

Searching for partial Hadamard matrices

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In honour of Kathy Horadam.

In Memoriam: This paper is dedicated to the late Warwick Richard de Launey (Oct. 1, 1958 to Nov. 8, 2010), for his outstanding contributions in Design Theory and related topics.

Abstract Three algorithms looking for pretty large partial Hadamard matrices are described. Here “large” means that hopefully about a third of a Hadamard matrix (which is the best asymptotic result known so far, [8]) is achieved. The first one performs some kind of local exhaustive search, and consequently is expensive from the time consuming point of view. The second one comes from the adaptation of the best genetic algorithm known so far searching for cliques in a graph, due to Singh and Gupta [21]. The last one consists in another heuristic search, which prioritizes the required processing time better than the final size of the partial Hadamard matrix to be obtained. In all cases, the key idea is characterizing the adjacency properties of vertices in a particular subgraph G_t of Ito’s Hadamard Graph $\Delta(4t)$ [18], since cliques of order m in G_t can be seen as $(m + 3) \times 4t$ partial Hadamard matrices.

Keywords Hadamard matrix · clique · Hadamard Graph

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1 Introduction

Hadamard matrices consist in $\{1, -1\}$ -square matrices whose rows are pairwise orthogonal. This nice property makes Hadamard matrices being objects for multiple applications (see [13] and [14] for instance).

It may be straightforwardly checked that such a matrix must be of size 1, 2 or a multiple of 4. The Hadamard Conjecture claims that a matrix of this type exists for every size multiple of 4. Many attempts have been devoted to prove this conjecture (both from a constructive way [14] and also from a theoretical point of view in terms of asymptotic results of existence [9, 11]), but it remains unsolved so far.

From the practical point of view, taking into account possible applications, sometimes there is no need to consider a full Hadamard matrix. In fact, it suffices to meet a large amount of pairwise orthogonal rows [2]. This has originated the interest in constructing *partial Hadamard matrices* PH , that is, $m \times n$ $(1, -1)$ -matrices PH satisfying $PH \cdot PH^T = nI_m$, for $m \leq n$. We call m the *depth* of PH .

From the orthogonality law, it is readily checked that the number n of columns must be 1, 2 or a multiple of 4.

Notice that a partial Hadamard matrix does not need to be a submatrix of a proper Hadamard matrix (for instance, cliques listed in Table 3 for $7 \leq t \leq 10$ are maximal but not maximum; in the sense that although no larger cliques exist containing them, there exist larger cliques, for example, those related to full Hadamard matrices).

Although partial Hadamard matrices are as useful as Hadamard matrices themselves with regards to practical purposes, unfortunately it seems that their explicit construction is equally hard as well.

De Launey proved in [8] that partial Hadamard matrices of size about a third of a $4t \times 4t$ Hadamard matrix exist for large t . The proof gives a polynomial time algorithm in t for constructing such a matrix. Furthermore, De Launey and Gordon proved in [10] that about a half of a Hadamard matrix $4t \times 4t$ exists for large t , assuming that the Riemann hypothesis is true. The idea is decomposing $2t - i$ as the sum of i odd prime numbers p_i , $2 \leq i \leq 3$, so that the juxtaposition of the corresponding Paley conference matrices provides a partial Hadamard matrix of depth $2 \min\{p_i\} + 2$. Unfortunately, none of these methods can provide a partial Hadamard matrix of depth greater than half of a full Hadamard matrix.

In this paper, we present three new algorithms for constructing partial Hadamard matrices of size $m \times 4t$. The first one performs some kind of local exhaustive search, and consequently is expensive from the time consuming point of view. The second one comes from the adaptation of the best genetic algorithm known so far searching for cliques in a graph, due to Singh and Gupta [21]. The third one consists in another heuristic search, which prioritizes the required processing time better than the final size of the partial Hadamard matrix obtained so far. The idea is looking for large cliques (i.e. subgraphs

whose vertices are pairwise adjacent) in a subgraph G_t of Ito's Hadamard Graph $\Delta(4t)$ [18].

Although the results showed in [8] and [10] are impressive and meaningfully better than any obtained from the algorithms described in this paper, it is a remarkable fact that our algorithms may provide partial Hadamard matrices of depth greater than half of a full Hadamard matrix. Furthermore, it is possible (and desirable) to run our algorithms taking as input data partial Hadamard matrices obtained by the procedures in [8, 10], so that deeper partial Hadamard matrices are constructed (see Table 4.2).

The paper is organized as follows.

The graph G_t and its properties are described in Section 2. Section 3 is devoted to the description of the local exhaustive algorithm looking for cliques in G_t . In Section 4, the two heuristics searching for cliques in G_t are described. Last section is devoted to conclusions.

2 The graph G_t

In what follows, for clarity in the exposition, we will simply use $+$ and $-$ instead of 1 and -1 .

Hadamard Graphs were introduced by Ito in [18]. Originally they referred to the graph $\Delta(4t)$ whose vertices are the $(1, -1)$ -vectors of length $4t$ consisting of an even number of 1s. The adjacency relation consists in orthogonality.

We call Hadamard graph to the subgraph G_t of $\Delta(4t)$ induced by the $(1, -1)$ -vectors simultaneously orthogonal to the three first rows of a normalized Hadamard matrix,

$$\begin{pmatrix} + \dots + & + \dots + & + \dots + & + \dots + \\ + \dots + & + \dots + & - \dots - & - \dots - \\ + \dots + & - \dots - & + \dots + & - \dots - \\ \dots & \dots & \dots & \dots \end{pmatrix}$$

These orthogonality conditions straightforwardly characterize the form of the vertices in G_t .

Lemma 1 *The vertices of G_t consist of $(1, -1)$ -vectors of length $4t$ where the $2t$ negative entries are distributed following this pattern,*



so that exactly k , $t - k$, $t - k$ and k negative entries occur among every t positions, for some $0 \leq k \leq t$.

We may then classify the set of vertices in G_t attending to the number k of negative entries which appear in positions 1 through t . In what follows, a k -vertex in G_t refers to a vertex with precisely k negative entries among positions 1 to t .

Lemma 2 In particular, the number of vertices in G_t is $|G_t| = \sum_{k=0}^t \binom{t}{k}^4$.

The tables below give the number of k -vertices ($n.v.$) and their degree δ (number of adjacent vertices), for $1 \leq t \leq 7$ and $0 \leq k \leq t$. The column *total* refers to the number of vertices and edges in G_t (notice that the number of edges is half the summation of the degree of every vertex). It is evident that for a fixed value of k , every k -vertex has the same degree (since permuting some columns does not affect to the orthogonality relation).

Table 1 Vertices and edges in G_t .

t = 1		
k	0	total
n.v.	1	2
δ	0	0

t = 2				
k	0	1	2	total
n.v.	1	16	1	18
δ	16	8	16	80

t = 3					
k	0	1	2	3	total
n.v.	1	81	81	1	164
δ	0	64	64	0	5184

t = 4						
k	0	1	2	3	4	total
n.v.	1	256	1296	256	1	1810
δ	1296	648	648	648	1296	587088

t = 5							
k	0	1	2	3	4	5	total
n.v.	1	625	10000	10000	625	1	21252
δ	0	6912	6912	6912	6912	0	73440000

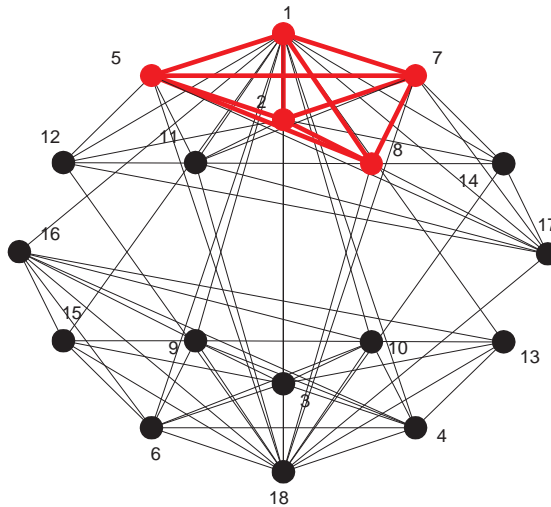
t = 6								
k	0	1	2	3	4	5	6	total
n.v.	1	1296	50625	160000	50625	1296	1	263844
δ	160000	80000	79808	79712	79808	80000	160000	10521080000

t = 7									
k	0	1	2	3	4	5	6	7	total
n.v.	1	2401	194481	1500625	1500625	194481	2401	1	3395016
δ	0	960000	960000	960000	960000	960000	960000	0	1629606720000

It is readily checked that the size of G_t grows exponentially on t . Since cliques of size m in G_t translate to partial Hadamard matrices $(m+3) \times 4t$, we would like to search for large cliques in G_t . Since the largest clique in $\Delta(4t)$ is at most of size $4t$ (see [17] for details), the largest clique in G_t is at most of size $4t - 3$. Cliques meeting the upper bound would correspond to full Hadamard matrices.

Example 1 For instance, consider the graph G_2 , obtained from $t = 2$. The picture below shows a clique of size 5, so that adding the three normalized rows we obtain a full Hadamard matrix of size 8×8 .

- (- - + + + + - -) = 1
- (- + - + - + - +) = 2
- (- + - + - + + -) = 3
- (- + - + + - - +) = 4
- (- + - + + - + -) = 5
- (- + + - - + - +) = 6
- (- + + - - + + -) = 7
- (- + + - + - - +) = 8
- (- + + - + - + -) = 9
- (+ - - + - + - +) = 10
- (+ - - + - + + -) = 11
- (+ - - + + - - +) = 12
- (+ - - + + - + -) = 13
- (+ - + - - + - +) = 14
- (+ - + - - + + -) = 15
- (+ - + - + - - +) = 16
- (+ - + - + - + -) = 17
- (+ + - - - - + +) = 18



□

A *maximum clique* is a clique with the maximum cardinality (which is called the maximum clique number). This notion is different from that of maximal clique, which refers to a clique which is not a proper subset of any other clique. Thus maximal cliques need not be maximum ones (as we had already noticed in the introduction), though the converse is always true.

Given a graph, the maximum clique problem (MCP) is to find a maximum clique, and it is NP-complete [6]. Unfortunately, there is no polynomial-time algorithm for approximating the maximum clique within a factor of $n^{1-\epsilon}$ unless $P=NP$ [12], where n is the number of the vertices of the graph. Moreover, there is no polynomial-time algorithm approximating the clique number within a factor of $\frac{n}{(\log n)^{1-\epsilon}}$ unless $NP=ZPP$ [19].

Anyway, our purpose here is to design an algorithm for constructing sufficiently large cliques in G_t , at least of depth greater than a third of a full Hadamard matrix. To this end, we need to study the properties of G_t in a more detailed way.

In what follows, for brevity, we will adopt the additive notation for representing Hadamard matrices, so that the 1s turn to 0s and the -1s turn to 1s.

This way, k -vectors in G_t are now described as $(0, 1)$ -vectors of length $4t$ consisting of precisely $2t$ ones (and hence $2t$ zeros), which are distributed in the following way: there are exactly k ones in positions 1 through t , other $t - k$ ones in positions $t + 1$ through $2t$, another $t - k$ ones in positions $2t + 1$ through $3t$, the last k ones being located in positions $3t + 1$ through $4t$.

Each of these k -vectors may be straightforwardly codified as an integer, assuming that the k -vector is the binary representation of a decimal number. Therefore cliques are codified as lists of integers, each of them being the deci-

mal representation of a binary number consisting of $2t$ ones and length less or equal to $4t$.

Lemma 3 *Actually, it can be assumed that $0 \leq k \leq \lfloor \frac{t}{2} \rfloor$.*

Proof This is a straightforward consequence of the fact that the negation of a row does not affect to the set of its orthogonal vectors. ■

That being so, the full set of vertices adjacent to a given k -vertex \mathbf{v} may be obtained by calculating those s -vectors \mathbf{w} orthogonal to \mathbf{v} , for $0 \leq s \leq \lfloor \frac{t}{2} \rfloor$, and then adding their complements. Notice that with the additive notation at hand, a k -vector \mathbf{v} and a s -vector \mathbf{w} are orthogonal if and only if they share exactly $2t$ bits.

We now describe a procedure for determining a set $\delta_{\mathbf{v}}$ of generators for the adjacency list related to a fixed k -vector \mathbf{v} , that is, generating those s -vectors \mathbf{w} orthogonal to \mathbf{v} .

In order to compute the total amount of coincidences between \mathbf{v} and \mathbf{w} , one may split the vectors by quarters, and count the amount i of 1-bits (for the first and last quarters) and 0-bits (for the second and third quarters) that these vectors share in each of these basic quarters.

Lemma 4 *At the first and fourth (resp., the second and third) quarters the number i of coincidences in 1s (resp, in 0s) runs in the range $[\max(0, s + k - t), \min(k, s)]$. Actually, assuming the conditions in Lemma 3, $i \in [0, \min(k, s)]$.*

Lemma 5 *At each quarter, the number α_i of total coincidences (both in 1s and 0s) satisfies $\alpha_i = t - s - k + 2i$, and runs in the range $[|t - k - s|, t - |s - k|]$. Actually, assuming the conditions in Lemma 3, $\alpha_i \in [t - s - k, t - |s - k|]$.*

Proof Assume that at a given quarter the vectors \mathbf{v} and \mathbf{w} share exactly i 1-bits. Then \mathbf{w} has $k - i$ 0-bits in those positions where the remaining 1-bits of \mathbf{v} are located. Analogously, \mathbf{v} has $s - i$ 0-bits in those positions where the remaining 1-bits of \mathbf{w} are located. Thus \mathbf{v} and \mathbf{w} share exactly $t - i - (k - i) - (s - i) = t - k - s + i$ 0-bits. Since \mathbf{v} and \mathbf{w} share i 1-bits and $t - k - s + i$ 0-bits, the total number of coincidences is $\alpha_i = t - k - s + 2i$. ■

Corollary 1 $\alpha_{i+1} = \alpha_i + 2$.

Let denote $n = \min(k, s)$. In the conditions above, the set of total coincidences is given by $t - s - k = \alpha_0 < \dots < \alpha_n = t - |s - k|$. We may now describe the set of s -vectors adjacent to a given k -vector.

Proposition 1 *The set of vectors orthogonal to a given k -vector corresponds to the full set of distributions of vectors satisfying tuples of total coincidences $(\alpha_{i_1}, \alpha_{i_2}, \alpha_{i_3}, \alpha_{i_4})$ such that $\alpha_{i_1} + \alpha_{i_2} + \alpha_{i_3} + \alpha_{i_4} = 2t$.*

Proposition 2 *The set of tuples $(\alpha_{i_1}, \alpha_{i_2}, \alpha_{i_3}, \alpha_{i_4})$ which give rise to orthogonal s -vectors are characterized as the solutions of the following system of diophantine equations*

$$\begin{cases} x_0\alpha_0 + \dots + x_n\alpha_n = 2t \\ x_0 + \dots + x_n = 4 \\ x_i \in \mathbb{Z} : 0 \leq x_i \leq 4 \end{cases} \quad (1)$$

Here, $n = \min(k, s)$ and x_i indicates how many coincidences of the type α_i must occur among the four quarters.

We now give a constructive way to solve the system above.

Proposition 3 *There exists a solution for the system (1) iff $4\alpha_0 \leq 2t \leq 4\alpha_n$.*

Proof From Corollary 1, we know that the difference between two consecutive α_{i_j} is 2.

Since $4\alpha_0$, $2t$ and $4\alpha_n$ are even and taking into account Corollary 1, we conclude that every even number in the range $[4\alpha_0, 4\alpha_n]$ may be (not uniquely, in general) written as a combination $\alpha_{i_1} + \alpha_{i_2} + \alpha_{i_3} + \alpha_{i_4}$ for some values $\alpha_0 \leq \alpha_{i_1} \leq \alpha_{i_2} \leq \alpha_{i_3} \leq \alpha_{i_4} \leq \alpha_n$. ■

The condition above may be straightforwardly generalized for the case of solutions related to tuples of the type $(\alpha_{i_1}, \alpha_{i_2}, \alpha_{i_3}, \alpha_{i_4})$, $\alpha_{i_1} \leq \alpha_{i_2} \leq \alpha_{i_3} \leq \alpha_{i_4}$.

Corollary 2 *Fixed t and $0 \leq k, s \leq \lfloor \frac{t}{2} \rfloor$, the set sol of solutions to the system (1) may be constructed in the following way:*

```

sol ← ∅
α₀ ← t - k - s
αₙ ← t - |k - s|
for i₁ from max{α₁, 2t - 3αₙ} to min{αₙ, ⌊ $\frac{2t}{4}$ ⌋} with step 2 do
  for i₂ from max{i₁, 2t - i₁ - 2αₙ} to min{αₙ, ⌊ $\frac{2t-i_1}{3}$ ⌋} with step 2
  do
    for i₃ from max{i₂, 2t - i₁ - i₂ - αₙ} to min{αₙ, ⌊ $\frac{2t-i_1-i_2}{2}$ ⌋} with
    step 2 do
      sol ← sol ∪ {{i₁, i₂, i₃, 2t - i₁ - i₂ - i₃}}
    od
  od
od

```

Given a tuple $(\alpha_{i_1}, \alpha_{i_2}, \alpha_{i_3}, \alpha_{i_4})$ solution to (1), construct the four matrices N_k whose rows are those vectors satisfying α_{i_k} total coincidences with the corresponding quarter of \mathbf{v} . By construction, the juxtaposition of any of the rows of these matrices gives a vector orthogonal to \mathbf{v} .

Proposition 4 *A set $\delta_{\mathbf{v}}$ of generators for the adjacency list of \mathbf{v} may be straightforwardly constructed in terms of matrices of the type above.*

In spite of the fact that the size (both in edges and vertices) of G_t grows exponentially in t , the procedure described in Proposition 4 is a cheaper way (in terms of both time and space) of saving this information.

We will illustrate now how the proposition above works by means of an example. In order to simplify the reading, in what follows we will use a vertical line $|$ to separate the different quarters of a k -vector.

Example 2 Let us consider the case $t = 5$, $k = 2$ and $\mathbf{v} = 684646$ (its binary representation gives the 2-vector $\mathbf{v} = (10100|11100|10011|00110)$). We are going to calculate the full set of s -vectors orthogonal to \mathbf{v} , for $0 \leq s \leq 2 = \lfloor \frac{5}{2} \rfloor$ (recall that the remaining orthogonal vectors are obtained by simply interchanging the 0-bits and 1-bits, since they are the negation of the vectors just calculated).

1. Case $s = 0$.

From Lemma 4, we know that there is just one value for the number i of coincidences in 1-bits, namely $i = 0$. Consequently, there is just one value α_i , namely $\alpha_0 = 3$.

Since $4\alpha_0 = 12 \neq 10 = 2 \cdot 5$, the system (1) has no solutions, so there is no 0-vector orthogonal to \mathbf{v} .

This was evident from the very beginning, since there is only one 0-vector, $\mathbf{w} = 32736$ (i.e. $\mathbf{w} = (00000|11111|11111|00000)$), and it is not orthogonal to \mathbf{v} .

2. Case $s = 1$.

From Lemma 4, we know that $i \in \{0, 1\}$, and hence $\alpha_i \in \{2, 4\}$. The set of different ways in which four α_i may be orderless chosen to sum 10 is described by the system (1),

$$\begin{cases} 2x_0 + 4x_1 = 10 \\ x_0 + x_1 = 4 \end{cases}$$

Since $4\alpha_0 = 8 \leq 10 \leq 4\alpha_1 = 16$, there exist solutions for the system. In fact, there is just one solution, $(x_0, x_1) = (3, 1)$, which corresponds to the following distribution of total coincidences (up to reordering): $(2, 2, 2, 4)$.

In order to explicitly construct those 1-vectors \mathbf{w} meeting the distribution $(2, 2, 2, 4)$, we have to find those 1-vectors with 0 coincidences with \mathbf{v} in 1-bits in the first quarter, 0 coincidences in 0-bits in the second and third quarters, and 1 coincidence in 1-bits in the fourth quarter.

Since \mathbf{v} is a 2-vector, in the first quarter there are $\binom{5-2}{1}$ choices for placing the 1-bit of \mathbf{w} among the 0-bits of \mathbf{v} . Analogously, there are $\binom{5-2}{1}$ choices for placing the 0-bit of \mathbf{w} among the 1-bits of \mathbf{v} in the second and third quarters. And there are $\binom{2}{1}$ choices for placing the 1-bit of \mathbf{w} among the 1-bits of \mathbf{v} .

In conclusion, the set of 1-vectors meeting the distribution of total coincidences $(2, 2, 2, 4)$ is generated by the juxtaposition of any of the rows of the following matrices

$$\begin{pmatrix} 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 1 \end{pmatrix} \times \begin{pmatrix} 0 & 1 & 1 & 1 & 1 \\ 1 & 0 & 1 & 1 & 1 \\ 1 & 1 & 0 & 1 & 1 \end{pmatrix} \times \begin{pmatrix} 0 & 1 & 1 & 1 & 1 \\ 1 & 1 & 1 & 0 & 1 \\ 1 & 1 & 1 & 1 & 0 \end{pmatrix} \times \begin{pmatrix} 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 \end{pmatrix}$$

Similar schemes are achieved with the remaining orderings of the valid distribution of total coincidences, $(2, 2, 4, 2)$, $(2, 4, 2, 2)$ and $(4, 2, 2, 2)$. In fact, they may be obtained by simply permuting and/or negating some suitable columns of the distribution above.

3. Case $s = 2$.

From Lemma 4, we know that $i \in \{0, 1, 2\}$, and hence $\alpha_i \in \{1, 3, 5\}$. The set of different ways in which four α_i may be orderless chosen to sum 10 is described by the system (1),

$$\begin{cases} x_0 + 3x_1 + 5x_2 = 10 \\ x_0 + x_1 + x_2 = 4 \end{cases}$$

Since $4\alpha_0 = 4 \leq 10 \leq 4\alpha_2 = 20$, there exist solutions for the system. In fact, there are just two solutions, $(x_0, x_1, x_2) \in \{(2, 1, 1), (1, 3, 0)\}$, which correspond to the following distribution of total coincidences (up to re-ordering): $(1, 1, 3, 5)$ and $(1, 3, 3, 3)$.

In order to explicitly construct those 2-vectors \mathbf{w} meeting the distribution $(1, 1, 3, 5)$, we have to find those 2-vectors with 0 coincidences with \mathbf{v} in 1-bits in the first quarter, 0 coincidences in 0-bits in the second quarter, 1 coincidence in 0-bits in the third quarter, and 2 coincidences in 1-bits in the fourth quarter.

Since \mathbf{v} is a 2-vector, in the first quarter there are $\binom{5-2}{2}$ choices for placing the 1-bits of \mathbf{w} among the 0-bits of \mathbf{v} . Analogously, there are $\binom{5-2}{2}$ choices for placing the 0-bits of \mathbf{w} among the 1-bits of \mathbf{v} in the second quarter. Analogously, in the third quarter, there are $\binom{2}{1}$ choices for placing one 0-bit of \mathbf{w} among the 0-bits of \mathbf{v} , and for each of them, there are $\binom{5-2}{1}$ choices for placing the second 0-bit of \mathbf{w} among the 1-bits of \mathbf{v} . Finally, there are $\binom{2}{2}$ choices (just one!) for placing the 1-bits of \mathbf{w} among the 1-bits of \mathbf{v} .

In conclusion, the set of 2-vectors meeting the distribution of total coincidences $(1, 1, 3, 5)$ is generated by the juxtaposition of any of the rows of

the following matrices

$$\begin{pmatrix} 0 & 0 & 0 & 1 & 1 \\ 0 & 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 & 0 \end{pmatrix} \times \begin{pmatrix} 1 & 0 & 0 & 1 & 1 \\ 0 & 1 & 0 & 1 & 1 \\ 0 & 0 & 1 & 1 & 1 \end{pmatrix} \times \begin{pmatrix} 1 & 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 & 1 \\ 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \end{pmatrix} \times (0 \ 0 \ 1 \ 1 \ 0)$$

Similar schemes are achieved from the remaining orderings of the distribution (1, 1, 3, 5).

Analogously, one may conclude that the set of 2-vectors meeting the distribution of total coincidences (1, 3, 3, 3) (and in a similar way its reorderings as well) is generated by the juxtaposition of any of the rows of the following matrices

$$\begin{pmatrix} 0 & 0 & 0 & 1 & 1 \\ 0 & 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 & 0 \end{pmatrix} \times \begin{pmatrix} 1 & 1 & 0 & 0 & 1 \\ 1 & 0 & 1 & 0 & 1 \\ 0 & 1 & 1 & 0 & 1 \\ 1 & 1 & 0 & 1 & 0 \\ 1 & 0 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \end{pmatrix} \times \begin{pmatrix} 1 & 0 & 1 & 1 & 0 \\ 1 & 0 & 1 & 0 & 1 \\ 0 & 0 & 1 & 1 & 1 \\ 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 0 & 1 \\ 0 & 1 & 0 & 1 & 1 \end{pmatrix} \times \begin{pmatrix} 0 & 0 & 1 & 0 & 1 \\ 0 & 1 & 1 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 1 & 1 \\ 0 & 1 & 0 & 1 & 0 \\ 1 & 0 & 0 & 1 & 0 \end{pmatrix}$$

□

We have just described a procedure for determining a set $\delta_{\mathbf{v}}$ of generators for the adjacency list related to a fixed k -vector \mathbf{v} , $0 \leq k \leq \lfloor \frac{t}{2} \rfloor$. In spite of the fact that the size (both in edges and vertices) of G_t grows exponentially in t , this is a cheaper way (in terms of both time and space) of saving this information.

Once we know how the adjacency relation in G_t looks like, we are in conditions to describe an algorithm looking for cliques in G_t .

3 Local exhaustive search

From the results described in the precedent Section, one may straightforwardly design an algorithm searching for a maximal (probably not maximum) clique in G_t . Starting from a clique C initially consisting of a random vertex \mathbf{v} in G_t , it suffices to repeatedly add a new vertex \mathbf{w} to C , randomly chosen among those vertices simultaneously orthogonal to the vertices already in C .

This is somehow a local exhaustive search. Exhaustive, in the sense that repeatedly the full set of vertices simultaneously orthogonal to the nodes of a given clique is constructed. Local, in the sense that just one vertex among the full set of candidates is actually used.

We next include a pseudo-code for this algorithm.

Algorithm 1 Searching for cliques in G_t .

Input: an integer t

Output: a maximal clique in G_t

Select a k -vertex \mathbf{v} in G_t

$clique \leftarrow \{\mathbf{v}\}$

$adj \leftarrow \delta_{\mathbf{v}}$

while adj is not empty{

$\mathbf{v} \leftarrow$ a random s -vertex in adj

$clique \leftarrow clique \cup \{\mathbf{v}\}$

$adj \leftarrow adj \cap \delta_{\mathbf{v}}$

}

$clique$

The complexity of the algorithm relies on the operations $\delta_{\mathbf{v}}$ and $adj \cap \delta_{\mathbf{v}}$. From Proposition 3, $\delta_{\mathbf{v}}$ may be constructed in polynomial-time. Unfortunately, the size of adj increases exponentially, and so the algorithm is both time and space consuming.

Improved versions of the algorithm might be implemented, depending on a deeper knowledge of how orthogonality on k -vertices works.

We now include some execution tables.

All the calculations of this section have been worked out in MATHEMATICA 4.0, running on a *Pentium IV 2.400 Mhz DIMM DDR266 512 MB*.

The table below shows, for every $2 \leq t \leq 10$, the number of essays which have been executed looking for cliques in G_t , the average time required in these calculations, the average size of these cliques, the largest size found so far, the time required in this calculation and one instance among the largest cliques already found.

Table 2 Results obtained from Algorithm 1.

t	Essays	Av. Time	Av. Size	Lar. S.	Time	Clique
2	10	0.0232''	5	5	0.016''	166, 101, 106, 169, 60
3	10	0.039''	9	9	0.031''	2396, 730, 881, 940, 1386, 2482, 1433, 2281, 1268
4	10	0.368''	13	13	0.327''	22166, 22874, 11698, 34776, 13251, 19428, 49971, 13116, 39594, 43606, 38246, 7793, 26218
5	10	0.369''	11	17	0.468''	615882, 81761, 124596, 682665, 315178, 323811, 183761, 808837, 405190, 572306, 350936, 677490, 193356, 813428, 219558, 406968, 564460

t	Essays	Av. Time	Av. Size	Lar. S.	Time	Clique
6	10	4.128''	13.8	21	3.198''	1943217, 2913196, 4896610, 1866067, 13689735, 5584078, 10118748, 4943241, 3324617, 6759253, 5685752, 8874722, 14710001, 8830356, 6614554, 4840148, 8771401, 3272036, 3364754, 13712184, 11117018
7	10	12.19''	12.8	17	20.53''	30121113, 153038560, 15673110, 73300362, 41266505, 117929485, 86698833, 43440080, 105500358, 176876844, 41595557, 156361628, 172841777, 119125298, 205299228, 79251369, 210612677
8	4	1'39''	13.75	15	59.37''	1305024466, 1295442290, 2999574898, 3795589971, 3631000788, 3248355466, 364489541, 2896517604, 2629324346, 1255832164, 504314142, 3570677031, 965647459, 1387503024, 1483592489
9	4	13'46''	14.25	16	6'34''	56453847575, 43074435680, 41936051018, 22138975396, 23156633420, 41987793978, 37225385892, 18981806746, 45452914326, 7371644105, 53995320335, 52910835425, 60376161688, 19823315036, 10578923147, 28478917930
10	2	4 ^h 50'6''	16	16	3 ^h 0'50''	611551599738, 585720653408, 381375537029, 727566346115, 90629862411, 851419790210, 418284730924, 524680378162, 364580931042, 154503136551, 747357767564, 199828304181, 99982406086, 319408643342, 422206490833, 34030595756

As the table below shows, it is remarkable that the sizes of the largest cliques found so far are greater than $\lfloor \frac{4t}{3} \rfloor - 3$ (a third of a full Hadamard matrix of size $4t$) and even $2t - 3$ (a half of a full Hadamard matrix of size $4t$), which are the best asymptotic bounds on the depth of partial Hadamard matrices known so far.

Table 3 Comparing sizes of cliques.

t	2	3	4	5	6	7	8	9	10
$\lfloor \frac{4t}{3} \rfloor - 3$	-1	1	2	3	5	6	7	9	10
$2t - 3$	1	3	5	7	9	11	13	15	17
Lar. S.	5	9	13	17	21	17	15	16	16

Although our procedure gives large partial Hadamard matrices (of depth greater than half of a full Hadamard matrix), it is very expensive both in space and time.

It would be desirable to find a way to design a procedure running significantly faster and which nevertheless leads to large partial Hadamard matrices as well. We describe such an algorithm in the following section.

4 Heuristic searches

In this section we describe two heuristics for searching for cliques in G_t .

The first of them is a straightforward adaptation of the best (as far as we know) genetic algorithm for solving the maximum clique problem (MCP). Since it is very expensive in time, we then describe a second heuristic, which is much faster, in exchange of precision (in the sense that not sufficiently large cliques are obtained).

Nevertheless, it is a remarkable fact that this last procedure admits as input data a clique already constructed. Consequently, one could eventually obtain a larger clique. Experimental results suggest that this actually happens more times than one could initially think (see Table 4.2). In fact, it seems to be a good idea to combine this fast search with other more precise procedures.

4.1 Classical GAs for MCP

As we commented before, finding the maximum clique of a graph is a NP-Hard problem, and consequently all known exact algorithms for this problem will run in time that grows exponentially with the number of vertices in the graph. This makes these algorithms infeasible even in case of moderately large problem instances. Therefore most of the efforts to solve the maximum clique problem are based on heuristic approaches.

In [21] a heuristic based steady-state genetic algorithm for the maximum clique problem is described. The steady-state genetic algorithm generates cliques, which are then extended into maximal cliques by the heuristic. After comparison with the three best evolutionary approaches for the maximum clique problem, they find out that their algorithm outperforms all the three evolutionary approaches in terms of best and average clique sizes found on majority of DIMACS benchmark instances (which are the canonical family of graphs used to test MCP-algorithms).

The main features of the genetic algorithm in [21] consist in:

- *Chromosome representation.* A n -length bit vector represent a chromosome (i.e. a clique), so that a value of 1 at the i th position indicates that the vertex i is in the clique.
- *Crossover.* They use fitness based crossover, so that a child is constructed bit by bit, receiving each time the bit from one of its parents, with probability proportional to the fitness of the parents. The vector obtained so far may not be a clique, so a repairing function is needed to transform the child into a clique.

- *Repair*. First, all 1 bits corresponding to vertices with significantly low degree (in comparison with the provisional fittest individual) are changed to 0. Then, the repairing procedure introduced by Marchiori in [20] is used, so that repeatedly a vertex of the child is selected at random, and either it or all the vertices not adjacent to it are deleted (i.e. the corresponding bits are fixed to 0), until the child becomes a clique.
- *Mutation*. Mutation consists in simple bit flip mutation, where each bit in the chromosome is flipped with a pre-fixed probability p_m . Once again, the repairing function is needed to guarantee that a valid chromosome (i.e. a clique) is obtained.
- *Extension*. Once a valid chromosome (i.e. a clique) is constructed, an extension function is applied, in order to extend the given clique to a maximal clique. The idea is repeatedly adding a vertex with highest degree among the set S of vertices simultaneously adjacent to the vertices already in the clique. When the size of the set S is small enough, then the exhaustive search of Carraghan and Pardalos [7] is performed.
- *Fitness*. The fitness of a chromosome is equal to the size of the clique that it represents.
- *Selection*. They use binary tournament selection, where the candidate with better fitness is selected with a pre-fixed probability p_b .
- *Replacement policy*. No duplicate chromosomes are permitted in the population. When a new child is constructed, it always replaces the worst member of the population, irrespective of its own fitness.

It seems natural trying to adapt this algorithm to our case. Unfortunately, one cannot afford to explicitly construct the adjacency lists of G_t , for values $t > 5$, since they grow exponentially in t , as we showed in the section before.

So the extension function described in [21] cannot be applied in the case of the graph G_t . Nevertheless, we can use instead the algorithm proposed in the previous section.

Algorithm 2 *GA looking for cliques in G_t .*

Substitute the extension function in [21] by Algorithm 1.

We show now some executions for $2 \leq t \leq 9$, where the size of the population is fixed to 5 and the maximum number of generations is fixed to 20.

Table 4 Results obtained from Algorithm 2.

t	Time	# generations	$\#\{C : C \text{ is maximal}\}$	$ C $	PH size
2	0, 171''	0	5	5	8
3	0, 359''	0	5	9	12
4	1, 872''	0	5	13	16
5	3, 931''	0	3	17	20
6	19, 36''	0	3	21	24
7	4' 10''	20	3	17	20
8	24' 37''	20	1	21	24
9	4 ^h 36''	20	1	18	21

We next include explicitly the cliques found so far. For brevity, we give the decimal number representations of the binary $4t$ -vectors which form each clique.

Table 5 Cliques obtained from Algorithm 2 listed explicitly.

t	Clique
2	89, 169, 195, 149, 101
3	2396, 922, 3347, 3214, 2635, 2290, 2854, 2473, 1386
4	11633, 27850, 20148, 40089, 29719, 6098, 14940, 43414, 22981, 40038, 15011, 42693, 13740
5	355028, 694485, 626266, 436558, 57188, 250510, 647277, 308937, 189682, 809194, 832054, 113080, 211555, 381267, 603590, 684888, 584579
6	9162129, 15599647, 12071353, 7947574, 2834188, 10323501, 6722981, 7449237, 5936794, 3845219, 2986835, 13186247, 14739211, 5822797, 5711193, 13280116, 14785656, 11687509, 9747734, 11764174, 13835043
7	206229172, 136297864, 145421137, 239938137, 244421436, 78464909, 111023826, 96903644, 49849529, 150232156, 47868686, 213067927, 46619057, 237397306, 193760535, 174494351, 223891867
8	925672665, 545242888, 131329093, 1388111142, 3800772080, 2494264851, 2084807742, 3004829231, 432983728, 1265186469, 1437667228, 2976213301, 766141292, 455842134, 3399920157, 3380112474, 2022530125, 1674167067, 3521287529, 517486905, 1394045560
9	6263028814, 17380851458, 66723786135, 13185706648, 61523714894, 11518454374, 28777615826, 31813316858, 7484361626, 45216625720, 10357786275, 32845624107, 64532207782, 48511720424, 46756144798, 24818822896, 53243861654, 27484036889

A comparison with the results obtained in the section before, reveals that the genetic algorithm is not as useful as desired.

On one hand, the only improvements are obtained for the values $t = 8, 9$, and they are not significantly impressive. Moreover, it seems that quality (in terms of the size of the cliques obtained) relies on the extension function rather than in the genetic procedure itself.

On the other hand, each run of the extension function is very time-consuming, so the required time for executing a full run of the genetic algorithm grows drastically. And there is no a dramatic increase in the size of the obtained cliques in return.

It would be desirable to look for a faster way of extending cliques, attending to the particular properties of our graph G_t . We tackle with this question in the next section.

4.2 A fast heuristic search

In order to get a faster heuristic search, we need to have a deeper look at the adjacency relations between the vertices in G_t .

We first translate Proposition 1 (which characterizes the set of s -vectors orthogonal to a given k -vector in terms of distributions of total coincidences

$(\alpha_{i_1}, \alpha_{i_2}, \alpha_{i_3}, \alpha_{i_4})$, in terms of distributions (i_1, i_2, i_3, i_4) of coincidences in 1s (for the first and last quarters) and 0s (for the second and third quarters).

Proposition 5 *The set of s -vectors orthogonal to a given k -vector corresponds to the full set of distributions of s -vectors satisfying tuples of coincidences in 1s (first and fourth quarters) and 0s (second and third quarters) (i_1, i_2, i_3, i_4) such that $i_1 + i_2 + i_3 + i_4 = 2s + 2k - t$. Furthermore, this is possible iff $2s + 2k - t \geq 0$.*

Proof From Proposition 1, we know that the set of s -vectors orthogonal to a given k -vector is characterized by those distributions of total coincidences $(\alpha_{i_1}, \alpha_{i_2}, \alpha_{i_3}, \alpha_{i_4})$ such that $\alpha_{i_1} + \alpha_{i_2} + \alpha_{i_3} + \alpha_{i_4} = 2t$.

Since $\alpha_i = t - s - k + 2i$ from Lemma 5, the relation above comes to be

$$4t - 4k - 4s + 2i_1 + 2i_2 + 2i_3 + 2i_4 = 2t \Leftrightarrow i_1 + i_2 + i_3 + i_4 = 2s + 2k - t.$$

Now, on one hand, since $0 \leq i_j \leq \min(k, s)$, the value $i_1 + i_2 + i_3 + i_4$ runs over the range $0 \leq i_1 + i_2 + i_3 + i_4 \leq 4 \min(k, s)$.

On the other hand, since $0 \leq s, k \leq \lfloor \frac{t}{2} \rfloor$, it is clear that $2s + 2k - t \leq 2 \min(k, s)$.

Thus, provided $2s + 2k - t \geq 0$, this value is in the range valid for $i_1 + i_2 + i_3 + i_4$, and therefore there exists a distribution of coincidences in 1s (at first and fourth quarters, i_1 and i_4 respectively) and 0s (at second and third quarters, i_2 and i_3 respectively), such that $i_1 + i_2 + i_3 + i_4 = 2s + 2k - t$. ■

Now it is apparent that not all possible values s in the range $0 \leq s \leq \lfloor \frac{t}{2} \rfloor$ do provide s -vectors orthogonal to a given k -vector.

Proposition 6 *Fixed a k -vector \mathbf{v} , there exist s -vectors orthogonal to \mathbf{v} iff $s \in [\lfloor \frac{t}{2} \rfloor - k, \lfloor \frac{t}{2} \rfloor]$.*

Proof The upper bound is given in Lemma 3.

On the other hand, from Proposition 5, there exist s -vectors orthogonal to a given k -vector iff $0 \leq 2s + 2k - t$. Consequently, $s \geq \frac{t}{2} - k$, that is, $s \geq \lceil \frac{t}{2} \rceil - k$. ■

Furthermore, we may straightforwardly precise the number of s -vectors orthogonal to a given k -vector, for some fixed $s \in [\lceil \frac{t}{2} \rceil - k, \lfloor \frac{t}{2} \rfloor]$.

Lemma 6 *Fixed a valid distribution (i_1, i_2, i_3, i_4) , the number of s -vectors orthogonal to a given k -vector is given by the expression:*

$$\binom{k}{i_1} \binom{t-k}{s-i_1} \binom{k}{i_2} \binom{t-k}{s-i_2} \binom{k}{i_3} \binom{t-k}{s-i_3} \binom{k}{i_4} \binom{t-k}{s-i_4}$$

Table 6 Distribution of s -vectors orthogonal to a k -vector.

		$t = 3$		$t = 4$			$t = 5$		
		$k = 0$	$k = 1$	$k = 0$	$k = 1$	$k = 2$	$k = 0$	$k = 1$	$k = 2$
$s = 0$		0	0	0	0	1	0	0	0
$s = 1$		0	32	0	81	96	0	0	216
				1296	486	454	0	3456	3240

		$t = 6$				$t = 7$			
		$k = 0$	$k = 1$	$k = 2$	$k = 3$	$k = 0$	$k = 1$	$k = 2$	$k = 3$
$s = 0$		0	0	0	1	0	0	0	0
$s = 1$		0	0	256	486	0	0	0	768
$s = 2$		0	10000	14688	15795	0	0	40000	57024
$s = 3$		160000	60000	49920	47148	0	480000	440000	422208

		$t = 8$				
		$k = 0$	$k = 1$	$k = 2$	$k = 3$	$k = 4$
$s = 0$		0	0	0	0	1
$s = 1$		0	0	0	625	1536
$s = 2$		0	0	50625	147000	183904
$s = 3$		0	1500625	2352000	2601000	2655744
$s = 4$		24010000	9003750	7183750	6483750	6297030

		$t = 9$				
		$k = 0$	$k = 1$	$k = 2$	$k = 3$	$k = 4$
$s = 0$		0	0	0	0	0
$s = 1$		0	0	0	0	2000
$s = 2$		0	0	0	243000	464000
$s = 3$		0	0	7203000	11210000	12912000
$s = 4$		0	76832000	69629000	65367000	63430000

		$t = 10$					
		$k = 0$	$k = 1$	$k = 2$	$k = 3$	$k = 4$	$k = 5$
$s = 0$		0	0	0	0	0	1
$s = 1$		0	0	0	0	1296	3750
$s = 2$		0	0	0	194481	858600	1200625
$s = 3$		0	0	9834496	32773650	48326400	53560000
$s = 4$		0	252047376	407209600	453248775	468312600	472003750
$s = 5$		4032758016	1512284256	1180754176	1041640236	978746976	960098756

The following tables show the number of s -vectors orthogonal to a given k -vector, for $3 \leq t \leq 10$, $0 \leq k \leq \lfloor \frac{t}{2} \rfloor$, and $0 \leq s \leq \lfloor \frac{t}{2} \rfloor$.

In particular, these results suggest that large cliques in G_t should consist of k -vectors, for large values of k , close to $\lfloor \frac{t}{2} \rfloor$.

This seems to be so, as the calculations below suggest.

For each $3 \leq t \leq 9$, we choose at random a Hadamard matrix of order $4t$ from Sloane's online library [22], say `had.12`, `had16.4`, `had20.hall.n`, `had24.pal`, `had28.pal2`, `had32.pal`, `had36.pal2`.

We now normalize these matrices, by means of the following algorithm. Notice that since just negation and permutation of columns are used, the Hadamard character of the matrix is preserved.

Algorithm 3 Hadamard normalization

- Negate those columns consisting of a first negative entry.
- Now, locate those columns i , $1 \leq i \leq 2t$, consisting of a second negative entry. Locate those columns j , $2t + 1 \leq j \leq 4t$, consisting of a second positive entry. Interchange them.
- Proceed as the step before, now by quarters. As a result, you will obtain a normalized Hadamard matrix.

Now we randomly fix a $\lfloor \frac{t}{2} \rfloor$ -vector among the rows of these matrices (for instance, the first such occurrence). The table below shows the distribution of the values s , for the s -vectors of the remaining rows. In addition, we also include the distribution of (not ordered!) total coincidences $(\alpha_{i_1}, \dots, \alpha_{i_4})$.

Table 7 Rows in Hadamard matrices are k -rows, for $k \in \{\lfloor \frac{t}{2} \rfloor - 1, \lfloor \frac{t}{2} \rfloor\}$.

t	row	$s = \lfloor \frac{t}{2} \rfloor$	$s = \lfloor \frac{t}{2} \rfloor - 1$	# {total coincidences}
3	4	8	0	(1, 1, 1, 3) → 8
4	6	8	4	(2, 2, 2, 2) → 4
				(0, 2, 2, 4) → 4
5	5	15	1	(1, 1, 3, 3) → 4
				(1, 3, 3, 3) → 12
6	4	11	9	(1, 1, 3, 5) → 3
				(2, 2, 2, 4) → 1
				(2, 2, 4, 4) → 9
				(2, 2, 2, 6) → 1
7	5	21	3	(0, 4, 4, 4) → 1
				(1, 3, 3, 5) → 6
				(3, 3, 3, 3) → 3
				(3, 3, 3, 5) → 16
				(1, 3, 5, 5) → 3
8	4	12	16	(1, 3, 3, 7) → 2
				(2, 2, 4, 6) → 2
				(2, 4, 4, 4) → 1
				(2, 4, 4, 6) → 12
9	4	26	6	(3, 3, 3, 7) → 2
				(3, 5, 5, 5) → 20
				(1, 5, 5, 7) → 6
				(2, 4, 6, 6) → 6

The table above suggests that one should focus on k -vectors for $k \in \{\lfloor \frac{t}{2} \rfloor - 1, \lfloor \frac{t}{2} \rfloor\}$. Furthermore, the vector of total coincidences per quarter uses to be homogeneously distributed.

With these ideas at hand, we next design a *fast* heuristic searching for (or eventually extending) cliques in G_t .

Algorithm 4 *Fast heuristic for extending cliques in G_t .*

Input: a clique C in G_t

Output: a clique C' in G_t containing C

```

 $C' = C$ 
for  $k$  from  $\lfloor \frac{t}{2} \rfloor$  to  $\lfloor \frac{t}{2} \rfloor - 1$  step  $-1$  do
   $iter = 0$ 
  while  $iter < t$  do
     $\{bool, v\} = \text{buildgrapas}(C', k)$ 
    If  $bool$  then  $iter = 0$ ;  $C' = C' \cup \{v\}$  else  $iter = iter + 1$ 
  od
od
 $C'$ 

```

The function `buildgrapas` tries to construct an s -vector quarter by quarter (in a random ordering), attending to the following aspects:

- Select a number of total coincidences for the quarter, according to the range valid at this step (i.e. such that equation (1) can be satisfied), and with probability proportional to the number of its appearances in the set of solutions described in Corollary 2.
- Once the desired number of total coincidences has been fixed, a genetic procedure is performed, for constructing a valid quarter (i.e. such that (1) can be satisfied). This heuristic consists of populations of $4t$ individuals. If no valid quarter is found after $4t$ generations, the search ends with a failure. In this case, the last quarter constructed so far is deleted, and the process goes on from this point. This situation is limited to occur at most t times.
- This search is performed at most 10 times. If no valid vector is constructed after these 10 attempts, the search stops and a FALSE boolean is returned.

The table below shows, for every $2 \leq t \leq 10$, the number of essays which have been executed looking for cliques in G_t , the average time required in these calculations, the average size of these cliques, the largest size found so far, the time required in this calculation and one instance among the largest cliques already found.

Table 8 Results obtained from Algorithm 4.

t	Essays	Av. Time	Av. Size	Lar. S.	Time	Clique
2	10	1.4''	5	5	1.4''	86, 101, 149, 89, 60
3	10	0.565''	9	9	0.5''	1452, 2396, 1393, 874, 756, 2482, 921, 1242, 2281
4	10	19.603''	11	12	17.28''	25542, 15462, 13769, 39626, 50538, 22099, 38294, 22188, 22876, 52421, 22947, 27802

t	Essays	Av. Time	Av. Size	Lar. S.	Time	Clique
5	10	27.369''	9	17	76.924''	193425, 586090, 808611, 420073, 350674, 408358, 222834, 109987, 315192, 341833, 604856, 662897, 171722, 308468, 121445, 218540, 552900
6	10	51.38''	7.6	10	56.87''	13215089, 13015273, 10053835, 12875531, 12954262, 6768979, 3454163, 9730420, 3324617, 6759253, 5685752, 8874722, 999010, 906181
7	10	1'23''	8	9	1'46''	159860692, 161016643, 73886147, 142481171, 173143250, 170760901, 21953176, 43986594, 203259148
8	10	2'11''	7.6	9	2'53''	866473426, 1497876124, 1273533381, 1697995341, 1439971764, 3784746441, 2345981979, 2309832360, 242628440
9	10	3'02''	7.8	9	3'05''	56095030680, 38163367817, 41103334725, 54854789721, 22744355553, 45279148512, 4785499937, 52133944916, 60209197830

Although the size of the cliques obtained so far are smaller than those constructed by the precedent procedures, it is a remarkable fact that this algorithm is substantially faster. In fact, this procedure should be considered as an extension function for cliques better than a procedure itself for constructing cliques starting from the empty graph.

This idea is supported by the calculations showed in the table below, where cliques C of size $|C| \leq 2t$ in G_t constructed by the procedures described in [8, 10] (after normalization by Algorithm 3) are extended to larger cliques C' (of size $|C'| \geq 2t$, more than a half of a full Hadamard matrix!) with Algorithm 4.

Table 9 Algorithm 4 applied to $PH_{m \times 4t}$ in [10] produces $PH_{(m+n) \times 4t}$, with $m + n \geq 2t$.

t	$ C $	$ C' $	time	added vertices
4	5	12	17.97''	21930, 50745, 25500, 13107, 37740, 42330, 51510
5	5	7	19.38''	118659, 341714
6	9	15	1'07''	3099915, 9123660, 8841105, 10606050, 4844385, 4692870
7	9	9	1'03''	
8	13	17	2'51''	1923517785, 3032697660, 1695521520, 2956808130

Notice that for $t = 7$, the input clique has not been extended to a larger one. We suspect that the input clique is maximal, and therefore a larger clique containing it could not exist.

5 Conclusions

In this paper we have described three algorithms looking for pretty large partial Hadamard matrices (i.e. about a third of a full Hadamard matrix), in terms of cliques of the Hadamard Graph G_t .

The first one (Algorithm 1) performed some kind of local exhaustive search, and consequently is expensive from the time consuming point of view. So we decided to design some heuristic for constructing partial Hadamard matrices.

Our first approach (Algorithm 2) consisted in an adaptation of Singh and Gupta's genetic algorithm for the Maximum Clique Problem. Unfortunately, it did not work properly, since it used Algorithm 1 for extending cliques, and consequently was very expensive in time as well.

Algorithm 4 prioritizes the required processing time better than the final size of the partial Hadamard matrix to be obtained. Experimental results show that this algorithm may output pretty large partial Hadamard matrices (larger than half a full Hadamard matrix!), provided a suitable initial clique is given as input data.

All the algorithms that we have presented here are based on the properties of the Hadamard Graph G_t which have been described in Section 2.

It would be an interesting question whether different techniques and methods could be considered for designing alternative algorithms searching for large partial Hadamard matrices. For instance, one could ask about the techniques and methods which have been shown to be useful when manipulating full Hadamard matrices.

Unfortunately, this will not be the case, in general. For instance, consider the case of the cocyclic approach.

More concretely, the cocyclic framework has arisen as a promising way to construct (cocyclic) Hadamard matrices [14, 1, 3, 4]. One could ask whether the cocyclic framework is also a good place to look for partial Hadamard matrices. Actually, this is not the case.

Proposition 7 *The depth of any partial Hadamard matrix which is a submatrix of a cocyclic matrix M_f is at most a half of the size of M_f .*

Proof Attending to the proof of the cocyclic Hadamard test in [16] (see Lemma 1.4 on p. 281), fixed a multiplicative group $G = \{g_1 = 1, \dots, g_n\}$ and a cocyclic matrix $M_f = (f(g_i, g_j))$ over G , rows $g_i \neq g_k$ in M_f are orthogonal if and only if the summation of the row $g_i g_k^{-1} (\neq g_1)$ is zero (and consequently, the summation of the row $g_k g_i^{-1}$ as well).

If a row $g_k \neq g_1$ in M_f fails to sum zero, then, for each $1 \leq i \leq n$, the pair of rows $\{g_i, g_k^{-1} g_i\}$ (and also $\{g_i, g_k g_i\}$) fails to be orthogonal. By partitioning the rows of M_f into pairs of the type $\{g_i, g_k^{-1} g_i\}$, it turns out that such a pair contributes at most one row to a partial Hadamard matrix included in M_f . Consequently, the depth of any partial Hadamard matrix which is a submatrix of M_f is at most $\frac{n}{2}$, as claimed.

It would be interesting to think about the way in which k -vertices in G_t could be combined in order to get larger cliques.

Nevertheless, it would be also interesting to investigate whether improved versions of the algorithms described in this paper could be designed, attending to other considerations.

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