

A Genetic Approach for the Efficient Numerical Analysis of Microwave Circuits

Luciano Tarricone

D.I.E.I., Via G. Duranti, 93, 06125, Perugia, Italy.

Abstract— The development of efficient and effective algorithms for sparse matrix bandwidth minimization is of paramount importance for the enhancement of many numerical techniques for the analysis of microwave circuits. The task of bandwidth reduction is computationally hard. Several approaches have already been proposed, but the problem is still open.

In this paper, a genetic solution is proposed. The genetic algorithm is described, as well as its main characteristics (choice of chromosomes, genetic operations, etc.). Results demonstrate that the advantages of the genetic approach vanish because of the huge computational effort required. This severe limitation is removed thanks to the natural amenability of genetic algorithms to a parallel implementation. Results in the paper prove that a parallel genetic approach is a state-of-the-art solution to the problem of bandwidth reduction of sparse matrices encountered in electromagnetic numerical methods.

I. INTRODUCTION

The use of numerical methods is nowadays the most typical way to approach the design of complex microwave circuits with a high degree of accuracy, with a low cost and a substantial reduction of times for trimming and tuning. The solution of a linear system of equations

$$Ax = B \quad (1)$$

is quite often the computational core of numerical methods [1]. In some cases, the system (1) is solved many times, with different right-hand-sides B and the same matrix A , and generally the matrix properties affecting the efficiency of the solution are

- its pattern
- its condition number

In many MW applications, both items have a predictable behaviour. For instance, some numerical approaches typically produce sparse matrices (such as in the case of Mode-matching [1], or Finite Element Methods [2]), with a distribution of non-zero elements which can be in some cases predicted. Other approaches, such as the discretization with the Method of Moments (MoM) of mixed-potential integral equations (MPIE) for planar circuits, generate impedance matrices which can be turned, with suitable thresholding actions over its entries, into sparse matrices with a typical blocked-banded pattern. The use of wavelet expansions, for instance in conjunction with a MoM discretization of the solving equations, can improve the condition number (when

orthogonal wavelets are used) and increase the matrix sparsity.

Several efforts have been produced to suitably treat the matrix properties, so that efficient linear algebra can be performed inside electromagnetic (EM) codes: the use of appropriate solvers [3], [4], [5], or analytical/numerical approaches for reducing the filling-in of the moment matrix [6], or the coupled use of appropriate solvers with high-performance architectures [7], just to mention some recent works.

It has been demonstrated [8] that, in many cases, the most robust and efficient strategy is based on an appropriate numbering of the problem's unknowns (x in (1)), so that the system is reduced to a banded system with reduced bandwidth. This allows the use of a banded direct factorize-and-solve algorithm, with high efficiency (its complexity depends quadratically on the matrix bandwidth [9]).

As a matter of fact, the efficiency and effectiveness of algorithms for sparse matrix bandwidth reduction is crucial for the high-performance analysis of MW circuits. The identification of an optimum permutation matrix P so that

$$(PAP^T)(Px) = PB \quad (2)$$

is a banded system with minimum bandwidth is an NP-hard task [10], and amenable for a possible solution with a genetic algorithm.

In this paper, we propose a genetic method for the reduction of bandwidth of sparse matrices attained in different MW numerical methods. In Section II, we describe the problem and its general issues. In Section III we describe the proposed genetic solution. In Section IV we compare its results with other bandwidth reducers. In Section V we briefly discuss a parallel version of the genetic approach, and finally draw some conclusions.

II. THE PROBLEM OF BANDWIDTH REDUCTION: WHY USING GENETIC ALGORITHMS

Referring to equation (1), the problem is the following: consider the bandwidth β of the A matrix,

$$\beta = \max |i - j| \quad \forall i, j \mid a_{ij} \neq 0 \quad (3)$$

A sparse matrix of dimension N with symmetrical zero-non-zero-pattern can be represented by a graph, as in Fig. 1, once that each row/column is numbered. A vector $\Pi = \{\pi_1, \pi_2, \dots, \pi_N\}$ is a possible numbering, and

is represented by a permutation of the initial numbering $\{1, 2, \dots, N\}$. The solution of the problem is represented by an optimum Π_{opt} so that

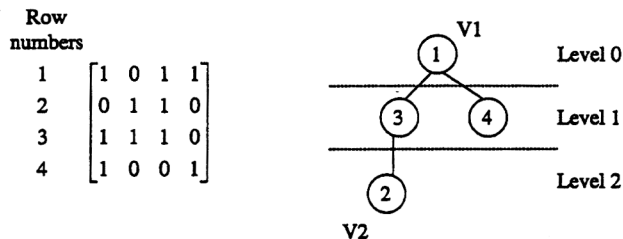
$$\beta(\Pi_{opt}) = \min(\beta(\Pi)) \quad \forall \Pi \quad (4)$$

In case of non symmetrical zero-non-zero pattern, this graph representation has some troubles, and is, as far as we know today, substantially useless.

The solutions to the bandwidth minimization problem proposed in the literature till now can be divided into two main classes:

- Solutions based on a graph representation
- Alternative solutions

The most important approach based on *graph representation* is the one proposed by Cuthill and McKee (CM) in 1969 [11]. They proposed some efficient heuristics to identify Π_{opt} , by introducing: 1) a partitioning of the graph into levels 2) new vertices at a maximum distance 3) heuristical rules for cutting some edges, and creating new ones (see Fig. 1). Several upgrades of the CM approach have been proposed. The one by Gibbs, Poole and Stockmeyer (GPS) [12] is extremely efficient, even though it has recently been overcome by the one by Esposito, Malucelli and Tarricone (EMT) [8], [13], which has been defined as the current state-of-the-art for the bandwidth minimization of matrices generated by EM codes [14].



Permutation: (1,2,3,4) becomes (1,4,3,2)

Corresponding matrix and graph:

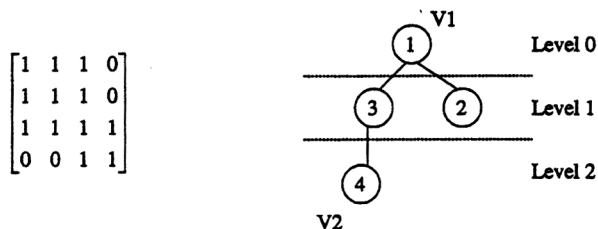


Fig. 1. A sparse matrix with symmetrical zero-non-zero pattern can be represented by a graph, once rows/columns have been numbered. A level partitioning can be identified on the graph, once two vertices V1 and V2 have been selected. A permutation or renumbering of rows/columns modifies the matrix pattern and the graph layout, with effects on the matrix bandwidth.

The *alternative approaches* proposed till now are based on combinatorial techniques based on global optimization. Examples are the use of simulated-annealing

(SA) [15] and of Tabu-Search (TS) [16]. In both cases, heuristical laws are introduced, in conjunction with an appropriate use of data structures to take into account the evolution of the search, so that the risk of being trapped into local optima is reduced.

Despite the strong efforts performed till now, several problems are still open. For instance, CM and GPS have severe troubles with some pathological cases arising from FEM simulation of boxed microstrip lines, or MM analysis of rectangular waveguide circuits [1], [17]. Moreover, they cannot cope with the problem of non-symmetrical structures of matrices encountered, for instance, in some cases when wavelet expansions are used with the MoM [4]. The EMT approach has solved these problems, but its performance on non-symmetrical matrices can be enhanced. As for SA and TS approaches, they are quite appropriate to overcome the problem of non-symmetrical patterns, but their numerical weight is still too much to make their use appealing in routinely-used CAD tools.

On such bases, an experimentation of a genetic approach (GA) to the problem is quite interesting. In fact, especially for large matrices, the use of appropriate global search strategies, with the possibility of embedding complex heuristical laws, is essential for finding satisfactory solutions. Moreover, a GA is naturally amenable to represent non-symmetrical problems, with a consequent advantage with respect to graph approaches. It is also easier to implement than graph approaches. Finally, its expectable drawback, i.e. its numerical weight, can easily be circumvented by a migration to parallel platforms (GA is intrinsically amenable to a parallel design).

III. THE GENETIC SOLUTION

Genetic algorithms are nowadays commonly used in the design and optimization of EM circuits [18]. We address to the pioneeristic works of Goldberg [19] and Holland [20] for the basic concepts, and describe here the main features of the GA proposed here.

A. Choice of chromosomes

As put forwards in (4), the problem unknown is a vector of natural numbers called Π_{opt} . Consequently, it is natural to define chromosomes as strings of natural numbers, of the same dimension of A matrix. This choice has a major drawback. In fact, during the usual operations over chromosomes, for instance when performing cross-overs, we risk the generation of non-feasible chromosomes, such as permutations of Π with repeated numbers. On the other side, cross-over, as quite well-known, is of fundamental importance for the efficiency and effectiveness of the GA. Therefore, in order to avoid the problems of repeated numbers after crossing-over, a set of data structures, and dedicated algorithms, have been designed. The data structures are: 1) the current permutation vector Π ; 2) an auxiliary vector Aux initialized with a certain permutation without repeated

numbers; 3) a vector $New\Pi$ with the generated permutation. It must be stressed that $New\Pi$ can host permutations with repeated natural numbers. The dedicated algorithms allow the generation of permutations with repeated numbers, and their transformation into permutations without repeated numbers, so that a biunivocal correspondence is guaranteed between each $New\Pi$ instance and each feasible Π instance.

Before describing the algorithms, we introduce a function $foundpos(\Pi(1))$, which finds out the position inside Aux of the first entry $\Pi(1)$ of array Π . For instance, if we have $\Pi = \{3, 1, 5, 4, 2\}$, and $Aux = \{1, 2, 3, 4, 5\}$, $foundpos(\Pi(1)) = foundpos(3) = 3$. We also introduce a function $delete(arr(i))$, which deletes the entry i from array arr . For instance, if we have $Aux = \{1, 2, 3, 4, 5\}$, $delete(Aux(3))$ turns Aux into $\{1, 2, 4, 5\}$ (its dimension has been reduced by one).

The algorithm for generating a modified permutation with repeated numbers is now described. The joint use of $New\Pi$ and Aux data structures guarantees a biunivocal correspondence between each instance of $New\Pi$ and one instance of Π (i.e. a permutation vector without repeated numbers):

```
for i=1,N
  NewΠ(i) = foundpos(Π(1))-1
  delete(Aux(NewΠ(i)+1))
  delete(Π(1))
end
```

The implementation of this algorithms results, for instance, in the following steps for a given current permutation and auxiliary permutation:

Π	Aux	$New\Pi$
31542	12345	2
1542	245	20
42	24	202
2	2	2021
-	-	20210

As apparent, the final $New\Pi$ vector has some repeated numbers. Its use, in conjunction with Aux , is sufficient to convert it into the corresponding Π . The conversion is performed by simply reverting the algorithm to generate the modified permutation.

B. Initial Population

The proposed implementation of the GA has been proved to be nearly insensitive to the chosen starting population, provided that its cardinality is suitable with respect to the size of the problem (the matrix dimension N).

As already observed for different combinatorial heuristics [21], no deterministic laws have been determined to describe the convergence of the GA with respect to the population generation, as well as to its cardinality. In the current implementation, we generate a starting population by random extraction of permutation vectors from the starting choice $\Pi = \{1, 2, \dots, N\}$.

C. Cost function

The choice of a suitable cost function is of paramount importance for the convergence of a combinatorial optimization task. The bandwidth minimization can be performed with different choices of the cost function. One of the most important issues is the selection of a cost function so that as few different solutions Π as possible have equal cost, and risk to be considered as equivalent. For instance, the very trivial choice of a cost function

$$c(\Pi) = \beta(\Pi) \quad (5)$$

where the bandwidth corresponding to a certain permutation vector is the cost, is not satisfactory at all. An enhancement can be the following choice:

$$c(\Pi) = w_1\beta(\Pi) + w_2N_\beta \quad (6)$$

where N_β is the number of rows/columns that have maximum bandwidth β , whilst w_1 and w_2 are tunable weights. Of course, in case of unsymmetrical patterns, the same function can be transformed into

$$c(\Pi) = (w_{1L}\beta_L(\Pi) + w_{2L}N_{\beta L}) + (w_{1U}\beta_U(\Pi) + w_{2U}N_{\beta U}) \quad (7)$$

where subscripts U and L correspond to "upper" and "lower" part of the matrix (with respect to the main diagonal). The three proposed choices are still not completely satisfactory: even in the case of (6) or (7) there are many different permutation vectors corresponding to the same value of $c(\Pi)$.

Some new ideas have been proposed in [15], and suggest the following solution to the problem of a suitable cost function:

$$c(\Pi) = \sum_{i,j} F(N, |i-j|) \quad (8)$$

where N is the matrix size, and F is the following function:

$$F(N, |i-j|) = \begin{cases} N & |i-j| = 0, 1 \\ (N - |i-j|) \cdot (F(N, |i-j|) - 1) & \text{elsewhere} \end{cases} \quad (9)$$

The choice of (8) guarantees an adequate partitioning of the searching space, with a substantial reduction of the risk of equivalence among different permutations. This is the cost function implemented in the proposed GA.

D. Convergence Criterion

The sparse matrix bandwidth reduction is typically used in order to improve the solution time of linear systems by using banded solvers, which have a quadratic complexity with respect to the matrix bandwidth. Therefore, it is possible to evaluate the effectiveness of each iteration by comparing the time needed for a single iteration, with respect to the induced reduction of the solution time. This practical parameter, averaged over a certain number of iterations, is appropriate to evaluate when the bandwidth reduction should be stopped.

E. Genetic Operators

We use three operators: selection, crossover and mutation.

E.1 Selection

We adopt the most typical way of performing selection, i.e. on a cost-proportional basis. This means that N_{sel} elements of the population are randomly chosen, and the one with the lowest cost is selected.

E.2 Crossover

The basic idea is of generating hybrid chromosomes, by crossing together two selected chromosomes. This idea is here coupled with another empirical observation: for each matrix pattern, some rows/columns are more effective than others when performing the permutation. Therefore, when the optimum or quasi-optimum position is found for them, the corresponding information should be preserved in the permutation vector. The natural translation of this idea is the principle of building-blocks, further described.

Now we quickly describe *when* and *how* crossover is to be performed.

- When crossover is to be performed: this is decided following a probabilistic approach [22]. Two vectors from the old population are selected in accordance with the selection operator. One random number p_1 is generated. The two vectors are inserted into the new population if $p_1 \geq 1 - p_c$. A second random number p_2 is generated, and crossover performed if $p_2 \geq p_c$. The value of p_c is a heuristically tunable parameter.
- How crossover is performed: two random numbers are generated to identify the beginning and the end of the crossing site. Two new chromosomes are attained by exchanging the crossing sites between the two vectors. For instance, if we indicate with n_1 and n_2 the two random numbers, and with Π_1 and Π_2 the two permutation vectors, the entries $\Pi_1(n_1, \dots, n_2)$ are swapped with $\Pi_2(n_1, \dots, n_2)$. In accordance with the principle of *preserving building blocks* [23], we know that a purely random choice of the crossing site is often unsatisfactory. Therefore, by using some statistical data about the role of each element of the permutation vector Π during the search, some positions inside the chromosome are prevented from destruction during crossover. The protected positions typically correspond to rows/columns of the matrix giving a low contribution to the value of the cost function (8). For instance, referring to the previous example, if a position within the range (n_1, \dots, n_2) is ranked as a building-block, no swapping is performed on it. Of course, when performing crossover, the data structures *Aux* and *NewPi* must be suitably managed, so that the modified permutation can be turned into a permutation vector Π without repetitions. The algorithm mentioned in Section III.A

is still valid, and must only be adjusted to cope with the problem of beginning and ending point of the crossing site.

E.3 Mutation

Three kinds of mutations are performed: swap, left and right shift. One tunable parameter p_m is chosen, and two random numbers pos_1 and pos_2 generated. A new random number is generated. If it is larger than p_m , genes pos_1 and pos_2 in the chromosome are swapped, and a left and right shift is performed over the partition of vector starting at pos_1 and ending at pos_2 .

When mutation is performed, the principle of preserving building blocks is not respected. Moreover, a *distance-dependent* mutation is implemented [24]. In fact, it is well known that, especially when small populations of chromosomes are used, the use of a fixed value of p_m does not prevent from the premature convergence over local minima. Therefore, the value of p_m is dynamically adapted, in order to avoid being trapped into unsatisfactory solutions.

IV. RESULTS ON SERIAL PLATFORMS

We propose two types of results. The former one refers to matrices encountered in the analysis of 1) rectangular waveguides inhomogeneously filled with dielectric (Fig. 2) or 2) boxed microstrip lines (Fig. 3). A revisited version of a public-domain FEM code, called EMAP1, based on a variational scalar formulation [25], is used.

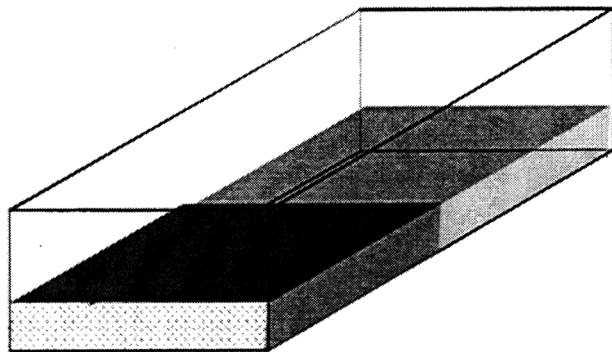


Fig. 2. A rectangular waveguide inhomogeneously filled with dielectric. Different dielectrics and geometries have been chosen. One of the examples is shown in the figure.

The latter refers to matrices generated during the analysis of microstrip circuits with an MPIE-MoM formulation [26]. In all the proposed cases, the performance of the GA is compared with a commercial CM approach available in MATLAB, a GPS and TS solution implemented by the author, and with the previously mentioned EMT solution described in [8], [13].

A. FEM Analysis

Table I proposes results for problems such as the one in Fig. 2. A standard WR90 is studied in the range 8-

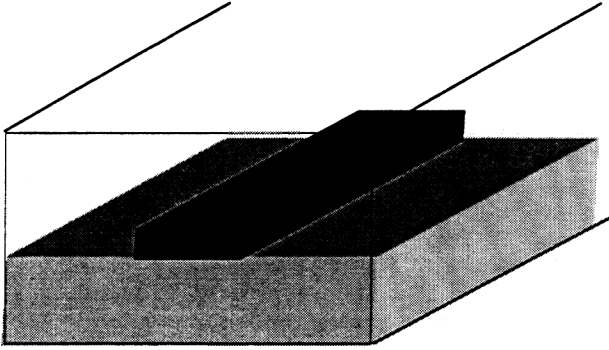


Fig. 3. A boxed microstrip line. Different cases with different dimensions and dielectric layers have been simulated.

12GHz, and the electric field distribution evaluated with different dielectric fillings.

N	In. β	GPS	CM	EMT	TS	GA
284	92	115	74	62	62	62
374	107	122	102	72	106	96
639	151	178	172	87	102	91
1231	251	247	242	199	233	212

Table I: Results for different matrices generated during a FEM analysis of inhomogeneously filled rectangular waveguides. Matrix size N , initial bandwidth β , and final bandwidth attained with different approaches are reported.

As apparent from Tab. I, GPS and CM have a critical behaviour with some pathological cases. The EMT approach is the more robust, even though the GA is quite effective as well. An essential issue is the time needed to achieve the solution. It is reported in Tab. II, on a Pentium 166MHz:

N	GPS	CM	EMT	TS	GA
284	0.218	0.22	0.215	6.9	7.2
374	0.74	0.87	0.560	19.1	18.9
639	2.4	3.2	1.44	498	480
1231	18.8	16	3.74	g.t. 10000	g.t. 10000

Table II: Times to find out the optimum Π for the cases in Tab. I.

Tab. II clearly demonstrates the real limitation of the GA: it is quite effective, but too computationally heavy. For instance, if we consider that the FEM generates banded matrices, we can compare the standard use of banded direct solver (BDS) without bandwidth reduction (i.e. what EMAP1 routinely does), with the case of a banded direct solver (BDS) used after bandwidth reduction. The time (in seconds) needed for a 100 frequency-point analysis is reported in Tab. III:

N	EMAP1	EMT+DBS	GA+DBS
374	264.8	186.1	242
639	798.4	395.2	961
1231	12270	1376	g.t. 30000

Table III: Times in seconds to analyze at 100 frequency points some circuits with the FEM-code EMAP1, with respect to the use of bandwidth reduction in conjunction with a direct banded solver (DBS).

It is easily seen that when the problem dimension grows up the numerical complexity of the GA becomes a substantial limitation, whilst the EMT approach is quite advantageous. Similar results are attained in the case of circuits such as the one in Fig. 3. Table IV reports some results, with the same scheme of Tab. III:

N	EMAP1	EMT+DBS	GA+DBS
484	284.8	24.6	212.1
720	737.5	162.7	13211

Table IV: Times in seconds to analyze at 100 frequency points some circuits with the FEM-code EMAP1, with respect to the use of bandwidth reduction in conjunction with a direct banded solver (DBS).

The matrices generated in the case of boxed microstrip lines have a smaller bandwidth with respect to the case of inhomogeneously waveguides, and this explains the reduced simulation times.

B. MPIE/MoM Analysis

We refer to a MPIE formulation using closed-form spatial-domain Green's functions, discretized with a Galerkin MoM with roof-top functions. As described in [26], the analysis of microstrip circuits with this approach originally generates dense impedance matrices; anyway, a thresholding action can be performed over the matrix, so that all entries smaller than a certain value are zeroed. This can imply a very small approximation error (around 1%) provided that a suitable threshold is identified. In the large majority of cases, a value of 10^{-6} with respect to the largest entry in the matrix is appropriate, and a matrix sparsity between 70 and 85 % is achieved.

Referring to the circuits of Fig. 4, we report results in Tab V, where we compare times for the analysis of the circuit by using an iterative sparse solver (ISS), with respect to the use of different bandwidth reduction approaches in conjunction with DBS. Both the ISS and the DBS come from the same public domain library (Lapack). A dispersion curve of 100 frequency point is evaluated for both circuits. The single-stub circuit operates in the range 7.5-12 GHz, the double stub between 8 and 18 GHz.

N	ISS	EMT+DBS	GA+DBS
280	113.4	23.6	57.1
448	312.5	84.1	412

Table V: Times in seconds to analyze at 100 frequency points the two circuits in Fig. 4 with the MPIE/MoM with ISS, with respect to the use of MPIE/MoM with bandwidth reduction in conjunction with a DBS.

Also in this case, it is apparent that the performance of the GA is less attractive than the EMT's one, and, above all, it decreases when enlarging the size of the problem.

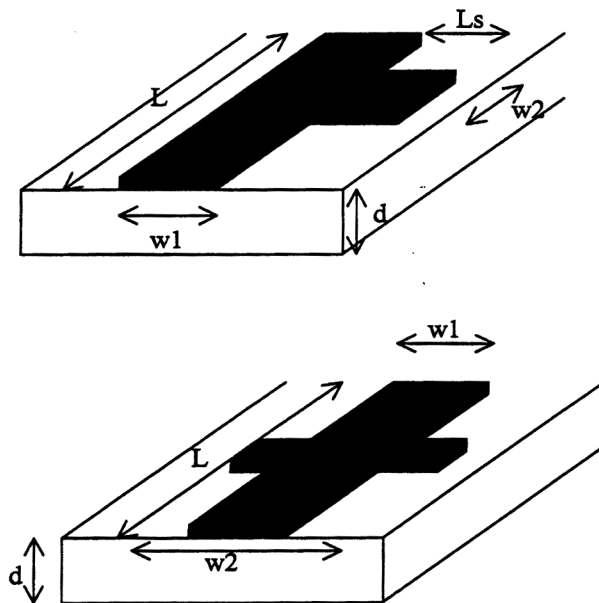


Fig. 4. The two circuits analyzed with the MPIE/MoM. For the single stub $\epsilon_r = 10.65$, $d=1.27\text{mm}$, $w_1=w_2=1.44\text{mm}$, $L=17.28\text{mm}$, $L_s=2.16\text{mm}$. For the double stub $\epsilon_r = 9.9$, $d=10\text{mm}$, $w_1=9.2\text{mm}$, $w_2=23\text{mm}$, $L=110.6\text{mm}$.

V. PARALLEL GA SOLUTION

The recent progresses in parallel computing, and above all the development of low-cost and efficient parallel platforms, such as clusters of PCs, can change the perspective opened by the previous observations. As apparent in previous sections, the several advantages of the GA, i.e. its easy implementation, its amenability to cope with pathological cases, as well as to deal with non-symmetrical or unstructured patterns, are ineffectual, due to its large numerical complexity. Luckily, the nature of GA renders it intrinsically amenable to a parallel design. The large majority of tasks inside it, such as the generation of a farm of initial populations and the evolution of each population, can be performed in parallel on different processors. The percentage of potentially-parallel tasks, with respect to the overall serial work, ranges between 80 and 95 %, depending on the problem size (Π dimension) and the selection of some heuristical parameters, such as p_m and p_c .

Therefore, a parallel version of the GA, called PGA, has been implemented using Parallel Virtual Machine (PVM) programming interface, on an IBM SP2 with 8 nodes. The PGA performs a parallel generation of a farm of initial populations, and periodically collects the results of the evolutionary search from each population, so that cross-over and mutations are performed over chromosomes from different populations, with an increase of the level of hybridization. This can be described as a first *coarse* level of parallelism. A second *fine* level of parallelism is represented by the evaluation of the cost function, which is performed in parallel. This task is quite heavy, especially when large problems are attacked, and can be performed in parallel with a suitable block-decomposition of both the matrix and the permutation vector Π .

A. Results with PGA

In Tab. VI results of PGA for the matrices encountered in the FEM analysis are reported (see Tab. I). The achieved bandwidth, and the computing time when using 8 SP2 nodes, are reported.

N	In. β	Opt. β	Time (s)
284	92	54	1.4
374	107	66	2.5
639	151	74	54
1231	251	151	1123

Table VI: Results for PGA on matrices from FEM analysis of MW circuits. Matrix size N , initial bandwidth β , and final bandwidth are reported.

As shown in Tab. VI, computing times are reduced, and the effectiveness of bandwidth reduction is improved. The use of PGA results in the times reported in Tab. VII for a 100-frequency-point dispersion curve of circuits as in Fig. 2 (compare with Tab. III):

N	EMAP1	EMT+DBS	PGA+DBS
374	264.8	186.1	193.1
639	798.4	395.2	422.7
1231	12270	1376	1642

Table VII: Times in seconds to analyze at 100 frequency points some circuits with the FEM-code EMAP1, with respect to the use of parallel bandwidth reduction in conjunction with a direct banded solver (DBS).

As demonstrated in Tab. VII, the performance of PGA turns the genetic approach into an effective method to reduce the time for the numerical analysis of MW circuits, thanks to the substantial decrease of bandwidth reduction time, as well as to the improvement in the effectiveness of the search. PGA's efficiency is similar to the state-of-the-art EMT's one. Speed-ups in the simulation times up to a factor 8 have been observed.

VI. CONCLUSIONS

A genetic solution (GA) to the problem of sparse matrix bandwidth minimization has been proposed. The main characteristics of the approach have been described, with respect to the choice of chromosomes, genetic operators, and other heuristical parameters. A suite of functions has been developed so that the crossover can be performed without risks of non-feasible chromosome generation. Results have proved that the GA, despite of its several attractive features (simplicity, flexibility, amenability to global optimization), is not efficient enough to be considered as an appropriate tool for CAD environments of MW circuits. Thanks to its natural parallelism, the approach has been migrated towards parallel platforms (PGA), with a substantial increase in its efficiency and effectiveness, which are similar to those of state-of-the-art bandwidth reducers based on graph theory (EMT).

On the other side, the GA and PGA are rather simple to be implemented, whilst EMT is complex and deserves a deep knowledge of graph theory. Furthermore, it is reasonable to expect a substantial increase in the scalability and efficiency of clusters of PCs in the next future, thanks to the continuous evolution of switch and fast-ethernet technologies. As a matter of fact, with very affordable costs, parallel environments for the analysis of EM circuits can be predicted as the natural future infrastructure for MW CAD of large and complex circuits. In conclusions, the opening of such new perspectives turns the genetic approach into a candidate solution to improve the efficiency of numerical methods for EM circuits via sparse matrix bandwidth reduction.

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