

Teitel and Domany Respond: The exact calculation of Maritan and Stella^{1,2} (MS) not only confirms the dynamic phase transition found by our numerical and perturbative renormalization-group (RG) calculations,³ but rather beautifully agrees with ours in all physical details. The confusion, which leads MS to believe that their results “largely disagree” with ours, results from oversight of the fact that *different RG schemes in general lead to different fixed-point values and RG flows*. While fixed-point values are not universal, and depend on the RG scheme implemented, all physical quantities should agree if calculated properly. Such is the situation here. Both calculations, when used for the initial model parametrized by $\epsilon_0=1$, $\epsilon_{i+1}/\epsilon_i=R$, yield an anomalous regime for $R < \frac{1}{2}$ with the autocorrelation function $P_0(t) \sim t^{-x(R)}$, and a normal diffusive regime for $R > \frac{1}{2}$ with $P_0(t) \sim t^{-1/2}$. The resulting exponent $x(R)$ is the same for both methods. Furthermore, the exact MS recursion relations can be used to calculate the diffusion constant D by the method outlined in our paper.³ This is done by use of ϵ_1 (instead of R) as the scaling parameter, with the MS results for (1) the n th iterate² $\epsilon_1^{(n)} = R[1 - (2R)^{n+1}]/(1 - 2R)$, and (2) the eigenvalue scaling factor¹ $\lambda'(\epsilon_1) = \alpha(\epsilon_1)\lambda(\epsilon_1)$ with $\alpha(\epsilon_1) = 4 + 2/\epsilon_1$, in conjunction with our relations³ $P_0(t, R) = P_0(Dt, R^*)$ and

$$D = \prod_{n=0}^{\infty} 4/\alpha(\epsilon_1^{(n)}).$$

One gets this way $D = 2(R - \frac{1}{2})/R$ for $R > \frac{1}{2}$, in full agreement with the exact answer as found by different methods in our paper.

The main apparent disagreement concerns our fixed point $R^*=1$, the equal-barrier model. For this value the problem is translationally invariant. Our RG of decimating every other *site* does not break this symmetry, while the MS procedure of decimating every other *pair of sites* does. Since symmetries are conserved unless explicitly broken by the RG procedure, $R^*=1$ must be a fixed point of our RG. On the other hand, the MS procedure maps the equal-barrier problem to one of a doubled unit cell, with alternating couplings $\epsilon_0=1$ and $\epsilon_1 \neq \epsilon_0$. However, since the MS procedure is *exact*, the physics of the equal-barrier model must be restored, and this happens by $\epsilon_1 \rightarrow \epsilon_1^* = \infty$, which is nothing but a model of pairs of sites with no barrier (i.e., infinite transition rate) between them, coupled by barriers $\epsilon_0=1$ between neighboring pairs. Obviously this is precisely equivalent in all physical details to the equal-barrier model.

MS err² when they say that their fixed-point structure differs from ours. Our fixed line $R^*=R$ for $0 \leq R \leq \frac{1}{2}$ maps onto their fixed line $\epsilon_1^*=R/(1-2R)$, $\epsilon_{i+1}^*/\epsilon_i^*=R$, $i \geq 1$, as they seem to agree.

However, for $\frac{1}{2} < R$ they claim they have a “fixed line” $\epsilon_1^* = \infty$, $\epsilon_{i+1}^*/\epsilon_i^* = R$. This “line,” however, is just a point, i.e., $1/\epsilon_i^* = 0$, $i \geq 1$ ($\epsilon_0^*=1$ by construction). The fact that models characterized by different initial R approach this point in different directions, i.e., $\epsilon_{i+1}^{(n)}/\epsilon_i^{(n)} = R$, is irrelevant to the final $n \rightarrow \infty$ behavior. The ordinary diffusion fixed point of their model just corresponds to the case $R^* = \infty$ of the original model, which is identical in all respects to our $R^*=1$ fixed point, as explained above.

Our calculation is based on the idea (confirmed by our numerical checks, and now by MS) that the problem has only one relevant scaling variable (our R , their ϵ_1). Thus for the initial physical problem $\epsilon_i = R^i$, $i \geq 0$, one can construct a β function on the physical (one dimensional) parameter space $R' = \beta(R)$, such that the long-time behavior of a system with parameter R will be identical to that of a system half the size but with parameter R' . The “identical behavior” is guaranteed by matching the low-lying eigenvalues of the master equation. Such a β function, augmented by the necessary functions which describe how properties rescale when we go from R to R' [in our case the eigenvalue rescaling factor $\alpha(R)$], provide a complete description of the long-time properties of the system as the flows in the infinite-dimensional ϵ_i space of a particular RG scheme.

Since our matching procedure in no way breaks the translational symmetry of the original problem (as does MS), we expect, and find, our results to agree with those obtained from the RG procedure based on decimation of every other site, whenever such decimation can be carried out successfully (i.e., $R \ll 1$ and $R \simeq 1$). In particular, we have $R^*=1$ as the fixed point characterizing ordinary diffusion. However, we stress that our procedure is independent of the decimation scheme and can be implemented at general R , where decimation of every other site fails (because of generation of nonhierarchical couplings).

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Received 20 January 1986

PACS numbers: 64.70.-p, 05.40.+j, 61.40.+b

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²A. Maritan and A. L. Stella, preceding Comment [Phys. Rev. Lett. **56**, 1754 (1986)].

³S. Teitel and E. Domany, Phys. Rev. Lett. **55**, 2176 (1985).