Finding Dense Subgraphs for Sparse Undirected, Directed, and Bipartite Graphs

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***Abstract*— This paper presents a method for identifying a set of dense subgraphs of a given sparse graph. Within the main applications of this "dense subgraph problem", the dense subgraphs are interpreted as communities, as in, e.g., social networks. The problem of identifying dense subgraphs helps analyze graph structures and complex networks and it is known to be challenging. It bears some similarities with the problem of reordering/blocking matrices in sparse matrix techniques. We exploit this link and adapt the idea of recognizing matrix column similarities, in order to compute a partial clustering of the vertices in a graph, where each cluster represents a dense subgraph. In contrast to existing subgraph extraction techniques which are based on a complete clustering of the graph nodes, the proposed algorithm takes into account the fact that not every participating node in the network needs to belong to a community. Another advantage is that the method does not require to specify the number of clusters; this number is usually not known in advance and is difficult to estimate. The computational process is very efficient, and the effectiveness of the proposed method is demonstrated in a few real-life examples.**

***Index Terms*— Dense subgraph, social network, community, bipartite graph, matrix reordering, hierarchical clustering, partial clustering.**

I. Introduction

A challenging problem in the analysis of graph structures is the *dense subgraph problem*, where given a sparse graph, the objective is to identify a set of meaningful dense subgraphs. This problem has attracted much attention in recent years due to the increased interest in studying various complex networks, such as the World Wide Web (information network), social networks, and biological networks, etc. The dense subgraphs are often interpreted as "communities" [1]–[4], based on the basic assumption that a network system consists of a number of communities, among which the connections are much fewer than those inside the same community.

The recent data mining literature has seen various techniques for approaching this problem from different aspects. With the knowledge of a few important nodes as sources, the Web can be considered a flow network and max-flow/min-cut algorithms can be applied to identify communities centered at the source nodes [3]. In [5], a greedy randomized adaptive search procedure is proposed to detect massive dense subgraphs with high densities. In [6], bipartite graphs are considered and dense subgraphs are iteratively grown by using local search heuristics. A graph clustering approach [7], based on expansions and inflations of the stochastic matrix, was proposed to identify intrinsic clusters in the graph. In many biological networks, communities that consist of a chain of adjacent cliques are of special interest, and many methods have been proposed for the detection of such communities [8], [9]. It is beyond the scope of this paper to list the many existing approaches in such emerging applications.

Among the techniques studied, a popular methodology is to exploit graph partitioning techniques for outputting a set of partitions, each of which is interpreted as a community. A broad set of partitioning techniques, such as hierarchical clustering [10], [11], spectral partitioning [12], [13], and multilevel graph partitioning (e.g. METIS [14]), have been proposed or adapted for this purpose. A common drawback for these methods is that the number k of partitions is a mandatory input parameter, and the change of k may result in a very different partitioning result, except for perhaps hierarchical based approaches. In most applications, the number k is not known a priori. A number of researchers proposed to remedy this difficulty by tracking a goodness measure of the partitioning as a function of k. Some measures, such as the conductance [4] and the modularity [11], are empirically studied to have local peaks or valleys, hence an optimal value for k is possible to obtain. However, this remedy may not always be practical due to its expensive computational cost. Furthermore, most of these methods yield a *complete clustering* of the data. A more crucial question when attempting to discover communities in this way is: "Why should every node belong to some community?"

In this paper, we propose a schematic approach to understand the structure of a graph and identify its dense components. Its main features are (i) a partial clustering of the graph vertices where each cluster represents a dense subgraph, (ii) a density concept with which communities are quantitatively measured, and (iii) a hierarchy of the vertices such that a density threshold can be conveniently modified and the corresponding subgraphs can be computed in real time. Indeed, there have been many density-based approaches proposed in the past (e.g., [5], [9]), but none possesses such a combination of features. An advantage of our approach is that a complete clustering of the vertices is avoided, even with the presence of a hierarchy as an outcome. (A hierarchy can be cut at some level to form a complete clustering.) The real merit of this approach is that we can navigate the hierarchy and adjust the density threshold (at almost no time cost) until a desirable result is achieved. Note that the term "dense" is somewhat ambiguous. The interpretation of this term in the study of social networks seems to be in a relative sense: A community is defined simply because the inner connections are much denser than the intra connections; however, the inner connections (the subgraph itself) may still be sparse. On the other hand, the term "density" is rigorous and it can be defined on mathematical terms. In this paper, we opt to identify subgraphs whose densities are beyond a certain threshold.

We point out that the problem studied here is different from the *densest subgraph problem* [15], [16] or the *densest k-subgraph problem* [17]–[19], both of which aim at identifying the subgraph

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which has the *highest* density. Instead, we are interested in finding a number of subgraphs that have a high enough density (not necessarily the densest). Of course, one possible approach to our problem consists of a gradual procedure whereby the densest subgraph is extracted and then removed from the original graph, and the process is repeated on the resulting reduced graph as many times as desired. However, the removal of the densest subgraph from the original graph may lead to a number of undesirable results. For example, the resulting subgraphs may have extremely different densities, and/or sizes. Our approach, being more global and progressive, is not prone to such extreme imbalances. It may be possible to adapt these techniques for the problem at hand but this will not be investigated here.

II. Dense Subgraphs Extraction

Given a sparse graph $G(V, E)$ which consists of the vertex set V and the edge set E, we are interested in identifying dense subgraphs of G. To be precise, the candidate subgraphs should have densities higher than a threshold value in order to be interesting. We consider the following three types of graphs, with an appropriate definition of *density* for each one.

1) Undirected graphs. Undirected graphs are the most common models of networks, where the directions of the connections are unimportant, or can be safely ignored. A natural definition of the graph density is the ratio of $|E|$ over the cardinality of the edge set of the complete graph with the same vertex set V, i.e.,

$$d_G = \frac{|E|}{|V|(|V|-1)/2}. \tag{1}$$

Note that $d_G \in [0, 1]$, and a subgraph has the density one if and only if it is a clique.

2) Directed graphs. The density of a directed graph is defined as

$$d_G = \frac{|E|}{|V|(|V|-1)}, \tag{2}$$

since the maximum number of possible directed edges cannot exceed $|V|(|V|-1)$. In other words, the density of a directed graph also lies in the range from 0 to 1. It is interesting to note that if we "undirectify" the graph, i.e., remove the directions of the edges and combine the duplicated resulting edges, we yield an undirected graph $\tilde{G}(V, \tilde{E})$ with the edge set $\tilde{E}$. Then,

$$\frac{1}{2} d_{\tilde{G}} \le d_G \le d_{\tilde{G}}.$$

An immediate consequence is that if we extract the subgraphs of the undirected version of the graph given a density threshold, we essentially obtain directed subgraphs with densities at least half of the threshold.

3) Bipartite graphs. A bipartite graph is an undirected graph whose vertex set V can be partitioned in two disjoint subsets V_1 and V_2, such that every edge connects a vertex from V_1 and one from V_2. There are several reasons to consider bipartite graphs separately from general undirected graphs. The most important one is that a bipartite graph is generally used to model the connections between two different types of entities in a data set, such as the relationship between documents and terms, that between customers and products, etc. Also, as will soon be discussed, the proposed dense subgraph extraction algorithm for a general undirected graph does not directly apply to the bipartite graph case. Finally, the density of a bipartite graph, as computed by formula (1) can never reach one for bipartite graphs. In fact it is an easy exercise to show that the density of an arbitrary bipartite graph, as defined by formula (1) cannot exceed the maximum value of $0.5|V|/(|V|-1)$, which is close to 1/2 for large graphs. Thus, we consider a the following alternative definition for the density of a bipartite graph:

$$d_G = \frac{|E|}{|V_1| \cdot |V_2|}. \tag{3}$$

According to this definition, $d_G \in [0, 1]$, and a subgraph has the density one if and only if it is a biclique.

The adjacency matrix A of the above three types of graphs has specific patterns. Throughout the paper, we assume that A is sparse, because we are considering subgraphs of a *sparse* graph. We also assume that the entries of A are either 0 or 1, since the weights of the edges are not taken into account for the density of a graph. In all cases, the diagonal of A is empty, since we do not allow self-loops. For undirected graphs, A is symmetric, whereas for directed graphs, A is only square. A natural matrix representation of a bipartite graph is a rectangular matrix B, where $B(i, j)$ is nonzero if and only if there is an edge connecting $i \in V_1$ and $j \in V_2$. The adjacency matrix for such a bipartite graph is indeed

$$A = \begin{bmatrix} 0 & B \\ B^T & 0 \end{bmatrix},$$

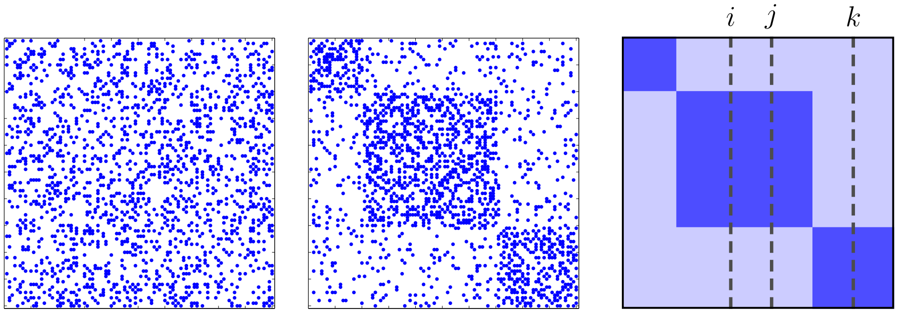
where the vertices from V_1 are ordered before those from V_2. Note that the diagonal blocks of A are zero for a bipartite graph. Also, note that there are situations where we do not know that the given undirected graph is bipartite in advance, i.e., A is given in a permuted form where the above 2×2 block structure is not revealed. In such a case, a simple strategy adapted from the breadth first search can be used to check if the inherent undirected graph is bipartite, and if so to extract the two disjoint subsets.

The dense subgraphs extraction methods proposed in this paper are inspired by the so-called *matrix blocking* problem [20], [21], which is introduced along with an efficient technique in the next subsection. Naively applying the technique to our problem may not be effective; nevertheless, the technique bears the basic ideas and ingredients of the main algorithms proposed later for the dense subgraph problem.

A. Matrix Blocking

Blocking is a vital ingredient of preconditioning methods. In such methods an approximate Gaussian elimination, i.e., an Incomplete LU (ILU) factorization is performed. This approximation is then used to improve the convergence of an iterative method [22]. Block ILUs perform this elimination with dense blocks and so the matrix is stored in a block format. The blocking of the matrix may be exact and known in advance or an approximate blocking may be sought by some automatic tool as is done in [21]. The main motivation for these techniques is that block preconditiong methods are known to yield better convergence than scalar ones, see [21], [22] and references therein. In addition, they are more economical since they tend to use more compact storage schemes. Fig. 1(b) illustrates the effects of blocking, where the nonzero entries of A are moved toward the diagonal.

A simple yet effective blocking algorithm [21] exploits the similarities between a pair of columns in the *pattern matrix* P



(a) A. (b) A after reordering. (c) Three columns of the reordered matrix A.

Fig. 1. A blocking of a sparse symmetric matrix A.

of A. Recall that P is obtained from A by simply replacing its nonzero entries by ones. The rationale behind this is that the nonzero patterns of two columns corresponding to the same block should be more similar than those of the two columns that correspond to different blocks. To be specific, let some dense block of the reordered P correspond to a subset of vertices V_s. Also, let $i, j \in V_s$ and $k \notin V_s$; see Fig. 1(c). The heuristic is that the cosine of the angle between the i-th and the j-th columns of P is large, whereas that of the i-th and the k-th (or the j-th and the k-th) columns is small, since i and j correspond to the same dense block but k does not. The blocking algorithm is to find maximal subsets of V such that inside the same subset, for each vertex i, there exists a vertex $j \neq i$ such that the cosine of $P(:, i)$ and $P(:, j)$ is larger than a predefined threshold.

The adjacency matrix of an undirected graph plays exactly the same role as P here. Roughly speaking, the goal of dense subgraph extraction is to reorder the adjacency matrix and to find the dense diagonal blocks, each of which represents a dense subgraph. One is tempted to directly apply the above algorithm on the adjacency matrix of a given graph. However, a difficulty arises when choosing an appropriate similarity threshold. A further concern is that each block should employ a different threshold. For example, two columns corresponding to a larger block have a higher probability of yielding a larger cosine than those corresponding to a smaller block.

B. The Case of Undirected Graphs

Consider the matrix M that stores the cosines between any two columns of the adjacency matrix A:

$$M(i,j) = \frac{\langle A(:,i), A(:,j)\rangle}{\|A(:,i)\| \, \|A(:,j)\|}. \tag{4}$$

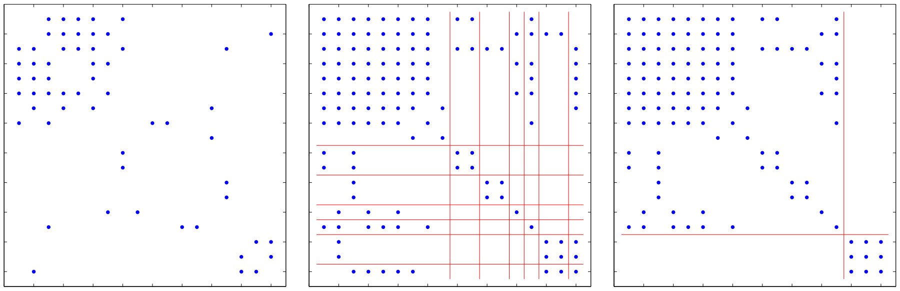
By reordering and partitioning the rows and columns of M in the same way as A, the above mentioned algorithm (by using a predefined similarity threshold) effectively yields a specially structured M: Entries outside the diagonal blocks of M, are all smaller than the threshold, whereas inside each non-trivial diagonal block, there exists at least one entry larger than the threshold for each row/column. Fig. 2(b) shows an illustration.

To avoid setting a fixed similarity threshold, we consider all possible ones as represented by the nonzero entries of M (excluding the diagonal of M, where the similarities between a column and itself is not useful at all). Going in ascending order of these entries, we set them to zero one by one. At some point after a few entries have been zeroed, M becomes a 2×2 block-diagonal matrix: the two off-diagonal blocks are completely zero (Fig. 2(c)). The last entry that was set to zero is a critical threshold, since by this value the rows and columns of M are partitioned in two subsets, and no smaller values can yield a partitioning. Once this initial partitioning is obtained, the zero-setting procedure is performed recursively on the two resulting partitions.

The above procedure can be precisely stated in the language of hierarchical clustering. Given an undirected graph $G(V, E)$ and its adjacency matrix A, we construct a weighted graph $G'(V, E')$ whose weighted adjacency matrix M is defined in (4). Assume without loss of generality that G' is connected (otherwise process each connected component of G' separately). A top-down hierarchical clustering of the vertex set V is performed by successively deleting the edges $e' \in E'$, in ascending order of the edge weights. When G' first becomes disconnected, V is partitioned in two subsets, each of which corresponds to a connected component of G'. Then, the edge-removal process is continued on these two components to partition them in turn.

One detail that is left is to decide when to terminate the recursions. Recall that the objective is to find meaningful dense subgraphs of G. Therefore, the usual termination criterion—stopping when each partition contains only one vertex—is not necessary. Instead, termination will take place when the density of the partition passes a certain density threshold $d_{\min}$. Thus, a subset of the vertices is no longer partitioned if the corresponding subgraph has a density $\geq d_{\min}$. The only exception is that some subsets never meet this requirement and are recursively partitioned until they result in trivial subgraphs consisting of singletons. These singletons bear no interest and are ignored.

Algorithm 1 summarizes the proposed method. As an example, we consider a graph with 18 vertices and 29 edges as shown in Fig. 3(a). (This example comes from a figure in [4].) A visual inspection results that the graph has a dense component that contains vertices 1 to 7 (and possibly vertex 10), as well as a plausible dense, though small, component $\{14, 15, 16\}$. The first step is to compute the similarity matrix M and to sort its nonzero entries, as listed in (b). We construct the graph G' using the weighted adjacency matrix M. Starting from the smallest entry in the list, we remove edges of G' one by one until G' becomes disconnected. The two resulting subsets of vertices are: $\{1, \ldots, 13, 17, 18\}$ and $\{14, 15, 16\}$. The latter subset happens to yield a subgraph that has a density higher than the desired threshold 0.75. Hence, it is output as a dense subgraph. On the other hand, the former subset does not yield a subgraph satisfying



(a) A.

(b) M and its blocking.

(c) M with the first batch of nonzero entries set to zero.

Fig. 2. An adjacency matrix A and its similarity matrix M. Plot (b) shows a partitioning of M by using a similarity threshold 0.5. Plot (c) shows the first partitioning of M in a recursive partitioning.

Algorithm 1 Finding Dense Subgraphs of a Sparse Undirected Graph

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Input: Sparse undirected graph $G$, density threshold $d_{\min}$.
 1: Construct $G'$ with the weighted adjacency matrix $M$ as
    defined in (4).
 2: Let $C$ be the array of tuples $(i, j, M(i,j))$, for all nonzero
    $M(i,j)$ and $i < j$, sorted in ascending order of $M(i,j)$.
 3: Run DENSE-SUBGRAPHS($G$, $G'$, $C$, $d_{\min}$).

 4: function DENSE-SUBGRAPHS($G$, $G'$, $C$, $d_{\min}$)
 5:     $k \leftarrow 0$
 6:     while $G'$ is connected do
 7:         Delete edge $\{C[k].i, C[k].j\}$.
 8:         $k \leftarrow k + 1$
 9:     end while
10:     Let the two connected components of $G'$ be
          $G'_s(V_s, E'_s)$ and $G'_t(V_t, E'_t)$.
11:     Let the two corresponding subgraphs of $G$ be
          $G_s(V_s, E_s)$ and $G_t(V_t, E_t)$.
12:     if $d_{G_s} \geq d_{\min}$ then
13:         Output $G_s$ as a dense subgraph.
14:     else if $|V_s| > 1$ then
15:         Let $C_s$ be the subarray of $C$, where $C_s[k].i \in V_s$
              and $C_s[k].j \in V_s$ for all $k$.
16:         DENSE-SUBGRAPHS($G_s$, $G'_s$, $C_s$, $d_{\min}$)
17:     end if
18:     Repeat lines 12–17 with $V_s$, $G_s$, $G'_s$, $C_s$ replaced
          by $V_t$, $G_t$, $G'_t$, $C_t$.
19: end function
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the density requirement, so it is successively partitioned, until the subset $\{2, 5, 3, 1, 4, 7, 6\}$ is reached. This gives the other dense subgraph. Fig. 3(c) shows the resulting hierarchy/dendrogram. The output dense subgraphs are kept being partitioned in the hierarchy just for illustration purposes.

Note that although the described algorithm is derived from the idea of matrix blocking, it turns out that it can be explained from another angle, which has been for long understood by sociologists: Build a dendrogram of the graph vertices, and interpret the clustering information from the dendrogram [23]. Yet there are two main differences here. The first is the similarity measure used for building the dendrogram. The interpretation of the cosine similarity we use here is that if two vertices share many neighbors and the shared neighbors constitute a large portion of all the neighbors of the two vertices, then they two have a higher tendency to be grouped together, or a lower tendency to be separated. Thus, they should belong to a community/subgraph. The second is the interpretation of the dendrogram. Instead of outputting the dendrogram as is, or cutting the dendrogram at a specific level to yield a predefined number of clusters, we walk the dendrogram in a top-down fashion and return clusters only when they have high densities. All the returned clusters, when combined, do not constitute a complete partitioning of the graph; they only represent the dense parts of the graph.

C. The Case of Directed Graphs

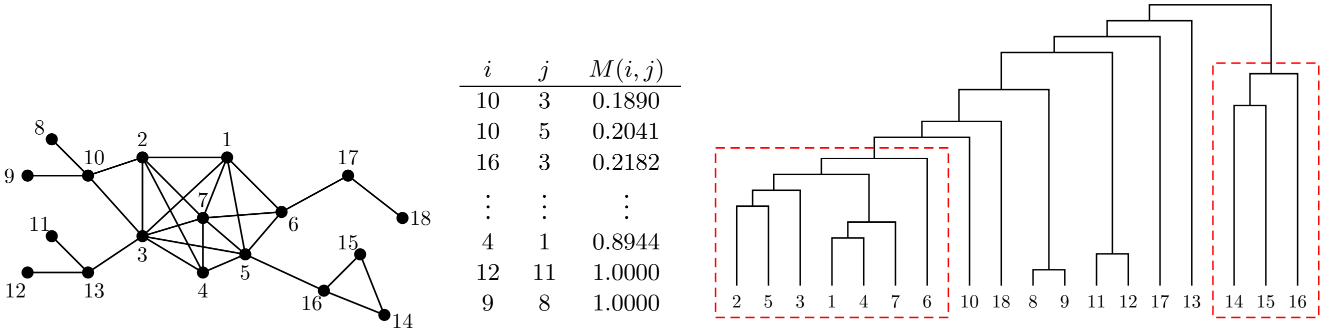
The adjacency matrix A of a directed graph is square but not symmetric. When Algorithm 1 is applied to a non-symmetric adjacency matrix, it will result in two different dendrograms, depending on whether M is computed as the cosines of the columns of A, or the rows of A. There may be applications where the direction is required and one can choose to perform the analysis with either A (outgoing edges) or its transpose (incoming edges). However, in most applications, symmetrizing the graph is a sensible strategy because an incoming edge and outgoing edge have a similar "cost" (think in terms of communications in parallel algorithms for example). This is often performed for the somewhat related problem of graph partitioning for example. In the following we symmetrize the matrix A and use the resulting symmetric adjacency matrix to compute the similarity matrix M. The rest of the procedure follows Algorithm 1.

Note that this technique is equivalent to removing the directions of the edges in G, and extracting dense components from the undirected version of the graph. As discussed at the very beginning of this section, given an input parameter $d_{\min}$, the output directed subgraphs have densities guaranteed to be at least $d_{\min}/2$. If the occurrence of edge pairs (v_1, v_2) and (v_2, v_1), where v_1 and v_2 are two vertices, is rare, the densities of the output subgraphs will even be much higher.

D. The Case of Bipartite Graphs

Unfortunately, Algorithm 1 does not work for a bipartite graph where the vertex set V consists of two disjoint subsets V_1 and V_2. To see this, consider its adjacency matrix

$$A = \begin{bmatrix} 0 & B \\ B^T & 0 \end{bmatrix},$$



i	j	$M(i,j)$
10	3	0.1890
10	5	0.2041
16	3	0.2182
$\vdots$	$\vdots$	$\vdots$
4	1	0.8944
12	11	1.0000
9	8	1.0000

(a) The graph G.

(b) Sorted nonzeros of M.

(c) The dendrogram.

Fig. 3. Two dense subgraphs (encapsulated in the red dashed frames) are found for a sparse undirected graph as shown in (a). The density threshold $d_{\min} = 0.75$.

where $B(i,j) = 1$ if there is an edge connecting $i \in V_1$ and $j \in V_2$, and $B(i,j) = 0$ otherwise. Then, the matrix M defined in (4) has the following form:

$$M = \begin{bmatrix} M_1 & 0 \\ 0 & M_2 \end{bmatrix}, \tag{5}$$

where M_1 (resp. M_2) contains the cosine similarities between the rows (resp. columns) of B. That is, without any edge removal of the graph G' (using M as the weighted adjacency matrix), the vertex set is already partitioned into two subsets: V_1 and V_2. Any subsequent hierarchical partitioning will only further subdivide these two subsets separately. This dilemma arises because we characterize the graph vertices inside a community by using the concept of “sharing neighbors”. The only opportunity for two vertices to share common neighbors in a bipartite graph is that they both belong to a same subset V_i. However, when considering a subgraph which consists of vertices from a single V_i, this subgraph always has a zero density, thus eventually no subgraphs will be output from the algorithm.

One way to overcome the difficulty of Algorithm 1 when applied to bipartite graphs, is to perform a partial clustering separately for the rows and for the columns of B, by using the same similarity idea of Algorithm 1. In essence this is similar to the first approach suggested for directed graphs where the application warrants to differentiate between incoming and outgoing edges. It is equivalent to finding subsets of V_i where vertices share similar neighbors (from the complement of V_i). However, separate subsets do not directly imply a dense subgraph of the original bipartite graph, i.e., for both sides of the bipartite graph. Alternatively, we opt to use an approach that shares the spirit of co-clustering: Find two subsets, $V_s \subset V_1$ and $V_t \subset V_2$, *simultaneously*, such that they are densely connected.

A reasonable strategy for purpose is to augment the original bipartite graph by adding edges between some of the vertices that are connected by a path of length two. Clearly, this will add edges between vertices of the same V_i, making the graph a regular undirected graph. This will not change the density structure of the bipartite graph itself; rather, it encourages the discovery of the dense components. If V_s and V_t are densely connected, we can add enough edges between the vertices in V_s and also edges between those in V_t, then all the vertices in $V_s \cup V_t$ will appear so densely connected that $V_s \cup V_t$ can be easily extracted by a blocking algorithm. Fig. 4 illustrates an extreme case. The bipartite graph consists of three bicliques. If we artificially fill in edges between vertices inside the same biclique as shown in (b), then a blocking algorithm will easily recognize the three cliques in (c) and hence extract the three corresponding bicliques.

The question is what edges to add, since we do not know V_s and V_t. The similarity matrices M_1 (and M_2) in (5) are especially useful for answering this question. Consider two vertices, $v_{s_1}, v_{s_2} \in V_s$, for example. The fact that V_s and V_t are densely connected implies the high likelihood that v_{s_1} and v_{s_2} share similar neighbors. In other words, the two columns in A, which v_{s_1} and v_{s_2} correspond to, have a large cosine similarity. Therefore, it is natural to add an edge between v_{s_1} and v_{s_2}. From the perspective of the similarity matrix, this is to choose the largest entries of M and add them to A. To be precise, we modify the adjacency matrix A of a given bipartite graph into

$$\hat{A} = \begin{bmatrix} \hat{M}_1 & B \\ B^T & \hat{M}_2 \end{bmatrix}, \tag{6}$$

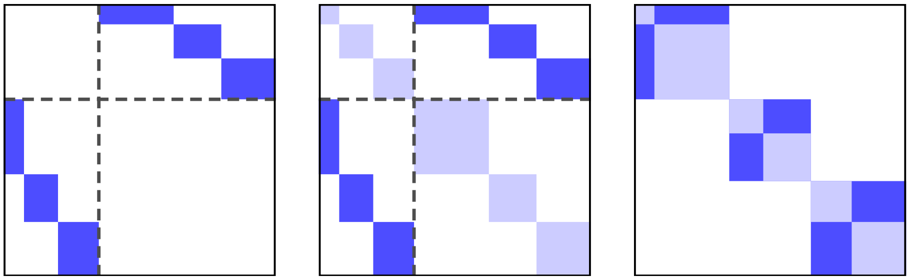
where $\hat{M}_1$ (resp. $\hat{M}_2$) is obtained by erasing the diagonal and keeping only the $2|E|$ largest nonzero entries of M_1 (resp. M_2), and $|E|$ is the number of edges in the original graph (i.e., it equals the number of nonzeros of B).

Once the densification process yields the modified adjacency matrix $\hat{A}$, which represents the augmented graph, we proceed to calculate the similarity matrix $\hat{M}$:

$$\hat{M}(i,j) = \frac{\left\langle \hat{A}(:,i), \hat{A}(:,j) \right\rangle}{\left\| \hat{A}(:,i) \right\| \left\| \hat{A}(:,j) \right\|}, \tag{7}$$

which is used to build the hierarchy for the vertex set $V = V_1 \cup V_2$. Algorithm 2 summarizes the steps. Note that the procedure DENSE-SUBGRAPHS(G, G', C, $d_{\min}$) has been introduced in Algorithm 1.

A toy example is shown in Fig. 5. The blue-green coloring indicates the two disjoint subsets: $V_1 = \{1, 2, \ldots, 8\}$ and $V_2 = \{9, 10 \ldots, 13\}$. A visual inspection results that the bipartite graph consists of two dense components: all the vertices to the left of 6 (including 6) contribute to one component, and the rest of the vertices (arranged in a hexagon shape) form the other. The densification of the graph, as shown in (b), further convinces the conjecture of the two dense components. Using the modified weighted adjacency matrix $\hat{A}$, we compute $\hat{M}$ and perform a hierarchical clustering similar to the one shown in Fig. 3(c). By using a density threshold $d_{\min} = 0.5$, it happens that two dense

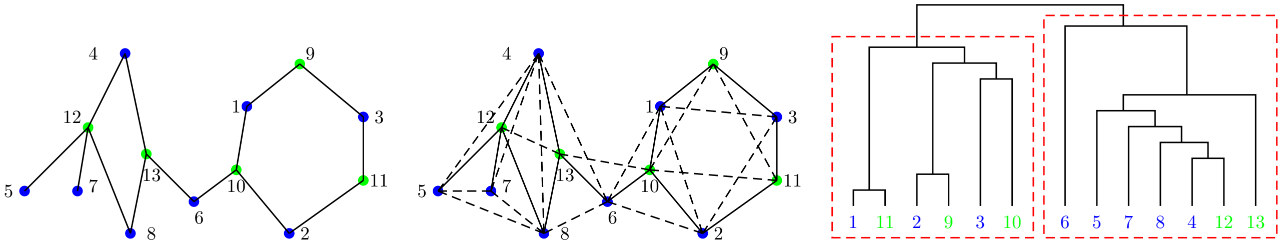


(a) Adjacency matrix A.

(b) A after edge fill-in.

(c) Blocking of the matrix in (b).

Fig. 4. A bipartite graph with the effect of edge fill-in.



(a) Bipartite graph G.

(b) Densification of G. Weights of the fill-in edges (dashed) have not been shown.

(c) The dendrogram constructed from (b).

Fig. 5. Two dense subgraphs (encapsulated in the red dashed frames) are found for a sparse bipartite graph as shown in (a). The density threshold $d_{\min} = 0.5$.

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Algorithm 2 Finding Dense Subgraphs of a Sparse Bipartite Graph
Input: Sparse bipartite graph $G$, density threshold $d_{\min}$.
1: [Densification:] Modify the adjacency matrix $A$ of $G$ into $\hat{A}$ as defined in (6).
2: Construct $G'$ with the weighted adjacency matrix $\hat{M}$ as defined in (7).
3: Let $C$ be the array of tuples $(i, j, \hat{M}(i,j))$, for all nonzero $\hat{M}(i,j)$ and $i < j$, sorted in ascending order of $\hat{M}(i,j)$.
4: Run DENSE-SUBGRAPHS($G$, $G'$, $C$, $d_{\min}$).
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subgraphs are extracted, exactly the same as what we conjecture by visual inspection: $\{1, 2, 3, 9, 10, 11\}$ and $\{4, 5, 6, 7, 8, 12, 13\}$.

A question may be asked why one shall not use Algorithm 2 as a universal solution for all the three types of graphs: undirected, directed, and bipartite. Indeed, in all cases the graph is canonically associated with a matrix (either the square matrix A for undirected/directed graphs, or the rectangular matrix B for bipartite graphs). As was stressed earlier, this approach would build the hierarchy for both the rows and the columns of B. this simultaneity of the blocking on each side of the bipartite graph is a feature in a way that is similar to the problem of co-clustering. On the other hand, for a general undirected graph, both sides of the matrix A represent the same set of vertices, in which case a co-clustering is not sensible.

III. Implementation and Computational Costs

Despite the conceptual simplicity of the ideas described in the previous section, a careful design is needed to obtain efficient algorithms. This section discusses several important details that will lead to an efficient implementation. The computational complexities of these implementations will also be considered. As will soon be seen, most of the steps have a computational cost only linear to the number of vertices in the graph, except that in addition we need to sort an array of size also linear in this number. Thus, the proposed methods have the potential of being scalable to very large data sets. However, it is noted that there may be large prefactors in this simple big-O notation. As a result, to complement this incomplete theoretical analysis, we show in Section IV-B actual run times for a collection of real-life graphs from various application domains.

Some additional notation is needed. For a given graph $G(V, E)$, the number of vertices is $|V|$, and the number of edges is $|E|$. Since G is sparse, we typically assume that $|E| = O(|V|)$. If the graph is undirected, then the adjacency matrix A has $n = |V|$ rows/columns and $\mathrm{nz}(A) = 2|E|$ nonzero entries. If the graph is directed, then A has $n = |V|$ rows/columns and $\mathrm{nz}(A) = |E|$ nonzeros. Further, if the graph is bipartite, the two disjoint subsets have cardinalities $|V_1| = n_1$ and $|V_2| = n_2$. Thus, the matrix B has size $n_1 \times n_2$ with $\mathrm{nz}(B) = |E|$ nonzero entries. The adjacency matrix A of a bipartite graph has size $n \times n = (n_1 + n_2) \times (n_1 + n_2)$ with $\mathrm{nz}(A) = 2|E|$ nonzero entries. In all cases, we have $\mathrm{nz}(A) = O(n)$.

A. The Computation of M ($\hat{M}$)

According to Eqn. (4), a naive way of computing M has the time complexity $O(\mathrm{nz}(A)^2) = O(n^2)$, since to compute an entry $M(i,j)$ takes time proportional to the sum of the numbers of nonzeros of $A(:,i)$ and $A(:,j)$. However, note that M is equal to $X^T X$, where X is the matrix A with each column normalized. A further investigation of Eqn. (6) (or (5)) indicates that the matrices M_1 and M_2 also take the form $X^T X$. Thus, an efficient way of computing M and $\hat{M}$ is to exploit the fact that X is sparse.

In the sequel, we consider how to multiply a sparse matrix X by its transpose:

$$Y = X^T X := ZX,$$

where $Z = X^T$. The most efficient way in practice is to compute Y row by row. Note that

$$Y(i,:) = \sum_j Z(i,j)X(j,:).$$

Thus, we first transpose X into Z, then for each row i of Z, we compute a weighted sum of the rows of X which correspond to the nonzero elements in row i of Z. A particular issue is how to compute this weighted sum in time proportional to the total number of nonzeros involved, instead of to the length of a row of X. The technique is to pre-allocate two working arrays a and b, each of which has a size the same as a row of X. When computing row i of Y, we find the nonzero entries $Z(i,j)$, and for each j, we add the nonzeros of $X(j,:)$ multiplied by $Z(i,j)$ into the working array a, and store the information of which locations of a has been changed in the working array b. Then after the weighted sum is computed, we use the information in b to reset the array a to zero and also erase the content in b, then proceed to the next i.

Let the maximum number of nonzeros per row of X be p. Then the upper bound of the time cost of the above technique for computing $X^T X$ is $O(p \cdot \mathrm{nz}(X))$, since to compute the i-th row of Y takes time $O(p \cdot \mathrm{nz}(Z(i,:)))$. In the average case, p can be considered a constant, thus the total time cost simplifies to $O(\mathrm{nz}(X))$. Also, transposing X has the same time complexity. In the graph language, X is the column-normalized A (or A^T), and p means the maximum number of neighbors for a vertex. Thus, the time cost of computing M (or $\hat{M}$) is $O(\mathrm{nz}(A)) = O(n)$.

We should note that the above method is a standard technique used for sparse matrix-matrix multiplications (cf. e.g., [22]). Perhaps the only important point to retain is the surprising fact that it takes time only linear in n to multiply two sparse matrices, assuming that the maximum number p of nonzeros per row is bounded by a constant. It is noted that for some real-life graphs the degree of a vertex may follow a power low distribution, which means that p can become large for large graphs of a given application. Nevertheless, in practice it is rare that p will be $O(n)$, which leads to the situation that the computational cost will rise to the forbidding $O(n^2)$.

B. The Computation of the Hierarchy/Dendrogram

The routine DENSE-SUBGRAPHS (cf. Algorithm 1) essentially computes a hierarchy of the graph vertices in a top-down fashion. Recursive calls of this routine are very time consuming since between lines 5 and 9, with each removal of an edge in G', a graph traversal procedure (such as the breadth first search) is needed to examine the connectivity of the graph. However, as the two toy examples (cf. Fig. 3(c) and 5(c)) suggest, it is entirely possible to build the dendrogram T in an opposite way: the bottom-up fashion.

The key is the array C which is sorted in ascending order of the nonzero entries $M(i,j)$ (or $\hat{M}(i,j)$)[1]. It indicates the order of the merges in the hierarchy/dendrogram T. Initially, each vertex $v \in V$ is a separate tree in the forest. Beginning from the end of the array C, each time we have a pair (i,j). We find the roots r_i and r_j of i and j, respectively. If r_i and r_j are different, we make a new root r with the left child r_i and the right child r_j (see Fig. 6). After iterating the whole array C, a single tree is returned, which is nothing but T.

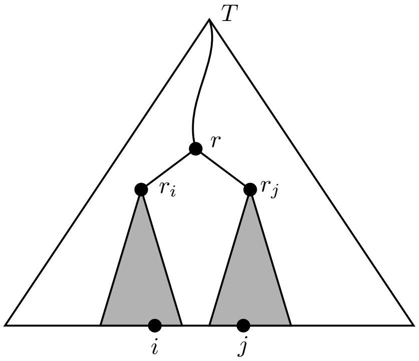


Fig. 6. The dendrogram T as a binary tree. Node r is the lowest common ancestor of i and j, and r_i and r_j are the children of r.

Note that the above process is equivalent to monitoring the connected components of a graph when edges are successively inserted (a.k.a. incremental connected components [24]). Initially we have a virtual graph with the vertex set V but without edges. When reversely iterating the array C, we merge the two subsets s_i and s_j, which i and j belongs to respectively, if $s_i \neq s_j$. Finally, a single set, which contains all the vertices in V, is returned.

Therefore, we can utilize the two standard disjoint-set operations SET-FIND and SET-UNION to assist the process of building T. When we iterate C and get a pair (i,j) each time, we first do SET-FIND(i) → s_i and SET-FIND(j) → s_j. If $s_i = s_j$, nothing is done. On the other hand, if $s_i \neq s_j$, we call SET-UNION to combine s_i and s_j. Meanwhile, we make a new node r which has the r_i and r_j (stored with the disjoint-set data structure) as the two children, and associate r with the combined set $s = s_i \cup s_j$.

The total time of the above process can be split in two parts: (a) the time of all the SET-FIND and SET-UNION calls, and (b) the gross time to build T. Part (a) is indeed the incremental connected component process, which takes time $O(n + \mathrm{nz}(M))$, since the graph G' has n vertices and $O(\mathrm{nz}(M))$ edges. Part (b), which consists of making new nodes and assigning children, has a time complexity linear to the size of T, which is $O(n)$.

We still can improve the performance. Recall that the whole bottom-up process is nothing but to yield the graph G' from a collection of isolated vertices by successively inserting edges. We can stop the insertion of edges at some point. This essentially yield an incomplete hierarchy, which is the part of T below some level. We opt to stop after we have inserted $O(n)$ edges. In practice, the number of inserted edges can be simply set as $\mathrm{nz}(A)$, or as $\tau \cdot \mathrm{nz}(A)$ by introducing some coefficient parameter τ. This may greatly reduce the cost of part (a) from $O(n + \mathrm{nz}(M))$ to $O(n)$, and also some minimal cost of part (b). By doing this, the negative impact on the final dense subgraphs extraction process is hoped to be minimal, since we only miss, if any, large subgraphs that have not been formed by merging in the hierarchy. We still are able to extract the dense parts of the hypothetically missing large subgraphs. Another advantage is that instead of sorting the nonzeros of M in $O(\mathrm{nz}(M)\log(\mathrm{nz}(M)))$ time to make the array C, we only need to sort the $O(n)$ largest nonzeros in $O(n \log n)$ time.

[1] To reduce the complication in reading, we thereafter omit the text "(or $\hat{M}$)" in this subsection. Readers are reminded that whenever the analysis is applied to a bipartite graph, all the notions involving M should be replaced by $\hat{M}$.

C. Collecting Density Information and Extracting Dense Subgraphs

Recall that in the hierarchy T, each internal node r represents a subgraph of G whose vertices are the leaf nodes of the subtree rooted at r. The dense subgraphs extraction process starts from visiting the root of T. If the subgraph corresponding to the current node has the density higher than the input threshold $d_{\min}$, it is output; otherwise the two children of the current node are visited and the whole process is recursive. Thus, the extraction process is equivalent to a traversal of T and is very cheap, given that the densities of all the subgraphs have been computed and stored in the internal nodes r.

In the following we discuss how the subgraph densities are computed. For each internal node r of T, it is sufficient to store two values: the number n_r of vertices the corresponding subgraph contains, and the number e_r of edges. The number of vertices can be easily computed in a recursive way: $n_r = n_{r_i} + n_{r_j}$, where r_i and r_j are the two children of r. However, the computation of e_r is not that straightforward. It is the sum of e_{r_i}, e_{r_j} and $e_{c(r_i,r_j)}$, where $e_{c(r_i,r_j)}$ is the number of edges crossing the subgraphs r_i and r_j represent. Thus, the computation of e_r can be split in two phases. The first phase is to compute $e_{c(r_i,r_j)}$ for each internal node r. The second phase is to recursively compute $e_r = e_{r_i} + e_{r_j} + e_{c(r_i,r_j)}$ for node r from its two children.

Further explanations on how $e_{c(r_i,r_j)}$ is counted are in order. Recall in Fig. 6 that r is the lowest common ancestor (LCA) of i and j. Thus, we initialize $e_r = 0$ for all r. For each edge $\{i, j\}$ in the undirected graph (either the original graph, the undirectified graph, or the densified graph), we find the lowest common ancestor r of i and j and add 1 to e_r. After iterating all the edges, the temporary e_r value for each internal node r in the hierarchy is exactly $e_{c(r_i,r_j)}$, thus finishing phase one as mentioned in the previous paragraph.

Currently, the most efficient LCA data structure answers queries in constant time after a linear time preprocessing [25], [26]. Thus, the time cost for phase one is $O(n + \mathrm{nz}(A)) = O(n)$, since the tree T has $O(n)$ nodes and we need to find the lowest common ancestors for $O(\mathrm{nz}(A))$ pairs. This complexity applies to all the three types of graphs, since even after modifications (either undirectification or densification), the adjacency matrix of the graph always has $O(\mathrm{nz}(A))$ nonzeros. Therefore, the time cost of computing n_r and e_r for all nodes r in the hierarchy takes time $O(n)$. This is also the cost of the final dense subgraphs extraction process, which simply consists of a traversal of T.

In summary, the improved versions of the two algorithms presented in Sec. II are shown in Algorithms 3 and 4, by incorporating the above discussions. These supersede Algorithms 1 and 2 in the rest of the paper. In the pseudocodes, the hierarchy/dendrogram T is a tree with the root $T.root$. A node r in the tree has the left child $left$, the right child $right$, and the density $density$ which is computed from num_vertex (n_r) and num_edge (e_r) according to the appropriate definition of density introduced at the beginning of Sec. II.

Algorithm 3 Finding Dense Subgraphs of a Sparse Undirected Graph (Improved Version of Algorithm 1)

```
Input: Sparse undirected graph $G$, density threshold $d_{\min}$.
Compute the matrix $M$ as defined in (4).
Sort the largest $t$ nonzero entries of $M$ in decreasing order, where $t = \mathrm{nz}(A)$. Denote $C$ the sorted array.
Construct the hierarchy $T$ according to the sorted vertex pairs designated by $C$.
COUNT-VERTICES-AND-EDGES($T$, $G$)
Compute $r.density$ for all nodes $r$ of $T$ according to (1).
EXTRACT-SUBGRAPHS($T.root$)

function COUNT-VERTICES-AND-EDGES($T$, $G$)
    Initialize $r.num\_edge \leftarrow 0$ for all nodes $r$ of $T$.
    Construct the LCA data structure for $T$.
    for all edge $\{i, j\}$ of $G$ do
        Find the lowest common ancestor $r$ of $i$ and $j$.
        $r.num\_edge \leftarrow r.num\_edge + 1$
    end for
    COUNT-VERTICES-AND-EDGES-WRAP-UP($T.root$)
end function

function COUNT-VERTICES-AND-EDGES-WRAP-UP($r$)
    if $r.left \neq nil$ and $r.right \neq nil$ then
        COUNT-VERTICES-AND-EDGES-WRAP-UP($r.left$)
        COUNT-VERTICES-AND-EDGES-WRAP-UP($r.right$)
    end if
    if $r.left \neq nil$ and $r.right \neq nil$ then
        $r.num\_vertex \leftarrow$
          $r.left.num\_vertex + r.right.num\_vertex$
        $r.num\_edge \leftarrow$
          $r.left.num\_edge + r.right.num\_edge + r.num\_edge$
    else
        $r.num\_vertex \leftarrow 1$
    end if
end function

function EXTRACT-SUBGRAPHS($r$)
    if $r.density > d_{\min}$ then
        Output the leaves of the subtree rooted at $r$.
    else if $r.left \neq nil$ and $r.right \neq nil$ then
        EXTRACT-SUBGRAPHS($r.left$)
        EXTRACT-SUBGRAPHS($r.right$)
    end if
end function
```

IV. Experimental Results and Applications

This section shows a few experimental results to illustrate the efficiency and the effectiveness of the proposed algorithms for extracting dense subgraphs. The experiments were performed under a Linux desktop with four AMD Opteron Processors (2.20GHz) and 16GB memory. The programs were not parallel and used only one processor. The algorithms were implemented in C/C++, and the programs were compiled using g++ with -O2 level optimization.

A. Simulations and Accuracies

In this subsection we show the dense subgraphs extraction results of two simulated graphs. A visualization is shown in Fig. 7. The graphs were randomly generated subject to the parameters given in Tab. I. The simulated undirected graph has three dense components/subgraphs, and the bipartite graph has four. We computed the densities of the dense components for each graph, and used the smallest of the densities as the input parameter $d_{\min}$ to our algorithms. The aim of this experiment

Algorithm 4 Finding Dense Subgraphs of a Sparse Bipartite Graph (Improved Version of Algorithm 2)

```
Input: Sparse bipartite graph $G$, density threshold $d_{\min}$.
[Densification:] Modify the adjacency matrix $A$ of $G$ into $\hat{A}$ as defined in (6).
Compute the matrix $\hat{M}$ as defined in (7).
Sort the largest $t$ nonzero entries of $\hat{M}$ in decreasing order, where $t = \mathrm{nz}(\hat{A})$. Denote $C$ the sorted array.
Construct the hierarchy $T$ according to the sorted vertex pairs designated by $C$.
COUNT-VERTICES-AND-EDGES($T, G$). [Instead of counting the number of vertices $r.num\_vertex$ for each subgraph, count the number of vertices that belong to $V_1$ and $V_2$ for each subgraph, in a similar way.]
Compute $r.density$ for all nodes $r$ of $T$ according to (3).
EXTRACT-SUBGRAPHS($T.root$)
```

is to show that the proposed algorithms are able to discover the intended dense components when a good parameter is provided. Other experiments for the situation when the density threshold is unknown in advance will be discussed in later subsections.

TABLE I
SIMULATION PARAMETERS FOR THE GRAPHS IN FIG. 7. FOR THE UNDIRECTED GRAPH, EACH (s, t) PAIR MEANS A (SUB)GRAPH WITH s VERTICES AND APPROXIMATELY t EDGES. FOR THE BIPARTITE GRAPH, EACH (s_1, s_2, t) PAIR MEANS A (SUB)GRAPH WITH $s_1 + s_2$ VERTICES AND APPROXIMATELY t EDGES.

Graph	Undirected	Bipartite
Whole	(100, 2000)	(100, 170, 1940)
Component 1	(25, 420)	(20, 40, 370)
Component 2	(30, 550)	(20, 35, 280)
Component 3	(20, 290)	(17, 30, 260)
Component 4		(15, 45, 340)

The criterion we use to measure the "accuracy" of the extracted dense subgraphs is the F-score. Here, the term "accuracy" only states how much the extracted subgraphs deviate from the intended dense components. Indeed, a precise determination of the dense subgraphs in each simulated case does not exist. As long as the output subgraphs have densities higher than the input threshold, there is no harm in considering that the result is as good as the "ground truth". For each dense component i in the intended construction, let V_i be its vertex set. We compare V_i with the extraction result $\tilde{V}_i$, and the F-score is defined as

$$F_i = \frac{2}{\dfrac{1}{precision} + \dfrac{1}{recall}} = \frac{2}{\dfrac{|V_i|}{|V_i \cap \tilde{V}_i|} + \dfrac{|\tilde{V}_i|}{|V_i \cap \tilde{V}_i|}}.$$

Tab. II shows the average F-score for each component i by simulating the graphs 100 times. It can be seen that the extraction results match the intended constructions quite well.

TABLE II
ACCURACY OF THE EXTRACTED DENSE SUBGRAPHS. THE UPPER TABLE IS FOR THE UNDIRECTED GRAPH, AND THE BOTTOM ONE IS FOR THE BIPARTITE GRAPH.

Dense component	1	2	3
Average F-score	0.9844	0.9882	0.9694

Dense component	1	2	3	4
Average F-score	0.9720	0.9310	0.9755	0.9730

B. Real Graphs and Running Times

We tested the performance of our algorithms on real-life graphs with different sizes and from various application domains. The graphs are listed in Tab. III; they include a social network (`polblogs`), a biological network (`yeast`), a citation network (`hep`), a trust network (`epinions`), an information network (`NDwww`), and graphs that represent the relationships between words (`Reuters911`, `foldoc`, `dictionary28`), between users and movies (`MovieLens`), and between words and documents (`newsgroup`, `cmuSame`, `cmuDiff`, `cmuSim`). In this subsection, we are mainly interested in the running times of the algorithms as opposed to the graph sizes. Some of the graphs will be mentioned again in later subsections for analyzing the extraction results and understanding community structures. For such graphs, more information related to the semantics of the graphs will be presented when appropriate.

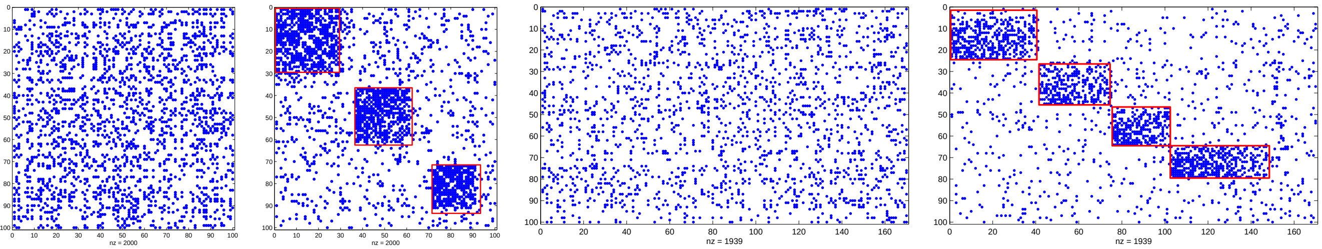
TABLE III
SOME REAL-LIFE GRAPHS.

Graph	Description and Link
`polblogs` [27]	A directed network of hyperlinks between weblogs on US politics. `http://www-personal.umich.edu/~mejn/netdata/`
`yeast` [28]	Protein-protein interaction network. `http://vlado.fmf.uni-lj.si/pub/networks/data/bio/Yeast/Yeast.htm`
`Reuters911` [29]	Reuters terror news network. `http://www.cise.ufl.edu/research/sparse/matrices/Pajek/Reuters911.html`
`foldoc`	... free on-line dictionary of computing ... `http://www.cise.ufl.edu/research/sparse/matrices/Pajek/foldoc.html`
`hep`	The citation graph of the hep-th portion of arXiv. `http://www.cs.cornell.edu/projects/kddcup/datasets.html`
`epinions` [30]	Trust network of the users on Epinions.com. `http://www.trustlet.org/wiki/Downloaded_Epinions_dataset`
`dictionary28`	... dictionary ... `http://www.cise.ufl.edu/research/sparse/matrices/Pajek/dictionary28.html`
`NDwww` [31]	Webpages within nd.edu domain. `http://vlado.fmf.uni-lj.si/pub/networks/data/ND/NDnets.htm`

`cmuSame` [32]
`cmuDiff`
`cmuSim`
	The 20 Newsgroups data set (three subsets).

`MovieLens` [33]	The MovieLens data set. `http://www.grouplens.org/taxonomy/term/14`
`newsgroup` [34]	The 20 Newsgroups data set. `http://people.csail.mit.edu/jrennie/20Newsgroups/`

The running times are shown in Tab. IV. Two aspects of the experimental design are noted. First, the density threshold $d_{\min}$ is the least important parameter in this experiment, since it affects only the extraction time (the last column in the table), which is almost negligible compared with other times. This meanwhile indicates that the parameter $d_{\min}$ does not constitute a weakness



(a) An undirected graph. (b) Dense subgraphs of (a). (c) A bipartite graph. (d) Dense subgraphs of (c).

Fig. 7. The extracted dense subgraphs of two simulated graphs.

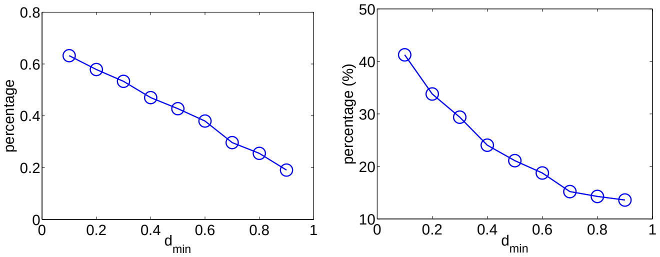
of our algorithms—we can always tune the parameter in real time. We fixed $d_{\min}$ to be 0.1 in this experiment. The second aspect is the parameter τ, where recall that in Sec. III-B we insert $\tau \cdot \mathrm{nz}(A)$ edges in the incremental connected component process. This constructs an incomplete, yet probably sufficient, hierarchy T. The parameter τ directly affects the sorting time and the time to compute the hierarchy. In most of the cases $\tau = 1$ is sufficient to yield meaningful dense subgraphs, except that in a few cases we tune the parameter to an appropriate value such that desirable subgraphs are extracted. The values of τ are listed in the table.

From Tab. IV we see that the proposed algorithms are efficient. A large part of the running time is spent on the matrix-matrix multiplication (computing M or $\hat{M}$), which is not difficult to parallelize. Note that all the graphs are run on a single desktop machine. In the future we will investigate parallel versions of the algorithms that can deal with massive graphs, at a minimal run time.

C. Power Law Distribution of the Dense Subgraph Sizes

To further understand the extraction results, we plot in Fig. 8 the distribution of the dense subgraph sizes. We experimented with two graphs: a collaboration network (`hep`) and a dictionary graph (`dictionary28`), using various density thresholds. Within each plot, the horizontal axis is the size of a subgraph, and each plotted point shows the number of dense subgraphs of this size. Remarkably, all the plots seem to indicate that the subgraph sizes follow the power law distribution—roughly speaking, the number $P(x)$ of dense subgraphs is a power function of the subgraph size x, in the form $P(x) \propto x^{\gamma}$ with $\gamma < 0$. This adds yet one more instance to the family of power laws previously discovered on social and information networks [35], [36], the most notable of which is the power law distribution of the vertex degrees. Each plot of Fig. 8 also shows a line that is the least squares fit to the plotted data in log-log scale. The slope of the line, which is essentially the exponent γ, is typically in the range from -3.5 to -1.5.

It is clear from our algorithms that the extracted dense components resulting from a larger $d_{\min}$ are all subgraphs of those resulting from a smaller $d_{\min}$. This effectively means that in the power law expression $P(x) \propto x^{\gamma}$, the exponent γ tends to decrease as the threshold $d_{\min}$ increases, since the extracted subgraphs become smaller and smaller. This can be seen from Fig. 8, where in general the fitted line becomes steep when $d_{\min}$ is increasing. Further, the total number of vertices that belong to the extracted subgraphs will naturally decrease. A plot (Fig. 9) indicates that this decrease looks linear.



(a) `hep` (b) `dictionary28`

Fig. 9. Percentage of vertices that belong to the extracted dense subgraphs.

D. A Blog Network Example

In this subsection we analyze the structure of a blog network `polblogs`. The data set, a network that connects bloggers of different political orientations, was originally constructed around the time of the 2004 U.S. presidential election, to study the interactions between the two groups: liberal and conservative [27]. The graph contains 1,490 vertices, among which the first 758 are liberal blogs, and the remaining 732 are conservative. An edge in the graph indicates the existence of citations between the two blogs. As can be seen from Figure 10(a), there are much denser links between blogs that hold the same political orientation than between those with different leanings.

We ran our algorithm on this graph by using different density thresholds. A typical result is shown in plot (b), where $d_{\min} = 0.4$. Indeed, for all the thresholds we tried, only two dense subgraphs (of size larger than 4) were identified. These two subgraphs perfectly correspond to the two politically oriented groups: The smaller subgraph (except for one vertex in the situation of low density thresholds) consists of conservative blogs, whereas the larger subgraph consists of liberal blogs. Hence, these two subsets of blogs are truly representative of the two groups.

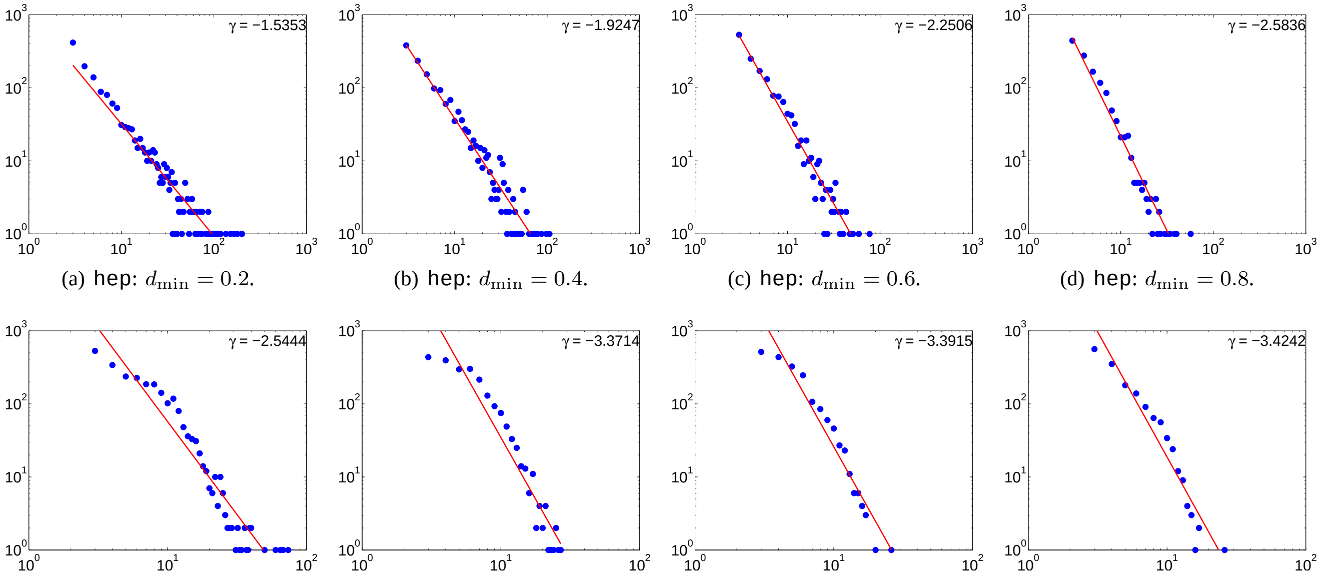
It is observed that the density of the smaller subgraph is in general larger than that of the larger subgraph. One conclusion from this is that conservative blogs tend to make a larger number of citations to each other than liberal ones. This happens to be in agreement with the point made in [27] that "right-leaning (conservative) blogs have a denser structure of strong connections than the left (liberal)", a result of a different analysis using the number of citations between different blogs. However, since the size of the liberal subgraph is much larger than that of the conservative (cf. plot (c)), an alternative conclusion is that more liberal blogs are willing to cite each other than conservative ones. This is somehow opposite to the dense citations in conservative blogs.

TABLE IV
RUNNING TIMES (UNIT: SECONDS) FOR THE GRAPHS IN TABLE III.

Graph	Type	$\lvert V\rvert$	$\lvert E\rvert$	τ	Similarity[a]	Sorting[b]	Hierarchy[c]	Density[d]	Extraction[e]
`polblogs`	directed	1,490	19,022	1	0.07	0.06	0.00	0.01	0.00
`yeast`	undirected	2,361	6,646	1	0.00	0.03	0.00	0.01	0.00
`Reuters911`	undirected	13,332	148,038	1	1.58	0.59	0.02	0.05	0.00
`foldoc`	directed	13,356	120,238	1	0.21	0.18	0.01	0.04	0.00
`hep`	directed	27,770	352,768	1	2.10	1.14	0.06	0.15	0.00
`epinions`	directed	49,288	487,182	3	3.86	2.04	0.12	0.17	0.02
`dictionary28`	undirected	52,652	89,038	1	0.22	0.11	0.04	0.08	0.01
`NDwww`	directed	325,729	1,469,679	30	13.98	42.07	2.46	0.67	0.07

Graph	Type	$\lvert V_1\rvert$	$\lvert V_2\rvert$	$\lvert E\rvert$	τ	Similarity[a]	Sorting[b]	Hierarchy[c]	Density[d]	Extraction[e]
`cmuSame`	bipartite	3,000	5,932	263,325	1	11.81	0.51	0.01	0.08	0.00
`cmuDiff`	bipartite	3,000	7,666	185,680	1	2.94	0.55	0.02	0.06	0.00
`cmuSim`	bipartite	3,000	10,083	288,989	1	5.46	1.03	0.01	0.10	0.00
`MovieLens`	bipartite	3,706	6,040	1,000,209	10	40.26	5.59	0.58	0.28	0.00
`newsgroup`	bipartite	18,774	61,188	2,435,219	1	140.32	11.15	0.21	0.87	0.02

[a] The time to compute M or $\hat{M}$, including the modification of A in the bipartite graph case (cf. Sec. III-A).
[b] The time to sort $\tau \cdot \mathrm{nz}(A)$ nonzeros of M or $\hat{M}$ (cf. Sec. III-B).
[c] The time to construct the hierarchy T (cf. Sec. III-B).
[d] The time to compute the densities of all the subgraphs in the hierarchy (cf. Sec. III-C).
[e] The time to extract the dense subgraphs given a density threshold (cf. Sec. III-C).



(a) `hep`: $d_{\min} = 0.2$. (b) `hep`: $d_{\min} = 0.4$. (c) `hep`: $d_{\min} = 0.6$. (d) `hep`: $d_{\min} = 0.8$.

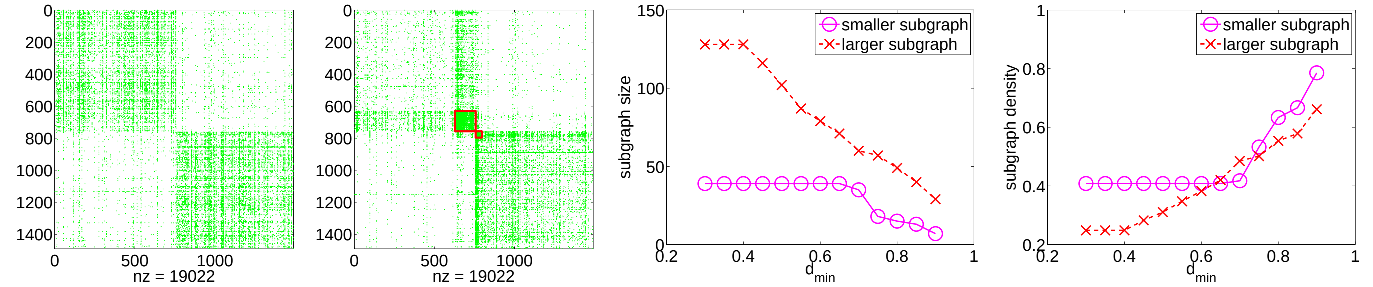
(e) `dictionary28`: $d_{\min} = 0.2$. (f) `dictionary28`: $d_{\min} = 0.4$. (g) `dictionary28`: $d_{\min} = 0.6$. (h) `dictionary28`: $d_{\min} = 0.8$.

Fig. 8. Statistics of the extracted dense subgraphs for different density thresholds. The vertical axis is the number of subgraphs, and the horizontal axis is the subgraph cardinality. The plots are in log-log scale. Each red line is a least squares fit to the data, with its slope γ indicated at the upper right corner of each plot.

It is interesting to note here that plot (c) can suggest a way to select an "optimal" threshold $d_{\min}$. In this particular case, $d_{\min} = 0.4$ seems optimal, because beyond this point, the size of one of the subgraphs starts decreasing significantly, whereas there is no change when $d_{\min}$ grows from smaller values.

E. A Text Network Example

Words can be organized to form a network, where the structures of the relations between words can be exploited in order to analyze word usage and to understand linguistics. The data set `Reuters911` "is based on all stories released during 66 consecutive days by the news agency Reuters concerning the September 11 attack on the U.S., beginning at 9:00 AM EST 9/11/01." (See the link in Tab. III for the description.) It consists of 13,332 words from these news reports, and two words are connected if they appear in the same semantic unit (sentence here). By our technique (using a density threshold $d_{\min} = 0.5$), we extracted words that tend to be used together under such a context, such as those related to politics: `house of reps`, `senate`, `house`, `committee`, `capitol`, `hill`, `congressional`, `republican`, `senator`, `democrat`, those related to Arabic countries and names: `tunisia`, `yahya`, `benaissa`, `ben`, `habib`, `morocco`, `riziq`, `syihab`, and those related to the



(a) Original graph.

(b) Two dense subgraphs.

(c) Subgraph size.

(d) Subgraph density.

Fig. 10. Dense subgraph extraction of a political blog network as shown in (a). Only two subgraphs (of size larger than 4) are identified for all the density thresholds experimented with. Plot (b) shows the two subgraphs (using $d_{\min} = 0.4$) in red boxes. Plots (c) and (d) show the changes in the sizes and the densities as $d_{\min}$ varies.

economic impacts: `market`, `stock`, `exchange`, `trade`, `wall street`.

Perhaps the most important group of words (the largest extracted subgraph) is listed in Tab. V. They can be used as key words to summarize the 911 tragedy and the stories behind it.

TABLE V

THE LARGEST GROUP OF WORDS THAT TEND TO APPEAR TOGETHER IN 911-RELATED NEWS REPORTS.

attack	united states	pres bush	official	people
washington	afghanistan	taliban	country	bin laden
afghan	american	kabul	al quaeda	force
troop	tuesday	wednesday	military	day
week	government	friday	thursday	monday
nation	support	pakistan	saudi-born	strike
new york	city	time	terrorism	terrorist
security	report	war	world	sunday
raid	network	new	air	alliance
opposition	capital	america	pakistani	militant
hijack	suicide	hijacker	aircraft	plane
flight	authority	leader	bomb	pentagon
kandahar	southern	stronghold	anthrax	case
bacterium	target	airport	possible	white house
group	information	campaign	operation	jet
fbi	letter	mail	test	dissident
deadly	month	part	threat	federal
tower	twin	110-story	world trade ctr	sept
state	saturday	islamic	muslim	11
man	member	fighter	agency	

F. A Bipartite Graph Example

Bipartite graph models are common in text mining, recommender systems, and other research fields. We show the `newsgroup` example where the dense subgraph extraction results can be interpreted as a partial co-clustering of the terms and the documents. Unlike existing co-clustering approaches [37]–[40] that return a complete clustering of the data matrix, our method returns only a subset of the entities where dense connections exist in each cluster.

The data set `newsgroup` (see Tab. III) is organized as a term-document matrix, where there are approximately 18,774 documents from 20 different newsgroups. The dictionary (number of terms) has size 61,188. The matrix represents a sparse graph where connections are drawn between two types of entities: terms and documents. We extracted dense subgraphs using the parameter $d_{\min}$ ranging from 0.1 to 0.9, and required that a subgraph should consist of at least 5 documents and 3 terms. To measure the clustering quality of the documents, we compute the entropy and the purity [41] of the document clusters. Fig. 11 shows the plot. It indicates that the document clusters are pure, especially when the density threshold is high. The plot also shows the total number of clustered documents. It varies from 10% to 30% of the whole document set. From the document clusters, we inspect the corresponding terms. We use the extraction results of $d_{\min} = 0.9$. In Tab. VI, we list the largest four term clusters, and the newsgroup to which they (or most of them) correspond. It can be seen that the words are very relevant to the topics of the newsgroups.

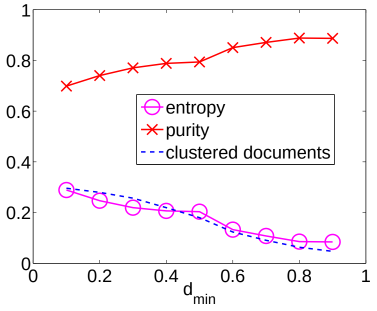


Fig. 11. Clustering quality of the documents in `newsgroup`: entropy and purity. “Clustered documents” is the percentage of documents that are clustered.

TABLE VI

THE LARGEST TERM CLUSTERS AND THE CORRESPONDING NEWSGROUPS.

talk.politics.mideast	talk.politics.guns	sci.crypt	misc.forsale
injuries	overwhelmed	transfering	cruising
comatose	conceded	betwen	barreling
boyhood	crudely	keyboards	liscence
pranks	detractors	numlock	occurance
devalued	outraged	micronics	reknowned
murderous	revocation	speedier	copious
municipalities	mailbombing	phantom	loper
shaman	confidentiality	preffered	armadillo
⋮	⋮	⋮	⋮
(368 in total)	(29 in total)	(28 in total)	(28 in total)

V. CONCLUDING REMARKS

We have proposed a method to extract meaningful dense subgraphs from a given sparse graph (either undirected, directed, or bipartite). There are two major distinctions between the proposed method and previous ones that exploit complete clustering techniques. First, the output subgraphs are guaranteed to have high densities (above a certain prescribed threshold). Second, the number of clusters, which is in general difficult to estimate, is no longer a required parameter. The proposed algorithm is inspired by a matrix approximate blocking technique which utilizes the cosine similarity of matrix columns. It effectively builds a hierarchy for the graph vertices, and computes a partial clustering for them. The real-life examples of Section IV indicate that the uses of the algorithm are flexible and the results are meaningful.

In the proposed algorithm, we introduced a density threshold parameter $d_{\min}$ to control the density of the output subgraphs. This parameter provides the flexibility needed to interactively explore the graph structure and the resulting communities. It can be tuned in real time, and results are easily visualized. The blog example in Sec. IV-D has shown the appeal of exploiting such a tunable parameter in understanding the extraction results.

The experiment in Sec. IV-C unraveled what appears to be a new power law for large sparse graphs: the power law distribution of the dense subgraph sizes. It is still unclear if this interesting phenomenon is intrinsic to real-life complex systems. This newly discovered structure may have an influence on understanding the sizes of the communities in social networks.

A future avenue of research is to design algorithms to identify overlapping dense subgraphs. Many social and biological networks have shown empirically overlapping structures, where communities do not have a distinct borderline. The identification of such characters that connect different communities together may help better understand the network systems. We intend to explore how the algorithm proposed in this paper can be adapted for this task.

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