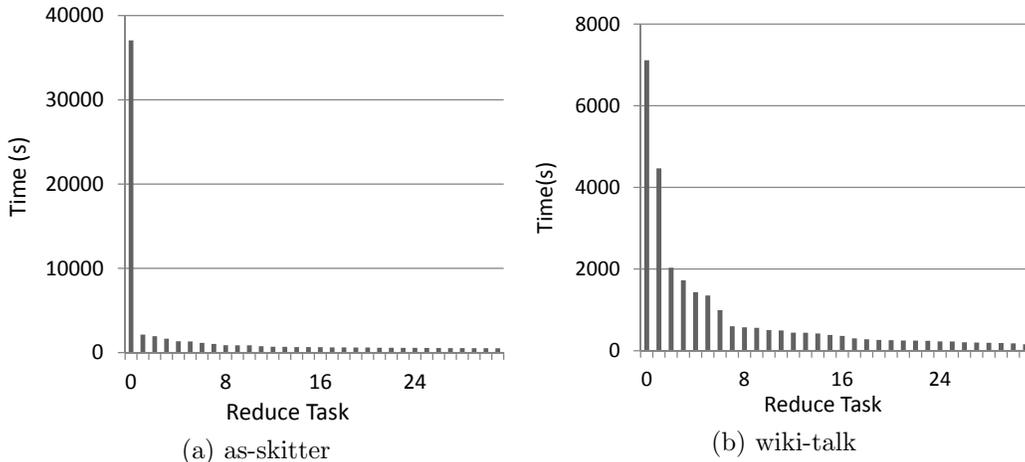


Figure 1: Completion times of reduce tasks for the naïve parallel algorithm, demonstrating poor load balancing. There is one bar for each of 32 reduce tasks, showing the time taken in seconds for the task.

only if  $\forall u \in C$ ,  $\text{rank}(v) \leq \text{rank}(u)$ . i.e.,  $v$  has the smallest rank among all vertices in  $C$ . Otherwise  $C$  is simply discarded by  $v$ . Since only one vertex satisfies this condition for each clique  $C$ , each clique will be output exactly once. This removes the need for post-processing to eliminate duplicates.

*Eliminating Redundant Work.* However, the above does not as easily solve Problem II (redundant work). Consider a clique  $C$  that has  $k$  vertices. While the above approach ensures that  $C$  is output only once, it is still computed by  $k$  different reduce tasks, and discarded by all but one of them. Eliminating this redundancy is more challenging, especially in a system such as MapReduce, since it is not possible for different reduce tasks to communicate and share state with each other. Our approach to this problem is to use the total ordering on vertices in conjunction with a modification to a sequential algorithm due to Tomita et al. [24], which will allow us to ignore search paths that involve vertices with a smaller value of  $\text{rank}$ . We discuss this further in the following sections.

*Improving Load Balance.* Let  $\sigma$  be a specific ranking function used to order vertices in  $G$ . For each vertex  $v \in V$ , there is a subproblem  $G_v$ , as defined above. Let  $\zeta_v$  denote the set of all maximal cliques in  $G_v$ . With the above approach to reducing redundant work and avoiding duplicates, the reducer responsible for vertex  $v$  (which receives  $G_v$  as an input) is

not required to enumerate all of  $\zeta_v$ . Instead the reducer for  $v$  only has to enumerate those maximal cliques  $C \in \zeta_v$  where  $v$  is the smallest vertex in  $C$  according to the total order induced by  $\sigma$ . Let  $\zeta_v(\sigma) \subseteq \zeta_v$  be the set of maximal cliques  $C$  such that  $v$  is the smallest vertex in  $C$  according to  $\sigma$ ;  $\zeta_v(\sigma)$  is the set of maximal cliques that are required to be enumerated from the subproblem  $G_v$ . A key observation is that we can tailor our sequential algorithm for subproblem  $G_v$  such that it is able to avoid the work done to enumerate cliques that are in  $\zeta_v$  but not in  $\zeta_v(\sigma)$ .

As a result of this, the computational cost of subproblem  $G_v$  depends on two factors: the number and sizes of cliques in  $\zeta_v$ , and the rank of  $v$  in the total order relative to other vertices in  $G_v$ . The higher is the rank of  $v$  in the total order, the fewer cliques in  $\zeta_v$  it is responsible for.

In deciding the **rank** function, in order to keep the sizes of subproblems approximately balanced, the intuition is to assign a high value of **rank** for a vertex  $v$  for which  $|\zeta_v|$  is large, and a small value of **rank** if  $|\zeta_v|$  is small. Therefore, we define the “ideal” total order as follows: *If  $|\zeta_u| > |\zeta_v|$  then  $u$  is ranked higher in the total order than  $v$ .* Overall, this increases the work done by vertices with a lower rank (for which the size of  $\zeta_v$  is small) and decreases the work done by vertices with a larger rank (for which the size of  $\zeta_v$  is large), resulting in a more even distribution of work. A difficulty with working with this ideal total order is that computing  $|\zeta_v|$  is an expensive task in itself. It is not reasonable to spend too much effort in computing  $|\zeta_v|$  exactly, since it is only used within an optimization. Instead, we base our ranking of vertices on metrics that are more easily computed, but provide some guidance on the number of cliques a vertex is a part of. We consider the following strategies for approximating the ordering described above.

- The Degree Ordering is defined through the following function. For vertex  $v$ ,  $\mathbf{rank}(v) = (d, v)$ , where  $d$  is the degree of  $v$ , and  $v$  the vertex identifier. Given two distinct vertices  $v_1$  and  $v_2$ , and their ranks  $\mathbf{rank}(v_1) = (d_1, v_1)$  and  $\mathbf{rank}(v_2) = (d_2, v_2)$ :  $\mathbf{rank}(v_1) > \mathbf{rank}(v_2)$  if either  $d_1 > d_2$ , or if  $d_1 = d_2$  and  $v_1 > v_2$ ; otherwise,  $\mathbf{rank}(v_1) < \mathbf{rank}(v_2)$ . Given two vertices, it is easy to evaluate their relative position in the total order, since

the degree of each vertex is readily available as the size of the neighbor list of the vertex. One can expect that the higher the degree of  $v$ , the larger is the size of  $\zeta_v$ , though this may not always be true.

- The **Triangle Ordering** is defined as  $\mathbf{rank}(v) = (t, v)$ , where  $t$  is the number of triangles (cliques of size 3) the vertex is a part of, and  $v$  is the vertex id. The relative ordering among tuples is defined the same way as in the degree ordering.

When compared with the degree ordering, the triangle ordering can be expected to produce a total order that is closer to the ordering produced through the use of  $|\zeta_v|$ . Hence, it has the advantage that it can be expected to yield better load balance. However, it has the downside that it is an additional overhead to count the number of triangles that a vertex is a part of (another MapReduce task).

We also consider two other simple ordering strategies that are agnostic of the number of cliques a vertex is a part of.

- The **Lexicographic Ordering** is defined as  $\mathbf{rank}(v) = v$ . It is assumed that the vertex ids themselves are unique and are chosen from a totally ordered set.
- The **Random Ordering** is defined as  $\mathbf{rank}(v) = (r, v)$ , where  $r$  is a random number between 0 and 1, and  $v$  is the vertex id. Note that  $r$  is the most significant set of bits, with  $v$  only used as a tiebreaker in the event the  $r$  values of two vertices are equivalent.

#### 4.2. Tomita et al. Sequential MCE Algorithm

*PECO* uses the Tomita *et al.* sequential maximal clique enumeration algorithm (TTT) [24]. The algorithm has a running time of  $O(3^{\frac{n}{3}})$ , which is worst case optimal, due to known lower bounds [32]. Although only guaranteed to be optimal in the worst case, in practice, it is found to be one of the fastest on typical inputs. We present a brief description of the TTT algorithm here.

TTT is based on the Bron-Kerbosch depth first search algorithm [16]. Algorithm 1 shows the **Tomita** recursive function. The function takes as parameters a graph  $G$  and the sets  $K$ ,

**Cand**, and **Fini**.  $K$  is a clique (not necessarily maximal), which the function will extend to a larger clique if possible. **Cand** is the set  $\{u \in V : u \in \Gamma(v), \forall v \in K\}$ , or simply  $u \in \mathbf{Cand}$  must be a neighbor of every  $v \in K$ . Therefore, any vertex in **Cand** could be added to  $K$  to make a larger clique. **Fini** contains all the vertices which were previously in **Cand** and have already been used to extend the clique  $K$ .

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**Algorithm 1:** Tomita( $G, K, \mathbf{Cand}, \mathbf{Fini}$ )

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**Input:**  $G$  - a graph  
 $K$  - a non-maximal clique to extend  
**Cand** - the set of vertices that could be used to extend  $K$   
**Fini** - the set of vertices previously used to extend  $K$

- 1 **if** ( $\mathbf{Cand} = \emptyset$ ) & ( $\mathbf{Fini} = \emptyset$ ) **then**
- 2     report  $K$  as maximal
- 3     return
- 4 **pivot**  $\leftarrow u \in \mathbf{Cand} \cup \mathbf{Fini}$  that maximizes the intersection  $\mathbf{Cand} \cap \Gamma(u)$
- 5 **Ext**  $\leftarrow \mathbf{Cand} - \Gamma(\mathbf{pivot})$
- 6 **for**  $q \in \mathbf{Ext}$  **do**
- 7      $K_q \leftarrow K \cup \{q\}$
- 8      $\mathbf{Cand}_q \leftarrow \mathbf{Cand} \cap \Gamma(q)$
- 9      $\mathbf{Fini}_q \leftarrow \mathbf{Fini} \cap \Gamma(q)$
- 10    Tomita( $G, K_q, \mathbf{Cand}_q, \mathbf{Fini}_q$ )
- 11     $\mathbf{Cand} \leftarrow \mathbf{Cand} - \{q\}$
- 12     $\mathbf{Fini} \leftarrow \mathbf{Fini} \cup \{q\}$
- 13     $K \leftarrow K - \{q\}$

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The base case for the recursion occurs when **Cand** is empty. If **Fini** is also empty, then  $K$  is a maximal clique. If not, then a vertex from **Fini** could be added to  $K$  to form a larger clique. However, each vertex in **Fini** has already been explored, adding it would re-explore a previously searched path. Therefore, if **Fini** is non-empty, the function returns without reporting  $K$  as maximal. Otherwise, at each level of the recursion, a  $u \in \mathbf{Cand} \cup \mathbf{Fini}$  with the property that it maximizes the size of  $\Gamma(u) \cap \mathbf{Cand}$  is selected to be the **pivot** vertex. The set **Ext** is formed by removing  $\Gamma(\mathbf{pivot})$  from **Cand**. Each  $q \in \mathbf{Ext}$  is used to extend the current clique  $K$  by adding  $q$  to  $K$  and updating the **Cand** and **Fini** sets. These updated sets are then used to recursively call the function. Upon returning,  $q$  is removed from **Cand** and  $K$ , and it is added to **Fini**. This is repeated for each  $q \in \mathbf{Ext}$ .

Using the vertices from `Ext` instead of `Cand` to extend the clique prunes paths from the search tree that will not lead to new maximal cliques. The vertices in  $\Gamma(\text{pivot})$  can be ignored at this level of recursion as they will be considered for extension when processing the recursive call for  $K \cup \{\text{pivot}\}$  (for a proof see [24]).

One of the key points to note about the TTT algorithm is that *no cliques which contain a vertex in `Fin` will be enumerated by the function*. *PECO* uses this to avoid duplicate enumeration of cliques across reduce tasks.

#### 4.3. *PECO: Parallel Enumeration of Cliques using Ordering*

We now provide details of our algorithm. It is assumed that the input is an undirected graph  $G$  stored as an adjacency list. For each vertex  $u$ , the adjacency list contains the list of vertices adjacent to  $u$ . If the input is instead presented as a list of edges, it can be converted into an adjacency list by a single, relatively inexpensive round of Map and Reduce.

Our algorithm consists of a single round of Map and Reduce. Algorithm 2 describes the `map` function of *PECO*. The function takes as input a single line of the adjacency list. Upon reading a vertex  $v$  and  $\Gamma(v)$ , it sends  $\langle v, \Gamma(v) \rangle$  to each neighbor of  $v$ . This information is enough for the reducer for vertex  $v$  to construct the graph  $G_v$ .

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#### **Algorithm 2:** PECO Map(key, value)

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**Input:** `key` - line number of input file  
`value` - an adjacency list entry of the form  $\langle v, \Gamma(v) \rangle$

- 1  $v \leftarrow$  first vertex in `value`
- 2  $\Gamma(v) \leftarrow$  remaining vertices in `value`
- 3 **for**  $u \in \Gamma(v)$  **do**
- 4     `emit`( $u, \langle v, \Gamma(v) \rangle$ )

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Algorithm 3 describes the `reduce` function of *PECO*. The reduce task for vertex  $v$  receives as input the adjacency list entry for each  $u \in \Gamma(v)$ , and constructs the induced subgraph  $G_v$ . Depending on the ordering selected, the total ordering among vertices in  $G_v$  is determined (note that in some cases, generating this total order may itself take an additional MapReduce computation, but this does not change the essence of the algorithm). The reduce task then

creates the three sets needed to run **Tomita**:  $K$ , the current (not necessarily maximal) clique to extend, begins as  $\{v\}$ , since this task is only required to output cliques that contain  $v$ .

Let  $L(v)$  denote the set  $\{u \in \Gamma(v) \mid \text{rank}(u) < \text{rank}(v)\}$ . Note that the reduce task for  $v$  should not output any maximal clique that contains a vertex from  $L(v)$ . One way to do this is to enumerate all maximal cliques in  $G_v$ , and filter out those that contain a vertex from  $L(v)$ . But this can be expensive, and leads to redundant work, as described in [II] above.

Our approach is to add the entire set of vertices in  $L(v)$  to the **Fini** set, so that **Tomita** will not search for maximal cliques that contain a vertex from  $L(v)$ . A subtle point here is that it is not correct to simply delete the vertices  $L(v)$  from  $G_v$  and search the residual graph, since this will lead to the enumeration of cliques that may not be maximal in  $G_v$ , and hence not maximal in  $G$ . These steps are described in lines 6-11 of the algorithm below.

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**Algorithm 3:** PECO Reduce( $v, \text{list}(\text{value})$ )

---

**Input:**  $v$  - enumerate cliques containing this vertex  
 $\text{list}(\text{value})$  - adjacency list entries for each  $u \in \Gamma(v)$

- 1  $G_v \leftarrow$  induced subgraph on vertex set  $v \cup \Gamma(v)$
- 2  $\text{rank} \leftarrow$  generated according to ordering selected
- 3  $K \leftarrow \{v\}$
- 4  $\text{Cand} \leftarrow \Gamma(v)$
- 5  $\text{Fini} \leftarrow \{ \}$
- 6 **for**  $u \in \Gamma(v)$  **do**
- 7     **if**  $\text{rank}(u) < \text{rank}(v)$  **then**
- 8          $\text{Cand} \leftarrow \text{Cand} - \{u\}$
- 9          $\text{Fini} \leftarrow \text{Fini} \cup \{u\}$
- 10 **Tomita**( $G_v, K, \text{Cand}, \text{Fini}$ )

---

#### 4.4. Correctness

We first note that it is easy to verify that the *PECO* map function (Algorithm 2) correctly sends  $G_v$  to the reduce task responsible for processing vertex  $v$ .

**Claim 4.1.** *The reduce function for vertex  $v$  (algorithm 3) enumerates every maximal clique  $C$  such that (1)  $v$  is contained in  $C$  and (2) For every vertex  $u \in C$ ,  $\text{rank}(v) \leq \text{rank}(u)$ . Further, no other maximal clique is enumerated by the reduce function for  $v$ .*

*Proof.* Note that  $G_v$  and a consistent total order on vertices are correctly received as input by the reducer for  $v$ . Let  $C$  be a maximal clique that satisfies the above two conditions. Since  $v \in C$ , the subgraph  $G_v$  will contain  $C$ . The `if` statement in line 7 will never evaluate to true for  $u \in C$  since  $v$  is the smallest vertex in  $C$ . Thus, every vertex in  $C$  will be in the `Cand` set when a call to `Tomita` is made. As a result,  $v$  will enumerate  $C$ , due to the correctness of the `Tomita` algorithm. Similarly, it is possible to show that no other maximal clique is output by this reduce function.  $\square$

**Claim 4.2.** *PECO (1) Outputs every maximal clique in  $G$ . (2) Does not output the same clique more than once. (3) Does not output a non-maximal clique.*

*Proof.* For (1) and (2). Let  $\zeta$  be the set of all maximal cliques in  $G$ . Consider  $C \in \zeta$ . From Claim 4.1,  $C$  is output once by the reducer for vertex  $v$  such that  $V$  is ranked earliest in the total order among all vertices in  $C$ . Further,  $C$  is not output by the reducer for any other vertex.

For (3). The reduce task for  $v$  has  $G_v$ , the subgraph induced by  $\{v\} \cup \Gamma(v)$ , and outputs all maximal cliques in this subgraph. Consider one such output clique, say  $C$ ; we claim that  $C$  is also maximal in  $G$ . The proof is by contradiction; suppose that  $C$  was not maximal in  $G$ . Then there is a vertex  $w \notin C$  that is adjacent to every vertex in  $C$ . Then vertex  $w \in \Gamma(v)$ , and hence  $w$  is also present in  $G_v$ . This implies that  $C$  is not maximal in  $G_v$ , which is a contradiction.  $\square$

#### 4.5. Analysis

We analyze the communication and memory costs of the algorithm.

*Communication.* The communication cost is equal to the amount of data output by the map tasks, since this data must be sent across the network to the corresponding reduce tasks. Examining the *PECO* map function, it is clear that the adjacency list entry for vertex  $v$  will be sent to each vertex in  $\Gamma(v)$ . Let  $\deg(v)$  denote the degree of  $v$ . The communication cost due to transmitting the neighbor list of  $v$  is proportional to  $(\deg(v))^2$ . Hence the total communication cost is:

$$\text{Comm. Cost} = \Theta \left( \sum_{v \in V} (\text{deg}(v))^2 \right) \quad (1)$$

One way to reduce communication costs is to divide the graph into fewer subgraphs. In contrast with the current method, which makes as many subproblems as the number of vertices, it is possible to divide the graph into fewer overlapping subgraphs, and still apply a similar technique for each individual subgraph, involving ordering of vertices. This will lead to lesser communication; for instance, if there is only one subproblem, then the total communication is of the order of the number of edges in the graph. We tried this approach of having fewer subproblems. But there were two issues with this approach: (1) the load balance was worse, and (2) there is a higher overhead to construct the vertex ordering. Overall, it performed much worse than our current algorithm.

*Memory.* The map function is trivial, and uses memory equal to the size of a single adjacency list entry, which is of the order of the maximum degree of a vertex in the graph. The reduce function for vertex  $v$  requires space equal to the size of the induced subgraph  $G_v$ . In the worst case,  $G_v$  can be as large as the input graph, if there is a single vertex that is connected to all other vertices. Fortunately, such cases seldom occur with large graphs, and in typical cases,  $G_v$  is much smaller.

## 5. Experiments

We ran experiments measuring the performance of *PECO* on a Hadoop cluster. The experiments used real-world graphs from the Stanford large graph database [40], as well as synthetic random graphs generated according to the Erdős-Rényi model. The test graphs used are given in Table 1 along with some basic properties. The soc-sign-epinion [2], soc-epinion [41], loc-gowalla [42], and soc-slashdot0902 [1] graphs are social networks, where vertices represent users and edges represent friendships. cit-patents [43] is a citation graph for U.S. patents granted between 1975 and 1999. In the wiki-talk graph [2] vertices represent users and edges represent edits to other users' talk pages. web-google [1] is a web graph

with pages represented by vertices and hyperlinks by edges. The as-skitter graph [44] is an internet routing topology graph collected from a year of daily traceroutes. For the purpose of clique enumeration, these graphs are all treated as undirected graphs. The wiki-talk-3 and as-skitter-3 graphs are the wiki-talk and as-skitter graphs, respectively, with all vertices of degree less than or equal to 2 removed. Two random graphs are also used in the experiments. UG100k.003 is a random graph with 100,000 vertices and a probability of 0.003 of an edge being present, while UG1k.3 has 1,000 vertices and a probability of 0.3. Table 2 shows the maximum and average size of the enumerated cliques for every input graph.

The experiments were run on a Hadoop [15, 45, 46] cluster with 62 HP DL160 compute nodes each with dual quad core CPUs and 16GB of RAM. Hadoop was configured to use multiple cores so that multiple map or reduce tasks can run in parallel on a single compute node. Note that each reduce task only runs on a single core, so that when we say “10 reduce tasks”, the total degree of parallelism (number of cores) in the reduce step is 10. The number of map / reduce tasks that can run on a single compute node can be configured by setting appropriate parameters.

Graph	# vertices	# edges	# cliques	Max degree	Avg degree
soc-sign-epinion	131,580	711,210	22,067,495	3,558	10.8
loc-Gowalla	196,591	950,327	1,005,048	14,730	9.6
soc-slashdot0902	82,168	504,231	642,132	2,552	12.3
soc-Epinions	75,879	405,746	1,681,235	3,044	10.7
web-google	875,713	4,322,051	939,059	6,332	9.9
cit-Patents	3,774,768	16,518,947	6,061,991	793	8.8
wiki-talk	2,294,385	4,659,565	83,355,058	100,029	3.9
wiki-talk-3	626,749	2,894,276	83,355,058	46,257	9.2
as-skitter	1,696,415	11,095,298	35,102,548	35,455	13.1
as-skitter-3	1,478,016	10,877,499	35,102,548	35,455	14.7
UG100k.003	100,000	14,997,901	4,488,632	380	300
UG1k.30	1,000	149,851	15,112,753	349	299.7

Table 1: Statistics of Test Graphs

Graph	Maximum size of a clique	Average size of a clique
soc-sign-epinion	94	22.7
loc-gowalla	29	7.4
soc-slashdot0902	27	12.3
soc-epinions	23	9
web-google	44	5.7
cit-patent	11	4.2
wiki-talk-3	26	13.8
as-skitter-3	67	21.1
UG100k.003	4	3
UG1k.30	10	5.8

Table 2: Clique Statistics of Test Graphs

### 5.1. Comparison of Ordering Strategies

In order to compare different ordering strategies, each was run on the set of test graphs. To limit the focus to the quality of the orderings produced, the runtimes of different reduce tasks are examined first, ignoring the map and shuffle phases. The different strategies do not vary in their map functions and limiting the focus to only the reduce task will remove the impact of network traffic on the running times. Table 3 shows the completion time of the longest running reduce task for each graph and ordering strategy.

Graph	Degree	Triangle	Random	Lex.
soc-sign-epinions	800	784	1843	1615
loc-gowalla	36	29	45	130
soc-slashdot0902	16	16	23	32
soc-epinions	25	21	32	41
web-google	70	65	86	79
cit-patent	64	59	64	63
wiki-talk-3	823	610	2999	7113
as-skitter-3	2091	2326	14009	> 37052
UG100k.003	226	223	238	269
UG1k.3	103	101	98	107

Table 3: Completion time (seconds) of the longest reduce task for the combinations of graphs and ordering strategies. “Lex” stands for Lexicographic ordering.

It is clear from Table 3 that the degree and triangle orderings are superior to the other two strategies, in their overall impact on the reduce times. This is particularly evident on the

more challenging graphs such as soc-sign-epinions, wiki-talk-3, and as-skitter-3 where these orderings see a reduction in time of over 50% when compared to the random or lexicographic orderings.

We note that for graphs where different vertex neighborhoods have a similar structure to each other, the ordering strategy does not matter much. For example, the UG1k.3 graph is a Erdos-Renyi random graph, where different vertices have similar neighborhoods. On such graphs, different subproblems are already of a similar size, and such a graph leads similar reducer runtimes, irrespective of the ordering used. However, on graphs where different neighborhoods are unbalanced, the advantage of the degree and triangle orderings are clear. For example, in the soc-sign-epinions graph, degree and triangle orderings perform much better than lexicographic and random orderings. This graph has different neighborhoods that are unbalanced; to see this, note that the maximum vertex degree is 3558 while the average degree is only 10.8. A similar behavior is observed with the loc-Gowalla graph.

Table 4 shows the total run time of the algorithm, (i.e. the total time from start to finish, including all map, shuffle, and reduce phases) for each ordering strategy.

Graph	# Reducers	Degree	Triangle	Random	Lex.
soc-sign-epinions	8	840	828	1875	1646
loc-gowalla	8	122	112	211	280
soc-slashdot0902	8	45	50	52	64
soc-epinions	8	55	53	62	70
web-google	8	126	168	144	140
cit-patent	8	113	150	111	109
wiki-talk-3	32	10667	20465	12229	16647
as-skitter-3	32	8140	17659	20588	> 37052
UG100k.003	8	353	503	376	421
UG1k.3	16	135	129	135	136

Table 4: Total running times (seconds) for different combinations of graphs and ordering strategies. “Lex” stands for Lexicographic ordering.

When the pre-processing step is also considered, the triangle ordering no longer performs as well as the degree ordering. This is most evident in the wiki-talk-3 and as-skitter-3 completion times, where the map and shuffle phase contribute to a large portion of the total

time. As a result, the degree ordering sees the lowest total running times.

### 5.2. Load balancing

We now present results on the load balancing behavior of different ordering strategies. Figure 2 shows the completion times of different reduce tasks for the degree ordering and the lexicographic ordering on the soc-sign-epinion and loc-gowalla graphs, and Figure 3 shows the number of maximal cliques enumerated by different reducers, for the degree ordering and the lexicographic ordering strategies. For both sets of experiments, we used 8 reducers.

It is clear that the distribution of work has better load balance with the degree ordering than with lexicographic ordering. For instance, for the soc-sign-epinion graph (Figure 3a) we see that reducer 1 emits about 5 million maximal cliques for lexicographical ordering whereas reducer 8 emits less than 500 thousand maximal cliques, only one tenth of the number that reducer 1 emitted. Similarly, for the loc-gowalla graph (Figure 3b) with lexicographical ordering, we note that reducer 1 emits approximately 325 thousand maximal cliques whereas reducer 8 emits only about 70 thousand maximal cliques. Such large differences are not observed when degree ordering is used. A similar behavior is observed in Figure 2, which shows that the runtimes of different reducers varies widely for the lexicographic ordering strategy but it relatively even for the degree ordering strategy.

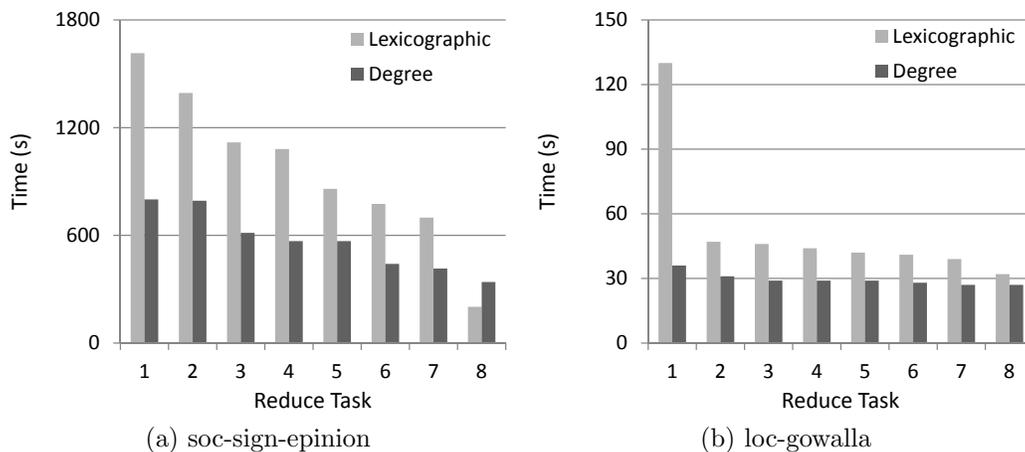


Figure 2: A comparison of reduce task completion times between the lexicographic ordering and degree ordering on the soc-sign-epinion and loc-gowalla graphs.

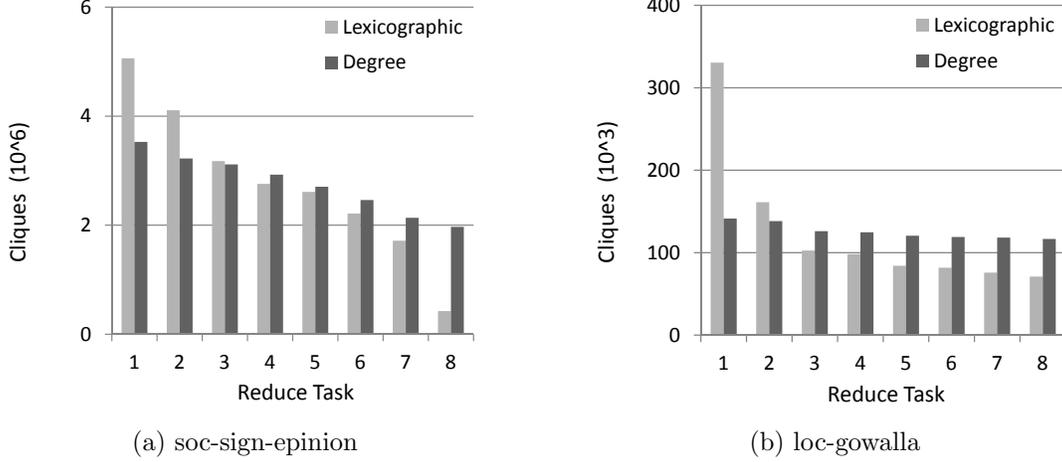


Figure 3: A comparison of the total number of maximal cliques emitted by each reducer for the lexicographic ordering and degree ordering on the soc-sign-epinion and loc-gowalla graphs.

Interestingly, degree ordering also leads to a decrease in the total runtime when compared with lexicographic ordering. So the decrease in runtime is a result of two factors, better load balancing and reduced total work. To evaluate the impact of the two factors, we propose the following measures. The total work for ordering strategy `order` is defined as  $T(\text{order}) = \sum_{i=1}^{\#\text{Tasks}} t_i$ , where  $t_i$  is the time taken by reducer  $i$ .

To measure load balancing, the first step is to normalize the reduce task running times to determine the proportion of the overall work that each task is responsible for. For reduce task  $i$ , let  $P_i(\text{order})$  represent the proportion of overall work  $i$  is responsible for when applying ordering `order`, i.e.  $P_i(\text{order}) = \frac{t_i}{T(\text{order})}$ , and further for each task  $i$ , we define  $P(\text{order}) = \{P_i(\text{order})\}$ . Then, one way to measure the load balance of an ordering is by the standard deviation of  $P(\text{order})$ . Let,  $L(\text{order})$  be the load balance of an ordering, defined as:  $L(\text{order}) = \text{stdev}(P(\text{order}))$ . Thus, two orderings may have the same load balance but differ in total runtime, because they differ in total work. Alternatively, two orderings may have the same total work, but differ in total runtime, because they differ in load balance.

Table 4 shows  $T$  and  $L$  for the degree and lexicographic orderings on the soc-sign-epinions graph. Comparing  $T(\text{deg})$  and  $T(\text{lex})$ , it is evident that there is a reduction in enumeration time from lexicographic to degree. Similarly, the degree ordering has a smaller  $L$  value than

lexicographic, indicating a better load balance. Overall, our finding was that on the soc-sign-epinions graph, the degree ordering significantly improves both load balance and enumeration time when compared to the lexicographic ordering. On graph UG1k.3 an improvement is seen in enumeration time, but not in load balancing.

Task	$t_i(\text{deg})$	$P_i(\text{deg})$
0	646	0.18
1	602	0.17
2	454	0.13
3	442	0.12
4	396	0.11
5	382	0.11
6	348	0.10
7	330	0.09
$T, L$	3600	0.03

(a) Degree Ordering

Task	$t_i(\text{lex})$	$P_i(\text{lex})$
0	1210	0.20
1	1081	0.17
2	1010	0.16
3	940	0.15
4	730	0.12
5	643	0.10
6	387	0.16
7	180	0.03
$T, L$	6181	0.05

(b) Lexicographic Ordering

Figure 4: Load balancing and time reduction statistics for the soc-sign-epinions graph.

### 5.3. Scalability with Number of Processors

We now present results from experiments on the scalability of *PECO* with increasing numbers of processors. *PECO* is run on several graphs using 1, 2, 4, 8, 16, 32, and 64 reduce tasks. Figures 5a and 5c show the speedup of the reduce step on the soc-sign-epinions and web-google graphs, respectively. Both graphs show good speedup, with the web-google graph achieving a speedup up of 42 on 64 reduce tasks. Figure 5b and 5d show the speedup for the two graphs when considering the entire job time. The soc-sign-epinions graph sees little change from the reduce task only graph, as communication costs contribute little to the overall running time. However, the web-google graph sees a larger impact, as the communication cost makes up a larger portion of the total run time.

The soc-sign-epinions and web-google graphs are relatively small when compared to the as-skitter graph. In order to better examine the scalability of both the communication and enumeration aspects of the algorithm, the speedup of the degree ordering is examined on the as-skitter-3 graph. Figure 6a shows the speedup of just the reduce tasks. A speedup of

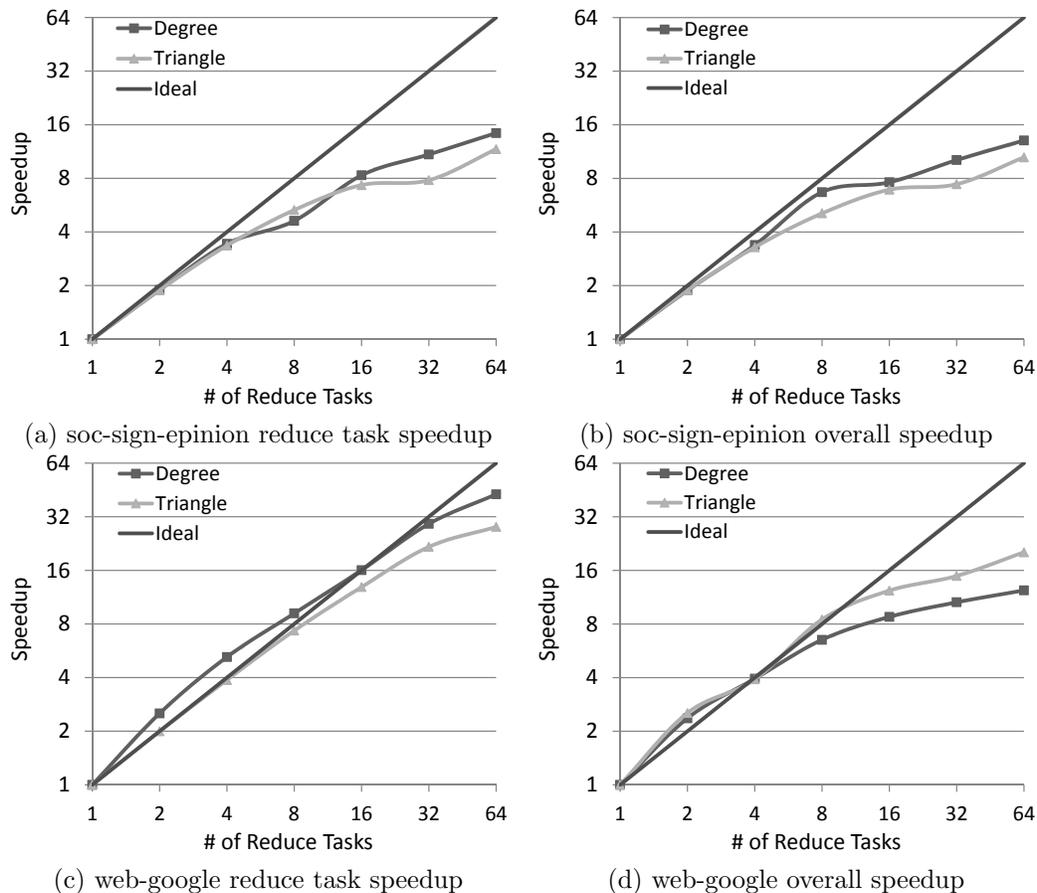


Figure 5: *PECO* scalability for the degree and triangle ordering strategies.

22 with 64 reduce tasks is achieved. When the running time of the entire job is considered (Figure 6b), the speedup increases slightly to 24, demonstrating that the communication aspect of the algorithm scales well on large graphs. Figure 6c compares the completion times of the reduce phase to those of the overall running time.

#### 5.4. Comparison with Prior Work

We implemented the WYZW Algorithm, a parallel algorithm for MCE designed for MapReduce due to Wu *et al.* [29], and compared its performance with that of *PECO*. The WYZW Algorithm divides the input graph into many subgraphs and independently processes each subgraph to enumerate cliques. This can emit non-maximal cliques which have to be filtered away by an additional post-processing step. For these experiments, we used a smaller Hadoop cluster with 50 compute nodes, each a Quad-Core AMD Opteron(tm)

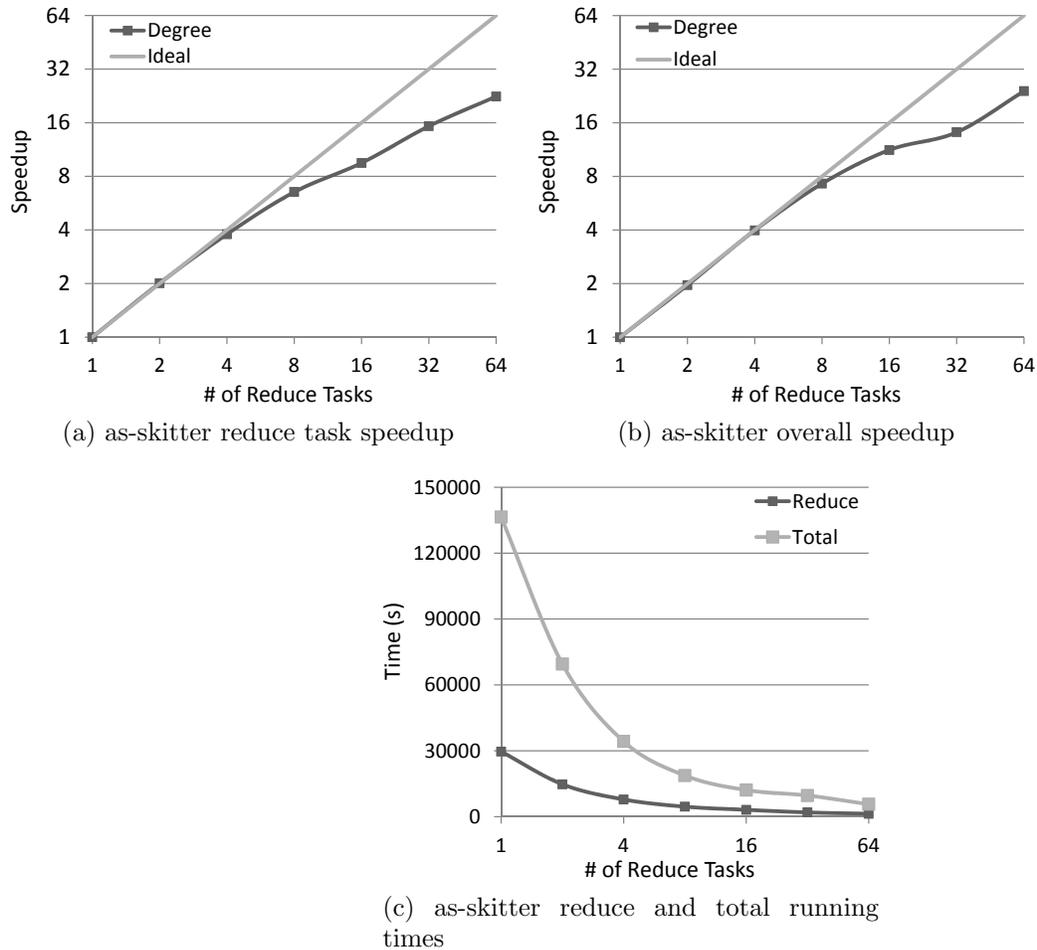


Figure 6: *PECO* large graph scalability

Processor 2354 and 8 GB of RAM.

Figure 7 shows the runtimes of *PECO* and *WYZW* when the number of reducers vary from 20 till 120. On the soc-epinions graph with 120 reducers, *PECO* runs approximately 127 times faster than *WYZW*, while it is about 42 times faster on 20 reducers, while using the same underlying sequential algorithm for both *WYZW* and *PECO*. The advantage of *PECO* over *WYZW* increases with the degree of parallelism (number of reducers). One of the reasons for this is the better load balancing of *PECO*, which allows it to use more processors more effectively. With *WYZW*, there were a few reducers that ran for a long time while the others finished quickly, and the runtime did not get significantly better as the number of reducers was increased.

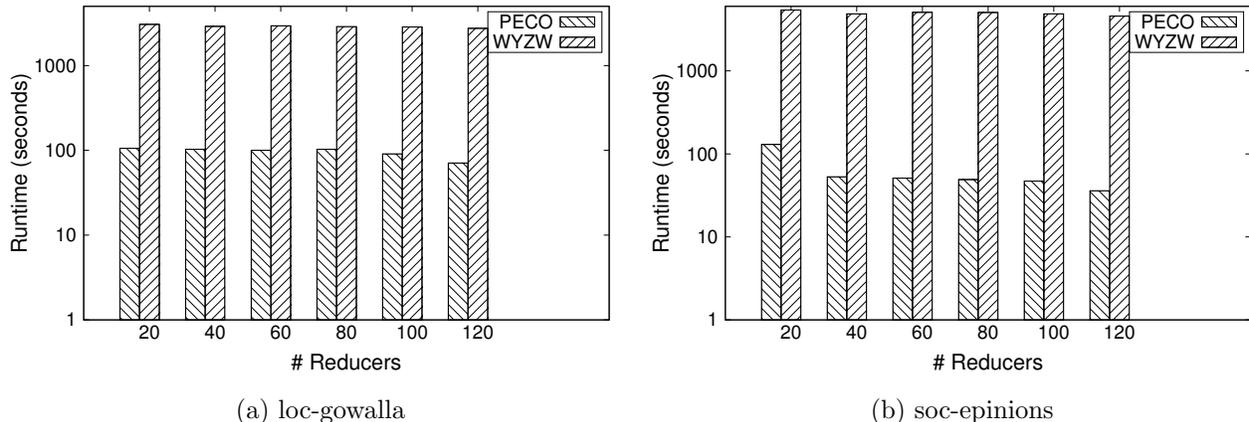


Figure 7: Runtime analysis of *PECO* vs *WYZW* for different reducer values on various input graphs. Note that the plot is in logarithmic scale.

A similar result was observed with the loc-gowalla graph (see Figure 7). Using 120 reducers, other input graphs that were processed by *PECO* include web-google (58 sec for *PECO*), wiki-talk-3 (1013 sec), and as-skitter3 (5930 sec). But none of these were completed by *WYZW* within 6 hours.

## 6. CONCLUSION

MCE is an important primitive in mining dense substructures from a graph, with many applications. As a result, sequential enumeration algorithms have been heavily studied. However, as graph sizes have continued to increase, sequential algorithms are no longer sufficient, and a need for parallel algorithms has arisen.

We presented *PECO*, a novel parallel algorithm for MCE. *PECO* addresses three key issues with parallelizing MCE, load balancing, eliminating redundant work, and eliminating the need for a post processing step. The parallel algorithm uses an appropriately constructed total ordering over the vertices in conjunction with a sequential MCE algorithm; the ordering is used to not only decide which cliques to enumerate within each task, but also to eliminate redundant search paths within the enumeration search tree in the task. By making the ordering sensitive to the size and complexity of the subgraph assigned to the task, the algorithm improves load balancing. Previous works require post-processing steps to remove

duplicate and non-maximal cliques, and do not address the issue of load balancing.

Experiments performed on large real world graphs demonstrate that *PECO* can enumerate cliques in graphs with millions of edges and scales well with the number of processors. A comparison of ordering strategies showed that orderings based on vertex degree and number of triangles perform the best, reducing both enumeration time and improving load balancing.

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## References

- [1] J. Leskovec, K. J. Lang, A. Dasgupta, M. W. Mahoney, Community structure in large networks: Natural cluster sizes and the absence of large well-defined clusters, *Internet Mathematics* 6 (1) (2009) 29–123.
- [2] J. Leskovec, D. Huttenlocher, J. Kleinberg, Signed networks in social media, in: *Proceedings of the 28th international conference on Human factors in computing systems, CHI '10*, ACM, 2010, pp. 1361–1370.
- [3] G. Palla, I. Dernyi, I. Farkas, T. Vicsek, Uncovering the overlapping community structure of complex networks in nature and society., *Nature* 435 (7043) (2005) 814–818.
- [4] O. Rokhlenko, Y. Wexler, Z. Yakhini, Similarities and differences of gene expression in yeast stress conditions, *Bioinformatics* 23 (2) (2007) e184–e190.
- [5] E. Harley, A. Bonner, Uniform integration of genome mapping data using intersection graphs, *Bioinformatics* 17 (6) (2001) 487–494.

- [6] Y. Chen, G. M. Crippen, A novel approach to structural alignment using realistic structural and environmental information, *Protein Science* 14 (12) (2005) 2935–2946.
- [7] H. M. Grindley, P. J. Artymiuk, D. W. Rice, P. Willett, Identification of tertiary structure resemblance in proteins using a maximal common subgraph isomorphism algorithm, *Journal of Molecular Biology* 229 (3) (1993) 707–721.
- [8] P. F. Jonsson, P. A. Bates, Global topological features of cancer proteins in the human interactome, *Bioinformatics* 22 (18) (2006) 2291–2297.
- [9] S. Mohseni-Zadeh, P. Brzellec, J.-L. Risler, Cluster-c, an algorithm for the large-scale clustering of protein sequences based on the extraction of maximal cliques, *Computational Biology and Chemistry* 28 (3) (2004) 211–218.
- [10] B. Zhang, B.-H. Park, T. Karpinets, N. F. Samatova, From pull-down data to protein interaction networks and complexes with biological relevance, *Bioinformatics* 24 (7) (2008) 979–986.
- [11] M. Hattori, Y. Okuno, S. Goto, M. Kanehisa, Development of a chemical structure comparison method for integrated analysis of chemical and genomic information in the metabolic pathways, *Journal of the American Chemical Society* 125 (39) (2003) 11853–11865.
- [12] M. J. Zaki, S. Parthasarathy, M. Ogihara, W. Li, New algorithms for fast discovery of association rules, in: *In 3rd Intl. Conf. on Knowledge Discovery and Data Mining*, AAAI Press, 1997, pp. 283–286.
- [13] J. Dean, S. Ghemawat, Mapreduce: simplified data processing on large clusters, in: *Proceedings of the 6th conference on Symposium on Operating Systems Design & Implementation - Volume 6*, USENIX Association, 2004, pp. 10–10.
- [14] J. Dean, S. Ghemawat, Mapreduce: simplified data processing on large clusters, *Communications of the ACM* 51 (2008) 107–113.

- [15] Hadoop, <http://hadoop.apache.org/>.
- [16] C. Bron, J. Kerbosch, Algorithm 457: finding all cliques of an undirected graph, *Commun. ACM* 16 (1973) 575–577.
- [17] F. Cazals, C. Karande, A note on the problem of reporting maximal cliques, *Theoretical Computer Science* 407 (1-3) (2008) 564–568.
- [18] N. Chiba, T. Nishizeki, Arboricity and subgraph listing algorithms, *SIAM J. Comput.* 14 (1985) 210–223.
- [19] E. Lawler, J. Lenstra, A. R. Kan, Generating all maximal independent sets: Np-hardness and polynomial-time algorithms, *SIAM Journal of Computing* 9.
- [20] D. Eppstein, M. Löffler, D. Strash, Listing all maximal cliques in sparse graphs in near-optimal time, in: *Algorithms and Computation*, Vol. 6506 of *Lecture Notes in Computer Science*, Springer Berlin / Heidelberg, 2010, pp. 403–414.
- [21] Ina, Koch, Enumerating all connected maximal common subgraphs in two graphs, *Theoretical Computer Science* 250 (1-2) (2001) 1–30.
- [22] D. S. Johnson, M. Yannakakis, C. H. Papadimitriou, On generating all maximal independent sets, *Information Processing Letters* 27 (3) (1988) 119–123.
- [23] K. Makino, T. Uno, New algorithms for enumerating all maximal cliques, in: *Algorithm Theory - SWAT 2004*, Vol. 3111 of *Lecture Notes in Computer Science*, Springer Berlin / Heidelberg, 2004, pp. 260–272.
- [24] E. Tomita, A. Tanaka, H. Takahashi, The worst-case time complexity for generating all maximal cliques and computational experiments, *Theor. Comput. Sci.* 363 (2006) 28–42.
- [25] S. Tsukiyama, M. Ide, H. Ariyoshi, I. Shirakawa, A new algorithm for generating all the maximal independent sets, *SIAM J. Comput.* 6 (3) (1977) 505–517.

- [26] Y. Zhang, F. Abu-Khzam, N. Baldwin, E. Chesler, M. Langston, N. Samatova, Genome-scale computational approaches to memory-intensive applications in systems biology, in: Supercomputing, 2005. Proceedings of the ACM/IEEE SC 2005 Conference, 2005, pp. 12–12.
- [27] N. Du, B. Wu, L. Xu, B. Wang, X. Pei, A parallel algorithm for enumerating all maximal cliques in complex network, in: Data Mining Workshops, 2006. ICDM Workshops 2006. Sixth IEEE International Conference on, 2006, pp. 320–324.
- [28] M. C. Schmidt, N. F. Samatova, K. Thomas, B.-H. Park, A scalable, parallel algorithm for maximal clique enumeration, *J. Parallel Distrib. Comput.* 69 (2009) 417–428.
- [29] B. Wu, S. Yang, H. Zhao, B. Wang, A distributed algorithm to enumerate all maximal cliques in mapreduce, in: Frontier of Computer Science and Technology, 2009. FCST '09. Fourth International Conference on, 2009, pp. 45–51.
- [30] L. Lu, Y. Gu, R. Grossman, dmaximalcliques: A distributed algorithm for enumerating all maximal cliques and maximal clique distribution, in: Data Mining Workshops (ICDMW), 2010 IEEE International Conference on, 2010, pp. 1320–1327.
- [31] S. Ghemawat, H. Gobiuff, S.-T. Leung, The Google File System, in: Proceedings of the 19th ACM Symposium on Operating Systems Principles, SOSP '03, ACM, 2003, pp. 29–43.
- [32] J. Moon, L. Moser, On cliques in graphs, *Israel Journal of Mathematics* 3 (1965) 23–28.
- [33] F. Kose, W. Weckwerth, T. Linke, O. Fiehn, Visualizing plant metabolomic correlation networks using clique-metabolite matrices., *Bioinformatics* 17 (12) (2001) 1198–1208.
- [34] J. Cheng, Y. Ke, A. W.-C. Fu, J. X. Yu, L. Zhu, Finding maximal cliques in massive networks by  $h^*$ -graph, in: Proceedings of the 2010 international conference on Management of data, SIGMOD '10, ACM, 2010, pp. 447–458.

- [35] N. Modani, K. Dey, Large maximal cliques enumeration in sparse graphs, in: Proceedings of the 17th ACM conference on Information and knowledge management, CIKM '08, 2008, pp. 1377–1378.
- [36] Y. Gu, R. L. Grossman, Sector and sphere: the design and implementation of a high-performance data cloud, *Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences* 367 (1897) (2009) 2429–2445.
- [37] A. Angel, N. Koudas, N. Sarkas, D. Srivastava, M. Svendsen, S. Tirthapura, Dense subgraph maintenance under streaming edge weight updates for real-time story identification, *The VLDB Journal* (2013) 1–25.
- [38] M. K. Agarwal, K. Ramamritham, M. Bhide, Real time discovery of dense clusters in highly dynamic graphs: Identifying real world events in highly dynamic environments, *PVLDB* 5 (10) (2012) 980–991.
- [39] B. Bahmani, R. Kumar, S. Vassilvitskii, Densest subgraph in streaming and mapreduce, *PVLDB* 5 (5) (2012) 454–465.
- [40] J. Leskovec, Stanford large network dataset collection, <http://snap.stanford.edu/data/index.html>, accessed 4 June 2012. Downloaded soc-Epinions1.txt.gz, Slashdot0902.txt.gz, Wiki-Talk.txt.gz, cit-Patents.txt.gz, web-Google.txt.gz, askitter.txt.gz, soc-sign-epinions.txt.gz, and loc-gowalla\_edges.txt.gz.
- [41] M. Richardson, R. Agrawal, P. Domingos, Trust management for the semantic web, in: *The Semantic Web - ISWC 2003*, Vol. 2870 of Lecture Notes in Computer Science, Springer Berlin / Heidelberg, 2003, pp. 351–368.
- [42] E. Cho, S. A. Myers, J. Leskovec, Friendship and mobility: user movement in location-based social networks, in: Proceedings of the 17th ACM SIGKDD international conference on Knowledge discovery and data mining, KDD '11, ACM, 2011, pp. 1082–1090.

- [43] B. H. Hall, A. B. Jaffe, M. Trajtenberg, The nber patent citation data file: Lessons, insights and methodological tools, Nber working papers, National Bureau of Economic Research, Inc (Oct 2001).  
URL <http://ideas.repec.org/p/nbr/nberwo/8498.html>
- [44] J. Leskovec, J. Kleinberg, C. Faloutsos, Graphs over time: densification laws, shrinking diameters and possible explanations, in: Proceedings of the eleventh ACM SIGKDD international conference on Knowledge discovery in data mining, KDD '05, ACM, 2005, pp. 177–187.
- [45] T. White, Hadoop: The Definitive Guide, O'Reilly Media, Inc., 2010.
- [46] K. Shvachko, H. Kuang, S. Radia, R. Chansler, The hadoop distributed file system, in: 2010 IEEE 26th Symposium on Mass Storage Systems and Technologies (MSST), 2010, pp. 1 –10.