2017

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**Keywords**

Algorithm design and analysis, Clustering algorithms, Social network services, Parallel algorithms, Data mining, Optimization, Proteins

**Disciplines**

Electrical and Computer Engineering

**Comments**

This is a manuscript of an article published as Mukherjee, Arko, and Srikanta Tirthapura. "Enumerating maximal bicliques from a large graph using mapreduce." IEEE Transactions on Services Computing, Volume: 10, Issue: 5, Page(s): 771 - 784, Sept.-Oct. 1 2017. 10.1109/TSC.2016.2523997. Posted with permission.

# Enumerating Maximal Bicliques from a Large Graph Using MapReduce

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**Abstract**—We consider the enumeration of maximal bipartite cliques (bicliques) from a large graph, a task central to many data mining problems arising in social network analysis and bioinformatics. We present novel parallel algorithms for the MapReduce framework, and an experimental evaluation using Hadoop MapReduce. Our algorithm is based on clustering the input graph into smaller subgraphs, followed by processing different subgraphs in parallel. Our algorithm uses two ideas that enable it to scale to large graphs: (1) the redundancy in work between different subgraph explorations is minimized through a careful pruning of the search space, and (2) the load on different reducers is balanced through a task assignment that is based on an appropriate total order among the vertices. We show theoretically that our algorithm is work optimal, i.e., it performs the same total work as its sequential counterpart. We present a detailed evaluation which shows that the algorithm scales to large graphs with millions of edges and tens of millions of maximal bicliques. To our knowledge, this is the first work on maximal biclique enumeration for graphs of this scale.

**Index Terms**—Graph mining, maximal biclique enumeration, mapreduce, hadoop, parallel algorithm, biclique

## 1 Introduction

A graph is a natural abstraction to model relationships in data, and massive graphs are ubiquitous in applications. Massive graphs have been widely used in modeling real world scenarios such as social networks (e.g., [1], [2]), information retrieval from the web (e.g., [3]), citation networks (e.g., [4]) and physical simulation and modeling (e.g., [5]). Finding patterns and insights from such data can often be reduced to mining substructures from massive graphs. We consider scalable methods for discovering densely connected subgraphs within a large graph. Mining dense substructures such as cliques, quasi-cliques, bicliques, quasi-bicliques etc. is an important and widely studied research area (see [6], [7], [8], [9]).

We focus on a fundamental dense substructure called a *biclique*. A biclique in an undirected graph $G = (V, E)$ is a pair of subsets of vertices $L \subseteq V$ and $R \subseteq V$ such that (1) $L$ and $R$ are disjoint and (2) there is an edge $(u, v) \in E$ for every $u \in L$ and $v \in R$. For instance, consider the following graph relevant to an online social network, where there are two types of vertices, users and webpages. There is an edge between a user and a webpage if the user "likes" the webpage on the social network. A biclique in this graph consists of a set of users $U$ and a set of webpages $W$ such that every user in $U$ has liked every page in $W$. Uncovering such a biclique yields a set of users who share a common interest, and is valuable for understanding and predicting the actions of users on this social network. Usually, it is useful to identify *maximal bicliques* in a graph, which are those bicliques that are not contained within any other larger bicliques. See Fig. 1 for an example. *We consider the problem of enumerating all maximal bicliques from a graph (henceforth referred to as MBE).*

Many applications in mining data from the web and online social networks have relied on biclique enumeration on an appropriately defined graph. [10] considered the "click-through" graph for the analysis of web search queries. This graph has two types of vertices, web search queries and web pages. There is an edge from a search query to every page that a user has clicked in response to the search query. MBE was used in clustering queries using the click through graph. MBE has been used by [11] in social network analysis, in detection of communities in social networks and the web by [12], [13], and in finding antagonistic communities in trust-distrust networks by [14].

In bioinformatics, MBE has been used in constructing the phylogenetic tree of life (see [15], [16], [17], [18]), in discovery and analysis of structure in protein-protein interaction networks (see [19], [20]), analysis of gene-phenotype relationships by [21], prediction of miRNA regulatory modules as described by [22], modeling of hot spots at protein interfaces by [23], and in the analysis of relationships between genotypes, lifestyles, and diseases by [24]. In other contexts, MBE has been used in Learning Context Free Grammars ([25]), finding correlations in databases ([26]), data compression ([27]), role mining in role based access control ([28]), and process operation scheduling ([29]).

However, current state of the art methods for MBE have not been shown to scale to large graphs and have the following drawbacks. First, most methods are sequential algorithms that are unable to use the power of multiple processors; there is very little work on parallel methods for MBE. For handling large graphs, it is imperative to have methods that can process a graph in parallel. Next, they have been evaluated only on relatively small graphs with a few thousand vertices and a few thousand

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*Manuscript received 13 June 2015; revised 16 Nov. 2015; accepted 25 Jan. 2016. Date of publication 3 Feb. 2016; date of current version 6 Oct. 2017. For information on obtaining reprints of this article, please send e-mail to: reprints@ieee.org, and reference the Digital Object Identifier below. Digital Object Identifier no. 10.1109/TSC.2016.2523997*

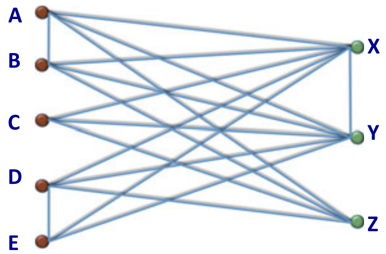



Fig. 1. Maximal bicliques.

bicliques. For instance, the popular "consensus" method for biclique enumeration by [6] presents experimental data only on random graphs of a low density with up to 2,000 vertices and a few thousand maximal cliques. Other works such as [30], [31] are similar.[1]

Our goal is to design a parallel method that can enumerate maximal bicliques in large graphs, with millions of edges and tens of millions of maximal bicliques, and which can scale with the number of processors.

### 1.1 Contributions

We present a parallel algorithm for MBE. At a high level, our algorithm clusters the input graph into overlapping subgraphs that are typically much smaller than the input graph, and processes these subgraphs using different parallel tasks. For the above cluster generation approach to be effective on large graphs, we needed to solve two problems.

The first problem is the overlap in work within different tasks. For biclique enumeration, it is usually not possible to assign disjoint subgraphs to different tasks, and subgraphs assigned to different tasks will overlap, sometimes significantly. The challenge is to ensure that work done in different tasks overlap as little as possible with each other. We accomplish this through a careful partitioning of the search space so that even if different tasks are processing overlapping subgraphs, they still explore disjoint portions of the search space.

The second problem is load balancing among different tasks. With a graph analysis task such as biclique enumeration, the complexities of different subgraphs vary significantly, roughly depending on the density of edges in the subgraph. With a naive assignment of subgraphs to tasks, this will lead to a case where most tasks finish quickly, while a few take a long time, leading to a poor parallel performance. We present a solution to keep the load more balanced, using an ordering of vertices that reduces enumeration load on subgraphs that are dense, and increases the load on subgraphs that are sparse, leading to a better load balance overall. We present two different ordering techniques to achieve this load balance, one based on the size of the neighborhood of the vertex (Algorithm CD1) and the other based on the size of the 2-neighborhood of the vertex (Algorithm CD2).

We provide a theoretical analysis of our algorithms, including proofs of correctness and analysis of computation and communication. Significantly, we show that our parallel algorithms are *work-optimal*, i.e., the total computation cost across all processors is the same as that of a sequential algorithm for MBE.

We also consider the related problem of generating only large maximal bicliques, which have at least a certain number of vertices. Our parallel algorithms can be easily adapted to this case, using appropriate changes to underlying sequential algorithms.

We also considered another approach to parallel MBE, using a direct parallelization of the "consensus" algorithm due to [6], which is probably the most commonly used sequential algorithm for MBE. We found that this method (i.e., parallelization of the consensus algorithm) takes substantially greater runtime than our clustering based method.

We design our algorithms for the MapReduce framework ([32], [33]) and implement it using Hadoop MapReduce. We present detailed experimental results on real-world and synthetic graphs. Overall, the cluster generation approach using a sequential algorithm based on depth-first-search (DFS), when combined with our pruning and load balancing optimizations, performs the best on large graphs, and provides speedups of an order of magnitude over simple approaches to parallelization. This algorithm can process graphs with millions of edges and tens of millions of maximal bicliques, and can scale out with the cluster size. To our knowledge, these are the largest reported graph instances where bicliques have been successfully enumerated.

### 1.2 Prior and Related Work

There are two general approaches to sequential algorithms for MBE, the "consensus" method due to [6], and methods based on recursive depth-first-search combined with branch-and-bound (see [30], [31], [34]).

The consensus method ([6]) is a very popular iterative algorithm for MBE. In this method, the algorithm starts off with a set of simple maximal bicliques and then expands to the set of all maximal bicliques through a sequence of repeated cross-products, as we explain in the following sections. We developed a direct parallelization of the consensus algorithm, but we found that this method performs poorly compared with our cluster generation approach; details are presented in subsequent sections.

Among the DFS based approaches, [30] presents an approach based on a connection with mining closed patterns in a transactional database and [31] present a more direct algorithm based on depth first search. Our parallel algorithm uses a sequential algorithm for processing bicliques within each task, and we considered both the consensus and the DFS based algorithms; the DFS-based algorithms ran faster overall, and it was easier to optimize the DFS based methods.

Another approach to MBE is through a reduction to the problem of enumerating maximal cliques, as described by [35]. Given a graph $G$ on which we need to enumerate maximal bicliques, a new graph $G'$ is derived such that through enumerating maximal cliques in $G'$ using an algorithm such as by [36], [37], it is possible to derive the maximal bicliques in $G$. However, this approach is not practical for large graphs since in going from $G$ to $G'$, the number of edges in the graph increases significantly.

1. In our experiments, we observed that the consensus method and the other current methods are unable to process our input graphs in a reasonable time.

Parallel algorithms for maximal clique enumeration have been proposed by [38], [39]. Like our method, these also perform optimizations in the depth first search paths to reduce redundancy. However, these optimizations are specific to the algorithm used and are different from the ones that we use. Note that the maximal clique is a structure that is more "local" than a maximal biclique in the sense that a maximal clique is present within the 1-neighborhood of a vertex in a graph while a maximal biclique goes beyond the 1-neighborhood but is contained in a 2-neighborhood of a vertex. Hence, the difficulty of obtaining an effective parallelization of MBE is higher than that of Maximal Clique Enumeration.

Makino and Uno [40] describe methods to enumerate all maximal bicliques in a *bipartite graph*, with the delay between outputting two bicliques bounded by a polynomial in the maximum degree of the graph. Zhang et al. [41] describe a branch-and-bound algorithm for the same problem. However, these approaches do not work for general graphs, as we consider here.

There is a variant of MBE where we only seek *induced* maximal bicliques in a graph. An induced maximal biclique is a maximal biclique which is also an induced subgraph. A maximal biclique $\langle L, R\rangle$ in graph $G$ is an induced maximal biclique if $L$ and $R$ are themselves independent sets in $G$. We consider the *non-induced* version, where edges are allowed in the graph between two vertices that are both in $L$, or both in $R$ (such edges are of course, not a part of the biclique). The set of maximal bicliques that we output will also contain the set of induced maximal bicliques, which can be obtained by post-processing the output of our algorithm. Note that for a bipartite graph, every maximal biclique is also an induced maximal biclique. Algorithms for Induced MBE include work by [42], [43], and [44].

To our knowledge, the only prior work on parallel algorithms for MBE is by [45]. However, this work does not explore aspects of load balancing and total work such as we do. Moreover, their evaluations are not for large graphs; the largest graph they consider has 500 vertices and about 9,000 edges. They do not present any provable properties of their algorithm. Also, their work represents the graph as an adjacency matrix in the memory, whereas we use adjacency list, which takes lesser space and is more practical for large graphs.

MBE is related to, but different from the problem of finding the largest sized biclique within a graph (maximum biclique). There are a few variants of the maximum biclique problem, including maximum edge biclique, which seeks the biclique in the graph with the largest number of edges, and maximum vertex biclique, which seeks a biclique with the largest number of edges; for further details and variants, see work by [46]. MBE is harder than finding a maximum biclique, since it enumerates all maximal bicliques, including all maximum bicliques.

## 2 Preliminaries

We present a precise problem definition and briefly review the MapReduce parallel programming model.

### 2.1 Problem Definition

We consider a simple undirected graph $G = (V, E)$ without self-loops or multiple edges, where $V$ is the set of all vertices and $E$ is the set of all edges of the graph. Let $n = |V|$ and $m = |E|$. Graph $H = (V_1, E_1)$ is said to be a sub-graph of graph $G$ if $V_1 \subset V$ and $E_1 \subset E$. $H$ is known as an induced subgraph if $E_1$ consists of all edges of $G$ that connect two vertices in $V_1$. For vertex $u \in V$, let $\eta(u)$ denote the vertices adjacent to $u$. For a set of vertices $U \subseteq V$, let $\eta(U) = \bigcup_{u\in U}\eta(u)$. For vertex $u \in V$ and $k > 0$, let $\eta^k(u)$ denote all vertices that can be reached from $u$ in $k$ hops. For $U \subseteq V$, let $\eta^k(U) = \bigcup_{u\in U}\eta^k(u)$. We call $\eta^k(U)$ as the $k$-neighborhood of $U$. For a set of vertices $U \subseteq V$, let $\Gamma(U) = \bigcap_{u\in U}\eta(u)$.

TABLE 1
Summary of Notation

| Notation | Description |
|---|---|
| $G = (V, E)$ | A simple undirected graph with vertex set $V$ and edge set $E$ |
| $n, m$ | Number of vertices and number of edges, respectively. |
| $\Delta$ | Maximum degree of a vertex in $G$ |
| $B = \langle L, R\rangle$ | Biclique with edges connecting vertex set $L$ with vertex set $R$ |
| $s$ | Size threshold for $\lvert L\rvert + \lvert R\rvert$ |
| $\eta(u)$ | Set of vertices in $G$ adjacent to vertex $u$ |
| $\eta(U)$ | $\bigcup_{u\in U}\eta(u)$ |
| $\eta^k(u)$ | All vertices that can be reached from $u$ in $k$ hops |
| $\eta^k(U)$ | $\bigcup_{u\in U}\eta^k(u)$ |
| $\Gamma(U)$ | $\bigcap_{u\in U}\eta(u)$ |

A *biclique* $B = \langle L, R\rangle$ is a subgraph of $G$ containing two non-empty and disjoint vertex sets, $L$ and $R$ such that for any two vertices $u \in L$ and $v \in R$, there is an edge $(u, v) \in E$. A biclique $M = \langle L, R\rangle$ in $G$ is said to be a maximal biclique if there is no other biclique $M' = \langle L', R'\rangle \neq \langle L, R\rangle$ such that $L \subset L'$ and $R \subset R'$. The Maximal Biclique Enumeration Problem (MBE) is to enumerate all maximal bicliques in $G$. Table 1 summarizes the notation used in the paper.

### 2.2 Sequential Algorithms

We describe the two general approaches to sequential algorithms for MBE that we consider, one based on depth first search (see [31]) and another based on a "consensus algorithm" (see [6]).

#### 2.2.1 Sequential DFS Algorithm

The basic sequential depth first approach that we use is described in Algorithm 1, based on work by [31]. It attempts to expand an existing maximal biclique into a larger one by including additional vertices that qualify, and declares a biclique as maximal if it cannot be expanded any further. The algorithm takes the following inputs: (1) the graph $G = (V, E)$, (2) the current vertex set being processed, $X$, (3) $T$, the tail vertices of $X$, i.e., all vertices that come after $X$ in lexicographical ordering and (4) $s$, the minimum size threshold below which a maximal biclique is not enumerated. $s$ can be set to 1 so as to enumerate all maximal bicliques in the input graph. However, we can set $s$ to a larger value to enumerate only large maximal bicliques such that for $B = \langle L, R\rangle$, we have $|L| \geq s$ and $|R| \geq s$. The size threshold $s$ is provided as user input. The other inputs are initialized as follows: $X = \varnothing$, $T = V$.

**Algorithm 1.** MineLMBC($G$, $X$, $T$, $s$)

**for all the** *vertex* $v \in T$ **do**
  **if** $|\Gamma(X \cup \{v\})| < s$ **then**
    $T \leftarrow T \setminus \{v\}$
**if** $|X| + |T| < s$ **then**
  **return**
Sort vertices in $T$ as per ascending order of $|\eta(X \cup \{v\})|$;
**for all the** *vertex* $v \in T$ **do**
  $T \leftarrow T \setminus \{v\}$
  **if** $|X \cup \{v\}| + |T| \geq s$ **then**
    $N \leftarrow \Gamma(X \cup \{v\})$
    $Y \leftarrow \Gamma(N)$
    Biclique $B \leftarrow <Y, N>$
    **if** $(Y \setminus (X \cup \{v\})) \subseteq T$ **then**
      **if** $|Y| \geq s$ **then**
        Emit $B$ as a maximal biclique
      MineLMBC($G, Y, T \setminus Y, s$)

The algorithm recursively searches for maximal bicliques. It increases the size of $X$ by recursively adding vertices from the tail set $T$, and pruning away those vertices from $T$ which cannot be added to $X$ to expand the biclique. From the expanded $X$, the algorithm outputs the maximal biclique $<\Gamma(\Gamma(X)), \Gamma(X)>$. The algorithm is shown [31] to have computational complexity of $O(n\Delta N)$, where $n$ is the number of vertices in the graph, $\Delta$ is the maximum vertex degree and $N$ is the number of maximal bicliques emitted.

### 2.2.2 *Consensus Algorithm*

Alexe et al. [6] present an iterative approach to MBE. This algorithm starts off with a set of simple "seed" bicliques. In each iteration, it performs a "consensus" operation, which involves performing a cross-product on the set of current candidates bicliques with the seed bicliques, to generate a new set of candidates, and the process continues until the set of candidates does not change anymore. After each stage, the newly found bicliques can be expanded to find new maximal bicliques. After each step, the duplicate maximal bicliques can be dropped. It is proved that these algorithms exactly enumerate the set of maximal bicliques in the input graph. Algorithm 2 shows the sequential consensus Algorithm. For further details, we refer the reader to [6].

The consensus approach has a good theoretical guarantee, since its runtime depends on the number of maximal cliques that are output. In particular, the runtime of the MICA version of the algorithm is proved to be bounded by $O(n^3 \cdot N)$ where $n$ is the number of vertices and $N$ total number of maximal bicliques in $G$. The consensus algorithm has been found to be adequate for many applications and is quite popular.

## 2.3 Parallel Processing Framework

*MapReduce* (see [32], [33]) is a popular framework for processing large data sets on a cluster of commodity hardware. A MapReduce program is written through specifying map and reduce functions. The map function takes as input a key-value pair $\langle k, v\rangle$ and emits zero, one, or more new key-value pairs $\langle k', v'\rangle$. All tuples with the same value of the key are grouped together and passed to a reduce function, which processes a key $k$ and all values 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. For further details and examples of use, see [32], [33], [47]. We used Hadoop, an open source implementation of MapReduce ([48]). Hadoop is built on top of a distributed file system HDFS ([49]). While we evaluated an implementation on top of MapReduce, the idea in our parallel algorithm is more generally applicable and can easily be adapted to other frameworks such as Pregel ([50]) and Spark ([51]).

**Algorithm 2.** Sequential Consensus Algorithm

Load Graph $G = (V, E)$
$R \leftarrow$ Collection of all Stars in $G$ `// Biclique formed by a vertex and its neighbors`
$S \leftarrow \varnothing$
**for all the** $b \in R$ **do**
  $m \leftarrow$ Extend $b$
  $S \leftarrow S \cup m$
$O \leftarrow S$; `// Add seed set to the output`
$P \leftarrow S$; `// Initialize set PREV with SEED`
**repeat**
  $T \leftarrow$ Consensus between all maximal bicliques in $S$ and $P$;
  $C \leftarrow \varnothing$;
  **for all the** $b \in T$ **do**
    $m \leftarrow$ Extend biclique $b$
    **if** $m$ is not a duplicate **then**
      $C \leftarrow C \cup m$
  $O \leftarrow O \cup C$
  $P \leftarrow C$
**until** $N$ is Empty

# 3 Parallel Algorithms for MBE

We describe our parallel algorithms for MBE, and give an outline of how these are implemented using MapReduce. We first present a basic cluster generation approach, *which can be used with any sequential algorithm for MBE*, followed by enhancements to the basic cluster generation approach.

## 3.1 Basic Cluster Generation Approach

For each $v \in V$, let subgraph (cluster) $C(v)$ be defined as the induced subgraph on all vertices in $\eta^2(v)$. We first note the following.

**Lemma 1.** *For any biclique $B$ in $G$ and a vertex $v$ in $B$, $B$ is maximal in $G$ if and only if $B$ is maximal in $C(v)$.*

**Proof.** Suppose $B$ is maximal in $G$. Then we first note that $B$ is a subgraph of $C(v)$. To see this, suppose that $B = \langle L, R\rangle$, and without loss of generality, suppose $v \in L$. Then each vertex in $R$ is in $\eta(v)$, and must be in $C(v)$. Similarly, each vertex in $L$ is in $\eta^2(v)$, and must be in $C(v)$. Since $C(v)$ is a vertex-induced subgraph, it must contain all edges as well as the vertices of the biclique $B$. Next we show $B$ must be a maximal biclique in $C(v)$. Suppose not, and $B$ was contained in another biclique $B'$ in $C(v)$. Since $B'$ is also present in $G$, this implies that $B$ is not maximal in $G$, which is a contradiction.

Consider a biclique $M = \langle L, R\rangle$ that is maximal in $C(v)$, and suppose $v \in L$. We show that $M$ is a maximal biclique in $G$. Clearly, $M$ is present in $G$, so it only remains to be proved that $M$ is maximal in $G$. Suppose not, and there was a biclique $M' = \langle L', R' \rangle$ in $G$ such that $L' \subset L$ and $R' \subset R$, and $M \neq M'$. We note that $v \in L'$, and hence every vertex in $R'$ and $L'$ are contained in $\eta^2(v)$. Hence, every vertex in $M'$ is contained in $C(v)$, and since $C(v)$ is a vertex-induced subgraph, every edge of $M'$ is also contained in $C(v)$. This implies that $M$ is not a maximal biclique in $C(v)$, which is a contradiction. □

### 3.2 Algorithm CDFS – Suppressing Duplicates

With the above observation, a basic parallel algorithm for MBE first constructs the different clusters $\{C(v) | v \in V\}$, and then enumerates the maximal bicliques in the different clusters in parallel, using any sequential algorithm for MBE for enumerating the bicliques within each cluster.

While each maximal biclique in $G$ is indeed enumerated by the above approach, the same biclique may be enumerated multiple times. To suppress duplicates, the following strategy is used: a maximal biclique $B$ arising from cluster $C(v)$ is emitted only if $v$ is the smallest vertex in $B$ according to a lexicographic total order on the vertices. The basic cluster generation framework is generic and can be used with any sequential algorithm for MBE. We have used a variant of the DFS-based sequential algorithm due to [31], as well as the sequential consensus algorithm due to [6]. We call the above basic clustering algorithm using DFS-based sequential algorithm as "CDFS".

**Observation 1.** Algorithm CDFS enumerates every maximal biclique in graph $G = (V, E)$ exactly once.

There are two significant problems with the CDFS algorithm described above. First is *redundant work*. Although each maximal biclique in $G$ is emitted only once, through suppressing duplicate output, it will still be generated multiple times, in different clusters. This redundant work significantly adds to the runtime of the algorithm. Second is an *uneven distribution of load* among different subproblems. The load on subproblem $C(v)$ depends on two factors, the complexity of cluster $C(v)$ (i.e., the number and size of maximal bicliques within $C(v)$) and the position of $v$ in the total order of the vertices. The earlier $v$ appears in the total order, the greater is the likelihood that a maximum biclique in $C(v)$ has $v$ has its smallest vertex, and hence the greater is the responsibility for emitting bicliques that are maximal within $C(v)$. A lexicographic ordering of the vertices will lead to a significantly increased workload for clusters $C(v)$ where $v$ appears early in the total order and a correspondingly low workload for clusters $C(v)$ where $v$ occurs earlier in the total order.

### 3.3 Algorithm CD0 – Reducing Redundant Work

In order to reduce redundant work done at different clusters, we begin with the basic cluster generation approach and modify the sequential DFS algorithm for MBE that is executed at each reducer. We first observe that in cluster $C(v)$, the only maximal bicliques that matter are those with $v$ as the smallest vertex; the remaining maximal bicliques in $C(v)$ will not be emitted by this reducer, and need not be searched for here. We use this to prune the search space of the sequential DFS algorithm used at the reducer. The algorithm at the reducer is presented in Algorithms 7 and 8.

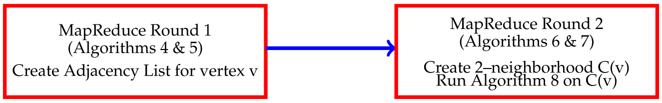



Fig. 2. Execution flow for Algorithm 3 (CD0).

The above algorithm, the "optimized DFS clustering algorithm", or "CD0" for short, is described in Algorithm 3. This takes two rounds of MapReduce. The first round, described in Algorithms 4 (map) and 5 (reduce), is responsible for generating the 1-neighborhood for each vertex. The second round, described in Algorithms 6 (map) and 7 (reduce) first constructs the clusters $C(v)$ and runs the optimized sequential DFS algorithm at the reducer to enumerate local maximal bicliques. We assume that the graph is presented as a file in HDFS organized as a list of edges with each line in the file containing one edge. The flow of execution of this Algorithm is described in Fig. 2.

All search paths in the algorithm which lead to a maximal biclique having a vertex less than $v$ can be safely pruned away. Hence, before starting the DFS, we prune away all vertices in the Tail set that are less than $v$, as described in Algorithm 7. Also, in DFS Algorithm 8, we prune the search path in Line 12 if the generated neighborhood contains a vertex less than $v$ – maximal bicliques along this search path will not have $v$ as the smallest vertex. Finally in Line 19 of Algorithm 8, we emit a maximal biclique only if the smallest vertex is the same as the key of the reducer in Algorithm 7.

**Algorithm 3.** Algorithm CD0

**Input:** Edge List of $G = (V, E)$

Execution Flow as per Fig. 2

**Algorithm 4.** Algorithm CD0 Round One – Map

**Input:** Edge $(x, y)$

```
// Generate Adjacency List for vertices x and y
Emit (key ← x, value ← y)
Emit (key ← y, value ← x)
```

**Algorithm 5.** Algorithm CD0 Round One – Reduce

**Input:** $key = v$, $value = \{v_1, v_2, \cdots, v_d\}$

```
// Generate Adjacency List for vertex v
N ← ∅;
for all the val ∈ value do
    N ← N ∪ val;
    // Add the neighbors of key to N
Emit (key ← v, value ← N)
```

**Algorithm 6.** Algorithm CD0 Round Two – Map

**Input:** $key = v, value = N$

```
// Create Two Neighborhood for vertex v
Emit (key ← v, value ← N);
for all the y ∈ N do
    Emit (key ← y, value ← ⟨v, N⟩)
```

**Algorithm 7.** Algorithm CD0 Round Two – Reduce

**Input:** $key = v$, $value = \{\eta(v), \eta(v_1), \eta(v_2), \ldots, \eta(v_d)\}$

`// Create Two Neighborhood for vertex v from the values received`

$G' = (V', E') \leftarrow$ Induced subgraph on $\eta^2(v)$

$X \leftarrow key$

$T \leftarrow V' \setminus \{key\}$

**for all the** vertex $t \in T$ **do**

  **if** $t < key$ **then**

    $T \leftarrow T \setminus \{t\}$

$O \leftarrow$ Mapping between vertex identifiers and their lexicographical ordering;

Algorithm 8 ($G'$, $X$, $T$, $key$, $s$, $O$)

**Algorithm 8.** CD0_Sequential($G'$, $X$, $T$, $key$, $s$, $O$)

**Input:** $G'$, $X$, $T$, $key$,$s$, $O$

1 `// The sequential Algorithm to be run independently on each cluster for the parallel Algorithm`

2 **if** X = { *key* } **then**

3   $N \leftarrow \Gamma(X)$ `// Same as` $\Gamma(key)$

4   $Y \leftarrow \Gamma(N)$

5   **if** $Y = X$ **then**

6     Biclique $B \leftarrow\ <Y, N>$

7     **if** $|Y| \geq s \wedge |N| \geq s$ **then**

8       $v_s \leftarrow$ Smallest vertex in $B$ as per the ordering in $O$

9       **if** $v_s = key$ **then**

10         `// Maximal biclique found`

11         Emit ($key \leftarrow \varnothing$,$value \leftarrow B$)

12     **else**

13       **return**

14 **for all the** *vertex* $v \in T$ **do**

15   **if** $|\Gamma(X \cup \{v\})| < s$ **then**

16     $T \leftarrow T \setminus \{v\}$

17 **if** $|X| + |T| < s$ **then**

18   **return**

19 Sort vertices in $T$ as per ascending order of $|\Gamma(X \cup \{v\})|$

20 **for all the** *vertex* $v \in T$ **do**

21   $T \leftarrow T \setminus \{v\}$

22   **if** $|X \cup \{v\}| + |T| \geq s$ **then**

23     $N \leftarrow \Gamma(X \cup \{v\})$

24     $Y \leftarrow \Gamma(N)$

25     **if** $Y$ *contains vertices smaller than key as per the ordering in* $O$ **then**

26       continue

27     Biclique $B \leftarrow\ <Y, N>$

28     **if** $(Y \setminus (X \cup \{v\})) \subseteq T$ **then**

29       **if** $|Y| \geq s$ **then**

30         $v_s \leftarrow$ Smallest vertex in $B$ as per the ordering in $O$

31         **if** $v_s = key$ **then**

32           `// Maximal biclique found`

33           Emit ($key \leftarrow \varnothing$,$value \leftarrow B$)

34     CD0_Sequential($G'$, $Y$, $T \setminus Y$, $key$, $s$, $O$)

Since Algorithm 8 is a pruned version of the sequential DFS Algorithm 1, the computation complexity of Algorithm 8 is $O(n_c \cdot \Delta_v \cdot N(v))$, where $n_c$ is the number of vertices in $C(v)$, $\Delta_v$ is the maximum degree of all vertices in $C(v)$ and $N(v)$ is the number of maximal bicliques in G, containing $v$. Since $\Delta_v$ cannot be greater than $n_c$, we can also write the computation complexity as $O({n_c}^2 \cdot N(v))$.

**Lemma 2.** *Algorithm 3 generates all maximal bicliques in a graph.*

**Proof.** The correctness of this Lemma can be proved from Lemma 1. Algorithm 3 generates the 2-neighborhood induced sub–graph of each vertex in $G$. It then runs the optimized sequential DFS algorithm that enumerates for each C(v), all the maximal bicliques where v is the smallest vertex. □

**Lemma 3.** *The total work done by Algorithm 3 is equal to the work done by the sequential DFS Algorithm 1.*

**Proof.** Algorithm 3 calls Algorithm 8 once for each vertex $v \in V$ for the input graph $G = (V, E)$. Thus there is one instance of Algorithm 8 created in parallel for each vertex $v$ with input $C(v)$. Before we prove this, note that the the sequential DFS Algorithm 1 can be represented as a tree as follows. Let each recursive call to the method be a node in the tree. Let the value of the node be the set of vertices in the working set $X$ in Algorithm 1. Each recursive call establishes a parent–child relationship where the calling instance of the method becomes the parent. Now to prove this lemma, we show that the work done by parallel instance of Algorithm 8 for vertex $v$ is same as work done by the subtree of the sequential Algorithm 1 that starts with $X = v$.

Consider the root of the search tree for the sequential Algorithm 1. At the root the working set $X$ is $\varnothing$. Let us consider the root to be depth 0. Let us assume some predefined ordering strategy of the tail set “T”. Also, let us label the vertices $v_1 \ldots v_n$ following the ordering. Then for each vertex, $v \in V$, we have a branch that comes out of the root. Thus for depth 1, we have $(X_1 \leftarrow 1, T_1 \leftarrow V \setminus \{1\})$, $(X_2 \leftarrow 2, T_2 \leftarrow V \setminus \{1, 2\})$ and so on. Thus for each $v \in V$, we have $(X_v \leftarrow v,\ T_1 \leftarrow V \setminus \{1, 2, \ldots, v-1\})$. Hence for depth 1, we have the above mentioned $|V|$ calls.

Now we show that each such branch corresponds to the instance of the parallel Algorithm 8 such that the reducer $key = v$.

To prove this, we note the call made to Algorithm 8 with key $v$. Algorithm 8 is called with $X = key$ and $\forall t \in T,\ t > v$. Thus we prune $T$ such that $T \leftarrow V \setminus \{1, 2, \ldots, v-1\}$. This call is same as the branch of the search tree of Algorithm 1 that starts with *key*. The input graph to the parallel algorithm is different from the sequential one. However, from Lemma 1, this doesn't make a difference to the output of the parallel Algorithm.

Now, Algorithm 8 is different from Algorithm 1 in Lines 1-12 of Algorithm 8. However, we note that these lines simulate the call made in Algorithm 8 with $X = v$. All further recursive calls that follow are identical in both Algorithms 8 and 1. □

### 3.4 Algorithms CD1 and CD2 – Improving Load Balance

In Algorithm CD0, vertices were ordered using a lexicographic ordering, which is agnostic of the properties of the cluster $C(v)$. The way the optimized DFS algorithm works, the enumeration load on a cluster $C(v)$ depends on the

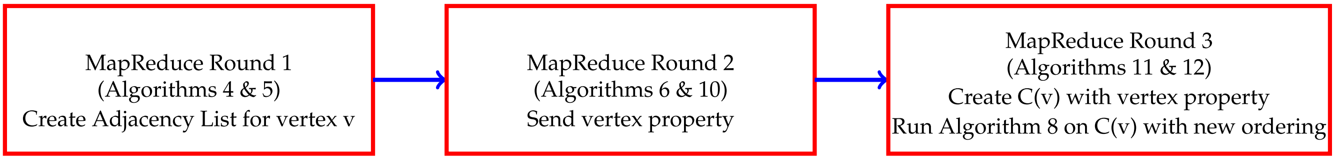



Fig. 3. Execution flow for Algorithm 9 (CD1/CD2).

number of maximal bicliques within this cluster as well as the position of $v$ within the total order. The earlier that $v$ is in the total order, the greater is the load on the reducer handling $C(v)$.

For improving load balance, our idea is to adjust the position of vertex $v$ in the total order according to the properties of its cluster $C(v)$. Intuitively, the more complex cluster $C(v)$ is (i.e., more and larger the maximal bicliques), the higher should be position of $v$ in the total order, so that the burden on the reducer handling $C(v)$ is reduced. While it is hard to compute (or even accurately estimate) the number of maximal bicliques in $C(v)$, we consider two properties of vertex $v$ that are simpler to estimate, to determine the relative ordering of $v$ in the total order: (1) Size of 1-neighborhood of $v$ (Degree), and (2) Size of 2-neighborhood of $v$.

Intuitively, we can expect that vertices with higher degrees are potentially part of a denser part of the graph and are contained within a greater number of maximal bicliques. The size of the 2-neighborhood is also the number of vertices in $C(v)$ and may provide a better estimate of the complexity of handling $C(v)$, but this is more expensive to compute than the size of the 1-neighborhood of the vertex.

The discussion below is generic and holds for both approaches to load balancing. To run the load balanced version of DFS, the reducer running the sequential algorithm must now have the following information for the vertex (key of the reducer) : (1) 2-neighborhood induced subgraph, and (2) vertex property for every vertex in the 2-neighborhood induced subgraph, where "vertex property" is the property used to determine the total order, be it the degree of the vertex or the size of the 2-neighborhood. The second piece of information is required to compute the new vertex ordering. However, the reducer of the second round does not have this information for every vertex in $C(v)$, and a third round of MapReduce is needed to disseminate this information among all reducers. We call the Algorithm using the size of 1–neighborhood of a vertex $v$ as the heuristic as CD1 and the one using the size of 2–neighborhood as CD2. The high level overviews of Algorithms CD1 and CD2 are described in Fig. 3. Following similar arguments as presented for Algorithm 8, Algorithms CD1/CD2 also has computation complexity of $O(n_c \cdot \Delta_v \cdot N(v)) = O({n_c}^2 \cdot N(v))$.

**Lemma 4.** *The total work done by parallel Algorithm 9 is equal to the work done by the sequential DFS Algorithm 1.*

**Proof.** Note that the only difference between Algorithm 9 and Algorithm 3 is how they order the vertices. Algorithm 3 uses lexicographical ordering of vertices where as Algorithm 9 uses either degree or size of 2–neighborhood. Hence, the proof follows from the proof of Lemma 3. This is because, the proof of Lemma 3 makes no assumption on the strategy used to order the vertices in the graph. □

---

**Algorithm 9.** Algorithms CD1 and CD2

**Input:** Edge List of $G = (V, E)$

Execution Flow as per Fig. 3

---

### 3.5 Communication Complexity

We consider the communication complexity of Algorithms CD0, CD1 and CD2. For input graph $G = (V, E)$, recall $n = |V|$ and $m = |E|$. Let $\Delta$ denote the largest degree among all vertices in the graph. Also, let $\beta$ denote the output size, defined as the sum of the numbers of edges of all enumerated maximal bicliques.

**Definition 1.** *The communication complexity of a MapReduce algorithm is defined as the sum of the total number of bytes emitted by all mappers and the total number of bytes emitted by all the reducers across all rounds.*

**Lemma 5.** *The communication complexity of Algorithm CD0 is $O(m \cdot \Delta + \beta)$.*

**Proof.** Algorithm CD0 has two rounds of MapReduce. In the first round the Map method (Algorithm 4) emits each edge twice, resulting in a communication complexity of $O(m)$. Similarly, the reducer (Algorithm 5), emits each adjacency list once. This also results in a communication complexity of $O(m)$. Hence total communication complexity of the first round is $O(m)$.

Now let us consider the second round of MapReduce. The total communication between the Map and Reduce methods (Algorithms 6 and 7 respectively) can be computed by analyzing how much data is received by all Reducers. Each reducer receives the adjacency list of all the neighbors of the key. Let $d_i$ be the degree of vertex $v_i$, for $v_i \in V$, $i = 1, .., n$. The adjacency list of vertex $v$ is sent to all vertices in that list. The size of adjacency list is $d_i$. This list is sent to $d_i$ vertices. Thus communication complexity for vertex $v_i$ becomes ${d_i}^2$. Total communication is thus $\sum_{i=1}^{n} {d_i}^2 = O\left(\Delta \cdot \sum_{i=1}^{n} d_i\right)$. Since $\sum_{i=1}^{n} d_i = 2 \cdot m$, the total communication becomes $O(m \cdot \Delta)$. The output from the final Reducer (Algorithm 7) is the collection of all maximal bicliques and hence the resulting communication cost is $O(\beta)$. Combining two rounds, total communication complexity becomes $O(m + m \cdot \Delta + \beta). = O(m \cdot \Delta + \beta)$. □

**Lemma 6.** *The communication complexity of Algorithm CD1 as well as CD2 is $O(m \cdot \Delta + \beta)$.*

**Proof.** First, note that both Algorithms CD1 and CD2 have the same communication complexity and observe that the first round uses the same Map and Reduce methods as CD0. Thus communication for Round 1 is $O(m)$. Again, note that Map method for Round 2 is same as CD0 and hence by Lemma 5, communication for Round 2 is $O(m \cdot \Delta)$.

The Reducer (Algorithm 10) of Round 2 sends the vertex property information to all its 2–neighbors. Thus every reducer receives information about all of its 2–neighbors. This makes the total output size of Reducer to be $O(m \cdot \Delta)$. The Map method of Round 3 (Algorithm 11) sends out the 2–neighborhood information as well as the vertex information to all vertices in 2–neighborhood. Thus communication cost becomes $O(m \cdot \Delta)$. The Reducer (Algorithm 12) emits all maximal bicliques and hence the resulting communication cost is $O(\beta)$. Thus total communication cost for Algorithms CD1 and CD2 is is $O(m \cdot \Delta + \beta)$. □

**Algorithm 10.** Algorithms CD1 and CD2 Round Two – Reduce

**Input:** $key = v$, $value = \{\eta(v), \eta(v_1), \eta(v_2), \cdots, \eta(v_d)\}$
`// Send vertex property of vertex v to required nodes`
$S \leftarrow$ 2-neighbors of $v$
$N \leftarrow$ Compute neighborhood of $v$ from $S$
`// Need to pass neighborhood for Round 3`
Emit ($key \leftarrow v$,$value \leftarrow N$)
`// Need to send vertex property to all 2-neighbors`
$p \leftarrow$ Value of vertex property of $v$ from $S$
**for all the** vertices $s \in S$ **do**
  Emit($key \leftarrow s$,$value \leftarrow [v, p]$)

**Algorithm 11.** Algorithms CD1 and CD2 Round Three – Map

**Input:** $key = v$, $value = N$ OR $key = s$, $value = v, p$
`// Create Two Neighborhood along with vertex property`
**if** $key = v$ **then**
  Emit ($key \leftarrow v$,$value \leftarrow N$)
  **for all the** $y \in N$ **do**
    Emit ($key \leftarrow y$,$value \leftarrow \langle v, N\rangle$)
**else**
  Emit ($key \leftarrow s$,$value \leftarrow [v, p]$)

**Algorithm 12.** Algorithms CD1 and CD2 Round Three – Reduce

**Input:** $key = v$, $value = \{\eta^2(v)$ along with vertex properties$\}$
`// Create Two Neighborhood along with vertex property`
$G' = (V', E') \leftarrow$ Induced subgraph on $\eta^2(v)$
$Map \leftarrow$ HashMap of vertex and vertex property created from $value$ required to compute the new ordering
$X \leftarrow key$
$T \leftarrow V' \setminus \{key\}$
**for all the** *vertex* $t \in T$ **do**
  **if** $t < key$ *in the new ordering* **then**
    $T \leftarrow T \setminus \{t\}$
  Algorithm 8($G'$, $X$, $T$, $key$, $s$, $Map$)

## 4 Parallel Consensus

We describe another approach, a direct parallelization of the consensus sequential algorithm of [6]. The motivation for trying this approach was that the cluster generation approach requires each cluster $C(v)$ to have the entire 2-neighborhood of $v$, whereas the parallel consensus approach does not require the generation of 2-neighborhood of vertices. Note that although this algorithm takes less memory per reducer than the cluster generation algorithm, we found the parallel consensus algorithm to be much slower, overall, than Algorithms CD1/CD2. We present the parallel consensus algorithm in this section.

Unlike the parallel DFS algorithm which works on subgraphs of $G$, the consensus algorithm is always directly dealing with bicliques within graph $G$. At a high level, it performs two operations repeatedly (1) a "consensus" operation, which creates new bicliques by considering the combination of existing bicliques, and (2) an "extension" operation, which extends existing bicliques to form new maximal bicliques. There is also a need for eliminating duplicates after each iteration, and also a step needed for detecting convergence, which happens when the set of maximal bicliques is stable and does not change further.

We developed a parallel version of each of these operations, by performing the consensus, extension and duplicate removal using MapReduce.

**Algorithm 13.** Parallel Consensus Algorithm – Driver Program

1 Load Graph G = (V, E)
2 $R \leftarrow$ Star bicliques from $G$ `// Biclique formed by a vertex and its neighbors`
3 $S \leftarrow$ Extend all bicliques in $R$ using MapReduce
4 Eliminate duplicates from $S$ using MapReduce
5 $O \leftarrow O \cup S$
6 $P \leftarrow S$
7 **repeat**
8   $T \leftarrow$ Consensus among all maximal bicliques in $S$ and $P$ using MapReduce
9   $C \leftarrow$ Extend all bicliques in $T$ using MapReduce
10   Eliminate duplicates from $C$ using MapReduce
11   $O \leftarrow O \cup C$
12   $P \leftarrow C$
13 **until** $N$ is $\varnothing$

Our Algorithm is described in Algorithm 13. Algorithms 14 and 15 (map and reduce) describe the consensus operation using MapReduce. Note that in Algorithm 13, line 8 performs consensus between each pair of biclique in sets S (seed set) and P (set of bicliques from previous round of iteration). To perform consensus between the all bicliques from the sets S and P naively, it would require $|S| \star |P|$ consensus operations. However, we reduce the total number of consensus operations using the following observation: If there are no common vertices between two bicliques, in that case the consensus output between the concerned two bicliques is the NULL set. This is because the intersection operation in the consensus will result in NULL. This helps us to "group" the bicliques in $n = |V|$ sets, one for each vertex of the graph. A biclique is a part of the group for vertex $v$, if $v$ is contained in the biclique. The map method helps to achieve this by "grouping" all bicliques having a particular vertex in common, thus eliminating the need of doing unnecessary consensus operations. Next we explain the extension operation. To reduce memory requirement, we required four rounds of MapReduce to perform the extension. The intention of the process is to bring together only those neighborhood information, which is required to extend a biclique. Algorithms 16 and 17 describe the map and reduce algorithms for the first round. Recall that the extension operation requires computation of 2-neighborhood of both the left and right set of the vertices in the biclique. The first two rounds of MapReduce are used to compute the 1-neighborhood of both the sets and then the same two rounds are run one more time to obtain the 2-neighborhood information. Finally, the algorithm stops when no new maximal bicliques are found after completing an iteration. The Driver Algorithm 13 checks for the same and halts if no new maximal bicliques are found.

**Algorithm 14.** Parallel Consensus Algorithm – Consensus Map

```
for all the i such that i is an node in the left set of the biclique H do
    Emit (i, H)
for all the j such that j is an node in the right set of the biclique H do
    Emit (j, H)
```

**Algorithm 15.** Parallel Consensus Algorithm – Consensus Reduce

```
for all the x such that x is a seed biclique containing the key k do
    for all the y such that y is a biclique from previous round having the key k do
        if key = minimum common element of the bicliques x and y then
            C ← Potentially new maximal bicliques from consensus of x and y
            for all the c in C do
                Extend the biclique c to generate maximal biclique H
                Emit (∅, H)
```

**Algorithm 16.** Parallel Consensus Algorithm – Extension Map

```
B ← Input biclique
if B is a star then
    x ← Main vertex
    Emit (x,B)
if data is from consensus output then
    for all the vertices i such that i is in B do
        Emit (i,B)
```

## 5 Experimental Results

We implemented our parallel algorithms on a Hadoop cluster, using both real-world and synthetic datasets. The cluster has 28 nodes, each with a quad-core AMD Opteron processor with 8 GB of RAM. All programs were written using Java version 1.5.0 with 2 GB of heap space, and the Hadoop version used was 1.2.1.

We implemented the DFS based algorithms CDFS (clustering DFS with no optimizations), CD0 (clustering DFS with the pruning optimization), CD1 (clustering DFS with pruning and load balancing using degree), and CD2 (clustering DFS with pruning and load balancing using size of 2-neighborhood). Table 2 summarizes the various Depth First Search Algorithms that were compared.

TABLE 2
Different Versions of Parallel Algorithms Based on Depth First Search (DFS)

| Label | Algorithm |
|---|---|
| CDFS | Clustering based on Depth First Search (DFS) |
| CD0 | CDFS + Reducing redundant work, without load balancing |
| CD1 | CDFS + Reducing redundant work + load balancing using degree |
| CD2 | CDFS + Reducing redundant work + load balancing using Size of 2-neighborhood |

**Algorithm 17.** Parallel Consensus Algorithm – Extension Reduce

```
S ← ∅
for all the value for key do
    if value is a neighborhood information then
        N ← Neighborhood of vertex key
    else
        S ← S ∪ value
for all the bicliques b in S do
    h ← Hash value of biclique b
    Emit (h, b)
    Emit (h, N)
```

We also implemented the sequential DFS algorithm due to [31], and the sequential consensus algorithm (MICA) due to [6]. The sequential algorithms were not implemented on top of Hadoop and hence had no associated Hadoop overhead in their runtime. But on the real-world graphs that we considered, the sequential algorithms did not complete within 12 hours, except for the p2p-Gnutella09 graph. In addition, we implemented the parallel clustering algorithm using the consensus-based sequential algorithm, and we also implemented an alternate parallel implementation of the consensus algorithm that was not based on the clustering method.

We used both synthetic and real-world graphs. A summary of all the graphs used is shown in Table 3. The real-world graphs were obtained from the SNAP collection of large networks (see [52]) and were drawn from social networks, collaboration networks, communication networks, product co-purchasing networks, and internet peer-to-peer networks. Some of the real world networks were so large and dense that no algorithm was able to process them. For such graphs, we thinned them down by deleting edges with a certain probability. This makes the graphs less dense, yet preserves some of the structure of the real-world graph. We show the edge deletion probability in the name of the network. For example, graph "ca-GrQc-0.4" is obtained from "ca-GrQc" by deleting each edge with probability $0.4$. Synthetic graphs are either random graphs obtained by the Erdos-Renyi model (see [53]), or random bipartite graphs obtained using a similar model. To generate a bipartite graph with $n_1$ and $n_2$ vertices respectively in the two partitions, we randomly assign an edge between each vertex in

TABLE 3
Properties of the Input Graphs Used, and Runtime (in Seconds) to Enumerate All Maximal Bicliques Using 100 Reducers

| Label | Input Graph | #vertices | #edges | #max–bicliques | Output Size | CDFS | CD0 | CD1 | CD2 |
|---|---|---|---|---|---|---|---|---|---|
| 1 | p2p-Gnutella09 | 8,114 | 26,013 | 20,332 | 203,779 | 113 | 60 | 79 | 80 |
| 2 | email-EuAll-0.6 | 125,551 | 168,087 | 292,008 | 4,580,577 | 42,023 | 4,188 | 415 | 406 |
| 3 | com-Amazon | 334,863 | 925,872 | 706,854 | 6,369,954 | 186 | 65 | 95 | 101 |
| 4 | amazon0302 | 262,111 | 1,234,877 | 886,776 | 7,276,888 | 396 | 264 | 102 | 97 |
| 5 | com-DBLP-0.6 | 251,226 | 419,573 | 1,875,185 | 41,407,481 | 1,659 | 285 | 239 | 314 |
| 6 | email-EuAll-0.4 | 175,944 | 252,075 | 2,003,426 | 55,685,463 | DNF | 33,300 | 3,140 | 2,196 |
| 7 | ego-Facebook-0.6 | 3,928 | 35,397 | 6,597,716 | 157,777,680 | 8,657 | 2,773 | 918 | 1,847 |
| 8 | loc-BrightKite-0.6 | 49,142 | 171,421 | 10,075,745 | 388,709,764 | 28,585 | 6,511 | 1,381 | 1,997 |
| 9 | web-NotreDame-0.8 | 150,615 | 300,398 | 19,941,634 | 471,150,086 | DNF | 27,827 | 1,044 | 1,577 |
| 10 | ca-GrQc-0.4 | 5,021 | 17,409 | 16,133,368 | 1,550,607,157 | 37,279 | 4,104 | 3,728 | 4,085 |
| 11 | ER-50K | 50,000 | 2,75,659 | 51,756 | 558,376 | 96 | 57 | 76 | 81 |
| 12 | ER-500K | 500,000 | 3,751,823 | 506,319 | 7,528,935 | 374 | 128 | 170 | 163 |
| 13 | Bipartite-50K-100K | 150,000 | 1,999,002 | 306,874 | 4,628,028 | 873 | 122 | 163 | 170 |
| 14 | Bipartite-75K-150K | 225,000 | 11,250,524 | 27,650,168 | 136,660,625 | DNF | 8,956 | 8,351 | 8,149 |

*DNF means that the algorithm did not finish in 12 hours. The size threshold was set as 1 to enumerate all maximal bicliques. Runtime includes overhead of all MapReduce rounds including graph clustering, i.e., formation of 2–neighborhood. Graphs 1-10 are real world graphs while the rest are synthetic graphs. We have used random graphs of various sizes between 50 and 500 K vertices, but do not show the details about all synthetic graphs in the table, due to space constraints. All runtimes shown are a mean of five individual runs of the Algorithm.*

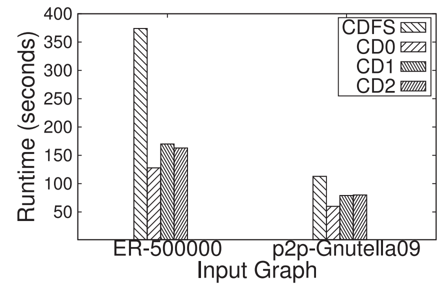
the left partition to each vertex in the right partition. A random Erdos-Renyi graph on $n$ vertices is named "ER-$\langle n \rangle$", and a random bipartite graph with $n_1$ and $n_2$ vertices in the bipartitions is called "Bipartite-$\langle n_1 \rangle$-$\langle n_2 \rangle$".

We seek to answer the following questions from the experiments: (1) What is the relative performance of the different methods for MBE? (2) How do these methods scale with increasing number of reducers? and (3) How does the runtime depend on the input size and the output size?

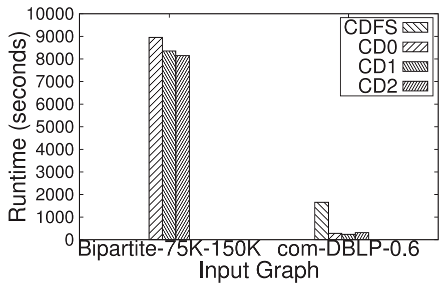
Fig. 4 presents a summary of the runtime data for the algorithms in Table 3. All data used for these plots was generated with 100 reducers. The runtime(s) given in Table 3 for various Algorithms were recorded by taking the mean over five individual runs. The runtime data given for the parallel algorithms include the time required to run all MapReduce rounds including time required to construct 2-neighborhood etc.

### 5.1 Impact of the Pruning Optimization

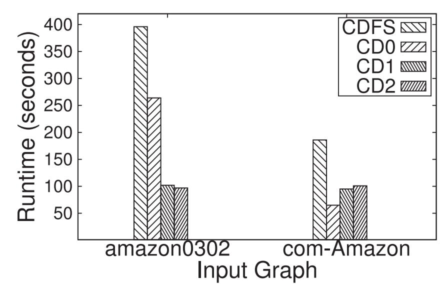
From Fig. 4, we can see that the optimizations to basic DFS clustering through eliminating redundant work make a significant impact to the runtime for all input graphs. For instance, in Fig. 4d, on input graph email-EuAll-0.6 CD0, which incorporates these optimizations, runs 10 times faster than CDFS, the basic cluster generation approach. Also, we can see from Table 3 that the input graphs email-EuAll-0.4, web-NotreDame-0.8 and Bipartite-75–150K could not be



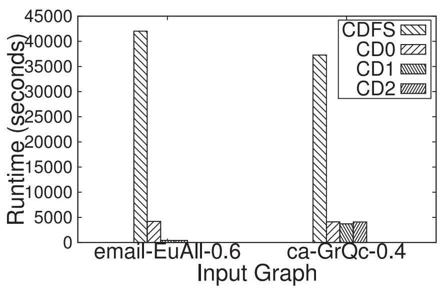

(a) ER-500K & p2p-Gnutella09



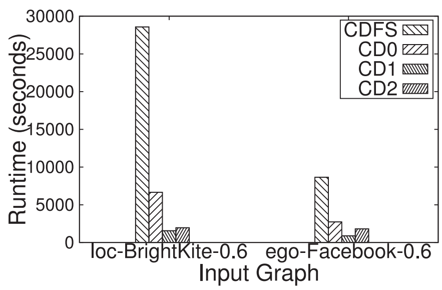

(b) web-NotreDame-0.8 & Bipartite-50K-100K



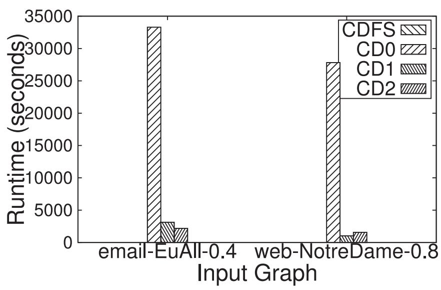

(c) amazon0302 & com-Amazon




(d) email-EuAll-0.6 & ca-GrQc-0.4




(e) loc-BrightKite-0.6 & ego-Facebook-0.6




(f) email-EuAll-0.4 & com-DBLP-0.6

Fig. 4. Runtime in seconds of parallel algorithms on real and random graphs. If an algorithm failed to complete in 12 hours the result is not shown. All algorithms were run using 100 reducers. All runtimes are a mean of five individual runs of the Algorithm. Runtime includes overhead of all MapReduce rounds including graph clustering, i.e., formation of 2–neighborhood.

TABLE 4
Mean and Standard Deviation Computation of All 100 Reducer Runtimes for Algorithms CD0, CD1 and CD2

| loc-BrightKite-0.6 | CD0 | CD1 | CD2 |
|---|---|---|---|
| Average | 637.27 | 387.77 | 393.68 |
| Variance | 1,259,680.12 | 81,447.47 | 111,443.13 |
| Standard Deviation | 1,122.35 | 285.39 | 333.83 |
| ego-Facebook-0.6 | CD0 | CD1 | CD2 |
| Average | 313.56 | 245.21 | 273.43 |
| Variance | 203,661.36 | 29,166.29 | 108,260.19 |
| Standard Deviation | 451.29 | 170.78 | 329.03 |

*The analysis is done for the reducer of the last Map Reduce round as it performs the actual depth first search.*

processed by Algorithm CDFS within 11 hours but could be processed by Algorithm CD0.

We measure the redundant processing that we avoid by using the optimized Algorithm CD0 rather than CDFS. To measure this we count the total number of recursive calls made to the depth first search method by the algorithms. We observe that the number of such recursive calls made by CDFS is an order greater than CD0. For example, for input graph ER-500K, CDFS makes about 16.5 million calls whereas CD0 makes only about 1 million calls. Similar results are obtained for real work input graphs. For example, for input graph ego-Facebook-0.6, CDFS makes about 133.5 million recursive calls while CD0 makes about only about 13.2 million. Hence we observe that our optimizations are successful in pruning the search tree by effectively removing redundant search paths.

## 5.2 Impact of Load Balancing

From Fig. 4, we observe that for graphs on which the algorithms do not finish very quickly (within 200 seconds), load balancing helps significantly. In Fig. 4d, for graph email-EuAll-0.6, the Load Balancing approaches (CD1 and CD2) are 10 to 10.3 times faster than CD0, which incorporates the pruning optimization, without load balancing. In Fig. 4b, we note that for input graph web–NotreDame-0.8, CD1 was 26.7 times faster than CD0 and CD2 was about 17.6 times faster. We can also observe the improvements in Load Balance from the reducer timings. For input graph email-EuAll-0.4, we observe that for CD0, most reducers finish in a few minutes. A very few took 2 hours. However, the last two reducers took 4.5 and 9.25 hours. By improving load balance in Algorithms CD1/CD2, we redistribute this work load bringing the parallel runtime of both Algorithms to below one hour.

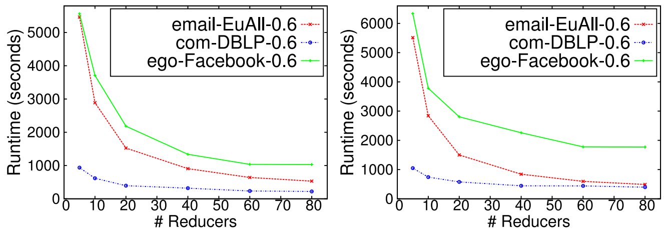
*For most input graphs, the versions optimized through load balancing and pruning (Algorithms CD1 and CD2) worked the best overall, and both these optimizations helped significantly in reducing the runtime.*

However, for graphs that completed quickly, load balancing performs slightly slower than Algorithm CD0 (see Fig. 4a). This can be explained by the additional overhead of load balancing (an extra round of MapReduce), which does not payoff unless the work done at the DFS step is significant.

There are two different approaches to load balancing, one based on the vertex degree (Algorithm CD1) and the other on the size of the 2-neighborhood of the vertex (Algorithm CD2). *From Fig. 4 we observed that no one approach was consistently better than the other, and the performance of the two were close to each other.* For some input graphs, like Email-EuAll-0.4, the 2-neighborhood approach (CD2) fared better than the degree approach (CD1), whereas for some other input graphs like web-NotreDame-0.8, the degree approach fared better.

To better understand the impact of load balancing, we calculated the mean and the standard deviation of the run time of each of the 100 reducers for the last round of MapReduce of Algorithms CD0, CD1 and CD2. We present results of this analysis for input graphs loc-BrightKite-0.6 and ego-Facebook-0.6 in Table 4. *The load balanced CD1 and CD2 have a much smaller standard deviation for reducer runtimes than CD0.*

We observe that random graphs have less variance in degree/size of 2–neighborhood than real world graphs. This leads to approximately balanced load on each node in the cluster, irrespective of how the work is distributed. Hence we don't get benefit out of the extra overhead involved in CD1 and CD2. Thus for randoms graphs, Algorithm CD0 performs better than Algorithms CD1/CD2.

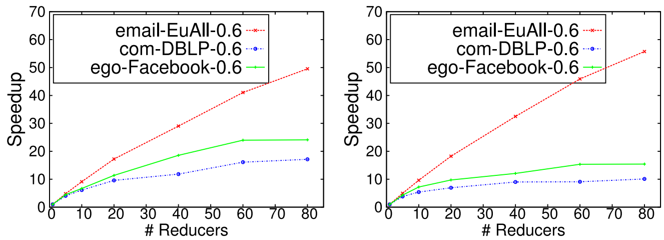



(a) Algorithm CD1 (b) Algorithm CD2

Fig. 5. Runtime versus number of reducers.

## 5.3 Scaling with Number of Reducers

In Fig. 5 we plot the runtime of CD1 and CD2 with increasing number of reducers. In Fig. 6, we also plot the speedup, defined as the ratio of the time taken with 1 reducer to the time taken with $r$ reducers, as a function of the number of reducers $r$. We observe that the runtime decreases with increasing number of reducers. Both CD1 and CD2 achieves acceptable speedup. For instance for Algorithm CD1 and input graph email-EuAll-0.6, for 5 reducers we get 4.8 speedup while for 80 reducers, we get 49.54 speedup. Similarly, for Algorithm CD2 and input graph email-EuAll-0.6, we achieve speedup of 4.9 with 5 reducers and 55.73 speedup with 80 reducers. This data shows that the algorithms are scalable and may be used with larger clusters as well.




(a) Algorithm CD1 (b) Algorithm CD2

Fig. 6. Speedup versus number of reducers.

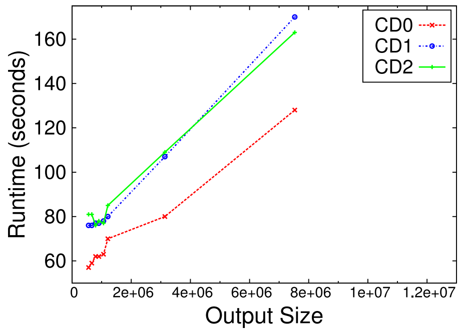



Fig. 7. Runtime versus Output Size for random graphs. All Erdos-Renyi random graphs were used. Output size of a single maximal biclique is defined as the number of edges in the biclique. The total output size is the sum of the output sizes taken over all the bicliques generated by the algorithm.

### 5.4 Relationship to Output Size

We observed the change in runtime of the algorithms with respect to the output size. We define the output size of the problem as the sum of the numbers of edges of all enumerated maximal bicliques. Fig. 7 shows the runtime of algorithms CD0, CD1, and CD2 as a function of the output size. This data is only constructed for random graphs, where the different graphs considered are generated using the same model, and hence have very similar structure. We observe that *the runtime increases almost linearly with the output size for all three algorithms CD0, CD1, and CD2*.

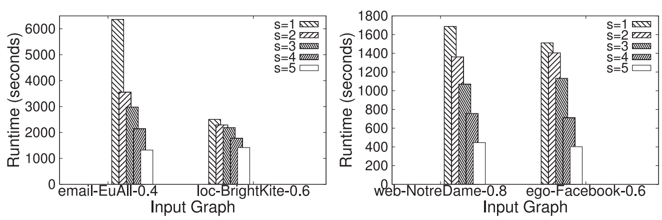
With real world graphs, this comparison does not seem as appropriate, since the different real worlds graphs have completely different structures; however, we observed that the runtimes of Algorithms CD1 and CD2 are well correlated with the output size, even on real world graphs.

### 5.5 Large Maximal Bicliques

Next, we considered the variant where only large bicliques, whose total number of vertices is at least $s$, are required to be emitted. Fig. 8 shows the runtime as the size threshold $s$ varies from 1 to 5. We observe that the runtime decreases significantly as the threshold increases. Also, Algorithms CD1 and CD2 were not able to enumerate all maximal bicliques from input graph email-EuAll-0.2 even after 12 hours. However, with size threshold 5, Algorithm CD1 took less than 6 hours to process this graph while Algorithm CD2 took about 3.5 hours.

### 5.6 Consensus versus Depth First Search

Finally we compare the two sequential techniques used in this work. The basic clustering method was used with the




(a) email-EuAll-0.4 loc-BrightKite-0.6

(b) web-NotreDame-0.8 ego-Facebook-0.6

Fig. 8. Runtime versus the size threshold for the emitted maximal bicliques. All experiments were performed using Algorithm CD1 and with 100 reducers.

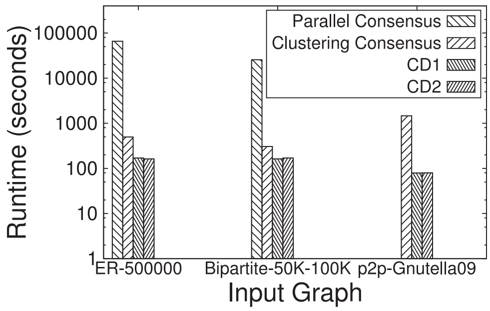



Fig. 9. Comparison of the parallel consensus and clustering consensus with Algorithms CD1 and CD2. We observe that the consensus algorithm performs poorly in comparison with CD1 and CD2.

consensus technique and compared with Algorithms CD1 and CD2. Fig. 9 shows the performance of Algorithms CD1 and CD2 against the consensus approach. We note that the cluster generation approach using the consensus technique performed very poorly compared with the DFS based algorithm. For example for the input graph p2p-Gnutella09, CD1 and CD2 took 79 and 80 seconds respectively (using 100 reducers). This is in contrast with the implementation of the clustering method using the consensus technique which took 1,469 seconds (again with 100 reducers). In all instances except for very small input graphs, clustering using consensus was 6 to 15 times slower than CD1 and CD2 or worse, and in many cases, clustering consensus did not finish within 12 hours while CD1 and CD2 finished within 1-2 hours.

We also compared the runtime of the more direct parallel implementation of the consensus technique as described in Algorithm 13. The direct parallel consensus, which uses a different parallelization strategy was 13 to 400 times slower than clustering consensus. For example, for input graph ER-500K, Algorithm CD1 finished processing in 170 seconds, whereas Algorithm 13 took over 18 hours. Further, it could not process the p2p-Gnutella09 input graph within 12 hours.

## 6 Conclusion

Maximal biclique enumeration is a fundamental tool in uncovering dense relationships within graphical data. We presented a scalable parallel method for mining maximal bicliques from a large graph. Our method uses a basic clustering framework for parallelizing the enumeration, followed by two optimizations, one for reducing redundant work, and another for improving load balance. Experimental results using MapReduce show that the algorithms are effective in handling large graphs, and scale with increasing number of reducers. To our knowledge, this is the first work to successfully enumerate bicliques from graphs of this size; previous reported results were mostly sequential methods that worked on much smaller graphs.

The following directions are interesting for exploration (1) How does this approach perform on even larger clusters, and consequently, larger input graphs? What are the bottlenecks here? and (2) Can these be extended to enumerate near-bicliques (quasi-bicliques) from a graph?

## Acknowledgments

This work was funded in part by the US National Science Foundation through grants 0834743 and 0831903 and is partially supported by the HPC equipment purchased through NSF MRI grant number CNS 1229081 and NSF CRI grant number 1205413. The views and conclusions contained in this document are those of the author(s) and should not be interpreted as representing the official policies, either expressed or implied of the US National Science Foundation.

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