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LETTER TO THE EDITOR

Cluster renormalisation study of site lattice animals in two and three dimensions

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Abstract. We have studied site lattice animals using the cluster renormalisation (CR) approach previously applied to bond animals. The exponent ν, characterising the asymptotic behaviour of the mean-square radius of gyration of site animals, and the fractal dimension $d_f = 1/\nu$, are determined in two and three dimensions. We find $\nu = 0.649 \pm 0.009$ and $\nu \simeq 0.51$ in two and three dimensions, respectively. In addition we have studied restricted valence site animals on a triangular lattice using a single-parameter CR approach.

The configurational statistics of lattice animals, i.e. connected clusters of sites or bonds on a d-dimensional lattice, in the asymptotic scaling limit when the number of sites (or bonds) in an animal tends to infinity, has been a subject of considerable recent interest, because of its applications in a variety of diverse problems including the cell growth problem (see Stauffer 1978, Peters *et al* 1979, and references therein), homogeneous turbulence in fluids (Hentschel and Procaccia 1982), spinodal decomposition (Klein 1981), percolation (see e.g. Stauffer 1979, 1981, Essam 1980, Gaunt 1980, and references therein) and the statistics of dilute branched polymers (Lubensky and Isaacson 1979, Family 1980, Family and Coniglio 1980, Parisi and Sourlas 1981).

One of the most important scaling properties of lattice animals, which serves to characterise their configurational properties, is the dependence of the mean-square radius of gyration $\langle R_N^2 \rangle$ on the number of elements N in an animal. In the limit $N \to \infty$, $\xi = \langle R_N^2 \rangle^{1/2}$ grows as

$$\xi \sim N^{\nu} \tag{1}$$

where ν is the exponent describing the power law divergence of this length. An alternative for characterising the conformation of a lattice animal is to relate it to an 'effective' or fractal dimension d_f (see e.g. Stanley 1977, Stauffer 1979, Mandelbrot 1982, and references therein). If we treat N as the 'mass' of an animal, since (mass) $\sim$ (radius)^{d_f}, then by relation (1),

$$d_f = 1/\nu. \tag{2}$$

If d_f is less than the spatial dimension d, the animals are highly ramified structures; if $d_f = d$, they are compact (Family and Coniglio 1980).

Recently a number of techniques, including Monte Carlo (Stauffer 1978, Herrmann 1979, Peters *et al* 1979, Gould and Holl 1981), series analysis (Peters *et al* 1979),

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field theory (Lubensky and Isaacson 1979, Parisi and Sourlas 1981), position space renormalisation group (Family 1980, Family and Coniglio 1980), finite size scaling (Derrida and de Sèze 1982), and Flory type approximation (Isaacson and Lubensky 1980, Daoud and Joanny 1981), have been used to estimate ν in various dimensions. In particular, Parisi and Sourlas (1981) found a connection between lattice animals and the Lee–Yang edge singularity problem and from it obtained the exact result $\nu = \frac{1}{2}$ in $d = 3$. However, their relation cannot be used in $d = 2$, and the present estimate $\nu = 0.61$–0.66 (see table 2) is not very conclusive. In view of the widespread interest in lattice animals, and because presently there is no consensus on the value of ν in $d = 2$—which is needed to understand turbulence in three dimensions (Hentschel and Procaccia 1982)—an independent calculation of ν would be of interest.

In this letter we present the first direct renormalisation group (RG) calculation of the exponent ν and the fractal dimension d_f for *site* lattice animals in $d = 2, 3$ using a RG approach—which we call the cluster renormalisation (CR)—previously applied (Family 1980) to bond lattice animals (dilute branched polymers). In addition, we use CR to study the restricted valence site animal problem (Gaunt *et al* 1979) on a triangular lattice. In a restricted valence animal the number of nearest neighbours of a site is restricted to be less than or equal to some prescribed value v, such that $v \leq z$, where z is the coordination number of the lattice. This problem is of interest as a model of steric hindrance in branched polymers and polymer gels. Recent studies (Whittington *et al* 1979) have shown that the dominant singularity of the generating function of site animals on a triangular lattice can be characterised by different exponents for $v = 2$ than for $v \geq 3$. In this letter we study the effect of valence on the exponent ν using a single parameter CR approach.

The essential ideas of the CR approach for lattice animals have been presented before (Family 1980) where they were applied to bond animals (dilute branched polymers) on a square lattice. In this approach we investigate the manner in which the global connectivity of lattice animals changes upon repeated length rescaling. We carry out the length rescaling by first dividing the lattice into cells of linear dimension b, as shown in figure 1, and rescaling to cells of linear dimension 1. Since in the lattice animal problem we are interested in the statistics of all distinct clusters starting at the origin of an infinite lattice, we only rescale a cell if it contains a *single cluster* originating at a *fixed origin* on the cell. In addition, since we are interested in the connectivity properties of lattice animals, we also use the general connectivity rule (for a review of the connectivity rule and its applications in polymer models, see Stanley *et al* (1982), and references therein) for rescaling an animal within a cell into a rescaled cell. For site lattice animals we define d types of connectivity rules on a d-dimensional cell and denote them by r_i, where $i = 0, 1, \ldots, d$. In r_0 a cell is rescaled to an occupied site, if it contains a single connected cluster that, starting from a fixed origin (which for all rules we choose to be the lower left-hand corner of the cell, as shown in figure 1), extends in any of the d possible directions across the cell; whereas r_i ($i \geq 1$) requires a site animal starting from the origin to span in i specific directions. We expect all these rules to converge to the same results in the large cell limit.

The RG transformations for site animals are constructed similarly to bond animals (Family 1980). We first assign a fugacity K to each site in an animal and then determine the generating function

$$R_i(K; b) = \sum_n c_i(n) K^n \tag{3}$$

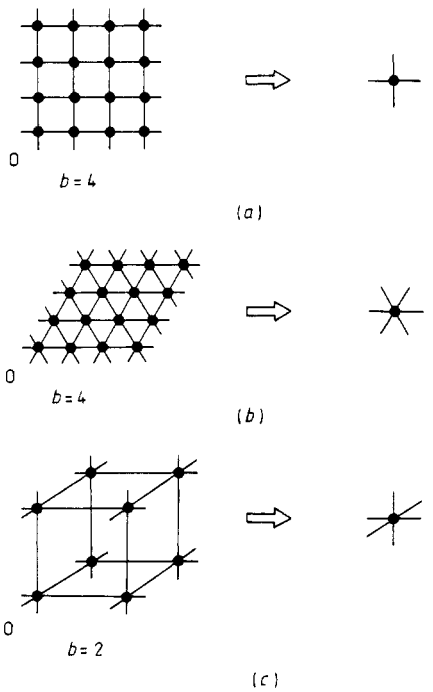

Figure 1. Examples of the types of cells used in CR calculations for (*a*) the square lattice, (*b*) the triangular lattice, and (*c*) the simple cubic lattice. Each cell contains b^d sites and under the RG transformation is rescaled to a single site. The origin of the cell where all site animals originate is denoted by O.

where $c_i(n)$ is the total number of site animals with n sites spanning according to rule r_i on a cell of side b. We define the recursion relation for the RG transformation by requiring that the generating function for the spanning animals is invariant on the original and rescaled levels. For connectivity rule r_i, this leads to a recursion relation of the form

$$K' = R_i(K; b) \tag{4}$$

where the renormalised fugacity K' is the generating function of a single site on the rescaled lattice.

We have used a computer program to determine the exact recursion relations for cells of size $b = 2$–5 on a square lattice using rules r_0, r_1 and r_2. These recursion relations each have two trivial (stable) fixed points at $K^* = K' = K = 0$ and ∞, and one critical (unstable) fixed point at an intermediate value of $K = K' = K^*$. The value of K at the unstable fixed point gives an estimate of the critical fugacity $K_c = 1/\mu$, where μ is the site lattice animal growth parameter (Sykes and Glen 1976). The exponent ν and the fractal dimension d_f are obtained from

$$\nu = d_f = \ln b / \ln \lambda \tag{5}$$

where λ is the eigenvalue of the linearised RG transformation.

In analogy with percolation (Reynolds *et al* 1978) and bond lattice animals (Family 1980), we also define a cell-to-cell transformation in which an implicit RG transformation from a cell of size b to a cell of size b' is constructed. Whereas the results for

the cell-to-site transformations are expected to improve with increasing b, the cell-to-cell transformation results improve as $b/b' \to 1$.

The results for K^* and ν with both types of transformations are given in table 1 for site lattice animals on the square lattice. From table 1 we see that the results of the cell-to-cell procedure improve as $b/b' \to 1$, and are in agreement with the estimates obtained by other techniques (see table 2).

Furthermore, from previous RG studies (Reynolds *et al* 1980, Eschbach *et al* 1981, Family and Reynolds 1981), it appears that the error in the cell-to-site finite b results vanishes as $b \to \infty$ in the following form:

$$\nu^{-1}(b) = \nu^{-1} + c_1(\ln b)^{-1} + c_2(\ln b)^{-2}. \tag{6}$$

Thus, the error decreases as b increases in a predictable fashion, and the results for $\nu(b)$ can be used to extrapolate the limiting behaviour ($b \to \infty$). Fitting the data of table 1 to (6), we have determined the best estimate for ν^{-1} for each of the three different rules separately. We find $\nu^{-1} = d_f = 1.59$, 1.54 and 1.48 for rules r_0, r_1 and r_2, respectively. However, a much better procedure is to combine the three sets of data, because asymptotically they are expected to converge to the same result. As shown in figure 2, we have determined ν^{-1} by finding the value of the intercept which gives the best overall fit to the three sets of data simultaneously. From this procedure we find $\nu^{-1} = d_f = 1.54 \pm 0.02$, i.e. $\nu = 0.649 \pm 0.009$. This result is listed in table 2

Table 1. The critical exponent ν and the fixed point K^* for site lattice animals on a square lattice, using (*a*) rule r_0, (*b*) rule r_1, and (*c*) rule r_2. The results are for a transformation from cells of side b to cells of side b', corresponding to a length rescaling of b/b'. The case $b' = 1$ is the cell-to-site transformation with a rescaling length b.

(*a*) Rule r_0.

b		$b'=1$	2	3	4
2	ν	0.7976			
	K^*	0.3247			
3	ν	0.7437	0.6684		
	K^*	0.3330	0.3388		
4	ν	0.7210	0.6583	0.6434	
	K^*	0.3236	0.3232	0.3111	
5	ν	0.7093	0.6532	0.6402	0.6372
	K^*	0.3132	0.3111	0.3013	0.2930

(*b*) Rule r_1.

b		$b'=1$	2	3	4
2	ν	0.7094			
	K^*	0.4142			
3	ν	0.6987	0.6784		
	K^*	0.3754	0.3483		
4	ν	0.6912	0.6697	0.6564	
	K^*	0.3487	0.3287	0.3134	
5	ν	0.6867	0.6657	0.6535	0.6485
	K^*	0.3302	0.3148	0.3029	0.2941

(*c*) Rule r_2.

b		$b'=1$	2	3	4
2	ν	0.6040			
	K^*	0.5321			
3	ν	0.6236	0.6658		
	K^*	0.4363	0.3716		
4	ν	0.6326	0.6686	0.6735	
	K^*	0.3869	0.3436	0.3213	
5	ν	0.6374	0.6701	0.6732	0.6776
	K^*	0.3573	0.3258	0.3091	0.2985

along with the estimates obtained by other techniques for site animals, bond animals, as well as bond animals without loops (i.e. branching trees), which are all expected to be in the same universality class.

Table 2. Comparison of the present CR result for ν and d_t for site lattice animals in $d = 2$ with the results obtained by other methods for (*a*) site animals, (*b*) bond animals and (*c*) bond animals without loops.

Method	ν	d_t
(*a*) *Site animals:*		
Cluster renormalisation	0.649 ± 0.009	1.54 ± 0.02
Monte Carlo	0.660 ± 0.007[a]	1.52 ± 0.02
	0.65[b]	1.54
	0.65 ± 0.02[c]	1.54 ± 0.05
Field theory	0.61[d]	1.64
Flory theory	0.625[e]	1.60
Finite size scaling	0.6408 ± 0.0003[f]	1.5605 ± 0.0007
(*b*) *Bond animals:*		
Cluster renormalisation	0.6370[g]	1.570
(*c*) *Bond animals without loops:*[h]		
Cluster renormalisation	0.6273[g]	1.594
Monte Carlo	0.615[i]	1.63

[a] Stauffer (1978), Herrmann (1979), [b] Peters *et al* (1979), [c] Gould and Holl (1981), [d] Parisi and Sourlas (1981), [e] Isaacson and Lubensky (1980), Daoud and Joanny (1981), [f] Derrida and de Sèze (1982), [g] Family (1980), [h] Animals with and without loops are in the same universality class (Lubensky and Isaacson 1979, Family 1980, Gaunt *et al* 1982), [i] Seitz and Klein (1981).

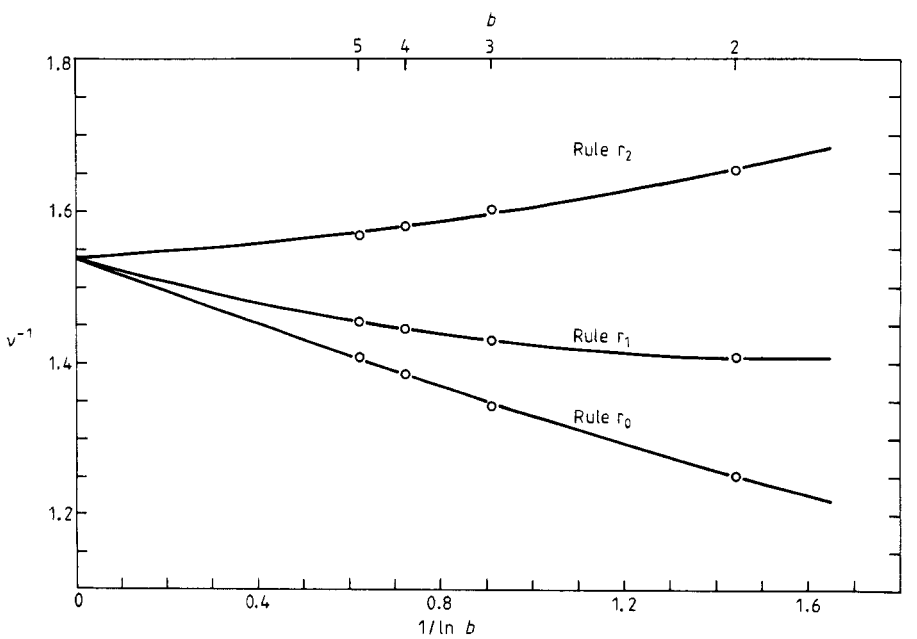

Figure 2. Plot of our estimates of ν^{-1} against $1/\ln b$ from table 1. The curves through the points are the best simultaneous quadratic fit to our three sets of data.

In $d = 3$, we have determined the recursion relations for site animals using rules r_0, r_1, r_2 and r_3 on a cell of size $b = 2$ on the simple cubic lattice. The values of ν and K^* obtained from these recursion relations are given in table 3. It is not possible to obtain a closed-form recursion relation for larger cells within a reasonable computer time. However, it is possible to give a rough estimate of ν in $d = 3$ in the following way. Let us define the ratio $f(b) = \nu/\bar{\nu}(b)$, where ν is the correct value of this exponent whereas $\bar{\nu}(b)$ is the average value of ν obtained from RG calculations with a cell of size b using rules r_0–r_d. From the data of tables 1 and 2 we find $f(2) \simeq 0.91$ in $d = 2$. Assuming that $f(2)$ is independent of d and using the value $\bar{\nu}(2) \simeq 0.56$ determined from the data in table 3, we find that $\nu \simeq 0.51$ in $d = 3$. Although this simple procedure is not expected to be too reliable, its estimate is in reasonable agreement with the exact result $\nu = 1/2$ (Parisi and Sourlas 1981), and the Monte Carlo result $\nu = 0.53 \pm 0.02$ (Gould and Holl 1981) for site animals and $\nu \simeq 0.46$ (Seitz and Klein 1981) for bond animals without loops, which are in the same universality class as bond animals (Lubensky and Isaacson 1979, Family 1980, 1982).

Table 3. The exponent ν and the fixed point K^* for site lattice animals on a simple cubic lattice with $b = 2$ using rules r_0–r_3.

Rule	r_0	r_1	r_2	r_3
ν	0.7120	0.5807	0.4928	0.4583
K^*	0.1824	0.2452	0.2973	0.3280

Proceeding to the restricted valence problem, we use the CR approach to investigate whether restricting the maximum allowed valence of sites in an animal on a triangular lattice changes the universality class.

We have determined the recursion relations for site animals with maximum valence $v = 2$–6 on cells of size $b = 2, 3$ on a triangular lattice (see figure 1) using rule r_1. For $v = 2$, the animals are the neighbour-avoiding walks (Whittington *et al* 1979) and were previously studied by the CR approach on the square and on the simple cubic lattices (Family 1981).

The recursion relations for $v = 2$ on a cell of size $b = 2$, using rule r_1, is

$$K' = K^2 + 2K^3 \tag{7}$$

which has a fixed point at $K^* = 0.5000$ and $\nu = 0.7565$. Because the $b = 2$ cell is too small, there is only one recursion relation for $v \geqslant 3$; namely

$$K' = K^2 + 3K^3 + K^4 \tag{8}$$

which has a fixed point at $K^* = 0.4142$ and $\nu = 0.7094$. For the cell of size $b = 3$, different recursion relations are obtained for $v = 2$–6. The results for ν and K^* for the $b = 3$ cell of the triangular lattice using rule r_1 are given in table 4 for $v = 2$–6.

The results of table 4 show that ν decreases as v increases. However, its maximum change occurs between $v = 2$ and 3, and for $v \geqslant 3$ it does not change very much. This is consistent with the series results (Whittington *et al* 1979), showing that site animals with $v = 2$ are in a different universality class from site animals with $v \geqslant 3$, and site animals with $v \geqslant 3$ are in the same universality class as unrestricted animals ($v = z$). These results are also consistent with a two-parameter CR calculation (Family 1980),

Table 4. The exponent ν and the fixed point K^* for restricted valence site animals on a $b = 3$ cell of the triangular lattice.

v	2	3	4	5	6
ν	0.7856	0.7176	0.7034	0.7003	0.7001
K^*	0.4902	0.3692	0.3566	0.3550	0.3549

showing that self avoiding-walks ($v = 2$ bond animals) are in a different universality class from bond lattice animals ($v = z$).

In summary, we have studied site lattice animals using the CR approach previously applied to bond animals (Family 1980), and have obtained the exponent ν and the fractal dimension d_f in $d = 2$ and 3. Our result $\nu = 0.649 \pm 0.009$ in $d = 2$ agrees very well with the finite-size scaling calculation (Derrida and de Sèze 1982). However, the estimate $\nu = 0.61$ obtained by Parisi and Sourlas (1981) using field-theoretic and extrapolation schemes, and the Flory result $\nu = 5/8 = 0.625$ (Isaacson and Lubensky 1980, Daoud and Joanny 1981), are outside the error bars. Our estimate $\nu \simeq 0.51$ in $d = 3$ is in reasonable agreement with the exact result $\nu = \frac{1}{2}$ (Parisi and Sourlas 1981), and the Monte Carlo results $\nu = 0.53 \pm 0.02$ (Gould and Holl 1981) for site animals and $\nu \simeq 0.46$ (Seitz and Klein 1981) for bond animals without loops.

We have also studied restricted valence site animals on the triangular lattice using a single-parameter CR approach. Our result suggests that site animals with $v = 2$ (neighbour-avoiding walks) are in a different universality class from site animals with $v \geqslant 3$, but site animals with $v \geqslant 3$ are in the same universality class as unrestricted animals ($v = z$).

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