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LETTER TO THE EDITOR

Position space renormalisation group for directed diffusion limited aggregation

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Abstract. We use a position space renormalisation group transformation to show that directed diffusion limited aggregation and directed animals are in different universality classes.

The problem of kinetic aggregation models of the type introduced by Witten and Sander (1981) has attracted much interest (Meakin 1983a, b). These models give an idealised description of the process in which diffusing particles aggregate to form clusters. A detailed analysis for smoke particle aggregates is given in Forrest and Witten (1979). In this letter we consider a directed form of the 'Witten–Sander' model which describes the aggregation of particles in the presence of a force field; for example the aggregation of smoke particles in a large electric field. Nadal *et al* (1984) have carried out Monte Carlo simulations for this model and shown that it has significantly different critical exponents from those of directed lattice animals. This implies that directed diffusion limited aggregation and directed lattice animals are in separate universality classes. We use a PSRG (position space renormalisation group) approach similar to the analysis by Gould *et al* (1983) of the 'Witten–Sander' model and isotropic lattice animals, to confirm this result. An estimate for the value of the critical exponent $\nu_{\|}$ is obtained.

We begin by describing the two models and then describe in detail the renormalisation group calculation. We consider both the directed animal and aggregation model on a two-dimensional square lattice. We place a source site at the origin and allow the cluster to grow only eastwards or northwards. Thus the cluster grows preferentially along the (1, 1) axis. For the animal problem each cluster with s sites has probability K^s where K is the fugacity of an occupied site. For the diffusion limited aggregation problem, the cluster is formed by releasing from infinity successive particles which each follow a directed random walk until they reach a possible next growth site for the cluster. In this case the probability depends not only on the number of sites but also on the walks available to each site. It is this difference in probabilities which implies that the two problems are in different universality classes. This is similar to the difference between a true self avoiding random walk and a self repelling chain (Amit *et al* 1983).

We perform our PSRG calculation using a 2×2 cell to site transformation on a square lattice similar to that of Gould *et al* (1983) for the isotropic system (for a recent review of these methods see Stanley *et al* 1982). In this transformation each 2×2 cell containing four sites is mapped onto a single site. The lattice spacing in the renormalised

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system is thus twice that in the original system. We place our seed particle at the bottom left-hand corner of the cell and define a cell to be spanned (occupied) if the top right-hand corner is also occupied. We notice that if we carry out this transformation on a particular configuration we may find that a connected configuration on the original lattice is no longer connected in the renormalised system. This is an interface effect between the cells and should decrease as the cell size is increased (Reynolds *et al* 1980, Stanley *et al* 1982). In figure 1 we show all the spanning clusters of sites on a 2×2 cell. For a directed animal it follows directly from this picture that the probability that the cell is spanned is

$$R_2(K)=2K^3+K^4. \tag{1}$$

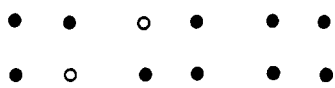

Figure 1. The set of spanning clusters of sites in a 2×2 cell. ● = occupied site; ○ = vacant site.

For the directed aggregation model we need to also define a bond lattice for the directed random walks. We choose the lattice shown in figure 2 and assign to each step of a walk a probability ω. By considering all possible ways of building each cluster using different walks, we can calculate the probability $R_2(K,\omega)$ that the cell is spanned:

$$R_2(K,\omega)=4\omega^2K^3(1+2\omega)+8\omega^3K^4(1+2\omega). \tag{2}$$

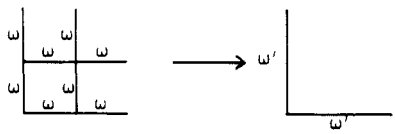

Figure 2. We show the 2×2 bond lattice for the directed random walks and the transformation to single bonds.

We can thus write down a recursion relation for K

$$K'=R_2(K,\omega). \tag{3}$$

We also need a recursion relation for ω and making the transformation shown in figure 2 then

$$\omega'=\omega^2+2\omega^3. \tag{4}$$

This equation has a fixed point at $\omega^*=\frac{1}{2}$ which is the exact fixed point for a directed random walk on a square lattice (Redner and Majid 1983). In order to look at the differences between the two models we consider an aggregation model in which the seed sites can be all possible directed animals. The new probability function for spanning clusters is

$$S_2(K,\omega)=2K^3+K^4+4\omega K^3(1+\omega+2\omega^2)+4\omega K^4(1+2\omega+2\omega^2+4\omega^3). \tag{5}$$

We calculate the new equation for ω by considering all walks on a cell which is already

partly occupied and find

$$\omega' = \omega^2 + 2\omega^3 + K^2\omega^2 + 2\omega^2 K(1+\omega). \tag{6}$$

In figure 3 we plot the behaviour of the recursion equations

$$K' = S_2(K, \omega) \tag{7}$$

and equation (6). We see that there are three non-trivial fixed points: one at $K = 0$, $\omega = \frac{1}{2}$ which is that of a directed walk, one at $\omega = 0$, $K = 0.62$ which is that for a directed animal and one at $K = 0.42$, $\omega = 0.34$ which corresponds to the directed diffusion limited aggregation problem. Thus the directed aggregation problem is in a different universality class from that of directed animals.

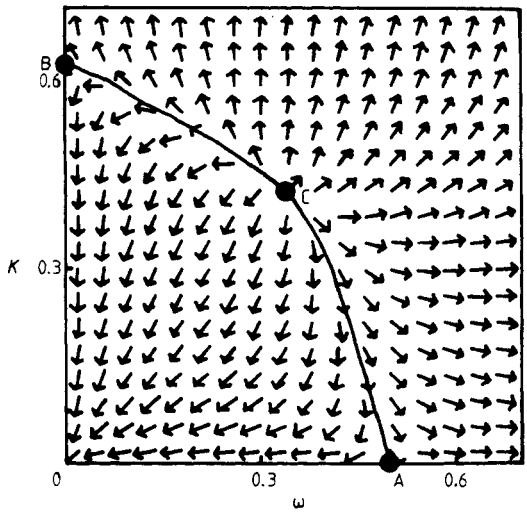

Figure 3. This diagram shows the behaviour of the recursion relations (6) and (7). The fixed point A is for directed walks, B for directed animals and C for directed aggregation.

We then calculated a value for the exponent $\nu_\parallel$ directly from our 2×2 results (2) and (4). If we define

$$\lambda_K = \partial R_2(K, \omega)/\partial K|_{K^*,\omega^*} \tag{8}$$

where K^* and ω^* are the fixed point solutions of equations (3) and (4) then

$$\nu_\parallel = \ln 2/\ln \lambda_K = 0.57. \tag{9}$$

We also repeated this calculation for a 3×3 cell to site transformation and a 3×3 to 2×2 cell to cell transformation. The results for these calculations are given in table 1. We always find $\nu_\parallel$ near to 0.6 compared with the Monte Carlo value of 0.52 (Nadal *et al* 1984). This discrepancy is not surprising and comes from two sources. The first is the strong interface effects between small cells which we mentioned earlier. We believe that these will not affect the qualitative behaviour of the system and therefore that the phase diagram will have the same structure as shown in figure 3 when the cell size is increased. However we do expect them to affect exponent values. The second source of error is that we have not allowed for the different scaling factors of the

Table 1. $\nu_{\parallel}$ for directed aggregation.

Method	K^*	ω^*	$\nu_{\parallel}$
2×2 cell to site	0.57	0.5	0.57
3×3 cell to site	0.43	0.5	0.59
3×3 to 2×2 cell to cell	0.34	0.5	0.62
3×3 to 2×2 cell to cell with patching	0.46	0.5	0.60
Monte Carlo			
Nadal *et al* (1984)	—	—	0.52 ± 0.02

parallel and perpendicular length scales in the problem. Herrmann *et al* (1983) have suggested an improved method which involves patching the cells together to form an infinite strip and allowing clusters which connect between neighbouring cells. He claims that if a sequence of values of K^* and $\nu_{\parallel}$ for increasing size cell to cell transformations is obtained then in the limit of infinite cell size the correct results are obtained. So good estimates can hopefully be obtained by examining the sequence. Unfortunately in the case of directed aggregation we have only 3×3 and 2×2 results and thus can obtain only one term in the sequence and cannot look at the limit of large cell size.

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