Genetic Algorithm for SU(2) Gauge Theory on a 2-Dimensional Lattice

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A hybrid algorithm is proposed for pure SU(N) lattice gauge theory based on Genetic Algorithms (GA)s and the Metropolis method. We apply the hybrid GA to pure SU(2) gauge theory on a 2-dimensional lattice and find the action per plaquette and Wilson loops being consistent with those given by the Metropolis and Heatbath methods. The thermalization of this newly proposed Hybrid GA is quite faster than in the Metropolis algorithm.

1. Introduction

The study of Genetic Algorithms based upon the theory of evolution originates with John Holland [1] in the mid-1970s. Applications in various fields have been proposed. In generic GAs, potential solutions are represented as symbolic strings and operators are defined on the analogy of selection and genetic mechanisms in Nature. A crossover operator of exchanging genes between individuals leads to the special feature of GAs in which discrete points in searching space are treated at once, while normal Metropolis (MP) or heat bath (HB) algorithms treat only one point. We proposed a hybrid GA and applied it to pure SU(2) gauge theory in 2 dimensions. Physical values obtained by our hybrid GAs, such as the action per plaquette and Wilson loops at each $\beta$ are consistent with those given by HBs. Our results show that the distinctive features of this new GAs leads to be the fast thermalization. The short calculation time are accomplished by the special encoding configurations on a lattice.

2. Genetic Algorithms for SU(N) Lattice gauge theory

In the language of GAs, a whole lattice corresponds to an individual, and the information on a field configuration is encoded in bit patterns which are treated as chromosome. The evaluation (fitness) function is the usual lattice action of SU(N) lattice gauge theory,

$$S[U] = \Sigma_p \left(1 - \frac{1}{N} ReTr U_p \right),$$

where $U_p$ is the element of SU(N) defined on a plaquette $p$ and $\beta$ is a coupling constant multiplying $S$ in the Boltzmann factor.

We would like to call our newly proposed algorithm “Hybrid Genetic Algorithm” (HGA), because it mixes a population update step of GAs with a normal Metropolis step applied to all members of the population. It combines heuristic methods for local search with GAs for global search with their respective advantages. In our algorithm, the GA starting from the $t^{th}$ generation is followed by the Metropolis step, leading to the next $(t+1)^{th}$ generation, namely

$$P_t \xrightarrow{\text{selection}} P_{\text{gene pool}} \xrightarrow{\text{recombination}} P'_{\text{gene pool}} \xrightarrow{\text{Metropolis}} P_{t+1},$$

where $P_t$ denotes the population at $t^{th}$ generation and $P_{\text{gene pool}}$ represents a number of $2N_{\text{pop}}$ genomes selected by Stochastic Universal Sampling which ensures unbiased selection [2]. In this scheme, among all genomes of $P_t$ laid on a pie chart with an area proportional to their fitness, $2N_{\text{pop}}$ members are picked up simultaneously into a gene pool by a single spin of a roulette wheel with $2N_{\text{pop}}$ equally-spaced pointers. Two genomes taken from the gene pool are recombined by the crossover operator to give two offsprings (children). The children are subject to a mutation step which consists of bitwise random flips described by a (small) mutation rate. To establish thermal equilibrium, we set up an accept/reject criterion in the next stage to fulfill the detailed balance condition: one does not replace automatically old individual of the previous
generation by new one but the better parent is replaced by the better child when the following condition is satisfied:

$$\min\{1, e^{-\beta (S_{\text{child}} - S_{\text{parent}})}\} > \xi, \quad (3)$$

where $\xi$ is a uniform random number. The population $P_{t+1}$ is then the result of one normal Metropolis step.

3. Thermalization

In order to compare the thermalization rate with MP, a 2-point crossover scheme is adopted with a crossrate 0.65 and a mutation rate 0.008. The population sizes are 16 for $\beta = 0.5$, 64 for $\beta = 2.0$ and 128 for $\beta = 8.0$. Fig. 1 shows the results of these runs for three $\beta$ values. In each figure, the horizontal dotted line shows the averaged action per plaquette for this $\beta$ over the last 1000 sweeps of 30,000 sweeps by the Heat-bath method. Square dots show the time history corresponding to our HGA, the lines show the MC history of pure MP. The convergence to equilibrium (the target values given by HB) for the runs of our HGA is faster in CPU time than MP. In particular, for large $\beta$ it is quite fast not being stuck due to low acceptance. The approach to equilibrium in the run with $\beta = 0.5$ is, however, non-monotonous due to hard fluctuations. In the case of small $\beta$s, most genomes in a population have very similar actions, which could have very similar genes or very different ones, an unexpected change of action is likely to be produced and accepted by the crossover operation. To avoid strong fluctuations caused by bad crossing, a closer analysis of the correlation between individuals is needed. Note that while MP treats just one lattice, HGA treats a population size of lattices at once.

4. Recombination Schemes and Genetic Parameters

We have tested two recombination schemes uniform crossover (UC) and 2-point crossover (2C) with respect to their effectivity. UC in which every locus of a genome is randomly occupied by a gene from one of the parents with a probability $p$ (or from the other with $1 - p$), leads to an increased diversity of offsprings. In the lattice gauge theory it can lead to an increase of action, caused by a frequent mismatch of the links. In $N_c$-point crossover a new genome is created from partitions of parents genomes. It has less advan-
5. Conclusion

We have designed a HGA and applied it to 2D SU(2) lattice gauge theory and calculated the action per plaquette and the Wilson loops. The results are shown in Fig. 3. For small $\beta \leq 2.0$ the action per plaquette obtained by HGA have been averaged over the last 32 generations out of 64 generations keeping a population size of 32, while for large $\beta$s (\geq 2.5) over 16 generations out of 32 generations with a population size of 128. The average of Wilson loops obtained with MP were taken over 1000 iterations of the best genome among the population in the 50th generation of HGA for $\beta$s between 2.0 \leq \beta \leq 4.0$ (of the best genome in the 30th generation for $\beta \geq 4.5$). Over the whole $\beta$ region the result of the physical averages are consistent with HB. They are obtained by HGA faster than by HB and normal MP, without any further optimization of the GA part of our procedure. We have shown the possibility and effectiveness of GA schemes for SU(N) lattice gauge theory. A more detailed discussion and analysis is needed to demonstrate the detailed balance properties. There is also enough room for further optimization of our algorithm.

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