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LETTER TO THE EDITOR

Non-algebraic domain growth in random magnets: a cell dynamical approach

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Abstract. We develop a novel numerical approach, based on a computationally efficient cell dynamical system (CDS) model, for studying the kinetics of ordering in systems (described by a non-conserved order parameter) with *quenched disorder*, evolving from unstable initial states. We use this model to study the kinetics of domain growth in a coarse-grained version of the random exchange Ising model. Our numerical data strongly indicate *quantitative* agreement with the theoretically predicted asymptotic growth law over a limited range of disorder amplitudes. We also compare our observations with those in laboratory experiments and make important predictions regarding dynamical scaling in these systems.

The kinetics of growth and pattern formation in spatially extended systems has been an active field of research over the last few years, not only because of the practical implications in metallurgy and materials science, but also because of the fundamental importance of the 'universal' growth laws and 'ubiquitous' dynamic scaling exhibited by these processes; for reviews, see [1]. Computer simulations have played a crucial role in elucidating the nature of such growth processes. Several interesting results have emerged for the first time from the computer simulation of model systems and many theoretical predictions have been verified by such computer experiments. In principle, it should be possible to observe the *asymptotic* growth laws through computer simulation provided (a) the true asymptotic regime is attained and (b) sufficiently accurate data over a wide enough time interval in this regime can be obtained within the available computer time. However, in practice, it is extremely difficult to fulfil these conditions using the conventional Monte Carlo (MC) techniques; the complexities involved have been discussed in detail elsewhere [2]. Computationally efficient modelling using coarse-grained cell dynamical system (CDS) models [3], first developed to study phase ordering in two-phase systems, has been applied successfully to many other similar problems [4]. In this letter we propose, for the first time, a non-trivial extension of this technique to deal with systems with quenched disorder and use it to study an outstanding growth problem in random magnetic systems, where the conventional MC method has had only limited success.

Conventional MC methods use the single spin-flip kinetic Ising model (Ising model with Glauber kinetics), which serves as a reliable model for investigating dynamical processes in many magnetic insulators. Investigation of ordering kinetics involves

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quenching the d-dimensional spin system from the high-temperature paramagnetic phase to a temperature T well below the co-existence curve and monitoring the characteristic domain size $\langle R\rangle(t)$ as a function of time t. It is well known [1] that the domain growth in the pure Ising model is controlled by curvature-driven interfacial motion which leads to the growth law $\langle R\rangle(t) \sim t^{1/2}$ (known as the Lifshitz-Cahn-Allen or LCA law). Quenched (immobile) disorder is introduced into the pure Ising model by either randomizing the strength of the spin-spin exchange interaction (i.e. random exchange Ising model or REIM [5]) or by introducing a site-dependent random field (i.e. random field Ising model or RFIM [6]). In this letter, we focus our attention on the case with random exchange. At late and intermediate times, domain growth in the Ising model with quenched disorder proceeds through thermally-activated hopping of the interface over energy barriers put up by the disorder. Let us denote the barriers against movement of interfaces at length scales $\langle R\rangle$ by $E(\langle R\rangle)$. Assuming that $E(\langle R\rangle)$ scales with a power of $\langle R\rangle$, Huse and Henley[7] (HH) obtained a growth law for the characteristic domain size

$$R(t) \sim (\ln t)^x. \tag{1}$$

Moreover, relating x with two other known exponents for the REIM, HH predicted that x is a *universal* quantity in the same sense as the other dynamic criticial exponents. Thus, in this scenario, the *asymptotic* growth law for the REIM is given by (1), where x depends on the dimensionality of the system but is independent of the temperature T and the actual amount of disorder. For example, $x = 4$ in $d = 2$. It is worth mentioning here that, in weakly-disordered systems, the interfacial curvature (rather than thermally-activated barrier hopping of the interface) is the rate-limiting mechanism of domain growth in the early stages. Consequently, a crossover froma power-law growth regime to the asymptotic logarithmic growth regime is expected as the domains grow with time. Eventually, the domains 'freeze' after attaining a temperature-dependent maximum size because the barriers on longer length scales are too strong to be overcome by the available thermal energy. (Although, in principle, domains can keep growing for ever at any non-zero temperature, the growth becomes so slow beyond a certain temperature-dependent maximum that, for all practical purposes, domains appear to be 'frozen' after attaining this size). Although the numerical data from the earlier Monte Carlo simulations [8] are in qualitative agreement with this scenario, a more recent attempt [9] to determine the exponent x turned out to be inconclusive mainly because of the scarcity of sufficiently accurate data over a wide enough interval of time in the asymptotic regime. Although the onset of the crossover to the logarithmic growth regime can be quickened by putting in stronger disorder ones does not get data over a wider interval of time becuase stronger disorder also leads more quickly to 'freezing'. Besides, it has recently been pointed out [10] that further subtle effects are introduced by the self-similarity of the structure in the presence of strong site-dilution. Thus, it seems that conventional MC methods would not be very successful in understanding the quantitative aspects of the problem. Therefore, in this letter we develop a CDS model, which is essentially a coarse-grained version of the REIM. We study the asymptotic domain growth law in this model and find it to be in accordance with the predictions of HH, albeit over a limited range of disorder. Moreover, to our knowledge, no attempt has been made so far to check the validity of dynamical scaling [1] in systems with quenched disorder. Our numerical results indicate that dynamical scaling holds for our CDS model and the form of the universal scaling function is independent of the amount of disorder.

We start with the time-dependent Ginzburg-Landau (TDGL) equation, which describes the temporal evolution of a system described by a non-conserved order parameter (e.g. a coarse-grained version of the pure Ising model with Glauber kinetics [11])

$$\frac{\partial\psi(\boldsymbol{r}, t)}{\partial t} = -L\frac{\delta H[\psi(\boldsymbol{r}, t)]}{\delta\psi(\boldsymbol{r}, t)} + \sigma(\boldsymbol{r}, t). \tag{2}$$

In (2), $\psi(\boldsymbol{r}, t)$ is the scalar order parameter at point $\boldsymbol{r}$ and time t; and L is a phenomenological parameter. For the pure Ising model, the coarse-grained free-energy functional $H[\psi(\boldsymbol{r}, t)]$ in (2) is usually taken to be of the ϕ^4-form, namely,

$$H[\psi(\boldsymbol{r}, t)] = \int \mathrm{d}\boldsymbol{r}\left(-\frac{\tau}{2}\psi(\boldsymbol{r}, t)^2 + \frac{g}{4}\psi(\boldsymbol{r}, t)^4 + \frac{K}{2}(\nabla\psi(\boldsymbol{r}, t))^2\right) \tag{3}$$

where τ, g and K are phenomenological constants which measure respectively the temperature T ($\tau \sim (T_c - T)$, where T_c is the critical temperature), the coupling constant, and the interfacial energy. The Gaussian white noise $\sigma(\boldsymbol{r}, t)$ satisfies the fluctuation-dissipation relation

$$\langle\sigma(\boldsymbol{r}, t)\sigma(\boldsymbol{r}', t')\rangle = 2TL\delta(\boldsymbol{r} - \boldsymbol{r}')\delta(t - t') \tag{4}$$

where we have taken the Boltzmann contant to be unity. The TDGL equation corresponding to the free-energy functional (3) (usually referred to as model A [12]) is then

$$\frac{\partial\psi(\boldsymbol{r}, t)}{\partial t} = L[\tau\psi(\boldsymbol{r}, t) - g\psi(\boldsymbol{r}, t)^3 + K\nabla^2\psi(\boldsymbol{r}, t)] + \sigma(\boldsymbol{r}, t). \tag{5}$$

For the case of the REIM, the coarse-grained free-energy functional is usually taken to be of the form[13]

$$H[\psi(\boldsymbol{r}, t)] = \int \mathrm{d}\boldsymbol{r}\left(-\frac{\tau(\boldsymbol{r})}{2}\psi(\boldsymbol{r}, t)^2 + \frac{g(\boldsymbol{r})}{4}\psi(\boldsymbol{r}, t)^4 + \frac{K(\boldsymbol{r})}{2}(\nabla\psi(\boldsymbol{r}, t))^2\right) \tag{6}$$

so that the phenomenological measures of the various parameters assume a spatial dependence. The spatial dependence is of the form of a random Gaussian fluctuation about a constant average, e.g. $\tau(\boldsymbol{r}') = \tau_0 + \delta\tau(\boldsymbol{r})$, $g(\boldsymbol{r}) = g_0 + \delta g(\boldsymbol{r})$, and so on. Then, the TDGL equation corresponding to (6) describes the dynamics of the coarse-grained version of the REIM. (This conclusion is supported by a derivation of the coarse-grained kinetic equation by applying the master equation approach [11] to the REIM [14].) For simplicity, we confine ourselves to the case where the interfacial energy is not spatially varying, i.e. $K(\boldsymbol{r}) \equiv K$. This restriction only affects the precise form of the interface between domains and does not change asymptotic results, which are independent of the precise form of the interface. Thus, we consider the TDGL equation

$$\frac{\partial\psi(\boldsymbol{r}, t)}{\partial t} = L[\tau(\boldsymbol{r})\psi(\boldsymbol{r}, t) - g(\boldsymbol{r})\psi(\boldsymbol{r}, t)^3 + K\nabla^2\psi(\boldsymbol{r}, t)] + \sigma(\boldsymbol{r}, t). \tag{7}$$

Equation (7) describes the temporal evolution of the coarse-grained version of the REIM which we consider in this letter. We will only consider the physically interesting case where $\tau(\boldsymbol{r})$ and $g(\boldsymbol{r})$ are positive at all points so that the homogeneous system is

thermodynamically unstable everywhere. Of course, the local minima of the order parameter will now be spatially varying functions. We can cast (7) in a dimensionless form by scaling as follows:

$$\psi = \sqrt{\frac{\tau_0}{g_0}}\,\psi' \qquad r = \sqrt{\frac{K}{\tau_0}}\,r'$$
$$t = \frac{1}{\tau_0 L}\,t' \qquad \sigma = L\sqrt{2T\tau_0\left(\frac{\tau_0}{K}\right)^{d/2}}\,\mu. \tag{8}$$

The corresponding dimensionless form of (7) is (dropping the primes)

$$\frac{\partial\psi(r,t)}{\partial t} = [1+\delta a(r)]\psi(r,t) - [1+\delta b(r)]\psi(r,t)^3 + \nabla^2\psi(r,t) + \sqrt{\varepsilon}\,\mu(r,t) \tag{9}$$

where $\delta a(r) = \delta\tau(r)/\tau_0$ and $\delta b(r) = \delta g(r)/g_0$ are random Gaussian fluctuations about zero. In (9), $\varepsilon = 2g_0 T\tau_0^{-2}(\tau_0/K)^{d/2}$ and $\mu(r,t)$ is a Gaussian noise satisfying $\langle\mu(r,t)\mu(r',t')\rangle = \delta(r-r')\delta(t-t')$.

The prescription for deriving a computationally efficient CDS model for a reaction-diffusion equation like (9) has been discussed extensively in the literature [3, 4]. Essentially, the procedure consists of integrating the deterministic local part of (9) (i.e. equation (9) without the diffusive and the noise terms) and using the solution of the deterministic local part to write down a CDS model for (9). The advantage of this prescription is that it enables the use of much larger mesh sizes than are possible with the conventional Euler discretization schemes. We do not go into further details of this procedure here. Rather, we directly write down the resultant CDS model,

$$\psi(r,t+\Delta t) = \frac{\alpha(r)A(r)\psi(r,t)}{\sqrt{\alpha(r)^2+\psi(r,t)^2(A(r)^2-1)}} + \frac{\Delta t}{(\Delta x)^2}\Delta_D\psi(r,t) + \sqrt{\varepsilon}\,\Delta t\mu(r,t)$$
$$= G_r(\psi(r,t)) + \frac{\Delta t}{(\Delta x)^2}\Delta_D\psi(r,t) + \sqrt{\varepsilon}\,\Delta t\mu(r,t) \tag{10}$$

where Δt and Δx are the mesh sizes in time and space respectively, and

$$\alpha(r) = \sqrt{\frac{1+\delta a(r)}{1+\delta b(r)}} \qquad A(r) = \exp[(1+\delta a(r))\Delta t]. \tag{11}$$

In (10), Δ_D is the isotropically discretized Laplacian at the discrete lattice point r. Using the robustness of cell dynamical modelling and the insensitivity of results to the precise form of the local relaxation function [3], we replace the function $G_r(x)$ by the piecewise linear function

$$f_r(x) = \begin{cases} A(r)x & |x| \leqslant \dfrac{\alpha(r)}{A(r)} \\ \alpha(r)\,\mathrm{sgn}(x) & |x| > \dfrac{\alpha(r)}{A(r)} \end{cases}. \tag{12}$$

This piecewise linear function ensures a more rapid relaxation to the local fixed points, thereby enabling quicker access to the asymptotic regime. Thus, we have the required computationally efficient CDS model

$$\psi(r,t+1) = f_r(\psi(r,t)) + D\Delta_D\psi(r,t) + B\sigma(r,t) \tag{13}$$

where the time is incremeneted in discrete steps; $D = \Delta t/(\Delta x)^2$; and $B = \Delta t\sqrt{\varepsilon}$. This is the model we have used to obtain the results described in this letter. There are five parameters in this model, namely the constants $A_0(=e^{\Delta t})$ and D; the noise amplitude

B; and the amplitudes of the two disorder terms $\delta a(\boldsymbol{r})$ and $\delta b(\boldsymbol{r})$. The choice of parameters is dictated by the requirements that (a) the scheme (13) be numerically stable; and (b) the results obtained be reasonable [3]. In this letter, we use the parameter values $A_0 = 1.3$ and $D = 0.125$. These parameter values have been considerably successful in elaborating the dynamics of ordering in the case without disorder [3]. Before we proceed, some discussion of this choice of values for A_0 and D is in order. Essentially, the values of A_0 and D affect only the width of the interface between domains and not the bulk of the domains. Asymptotically, as we have remarked earlier, the width of the interface (which is constant in time) is an irrelevant variable compared with the characteristic domain size (which grows in time). Thus, the only effect of the interface width is to introduce non-universal features in the scaled structure factors at early times. Asymptotically, scaled structure factors are independent of the interface width and, consequently, independent of the values of A_0 and D. This has been confirmed for the case without disorder [3] and we have also verified it for the case with disorder, though we do not present detailed results here. The asymptotic results presented below are independent of the values of A_0 and D over a broad range of values [3]. Details will be provided in an extended publication.

The choice of the noise amplitude raises a somewhat delicate question. In the case of ordering in pure systems, noise has been shown to be irrelevant for the asymptotic domain growth law [3]. However, as explained above, the HH prediction is based on the argument that growth in the presence of quenched disorder is driven by thermally assisted hopping of energy barriers. Therefore, we must consider the case where the noise amplitude (which mimics thermal fluctuations) is non-zero. Even the determinstic case gives rise to non-algebraic growth but this should not be quantitatively compared with the HH prediction, as it is not clear whether their scenario applies. Furthermore, as we show later, the patterns freeze rapidly in the deterministic case. Numerically, we choose the noise to be uniformly distributed with an amplitude $B = 0.2$, unless mentioned otherwise. (Results similar to those presented here are obtained for other reasonable noise amplitudes and a Gaussian distributed noise. We do not present these results here.) Finally, for simplicity, we consider only the case where the amplitudes of $\delta a(\boldsymbol{r}')$ and $\delta b(\boldsymbol{r})$ are equal. We have considered both uniformly and Gaussian distributed disorder. The results obtained are similar and all results presented here are for the case of quenched disorder uniformly distributed between $-C$ and $+C$, C being the amplitude of the disorder.

At this stage, we examine the physical implications of our parameter values. Recall that we had rescaled the TDGL equation (7) to arrive at the dimensionless form (9) and all parameters will have to be interpreted in terms of this rescaling. First, we consider A_0 and D, which are related to the mesh sizes in our new discretization scheme as $A_0 \equiv e^{\Delta t}$ and $D \equiv \Delta t/\Delta x^2$. The mesh sizes corresponding to the values $A_0 = 1.3$ and $D = 0.125$ are $\Delta t = 0.26$ and $\Delta x = 1.45$. These values are unreasonably large for a conventional simulation of the corresponding partial differential equation and can only be justified in the context of cell dynamical systems [3]. Next, we consider the role of the noise parameter B, which we have already discussed partly. Clearly, the amplitude of noise should not be so large as to destroy the local domain structure. Noise amplitudes $B \leqslant 0.4$ are reasonable and give well-formed domains. Finally, we discuss the disorder amplitude C. Typically, a disorder amplitude of $C = 0.30$ corresponds to a maximum variation of $0.3\tau_0$ in the local temperature variable $\tau(\boldsymbol{r})$ or a maximum variation of $0.3g_0$ in the local coupling variable $g(\boldsymbol{r})$. These fluctuations are physically reasonable in the context of experimental systems.

We have implemented the scheme (13) on a 128×128 lattice with periodic boundary conditions. The quantity usually calculated is the time-dependent structure factor, which is defined as

$$S(\boldsymbol{k}, t) = \langle \psi(\boldsymbol{k}, t) \psi(\boldsymbol{k}, t)^* \rangle \tag{14}$$

where $\psi(\boldsymbol{k}, t)$ is the Fourier transform of $\psi(\boldsymbol{r}, t)$ on the discrete lattice; the angular brackets denote an averaging over different initial conditions and then different disorder configurations; and the $*$ denotes complex conjugation. The wavevectors $\boldsymbol{k}$ take up the discrete values $2\pi(k_x, k_y)/128$, where k_x and k_y range from 1 to 128. For each fixed configuration of disorder, we obtain structure factors as averages over 20 different initial conditions. Then, we average over (typically) 20 different configurations of disorder. The time-dependent structure factors are circularly averaged to give the scalar function $S(k, t)$, which will be shown in subsequent figures. The characteristic domain size $\langle R \rangle(t)$ is defined as the reciprocal of the first moment of the scalarized structure factor $\langle R \rangle(t) = \langle k \rangle(t)^{-1}$, where $\langle k \rangle(t)$ is defined as

$$\langle k \rangle(t) = \frac{\int_0^{k_m} \mathrm{d}k \, kS(k, t)}{\int_0^{k_m} \mathrm{d}k \, S(k, t)} \tag{15}$$

where k_m is the magnitude of the largest wavevector we consider. The results presented here are for k_m equal to half the magnitude of the largest wavevector lying in the Brillouin zone of the lattice. The characteristic length scale thus measured is in units of the lattice spacing.

Figure 1 shows the square of the characteristic domain size, $\langle R \rangle(t)^2$, as a function of time t for four different values of the disorder amplitude $C(=0.0, 0.30, 0.35, 0.40)$ and the noise amplitude $B = 0.2$. The data for the pure system (corresponding to $C = 0.0$) obey the LCA growth law $\langle R \rangle(t) \sim t^{1/2}$ up to a time of about 1000 units. After that, finite-size effects affect the accuracy of our data [3]. We will take $\langle R \rangle_c \sim 20$ as an approximate cutoff beyond which we expect our results to be affected by the finite size of the system. Thus, we present here only data (for both pure and disordered systems) with $\langle R \rangle(t) \leq 20$. Figure 1 shows that the data for the disordered case cross over from a power-law growth regime to a slower growth regime; the stronger the disorder, the quicker the onset of crossover. The qualitative features of the data are similar to the corresponding features seen in earlier MC simulations [8, 9] of the REIM. In figure 1, we have shown results only for optimal values of disorder. For lower values of disorder, the growth law is indistinguishable from a LCA growth law for an extended period of time and then finite-size effects hamper the observation of the slow growth regime. For larger values of disorder, freezing occurs too quickly to exhibit an extended growth regime.

To check whether the HH prediction (equation (1)) is valid for our coarse-grained model, we have plotted $\langle R \rangle(t)$ versus $(\ln t)$ [4] in figure 2. Clearly, $\langle R \rangle(t)$ does not go as $(\ln t)^4$ for early times. This is as expected because the early time behaviour is dominated by curvature effects which give rise to a LCA growth law. For intermediate and late times, the data for $C = 0.30$ supports the HH prediction. However, the data for larger values of disorder (namely, $C = 0.35, 0.40$) are in agreement with equation (1) only over an intermediate regime of time. The deviation from (1) in the later stages does not necessarily imply any breakdown of the form (1); the true asymptotic growth for these stronger disorder values may have been masked by the dominating effects of freezing. Nevertheless, our data in this figure stongly suggest that the HH prediction would hold in the true asymptotic regime. This, we believe, is the first strong evidence

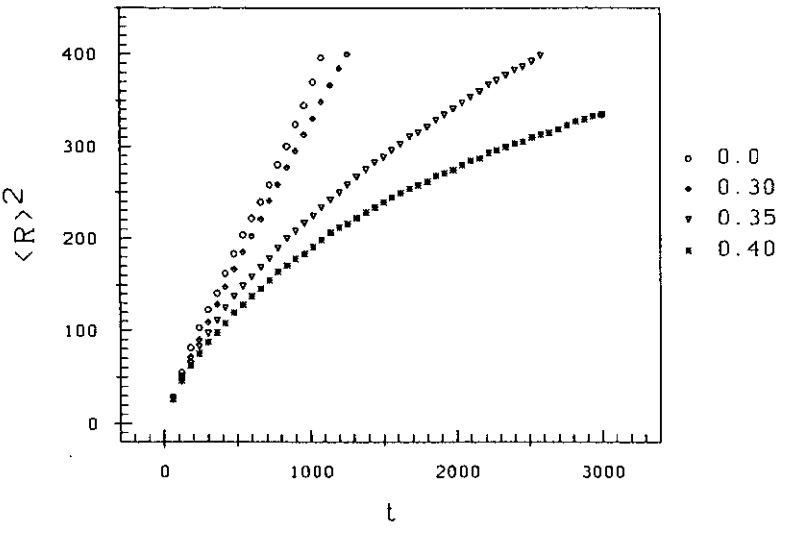

Figure 1. Square of the characteristic domain length, $\langle R\rangle^2$ plotted as a function of time t for disorder amplitudes $C=0.30$, 0.35 and 0.40 (denoted by the symbols indicated). For comparison, we also plot $\langle R\rangle^2$ versus t (denoted by circles) for the pure system corresponding to $C0.0$. The noise amplitude is always taken to be $B=0.2$.

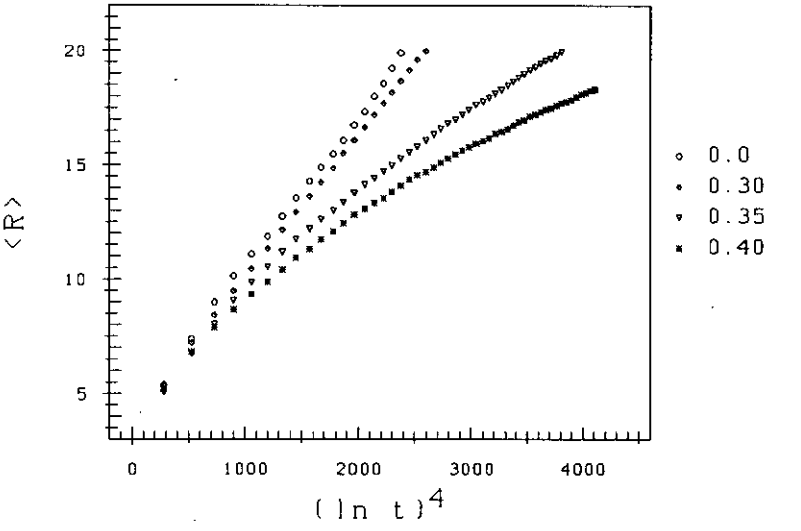

Figure 2. Characteristic domain size $\langle R\rangle$ versus $(\ln t)^4$ for the data from figure 1.

in favour of the theoretically predicted asymptotic growth law, albeit over a limited range of disorder values.

In figure 3, we show the domain growth for deterministic systems ($B=0.0$) with the same disorder values as in figure 1. The onset of freezing is much quicker than that in case of growth with noise. However, the forms of these curves are qualitatively similar to that of the curves in figure 1; the stronger the disorder, the quicker the

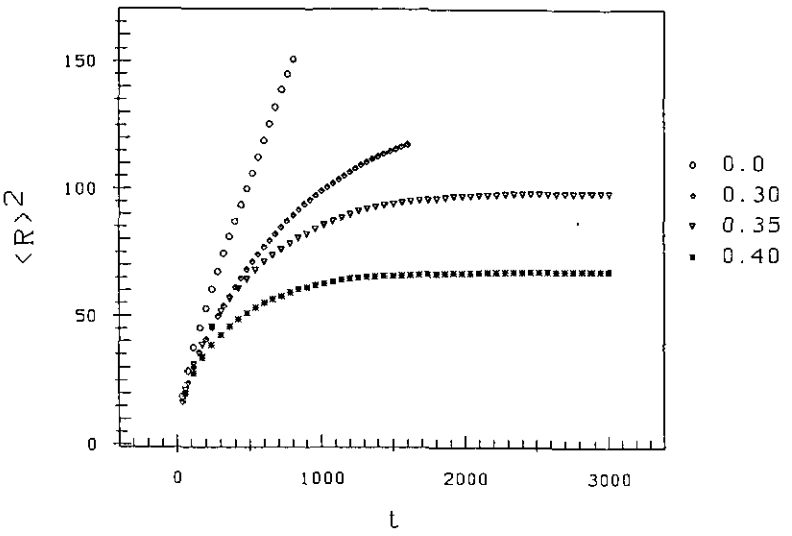

Figure 3. Square of the domain size, $\langle R \rangle^2$ plotted as a function of time t for the same disorder amplitudes as in figure 1 (denoted by the symbols indicated) but in the absence of noise ($B = 0.0$).

freezing. For smaller values of disorder, growth is seen over a somewhat larger period of time but it is not at all in accordance with the HH prediction. As pointed out earlier, this data should not be interpreted in terms of the HH prediction, because it is not clear whether their scenario applies to this case.

So far we have attempted to test the theoretical prediction of Huse and Henley [7]. Now, based on our simulation, we make some further predictions regarding the universal features of domain growth in random magnetic systems. We have tested for dynamical scaling by plotting (for different values of C) $S(k, t)\langle k \rangle^2$ versus $k/\langle k \rangle$ for different times. If dynamical scaling is valid, the data should collapse onto a single master curve. We have confirmed (results not presented here) that dynamical scaling is valid for all values of C considered here. Furthermore, the universal functions obtained in this fashion are independent of the amplitude of disorder. This is shown in figure 4(a), where we plot $S(k, t)\langle k \rangle^2$ versus $k/\langle k \rangle$ for data from $C = 0.0$ ($t = 1000$), $C = 0.30$ ($t = 1000$), $C = 0.35$ ($t = 3000$), and $C = 0.40$ ($t = 3000$). In figure 4(b), we plot $\ln(S(k, t)\langle k \rangle^2)$ versus $k/\langle k \rangle$ for the data from figure 4(a), indicating that the universal functions agree even in the tail regions. The independence of the universal function of the amplitude of disorder should be observable in laboratory experiments.

Finally, let us compare and contrast our results with the corresponding experimental observations. To our knowledge, there is only one such experimental work [15] reported in the literature and it does not support the HH prediction. The experiment has been performed on $Rb_2Co_pMg_{1-p}F_4$, which is a well characterized (effectively) two-dimensional antiferromagnet where strong anisotropy gives rise to Ising-like critical behaviour. Nevertheless, the domain walls in the latter system have a finite thickness. In our cell dynamical simulation also, the system has soft walls which harden (relative to the characteristic domain size) with the passage of time. Therefore, the system in our computer experiment is not very different from the real system studied in the laboratory experiment. However, there are at least two important differences:

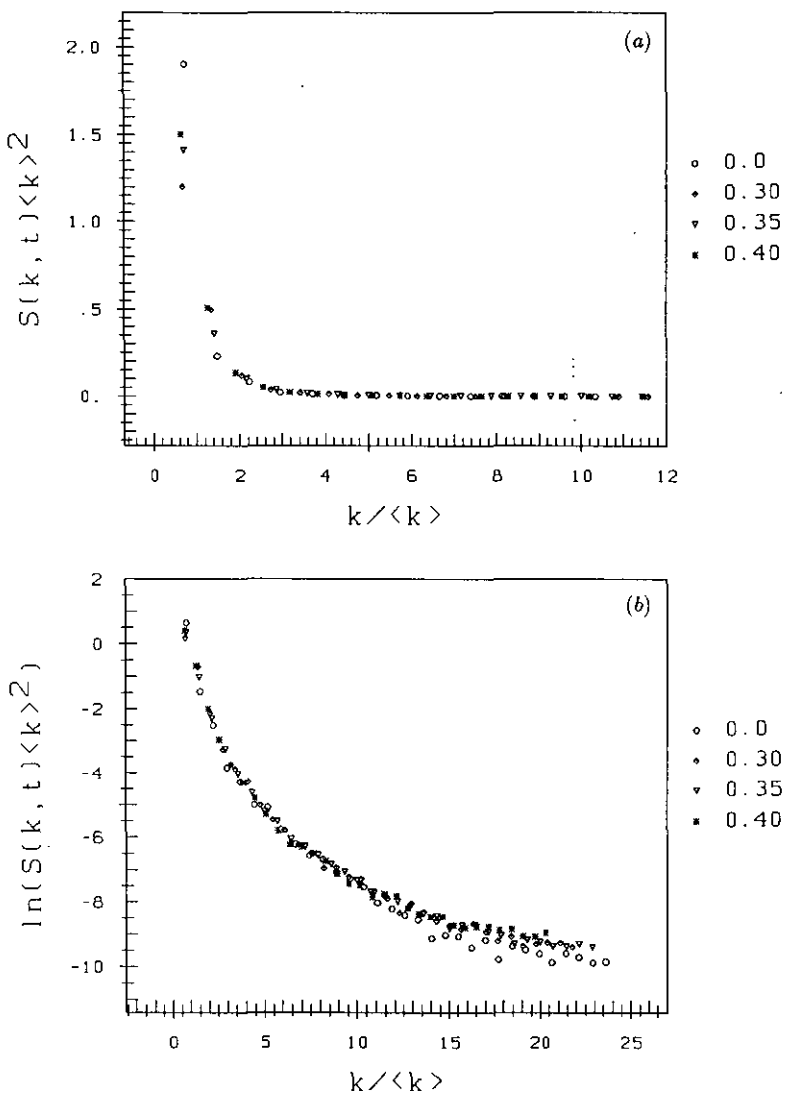

Figure 4. (*a*) Plot of $S(k, t)\langle k\rangle^2$ versus $k/\langle k\rangle$ for the data from disorder amplitudes $C = 0.0$ ($t = 1000$), $C = 0.30$ ($t = 1000$), $C = 0.35$ ($t = 3000$) and $C = 0.40$ ($t = 3000$). The different disorder amplitudes are denoted by the symbols indicated. The noise amplitude is always taken to be $B = 0.2$ (*b*) Data from (*a*), plotted on a semi-log scale, i.e. $\ln(S(k, t)\langle k\rangle)^2)$ is plotted against $k/\langle k\rangle$.

(i) The disorder enters the laboratory system through random *site* dilution (i.e. random substitution of the magnetic ions by non-magnetic ones), whereas the concepts of site and bond do not have any clear meaning in the coarse-grained picture of the cell-dynamic approach.

(ii) Since p in the samples used was very close to the corresponding percolation threshold p_c, the growth process was strongly affected by self-similarity of the underlying structure [10], whereas no such fractal effects influence growth in our cell-dynamic formulation.

Of course, it is difficult to be certain whether or not the laboratory experiment could really probe the asymptotic regime. Therefore, the disagreement with the predictions of HH and our numerical results may also be a consequence of the experimental results being in the crossover regime. We urge experimentalists to perform longer-time experiments and also to check for the validity of dynamical scaling.

We would like to end our discussion with a philosophical note on the recent rends in numerical methods in statistical physics. Recently, it has been possible [16] to resolve some of the controversies in the literature regarding the static critical behaviour of the REIM by using the various efficient non-local (cluster) algorithms [17] developed specifically for this purpose over the last few years. We have suceeded here in throwing light on the dynamical behaviour of a coarse-grained version of the REIM by using another non-local algorithm developed specifically for such studies.

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