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A Much Faster Algorithm for Finding a Maximum Clique with Computational Experiments

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Abstract: We present further improvements to a branch-and-bound maximum-clique-finding algorithm MCS (WALCOM 2010, LNCS 5942, pp.191–203) that was shown to be fast. First, we employ a variant of an efficient approximation algorithm KLS for finding a maximum clique. Second, we make use of appropriate sorting of vertices only near the root of the search tree. Third, we employ a lightened approximate coloring mainly near the leaves of the search tree. A new algorithm obtained from MCS with the above improvements is named & MCT. It is shown that & MCT is much faster than MCS by extensive computational experiments. In particular, & MCT is shown to be faster than MCS for gen400_p0.9_75, gen400_p0.9_65 and gen400_p0.9_55 by over 81,000, 39,000 and 19,000 times, respectively.

Keywords: maximum clique, branch-and-bound algorithm, bounding condition, computational experiments

1. Introduction

Given an undirected graph G, a *clique* is defined to be a complete subgraph of G in which all pairs of vertices are adjacent to each other. Finding a *maximum* clique, that is a clique of maximum cardinality, is a typical NP-hard problem [4]. So, it is very difficult to obtain the exact solution of this problem in general. In addition, it is also difficult to obtain even a satisfactory approximate solution [38]. Finding a maximum independent set in a graph is also equivalent to finding a maximum clique of its complementary graph. Here, finding a maximum clique in a graph has many important practical applications. These applications include coding theory [24], pattern recognition and image processing [9], [20], bioinformatics [5], [18], [33], design of wireless networks [16], and others [4], [36], [37].

Hence, much effort has been devoted to this problem theoretically and experimentally [4], [21], [37]. In particular, see [37] for a recent progress of algorithms for this problem. Furthermore, much faster algorithms are in great demand so that much more practical problems can be solved. Along this line, Tomita et al. developed a series of branch-and-bound algorithms MCQ [29], MCR [31] and MCS [32], [34] among others that run fast in practice. It was experimentally shown that MCS is relatively fast for many instances tested.

In this paper, we present improvements to MCS to make it

much faster. First, we turn back to our original MCS [25] that employs an approximation algorithm for the maximum clique problem at the beginning in order to obtain an initial lower bound on the size of a maximum clique, as noted at Concluding Remarks in Ref. [34]. We choose here another approximation algorithm called *k-opt local search* (KLS for short) by Katayama et al. [11] that runs in quite a short time. Second, we sort vertices as in MCR [31] and MCS [32] only appropriately near the root of the search tree. This technique is based on our successful earlier results [12], [19], [23]. Third, we employ lightened approximate coloring mainly near the leaves of the search tree [12]. A new algorithm obtained from MCS with the above improvements is named *5.MCT. It is shown that *5.MCT is much faster than MCS by extensive computational experiments.

The preliminary versions of this paper appeared in Refs. [8] and [35]. This paper is an extended version of Ref. [35] with a slight modification.

2. Definitions and Notation

- (1) We are concerned with a simple undirected graph G = (V, E) with a finite set V of vertices and a finite set E of edges that comprise *unordered* pairs (v, w) (= (w, v)) of distinct vertices. The set V of vertices is considered to be *ordered*, and the i-th element in V is denoted by V[i]. A pair of vertices v and w are said to be adjacent if $(v, w) \in E$.
- (2) For a vertex $v \in V$, let $\Gamma(v)$ be the set of all vertices that are adjacent to v in G = (V, E), i.e., $\Gamma(v) = \{w \in V \mid (v, w) \in E\}$. We call $|\Gamma(v)|$, the number of vertices adjacent to a vertex v, the *degree* of v. Here, the number of elements in a set S is denoted by |S|.
- (3) For a subset $R \subseteq V$ of vertices, $G(R) = (R, E \cap (R \times R))$ is an *induced* subgraph. An induced subgraph G(Q) is said to be a *clique* if $(v, w) \in E$ for all $v, w \in Q \subseteq V$, with $v \neq w$. In this case,

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we may simply say that Q is a clique. In particular, a clique which is not properly contained in any other clique is called *maximal*. A maximal clique of the maximum cardinality in a graph is called a *maximum clique*, and the number of vertices in a maximum clique in G(R) is denoted by $\omega(R)$.

An *independent set* is defined to be a subgraph in which any pair of vertices are not adjacent to each other.

3. Maximum Clique Algorithm MCS

3.1 The Branch-and-Bound Algorithm

One standard approach for finding a maximum clique is based upon the branch-and-bound depth-first search method. Each of the preceding algorithm MCQ [29], MCR [31], and MCS [32] is also a branch-and-bound one that begins with a small clique and continues by finding larger and larger cliques. To be precise, we maintain global variables Q and Q_{\max} , where $Q = \{p_1, p_2, \ldots, p_d\}$ consists of the vertices of the current clique and Q_{\max} consists of the vertices of the largest clique found so far. Let $R = V \cap \Gamma(p_1) \cap \Gamma(p_2) \cap \cdots \cap \Gamma(p_d) \subseteq V$ consist of candidate vertices that can be added to Q to enlarge Q. We begin the algorithm by letting $Q := \emptyset$, $Q_{\max} := \emptyset$, and R := V (the set of all vertices). We select a certain vertex p from R, add it to Q ($Q := Q \cup \{p\}$), and then compute $R_p := R \cap \Gamma(p)$ as the new set of candidate vertices. This procedure is applied recursively while $R_p \neq \emptyset$.

When $R_p = \emptyset$ is reached, then Q constitutes a maximal clique. If Q is maximal and $|Q| > |Q_{\max}|$ holds, then Q_{\max} is replaced by Q. We then backtrack by removing p from Q and R. We select a new vertex p from the resulting R and continue the same procedure until $R = \emptyset$.

Such a procedure is represented by a *search tree*, where the root is V and, whenever $R_p := R \cap \Gamma(p)$ is applied then R_p is a child of R. The edge between R and $R_p := R \cap \Gamma(p)$ is called a *branch*.

3.2 Approximate Coloring: Numbering

To make the above branch-and-bound algorithm efficient, it is most important to prune unnecessary searching with *low* overhead. For this purpose, we employed *greedy approximate* coloring or Numbering of the vertices in MCQ and MCR, as introduced in Refs. [7], [26], [27]. That is, each $p \in R$ is sequentially assigned a minimum possible positive integral value No[p], called the Number or Color of p, such that $No[p] \neq No[r]$ if $(p,r) \in E$. Consequently, we have the following property.

Proposition Let $\chi(R)$ be the minimum possible number of colors to color a subgraph induced by R. Then,

$$\omega(R) \le \chi(R) \le \operatorname{Max}\{No[p] \mid p \in R\}.$$

Hence, if $|Q| + Max\{No[p] \mid p \in R\} \le |Q_{max}|$ holds, we need not continue the search for R. This is a *bounding condition*.

At the beginning of MCQ, we sort vertices of V in descending order with respect to their degrees. In MCR and MCS, vertices of V are sorted in a similar but more sophisticated way.

After *Numbers* (*Colors*) are assigned to all vertices in R, let $Max\{No[r] \mid r \in R\} = maxno$ and $C_i = \{r \in R \mid No[r] = i\}$, where i = 1, 2, ..., maxno, that is, C_i is an independent set of vertices whose numbers are i. We sort the vertices in ascending order with

respect to their *Numbers* so that $R = C_1 \cup C_2 \cup \cdots \cup C_{maxno}$ as an ordered set of vertices.

Vertices are expanded for searching from the rightmost (with the *largest Number*) to the leftmost (with the *smallest Number*) on this R.

3.3 New Approximate Coloring

In order to make the above bounding condition work more efficiently, the algorithm MCS [25] first introduced the following **procedure** Re-NUMBER.

Because of the bounding condition mentioned in Section 3.2, if $No[r] \leq |Q_{\max}| - |Q|$, then it is not necessary to search from vertex r. When we encounter a vertex p with $No[p] > |Q_{\max}| - |Q|$, we attempt to change its Number to be less than or equal to $|Q_{\max}| - |Q|$ in the following manner. Let No_p denote the original value of No[p] and $No_{th} := |Q_{\max}| - |Q|$ stand for $No_{threshold}$. Attempt to find a vertex q in $\Gamma(p)$ such that $No[q] = k_1 \leq No_{th} - 1$, with $|C_{k_1}| = 1$. If such q is found, then attempt to find $Number\ k_2$ such that no vertex in $\Gamma(q)$ has $Number\ k_2$. If such number k_2 is found, then exchange the $Number\ of\ q$ so that $No[q] = k_2$. (If no vertex q with $Number\ k_2$ as above is found, then nothing is done.) When the $Number\ of\ vertex\ q$ is changed from k_1 to k_2 , No[p] is changed from No_p to k_1 ($\leq No_{th} - 1$); thus, $it\ is\ no\ longer\ necessary\ to\ search\ from\ p$.

The above procedure is named "Re-NUMBER" and is de-

```
procedure Re-NUMBER(p, No_p, No, C_1, C_2, ..., C_{maxno})
begin
 No_{th} := |Q_{max}| - |Q|;
 for k_1 := 1 to No_{th} - 1 do
  if |C_{k_1} \cap \Gamma(p)| = 1 then
    q := the element in (C_{k_1} \cap \Gamma(p)) ;
    for k_2 := k_1 + 1 to No_{th} do
      if C_{k_2} \cap \Gamma(q) = \emptyset then
        {Exchange the Numbers of p and q.}
       C_{k_2} := C_{k_2} \cup \{q\};
       No[q] := k_2;
       C_{No_p}:=C_{No_p}-\{p\};
       C_{k_1} := (C_{k_1} - \{q\}) \cup \{p\};
       No[p] := k_1;
       return
      fi
    od
  fi
 od
end { of Re-NUMBER}
```

Fig. 1 Procedure Re-NUMBER.

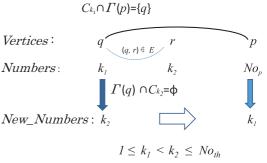


Fig. 2 ReNumbering.

3.4 EXTENDED INITIAL SORT-NUMBER

At the beginning of MCR and MCS, the given set V of n-vertices is sorted to $V = \{V[1], V[2], \ldots, V[n]\}$ so that a subgraph of G = (V, E) induced by a set of vertices $\{V[1], V[2], \ldots, V[i]\}$, it holds that V[i] aways has the minimum degree in $\{V[1], V[2], \ldots, V[i]\}$ for $1 \le i \le |V|$ as in Ref. [6]. Here, the degrees of their adjacent vertices are also taken into consideration. In addition, vertices are assigned initial Numbers. More precisely, the steps from $\{SORT\}$ to just above EXPAND(V, No) in Fig. 4 (Algorithm MCR) in Ref. [31] is named EXTENDED INITIAL SORT-NUMBER to V. Note that global variable Q_{max} can be updated by

then
$$Q_{\text{max}} := R_{\text{min}}$$

at line 5 from the bottom of Fig. 4 (Algorithm MCR) in Ref. [31]. Here, MCS introduced another new *adjunct ordered set* V_a of vertices in order to preserve the order of the vertices sorted by EXTENDED INITIAL SORT-NUMBER. Approximate coloring is carried out in the order of V_a from the left to the right. (See Fig. 4 in Ref. [34] for an illustration.)

3.5 Reconstruction of the Adjacency Matrix

Each graph is stored as an adjacency matrix in the computer memory. Sequential numbering is carried out according to the initial order of vertices in the adjunct ordered set V_a . Taking this into account, we *rename* the vertices of the graph and *reconstruct* the adjacency matrix so that the vertices are *consecutively ordered* in a manner identical to *the initial order of vertices* obtained at the beginning. (See Fig. 5 in Ref. [34] for an illustration.) The above-mentioned reconstruction of the adjacency matrix is to localize the memory usage, and it results in a more effective use of the cache memory.

The algorithm obtained by combining all the techniques described in this section is named MCS [25], [32], [34].

4. Improved Algorithms

4.1 An Approximate Solution as an Initial Lower Bound

When the algorithm MCS was first proposed in Ref. [25], the first part of MCS consisted of a procedure for finding an approximately maximum clique of the given graph. Its approximation algorithm named init-lb [25] is a local search algorithm based on our previous work [28]. It finds a near-maximum clique in a very short time, and the result is used as an <u>initial lower bound</u> of the size of a maximum clique. It demonstrated the effectiveness of an approximate solution for finding an exactly maximum clique. More precisely, when a sufficiently large near-maximum clique Q'_{max} is found, we let

$$Q_{\max} := Q'_{\max}$$

at the beginning of the original MCS [25]. Then $No_{th} := |Q_{\text{max}}|$ –

|Q| becomes large and the bounding condition becomes more effective

The final version of MCS presented in Refs. [32], [34] excluded the procedure (init-lb) for finding an approximately maximum clique. This is because it is important to examine the performance of the main body of MCS [32] itself independently of an approximation algorithm.

We have many approximation algorithms for finding a maximum clique [37], while finding a good approximate solution for the maximum clique problem is considered to be very hard as shown that the maximum clique problem is not polynomial-time approximable within $|V|^{1-\epsilon}$ for any ϵ unless NP = P[38]. The most important problem is a proper choice of the trade-off between the quality of the approximate solution and the time required to obtain it. We now turn back to our original MCS in Ref. [25] and choose another approximation algorithm called kopt local search (KLS) by Katayama et al. [11]. It does not necessarily give the best quality solution, but it runs in quite a short time and it is easy to control the above trade-off. Note that KLS uses a random number in it for selecting a vertex. The KLS repeats a number of local searches from different vertices of the given graph. In this repetition, we select a vertex with the largest degree one by one from the sorted vertices with respect to their degrees by EXTENDED INITIAL SORT-NUMBER. This is because a vertex with a large degree tends to be included in a maximum clique. When the number of repetitions becomes large, the quality of the solution increases but with increased running time.

In order to give a proper compromise between the high quality of the solution and the time required to obtain it for the given graph G = (V, E) with n = |V|, m = |E|, and dens = 2m/n(n-1) (density), we choosed the number rep of repetitions as follows by preliminary experiments in Ref. [35] with $d_0 = 1$:

$$rep = \min\{20n^{1/2} \times (\min\{dens, d_0\})^3, n\}$$
 for $n \ge 1$

A procedure for finding an approximate maximum clique of the given graph G = (V, E) under the above condition was named KLS(V, Q'_{max}) and its solution was given to Q'_{max} in Ref. [35]. The new MCS that was composed of a combination of the KLS procedure and MCS in Ref. [32] as above was named MCS₁.

In this paper, we take a slightly different approach from Ref. [35] by giving more thought to problems requiring more than 1 second to solve by MCS. Based on this intention, we try to improve the quality of the solution of KLS with a little more overhead. More exactly, we execute KLS just described above "5 times" with different random numbers (in parallel, conceptually) to get 5 (possibly different) solutions, but with $d_0 = 0.9$. And the final solution is set to be the best (largest) one among these 5 solutions. The total time required by the slightly extended KLS as above is about 5 times more than the time required by single execution of KLS in Ref. [35] but with possibly a better solution. Such a variant of KLS is named KLS5. We use in this paper KLS5(V, Q'_{max}) instead of KLS(V, Q'_{max}) in Ref. [35]. The KLS5(V, Q'_{max}) gives the (best of the 5) solution to Q'_{max} . The new MCS that is composed of a combination of the KLS5 procedure and MCS in Ref. [32] as above is named KLS5_MCS1 (&5.MCS1

Recently, Batsyn et al. [2] and Maslov et al. [17] also demonstrated the effectiveness of an approximate solution, independently. They used iterated local search (ILS) heuristic developed by Andrade [1].

4.2 EXTENDED INITIAL SORT-NUMBER near the Root of the Search Tree

It is shown that both search space and overall running time are reduced when vertices are sorted in ascending order with respect to their degrees prior to application of a branch-and-bound depth-first search for finding a maximum clique [6], [7], [27]. All of the preceding algorithms MCQ, MCR and MCS employ such sorting of vertices at the root level (*depth* = 0) of the search trees. Also clarified here is that if the vertices are sorted as above and followed by *Numbering* at every depth of the search tree then the resulting search space becomes more reduced but with much more overhead of time [12].

Therefore, it becomes important to choose a good trade-off between the reduction of the search space and the time to achieve it. In order to solve this trade-off, we confirmed in Refs. [12], [19] and [23] that it is effective to adaptively control the search method. For an earlier algorithm MCLIQ [27] that is a predecessor of MCQ, we proposed a technique to solve the trade-off and reduced the overall running time successfully as follows [12]:

- (i) At the first stage near the root of the search tree, we apply sorting of vertices followed by *Numbering*. (Ref. [12])
- (ii) In the second stage of the search tree, we apply *Numbering* without new sorting of vertices. (Just as in Ref. [27])
- (iii) In the third stage of the search tree near the leaves, we expand vertices by only inheriting the order of vertices and the previous *Numbers*. (Just as in Ref. [7])

The above techniques are promising for any algorithm for finding a maximum clique if we control these three stages appropriately. We apply the techniques of Ref. [12] to MCS. Here, we make full use of the adjunct ordered set V_a of vertices in MCS [32] in which vertices are sorted in ascending order with respect to their degrees from the rightmost (end) to the leftmost (front) by EXTENDED INITIAL SORT-NUMBER in Ref. [32]. In addition, we avoid the set R of vertices in MCS [32] in which vertices are sorted with respect to their Numbers. So, we are free from having to reconstruct such an R. From now on, we rename V_a as R, for simplicity. So, be careful that the set R in this paper corresponds to V_a in MCS [32], and not to R in MCS [32].

Hereafter, the NUMBERing procedure combined with Re-NUMBER is named NUMBER-R and is shown in **Fig. 3**. This is exactly the first half of the **procedure** Re-NUMBER-SORT in Fig. 2 of MCS [32].

A slightly stronger **procedure** Re-NUMBER1 is defined as the one obtained from **procedure** Re-NUMBER by replacing

```
"for k_2 := k_1 + 1 to No_{th} do" by "for k_2 := 1 to k_1 - 1 and k_1 + 1 to No_{th} do".
```

Another slightly modified **procedure** NUMBER-R+(R, No) is defined as the one obtained from **procedure** NUMBER-R(R, No) by replacing

```
procedure NUMBER-R(R, No)
        begin
           {NUMBER}
              maxno := 0:
              C_1 := \emptyset;
              for i := 1 to |R| do
                { Conventional greedy approximate coloring }
                p := R[i];
                k := 1:
                while C_k \cap \Gamma(p) \neq \emptyset
                   do k := k + 1 od
                if k > maxno then
                   maxno := k;
                   C_{maxno} := \emptyset
                fi
                C_k := C_k \cup \{p\};
                No[p] := k;
                { - Re-NUMBER starts - }
                No_{th} := |Q_{max}| - |Q|;
                if (k > No_{th}) and
                      (k = maxno) then
                   Re-NUMBER(p, k, No, C_1, C_2, ..., C_{maxno});
                   if C_{maxno} = \emptyset then
                      maxno := maxno - 1
                   fi
                { - Re-NUMBER ends - }
              od
        end { of NUMBER-R }
                   Fig. 3 Procedure NUMBER-R.
"if (k > No_{th}) and (k = maxno) then" by
"if (k > No_{th}) then"
"Re-NUMBER-R" by
"Re-NUMBER1"
```

in NUMBER-R(R, No). Thus, the condition for applying Re-NUMBER is relaxed in **procedure** NUMBER-R+(R, No).

At the first stage near and including the root of the search tree, we sort a set of vertices by EXTENDED INITIAL SORT-NUMBER to R followed by Numbering by NUMBER-R+(R, No). The procedure is shown in Fig. 5 with " $Th_1 = 0.4$, $Th_2 = 0$ " instead of " $Th_1 = 0.4$, $Th_2 = 0.1$ " at {Switches}. It is experimentally confirmed that NUMBER-R+(R, No) is better than NUMBER-R(R, No), since NUMBER-R+(R, No) is applied only a few times with better results but with more overhead than NUMBER-R(R, No).

This task of preprocessing (of sorting vertices followed by NUMBER-R) is time-consuming. So, as stated at the beginning of Section 4.2, it is important to change this first stage to the second stage at an appropriate switching depth that is near the root of the search tree. First, for a vertex $p \in R$ at a certain depth of the search tree, consider $newR := R_p = R \cap \Gamma(p)$ that is a child of R. If the ratio $|\{v \in newR \mid No[v] > No_{th}\}|/|newR|$ becomes large, then much more preprocessing time may be required. In addition, when dens (density) of the graph becomes larger it generally requires more time for finding a maximum clique and then much

```
procedure NUMBER-RL(R, No, newNo)
begin
   No_{th} := |Q_{max}| - |Q|;
   for i := 1 to |R| do
     C_i := \emptyset;
   od
   maxno := 1;
   for i := 1 to |R| do
     if No[R[i]] \leq No_{th} then
        k := No[R[i]];
        if k > maxno then maxno := k fi
        C_k := C_k \cup \{R[i]\};
        newNo[R[i]] := k;
      fi
   od
   for i := 1 to |R| do
     if No[R[i]] > No_{th} then
        p := R[i];
        k := 1;
        while C_k ∩ Γ(p) ≠ ∅
           do k := k + 1 od
        if k > maxno then
           maxno := k:
        C_k := C_k \cup \{p\};
        newNo[p] := k;
        if (k > No_{th}) then
            Re-NUMBER1(p, k, No, C_1, C_2, \dots, C_{maxno});
           if C_{maxno} = \emptyset then
              maxno := maxno - 1
           fi
        fi
     fi
   od
end { of NUMBER-RL}
```

Fig. 4 Procedure NUMBER-RL.

larger number of preprocessing steps is needed. As a result, we consider the following value:

$$T = \frac{|\{v \in newR \mid No[v] > No_{th}\}|}{|newR|} \times dens.$$

From preliminary experiments, we have chosen that if $T \ge 0.4$ then we continue the same procedure described for the first stage. Otherwise, we switch the stage to the second stage. Thus, we let $Th_1 := 0.4$ in Fig. 5. The new procedure obtained from Fig. 5 by replacing " $Th_1 := 0.4$, $Th_2 := 0.1$ " by " $Th_1 := 0.4$, $Th_2 := 0$ " at {Switches} is named LSMCS₂. Here, we control the stage = 1 so that it never returns back to stage = 1 after it changed to the second or the third $stage \ (\ne 1)$.

Konc and Janežič [13] also independently improved MCQ [29] successfully in a similar way.

4.3 Lightened Numbering Mainly near the Leaves of the Search Tree

Mainly near the leaves of the search tree, the ratio $|\{v \in newR \mid No[v] > No_{th}\}|/|newR|$ tends to be small. In this third stage, it is preferable to lighten the task of preprocessing before expansion of vertices. So, we only inherit the order of vertices from that in their parent depth, as in the second stage. In addition, we inherit the assigned *Numbers* from those assigned to their

```
procedure k5.MCT(G = (V, E))
begin
  global Th_1 := 0.4; Th_2 := 0.1; {Switches}
  global\ Q := \emptyset;
  global Q_{max} := \emptyset;
  global\ dens := 2|E|/|V|(|V|-1);\ \{density\}
  if dens \le 0.1 then
    k5.MCS<sub>1</sub>(G = (V, E));
  else
   Apply EXTENDED INITIAL SORT-NUMBER to V;
      { Q_{max} can be updated.}
   Reconstruct the adjacency matrix as described in [32];
   \mathrm{KLS5}(V,Q'_{max});
   if Q_{max} < Q'_{max} then
     Q_{max} := Q'_{max}
   NUMBER-R+(V, No);
       stage := 1;
   EXPAND(V, No, stage);
  output Q_{max} {Maximum clique}
end { of k5_MCT}
                Fig. 5 Procedure k5_MCT.
procedure EXPAND(R, No, stage)
begin
 for i := |R| downto 1 do
  p := R[i];
  if (stage = 1 \text{ and } |Q| + \max_{v \in R} \{No[v]\} > |Q_{max}|)
   or (stage \neq 1 \text{ and } |Q| + No[p] > |Q_{max}|) then
    O := O \cup \{p\};
    newR := R \cap \Gamma(p); {preserving the order}
    if newR \neq \emptyset then
     No_{th} := |Q_{max}| - |Q|;
     T := \frac{|\{v \in newR \mid No[v] > No_{th}\}|}{} \times dens;
                   newR
     if stage = 1 and Th_1 \le T then
      Apply EXTENDED INITIAL SORT-NUMBER to R;
      NUMBER-R+(newR, newNo);
      {The initial value of newNo has no significance.}
      newstage := 1:
     else if dens > 0.95 or Th_2 \le T then
      NUMBER-R(newR, newNo);
      newstage := 2;
      NUMBER-RL(newR, No, newNo);
      newstage := 3;
     EXPAND(newR, newNo, newstage)
    else if |Q| > |Q_{max}| then Q_{max} := Q fi
    Q := Q - \{p\};
    R := R - \{p\}; {preserving the order}
  fi
 od
end { of EXPAND }
              Fig. 6 Procedure EXPAND.
```

parents only if their *Numbers* are less than or equal to No_{th} . If we inherit all the assigned *Numbers* from those assigned to their parents as in Ref. [7] the resulting bounding condition becomes too weak. In order to remedy this weakness, if the inherited *Numbers* from those assigned to their parents are greater than No_{th} then we give them new *Numbers*. For vertices whose inherited *Numbers*

Table 1 Comparison of CPU times in MCS, k5_MCS1, k5_MCS2 and k5_MCT.

	Graph			KLS5		times [sec]				
Name	n	dens	ω	sol	MCS	k5_MCS ₁	k5_MCS2	k5.MCT	(MCS/k5_MCT) _t	
brock400_1	400	0.75	27	25	288	260	182	116	2.49	
brock400_2	400	0.75	29	25	124	104	77	47	2.66	
brock400_3	400	0.75	31	25	195	132	92	59	3.33	
brock400_4	400	0.75	33	25	103	101	73	46	2.23	
brock800_1	800	0.65	23	21	4,122	4,080	2,922	1,944	2.12	
brock800_2	800	0.65	24	21	3,683	3,484	2,499	1,629	2.26	
brock800_3	800	0.65	25	21	2,540	2,372	1,682	1,104	2.30	
brock800_4	800	0.65	26	20	1,768	1,758	1,256	819	2.16	
C250.9	250	0.90	44	44	1,171	946	779	405	2.89	
gen200_p0.9_44	200	0.90	44	44	0.17	0.39	0.39	0.29	0.60	
gen200_p0.9_55	200	0.90	55	55	0.46	0.32	0.32	0.32	1.43	
gen400_p0.9_55	400	0.90	55	55	22,536	80.8	89.3	1.18	19,098	
gen400_p0.9_65	400	0.90	65	65	57,385	6.81	7.04	1.44	39,851	
gen400_p0.9_75	400	0.90	75	75	108,298	2.44	2.43	1.33	81,427	
p_hat300-3	300	0.74	36	36	0.99	0.68	0.68	0.52	1.90	
p_hat500-3	500	0.75	50	50	57	35	33	18	3.11	
p_hat700-2	700	0.50	44	44	2.16	1.46	1.44	1.12	1.93	
p_hat700-3	700	0.75	62	62	900	470	440	217	4.16	
p_hat1000-2	1000	0.49	46	46	85	49	47	29	2.90	
p_hat1000-3	1000	0.74	68	68	305,146	111,587	96,207	39,134	7.80	
p_hat1500-2	1500	0.51	65	65	6,299	3,039	2,833	1,559	4.04	
san1000	1000	0.50	15	15	1.02	0.25	0.23	0.24	4.25	
san200_0.9_2	200	0.90	60	60	0.16	0.32	0.32	0.32	0.50	
san400_0.7_1	400	0.70	40	40	0.26	0.29	0.28	0.28	0.92	
san400_0.7_3	400	0.70	22	18	0.67	0.51	0.54	0.41	1.62	
sanr200_0.9	200	0.90	42	42	15.3	9.7	9.9	4.9	3.10	
sanr400_0.7	400	0.70	21	21	77	77	58	41	1.89	
DSJC1000.5	1000	0.50	15	15	141	137	125	94	1.50	
keller5	776	0.75	27	27	82,422	81,631	36,548	10,008	8.24	
frb30-15-1	450	0.82	30	30	740	434	464	75	9.84	
frb30-15-2	450	0.82	30	30	1,048	692	773	122	8.55	
frb30-15-3	450	0.82	30	28	670	678	729	124	5.39	
frb30-15-4	450	0.82	30	30	2,248	1,086	1,201	223	10.1	
frb30-15-5	450	0.82	30	30	972	741	780	105	9.29	
r200.8	200	0.80	24-27	24-27	1.64	1.47	1.31	0.90	1.82	
r200.9	200	0.90	39-44	39-44	26.5	19.0	19.2	10.7	2.48	
r200.95	200	0.95	58-66	58-66	19.4	12.0	12.5	10.9	1.78	
r250.8	250	0.80	26-28	26-28	19.6	17.5	13.9	8.8	2.23	
r300.8	300	0.80	28-29	28-29	160	133	96	59	2.73	
r400.7	400	0.70	21-22	21-22	75	67	50	35	2.15	
r400.8	400	0.80	30-31	30-31	6,467	5,527	3,437	1,997	3.24	
r500.7	500	0.70	22-23	21-23	733	692	473	326	2.25	
r1000.5	1000	0.50	15-16	14-15	134	133	123	92	1.46	
r1000.6	1000	0.60	19-20	18-19	6,591	6,569	4,862	3,456	1.91	

from their parents are greater than No_{th} we newly give them Num-bers by sequential numbering combined with Re-Numbering. For this Re-Numbering we adopt stronger Re-NUMBER1 instead of Re-NUMBER since Re-Numbering is required not so many times in this stage. The resulting procedure in this stage named **procedure** NUMBER-RL is shown in **Fig. 4**.

From preliminary experiments, we have chosen to turn to the new stage = 3 if the previously given value $T = (|\{v \in newR \mid No[v] > No_{th}\}|/|newR|) \times dens$ is less than 0.1. Then we let $Th_2 := 0.1$ in Fig. 5. The **procedure** NUMBER-RL is weaker than the previous **procedure** NUMBER-R for obtaining a strong bounding condition but requires less overhead than the previous one. However, if the given graph is too dense then **procedure** NUMBER-RL becomes too weak and the number of branches of the search tree grows quite large. So, we choose to go to new stage = 3 only if $dens \le 0.95$.

In addition, a simpler algorithm is generally better than sophisticated algorithms for sparse graphs. Thus, if $dens \le 0.1$ we choose simpler algorithm ks-MCS₁ without relying on techniques introduced after ks-MCS₁ in this paper.

The resulting algorithm obtained by taking the total techniques in Sections 4.1–4.3 to improve MCS [32] is named &MCT (The 'T' is for 'Total'.) and is shown in **Fig. 5** and **Fig. 6**.

5. Computational Experiments

In order to demonstrate the effectiveness of the techniques given in the previous section, we carried out computational experiments. All the algorithms were implemented in C language, where the underlining programs were slightly revised from those in Ref. [35]. The computer had an Intel core i7-4790 CPU of 3.6 GHz clock with 8 GB of RAM and 8 MB of cache memory. It worked on a Linux operating system with a compiler gcc -O3. The *dfmax running time for DIMACS benchmark instances* [10] for r300.5, r400.5 and r500.5 are 0.141, 0.900 and 3.442 seconds, respectively. All the results of the experiments are summarized in **Tables 1–4**. Each first column lists the benchmark graphs brock - keller5 in DIMACS [10], the frb family in BHOSLIB [3], and/or random graphs rn.p with the number of vertices=n and the edge probability=p. As for the CPU time, the averages are taken over 10 random graphs rn.p where p < 0.9. For random

Table 2	Comparison	of branches in	MCS, k5.MCS	1. k5.MCS2	and k5.MCT.
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	Graph			KLS5		branches	$s [\times 10^{-6}]$		
Name	n	dens	ω	sol	MCS	k5.MCS1	k5.MCS2	k5.MCT	(MCS/k5_MCT)
brock400_1	400	0.75	27	25	89	77	52	55	1.62
brock400_2	400	0.75	29	25	34	24	18	18	1.82
brock400_3	400	0.75	31	25	65	38	25	27	2.41
brock400_4	400	0.75	33	25	31	30	20	22	1.42
brock800_1	800	0.65	23	21	1,092	1,081	748	786	1.39
brock800_2	800	0.65	24	21	953	867	599	627	1.52
brock800_3	800	0.65	25	21	630	557	378	396	1.59
brock800_4	800	0.65	26	20	381	380	258	270	1.41
C250.9	250	0.90	44	44	255	197	154	188	1.35
gen200_p0.9_44	200	0.90	44	44	0.0355	0.0170	0.0167	0.0024	14.5
gen200_p0.9_55	200	0.90	55	55	0.11248	0.00073	0.00065	0.00060	188
gen400_p0.9_55	400	0.90	55	55	2,895	7.4348	8.1264	0.0002	11,626,243
gen400_p0.9_65	400	0.90	65	65	7,628	0.330	0.341	0.058	131,671
gen400_p0.9_75	400	0.90	75	75	17,153	0.054	0.052	0.002	8,354,874
p_hat300-3	300	0.74	36	36	0.23	0.07	0.07	0.09	2.63
p_hat500-3	500	0.75	50	50	7.9	4.3	4.1	5.6	1.41
p_hat700-2	700	0.50	44	44	0.339	0.126	0.121	0.197	1.72
p_hat700-3	700	0.75	62	62	88	43	40	54	1.64
p_hat1000-2	1000	0.49	46	46	12.6	6.6	6.3	10.0	1.26
p_hat1000-3	1000	0.74	68	68	27,212	9,026	7,822	9,027	3.01
p_hat1500-2	1500	0.51	65	65	560	253	234	400	1.40
san1000	1000	0.50	15	15	0.085	0.0005	0	0	1110
san200_0.9_2	200	0.90	60	60	0.042	0.0001	0	0	
san400_0.7_1	400	0.70	40	40	0.023	0.0002	0	0	
san400_0.7_3	400	0.70	22	18	0.124	0.041	0.050	0.054	2.32
sanr200_0.9	200	0.90	42	42	3.5	2.0	1.9	2.1	1.63
sanr400_0.7	400	0.70	21	21	30	29	21	23	1.31
DSJC1000.5	1000	0.50	15	15	52	49	43	45	1.14
keller5	776	0.75	27	27	13,148	13,152	5,519	4,495	2.93
frb30-15-1	450	0.82	30	30	157	82	85	38	4.12
frb30-15-2	450	0.82	30	30	229	135	148	65	3.55
frb30-15-3	450	0.82	30	28	147	146	153	73	2.01
frb30-15-4	450	0.82	30	30	509	214	232	121	4.22
frb30-15-5	450	0.82	30	30	203	143	146	57	3.58
r200.8	200	0.80	24-27	24-27	0.66	0.51	0.42	0.47	1.40
r200.9	200	0.90	39-44	39-44	6.5	4.4	4.1	5.2	1.25
r200.95	200	0.95	58-66	58-66	2.7	1.5	1.5	2.5	1.09
r250.8	250	0.93	26-28	26-28	7.0	6.0	4.5	4.9	1.42
r300.8	300	0.80	28-29	28-29	53	42	29	31	1.69
r400.7	400	0.70	21-22	21-22	28	24	17	18	1.54
r400.7	400	0.70	30-31	30-31	1,921	1,588	933	999	1.92
	500	0.80	22-23	21-23	261	241	159	170	1.54
r500.7		0.70			50				
r1000.5	1000		15-16	14-15		49	43	45	1.11 1.34
r1000.6	1000	0.60	19-20	18-19	2,137	2,111	1,513	1,594	1.34

graphs rn.p where $p \ge 0.9$, the averages are taken over 100 random graphs. The random graphs in this paper are not exactly the same as those in Ref. [35]. In the Tables, n and ω stands for the number of vertices and the size of the maximum clique, respectively. In addition, dens stand for density of a benchmark graph and p for a random graph rn.p. The columns sol and time below KLS5 show the solution and the computing time of KLS5, respectively.

5.1 Stepwise Improvement

Tables 1 and 2 show stepwise improvement from MCS to ${}_{k5}$ MCT for selected graphs chosen from the following Tables 3 and 4. In Table 1, $(MCS/{}_{k5}MCT)_t$ is the ratio of the CPU time required by MCS to that of ${}_{k5}MCT$. In Table 2, $(MCS/{}_{k5}MCT)_b$ is the ratio of the number of branches required by MCS to that of ${}_{k5}MCT$.

(1) Improvement from MCS to ks.MCS₁ by an approximate solution given by KLS5 in Section 4.1: The improvement is particularly quite effective for the gen graph family. ks.MCS₁ is faster than MCS for gen400-p0.9-75, gen400-p0.9-65, and

gen400_p0.9_55 by more than 44,000, 8,000, and 270 times, respectively. This technique is effective for almost all graphs but with few exceptions such as the MANN graph family.

- (2) Improvement from & MCS₁ to & MCS₂ by EXTENDED INITIAL SORT-NUMBER in Section 4.2: This technique is effective mainly for the brock graph family by around 1.4 times. For some graphs such as the gen and frb graph families, the effect is negative.
- (3) Improvement from \$1.5\text{MCS}_2\$ to \$1.5\text{MCT}\$ by Lightened Numbering in Section 4.3: This technique is effective for almost all graphs in reducing computing time in spite of increased numbers of branches in general. The \$1.5\text{MCT}\$ is faster than \$1.5\text{MCS}_2\$ for gen400_p0.9_55, frb30-15-5, frb30-15-2, and frb30-15-1 by more than 76, 7, 6, and 6 times, respectively, where their numbers of branches are also reduced.

5.2 Overall Improvement

Table 3 shows the result of the overall improvement from MCS to k5.MCT in computing time for the benchmark graphs. The column *time* below KLS5 shows the computing time for KLS5 that

Table 3 CPU time [sec] for benchmark graphs.

(Graph			KI	LS5	MCS	k5_MCT	BBMCX	MaxCLQ	ILS&MCS	BG14
Name	n	dens	ω	sol	time	[32]		[22]	[15]	[17]	[2]
brock200_1	200	0.75	21	21	0.09	0.36	0.30	0.18	0.34	4.42	2.51
brock400_1	400	0.75	27	25	0.41	288	116	150	205	188	302
brock400_2	400	0.75	29	25	0.41	124	47	68	96	94	132
brock400_3	400	0.75	31	25	0.41	195	59	120	160	145	211
brock400_4	400	0.75	33	25	0.41	103	46	68	100	72	87
brock800_1	800	0.65	23	21	1.07	4,122	1,944	2,690	4,562	3,998	4,216
brock800_2	800	0.65	24	21	1.09	3,683	1,629	2,415	4,002	3,462	3,778
brock800_3	800	0.65	25	21	1.07	2,540	1,104	1,587	2,510	2,361	2,649
brock800_4	800	0.65	26	20	1.08	1,768	819	1,100	1,853	1,685	1,868
C250.9	250	0.90	44	44	0.43	1,171	405	713	268		
C2000.5	2000	0.50	16	16	2.74	33,899	21,030				
gen200_p0.9_44	200	0.90	44	44	0.29	0.17	0.29	0.16	0.11	1.68	
gen200_p0.9_55	200	0.90	55	55	0.32	0.46	0.32	0.31	0.14	2.43	0.92
gen400_p0.9_55	400	0.90	55	55	1.18	22,536	1.18	19,362		46,504	2,965
gen400_p0.9_65	400	0.90	65	65	1.23	57,385	1.44	66,135	36,684	2,130	18
gen400_p0.9_75	400	0.90	75	75	1.32	108,298	1.33	47,176	9,984	84	7.8
MANN_a27	378	0.99	126	126	2.60	0.26	2.88	0.17	0.16	1.30	
MANN_a45	1035	0.99	345	344	79	53	128	32	23	17	55
p_hat300-3	300	0.74	36	36	0.31	0.99	0.52	0.66	1.16	6.72	3.62
p_hat500-3	500	0.75	50	50	1.11	57.1	18.4	33.3	39.6	50	60
p_hat700-2	700	0.50	44	44	0.57	2.16	1.12	1.53	3.61	59	29
p_hat700-3	700	0.75	62	62	2.28	900	217	680	879	552	767
p_hat1000-1	1000	0.25	10	10	0.02	0.23	0.22	0.19	1.60	218	
p_hat1000-2	1000	0.49	46	46	1.13	85	29	73	101	204	113
p_hat1000-3	1000	0.74	68	68	4.94	305,146	39,134				
p_hat1500-1	1500	0.25	12	11	0.08	1.82	1.46	1.95	10	478	422
p_hat1500-2	1500	0.51	65	65	4.77	6,299	1,559	3,852	8,027	5,346	5,434
san1000	1000	0.50	15	15	0.23	1.02	0.24	0.68	0.72	449	158
san200_0.9_2	200	0.90	60	60	0.32	0.16	0.32	0.07	0.10	12	
san400_0.7_1	400	0.70	40	40	0.28	0.26	0.28	0.14	0.13	16	7
san400_0.7_2	400	0.70	30	30	0.25	0.059	0.256	0.092	0.064	19	
san400_0.7_3	400	0.70	22	18	0.25	0.67	0.41	0.39	0.43	27	12
sanr200_0.7	200	0.70	18	18	0.07	0.15	0.16	0.08	0.17	5.05	1.03
sanr200_0.9	200	0.90	42	42	0.30	15.33	4.94	7.38	4.21	4.62	10.2
sanr400_0.5	400	0.50	13	13	0.07	0.35	0.31	0.19	0.69	35	18
sanr400_0.7	400	0.70	21	21	0.31	77	41	44	81	86	81
DSJC500.5	500	0.50	13	13	0.12	1.5	1.3	0.8	2.8	00	01
DSJC1000.5	1000	0.50	15	15	0.12	141	94	102	265		
keller5	776	0.75	27	27	1.65	82,422	10,008	30,299	4,982	5,777	82,508
frb30-15-1	450	0.73	30	30	0.76	740	75	1,029	560	3,777	02,500
frb30-15-2	450	0.82	30	30	0.75	1,048	122	672	758		
frb30-15-3	450	0.82	30	28	0.75	670	124	350	477		
frb30-15-4	450	0.82	30	30	0.75	2,248	223	1,157	955		
frb30-15-5	450	0.82	30	30	0.75	2,248 972	105	801	705		

is a part of the total CPU time. In Table 2 of Ref. [35], the *time* included the computing time from "Apply *EXTENDED INITIAL SORT-NUMBER* to V;" to "Reconstruct the adjacency matrix as described in Ref. [32]," since sorting of vertices is necessary before KLS5(V, $Q'_{\rm max}$). But, the *time* in this paper excludes the above preceding time so that KLS5 itself is clearer. Table 4 shows the same result for random graphs.

Tables 3–4 include the state-of-the-art result of BBMCX [22] by Segundo et al. that makes good use of a limited MaxSAT bound. Here, its computing time is calibrated in the established way in the Second DIMACS Implementation Challenge [10], where our computer is calculated to be 1.30 times faster than that in Ref. [22]. (See **Table 5** in Appendix for the detail, and that 1.30 > 1.298.) From Ref. [22], Tables 3–4 also include the calibrated computing time of MaxCLQ [14], [15] by Li and Quan that is based on MaxSAT. The calibrated computing time by ILS&MCS [17] and BG14 [2] are added on the assumption that the performance of each MCS is the same as that in this paper, for reference, too. The boldface entries indicate the fastest time in the row.

The result shows that the &s_MCT is faster than MCS for gen400_p0.9_75, gen400_p0.9_65 and gen400_p0.9_55 by over 81,000, 39,000 and 19,000 times, respectively. The &s_MCT is faster than MCS for frb30-15-4 by over 10 times. The &s_MCT is faster than MCS for frb30-15-1, frb30-15-5, frb30-15-2, keller5, p_hat1000-3, frb30-15-3 by over 5 times. The &s_MCT is faster than MCS for san1000, p_hat700-3, p_hat1500-2, brock400_3, r400.8, p_hat500-3, sanr200_0.9 by over 3 times. In Table 1, &s_MCT is faster than MCS by more than 2 times for the other 14 graphs including r300.8, r200.9, r500.7, r250.8 and r400.7.

Except for few special graphs such as in the MANN family and for easy graphs that can be solved in less than 1 second by MCS, ks_MCT is faster than or equal to MCS for all graphs in Tables 3 and 4.

The k5.MCT is faster than the other algorithms in Tables 3 and 4 for many instances. Note that MaxCLQ is fast for dense graphs. ILS&MCS [17] and BG14 [2] require more time than k5.MCT for most of the instances tested. One reason for this difference comes from the fact that our approximation algorithm, KLS, takes up only small portion of the total algorithm's computing time with

Table 4 CPU time [sec] for random graphs.

	Graph			KL	S5	MCS	k5_MCT	BBMCX	MaxCLQ
Name	n	dens	ω	sol	time	[32]		[22]	[15]
r150.9	150	0.90	35-39	35-39	0.14	0.40	0.30	0.26	0.13
r150.95	150	0.95	52-57	52-57	0.24	0.13	0.28	0.11	0.02
r200.7	200	0.70	17-19	17-19	0.07	0.17	0.17	0.09	0.18
r200.8	200	0.80	24-27	24-27	0.13	1.64	0.90	0.95	1.08
r200.9	200	0.90	39-44	39-44	0.29	26.5	10.7	14.8	6.2
r200.95	200	0.95	58-66	58-66	0.49	19.4	10.9	30.2	2.5
r250.7	250	0.70	18-19	18-19	0.11	1.07	0.75		
r250.8	250	0.80	26-28	26-28	0.20	19.6	8.8		
r300.6	300	0.60	15-16	15-16	0.09	0.47	0.41	0.21	0.58
r300.7	300	0.70	20-20	19-20	0.16	5.3	2.9	2.6	4.7
r300.8	300	0.80	28-29	28-29	0.30	160	59	89	87
r400.5	400	0.50	13-13	12-13	0.07	0.32	0.30		
r400.6	400	0.60	16-17	16-17	0.16	3.59	2.41		
r400.7	400	0.70	21-22	21-22	0.31	75	35		
r400.8	400	0.80	30-31	30-31	0.55	6,467	1,997		
r500.5	500	0.50	13-14	13-13	0.11	1.31	1.17	0.64	2.09
r500.6	500	0.60	17-18	16-17	0.26	18.0	11.3	10.1	22.1
r500.7	500	0.70	22-23	21-23	0.49	733	326	423	564
r600.4	600	0.40	11-11	10-11	0.05	0.36	0.35		
r600.5	600	0.50	14-14	13-14	0.17	4.21	3.29		
r600.6	600	0.60	17-18	17-18	0.40	85	48		
r1000.3	1000	0.30	9-10	8-9	0.03	0.46	0.46	0.38	2.03
r1000.4	1000	0.40	12-12	11-11	0.17	5.9	5.3	4.5	14.5
r1000.5	1000	0.50	15-16	14-15	0.54	134	92	103	231
r1000.6	1000	0.60	19-20	18-19	1.25	6,591	3,456		
r2000.2	2000	0.20	8-8	7-8	0.02	0.67	0.69		
r2000.3	2000	0.30	10-11	9-10	0.17	15.0	13.5		
r2000.4	2000	0.40	13-14	12-13	0.83	452	362		
r3000.1	3000	0.10	6-7	5-6	0.00	0.21	0.21	0.19	15
r3000.2	3000	0.20	9-9	7-8	0.05	3.62	3.48	4.34	34
r3000.3	3000	0.30	11-11	10-10	0.44	121	108		
r3000.4	3000	0.400	14-14	12-13	2.28	6,411	5,176		
r4000.1	4000	0.10	7-7	5-7	0.00	0.53	0.53		
r4000.2	4000	0.20	9-9	8-9	0.10	14.8	13.4		
r4000.3	4000	0.30	11-12	10-11	0.88	633	547	1.10	60
r5000.1	5000	0.10	7-7	5-6	0.01	1.13	1.13	1.19	68
r5000.2	5000 5000	0.20	9-10 12-12	8-8 10-11	0.20 1.55	2 260	39	68	578
r5000.3	10000		6-6	4-5		2,269	1,873		
r10000.05		0.05	7-7		0.01	1.883	1.886	20	601
r10000.1 r10000.2	10000 10000	0.10 0.20	10-10	6-7 8-9	0.04 0.87	13.7 1,331	13.1 1,136	20	684
r10000.2 r15000.05		0.20	6-6	8-9 5-5		6.96	1,136 6.96		
r15000.05 r15000.1	15000 15000	0.05	0-0 8-8	5-5 6-6	0.02 0.10	65.3	61.3	115	2,749
r15000.1 r15000.2	15000	0.10	8-8 10-11	0-0 9-9	2.18	10,565	9,488	113	2,749
r20000.2	20000	0.20	6-7	9-9 5-5	0.05	10,363	18.3		
r20000.03	20000	0.03	8-8	3-3 6-7	0.03	251	235		
120000.1	20000	0.10	0-0	0-7	0.17	231	433		

few exceptions, whereas their approximation algorithm, ILS [1] in ILS&MCS and BG14, consumes a considerable part of the total computing time. To be more precise, they run the ILS heuristic with 100,000 scans for all the considered instances except gen400_p0.9_55 and p_hat1000-3 for which they use 60 million scans because these two instances are computationally difficult. Their resulting approximate solution for gen400_p0.9_55 is 54, whereas our corresponding solution is 55 that is optimal.

In ks_MCT, even if we change the value of d_0 from 0.9 to 1 in rep we have no change of sol in Tables 1–4. So, reducing $d_0 = 1$ in MCT [35] to $d_0 = 0.9$ in ks_MCT is reasonable.

6. Concluding Remarks

In conclusion, &s_MCT has achieved significant improvement over MCS, that is, &s_MCT is much faster than MCS for graphs which require more than around 1 second to solve by MCS [32].

For comparison, the number of graphs for which &5.MCT is faster than MCS by more than 1000, 100, 10, and 5 times is 3, 3,

4, and 10, respectively, in Table 1, whereas the number of graphs for which MCT is faster than MCS by more than 1000, 100, 10, and 5 times is 2, 3, 3, and 9, respectively, among the same group of graphs [35]. This is an example to show that LEDMCT is slightly faster than MCT for graphs which require more than around 1 second to solve by MCS, but with few exceptions as in MANN family graphs. See Ref. [35] for the details of MCT.

Another improved MCT could be obtained by replacing simply

$$rep = \min\{20n^{1/2} \times dens^3, n\} \quad \text{for } n \ge 1$$

in Ref. [35] by

$$rep = 5 \times min\{20n^{1/2} \times dens^3, n\}$$
 for $n \ge 1$,

and we call it rs.MCT, where the modified KLS in this way is named KLSr5. This KLSr5 takes almost the same time as KLS5 for the same instance. As one example for gen400_p0.9_55, rs.MCT gets an approximately maximum clique of size 53 and requires the total of 135.9 seconds to obtain the final exact result

of 55, whereas ks_MCT gets an approximately maximum clique of size 55 (= exact solution) and requires a total of 1.18 seconds to obtain the final result as shown in Table 1. If we let rep := 23,852 in this rs_MCT then it just manages to get an approximately maximum clique of size 55 and requires the total of 19.16 seconds to obtain the final exact result. This shows another example of the advantage of ks_MCT over MCT, hence also over MCS.

It is left as an important problem to choose other better approximation algorithms for the maximum clique problem. The present algorithm can be easily extended for enumerating all maximal cliques of the maximum and near-maximum size with the technique of Ref. [30].

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 Table 5
 Each dfmax running time for instances [sec].

	k5_MCT	BBMCX				
	This paper	Segundo et al. [22]				
Graph	$\overline{T_1}$	$\overline{T_2}$	T_2/T_1			
r300.5	0.141	0.189	1.340			
r400.5	0.900	1.155	1.283			
r500.5	3.442	4.369	1.269			

Average: 1.298



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