

Density Matrix Renormalization Group Method applied to two crossed disordered chains within Anderson model

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Abstract : A variation of the Density Matrix Renormalization Group (DMRG) procedure, based on a simplified version suggested by Martin-Delgado et al., is developed to compute low states energies for two crossed chains within the simple tight binding model suggested earlier by P. Anderson. For comparison, our results obtained using the new procedure are presented along with those obtained by exact diagonalization. In order to make clear the procedure, some technical aspects of the implementation of the algorithm are given in detail.

Keywords: reduced density matrix, disordered system, tight-binding model.

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I. Introduction

The Density Matrix Renormalization Group (DMRG), developed by S. R. White in 1992 [1], is a powerful numerical method which permits us to obtain the ground-state and low-lying excited states wavefunctions of large-size systems with controlled high accuracy. S.White has considered that a system (block) must be connected to an other block (environment) to form a superblock, and therefore each part contributes to the ground state of the superblock through its own states. The basic idea of the DMRG is to use the concept of density matrix to decide which states from a given block that contribute the more to the wavefunction of the whole system. As the procedure is iterated the size of the system is increasing while the corresponding Hilbert space is kept constant.

Technically, the algorithm consists in a warm up phase where Hamiltonian operators for each block and connection operators in the system are renormalized and then stored to be used later. This is followed by a sweeping procedure which iterates the process on the full system until convergence is reached.

In fact, since its appearance, DMRG has proven a high level of accuracy when dealing with one-dimensional systems, in such a way that it became, in few years, a valuable numerical tool, among other numerical methods, to calculate energy spectrum and other dynamic correlation functions at finite temperatures of interacting 1-d quantum systems.

Still, the DMRG is called to prove its accuracy when applied to 2-d quantum systems and, eventually, 3-d ones.

Thus, various algorithms have been proposed to apply DMRG to two-dimensional quantum systems; see for example [2-7]. Most of these works use mappings on to effective one-dimensional models with long-range interactions, and the standard DMRG method is applied to the effective one-dimensional systems. In this spirit, the present paper is to give a new configuration of the DMRG method to treat a diffusive problem without any mapping:

a disordered two-crossed chains system within the very simple tight-binding Anderson model.

Our work is based on an earlier paper [8], where M.A. Martín-Delgado et al. have given a simplified version of White's Density Matrix Renormalization Group (DMRG) algorithm to find the ground state of single-particle quantum mechanics. They solved a discretized version of the single-particle Schrödinger equation, which allows them to obtain very accurate results for the lowest energy levels of a single particle under the action of three potentials: harmonic oscillator, anharmonic oscillator and double-well.

Our contribution consists in replacing the standard configuration, which consists in two connected blocks (system + environment), by a five-blocks system, representing the two crossed chains.

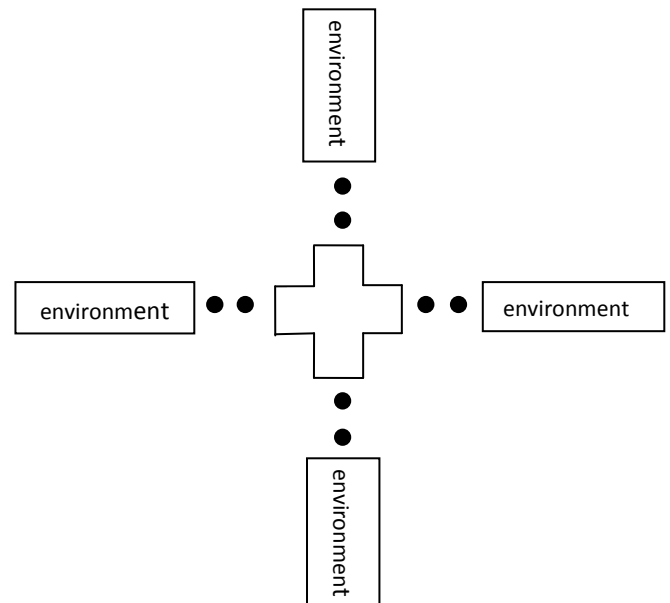


Figure 1: DMRG superblock configuration: five blocks and eight sites to add in each step of the procedure.

II. DMRG applied to two crossed chains

The present implementation consists in five blocks: right, left, upper and down blocks B_l^L , B_l^R , B_l^U and B_l^D with l sites (environment) plus a center block B_m^C with also m sites (system), as it is shown in figure 1.

2.1. Superblock Hamiltonian

In order to treat the $N_E \geq 1$ lowest energy levels, the environment B_l^L , B_l^R , B_l^U and B_l^D must contain N_E degrees of freedom. Clearly, the center block contains $2N_E - 1$ sites. Our choice for numbering sites in the superblock is such the horizontal sites are labeled with odd number from left to right, whereas the vertical sites are labeled with even number starting from up to down. The superblock Hamiltonian H_{SB} is therefore a $(6N_E + 7) \times (6N_E + 7)$ matrix given by

$$H_{SB} = \begin{pmatrix} H_{LU} & -v_L & -v_U & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -v_L^\dagger & h_{CL} & 0 & -1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ -v_U^\dagger & 0 & h_{CU} & 0 & -1 & -v_{CL}^\dagger & 0 & 0 & 0 & 0 & 0 \\ 0 & -1 & 0 & h_{CCL} & 0 & -v_{CU}^\dagger & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & -1 & 0 & h_{CCU} & -v_{CR}^\dagger & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -v_{CL} & -v_{CU} & H_C & -v_{CR} & -v_{CD} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -v_{CR}^\dagger & h_{CCR} & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -v_{CD}^\dagger & 0 & h_{CCD} & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & h_{CR} & 0 & -v_R^\dagger \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & h_{CD} & -v_D^\dagger \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -v_R & -v_D & H_{RD} \end{pmatrix} \quad (1)$$

where H_{LU} writes:

$$H_{LU} = \begin{pmatrix} H_L^{11} & 0 & H_L^{12} & 0 & \dots & H_L^{1N_E} & 0 \\ 0 & H_U^{11} & 0 & H_U^{12} & \dots & 0 & H_U^{N_E 1} \\ H_L^{21} & 0 & H_L^{22} & 0 & \dots & H_L^{2N_E} & 0 \\ 0 & H_U^{21} & 0 & H_U^{22} & \dots & 0 & H_U^{2N_E} \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ H_L^{N_E 1} & 0 & H_L^{N_E 2} & 0 & \dots & H_L^{N_E N_E} & 0 \\ 0 & H_U^{N_E 1} & 0 & H_U^{N_E 2} & \dots & 0 & H_U^{N_E N_E} \end{pmatrix} \quad (2)$$

H_{LU} is a $2N_E \times 2N_E$ matrix, built up by two embedded matrices H_L and H_U , each one representing the interactions inside the blocks B_L and B_U , respectively. Zeros in the matrix indicate lost links

between sites. Thus, H_{LU}^{12} , for example, is equal to zero because there is no link between the first and second sites.

Similarly, H_{RD} writes as

$$H_{RD} = \begin{pmatrix} H_R^{11} & 0 & H_R^{12} & 0 & \dots & H_R^{1N_E} & 0 \\ 0 & H_D^{11} & 0 & H_D^{12} & \dots & 0 & H_D^{N_E 1} \\ H_R^{21} & 0 & H_R^{22} & 0 & \dots & H_R^{2N_E} & 0 \\ 0 & H_D^{21} & 0 & H_D^{22} & \dots & 0 & H_D^{2N_E} \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ H_R^{N_E 1} & 0 & H_R^{N_E 2} & 0 & \dots & H_R^{N_E N_E} & 0 \\ 0 & H_D^{N_E 1} & 0 & H_D^{N_E 2} & \dots & 0 & H_D^{N_E N_E} \end{pmatrix} \quad (3)$$

It represents the interactions inside the blocks B_R and B_D . The symbols h_{CL} , h_{CU} , h_{CR} and h_{CD} represent the

added sites, at each iteration, to left, upper, right and down blocks, respectively. Also, h_{CCL} , h_{CCU} , h_{CCR}

and h_{CCD} are the added sites to the center block. The N_E -component column vectors v_L , v_U , v_R and v_D describe the interaction between the B_L , B_U , B_R and B_D and the sites next to them in the superblock. For example, v_L writes as $(v_L^1, 0, v_L^2, \dots, v_L^{N_E}, 0)$ and v_U writes as $(0, v_U^1, 0, v_U^2, \dots, 0, v_U^{N_E})$. The $2N_E - 1$ -component column vectors v_{CL} , v_{CU} , v_{CR} , and v_{CD}

describe the interaction between the center B_C and the sites next to it in the superblock. So that, v_U , for example, writes as $(v_{CU}^1, v_{CU}^2, \dots, v_{CU}^{N_E})$.

Then, the Hamiltonian H_{SB} in Eq.(1) describes the superblock:

$$\begin{array}{ccccccc} & & & B_l^U & & & \\ & & & \vdots & & & \\ & & & \bullet & & & \\ B_l^L & \bullet & \bullet & B_{2N_E+4nbr}^C & \bullet & \bullet & B_{\frac{N-7}{2}-N_E-2nbr-l}^R \\ & & & \vdots & & & \\ & & & \bullet & & & \\ & & & B_{\frac{N-7}{2}-N_E-2nbr-l}^R & & & \end{array}$$

Since the blocks $B_{\{L,U,R,D\}}$ and the block B_C contain N_E and $2N_E - 1$ effective sites, respectively, we need $nbr = \frac{N-6N_E-7}{8}$ warm-up steps to reach the desired

system length N . $H_{SB} = H_{SB}^{(l)}$ can be defined for $l = N_E, N_E + 1, \dots, N_E + nbr$.

2.2 . DMRG truncation

As in the previous section, we have to obtain the N_E lowest eigenstates of H_{SB} , which will be designated as:

$$\{(a_{L,i}^1, a_{U,i}^1, \dots, a_{L,i}^{N_E}, a_{U,i}^{N_E}, a_{CL,i}, a_{CU,i}, a_{CCL,i}, a_{CCU,i}, a_{C,i}, a_{CCR,i}, a_{CCD,i}, a_{CR,i}, a_{CD,i}, a_{R,i}^1, a_{D,i}^1, \dots, a_{R,i}^{N_E}, a_{D,i}^{N_E})\}_{i=1}^{N_E}$$

where $(a_{L,i}^1, \dots, a_{L,i}^{N_E})$, $(a_{U,i}^1, \dots, a_{U,i}^{N_E})$, $(a_{R,i}^1, \dots, a_{R,i}^{N_E})$ and $(a_{D,i}^1, \dots, a_{D,i}^{N_E})$ are N_E -component vectors and $a_{C,i}$ is $2N_E - 1$ -component vector. For $N_E = 3$, these vectors are then projected onto a set of 3 vectors of the block

B_L •, i.e., $\{(a_{L,i}, a_{CL,i})\}_{i=1}^3$, a set of 3 vectors of the block B_U •, i.e., $\{(a_{U,i}, a_{CU,i})\}_{i=1}^3$ and a set of 3 vectors of the block :

$$\begin{array}{ccc} & \bullet & \\ \bullet & B_C & \bullet \\ & \bullet & \end{array}$$

,i.e., $\{(a_{CCL,i}, a_{CCU,i}, a_{C,i}, a_{CCR,i}, a_{CCD,i})\}_{i=1}^3$. These three sets of vectors must be orthonormalized using a

Gram-Schmidt orthogonalization procedure and then dividing them by:

$$N_L^i = \sqrt{(a_{L,i}^1)^2 + (a_{L,i}^2)^2 + (a_{L,i}^3)^2 + (a_{CL,i})^2}$$

$$N_U^i = \sqrt{(a_{U,i}^1)^2 + (a_{U,i}^2)^2 + (a_{U,i}^3)^2 + (a_{CU,i})^2}$$

and

$$N_C^i = \sqrt{(a_{CCL,i})^2 + (a_{CCU,i})^2 + (a_{C,i}^1)^2 + (a_{C,i}^2)^2 + (a_{C,i}^3)^2 + (a_{CCR,i})^2 + (a_{CCD,i})^2}$$

respectively.

The new three sets are designated as $\{(\mathbf{a}'_{L,i}, \mathbf{a}'_{CL,i})\}_{i=1}^3$, $\{(\mathbf{a}'_{U,i}, \mathbf{a}'_{CU,i})\}_{i=1}^3$, and $\{(\mathbf{a}'_{CCL,i}, \mathbf{a}'_{CCU,i}, \mathbf{a}'_{C,i}, \mathbf{a}'_{CCR,i}, \mathbf{a}'_{CCD,i})\}_{i=1}^3$.

If there is no symmetry in the Hamiltonian, right and down matrices have to be renormalized in the same manner. A straightforward generalization of the renormalized block Hamiltonians in [8] yields the new effective Hamiltonians, H'_L and H'_U , and vectors v'_L and v'_U ; which write, for $N_E = 3$, as:

$$H'_L = \begin{pmatrix} a'_{L,1} & a'_{L,2} & a'_{L,3} & a'_{CL,1} \\ a'_{L,2} & a'_{L,2} & a'_{L,2} & a'_{CL,2} \\ a'_{L,3} & a'_{L,3} & a'_{L,3} & a'_{CL,3} \end{pmatrix} \begin{pmatrix} H_L^{11} & H_L^{12} & H_L^{13} & -v_L^1 \\ H_L^{21} & H_L^{22} & H_L^{23} & -v_L^2 \\ H_L^{31} & H_L^{32} & H_L^{33} & -v_L^3 \\ -v_L^1 & -v_L^2 & -v_L^3 & h_{CL} \end{pmatrix} \begin{pmatrix} a'_{L,1} & a'_{L,2} & a'_{L,3} \\ a'_{L,1} & a'_{L,2} & a'_{L,3} \\ a'_{L,1} & a'_{L,2} & a'_{L,3} \\ a'_{CL,1} & a'_{CL,2} & a'_{CL,3} \end{pmatrix} \quad (4)$$

$$H'_U = \begin{pmatrix} a'_{U,1} & a'_{U,2} & a'_{U,3} & a'_{CU,1} \\ a'_{U,2} & a'_{U,2} & a'_{U,2} & a'_{CU,2} \\ a'_{U,3} & a'_{U,3} & a'_{U,3} & a'_{CU,3} \end{pmatrix} \begin{pmatrix} H_U^{11} & H_U^{12} & H_U^{13} & -v_U^1 \\ H_U^{21} & H_U^{22} & H_U^{23} & -v_U^2 \\ H_U^{31} & H_U^{32} & H_U^{33} & -v_U^3 \\ -v_U^1 & -v_U^2 & -v_U^3 & h_{CU} \end{pmatrix} \begin{pmatrix} a'_{U,1} & a'_{U,2} & a'_{U,3} \\ a'_{U,1} & a'_{U,2} & a'_{U,3} \\ a'_{U,1} & a'_{U,2} & a'_{U,3} \\ a'_{CU,1} & a'_{CU,2} & a'_{CU,3} \end{pmatrix} \quad (5)$$

with

$$\begin{aligned} v'_{L,i} &= a'_{CL,i}, (i = 1, 2, 3) \\ v'_{U,i} &= a'_{CU,i}, (i = 1, 2, 3) \end{aligned} \quad (6)$$

Similarly, the new effective Hamiltonian, H'_C , and the vectors v'_{CL} , v'_{CU} , v'_{CR} and v'_{CD} are given by:

$$H'_C = \begin{pmatrix} a'_{CCL,1} & a'_{CCU,1} & \mathbf{a}'_{C,1} & a'_{CCR,1} & a'_{CCD,1} \\ a'_{CCL,2} & a'_{CCU,1} & \mathbf{a}'_{C,2} & a'_{CCR,1} & a'_{CCD,1} \\ a'_{CCL,3} & a'_{CCU,1} & \mathbf{a}'_{C,3} & a'_{CCR,1} & a'_{CCD,1} \end{pmatrix} \begin{pmatrix} h_{CCL} & 0 & -v_{CL}^\dagger & 0 & 0 \\ 0 & h_{CCU} & -v_{CU}^\dagger & 0 & 0 \\ -v_{CL} & -v_{CU} & H_C & -v_{CR} & -v_{CD} \\ 0 & 0 & -v_{CR}^\dagger & h_{CCR} & 0 \\ 0 & 0 & -v_{CD}^\dagger & 0 & h_{CCD} \end{pmatrix} \begin{pmatrix} a'_{CCL,1} & a'_{CCL,2} & a'_{CCL,3} \\ a'_{CCU,1} & a'_{CCU,1} & a'_{CCU,1} \\ \mathbf{a}'_{C,1} & \mathbf{a}'_{C,2} & \mathbf{a}'_{C,3} \\ a'_{CCR,1} & a'_{CCR,1} & a'_{CCR,1} \\ a'_{CCD,1} & a'_{CCD,1} & a'_{CCD,1} \end{pmatrix} \quad (7)$$

with

$$\begin{aligned} v'_{CL,i} &= a'_{CCL,i}, (i = 1, \dots, 5) \\ v'_{CU,i} &= a'_{CCU,i}, (i = 1, \dots, 5) \\ v'_{CR,i} &= a'_{CCR,i}, (i = 1, \dots, 5) \\ v'_{CD,i} &= a'_{CCD,i}, (i = 1, \dots, 5) \end{aligned} \quad (8)$$

2.2. Initialization, warm up and sweeping

In the present case, the system is enlarged by 8 sites at each step of iteration. Thus, the warm-up phase, with reflection symmetry, consists in iterating these operations:

1. The left and upper blocks are built and then enlarged by adding a single site.
2. The right and down enlarged blocks are obtained by just reflecting the left and upper blocks, respectively. In the case where there is no symmetry reflection, the former blocks (right and down ones) must be built independently.
3. The center block is built and then enlarged by adding a single site to each side (four sites).
4. All these operators must be stored to be used later.

5. The five enlarged blocks, including interactions between them, form the super-block Hamiltonian.
6. The latter Hamiltonian is diagonalized, and the N_E lowest eigenstates are obtained.
7. The new effective Hamiltonians and interaction vectors are then constructed.
8. Once the system size N is reached; then the center block continues to grow up by four sites at each iteration, whereas the left, upper, down and right blocks retrieve until the number of sites in each block is equal to N_E .
9. At each step below, the left, upper, down and right blocks used are just those stored before.
10. Then, the procedure is reversed: the left, upper, down and right blocks grow up while the center block retrieves until the number of sites in it is

just 5 sites. Similarly, the center blocks used are those stored as they have grown up before.

The image of the superblock at the end of these iterations is: four blocks representing a maximum of effective sites plus a center block with just 5 sites.

In order to improve accuracy of the results, a number of sweep cycles are needed, keeping fixed the system size. Due to the geometry of the present system, it was necessary for us to adjust the process of sweeping, the standard process being useless. Effectively, each sweeping cycle consists of two parts:

1. The left (right) and upper (down) blocks will retrieve down to their minimum size N_E , and the stored ones are used, while the center block grows up, using the procedure below, until its maximum number of sites is reached.
2. Then, a new set of operators corresponding to the left (right) and upper (down) blocks are generated, while the center block matrices are picked up from the stored ones.

After repeating these two steps many times, energy results will converge to the more accurate values that can be obtained by DMRG procedure.

III. Results

We consider the simple Anderson Hamiltonian in site representation:

$$H = \sum_i \varepsilon_i |i\rangle\langle i| + \sum_{\langle i,j \rangle} V |i\rangle\langle j| \quad (9)$$

with orthonormal states $|i\rangle$ corresponding to electrons located at sites i . V is the constant nearest-neighbor transfer integral with unit value and ε_i a site-diagonal random variable governed by a *normal* probability distribution *i.e.*

$$P(\varepsilon_i) = \begin{cases} \frac{1}{W}, & |\varepsilon_i| \leq \frac{W}{2} \\ 0, & \text{otherwise} \end{cases}$$

W is the disorder strength. Other probability distributions, such the Gaussian one, can be also used.

Despite its simplicity and since it was suggested by P.Anderson [9], the model has been widely used to study spectral and localization properties of disordered structures [10, 11], metal-insulator transition induced by disorder [12, 13], transport in general topologically disordered media [14], multifractal aspects of wavefunctions [15, 16] for interacting and non-interacting electron systems.

We begin our investigation with an ordered structure *i.e.* $\varepsilon_i = \varepsilon$. Unfortunately, there are no theoretical results to compare with; therefore, it is necessary to obtain the ground state and few excited states energies by exact diagonalization.

Table 1: The ground, first and second excited states energies $E_0(N)$, $E_1(N)$ and $E_2(N)$ for a free particle on a tight-binding model in a two-crossed chains, computed using exact diagonalization (ED) and DMRG method. The value of the diagonal entries in the diagonalized matrices is 2.0.

Method	N	E0(N)	E1(N)	E2(N)
ED	105	-0.309401076758301	$1.352328451610949 \times 10^{-2}$	$1.352328451611478 \times 10^{-2}$
DMRG	105	-0.309401076758301	$1.352328451611124 \times 10^{-2}$	$1.352328451611313 \times 10^{-2}$
ED	425	-0.309401076758508	$8.619875459942861 \times 10^{-4}$	$8.619875459979135 \times 10^{-4}$
DMRG	425	-0.309401076758506	$8.619875460086855 \times 10^{-4}$	$8.619875460089741 \times 10^{-4}$
ED	905	-0.309401076758518	$1.915318921536133 \times 10^{-4}$	$1.915318921562604 \times 10^{-4}$
DMRG	905	-0.309401076758502	$1.915318922078220 \times 10^{-4}$	$1.915318922102459 \times 10^{-4}$
ED	1465	-0.309401076758482	$7.327654175460374 \times 10^{-5}$	$7.327654175659017 \times 10^{-5}$
DMRG	1465	-0.309401076758503	$7.327654180964834 \times 10^{-5}$	$7.327654181053537 \times 10^{-5}$
ED	2025	-0.309401076758501	$3.839568650589582 \times 10^{-5}$	$3.839568651057789 \times 10^{-5}$
DMRG	2025	-0.309401076758502	$3.839568654973506 \times 10^{-5}$	$3.839568655256073 \times 10^{-5}$
ED	2505	-0.309401076758508	$2.510520401701136 \times 10^{-5}$	$2.510520402393568 \times 10^{-5}$
DMRG	2505	-0.309401076758506	$2.510520404624172 \times 10^{-5}$	$2.510520404886720 \times 10^{-5}$
ED	3065	-0.309401076758504	$1.677677228672380 \times 10^{-5}$	$1.677677230021150 \times 10^{-5}$
DMRG	3065	-0.309401076758505	$1.677677232041186 \times 10^{-5}$	$1.677677232175863 \times 10^{-5}$
ED	4025	-0.309401076758491	$9.732859440333661 \times 10^{-6}$	$9.732859445854112 \times 10^{-6}$
DMRG	4025	-0.309401076758504	$9.732859465153467 \times 10^{-6}$	$9.732859468420359 \times 10^{-6}$

Thus, results for the ground state, first and second excited states, obtained with both methods, are given in table 1. The number of targeted states is $N_E = 3$. Five sweeps are

generally sufficient to reach convergence. As it can be seen from the table, a high degree of agreement exists between exact diagonalization results and our DMRG

results for the ground state; it ranges from complete agreement (in the order of computational material) for a system size equal to 105 sites (15 digits) to 12 digits when the size of the system exceeds 4000 sites. For first and second excited states energies, the agreement is still significant, but in a bit less degree. In fact, for a system of 105 sites, which is relatively small, the agreement between the methods is up to 13 digits and it is apparently kept at this level in the case of a system size exceeding 4000 sites. Certainly, the decaying accuracy of results as the system size increases is still a general behavior of DMRG method, though results do not make it so clear. It is essentially due to our limiting computational facilities to deal with much larger systems.

By introducing disorder, *i.e.* ε_i are randomly distributed, the symmetry of left, right, up and down blocks is lost, and we have to renormalize all blocks separately. As it is just a matter of comparison of our results with those obtained by exact diagonalization, we restrict our study to a single value of W , taken to be equal to $W = 2.0$. Table 2 displays results of the first three lowest energies of a disordered structure obtained by both exact diagonalization and DMRG procedure. From the table we can see an accurate results obtained by our calculations compared to those obtained by exact diagonalization (up to 12 digits for a system with 2,425 sites), although the size of the structures is not so big to be considered as representing real materials. This is due in first place to computational restrictions, which were, let's remind, the major instigator to explore other ways in dealing with such huge systems.

Nevertheless, regarding the behavior of our results for those relatively small sizes, we may think that accuracy, by its decreasing aspect when system size increases, will not be completely lost before a considerable size is reached.

In other hand, this procedure enables us to obtain the ground state of a non-interacting disordered system by just multiplying the ground state value by the number of sites of the system (one electron per site). This value could be a rough estimation of energy scale for the ground state of an interacting disordered system.

IV. Conclusion

In this paper, we presented a DMRG procedure extension to compute low states energies of a two disordered crossed chains within the tight-binding model suggested by P. Anderson. The purpose of this work was to try to bring a different insight on a major challenging problem vis-à-vis the application of the DMRG procedure to systems with geometry other than 1-d. Instead of the standard two-blocks configuration, we have adopted a five-blocks configuration (four environment blocks and a system block in-between), with a bit different way to achieve warm-up phase and sweep cycles. Results obtained have shown that the new procedure works with a high precision within a certain accuracy. They have also shown a "decaying accuracy as size increases" behavior, proper to standard DMRG.

The present procedure can be applied to many-body problems (spin systems, fermionic and bosonic systems) but, unfortunately, it seems to be, as we have tried it, a big memory and time consumer.

Table 2: The ground, first and second excited states energies $E_0(N)$, $E_1(N)$ and $E_2(N)$ for a free particle on a tight-binding model in a two-crossed chains, computed using exact diagonalization (ED) and DMRG method. The disorder strength W is equal to 2.0.

Method	N	E0(N)	E1(N)	E2(N)
ED	105	-2.33492839367123	-2.31256015487412	-2.27633450482704
DMRG	105	-2.33492839248340	-2.31256015458150	-2.27633450453549
ED	425	-2.62707526909553	-2.51368257944855	-2.49551862249973
DMRG	425	-2.62707353842147	-2.51368257944855	-2.49551862249973
ED	825	-2.74034137548984	-2.66488808899811	-2.62707526909553
DMRG	825	-2.74034137548807	-2.66484686948334	-2.62707526909553
ED	1225	-2.68329769657425	-2.66115344781251	-2.63257708999018
DMRG	1225	-2.68329769655407	-2.66115344781251	-2.63257708999017
ED	2425	-2.64472106170087	-2.63084212954662	-2.61585544521942
DMRG	2425	-2.64472106170071	-2.63084212954661	-2.61585544521941
ED	3225	-2.74712495427613	-2.61737491050982	-2.59050557867426
DMRG	3225	-2.74712485946028	-2.61736733389125	-2.59050557867427

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