Efficient Algorithms for Node Disjoint Subgraph Homeomorphism Determination

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Abstract. Recently, great efforts have been dedicated to researches on the management of large scale graph based data such as WWW, social networks, biological networks. In the study of graph based data management, node disjoint subgraph homeomorphism relation between graphs is more suitable than (sub)graph isomorphism in many cases, especially in those cases that node skipping and node mismatching are allowed. However, no efficient node disjoint subgraph homeomorphism determination (ndSHD) algorithms have been available. In this paper, we propose two computationally efficient ndSHD algorithms based on state spaces searching with backtracking, which employ many heuristics to prune the search spaces. Experimental results on synthetic data sets show that the proposed algorithms are efficient, require relative little time in most of the testing cases, can scale to large or dense graphs, and can accommodate to more complex fuzzy matching cases.

1 Introduction

Recently, large scale graph based data management has received more and more research attentions, due to the broad application of graph based data. In the study of graph based data management, *graph based pattern matching*, i.e., to determine whether the structure of a pattern graph can match to that of a data graph, is the key of many problems about graph data management.

Existing graph pattern matchings can be classified into two preliminary categories: *exact matching* and *inexact matching*. Exact matching requires that the matched two graphs are isomorphic to each other; i.e., exact graph pattern matching is based on *graph isomorphism* relations between graphs. While the inexact graph matching is often considered as *subgraph isomorphism* between graphs, which means that pattern graph P matches to data graph G if and only if P is subgraph isomorphic to G.

However, in real applications, inexact graph pattern matching based on subgraph isomorphism cannot represent the fuzzy matching in some cases that *node skipping or node mismatching is allowed.* For example, as shown in Figure 1, although G_2 is not a subgraph of G_1, G_2 still can be regarded as matched to G_1 if node skipping or node mismatching is allowed. In other words, G_2 is matched to G_1 from the abstract topological structure perspective, because G_2 retains the abstract topological structure of G_1 if paths in G_1 can be contracted into the corresponding edges in G_2.

However, this kind of fuzzy matching is more desired in many real applications than subgraph isomorphism based inexact matching. For instance, the discovery of frequent

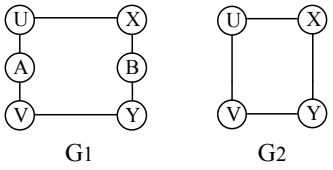


Fig. 1. Inexact Matching

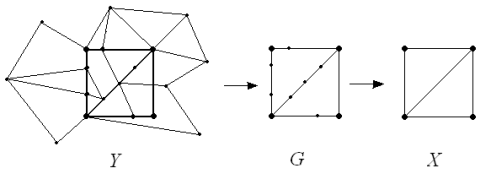


Fig. 2. Topological Minor

conserved subgraph patterns from protein interaction networks [1,2] is an important and challenging work in evolutionary and comparative biology, where 'conserved' just means the inexact graph pattern matching allowing node mismatch and node skipping. Similarly, in social network analysis, the direct connection between nodes usually is not the focus; instead, the high-level topological structure with independent paths contracted is of great interest.

Using *Graph Minor* theory [4], the abstract topological structure in many real applications can be described as *topological minor*, and the relation between abstract topological structure and its detailed original graph can be described as *node/vertex disjoint subgraph homeomorphism*. However, to determine whether a pattern graph P is a topological minor of data graph G is not a trivial thing, and this problem has been proved to be NP-complete when P and G are not fixed [3]. Although Robertson and Seymour [4] have proposed a framework to solve *minor containment* problem that is a generalization of topology containment problem and [5] has implemented the framework, no efficient algorithms have been dedicated to solve *ndSHD* (in other contexts, also known as *topological minor containment*, *homeomorphic embedding* or *topological embedding*), to the best of our knowledge.

To efficiently determine the node disjoint homeomorphism relation between two graphs, we propose two algorithms based on state space searching with backtrack, which integrate many heuristics into the searching procedure to prune the search spaces. The work in the paper is inspired by Ullmann's [6] subgraph isomorphism determination (SID) algorithm. However, for ndSHD, we need to do some more specific things. First, for ndSHD, not only *node mapping space* but also *edge-path mapping space* needs to be searched, whereas for SID only the former needs to be searched. Second, for ndSHD, according to the definition of topological minor, we need to perform pairwise independence determination of the paths to ensure the paths are disjoint. Third, for SID, only edge information is explored, while in ndSHD path information is explored too, which will be a great challenge to the efficiency of the algorithm since the amount of paths is exponential to the size of the graph.

In a summary, we make the following contributions in this paper:

1. We propose two efficient algorithms for node disjoint subgraph homeomorphism determination. To the best of our knowledge, it's the first paper dedicated to design practical efficient algorithms for node disjoint subgraph homeomorphism determination or topological minor containment determination problem.
2. We investigate the properties of topological minors, and employ these properties as the heuristics to prune the search space.
3. We present a systematic performance study of proposed algorithms. The experimental results show that the algorithms are efficient and scalable on synthetic data sets.

2 Preliminaries

We begin with some basic notations that are used in [7]. Let $G = (V, E, l)$ be a *vertex labeled graph*, where V is the set of vertices, E is the set of edges and $E \subseteq V \times V$, and l is a label function $l : V \to L$, giving every vertex a label.(In this paper, we only focus on vertex labeled graphs. Unlabeled graph can be considered as a labeled graph with all vertexes having the same vertex label.) The vertex set of G is referred to as $V(G)$, and its edges set as $E(G)$. A *path* P in a graph is a sequence of vertices v_1,v_2,...,v_k, where $v_i \in V$ and $v_i v_{i+1} \in E$. The vertices v_1 and v_k are linked by P and are called its *ends*. The number of edges of a path is its *length*, and the path of length k is denoted as P^k. A path is *simple* if its vertices are all distinct. Particularly, a group of paths are *independent* if none of the paths have an inner vertex on another path. In the other words, a path intersecting with other paths only at its ends can be called as an *independent path*. Be aware that the independent paths are the key to study topological minors of a graph.

2.1 Topological Minor

As described in [7], a topological minor of a graph is obtained by contracting the independent paths of one of its subgraphs into edges. For example, in Figure 2, X is a topological minor of Y, since X can be obtained by contracting the independent paths of G which is a subgraph of Y. Clearly, contracting independent paths helps simplify a (sub)graph without compromising its abstract topological information.

Formally, as shown in Figure 2, if we replace all the edges of X with independent paths between their ends, so that these paths are *pairwise node independent*, namely none of these paths has an inner vertex on another path, then G is a *subdivision* of X, denoted as $T(X)$. If G is a subgraph of Y, then X is a *topological minor* of Y. As a subdivision of X and a subgraph of Y, if G is obtained by replacing all the edges of X with independent paths with length from l to h, then G is a *(l, h)-subdivision* of X and T is a *(l, h)-topological minor* of Y.

Given two graph X and Y, if X is a topological minor of Y, then there exists a corresponding *node disjoint subgraph homeomorphism* from X into Y, which is a pair of injective mappings (f, g) from X into Y, where f is an injective mapping from vertex set of X into that of Y and g is an injective mapping from edges of X into simple paths of Y such that (1) for each $e(v_1, v_2) \in E(X)$, $g(e)$ is a simple path in Y with $f(v_1)$ and $f(v_2)$ as two ends;(2) all mapped paths are pairwise independent. In other words, if X is node disjoint subgraph homeomorphic to Y, all the edges of X can be mapped to a corresponding simple path of Y and all the mapped path are pairwise independent; all the nodes in X can be mapped to a corresponding node in Y(all the mapped nodes are called *branch nodes* of Y).

2.2 Problem Definition

As shown in Figure 3, given two vertex labeled graphs G_1 and G_2, given the minimal path length l and the maximal path length h, the problem is whether G_1 is a (l, h)-topological minor of G_2, i.e., G_1 is node disjoint homeomorphic to G_2 so that all mapped paths in G_2 have length from l to h. Obviously, this problem is a typical *determination problem*. When the answer is true, the homeomorphism mapping (f, g) also can be obtained. The solution to the determination problem also can be extended

to solve the *enumeration problem*, which is to find the entire valid homeomorphism mappings between two graphs.

The answer to the problem is sensitive to the given parameter (l, h). For example, in Figure 3, if (l, h) is $(2, 2)$, which means the edges in G_1 can only be mapped to the paths in G_2 with length 2, then nodes in G_1 can be mapped to the four nodes in shadow in G_2 and the five edge-path mappings are $12-218, 13-296, 14-234, 23-876, 34-654$. If (l, h) is $(3, 3)$, G_1 is not a topological minor of G_2. The influence of parameter (l, h) on topology containment determination has been discussed in [8] in detail.

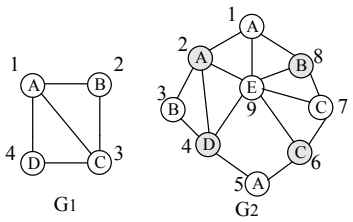


Fig. 3. Running Example

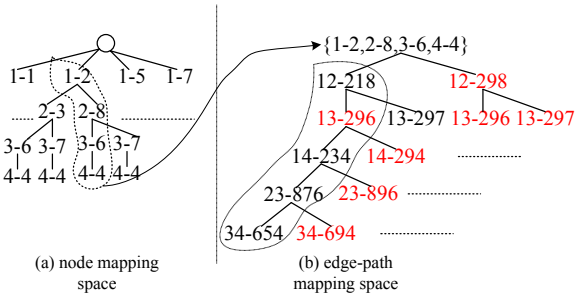


Fig. 4. Two Level State Space Searching

3 Algorithm Framework

To simplify the description of the algorithm, we first give some notations. Assume that vertex labeled graph $G_1 = (V_1, E_1, l_1)$ is a (l, h)-topological minor of vertex labeled graph $G_2 = (V_2, E_2, l_2)$ under the node disjoint subgraph homeomorphism (f, g), where $f : V_1 \rightarrow V_2$ and $g : E_1 \rightarrow P^l \cup ... \cup P^h$, the image of E_1 under mapping g is denoted as $g(E_1) = \{g(e)|e \in E_1\}$. The number of vertices and edges of G_1 and G_2 are n_1, m_1 and n_2, m_2, respectively. For the convenience of notation, we call G_1 as *minor graph*, and G_2 as data graph; without explicit statement, in the following discussion, G_1 always denote a minor graph, G_2 always denote a data graph.

3.1 A Rudimentary Algorithm

To determine whether G_1 is a (l, h) topological minor of G_2 is equivalent to find a pair of mapping (f, g) between these two graphs. The mapping f maps the nodes in G_1 to the nodes with the same label in G_2 so that g can map each edge of G_1 to a corresponding path in G_2. Obviously, the final solution of the determination, i.e., the complete mapping (f, g) between these two graphs, can be described as $\mathcal{M} = (NM, EPM)$,where $NM \subseteq V_1 \times V_2$ is the node match set and $EPM \subseteq E_1 \times (P^l \cup ... \cup P^h)$ is the edge-path match set. All the mapped nodes of G_2 can be denoted as $NM^{(2)}$, and all the mapped paths of G_2 can be denoted as $EPM^{(2)}$.

The process of finding the homeomorphism mapping can be suitably described by means of *State Space Representation* [9]. Each state s of the matching process can

be associated with a partial mapping solution $\mathcal{M}_s = (NM_s, EPM_s)$, where NM_s and EPM_s are the node match set and edge-path match set at state s, respectively. Obviously, $\mathcal{M}_s$ contains all the matches we have found so far and probably become a subset of some final match set $\mathcal{M}$.

Given the two vertex labeled graphs as shown in Figure 3, a naive two level state space searching procedure for a $(2, 2)$ topological mapping is shown as Figure 4, where the first level is to find a suitable node mapping solution (shown in the dotted box of Figure 4(a)) and the second level is to find a suitable edge-path mapping solution (shown in the dotted box of Figure 4(b)). The corresponding algorithm framework is shown as follows.

Algorithm ndSHD1(G_1,G_2,l,h)
Input: G_1,G_2:vertex labeled graphs; l:minimal path length; h:maximal path length.
Output: If G_1 is a (l, h)-topological minor of G_2 return *true* and return *the **first** found node disjoint subgraph homeomorphism* (f, g), otherwise return *false*.

```
1. Initial(M);/*Initialize SHD, Generate necessary path information, Initialize the
   basic data structures*/
2. Initial(R);
3. s ← ∅; /*initialize state as empty state*/
4. s ←NodeMappingSearch(s,M,R); /*node mapping space search*/
5. if not IsValid(s)
6.    return false;
7. else
8.    s ←EdgePathMappingSearch(s); /*edge-path mapping space*/
9. if not IsValid(s)
10.   return false;
11. else
12.   return true;
```

At first, we initialize two basic data structures : *node compatible matrix* M and *independent path matrix* R as well as its associated *path indexed structure*. Then we start the node matching process from the empty state. Each time we select a branch in the state space, a state s transits to a new successor state s' by adding a new match, which is a node pair or an edge path pair, to the partial solution. Each time a new match state arrives, M and R are updated so that the node mapping space and edge-path mapping space can be pruned. When a complete node mapping has been found, the matching process will come to the second level: edge-path matching space search. Similar to the search process in node mapping space, each time a branch is selected, an edge-path pair is added to the partial mapping solution and the independent path matrix is updated. The process continues until a complete edge-path mapping is found.

In the above searching process, if all the possible valid branches in the subspace rooted at current state s have been explored, but still no valid match can be found, the searching process *backtracks* to the parent state of s. And any time the procedure enters into *dead state* which will be discussed in 3.5, the whole process will stop and return false which means the two graphs do not satisfy the (l, h)-topological minor relationship.

3.2 Basic Data Structure

As described above, we need to two basic data structures, one is used to represent the node mapping information; the other is used to represent (l, h) independent path

information of G_2. For the former, we use node compatible matrix; the latter, we use independent path matrix as well as a path index structure. Both of them are changing with the transition of the matching state.

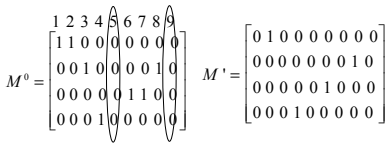


Fig. 5. M^0 and M'

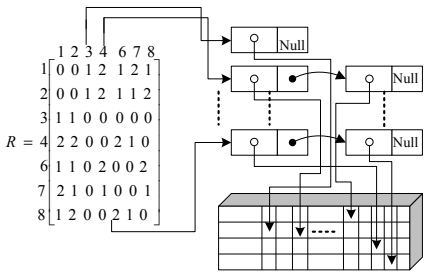


Fig. 6. R and its associated Path Indexed Structure

We define node compatible matrix $M = [m_{ij}]$ to be a n_1 (rows)$\times n_2$ (columns) matrix whose elements are 1's or 0's. At the final success state, we can get a final mapping matrix $M' = [m'_{ij}]$ whose elements are 1's or 0's, such that each row contains exactly one 1 and each column contains no more than one 1. The final mapping matrix represents a valid one to one mapping between nodes of G_1 and G_2, while the initial compatible matrix M^0 represents the probable mappings between nodes of G_1 and G_2. The initial node mapping and the final node mapping between G_1 and G_2 in Figure 3 is shown in Figure 5. Obviously for each element m'_{ij} of M', $(m'_{ij} = 1) \rightarrow (m^0_{ij} = 1)$.

Clearly, to reduce the number of 1's in M is the key to speed up the search procedure in node mapping space. Hence, the first key step is to construct an initial compatible matrix M^0 with as less 1's as possible. For this reason, we first introduce Lemma 1. Due to the limitation of space, the detailed proof is omitted in this paper.

Lemma 1. *The number of elements of the independent path set starting from a specified vertex $v_i \in V$ is no more than $d(v_i)$, where $d(v_i)$ denotes the degree of v_i.*

Since every path set starting from v_i necessarily pass through one or more edges incident with v_i, the independent path set starting from v_i has at most $d(v_i)$ elements. According to lemma 1, the node v in G_1 cannot be matched to those nodes in G_2 whose degree is less than $d(v)$. Therefore, we construct the initial compatible matrix M^0 in accordance with the following rule: $m^0_{ij} = 1$ if $l_1(v_i) = l_2(v_j) \wedge d(v_i) \leq d(v_j)$, otherwise 0. As shown in Figure 3, v_1 in G_1 cannot mapped to v_5 of G_2, although these two nodes have the same label.

When constructing Independent Path Matrix and its associated Path Indexed Structure, the first problem we face is whether we need to generate all the (l, h) path information of G_2. The answer is false, which is based on the following lemma.

Lemma 2. *If G_1 is a (l, h)-topological minor of G_2 under subgraph homeomorphism (f, g), then $g(E_1)$ only contains paths ending with those branch nodes in G_2.*

For example, in Figure 3, since v_5 in G_2 cannot be a branch node, then all paths starting from v_5 needn't to be enumerated. However, note that the path having v_5 as inner vertex can not be ignored.

Therefore, we only need to enumerate all the (l, h) paths between all *candidate branch node* pairs. These candidate branch nodes can be filtered out by matrix M^0. As shown in Figure 3, since column 5 and 9 have only 0's, v_5 and v_9 in G_2 cannot be branch nodes, thus could be filtered out and the remaining nodes in G_2 are just candidate branch nodes. The cardinality of the candidate branch node set is denoted as n_2'.

Then, we can define the independent path matrix $R = [r_{ij}]$ to be n_2'(rows)$\times n_2'$ (columns) matrix whose elements are positive integers or 0's, which represent the number of (l, h) paths between the node pair (v_i, v_j) in G_2. The corresponding detailed path information are stored in a list array *RLists*, where each list in RLists contains corresponding path addresses that point to the physical storage of the path. RLists can be considered as a path index structure that is built according to the end vertex pair of the path.

3.3 State Space Searching

The procedure of node mapping space searching and edge-path mapping space searching are similar to each other. These two procedures are shown as follows.

Algorithm Node/EdgePatbMappingSearch1 (s,M,R)
Input: s:the current matching state; M:the current node compatible matrix; R: the current independent path matrix.
Output: *found*: a boolean variable indicating whether a complete node/edge-path mapping has been found.

```
1. if(s is dead state)
2.   return false;
3. if(s is complete mapping state)
4.   return true;
5. let found←false
6. while(not found && Exists Valid node/edge-path Mapping Pair)
7.   m ←GetNextNodePair(); /*m ←GetNextEdgePathPair();*/
8.   s' ←BackupState(s);
9.   NM_s ← NM_s ∪ {m}; /*EPM_s ← EPM(s) ∪ {m}*/
10.  Refine(M,R);
11.  found←Node/EdgePathMappingSearch(s, M, R);
12.  if(found)
13.    return true;
14.  else
15.    s ←RecoverState(s');
16. return false;
```

From line 1-2, we can see that when a new state s arrives, s can be a *dead state* or *success state*(complete mapping state). The state space search arrives at a *success state* if all the node mappings or edge-path mappings have been found, which means $|NM_s| = |V_1|$ or $|EPM_s| = |E_1|$, where NM_s and EPM_s are the node match set and edge-path match set at state s. The node mapping state space search arrives at a *dead state* if there is a row with all 0's in node compatible matrix M of the current state, i.e. $\exists i, |NM_s| \leq i \leq n_1$,s.t. $\sum_{1 \leq j \leq n_2} m_{ij} = 0$. And the edge-path mapping state space search arrives at a *dead state* if there is no path between any one branch node pairs, i.e.,

$\exists i, |EPM_s| \leq i \leq n_1'$,s.t. $\prod_{(f^{-1}(node(i)),f^{-1}(node(j)))\in E_1} r_{ij} = 0$, where $node(i)$ gets the vertex corresponding to the ith column in matrix R, which can be easily determined from independent path matrix R of the current state.

Any time the search process enters into a success state or dead state, the procedure is over. If success state arrives, the complete mapping is found and the procedure returns true. If dead state arrives, the procedure returns false. On any other cases, the procedure will continue exploring the state space. The 1-11 lines describe the process.

Assume the process comes to a state s that is only a partial solution. Then as long as there exists a valid mapping pair, i.e., a node pair or an edge-path pair, we need to generate a new state by adding the new match (line 9) to the existing solution M_s. To enable backtracking, we need to backup the current state first (line 8), including the node compatible matrix, independent path matrix etc. Because after a new match added to the current solution, these two basic data structure will be refined to prune the following mapping space (line 10). Then DFS continues, until the search enters into dead state or success state. If we cannot find a success state in subtree space rooted at s, we recover the state s(line 15), and try the sibling state branches.

3.4 Refinement Procedure

To traverse all possible mapping branches is time consuming, so space pruning is essential for ndSHD. For this purpose, we devise two refinement procedures on R and M, respectively, the correctness of the former refinement is based on Lemma 3,4, and the latter is based on Lemma 5.

Lemma 3. *In the matching process, let s be the current state, if* $v \in NM_s^{(2)}$ *and* $\mathcal{M}_s$ *will be a partial solution of some final solution* $\mathcal{M}$*, then any path with* v *as inner vertex will not* $\in EPM^{(2)}$*.*

If $v \in NM_s^{(2)}$ and $NM_s^{(2)}$ will be a subset of some final solution, then v will a branch nodes of G_2. Since branch nodes can only be the end vertex of the final independent path set, thus any path with v as inner vertex will not belong to the final independent path set.

Lemma 4. *In the matching process, let s be the current state, if* $p \in EPM_s^{(2)}$ *and* $\mathcal{M}_s$ *will be a partial solution of some final solution* $\mathcal{M}$*, then any path passing trough the inner vertex of* p *will not* $\in EPM^{(2)}$*.*

Obviously, if $p \in EPM_s^{(2)}$, then all the path passing through any inner vertex of p will joint with p, so all these paths will not occur in $EPM^{(2)}$.

Lemma 3 implies that, if a vertex v in G_2 is added to the existing node match set, all the paths with v as inner vertex can be removed from RLists and the number in the corresponding element in R can be decreased. Lemma 4 implies that if we reach a new state by adding a new edge-path pair (e_{1i}, p_{2i}), all the path passing through any inner vertex of p_{2i} can be removed from RLists and the number in the corresponding element in R can be reduced.

As shown in Figure 3, if vertex v_2 in G_1 is mapped to v_8 in G_2, any path passing through v_8 could be removed from RList, thus the potential edge-path mapping space could be pruned. As shown in Figure 4, when $(13, 296)$ is added to the partial solution, the subtree rooted at node $(13-296)$ will be reduced, in the way that all the branches containing paths passing through vertex v_9 will be pruned.

Lemma 5. *In the matching process, let s be the current state, if $(v_i, v_j) \in NM(v_i \in V_1, v_j \in V_2)$ and $\mathcal{M}_s$ will be a partial solution of some final solution $\mathcal{M}$, then the following statements hold true:*

1. $\prod r_{j'k} > 0, where j' = Index(v_j), k \in Index(V)$ *and* $V = \{v_2 | v_1 \in Adjacent(v_i) \wedge (v_1, v_2) \in NM_s\}$.
2. $\forall v' \in V', \exists v \in V_2$ *such that* $l_2(v) = l_1(v')$ *and* $r_{j'k} > 0, wherj' = Index(v_j), k = Index(v)$ *and* $V' = \{v' | v' \in Adjacent(v_i) \cap (V_1 - NM_s^{(1)})\}$.
3. *The path set consisting of the paths to which all mentioned $r_{j'k}$'s in (1) and (2) indicate is independent.*

In the above statements, the function $Index(v)$ gets an index in R for a node v in G_2; and $Adjacent(v)$ obtains the adjacent nodes set of v.

Suppose that the partial solution of current state will grow to be one final successful solution, Lemma 5 implies that two node $v_i \in V_1$ and $v_j \in V_2$ is compatible if only the three conditions are satisfied, i.e., if any one is not satisfied, m_{ij} in node compatible matrix at state s, namely M^s, could be refined to be 0.

As shown in Figure 3, assume current matching state is s, and $NM_s = \{(1,2),(2,8)\}$. Condition 1 implies that if (3,7) can be added to NM, i.e., v_3 in G_1 can be mapped to v_7 in G_2, there must exist two independent paths from v_7 to v_2 and v_8 in G_2, otherwise m_{37} can be refined to be 0, thus the node mapping space could be pruned. Moreover, since v_3 and v_4 are adjacent in G_1, there must exist a corresponding path in G_2 from v_7 to some node with the same label as v_4 of G_1, otherwise m_{37} can be refined to be 0, which is stated in condition 2. Furthermore, all the above paths must be node disjoint, which is implied in condition 3. Obviously, if (l, h) is set as (2,2), paths connecting v_7 to v_2,v_4 and v_8 all pass through node E. Hence m_{37} in matrix M^s can be refined to be 0.

3.5 More Efficient Searching Strategy

A basic observation of the above refinement procedures is that the constraint resulting from an edge-path match will be more restricted than that resulting from a node match. Hence, a better strategy is to try edge-path match as early as possible, instead of performing edge-path match only after complete node match has been found. We denote these two strategy as s_1 (old strategy) and s_2(new strategy), respectively; and algorithms employing two strategies are denoted as *ndSHD1* and *ndSHD2*, respectively. Intuitively, in *ndSHD2* the searching procedure will meet with the dead state very early if the current searching path will not lead to a successful mapping solution, thus the searching procedure will fast backtrack to try another mapping solution.

As an example, assume that (l, h) is set as (2,2) and the current matching state is s such that $NM_s = \{(1,2),(2,8)\}$. Since v_1 and v_2 is adjacent in G_1, why we not try to match a path in G_2 for the edge $e(v_1, v_2)$? If we do so, there are only two suitable edge-path pairs $(12, 298)$ and $(12, 218)$. Then, once $(12, 298)$ has been added to EPM_s, all paths in G_2 passing through v_9 will be excluded from R and $Rlist$, thus the searching space could be pruned early. Furthermore, we can see that the current partial mapping solution will not be a part of a final successful solution, thus any other solution with this partial solution as subset will be pruned. And if we try the edge-path pair $(12, 218)$, we can eventually find a successful complete mapping solution.

The framework of the *ndSHD2* is similar to that of *ndSHD1*, which is omitted here. The detailed procedure of *ndSHD2* is shown in NodeMappingSearch2 and

EdgePatbMappingSearch2. Note that, in NodeMappingSearch2, after a new node match (v_i, v_j) has been added to NM_s, we can get an edge set consisting of edges that connect v_i to any vertex exiting in $NM_s^{(1)}$ (line 11), namely $E = \{(v_i, u) | u \in NM_s^{(1)} \cap Adjacent(v_i)\}$. If $E = \emptyset$ (for connected graph, it only happened at the initial stage of the first node match), we continue the node mapping searching procedure (line 12-13); otherwise, we switch to edge-path mapping search procedure to find valid path in G_2 for each edge in E (line 14-15). In EdgePatbMappingSearch2, if we can find valid paths for all the edges in E, the edge-path mapping search procedure returns true (line 3-4) and we will turn to the node mapping space search (line 13); otherwise, we continue the edge-path mapping search procedure (the while body).

Algorithm NodeMappingSearch2 (s,M,R)
Input and **Output** is the same as that in NodeMappingSearch1.

1. **if**(s is *complete mapping state*)
2. **return true**;
3. **if**(s is *dead state*)
4. **return false**;
5. let *found*←**false**
6. **while**(**not** *found* && Exists Valid node Mapping Pair)
7. m ←GetNextNodePair(); /*Get a next valid node pair*/
8. s' ←BackupState(s);
9. $NM_s \leftarrow NM_s \cup \{m\}$;
10. Refine(M,R);
11. E ←NewEdgeEmergent(s,G_1)
12. **if**($E = \emptyset$)
13. *found*←NodeMappingSearch2(s, M, R);
14. **else**
15. *found*←EdgePathMappingSearch2(s, M, R, E);
16. **if**(*found*)
17. **return true**;
18. **else**
19. s ←RecoverState(s');
20. **return** *found*;

Algorithm EdgePathMappingSearch2 (s,M,R,E)
Input and **Output** is the same as that in EdgeMappingSearch1 except E, which is the edges in G_1 induced by $NM_s^{(1)}$.

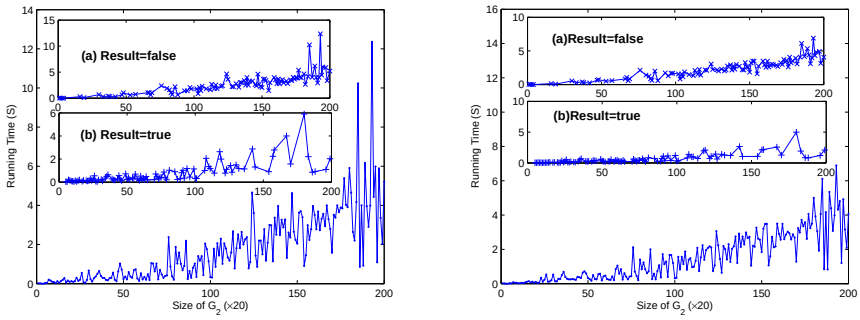
1. **if**(s is *dead state*)
2. **return false**;
3. **if**(s is *complete mapping state with respect to* E)
4. **return true**;
5. let *found*←**false**
6. **while**(**not** *found* && Exists Valid edge-path Mapping Pair)
7. m ←GetNextEdgePathPair(); /*Get a next valid edge-path pair*/
8. s' ←BackupState(s);
9. $EPM_s \leftarrow EPM_s \cup \{m\}$;
10. Refine(M,R);
11. *found*←EdgePathMappingSearch2(s, M, R, E);

12. **if**(*found*)
13. *found*←NodeMappingSearch2(s, M, R);
14. **else**
15. s ←RecoverState(s');
16. **return false**;

4 Experimental Evaluation

To test the efficiency of the algorithm, we generate the synthetic data sets according to the random graph [10] model that links each node pair by probability p. All generated graphs are vertex labeled undirected connected graphs. We also randomly label every node so that the vertex labels are uniformly distributed. We implement the algorithm in C++, and carry out our experiments on a Windows 2003 server machine with Intel 2GHz CPU and 1G main memory.

The efficiency of the algorithms is influenced by the following factors: N_1: node size of G_1, N_2: node size of G_2, M_1: average degree of G_1, M_2: average degree of G_2, (L, H): the minimal and maximal path length. The efficiency also can be influenced by the number of vertex labels. Obviously, large number of labels will exert great constraint on the initial node compatible matrix, thus reduce the runtime significantly. However, for determination algorithms, the runtime also may be influenced by the answer to the determination. Generally, if the answer is false, in the worst case the algorithm may need to traverse the entire mapping spaces, which is very time consuming. If the answer is true, then in the best case the algorithm may only need to try one complete match procedure. However, in the following experiments, we can see that result of the determination has limited impact on the runtime, which could partly be attributed to the strong pruning ability of the refinement procedure. Due to these pruning techniques, even the result is false, the procedure will backtrack as early as possible, thus the whole runtime is rarely impacted.



(a) $ndSHD1$ (b) $ndSHD2$

Fig. 7. Efficiency and scalability with respect to the growth of size of data graph (G_2). The inset of (a), (b) show runtime of all running cases that the determination result is *true*, *false* respectively.

First we will demonstrate the scalability with respect to the growth of the size of nodes of data graph G_2 via experiment Exp_1. We use a complete graph with 4 uniquely labeled nodes, denoted as C_4, as a minor graph; we generate overall 200 data graphs G_2 with node size varying from 20 to 4000 in an increment of 20. The average degree of each data graph is fixed as 4 and nodes of each graph are randomly labeled as one of overall 20 labels. L and H are fixed as 1 and 3, respectively, meaning that the path length is in the range of $[1, 3]$. Thus the parameters can be denoted as $N_1 4 M_1 3 M_2 4 L 1 H 3$. From Figure 7, we can see that *ndSHD1* and *ndSHD2* both are approximately linearly scalable with respect to the number of nodes in G_2, irrespective of the result of the determination result. Notice that for G_2 with about 4000 nodes and 8000 edges, the worst case of *ndSHD1*is no more than 13s, the worst case of *ndSHD2* is no more than 7s.

$Exp2$ is designed to show the scalability of *ndSHD1* and *ndSHD2* with respect to the size of G_1, where we fix some parameters as $M_1 4 N_2 4 k L 1 H 3$ and vary the size of G_1 from 6 to 82 in increment of 4 to generate 20 minor graphs. Each minor graph is uniquely labeled, meaning that the number of labels equals to that of nodes. Two data graphs are used, one has average degree M_2 as 8 and the other as 20. These two data graphs are randomly labeled as one of 200 labels. Figure 8(a) and (b) show the results with M_2 set as 8 and 20, respectively; and these two experiments are denoted as $Exp2_1$ and $Exp2_2$, respectively. The determination results of running case shown in Figure 8(a) are all false due to the relative sparsity of G_2; and determination results of all running cases shown in Figure8(b) are true due to relatively higher density of G_2. As can be seen, *ndSHD1* and *ndSHD2* both are approximately linearly scalable with respect to the number of nodes in G_1. We also can see that, when G_2 is sparse, the difference of performance between *ndSHD1* and *ndSHD2* are so minute that can not be discerned; whereas as G_2 becomes denser, running time of *ndSHD1* is not available, meaning that all running cases need time larger than one hour, while runtime increase of *ndSHD2* is not very substantial.

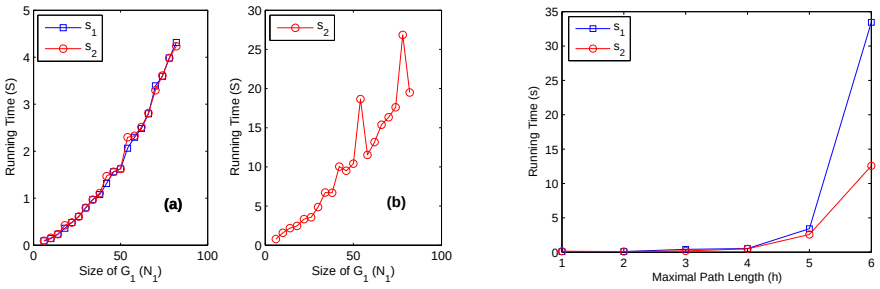


Fig. 8. Scalability with respect to the size of G_1.

Fig. 9. Scalability with respect to the upper bound of path length

$Exp3$ is designed to show the scalability with respect to the growth of density of G_2, parameters are fixed as $N_1 6 M_1 5 N_2 1 k L 1 H 3$. Minor graph are uniquely labeled; data graphs are randomly labeled as one of 20 labels. Table 1 shows the running time

when we vary M_2 from 2 to 20 in increment of 1. As can be seen, runtime of *ndSHD1* and *ndSHD2* both approximately increase linearly with the growth of M_2. However, we must note that for *ndSHD1*, there exists some outliers which consume too much time, e.g, when $M_2 = 17$, more than 10 minutes are needed, when $M_2 = 16$ running time is not available. Compared to *ndSHD1*, *ndSHD2* is more stable.

Table 1. Running time of $Exp3$

M_2	2	3	4	5	6	7	8	9	10	11
Result	0	0	0	0	1	1	1	1	1	1
s_1	0	0.14	0.31	1.78	21.67	19.69	1.77	1.23	83.66	661.33
s_2	0.016	0.14	0.33	1.05	11.41	0.97	0.92	1.27	2.14	3.77
M_2	12	13	14	15	16	17	18	19	20	
Result	1	1	1	1	1	1	1	1	1	
s_1	3.23	3.89	4.24	5.36	-	6508.7	7.75	10.06	9.77	
s_2	3.11	3.92	4.23	5.36	6.66	7.91	8.06	10.72	10.11	

Figure 9 shows the runtime of the algorithm with respect to (l, h). Parameters of this experiment (denoted as $Exp4$), are set as $N_1 4 M_1 3 N_2 1 k M_2 8 L 1$. The vertex labeling of minor graph and data graphs are the same as $Exp3$. As can been seen the broader the range is, the longer the running time is; and the runtime of *ndSHD1* and *ndSHD2* both increase dramatically with the growth of upper bound of path length. However, the increasing speed of *ndSHD2* is slower than that of *ndSHD1*, which implies that *ndSHD2* is more efficient than *ndSHD1* with respect to larger h. The super linearly growth of the runtime with the increase of upper bound of the path length can be partly attributed to the exponentially growth of the number of potential mapped paths. Luckily, in the real applications, larger upper bound is too unrestricted when performing fuzzy matching on graph data, thus usually upper bounds less than 3 are used.

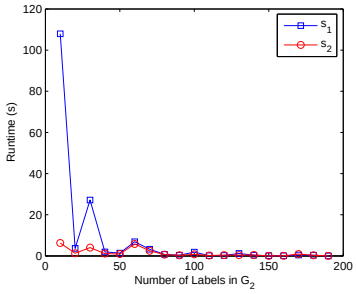


Fig. 10. Effect of label numbers of G_2 on the performance of *ndSHD1* and *ndSHD2*.

To examine the impact of number of vertex labels on the performance of *ndSHD1* and *ndSHD2*, we use a uniquely labeled graph with 6 nodes and 15 edges as minor

graph, a graph with 1000 nodes and 4000 edges as data graph. We randomly labeled the data graph from 10 labels to 200 labels in increment of 10 to generate 20 different labeled data graphs. L and H are set as 1 and 3, respectively. The result of this experiment (denoted as $Exp5$) is shown in Figure 10. Clearly, runtime of *ndSHD1* and *ndSHD2* substantially decrease with the growth of number of labels of G_2, which confirms to what we have expected, since larger number of labels in G_2 can reduce the node mapping space between minor graph and data graph. We also can see that *ndSHD2* outperforms *ndSHD1* to a great extent when label number is small.

To examine the stability of *ndSHD1* and *ndSHD2*, we recorded in Table 2 the statistics including *max*, *mean* and *standard deviation* of sample data used in the above experiments. We can see that in almost all the experiments, the standard deviation of *ndSHD2* is much less than that of *ndSHD1*, indicating that *ndSHD2* is more stable than *ndSHD1*.

In a summary, in some simple running cases, such as small size of minor graph, sparse data graphs, small value of upper bound of path length, larger number of labels in data graphs, both *ndSHD2* and *ndSHD1* are scalable and efficient. However, in more complex cases, *ndSHD2* will outperform *ndSHD1* substantially in all aspects, including scalability, efficiency and stability.

In Figure 11,we also illustrate the detailed searching procedure of two running cases to show the superiority of *ndSHD2* to *ndSHD1*. In both of these two cases, *ndSHD2* runs much faster than *ndSHD1*. Since the mapping searching procedure has been designed to be a recursive procedure, statistics about the recursive depth of each match (node-node match or edge-path match) will be a significant index indicating the performance of the algorithm. Hence, we recorded recursive depth of all matches in the searching procedure. Obviously, either narrow width of the exploring space or small value of the average backtrack depth, will lead to the less runtime of the algorithm. Hence ,from Figure 11, we can easily see the great advantage of *ndSHD2* over *ndSHD1*, which can be attributed to the small value of the width or average backtrack depth in the actual exploring space.

Table 2. Statistics of sample data in 5 experiments

	$Exp1$		$Exp2_1$		$Exp2_2$		$Exp3$		$Exp4$		$Exp5$	
statistics	s_1	s_2	s_1	s_2	s_1	s_2	s_1	s_2	s_1	s_2	s_1	s_2
max	12.36	6.89	4.312	4.234	-	26.84	6509	11.41	33.44	12.56	107.9	6.297
mean	1.727	1.49	1.709	1.73	-	10.06	408	4.32	6.325	2.675	8.312	1.392
std	1.788	1.396	1.344	1.331	-	7.24	1530	3.797	13.34	4.937	24.89	1.909

5 Conclusions

In this paper, we investigated the problem known as node disjoint subgraph homeomorphism determination; and proposed two practical algorithms to address this problem, where many efficient heuristics have been exploited to prune the futile searching space. The experimental results on synthetic data sets show that our algorithms are scalable and efficient. To the best of our knowledge, no practical algorithm is available to solve node disjoint subgraph homeomorphism determination.

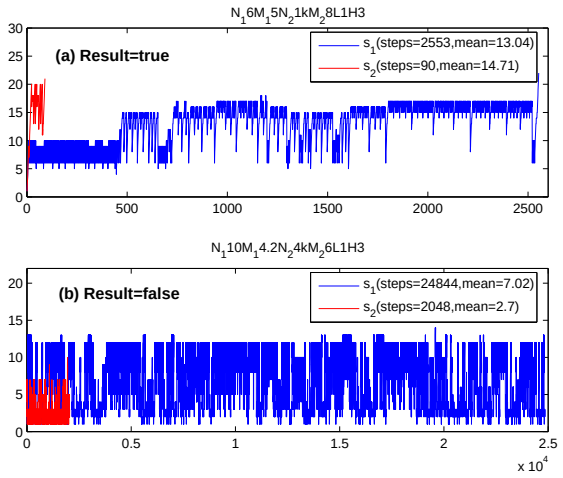


Fig. 11. Recursive depths of two running cases

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