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Calculation of the Quantum Entanglement Measure of Bipartite States, Based on Relative Entropy, Using Genetic Algorithms

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Quantum entanglement is an enigmatic and powerful property that has attracted much attention, since it provides new means of communication, such as quantum cryptography, quantum teleportation and superdense coding, and quantum computation. Therefore, the measure of entanglement of composite systems becomes crucial. For pure bipartite states the von Neumann entropy is a good measure and it is easily calculated; however, to quantify the entanglement of mixed states is a harder task. Some measures have been proposed, among them one based on relative entropy. This measure needs a minimization procedure. In this paper, we present an algorithm to calculate the quantum entanglement measure based on relative entropy, in which the required minimization procedure is done using a genetic algorithm. The main advantage of using a genetic algorithm is it is easier to implement than gradient methods are when the number of parameters is very large.

Key Words: quantum entanglement measures; relative entropy; genetic algorithms.

1. INTRODUCTION

In the last decade quantum information theory has attracted a lot of attention due to the possibility it provides for new ways of communicating without classical counterparts, such as quantum cryptography [1] and quantum teleportation [2]. At the heart of this theory is quantum entanglement, that is, the ability of composite quantum systems to show nonlocal correlation [2]. When the composite state is a pure state, σ, the entanglement, E, can be quantified using the von Neumann entropy of one of the individual parts of the system,

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$E \equiv S = -Tr(\rho_a \log \rho_a) = -Tr(\rho_b \log \rho_b)$, where $\rho_a = Tr_b\sigma$ and $\rho_b = Tr_a\sigma$, with a and b being the individual parts. This is a unique measure for bipartite pure-state entanglement, in the sense that any other measure based on asymptotic distillation and dilution of pure-state entanglement agrees on pure states with the von Neumann entropy [3]. However, when the composite state is a mixed state, Φ, that is, a statistical mixture of pure states, the work needed to quantify the entanglement is harder, involving now a set of quantum entanglement measures proposed elsewhere [2, 4–7]. The first two measures proposed were the entanglement of formation, E_F, and the distillable entanglement, E_D. The first one is defined as the least-expected entanglement of any ensemble of pure states that implements the mixed states whose entanglement we want to measure, $E_F(\Phi) = \min \sum_i p_i S(|\sigma_i\rangle\langle\sigma_i|)$, such that $\Phi = \sum_i p_i |\sigma_i\rangle\langle\sigma_i|$. The second one is the maximal number of maximally entangled states that can be obtained, from a mixed entangled state, by using a purification protocol that involves local operations and classical communication between the parties, and its value depends on the protocol of purification used. Any other entanglement measure, obeying certain natural axioms (two of them in the asymptotic regime), must be confined between E_F and E_D, $E_D \leq E \leq E_F$ [8]. Among them, one of the most direct and most used is the measure based on relative entropy. In order to calculate this measure, we need to search for the minimal relative entropy between the entangled state whose entanglement we want to quantify and all other possible disentangled states [5]. This minimal value can be found by evaluating numerically the gradient of the relative entropy and moving in the opposite direction of the gradient [6]. However, since the number of parameters is very large, this may not be an easy task, albeit, in the problem in question, there is only a global minimum [6]. In this paper, we use the computational technique named genetic algorithm to find the disentangled state that minimizes the relative entropy. This technique has been used successfully in several kinds of problems where the search for a minimal or a maximal value is necessary, even when local minima are present.

2. QUANTUM ENTANGLEMENT MEASURE

As mentioned earlier, we use relative entropy to calculate the entanglement, E. This measure is equal to the von Neumann reduced entropy when applied to pure states and it is an upper bound on the distillable entanglement. It was introduced by Vedral and coworkers [2, 5, 6] and, briefly, it can be described as follows: The entanglement of a composite quantum state Γ can be given by the minimal distance between it and a disentangled state,

$$E(\Gamma) = \min_{\rho \in d} D(\Gamma \parallel \rho), \tag{1}$$

where d is the set of all possible disentangled state. For distance D, not necessarily a metric, we can use the quantum relative entropy, given by [2, 5, 6]

$$D(\Gamma \parallel \rho) \equiv S(\Gamma \parallel \rho) = \mathrm{Tr}(\Gamma \ln \Gamma - \Gamma \ln \rho), \tag{2}$$

where Tr denotes the trace operation. Since we must search for the solution among all possible disentangled states, we use the most general formula of a disentangled state. For a

bipartite state, in which we concentrate our attention, the most general formula is [6]

$$\rho = \sum_{i=1}^{16} p_i \left(\rho_a^i \otimes \rho_b^i\right), \tag{3}$$

where the coefficients p_i obey the normalization condition

$$\sum_{i=1}^{16} p_i = 1. \tag{4}$$

Each p_i can be obtained using the parameterization [6]

$$p_i = \left[\sin(\psi_{i-1}) \prod_{j=i}^{15} \cos(\psi_j)\right]^2, \quad \text{with } \psi_0 = \pi/2. \tag{5}$$

Finally, ρ_a^i and ρ_b^i are pure states of the form

$$\rho_a^i = \begin{bmatrix} \cos^2(\theta_i) & \cos(\theta_i)\sin(\theta_i)\exp(i\xi_i) \\ \cos(\theta_i)\sin(\theta_i)\exp(-i\xi_i) & \sin^2(\theta_i) \end{bmatrix}, \tag{6}$$

$$\rho_b^i = \begin{bmatrix} \cos^2(\varphi_i) & \cos(\varphi_i)\sin(\varphi_i)\exp(i\phi_i) \\ \cos(\varphi_i)\sin(\varphi_i)\exp(-i\phi_i) & \sin^2(\varphi_i) \end{bmatrix}. \tag{7}$$

For each i, in Eq. (3), we have five variables: θ_i, ξ_i, φ_i, ϕ_i, and p_i; hence, the sum (3) has 80 variables. However, due to Eq. (4), only 15 p_is are independent; therefore, there are 79 parameters that need to be varied in order to find a minimal value of Eq. (1).

3. GENETIC ALGORITHMS

A genetic algorithm is a computational technique based on the evolution of the species. A possible solution to the problem is coded in a binary string, called a chromosome. An initial population of chromosomes is created (randomly) and processed by natural operators: natural selection, reproduction (*crossover*, exchange of parts of the binary string between chromosomes, and *mutation*, inversion of one of the bits of the binary string; for both, the position where the exchange and inversion takes place is chosen randomly), and evaluation of the fitness (how good the solution is). A good understanding of genetic algorithms can be obtained in Ref. [9]. With these rules, the good features of one solution can be transmitted to the next generation of chromosomes and better solutions can be found. Natural selection and reproduction are probabilistic stages and, hence, a genetic algorithm is a random process. In this way, we cannot predict when the best solution will be found and, therefore, we set a number of generations after which the program finishes.

4. SIMULATIONS

In our program we coded each angle in Eqs. (5)–(7) in a string of 10 bits, where the string 000 (hex) corresponds to the angle 0 rad and the string 3FF (hex) corresponds to the angle 2π rad. One chromosome is obtained by placing the 79 strings together, in sequence, and,

therefore, it has 790 bits. With this arrangement, our space of solutions has 2^{790} elements, making a brute-force method impossible, at least with the velocity of the present computers. The initial population has 150 chromosomes and the number of generations allowed depends on the accuracy desired. Using a larger number of bits per string, or a large number of generations, improves the precision, but the computational cost increases and the simulation becomes slower. The natural selection is done by a tournament in which we choose randomly three members of the population and the one that has the best fitness among them goes to reproduction. This step is repeated 113 times (60% of the initial population). In the reproduction we use a two-point crossover, with the crossover rate equal to 0.65, and mutation, with the mutation rate equal to 0.008. Aiming to increase the velocity of convergence of the algorithm, we employ elitism of the two best chromosomes; that is, they are guaranteed into the next generation. Finally, the fitness function is the proper quantum relative entropy, Eq. (2), since it is always positive. We tested our program using the Werner states [6, 7]

$$W = F|\psi^-\rangle\langle\psi^-| + \frac{1-F}{3}(|\psi^+\rangle\langle\psi^+| + |\phi^-\rangle\langle\phi^-| + |\phi^+\rangle\langle\phi^+|), \tag{8}$$

$$W = F\begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0.5 & -0.5 & 0 \\ 0 & -0.5 & 0.5 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} + \frac{1-F}{3}\begin{bmatrix} 1 & 0 & 0 & 0 \\ 0 & 0.5 & 0.5 & 0 \\ 0 & 0.5 & 0.5 & 0 \\ 0 & 0 & 0 & 1 \end{bmatrix}, \tag{9}$$

where the states on the right side of Eq. (8) are the states of Bell's base [4] and F, belonging to the interval [0.25, 1], is called fidelity. In Fig. 1 we can see the evolution of the solution of the entanglement for two simulations: The upper curve is for a Werner state with $F = 1$,

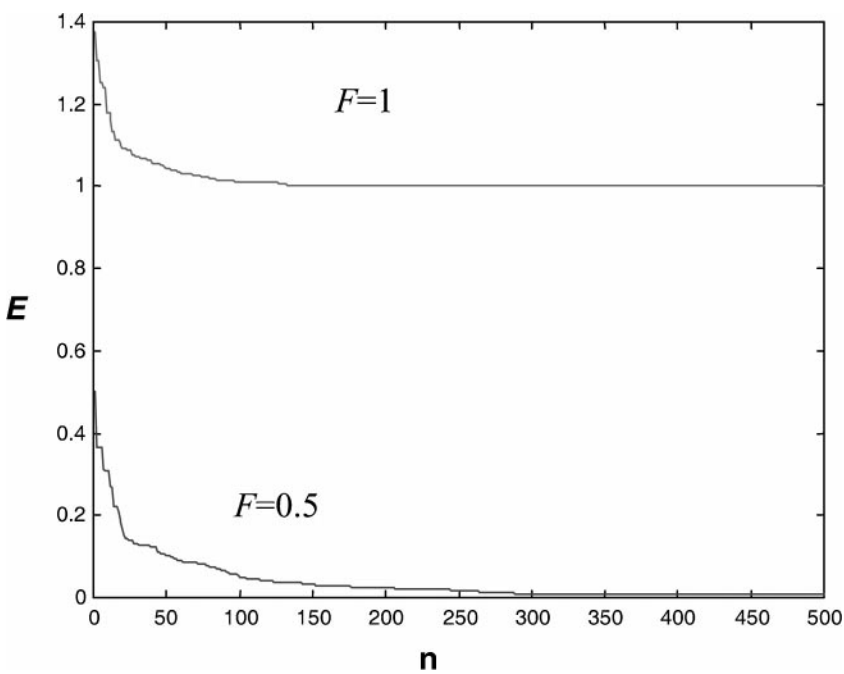

FIG. 1. Evolution of the solution for a maximally entangled state ($F = 1$) and a disentangled state ($F = 0.5$), where n is the number of generations.

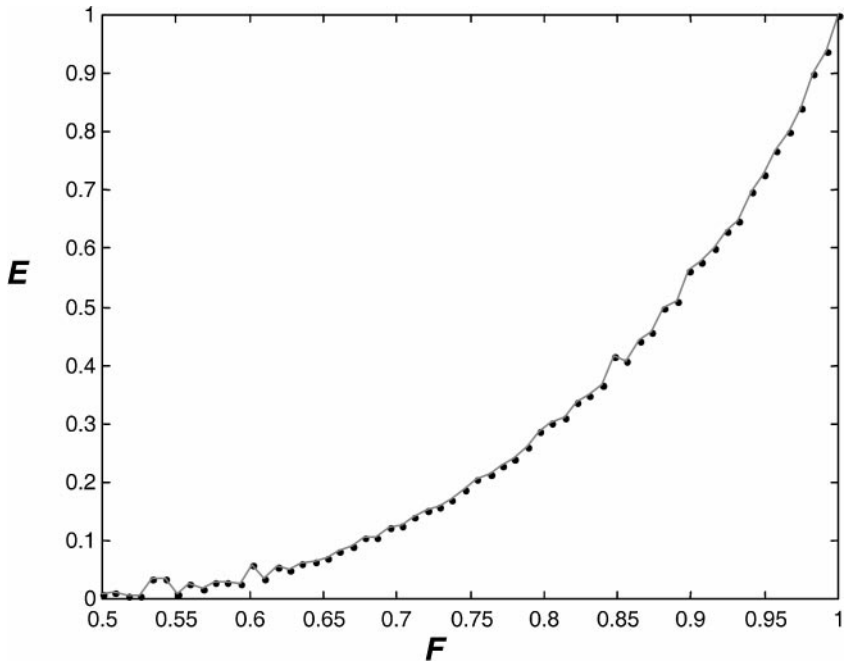

FIG. 2. Entanglement of Werner states (E), using relative entropy, versus fidelity (F) for 500 generations.

which is a maximally entangled state, and the lower curve is for a Werner state with $F = 0.5$, which is a disentangled state. As already mentioned, due to the stochastic nature of a genetic algorithm, we cannot predict in which generation the best solution will be found. This can be seen by comparing both curves in Fig. 1. In Fig. 2, the entanglement, E, for Werner states with F varying in the interval [0.5, 1], using 60 points and 500 generations, is shown. Its smoothness can be improved simply by increasing the number of generations used, as shown in Fig. 3, for 1200 generations, or by taking the average curve over several simulations, as shown in Fig. 4, in which we took the average curve over the simulations with 500, 700, and 1200 generations. The entanglement of Werner states using relative entropy is a well-known curve and the values shown in Figs. 3 and 4 are in good agreement with the curve presented in Ref. [6]. Let us consider now the family of states introduced in Ref. [10],

$$\Gamma = q|\Psi_1\rangle\langle\Psi_1| + (1-q)|\Psi_2\rangle\langle\Psi_2|, \tag{10}$$

$$|\Psi_1\rangle = a|00\rangle + \sqrt{1-a^2}|11\rangle, \tag{11}$$

$$|\Psi_2\rangle = a|10\rangle + \sqrt{1-a^2}|01\rangle, \tag{12}$$

where $0 < q, a < 1$ and the states $|00\rangle$, $|01\rangle$, $|10\rangle$, and $|11\rangle$ form the standard basis. The density matrix, Eq. (10), in the standard basis is

$$\Gamma = \begin{bmatrix} qa^2 & 0 & 0 & qa\sqrt{1-a^2} \\ 0 & (1-q)(1-a^2) & (1-q)a\sqrt{1-a^2} & 0 \\ 0 & (1-q)a\sqrt{1-a^2} & (1-q)a^2 & 0 \\ qa\sqrt{1-a^2} & 0 & 0 & q(1-a^2) \end{bmatrix}. \tag{13}$$

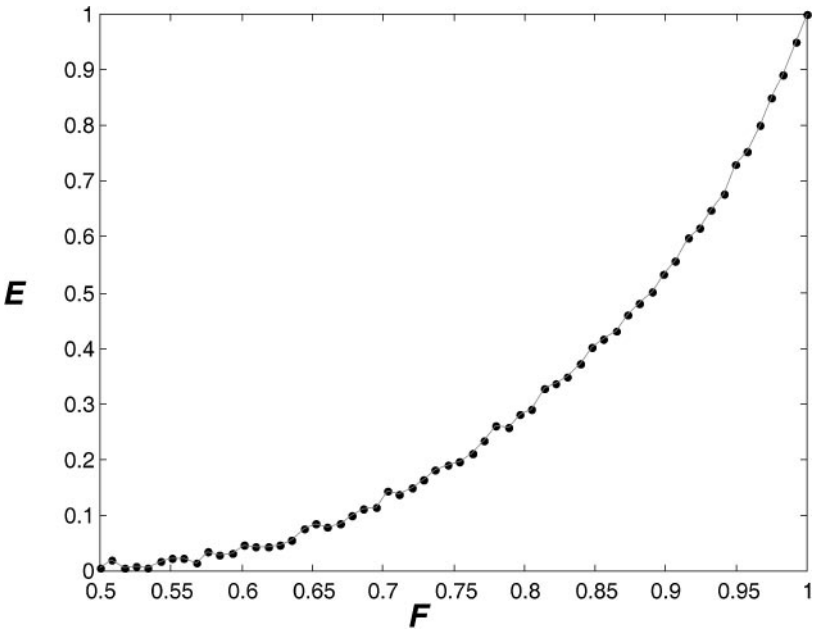

FIG. 3. Entanglement of Werner states (E), using relative entropy, versus fidelity (F) for 1200 generations.

In Fig. 5, we show the entanglement of formation (continuous line), E_F, and the entanglement based on the relative entropy (dotted line), E, calculated by our genetic algorithm. In this simulation we used $a = 0.75$ and q varying in the interval (0, 1). As we can see in Fig. 5, the entanglement of formation and the relative entropy have the same shape but, as

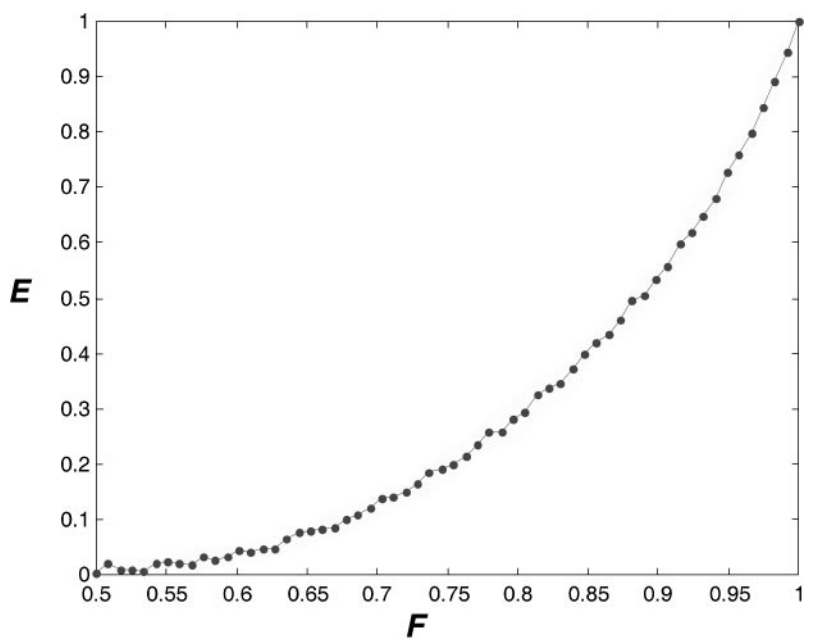

FIG. 4. Average curve (500, 700, and 1200 generations) for the entanglement of Werner states (E), using relative entropy, versus fidelity (F).

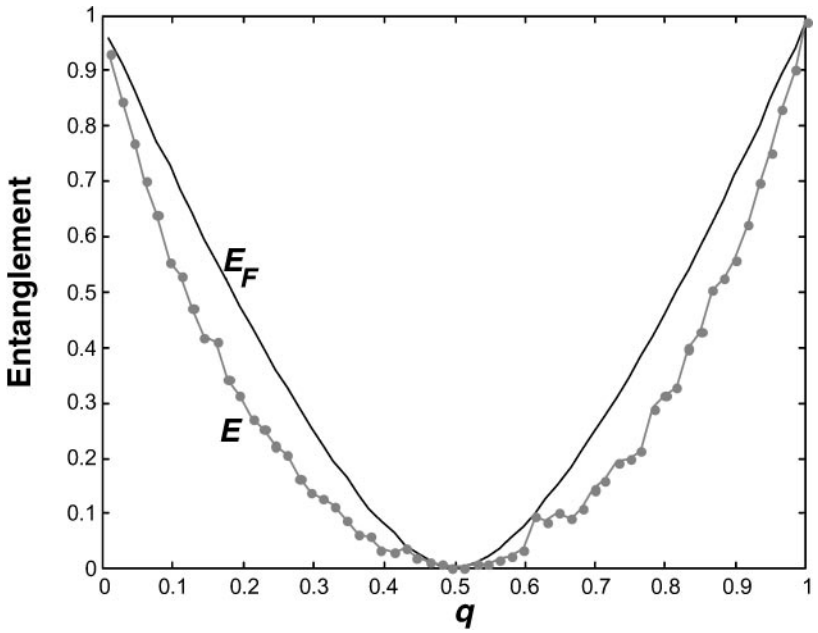

FIG. 5. Entanglement of formation (continuous line) and minimal relative entropy (dotted line) for the state in Eq. (13), with $a = 0.75$.

expected, the former is larger than the latter. Again, the smoothness of the curve shown in Fig. 5 can be improved by increasing the number of generations (3000) or the size of the population of chromosomes (75), but the price is a longer time needed for simulation.

5. ADVANTAGES AND DISADVANTAGES OF USING GENETIC ALGORITHMS

The implementation of a genetic algorithm is quite easy; in fact, with a smart encoding of the density matrix parameters of the disentangled state in a binary string, just a few lines of program can be implemented to solve the problem. The main drawback of a genetic algorithm is its velocity. As mentioned earlier, a genetic algorithm is a random process and we never know when the best solution will be achieved. We can work with the crossover rate, the type of crossover (one point or two points), and the population size, among other parameter, in order to increase the velocity of convergence of a genetic algorithm. We can also adopt some strategies to improve its performance. For example, the relative entropy can assume values much larger than 1, the maximum value of the entanglement. We can force the initial population to have a minimal number of chromosomes with a relative entropy (related to the state whose entanglement we wish to measure) at least not much larger than 1. We can also adopt the entanglement of formation of the state to be measured, which can be calculated analytically [11], as a stop criterion, since the relative entropy cannot be larger than that of the entanglement of formation. For bipartite states, the gradient method implemented in Ref. [6] is faster than our genetic algorithm. When we consider entangled systems with more than two subsystems (all of them two-level systems), called multiqubit systems, the number of parameters in the formula of a general disentangled state increases [6] and the problem may have local minima (this is not known yet). If they really exist, we

believe that in multiqubit systems a genetic algorithm is a good choice because it is robust against local minima. Furthermore, if a criterion of separability for the multiqubit system considered exists, a formulation for the most general disentangled state, for that system, is not necessary since we can discard the entangled states eventually created during the search for the solution. At last, a computer program to calculate the entanglement based on the relative entropy for multiqubit systems is almost equal to the computer program used to calculate the entanglement for bipartite states. The difference is the encoding of a disentangled state of the multiqubit system in a chromosome. This will be longer, since there are more state parameters to be encoded. As quoted before, the longer the chromosome, the slower the computer program runs (larger matrices are handled).

6. CONCLUSIONS

We explained, briefly, the quantum entanglement measure based on relative entropy. Following that, we used a technique of computational intelligence, named genetic algorithm, as an alternative method for searching the disentangled state that is at the minimal distance, in the sense explained in the text, from the state whose entanglement we want to measure. Our computer program showed results that agree with results presented in the literature and it can be used as a tool for numerical studies of quantum communication systems, based on quantum entanglement, or to find properties of the quantum entanglement. The major advantage of using a genetic algorithm is its easy implementation and its ability to find the best solution, even when there are local minima. The major disadvantage is its low velocity.

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