

## Monte Carlo simulation of ice models

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We study a number of Monte Carlo algorithms for the simulation of ice models, and compare their efficiency. One of them, a cluster algorithm for the equivalent three-color model, appears to have a dynamic exponent close to zero, making it particularly useful for simulations of critical ice models. We have performed extensive simulations using our algorithms to determine a number of critical exponents for the square ice and  $F$  models. [S1063-651X(98)09301-5]

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### I. INTRODUCTION

Ice models are a class of simple classical models of the statistical properties of the hydrogen atoms in water ice. In ice, the oxygen atoms are located on a lattice, and each oxygen atom has four hydrogen bonds to neighboring oxygen atoms, giving a fourfold-coordinated lattice. However, as has long been known, the proton (hydrogen atom) which forms a hydrogen bond is located not at the center point of the line between two oxygens, but at a point closer to one of the two. Bernal and Fowler [1] and Pauling [2] proposed that the protons are arranged according to two rules, known as the ice rules: (1) there is precisely one hydrogen atom on each hydrogen bond and (2) there are precisely two hydrogen atoms near each oxygen atom.

Ice models are a class of models mimicking the behavior of systems which obey these rules. The most widely studied ice model is the model on a square lattice in two dimensions. A version of this model was solved exactly by Lieb [3–5]. The exact solution gives us, for instance, the critical temperature and the free energy of the model. However, there are a number of quantities of interest which cannot be obtained from the exact solution, and for these quantities we turn to Monte Carlo simulation.

In this paper we introduce a number of Monte Carlo algorithms for the simulation of ice models, and compare their efficiency. We will show that one of them, the three-color cluster algorithm for square ice described in Sec. V, possesses a very small dynamic exponent (possibly zero), and so suffers very little from critical slowing down. We also extend this algorithm to the case of energetic ice models in Sec. VII. Using these algorithms we determine numerically several critical exponents which have not been accurately measured previously: the dimensionality of the percolating cluster of symmetric vertices in the  $F$  model at critical temperature, the scaling of the largest loop in the loop representation of both square ice and the  $F$  model at critical temperature, and the scaling of the trajectory of a wandering defect in square ice.

### II. ICE MODELS

Our ice model is as follows. Oxygen atoms are arranged on the vertices of a square grid, and between each oxygen

and its four neighbors there are hydrogen bonds, represented by the lines of the grid. Commonly, arrows are drawn on the bonds to indicate the positions of the protons: the arrow points towards the vertex which the proton is nearest to. The first ice rule above then corresponds to the condition that there should be exactly one arrow on each bond. The second ice rule says that each vertex should have exactly two arrows pointing towards it, and two pointing away. This gives us six types of vertices, and for this reason ice models are sometimes also referred to as six-vertex models. The six vertices are illustrated in Fig. 1.

In the first part of this paper we study the simplest six-vertex model, in which all types of vertices are assigned the same energy. This model is usually called “square ice.” The name is somewhat confusing, since other ice models on square lattices, such as the KDP and  $F$  models of Sec. VII, are not also called square ice. However, since the name is widely used, we will follow convention and use it here too. Because all configurations of square ice possess the same energy, the model’s properties are entirely entropically driven, and variations in temperature have no effect on its behavior. It turns out that the square ice model is equivalent to three other well-studied models in statistical physics: the three-coloring model, a random-surface model on a square lattice, and the “fully packed loop model” of Nienhuis.

#### A. Coloring models

Lenard [3,6] showed an important result about square ice which will help us in the design of an efficient Monte Carlo algorithm for the simulation of the model. Lenard demonstrated that the configurations of an ice model on a square lattice can be mapped onto the configurations of a lattice of squares colored using three different colors, with the restric-

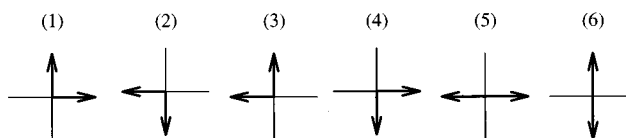


FIG. 1. The six possible vertex configurations of an ice model on a square lattice.

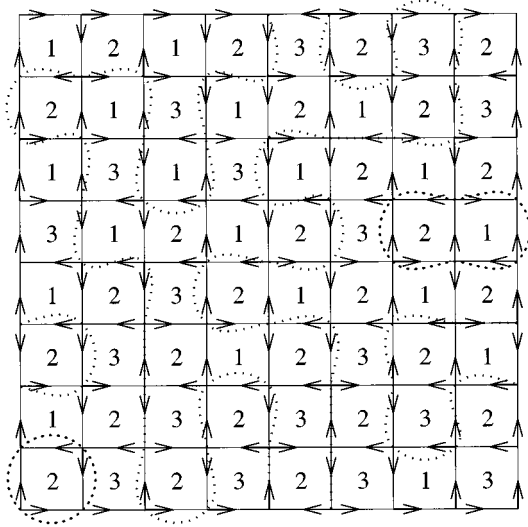


FIG. 2. A three coloring of a square lattice and its corresponding configurations of arrows and fully packed loops.

tion that no two nearest-neighbor squares have the same color. It is actually not very difficult to demonstrate this equivalence. The procedure for working out the configuration of the arrows of the ice model, given a suitable coloring of the plaquets on the lattice, is shown in Fig. 2, in which the three colors are represented by the numbers 1, 2 and 3. The rule is that we imagine ourselves standing on one of the squares of the lattice and looking toward one of the adjacent ones. If the number in the adjacent square is one higher (modulo 3) than the number in the square we are standing on, we draw an arrow on the intervening bond pointing to the right. Otherwise, we draw an arrow to the left. The procedure is then repeated for every other bond on the lattice.

Clearly the resulting configuration of arrows obeys the first ice rule; since neighboring plaquets must have different colors, the prescription above will place one and only one arrow on every bond. The second ice rule requires that each vertex has two ingoing and two outgoing arrows. If we walk from square to square in four steps around a vertex, then each time we cross a bond separating two squares, the color either increases or decreases by one, modulo 3. The only way to get back to the color we started with when we have gone all the way around is if we increase twice and decrease twice. This means that the vertex we walk around must have two ingoing and two outgoing arrows, exactly as we desire. Thus each configuration of the three-coloring model corresponds to a unique correct configuration of square ice.

We can also reverse the process, transforming an ice model configuration into a three-coloring configuration. We are free to choose the color of one square on the lattice as we wish, but once that one is fixed, the arrows on the bonds separating that square from each of its neighbors uniquely determine the color of the neighboring squares, and, by repeated application of the rule given above, the color of all the rest of the squares in the lattice. Thus the number of ways in which the squares of the lattice can be colored is exactly the number of configurations of the ice model on the same lattice, regardless of the size of the lattice, except for a factor of 3.

Given this three-color mapping, it is clear that the square ice model is also equivalent to the  $q=3$  Potts antiferromagnet on a square lattice in the limit of infinite coupling  $J$ ; the three colors correspond to the three states of the Potts model, and the infinite  $J$  ensures that no two adjacent sites can possess the same color.

### B. Random surfaces

Square ice is also equivalent to a random surface model in which heights are assigned to the plaquets of a square lattice. If we assign these heights in such a way that adjacent plaquets have heights which differ by exactly 1, then again there is a one-to-one mapping between the configurations of the ice model and the random surface: the mapping is identical to the three-color mapping of Sec. II A, except for the absence of the modulo operation. There has in fact been considerable recent interest in the connection between coloring (and Potts) models and models of random surfaces (see, for example, Ref. [7]), another reason for the development of efficient Monte Carlo algorithms for these problems.

### C. Fully packed loop models

The six-vertex model is also equivalent to the “fully packed loop model” [8,9], in which (nondirected) loops are formed by joining the vertices of the square lattice with “links” in such a way that each site on the lattice belongs to exactly one self-avoiding loop. To demonstrate this equivalence, consider the following rule. First, divide the lattice into even and odd sites in a checkerboard pattern. Now place links along all bonds whose arrows are pointing away from an even vertex. Since each such arrow must also point towards an odd vertex, and since each vertex has two ingoing and two outgoing arrows, this creates two links to every site on the lattice. Hence the lattice is fully covered by closed self-avoiding loops.

Proving the reverse result, that each configuration of loops corresponds to exactly one configuration of arrows, is equally simple: we place outgoing arrows on each bond adjoining an even site which is part of one of our loops. The direction of all the remaining arrows is then fixed by using the second ice rule.

## III. MONTE CARLO ALGORITHMS FOR SQUARE ICE

In this paper we develop a number of different Monte Carlo algorithms for calculating the average properties of ice models on square lattices. In the case of square ice, in which all configurations of the lattice have the same energy, the necessary steps for creating such an algorithm are (i) to choose a set of elementary moves which take us from one state of the model to another, (ii) to demonstrate that these moves can take us from any state of a finite lattice to any other in a finite number of steps (the condition of ergodicity), and (iii) to construct an algorithm from these moves such that in equilibrium the rate at which a particular move occurs which takes us from a state  $\mu$  to a state  $\nu$  is the same as the rate for the reverse move from  $\nu$  to  $\mu$  (the condition of detailed balance). It is then straightforward to show that, over a sufficiently long period of time, we will sample all states on a finite lattice with equal probability. However, the

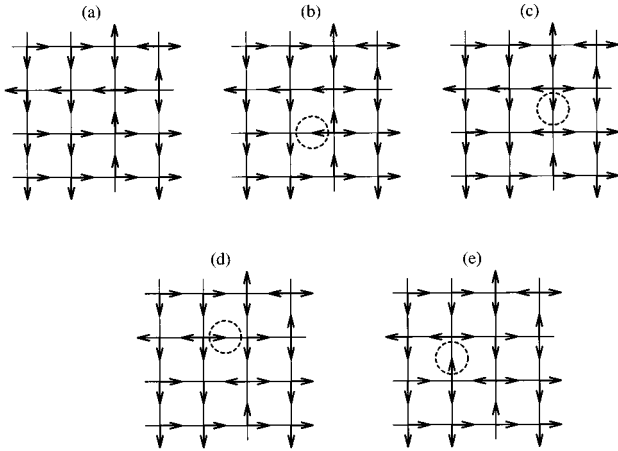


FIG. 3. Flipping arrows one by one along a line across the lattice allows us to change the configuration and still satisfy the ice rules. The only problems are at the ends of the line, but if the two ends eventually meet one another, forming a closed loop of flipped arrows, this problem goes away too.

choice of an elementary move is not obvious, since there is no local change we can make to the directions of the arrows on the lattice which will preserve the second ice rule. There is no equivalent of the reversal of a single spin in an Ising model, for example. In the next few sections we will consider four different candidate nonlocal update moves for square ice, which lead us to four different Monte Carlo algorithms of varying efficiency. Two out of these four algorithms have been described before by other authors, but it is still worth our going over them here, because in Sec. VII we will make use of some of the same ideas to develop algorithms for energetic ice models. These latter algorithms have not, to our knowledge, been described before.

#### A. Standard ice algorithm

First, we look at the standard algorithm for square ice [10,11], which involves reversing the arrows around a loop on the lattice. It is clear that one possible move which takes us from an allowed configuration of arrows in an ice model to another is the reversal of all the arrows in a loop chosen such that all arrows point in the same direction around the loop. Such a loop has one arrow pointing in and one pointing out of each participating vertex, so that the reversal of all of them preserves the number of arrows going in and out of each vertex. Notice that these loops are not the same loops as those in the fully packed loop model described above. In that case the arrows along the loop point in alternating directions, and their reversal would violate the second ice rule.

How do we find a loop in which all arrows point in the same direction around the loop? The most straightforward method is illustrated in Fig. 3. Starting with a correct configuration of the model (a), we choose a single vertex at random from the lattice. We then choose at random one of the two outgoing arrows at this vertex and reverse it (b). (We could just as well choose an ingoing arrow—either is fine.) This creates a violation of the second ice rule at the initial vertex, and also at a new vertex at the other end of the reversed arrow. In ice terminology these are referred to as ionic defects: the vertices with one and three outgoing ar-

rows correspond to  $\text{OH}^-$  and  $\text{H}_3\text{O}^+$  ions respectively. We can remove the defect at the new vertex by choosing at random one of the two outgoing arrows at this vertex and reversing it (c). (There are actually three outgoing arrows at this vertex, but one of them is the arrow we reversed in the first move, and we exclude this one from our set of possible choices to avoid having the loop retrace its steps.) This creates another defect at the other end of that arrow, and so forth. In this manner one of the two defects created by the reversal of the first arrow diffuses around the lattice (d), until by chance it finds itself back at the starting site once more, at which point it annihilates with the defect there, resulting in a new configuration of the lattice which satisfies the ice rules (e). The net result is the reversal of a loop of arrows on the lattice.

In the figure we illustrate the case of the smallest possible loop, which on the square lattice involves the reversal of just four arrows. However, provided the size of the lattice allows for it, the loops can be arbitrarily long, and for this reason we will refer to this algorithm as the “long loop algorithm.” At each step around the loop we have a choice to make between two possible arrows that we could reverse, and if we make these choices at random with equal probability we generate a species of random walk across the lattice. This walk could quite possibly take a long time to return to its starting point. However, on the finite lattices we use in our Monte Carlo simulations, we are guaranteed that the walk will eventually return. And long loops are not necessarily a bad thing, since, although they take longer to generate, they also flip a larger number of arrows, which allows the system to decorrelate quicker.

An alternative, but entirely equivalent scheme, makes use of so-called Bjerrum defects [12], rather than the ionic defects we have employed. A Bjerrum defect is a violation of the first ice rule: a bond containing two protons, one at either end of the bond (a Bjerrum  $D$  defect), or a bond containing no protons (a Bjerrum  $L$  defect). One can construct a Monte Carlo move using Bjerrum defects just as we did with ionic defects by removing an arrow from a bond, and placing it on another bond. This creates one  $D$  defect and one  $L$  defect. These defects can also wander around and eventually recombine, resulting in a new state of the lattice.

The process in which two defects (either ionic or Bjerrum) are created and diffuse around the lattice until they find one another again is actually very similar to what goes on in real ice. In real ice, changes in the proton configuration are mediated principally by the diffusion of Bjerrum defects around the lattice. The density of defects is very small—already at  $-10^\circ\text{C}$ , only about one in five million bonds is occupied by a Bjerrum defect, and the number of ionic defects is smaller even than this [13].

#### B. Ergodicity

We have now specified a move that will take us from one correct configuration of the arrows to another, and our proposed Monte Carlo algorithm for square ice is simply to carry out a large number of such moves, one after another. However, as we remarked above, we still need to demonstrate that the algorithm satisfies the criteria of ergodicity and detailed balance.

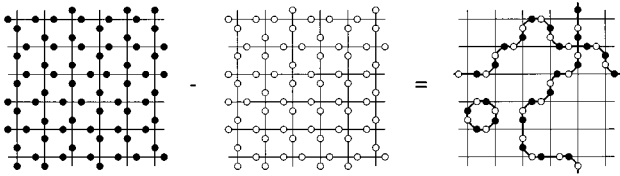


FIG. 4. The difference between any two configurations of the six-vertex model can be decomposed in a number of loops (which may run around the periodic boundaries). If all the arrows along these loops are reversed, we go from one configuration to the other.

First, consider ergodicity, whose proof is illustrated in Fig. 4. The figure shows how the difference between two configurations of the model on a finite lattice can be decomposed into the flips of arrows around a finite number of loops. We can demonstrate the truth of this statement for any two configurations by the following argument. Each of the vertices in Fig. 1 differs from each of the others by the reversal of an even number of arrows. This fact follows directly from the ice rules. Thus, if we take two different configurations of the model on a particular lattice and imagine drawing lines along the bonds on which the arrows differ, we are guaranteed that there will be an even number of such lines meeting at each vertex. Thus these lines must form a set of (possibly intersecting) loops covering a subset of the vertices on the lattice. It is not difficult to show that these loops can be chosen so that the arrows around each one all point in the same direction. Since the reversal of the arrows around these loops are precisely our Monte Carlo moves, and since there are a finite number of such loops, it follows that we can move from any configuration to any other in a finite number of steps, and thus the system is ergodic. Note that it is important to allow the loops to pass through the periodic boundary conditions for this to work [14].

### C. Detailed balance

Our Monte Carlo move consists of choosing a starting site  $S_0$  and reversing a loop of arrows starting at that site and ending,  $m$  steps later, at the same site  $S_m = S_0$ . The probability of selecting a particular site  $S_0$  as the starting site is  $1/N$ , where  $N$  is the number of sites on the lattice. The probability of making a particular choice from the two possible outgoing arrows at each step around the loop is  $\frac{1}{2}$  for each step, so that the probability that we chose a certain sequence of steps is equal to  $2^{-m}$ , and the probability of generating the entire loop is  $2^{-m}/N$ . For the reverse move, in which the same loop of arrows is flipped back again to take us from state  $\nu$  back to state  $\mu$ , the exact same arguments apply, again giving us a probability of  $2^{-m}/N$  for making the move, and hence detailed balance is observed. This, in combination with the demonstration of ergodicity above, ensures that our algorithm will sample all states of the model with equal probability.

## IV. AN ALTERNATIVE ALGORITHM, INVOLVING SMALLER LOOPS

A practical problem which arises in the algorithm presented above is that, if we simulate a large lattice, the probability that we return to the starting site  $S_0$  is quite small

once we have wandered sufficiently far away from it, and thus it may take a long time to generate even one move. In response to this problem, Rahman and Stillinger [10] proposed a second algorithm which also reverses the arrows around a closed loop of bonds, but which generates shorter loops. For obvious reasons we call this the ‘‘short loop algorithm.’’ Here we describe a slightly refined version of the algorithm due to Yanagawa and Nagle [11].

The short loop algorithm works in a similar way to the long loop algorithm: we choose a starting site  $S_0$  at random from the lattice, and reverse one of the outgoing arrows at that vertex, thereby creating two defects. We then reverse further arrows so that one of the defects wanders around the lattice randomly. However, rather than waiting until the two defects find one another again, we now continue only until the wandering defect encounters a site, call it  $S_m$ , which it has encountered before in its path across the lattice:  $S_m = S_l$  with  $l < m$ . From this point, we retrace our steps *backwards* down the old path of the defect, until we reach  $S_0$  again, reversing all the arrows along the way. The net result is that we reverse all the arrows along the path from site  $S_0$  to  $S_l$  twice (which means that they are the same before and after the move), and all the arrows in the loop from  $S_l$  to  $S_m$  once. Thus we have again reversed all the arrows around a loop. In contrast with the long loop algorithm however, the wandering defect does not have to find its way back to its original starting point; it only needs to find any site on its previous path. This guarantees that the length of its walk will never exceed  $N$  steps, and in practice the typical move is much shorter than this. (In fact, the number of steps tends to a finite limit as the lattice becomes large—see Sec. VI B.)

As with the previous algorithm, we need to demonstrate ergodicity and detailed balance. The proof of ergodicity is identical to that for the previous case: the difference between any two states on a finite lattice can be reduced to the reversal of the spins around a finite number of loops. Since the algorithm has a finite chance of reversing each such loop, it can connect any two states in a finite number of moves.

The proof of detailed balance is also similar to that for the long loop algorithm. Consider again a move which takes us from state  $\mu$  to state  $\nu$ . The move consists of choosing a starting site  $S_0$  at random, then a path  $P = \{S_0, \dots, S_l\}$  in which the arrows are left untouched, followed by a loop  $L = \{S_l, \dots, S_m\}$  in which we reverse the arrows. (Remember that the last site in the loop  $S_m$  is necessarily the same as the first  $S_l$ .) The probability that we chose  $S_0$  as the starting point is  $1/N$ , where  $N$  is the number of sites on the lattice. After that we have a choice of two directions at each step along the starting path and around the loop, so that the probability that we end up taking the path  $P$  is equal to  $2^{-l}$ , and the probability that we follow the loop  $L$  is  $2^{-(m-l)}$ . After the loop reaches site  $S_m = S_l$ , we do not have any more free choices. The probability that we move from a configuration  $\mu$  to configuration  $\nu$  by following a particular path  $P$  and loop  $L$  is thus

$$P(\mu \rightarrow \nu) = \frac{1}{N} 2^{-l} 2^{-(m-l)} = 2^{-m}. \quad (1)$$

For the reverse move, the probability of starting at  $S_0$  is again  $1/N$ , and the probability of following the same path  $P$

as before to site  $S_l$  is  $2^{-l}$  again. However, we cannot now follow the same loop  $L$  from  $S_l$  to  $S_m$  as we did before, since the arrows along the loop are reversed from what they were in state  $\mu$ . On the other hand, we can follow the loop in the reverse direction, and this again has probability  $2^{-(m-l)}$ . Thus we have

$$P(\nu \rightarrow \mu) = \frac{1}{N} 2^{-l} 2^{-(m-l)} = 2^{-m}, \quad (2)$$

exactly as before. This demonstrates detailed balance for the algorithm and, in combination with the demonstration of ergodicity, ensures that all possible states will be sampled with equal probability.

### V. MONTE CARLO ALGORITHMS FOR THE THREE-COLOR MODEL

We now have two Monte Carlo algorithms which correctly sample the states of the square ice model, and since, as we showed in Sec. II A, the states of this model can be mapped onto the states of the three-color lattice model, we can of course use the same algorithms to study the three-color model. In this section however, we will explore the other side of the same question: is there a natural Monte Carlo dynamics for the three-coloring model which could then be used to sample the states of the ice model? It turns out that there is, and the resulting algorithm provides not only an efficient way of simulating ice models, but will also prove useful when we move to the energetic ice models of Sec. VII, in which different types of vertices are assigned different energies.

In the three-coloring representation the degrees of freedom—the colors—are located on the plaquets of the lattice, rather than at the vertices, and, as we showed earlier, the ice rules translate into the demand that nearest-neighbor squares have different colors. Just as in the case of the square ice model, there is no obvious update move which will take us from state to state. Although there are some states in which the color of one square can be changed from one value to another without violating the ice rules, there are also states in which no such moves are possible, and therefore single-plaquet moves of this kind cannot reach these states, and so do not lead to an ergodic dynamics. Again then, we must resort to nonlocal moves, and the most obvious such move is to look for clusters of nearest-neighbor plaquets of only two colors, call them  $A$  and  $B$ , entirely surrounded by plaquets of the third color  $C$ . A move which exchanges the two colors  $A$  and  $B$  in such a cluster but leaves the rest of the lattice untouched satisfies the ice rules, and this suggests the following cluster-type algorithm for square ice:

- (1) We choose a plaquet at random from the lattice as the seed square for the cluster. Suppose this plaquet has color  $A$ .
- (2) We choose another color  $B \neq A$  at random from the two other possibilities.
- (3) Starting from our seed square, we form a cluster by adding all nearest-neighbor squares which have either color  $A$  or color  $B$ . We keep doing this until no more such nearest neighbors exist.
- (4) The colors  $A$  and  $B$  of all sites in the cluster are exchanged.

There are a couple of points to notice about this algorithm. First, the cluster possesses no nearest neighbors of either color  $A$  or color  $B$ , and therefore all its nearest neighbors must be of the third color  $C$ . In the simplest case, the seed square has no neighbors of color  $B$  at all, in which case the cluster consists of only the one plaquet. It is crucial to the working of the algorithm that such moves should be possible. If we had chosen instead to seed our cluster by picking two neighboring plaquets and forming a cluster with their colors, single-plaquet moves would not be possible, and we would find that the algorithm satisfied neither ergodicity nor detailed balance. Notice also that within the boundary of color  $C$ , the cluster of  $A$ 's and  $B$ 's must form a checkerboard pattern, since no two  $A$ 's or  $B$ 's can be neighbors.

We are now in a position to prove that our algorithm satisfies the conditions of ergodicity and detailed balance. In this case it turns out that detailed balance is the easier to prove. Consider, as before, a Monte Carlo move which takes us from a state  $\mu$  to a state  $\nu$ , and suppose that this move involves a cluster of  $m$  squares. The probability of choosing our seed square in this cluster is  $m/N$ , where  $N$  is the total number of plaquets on the lattice. The probability that we then choose  $B$  as the other color for the cluster is  $\frac{1}{2}$ , and after that there are no more choices: the algorithm specifies exactly how the cluster should be grown from here on. Thus the total probability for the move from  $\mu$  to  $\nu$  is  $m/(2N)$ . Exactly the same argument applies for the reverse move from  $\nu$  to  $\mu$  with the same values of  $m$  and  $N$ , and hence the rates for forward and reverse moves are the same. Thus detailed balance is obeyed.

The proof of ergodicity is a little trickier. It involves two steps. First, we show that from any configuration we can evolve via a finite sequence of reversible moves to a checkerboard coloring (a configuration in which one of the three colors is absent). Then we show that all checkerboard colorings are connected through reversible moves.

Any configuration of the lattice can be regarded as a number of checkerboard regions consisting of only two colors, divided by boundaries. This result is obvious, since each site of color  $A$  must have at least two neighbors with the same color, and therefore each square on the lattice belongs to a checkerboard domain of at least three squares. However, under the dynamics of our proposed Monte Carlo algorithm, the boundaries between these domains can move. If we have a domain of colors  $A$  and  $B$  and another of  $B$  and  $C$ , then by choosing one of the plaquets on the boundary as the seed square for our Monte Carlo move, and  $B$  as one of the colors for the cluster, we can make the boundary move one square in one direction or the other, with the direction depending on whether the other color for the cluster was  $A$  or  $C$ . In this way we can take a single simply connected cluster of one checkerboard pattern and, over a number of steps, grow its border until the cluster covers the entire lattice, leaving the lattice in a checkerboard state.

There are six of these checkerboard colorings, and from any one of them the others can easily be reached, since on a checkerboard the color of any square can be changed on its own without changing any other squares. Thus, for example, we can move from a checkerboard of colors  $A$  and  $B$  to one of  $A$  and  $C$  by changing all the  $B$ 's to  $C$ 's one by one. All other combinations can be reached by a similar process.

Since we can move from any state  $\mu$  to a checkerboard coloring and from any checkerboard to any other, all via reversible moves, it follows that our algorithm is ergodic.

The algorithm presented above, a single-cluster algorithm, resembles in spirit the Wolff single-cluster algorithm for the Ising model [15]. It is also possible to construct a multi-cluster algorithm for the three-coloring model, similar to the Swendsen-Wang algorithm for the Ising model [16]. In this algorithm we start by choosing at random a pair of colors  $A$  and  $B$ . Then we construct all clusters of nearest-neighbor spins made out of these two colors, and for each cluster we choose at random with 50% probability whether to exchange the two colors or not. This algorithm satisfies ergodicity for the same reason the single-cluster algorithm did—we can repeatedly choose two colors for the move until a single cluster grows to fill the entire lattice, giving a checkerboard pattern. But we can move from any checkerboard to any other, so that any state can be reached in a finite number of steps on a finite lattice. The algorithm also satisfies detailed balance: the probability of selecting a particular two out of the three colors for a move is  $\frac{1}{3}$ , and the probability of exchanging the colors in a particular set of clusters is  $2^{-n}$ , where  $n$  is the number of clusters. The probability for the reverse move is exactly the same, and hence detailed balance is upheld.

This full-lattice algorithm is in fact precisely the same as an algorithm proposed in 1990 by Wang, Swendsen, and Kotecky [17]. Although their algorithm was designed to simulate a Potts antiferromagnet, it can (as they pointed out) also be used to simulate square ice, via the correspondence between the two models pointed out in Sec. II A.

## VI. COMPARISON OF ALGORITHMS FOR SQUARE ICE

In previous sections, we proposed four algorithms for the simulation of square ice: the long loop algorithm, the short loop algorithm, the single-cluster three-coloring algorithm, and the full-lattice three-coloring algorithm. In this section we consider these algorithms one by one and compare their computational efficiency.

### A. Long loop algorithm

The long loop algorithm involves the creation of a pair of ionic defects, one of which diffuses around the lattice until it recombines with the first, in the process reversing all the arrows along the path of its diffusion. To assess the efficiency of this algorithm, we first measure the average number of steps which the wandering defect takes before it recombines as a function of the system size  $L$ . For an ordinary random walker on a square lattice, this number scales as  $L^2$ . In the case of the wandering defect however, we find that it scales instead as  $L^{1.67}$ —see Fig. 5 [18]. The amount of CPU time required per step in our algorithm increases linearly with the size of the loop, and hence we expect the CPU time per Monte Carlo step also to increase with system size as  $L^{1.67}$ . This is not necessarily a problem; since longer loops reverse more arrows as well as taking more CPU time, it is unclear whether longer is better in this case, or worse. To answer this question we need to consider the correlation time of the algorithm. We have measured the correlation time for

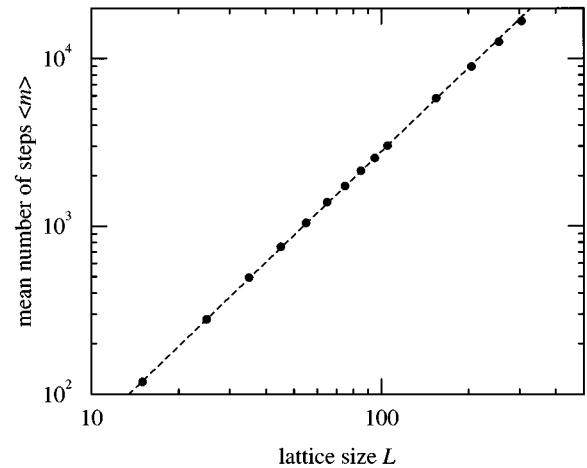


FIG. 5. The mean length  $\langle m \rangle$  of loops in the long loop algorithm as a function of system size  $L$ . We find that  $\langle m \rangle \sim L^{1.665 \pm 0.002}$ .

an observable  $\rho_{\text{sym}}$ , which we define to be the density of the symmetric vertices 5 and 6 in Fig. 1. As Fig. 6 shows, when we measure time in Monte Carlo steps we find a correlation time  $\tau_{\text{steps}} \sim L^{0.68 \pm 0.03}$ . It is, however, more common (and more convenient for the comparison of our algorithms) to measure time in “sweeps” of the lattice, which in this case means arrow flips per bond on the lattice. On average, each Monte Carlo step corresponds to  $\langle m \rangle / (dL^d)$  sweeps on a  $d$ -dimensional lattice, which means that the correlation time on our two-dimensional lattice goes as

$$\tau \sim L^{0.68} \frac{L^{1.67}}{L^2} = L^{0.35 \pm 0.03}. \quad (3)$$

This quantity measures the amount of computer effort we have to invest, per unit area of the lattice, in order to generate an independent configuration of the arrows.

The square ice model is a critical model, possessing an infinite correlation length [5]. Thus it comes as no surprise that the correlation time scales as a nonintegral power law with system size. The exponent  $z = 0.35$  is the dynamic ex-

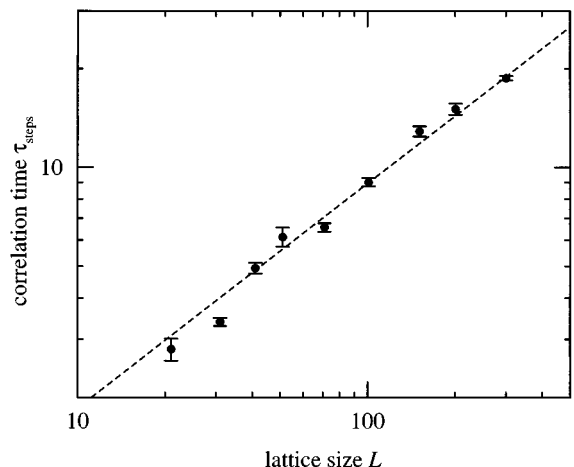


FIG. 6. The correlation time in Monte Carlo steps of the long loop algorithm as a function of system size  $L$ . The best fit straight line gives  $\tau_{\text{steps}} \sim L^{0.68 \pm 0.03}$ .

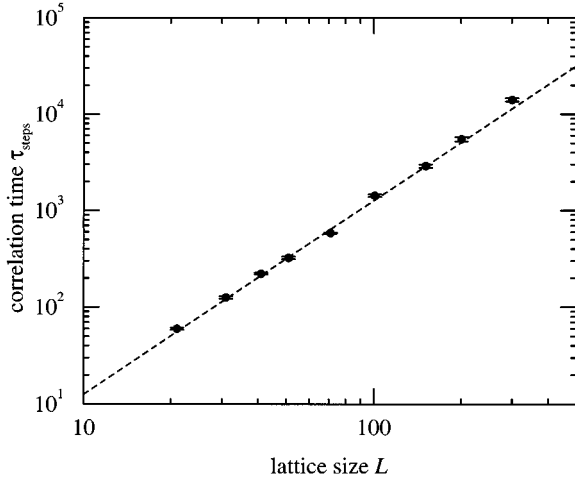


FIG. 7. The correlation time  $\tau_{\text{steps}}$  of the short loop algorithm measured in Monte Carlo steps as a function of system size. The best fit straight line gives  $\tau_{\text{steps}} \sim L^{2.00 \pm 0.01}$ .

ponent for the critical system—the anomalous scaling of the correlation time over and above the  $L^d$  scaling expected of a system far from criticality. As dynamic exponents go, this is a reasonably small one. The Metropolis algorithm for the normal Ising model in two dimensions for example has a dynamic exponent of about  $z = 2.17$  [19], making simulations of the model very time consuming for large lattices close to criticality. However, as we will see, some of our other algorithms for square ice do better still, possessing dynamic exponents not measurably different from zero.

### B. Short loop algorithm

The short loop algorithm of Sec. IV also involves creating a pair of defects, and having one of them diffuse around. Recall, however, that in this case the wandering defect only has to find *any* of the sites which it has previously visited in order to close the loop and finish the Monte Carlo step. If the diffusion were a normal random walk, then this process would generate loops of a finite average length. Although the diffusion of defects in square ice is not a true random walk, it turns out once more that the same result applies. Numerically we find that the average number of steps per move is  $\langle m \rangle = 13.1$ , independent of the lattice size, for a sufficiently large lattice. This figure includes the steps taken at the end of the move, which simply flip a number of arrows back to their starting configuration and therefore have no net effect on the state of the system (see Sec. IV). We find that typically about 58% of the arrows reversed during a move have to be restored in their original state. This is certainly a source of inefficiency in the algorithm.

The correlation time measured in Monte Carlo steps  $\tau_{\text{steps}}$ , for the same observable  $\rho_{\text{sym}}$  as above, increases as  $L^2$  (Fig. 7). Since the mean number of steps in a loop is independent of  $L$ , the correlation time per unit volume goes as

$$\tau \sim L^2 \frac{L^0}{L^2} = \text{const.} \quad (4)$$

Thus the short loop algorithm scales optimally with system size. To the accuracy of our simulations the dynamic exponent is  $z = 0.00 \pm 0.01$ .

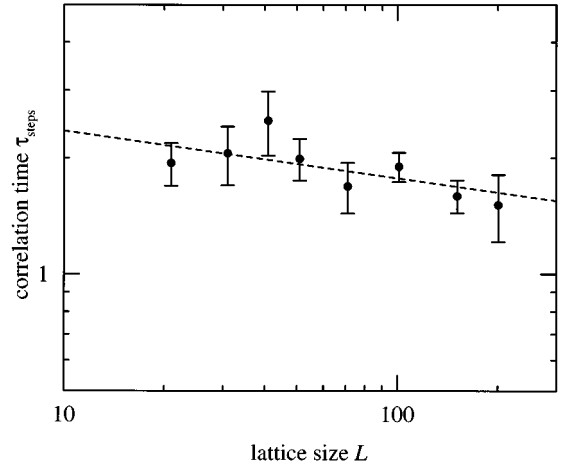


FIG. 8. The correlation time  $\tau_{\text{steps}}$  of the full-lattice three-coloring algorithm measured in Monte Carlo steps as a function of system size. The best fit straight line gives  $\tau_{\text{steps}} \sim L^{-0.12 \pm 0.07}$ .

### C. Single-cluster three-coloring algorithm

Our third algorithm is the single-cluster three-coloring algorithm outlined in Sec. II A. For this algorithm the average CPU time per Monte Carlo step scales as the average cluster size  $\langle c \rangle$ . Like the loop length in the long loop algorithm, this quantity scales up with increasing lattice size, and numerically we find that

$$\langle c \rangle \sim L^{1.5}. \quad (5)$$

The correlation time per Monte Carlo step goes as

$$\tau_{\text{steps}} \sim L^{1.8}, \quad (6)$$

and hence the correlation time in steps per site goes as

$$\tau \sim L^{1.8} \frac{L^{1.5}}{L^2} = L^{1.3}, \quad (7)$$

indicating that the single-cluster algorithm is a poor algorithm for studying square ice on large lattices.

### D. Full-lattice three-coloring algorithm

Our last algorithm, the full-lattice three-coloring algorithm, also described in Sec. II A, generates clusters in a way similar to the single-cluster algorithm, but rather than generating only one cluster per Monte Carlo step, it covers the whole lattice with them. For this algorithm we find numerically that the correlation time  $\tau_{\text{steps}}$  measured in Monte Carlo steps is approximately constant as a function of lattice size (Fig. 8). Since each Monte Carlo move updates sites over the entire lattice, the CPU time per move scales as  $L^2$ , and hence the correlation time in moves per site is

$$\tau \sim L^0 \frac{L^2}{L^2} = L^0. \quad (8)$$

Thus, like the short loop algorithm, this one possesses optimal scaling as lattice size increases, with a measured dynamic exponent of  $z = -0.12 \pm 0.07$ . (This figure agrees with

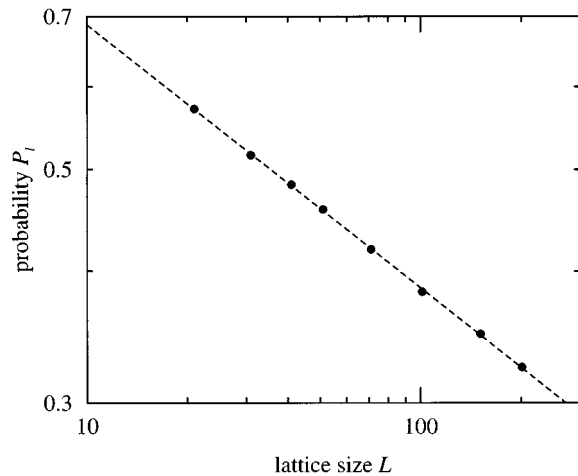


FIG. 9. The probability  $P_l$  that a site belongs to the longest loop in the fully-loop-covered representation of square ice, as a function of system size  $L$ . We find that  $P_l \sim L^{-0.251 \pm 0.002}$ .

the results for the  $q=3$  Potts antiferromagnet from Ref. [17], in which it is also found that the full-lattice algorithm has a zero dynamic exponent.)

Comparing the four algorithms, clearly the most efficient ones for large systems are the short loop algorithm and the full-lattice three-coloring algorithm. In both other algorithms, the computer time required to generate an independent configuration of the lattice increases with system size. The larger impact of the larger moves in these algorithms does not compensate for the extra effort invested in generating them. Between the short loop algorithm and the full-lattice three-coloring algorithm, it is harder to decide the winner, since both have the same scaling of CPU requirements with system size. Our results show in fact that the two algorithms are comparable in speed, both giving on the order of 1 000 000 site updates per second on the workstations used for this study. The loop algorithm is perhaps slightly faster (maybe 10%–20%) and has the advantage of working on lattices of other topologies as well as the square lattices used here. The three-coloring algorithm, on the other hand, is considerably more straightforward to program.

As an example of the use of our algorithms, we measured one of the simplest nontrivial critical exponents for the square ice model. As we showed in Sec. II C, each state of the square ice model corresponds to a configuration of a square lattice which is entirely covered by closed, non-self-intersecting loops. Using our full-lattice three-coloring algorithm, we measured the probability  $P_l$  that a particular site is visited by the largest loop in such a model as a function of lattice size  $L$ . The results are shown in Fig. 9. The data closely follow a power law:  $P_l \sim L^{-0.25}$ .

## VII. ENERGETIC ICE MODELS

There are a number of other systems besides  $\text{H}_2\text{O}$  with fourfold-coordinated hydrogen bonds, the most studied being potassium dihydrogen phosphate ( $\text{KH}_2\text{PO}_4$ ), also known as KDP. Slater [20] argued that KDP at low temperatures could be modeled using a six-vertex model in which vertices 1 and 2 in Fig. 1 are favored by giving them an energy  $-\epsilon$ , while all the others are given energy zero. Notice that it is possible

to form a domain on a square lattice consisting only of type-1 vertices, or only of type 2. Thus there are two degenerate ground states of the KDP model in which the lattice is entirely covered with vertices of one of these two types, and the model displays a symmetry-breaking phase transition from a high-temperature phase in which the two appear with equal probability to a low-temperature one in which one or the other dominates. A suitable order parameter to describe this transition is the polarization, or average direction of the arrows:

$$\mathbf{P} = \frac{1}{\sqrt{2N}} \sum_i \hat{\mathbf{n}}_i, \quad (9)$$

where the vector  $\hat{\mathbf{n}}_i$  is a unit vector in the direction of the  $i$ th arrow. In the thermodynamic limit the polarization will be zero above the critical temperature  $T_c$ , and nonzero below it with a direction either upwards and to the right, or downwards and to the left, and a magnitude which approaches unity as  $T \rightarrow 0$ .

Another widely studied energetic ice model is the so-called  $F$  model [21], in which vertices 5 and 6 in Fig. 1 are given a lower energy  $-\epsilon$ , and all the others are given energy zero. This model has a ground state in which vertices 5 and 6 alternate in a checkerboard pattern across the lattice. There are again two possible such ground states, depending on which type of vertex falls on the even sites of the checkerboard and which on the odd, and there is a symmetry-breaking phase transition from the high-temperature phase in which the two vertices fall on even and odd sites with equal probability. Since neither vertex 5 nor vertex 6 possesses any net polarization, the value of  $\mathbf{P}$  is zero in the thermodynamic limit for the  $F$  model, regardless of temperature. However, one can define an antiferroelectric order parameter which does become nonzero in the low-temperature phase [3,4].

A third energetic ice model which has attracted some attention recently is the staggered, body-centered solid-on-solid model [22,23]. In this model the square lattice is divided into even and odd sites, and the vertex types are divided into three groups. On even lattice sites, vertices of types 1 and 2 have energy  $\epsilon$  and types 3 and 4 have energy  $\epsilon'$ ; on odd lattice sites,  $\epsilon$  and  $\epsilon'$  are reversed, and vertices of types 5 and 6 have energy zero everywhere. The values of  $\epsilon$  and  $\epsilon'$  may be either positive or negative. In the height representation discussed in Sec. II B, this model is believed to describe roughening transitions in certain ionic crystals with the CsCl structure.

### Monte Carlo algorithms for energetic ice models

In Sec. VI we developed a variety of elementary ergodic moves for sampling the states of ice models on square lattices, and showed how these could be used to create Monte Carlo algorithms for the square ice model, in which all states have the same energy. We can use the same sets of elementary moves to create Monte Carlo algorithms for the energetic ice models as well. The simplest method is to employ a Metropolis-type scheme in which, instead of always carrying out every move generated by the algorithm, we carry them out with an acceptance probability  $P$  which depends on the



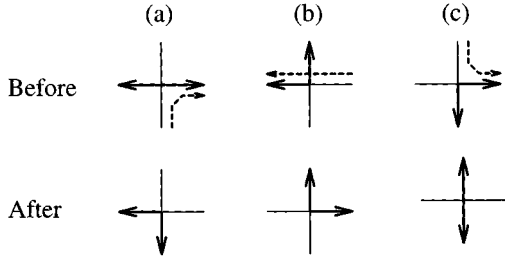


FIG. 10. Symmetric vertices become nonsymmetric if a loop passes through them (a). Nonsymmetric vertices stay nonsymmetric if the loop through them goes straight through (b), but become symmetric if the loop makes a turn (c).

energy difference  $\Delta E = E_\nu - E_\mu$  between the states  $\mu$  and  $\nu$  of the system before and after the move

$$P = \begin{cases} e^{-\beta\Delta E} & \text{if } \Delta E > 0 \\ 1 & \text{otherwise.} \end{cases} \quad (10)$$

Here we give examples of algorithms for the  $F$  model, but the same ideas can easily be adapted for use with other energetic ice models.

The Hamiltonian of the  $F$  model is given by

$$H = -\epsilon \sum_i (\delta_{v_i,5} + \delta_{v_i,6}), \quad (11)$$

where  $v_i$  is a number corresponding to the type of vertex at site  $i$ , using the numbering scheme illustrated in Fig. 1.

Let us first consider algorithms in which the proposed moves involve reversing the directions of the arrows around a loop on the lattice, as in the long and short loop algorithms of Secs. III and IV. For these moves the only vertices which change type (and hence energy) are those which the loop passes through. As is shown in Fig. 10, a symmetric vertex (type 5 or 6) always becomes nonsymmetric if the loop passes through it, thereby increasing the total energy. If the loop passes straight through a nonsymmetric vertex, the vertex remains nonsymmetric and its energy is unchanged. On the other hand, if the loop makes a turn as it passes through a nonsymmetric vertex, the vertex becomes symmetric and the energy decreases. Thus, given a particular loop, we can calculate the value of  $\Delta E$  by counting the number  $m$  of symmetric vertices which the loop passes through and the number  $n$  of nonsymmetric vertices in which it makes a  $90^\circ$  turn, and applying the formula

$$\Delta E = (m - n)\epsilon. \quad (12)$$

The density of symmetric vertices in the  $F$  model increases with decreasing temperature, so that the average number of symmetric vertices through which a loop passes grows as we go to lower temperatures. Since each symmetric vertex which we pass adds an amount  $\epsilon$  to  $\Delta E$ , it is clear that loop moves will carry an energy cost which increases with their length and that long loops will be very energetically costly, especially at low temperatures. This suggests that the short loop algorithm of Sec. IV will be more efficient for the simulation of the  $F$  model at finite temperature. In Fig. 11 we

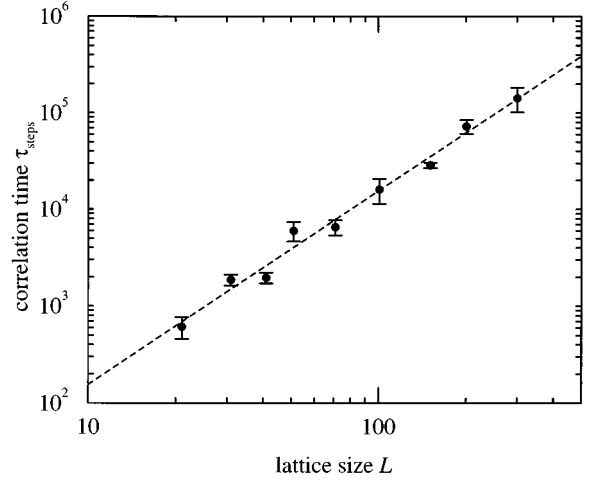


FIG. 11. The correlation time  $\tau_{\text{steps}}$  of the short loop algorithm for the  $F$  model measured in Monte Carlo steps, as a function of system size. The best fit straight line gives  $\tau_{\text{steps}} \sim L^{2.00 \pm 0.09}$ .

show the correlation time  $\tau_{\text{steps}}$  measured in Monte Carlo steps for this algorithm, and the best fit to these data gives us

$$\tau_{\text{steps}} \sim L^{2.0}. \quad (13)$$

As with square ice, the number of sites updated by a single Monte Carlo step tends to a constant for large lattices, so that the correlation time in steps per site is

$$\tau \sim L^{2.0} \frac{L^0}{L^2} = L^0. \quad (14)$$

To the accuracy of our simulations then, this algorithm has a zero dynamic exponent [24]. However, it turns out that this algorithm is still quite inefficient for temperatures in the region of the critical temperature and below. For example, at  $T_c$  the measured acceptance ratio is 36%, so that nearly two-thirds of the computational effort is wasted. For this reason we have investigated a number of other algorithms for simulating the  $F$  model.

How can we increase the acceptance ratio of our Monte Carlo algorithm? We would like to propose moves that are less likely to cost energy. For example, if we can encourage the loop to make turns in nonsymmetric vertices, we will on average end up with a lower final energy, since a reversal of the arrows around the loop will create more symmetric vertices. Unfortunately, it turns out to be quite complicated to formulate a correct algorithm along these lines, and the expression for the acceptance ratio becomes quite tedious. There is, however, an elegant alternative, which is to employ a three-coloring algorithm of the type discussed in Sec. V.

The equivalent of a symmetric vertex in the three-coloring model is a group of four squares in which both of the diagonally opposing pairs share the same color. In nonsymmetric vertices only one of these two diagonal pairs share the same color. Making use of this observation we can write the Hamiltonian of the  $F$  model [Eq. (11)] in the form

$$H = -\epsilon \sum_{[i,j]} (\delta_{c_i, c_j} - \frac{1}{2}) = N\epsilon - \epsilon \sum_{[i,j]} \delta_{c_i, c_j}, \quad (15)$$

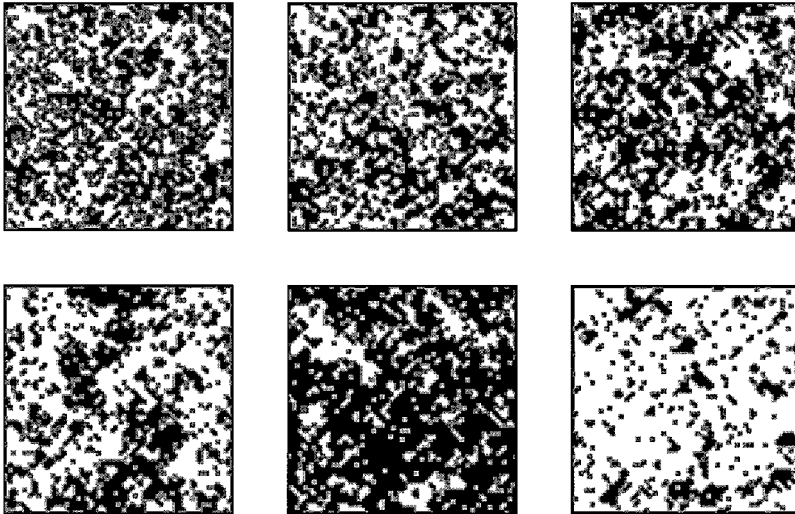


FIG. 12. Sample configurations of the  $F$  model for increasing  $\beta$ . Grey squares denote vertices of types 1, 2, 3, and 4. White vertices denote either vertices of type 5 on even lattice sites, or vertices of type 6 on odd lattice sites. Other vertices are black. Top row:  $\beta/\beta_c = 0.5, 0.8,$  and  $0.9$ . Bottom row:  $\beta/\beta_c = 1.0, 1.1,$  and  $1.2$ .

where the summation runs over all pairs of next-nearest-neighbor squares  $[i,j]$ , and  $c_i$  is the color of square  $i$ . We see that it is energetically favorable to have pairs of next-nearest-neighbor squares with the same color. We can make use of this observation to create an efficient algorithm for the three-coloring model. In this algorithm, as in the algorithms for square ice discussed in Sec. V, we build clusters of nearest-neighbor plaquets of two colors, but now, in addition, we also add to the cluster next-nearest-neighbor plaquets as well. In detail our algorithm is as follows.

(1) We choose a plaquet at random from the lattice as the seed square for the cluster. Suppose that this plaquet has color  $A$ .

(2) We choose another color  $B \neq A$  at random from the two other possibilities.

(3) Starting from our seed square, we form a cluster by adding all nearest-neighbor squares which have either color  $A$  or color  $B$ , and in addition we now also add to the cluster the squares which are next-nearest neighbors of some square  $i$  which is already in the cluster, provided they have the *same* color as square  $i$ . However, we make this latter addition with

a temperature-dependent probability  $\alpha < 1$ , whose value we calculate below in order to satisfy the condition of detailed balance. We go on adding squares to the cluster in this way until no more additions are possible.

(4) The colors  $A$  and  $B$  of all sites in the cluster are exchanged.

We can also make a full-lattice version of this algorithm in exactly the same way as for the square ice case. We choose two colors  $A$  and  $B$  at random, and create clusters all over the lattice from these two, using the method above.

It is straightforward to prove ergodicity for these algorithms. Since our three-coloring algorithms for square ice were ergodic (see Sec. V), and since each move in the square ice algorithms is also a possible move in our  $F$ -model algorithm (as long as  $\alpha < 1$ ), the result follows immediately.

Detailed balance is a little more tricky. We outline the argument here for the single-cluster version of the algorithm. As before, consider two states  $\mu$  and  $\nu$  which differ by the exchange of colors in a single cluster of  $m$  squares. The probability of choosing the seed square in this cluster is  $m/N$

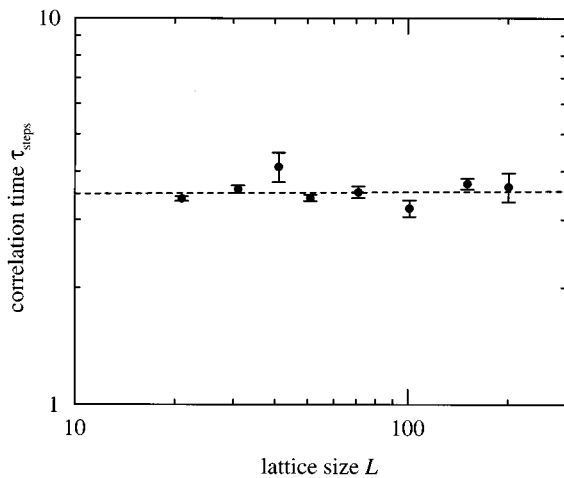


FIG. 13. The correlation time  $\tau_{\text{steps}}$  of the full-lattice three-coloring algorithm for the  $F$  model measured in Monte Carlo steps as a function of system size. The best fit straight line gives  $\tau_{\text{steps}} \sim L^{0.005 \pm 0.022}$ .

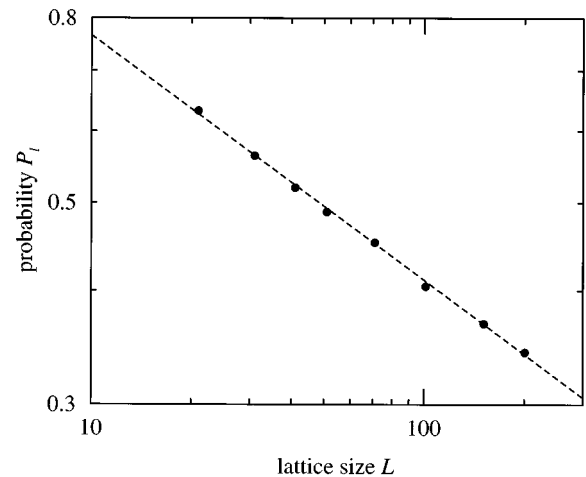


FIG. 14. The probability  $P_l$  that a site is visited by the longest loop, as a function of system size  $L$ , for the  $F$  model at critical temperature. At critical temperature we find that  $P_l \sim L^{-0.270 \pm 0.002}$ , which is very close to the exponent measured in the case of square ice (Sec. VI D).

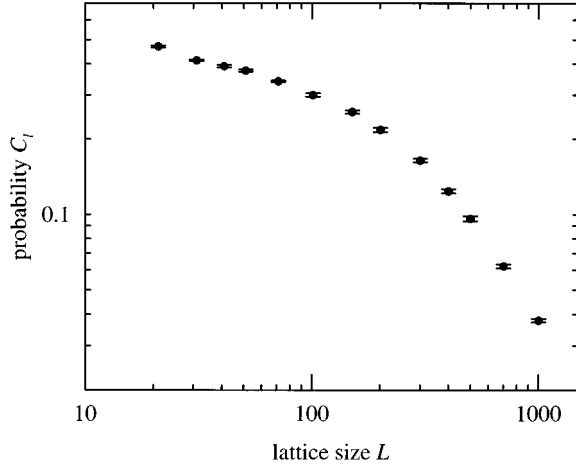


FIG. 15. The probability  $C_l$  that a site is part of the largest cluster, as a function of system size  $L$ , for the  $F$  model at critical temperature.

and the probability that we choose the correct second color to create this particular cluster is  $\frac{1}{2}$ , just as in the square ice case. However, we now also have a factor of  $\alpha$  for every square which we add to the cluster which is only a next-nearest neighbor of another and not a nearest neighbor. And we have a factor of  $1 - \alpha$  for every such site which we could have added but did not. Thus the overall probability of making the move from  $\mu$  to  $\nu$  is

$$P(\mu \rightarrow \nu) = \frac{m}{2N} \prod_{[i,j]_{\text{con}}} \alpha \prod_{[i,j]_{\text{dis}}} (1 - \alpha)^{\delta(c_i^{(\mu)}, c_j^{(\mu)})}, \quad (16)$$

where the two products run over pairs of next-nearest neighbors which are connected to or disconnected from the cluster, respectively. We will find it easier to work with the logarithm of this probability:

$$\begin{aligned} \ln P(\mu \rightarrow \nu) &= -\ln(m/2N) + \ln \alpha \sum_{[i,j]_{\text{con}}} 1 \\ &\quad + \ln(1 - \alpha) \sum_{[i,j]_{\text{dis}}} \delta(c_i^{(\mu)}, c_j^{(\mu)}). \end{aligned} \quad (17)$$

The expression for  $\ln P(\nu \rightarrow \mu)$  is identical except for the exchange of the labels  $\mu$  and  $\nu$ .

We want to know the ratio of the probabilities for the forward and reverse moves:

$$\ln \frac{P(\mu \rightarrow \nu)}{P(\nu \rightarrow \mu)} = \ln(1 - \alpha) \sum_{[i,j]_{\text{dis}}} \delta(c_i^{(\mu)}, c_j^{(\mu)}) - \delta(c_i^{(\nu)}, c_j^{(\nu)}). \quad (18)$$

The energy difference  $\Delta E$  between states  $\mu$  and  $\nu$  is equal to  $\epsilon$  times the change in the number of identically colored next-nearest-neighbor squares [see Eq. (15)]. The only contribution to this sum comes from next-nearest-neighbor pairs  $[i, j]$ , such that  $i$  belongs to the cluster and  $j$  does not, since all other pairs contribute the same amount to the Hamiltonian in state  $\mu$  as in state  $\nu$ . Thus

$$\Delta E = E_\nu - E_\mu = -\epsilon \sum_{[i,j]_{\text{dis}}} [\delta(c_i^{(\nu)}, c_j^{(\nu)}) - \delta(c_i^{(\mu)}, c_j^{(\mu)})]. \quad (19)$$

In order to satisfy the condition of detailed balance we want the ratio of the rates  $P(\mu \rightarrow \nu)$  and  $P(\nu \rightarrow \mu)$  to be equal to the ratio  $\exp(-\beta \Delta E)$  of the Boltzmann weights of the two states. Comparing Eqs. (18) and (19), we see that this can be arranged by setting  $\ln(1 - \alpha) = -\beta \epsilon$ , or

$$\alpha = 1 - e^{-\beta \epsilon}. \quad (20)$$

The proof of detailed balance for the full-lattice version of the algorithm follows from the single-cluster version, just as in the case of the square ice model.

In Fig. 12 we show some results of simulations of the  $F$  model using the full-lattice version of the algorithm described above. In this figure we have colored areas of the two low-energy domains (checkerboards of symmetric vertices) in black and white—type-5 vertices on even lattice sites and type-6 vertices on odd lattice sites are black, while type-6 vertices on even lattice sites and type-5 vertices on odd lattice sites are white. All other vertices are in gray.

The phase transition is clearly visible in the figure as a change from a state in which black and white appear with equal frequency to one in which one or the other dominates. Analytically it is known that this transition takes place at  $T_c = \epsilon / \ln 2$ . This number is rather difficult to measure numerically, however, since the phase transition is of infinite order; no matter how often you differentiate the energy or the density of symmetric vertices with respect to temperature, you will not see a singularity. Nonetheless there is a phase transition. For instance, the absolute value of the difference in density of black and white squares on an infinite lattice is strictly zero above the critical temperature, while nonzero below, ruling out any analytic behavior.

The full-lattice three-coloring algorithm does well at simulating the  $F$  model, even at the critical temperature. There is no measurable increase in the correlation time in number of lattice sweeps with system size at  $T_c$ ; our best estimate of the dynamic exponent is  $z = 0.005 \pm 0.022$  (see Fig. 13).

Because of the infinite order of the phase transition in the  $F$  model, we cannot define critical exponents in the normal fashion to describe power-law behavior of the order parameters as we approach criticality. However, there are a number of nontrivial exponents governing the behavior of the model at the critical temperature. As noted previously, the configurations of an ice model on a square lattice can be represented as sets of closed loops covering the entire lattice, and the  $F$  model corresponds to such a fully packed loop system in which the loops have “stiffness:” symmetric vertices correspond to straight segments of the loop and are energetically favored in the  $F$  model. Using our full-lattice three-coloring algorithm, we have measured the probability  $P_l$  that a site is visited by the largest loop in this representation of the model, just as we did for square ice in Sec. VI D. The results are presented in Fig. 14. At the critical temperature, the data are well fitted by a power law with an exponent of  $-0.27$ , very close to the value in the square ice case, indicating that in-

roduction of stiffness to the loops does not significantly influence the value of this exponent.

We have also used our Monte Carlo algorithm to measure as a function of system size  $L$  the probability  $C_l$  that at  $T_c$  a given site is part of the largest (percolating) cluster of nearest-neighbor symmetric vertices. The results are shown in Fig. 15. Interestingly, there is no clear power-law behavior in these data, despite the fact that the measurements were made at  $T_c$ . Possibly this is the result of strong finite-size effects in this system. Below the critical temperature, by contrast, the largest cluster is compact and scales as  $L^2$ .

### VIII. CONCLUSIONS

We have described a number of Monte Carlo algorithms for simulating ice models. One of them, the full-lattice three-coloring algorithm, is apparently able to simulate the  $F$  model without critical slowing down.

Using these algorithms, we have determined several ex-

ponents governing nonlocal quantities in square ice and the  $F$  model. We find that, in square ice, the average number of steps taken by a defect before it returns to its starting point scales as  $L^{1.67}$ . The probability that a site belongs to the largest loop in the loop representation of the model scales as  $L^{-0.25}$ . In the  $F$  model, the probability of belonging to largest loop scales with a very similar exponent  $L^{-0.27}$ , although the prefactor is different.

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