

Understanding and improving the Wang-Landau algorithm

Chenggang Zhou* and R. N. Bhatt

Department of Electrical Engineering, Princeton University, Princeton, New Jersey 08544, USA

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We present a mathematical analysis of the Wang-Landau algorithm, prove its convergence, and identify sources of errors and strategies for optimization. In particular, we found the histogram increases uniformly with small fluctuations after a stage of initial accumulation, and the statistical error is found to scale as $\sqrt{\ln f}$ with the modification factor f . This has implications for strategies for obtaining fast convergence.

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The Wang-Landau (WL) algorithm [1] has been applied to a number of interesting problems [1–6]. It overcomes some difficulties present in other Monte Carlo (MC) algorithms such as critical slowing down, and long relaxation times due to frustration and complex energy terrain. Similar to the Metropolis algorithm, the WL algorithm is a generic algorithm, independent of the details of the physical system. Many methods have been suggested to improve the algorithm for certain types of systems [7–9]. The same mechanism also appears in the recent research of molecular dynamics simulations [10]. Among the studies to characterize and improve the efficiency of the algorithm, Dayal *et al.* [11] shows the WL algorithm considerably reduces the tunneling time, and Trebst *et al.* [12] proposed an algorithm that performs better in terms of tunneling time. However, the WL algorithm has been used as an empirical method. Many important questions still remain unanswered: (i) How is the flatness of the histogram related to the accuracy? (ii) What is the relation between the modification factor and error? (iii) How does the simulation actually find out the density of states? The convergence of the WL algorithm should be guaranteed by a generic principle, in the same sense as the detailed balance assures the convergence of the Metropolis algorithm. However, the WL algorithm is different from the Metropolis algorithm, since it is not a Markov process.

In this paper we present our study of this algorithm from an analytical approach, and try to answer those questions raised above. Our analysis provides a proof of the convergence of the method, estimation for the errors and the computational time, along with some strategies for optimization and parallelization.

The goal of the WL algorithm is to accumulate knowledge about $\rho(E)$ during a Metropolis-type MC sampling. The Metropolis-type random walk is characterized by an acceptance ratio $\min\{1, g(E_j)/g(E_i)\}$, where $g(E)$ is a function of energy, similar to the Boltzmann factor in the usual Metropolis algorithm. E_i and E_j refer to energies before and after this transition. The acceptance ratio biases the free random walk and produces a final histogram $h(E)$, which is related to the

equilibrium distribution of the unbiased random walk $\rho(E)$ by $\rho(E)g(E)=h(E)$, provided that both sides of the identity are normalized. This identity is essentially a result of detailed balance. The WL algorithm divides $g(E_j)$ by a modification factor f after each transition, expecting $g(E)$ to converge to $1/\rho(E)$ and the histogram $h(E)$ to be flat.

$\rho(E)$ is *a priori* unknown in the simulation. We begin our analysis by clarifying the relevant parameters. Suppose the phase space of our physical model is divided into N macroscopic states with density (number of microscopic configurations) $\rho_i > 0$ for macroscopic state i ($i=1, 2, \dots, N$). (These macroscopic states could be labeled by energy, magnetization, or other macroscopic variables.) Each microscopic configuration in the phase space uniquely belongs to one macroscopic state. The histogram $h_i(t)$ with $1 \leq i \leq N$ is defined as the number of visits of each macroscopic state before the t th step of the simulation. Initially $h_i(1)=0$, after macroscopic state k is visited at time t , $h_i(t+1)=h_i(t)+\delta_{ik}$. In the original implementation [1], one record is inserted into the histogram every Metropolis trial flip. However, in addition to the modification factor, we have a second tunable parameter of the algorithm, separation S between successive records in the histogram, defined as the number of trial flips (random steps) that precede each increment of the histogram. S steps of the random walk should be regarded as a single transition from initial macroscopic state i to the final macroscopic state j . The transition from i to j includes S trial flips and each trial flip makes a transition from macroscopic state k_{n-1} to macroscopic state k_n ($k_0=i$ and $k_S=j$) with acceptance ratio $\min(1, \exp\{\ln f[h_{k_{n-1}}(t)-h_{k_n}(t)]\})$. At time t , macroscopic state k has a probability $p_k(t)$ to be picked out by the simulation. $p_k(t)$ is normalized so that vector $p(t) \in V_N$, where $V_N = \{x \in [0, 1]^N, \sum_{k=1}^N x_k = 1\}$ is an N -dimensional simplex. In the following derivation, we assume S is larger than the autocorrelation length of the random walk, thus i and j can be considered as independent random macroscopic states. The effect of autocorrelation will be discussed later. Although this assumption differs from real simulations, it is reasonable since the particular model under study is not specified. It is also asymptotically accurate for any model when S is large enough. With this assumption, the probability distribution $p(t)$ has an explicit expression,

$$p_i(t) = Z(t)^{-1} (\rho_i / \theta_i) f^{-h_i(t)}, \quad (1)$$

where $Z(t) = \sum_{k=1}^N (\rho_k / \theta_k) f^{-h_k(t)}$ is the normalization constant, and without loss of generality, we insert an initial guess θ_i

*Present address: Computer Science and Mathematics Division, Oak Ridge National Laboratory, P.O. Box 2008, MS6164, Oak Ridge, Tennessee 37830-6164, USA; Center for Simulational Physics, University of Georgia, Athens, Georgia 30602, USA.

into the simulation. In fact $f^{h_i(t)}$ serves as a guess for the simulation after t . Similarly the simulation can start from some “existing knowledge” represented by θ_i . If nothing is known about the density of states, then we start with $\theta_i=1$. With the probability distribution Eq. (1), the macroscopic state k has the probability $p_k(t)$ to be picked out in the next step. Once this happens, $p(t)$ is changed to $p(t+1)$ by

$$p_i(t+1) = p_i(t)f^{-\delta_{ik}}[1 - p_k(t) + p_k(t)f^{-1}]. \quad (2)$$

Here the Kronecker δ only suppresses $p_k(t)$ by a factor of f and the denominator comes from the change in $Z(t+1)$ such that the normalization of probability is preserved. We point out that the evolution of $p(t)$ is a Markov process, although the WL algorithm is not, because it makes references to its entire history.

We will prove that the $p(t)$ is attracted to the vicinity of uniform distribution ($p_i^{(0)}=1/N$) in the simulation. For this purpose, we define a measure of the difference between $p(t)$ and the uniform distribution $p^{(0)}$ by

$$\mu(t) = N \ln N + \sum_{i=1}^N \ln p_i(t). \quad (3)$$

One can check that $\mu(t) \leq 0$ and $\mu(t)=0$ only when $p(t) = p^{(0)}$. After the macroscopic state k is picked out, $\Delta\mu(t) = \mu(t+1) - \mu(t)$ is given by

$$\Delta\mu(t) = -\ln f - N \ln[1 - p_k(t) + p_k(t)f^{-1}]. \quad (4)$$

Obviously $\Delta\mu(t) > -\ln f$, and when $p_k(t) > (1-f^{-1/N})/(1-f^{-1}) \approx \ln f/N(1-f^{-1})$ (approximately $1/N$ when $f \rightarrow 1$), $\Delta\mu(t)$ is always positive. This shows that $\mu(t)$ increases when the simulation picks out macroscopic states with probabilities above average. However, there is a probability for $\mu(t)$ to decrease, in particular, at the center of attraction [$p(t)=p^{(0)}$], $\Delta\mu(t)$ is negative. As a result, rather than converging to the uniform distribution, $p(t)$ is expected to either fluctuate around the uniform distribution, or go away from it. Actually the second situation does not happen. To prove this, we first show that the expectation value $\mathbf{E}_{p(t)}\{\Delta\mu(t)\}$ (averaged over all possible moves) has a lower bound determined by $p(t)$: Using Eq. (4), the expectation value becomes

$$\mathbf{E}_{p(t)}\{\Delta\mu(t)\} = -\ln f + N \sum_{k=1}^N p_k(t) \ln \frac{1}{1 - p_k(t)(1 - f^{-1})}.$$

Since $0 < p_k(t)(1-f^{-1}) < 1$, we use the inequality $\ln(1-x)^{-1} > x$ for $x \in (0, 1)$ to give a lower bound for the logarithm, which turns out to be

$$\mathbf{E}_{p(t)}\{\Delta\mu(t)\} > -\ln f + N(1-f^{-1}) \sum_{k=0}^N p_k^2(t).$$

Typically $p_k(t)$ is of order $1/N$, where N is a large integer, so this lower bound is very close to the actual value. This lower bound can be further expressed in terms of the Euclidean distance between $p(t)$ and $p^{(0)}$, since $\|p(t) - p^{(0)}\|^2 = \|p(t)\|^2 - 1/N$, due to the normalization of $p(t)$. Therefore we have *Theorem 1*. If $\|p(t) - p^{(0)}\|^2 = N^{-1}[(1-f^{-1})^{-1} \ln f - 1] + \epsilon$, with

$\|\cdot\cdot\|$ being the Euclidean distance, the expectation value of $\Delta\mu(t)$ averaged over N possible moves is bounded from below $\mathbf{E}_{p(t)}\{\Delta\mu(t)\} > N(1-f^{-1})\epsilon$.

Theorem 1 states that for a probability distribution $p(t)$ outside the N -dimensional sphere B_ϵ defined by its condition, $\mu(t)$ always has a tendency to increase. Next we consider an ensemble of simulations, whose $p(t)$ has a certain distribution at time t , $F_t(p)$. The ensemble-averaged $\mu(t)$ is defined as $\langle\mu(t)\rangle = \int F_t(p)\mu(p)dp$. (Note in the integrand we treat μ as a function of p instead of time t .) We want to show that the evolution of $F_t(p)$ brings every simulation in the ensemble into the sphere B_ϵ . Define $D(p, p')$ as the probability of bringing distribution p' to p after one step. Obviously, $F_{t+1}(p) = \int_{V_N} D(p, p')F_t(p')dp'$, where the integral over p' is restricted to the simplex V_N .

We can express the ensemble average of $\mu(t+1)$, $\langle\mu(t+1)\rangle = \int_{V_N} F_{t+1}(p)\mu(p)dp$, with $F_t(p) : \langle\mu(t+1)\rangle = \iint_{V_N} \mu(p)D(p, p')F_t(p')dp' dp$. As a result of *Theorem 1*, if we assume at time t , every simulation is outside B_ϵ , i.e., $p' \notin B_\epsilon$, then $\int_{V_N} \mu(p)D(p, p')dp > \mu(p') + N(1-f^{-1})\epsilon$. Therefore $\langle\mu(t+1)\rangle > \int_{V_N} [\mu(p') + N(1-f^{-1})\epsilon]F_t(p')dp' = \langle\mu(t)\rangle + N(1-f^{-1})\epsilon$, which is the following corollary: *Corollary 2*. If the distribution F_t does not enter B_ϵ , i.e., $\text{supp}(F_t) \cap B_\epsilon = \emptyset$, then $\langle\mu(t+1)\rangle > \langle\mu(t)\rangle + N(1-f^{-1})\epsilon$.

This result implies that $\langle\mu(t)\rangle$ increases at least linearly as the simulation goes. However, if $\text{supp}(F_t)$ is always outside B_ϵ , $\mu(t)$ is therefore bounded from above by the maximum value of $\mu(p)$ on the boundary of B_ϵ . This contradiction tells us that part of the ensemble has to be pushed into B_ϵ so that $\text{supp}(F_t) \cap B_\epsilon \neq \emptyset$. We can exclude those parts of the ensemble already inside B_ϵ , and apply the same inference to the remaining part of the ensemble that is still outside B_ϵ . No matter where the simulation starts, the conclusion is that $p(t)$ sooner or later goes into B_ϵ . Once $p(t)$ is in the vicinity of $p^{(0)}$, it is unlikely to escape because $\Delta\mu(t)$ has a lower bound $\Delta\mu(t) > -\ln f$. If after a certain step $p(t)$ moves outside B_ϵ , we can immediately use *Corollary 2* to show that it is attracted back into B_ϵ . It is this attraction towards $p^{(0)}$ that reduces the tunneling time of the WL algorithm [11]. When $N(1-f^{-1}) \ll 1$, this attraction is weak, which explains why Ref. [11] finds the tunneling time of the WL algorithm saturates when f is less than a critical value determined by the system size.

When $p(t)$ is trapped near $p^{(0)}$, the histogram shows a uniform growth with fluctuation. $h_i(t) = \log_f(\rho_i/\theta_i) + t/N + r_i(t)$, where $r_i(t)$ is a random number with zero mean. The approximate density of states is measured from the histogram by $\rho_i'(t) = K\theta_i f^{h_i(t)}$, where K is a proper normalization constant. Figure 1 shows three snapshots of the histograms calculating the density of states of a two-dimensional Ising model on a lattice of size 32×32 with periodic boundary conditions. We have used $f=e^4$ in this simulation to reveal the fluctuation of the histogram in Fig. 1. The simulation visits energies (macroscopic states) with high density of states first, then extends the histogram to the whole spectrum. Once the whole spectrum is visited, the histogram grows uniformly with small fluctuation. Two important observations follow the results above: (i) A flat histogram is not

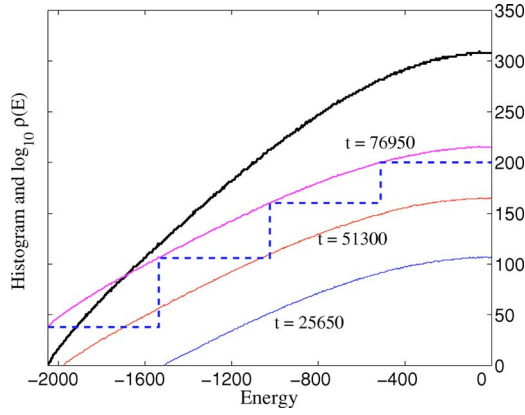


FIG. 1. (Color online) Snapshots of the histogram of a single random walker on a two-dimensional 32×32 Ising model. Three thin curves are histograms of three sequences of lengths labeled in the figure. The thick dark line is the $\rho(E)$ calculated from the last histogram ($t=76\,950$), which overlaps with the exact $\rho(E)$ within the accuracy of the width of the line on this figure. The length of the sequence is just the area under the histogram. The dashed staircase indicates a possible guess for $\rho(E)$ with four energy intervals (see text).

required for convergence; the histogram is ready for calculation of ρ' when it reaches a threshold $h_i(t) \gg \sigma_{r_i}$, for all i 's, where σ_{r_i} denotes the standard deviation of $r_i(t)$. (ii) The statistical error can be reduced by averaging over multiple results obtained with the same f , as well as reducing f . A proper estimation of the statistical error is from the condition of Theorem 1. Since $p(t)$ fluctuates around a ball centered at $p^{(0)}$ of radius $N^{-1/2}\pi(f) = \sqrt{N^{-1}[(1-f^{-1})^{-1}\ln f - 1]}$, we use $\pi(f)$ to give a reasonable estimation of the statistical error. $p(t)$ is related to $\rho'(t)$ by $p_i(t) = C\rho_i\rho_i'^{-1}(t)$, where C is a constant for all i 's. Plugging this into $\|p(t) - p^{(0)}\| \approx N^{-1/2}\pi(f)$, we arrive at

$$\sqrt{\frac{1}{N} \sum_{i=1}^N \left(\frac{NC\rho_i}{\rho_i'(t)} - 1 \right)^2} \approx \pi(f), \quad (5)$$

where NC is a constant allowed by the WL algorithm, which can be absorbed into $\rho_i'(t)$. The left side of this equation is the standard deviation of $\rho_i/\rho_i'(t)$, so an appropriate estimation of the typical relative error $\delta\rho_i'/\rho_i'$ is $\pi(f)$, which scales as $\sqrt{\ln f}$ when f is close to 1. [The difference between the expression here $(\rho' - \rho)/\rho'$ and the standard definition of relative error $(\rho' - \rho)/\rho$ is negligible, when the error is small.] Thus, we expect the fluctuation in the histogram to be $\sigma_{r_i} \approx \pi(f)/\ln f \sim 1/\sqrt{\ln f}$, because $d\rho_i'(t)/dh_i(t) = \rho_i'(t)\ln f$. This has been recently confirmed by numerical tests [13]. Our strategy for a single iteration simulation is to run until a minimum number of visits (at least $1/\sqrt{\ln f}$) have been accumulated for each macroscopic state, followed by measurements separated by a short simulation that decorrelates $r_i(t)$. Usually $1/\sqrt{\ln f}$ visits on each macroscopic state is enough. With K measurements, the statistical error in $\ln \rho_i'(t)$ is reduced to $\sqrt{\ln f/K}$. The total number of records in the histograms is thus at least

$$\sum_{i=1}^N h_i(t) \approx \sum_i \log_f \frac{\rho_i}{\min\{\rho_i\}} + \frac{NK}{\sqrt{\ln f}}. \quad (6)$$

The first term represents the number of records for the simulation to reach every macroscopic state. This term occupies the bulk of the histograms in Fig. 1. The second term of Eq. (6) represents the cost of K uncorrelated measurements. The measurements can be parallelized on a number of processors. The dashed staircase in Fig. 1 shows what happens if the energy is divided into four equal intervals, as Ref. [1] did for parallelization. As the spectrum is divided into four intervals assigned to four separate simulations, an interval with high density of states does not have to wait for those with low density of states to be visited. The histogram represented by the first term of Eq. (6) is reduced to the area of four triangles bounded by the staircase and the last histogram above it in Fig. 1. In terms of saving total computational time, an equivalent strategy is to use the staircase as an initial guess θ_i . Thus, four triangles are filled simultaneously, equivalent to doing four simulations sequentially. Dividing the energy range causes boundary errors [9], while a good initial guess of the functional form of the histogram does not have this problem.

Assuming N is roughly proportional to the total number of degrees of freedom, to the logarithm of the maximum density of states, and to the number of MC steps to generate an uncorrelated visit, the cost of CPU time for the first term in Eq. (6) is of order $O(N^3)$, while the cost of the second term is of order $O(N^2)$. (Logarithmic corrections might be present.) If we use a proper guess θ_i to begin the simulation, the CPU time cost for the first term can be substantially reduced to $O(N^2)$.

Now we discuss the effect of insufficient S that introduces autocorrelation between successive records in the histogram. At first sight, the total number of steps given by Eq. (6) is considerably reduced by using a large f . Multiple measurements also reduce the statistical error more quickly than reducing the value of f , so a small f seems to be unnecessary. However, there are *systematic* errors due to the correlation between adjacent records in the histogram when f is not small, or the separation S not large enough. We illustrate this systematic error in Fig. 2, which shows the total density of states for a fixed magnetization M , $\rho(M)$, of the Ising model on a 4×4 lattice, for which the exact result is: $\log_{10} \rho(M) = \log_{10} C_{16}^{8+M/2} + (1 - \delta_{0M}) \log_{10} 2$. States with M and $-M$ are grouped in the same macroscopic state for better statistics, so M is restricted to be a non-negative even integer. We demonstrate the effect of this correlation in Fig. 2 by showing the result of an extremely biased scheme that restores all 16 spins to total alignment after each record. As expected, the result (shown as downward triangles) is biased towards $M = 16$. The simulation actually calculates the probability of reaching state M starting from $M = 16$ within 16 trial flips, which deviates from the correct density of states. On the other hand, the accuracy of data shown as squares indicates that the desired probability distribution Eq. (1) is produced after 1600 trial flips. The data plotted with diamonds for a smaller f show that the systematic error is also reduced by

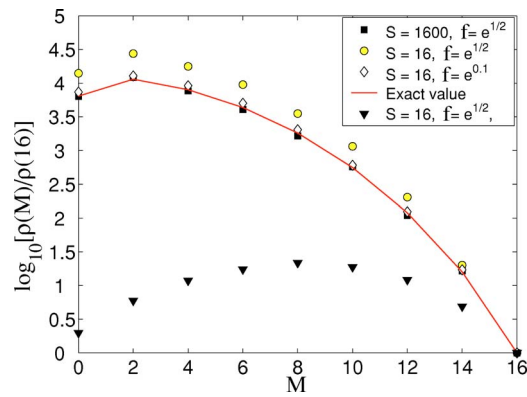


FIG. 2. (Color online) $\rho(M)$, the density of states for magnetization M of 16 Ising spins normalized to $\rho(M=16)$. The solid line connects the exact values, and the symbols were obtained with different parameters f and S as explained in the text. Data was averaged over 100 measurements, so the statistical errors are smaller than the symbols.

letting $f \rightarrow 1$, or equivalently, the minimum S required to eliminate the autocorrelation decreases with f . As an extreme case, if each trial flip is recorded ($S=1$), for the Ising model of Fig. 1, the histogram always grows quickly near $E=0$ and propagates to higher or lower energies very slowly. The systematic error due to the correlation is revealed, when the statistical error is reduced by multiple measurements with a

single f . At this point, either a smaller f , or larger S is necessary to improve the accuracy.

To summarize, we have given a proof of the convergence of the WL algorithm, and analyzed the sources of errors and optimization strategies. We find: (i) the density of states is encoded in the average histogram; (ii) the fluctuation of the histogram, proportional to $1/\sqrt{\ln f}$, where f is the modification factor, causes statistical error, which can be reduced by averaging over multiple $\rho'(t)$; (iii) the correlation between adjacent records in the histogram introduces a systematic error, which is reduced by small f , and also by minimizing the correlation, e.g., using large S , or cluster algorithms [14]. These findings suggest that numerical simulations can start with a large f , e.g., e^4 , and then reduce f in large steps in each stage, e.g., divide $\ln f$ by a factor of 10. Multiple measurements can be made in the final stage to reduce the statistical error effectively. However, results calculated with a single pair of f and S are prone to systematic error. One can extrapolate results calculated with different f and S to $f=1$ or $S=\infty$ to eliminate this error. If the error is believed to be small enough, one can also reduce f to 1 directly, which results in a histogram proportional to $\rho_i/\rho'_i(t)$, which is the ratio of the true density of states to the numerical results.

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