Comment on "Self-Similarity in Irreversible Kinetic Gelation"

In a recent Letter, Family reported on a Monte Carlo study of the fractal dimension of the irreversible kinetic gelation model on a two-dimensional lattice. He made the startling discovery that d_f depends upon the value of the initiator concentration c_I , decreasing from its percolation value $d_f \cong 1.9$ for large c_I to 1.7 for small c_I . He also made the intriguing suggestion that kinetic gelation might be in the same universality class as dif-

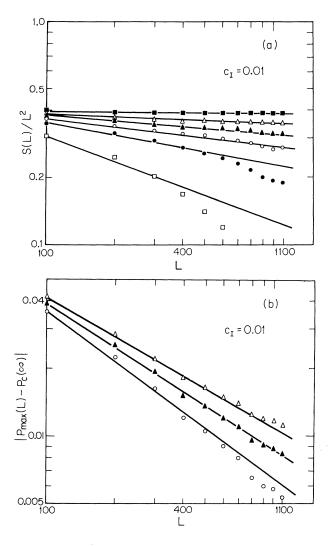


FIG. 1. (a) The fraction of sites belonging to the incipient infinite cluster vs L, and (b) finite-size-scaling plot for $|p_{\rm max}(L)-p_c^{\rm trial}|$ vs L. Here $p_c^{\rm trial}=0.235$ (solid squares) corresponds to $d_f=2$; 0.230 (open triangles) to $d_f=1.96$; 0.227 (solid triangles) to $d_f=1.91$; 0.224 (open circles) to $d_f=1.86$; 0.220 (solid circles) to $d_f=1.80$; and 0.210 (open squares) to $d_f=1.62$.

fusion-limited aggregation (DLA), for which $d_f \approx 1.7$ also, thus linking the major model for addition polymerization with the major model for aggregation and growth. We have undertaken our own study of kinetic gelation by the same Monte Carlo procedure, with the principal difference being that (i) we perform a more elaborate data analysis and (ii) we study systems roughly 7.5 times as large: We study systems of size L^2 for a sequence of L values up to 1100, while Family's study was limited to $L \leq 400$.

Figure 1(a) corresponds to Fig. 3 of Family, showing the L dependence of the fraction of sites $\rho(L)$ in the incipient infinite cluster for several trial values $p_c^{\rm trial}$. Since $\rho(L) \sim L^{d_f-d}$, we see that d_f-d depends strongly on $p_c^{\rm trial}$. From the full range of data, $L \leq 1100$, we can now clearly rule out $d_f \leq 1.80$. To fix d_f more precisely, we consider the prediction of finite-size scaling $|p_{\rm max}(L)-p_c|\sim L^{-1/\nu}$, where $p_{\rm max}(L)$ is the value of p that leads to a maximum in the mean cluster size. From Fig. 1(b) we see that $p_c^{\rm trial}=0.227$ is the best choice of percolation threshold, and so from Fig. 1(a) we conclude that $d_f=1.91\pm0.03$.

The above analysis was carried out for $c_I = 0.01$, the same value used by Family. We have also obtained data for other values of c_I and all our data are consistent with the possibility that d_f is independent of c_I , thus establishing that the "field-like scaling power" $y_h = d_f$ does not depend on initiator concentration.

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