

Enumerations of lattice animals and trees

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Abstract

We have developed an improved algorithm that allows us to enumerate the number of site animals on the square lattice up to size 46. We also calculate the number of lattice trees up to size 44 and the radius of gyration of both lattice animals and trees up to size 42. Analysis of the resulting series yields an improved estimate, $\lambda = 4.062570(8)$, for the growth constant of lattice animals, and, $\lambda_0 = 3.795254(8)$, for the growth constant of trees, and confirms to a very high degree of certainty that both the animal and tree generating functions have a logarithmic divergence. Analysis of the radius of gyration series yields the estimate, $\nu = 0.64115(5)$, for the size exponent.

KEY WORDS: Lattice animals; Exact enumeration; Computer algorithms

1 Introduction

The enumeration of lattice animals is a classical combinatorial problem of great interest in its own right [1]. Lattice animals are connected subgraphs of a lattice. A *site* animal can be viewed as a finite set of lattice sites connected by a network of nearest neighbor bonds. The fundamental problem is the calculation (up to translation) of the number of animals, a_n , with n sites. In the physics literature lattice animals are often called *clusters* due to their close relationship to percolation problems [2]. Series expansions for various percolation properties, such as the percolation probability or the average cluster size, can be obtained as weighted sums over the number of lattice animals, $g_{n,m}$, enumerated according to the number of sites n and perimeter m [3, 4]. In mathematics, and combinatorics in particular, the term polyominoes is frequently used. A polyomino is a set of lattice cells joined at their edges. So polyominoes are identical to site animals on the dual lattice. Furthermore, the enumeration of lattice animals has traditionally served as a benchmark for computer performance and algorithm design [5]–[12].

Lattice trees form a proper subset of lattice animals, and can be defined as those animals containing no circuits. Another way of defining trees is that a tree is a finite connected set of

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sites with the property that a walk starting from any given site cannot return to the original site without self-intersections. Lattice trees have been suggested as a model of branched polymers [13]. Lattice animals and trees are expected to belong to the same universality class [13, 14] and thus have the same critical exponents.

An algorithm for the calculation of $g_{n,m}$ has been published by Martin [6] and Redner [8]. It was used by Sykes and co-workers to calculate series expansions for percolation problems on various lattices. In particular Sykes and Glen [4] calculated $g_{n,m}$ up to $n = 19$ on the square lattice, and thus obtained the number of lattice animals, $a_n = \sum_m g_{n,m}$, to the same order. Redelmeier [7] presented an improved algorithm for the enumeration of lattice animals and extended the results to $n = 24$. This algorithm was later used by Mertens [10] to devise an improved algorithm for the calculation of $g_{n,m}$ and a parallel version of the algorithm appeared a few years later [11]. The next major advance was obtained by Conway [12] who used the finite lattice method with an associated transfer-matrix algorithm to calculate a_n and numerous other series up to $n = 25$ [15]. In unpublished work Oliveira e Silva [16] used the parallel version of the Redelmeier algorithm [11] to extend the enumeration to $n = 28$. In this work we use an improved version of Conway's algorithm to extend the enumeration to $n = 46$. We also calculate the number of lattice trees up to $n = 44$ and the radius of gyration of lattice animals and trees up to $n = 42$.

The quantities and functions we consider in this paper are: (i) the number of lattice animals a_n and the associated generating function, $\mathcal{A}(u) = \sum a_n u^n$; (ii) the number of lattice trees t_n with generating function, $\mathcal{T}(u) = \sum t_n u^n$; and (iii) the mean-square radius of gyration of animals or trees of size n , $\langle R^2 \rangle_n$. These quantities are expected to behave as

$$\begin{aligned} a_n &= A\lambda^n n^{-\tau}[1 + o(1)], \\ t_n &= T\lambda_0^n n^{-\tau}[1 + o(1)], \\ \langle R^2 \rangle_n &= Rn^{2\nu}[1 + o(1)], \end{aligned} \tag{1}$$

where λ and λ_0 are the reciprocals u_c^{-1} of the critical point of, respectively, the animal and tree generating functions. From numerical evidence it is well-established that $\tau = 1$.

In Section 2 we give a detailed description of the finite lattice method for enumerating lattice animals. Some initial results of the analysis of the series are presented in Section 3.

2 Enumerations of lattice animals and trees

The method we use to enumerate site animals and trees on the square lattice is based on the method used by Conway [12] for the calculation of series expansions for percolation problems, and is similar to methods devised by Enting for enumeration of self-avoiding polygons [17] or the algorithm used by Derrida and De Seze to study percolation and lattice animals [18]. In the following we give a detailed description of the algorithm used to count lattice animals. We then show how to generalise the method to calculate the radius of gyration and obtain series for lattice trees.

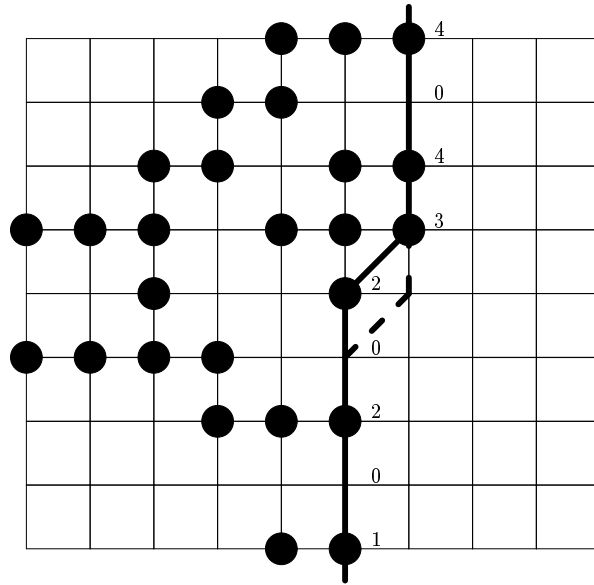


Figure 1: A snapshot of the intersection (solid line) during the transfer matrix calculation on the square lattice. Animals are enumerated by successive moves of the kink in the boundary, as exemplified by the position given by the dashed line, so that one site at a time is added to the rectangle. To the left of the boundary we have drawn an example of a partially completed animal. Numbers along the boundary indicate the encoding of this particular configuration.

2.1 Transfer matrix algorithm

The number of animals that span rectangles of width W and length L are counted using a transfer matrix algorithm. By combining the results for all $W \times L$ rectangles with $W \leq W_{\max}$ and $W + L \leq 2W_{\max} + 1$ we can count all animals up to $n = 2W_{\max}$. Due to symmetry we only consider rectangles with $L \geq W$ and thus count the contributions for rectangles with $L > W$ twice.

The transfer matrix technique involves drawing a boundary line through the rectangle intersecting a set of W sites. For each configuration of occupied or empty sites along the boundary we maintain a generating function for partially completed animals intersecting the boundary in that particular pattern. Animals in a given rectangle are enumerated by moving the boundary so as to add one site at a time, as shown in figure 1. Each configuration can be represented by a set of states $\{\sigma_i\}$, where the value of the state σ_i at position i must indicate first of all if the site is occupied or empty. An empty site is simply indicated by $\sigma_i = 0$. Since we have to ensure that we count only connected graphs more information is required if a site is occupied. In short we need a way of describing which other occupied sites on the boundary it is connected to via a set of occupied sites to the left of the boundary. The most compact encoding of this connectivity is [12]

$$\sigma_i = \begin{cases} 0 & \text{empty site,} \\ 1 & \text{occupied site not connected to others on the boundary,} \\ 2 & \text{first among a set of connected boundary sites,} \\ 3 & \text{intermediate among a set of connected boundary sites,} \\ 4 & \text{last among a set of connected boundary sites.} \end{cases} \quad (2)$$

Configurations are read from the bottom to the top. As an example the configuration along

the boundary of the partially completed animal in figure 1 is $\{102023404\}$.

In addition to the configuration of states along the boundary line we also have to specify whether or not the partially completed animals include sites on the lower and/or upper borders of the rectangle. This can simply be done by marking a configuration with a 0 if none of the borders have been touched, and a 1, 2 or 3 if, respectively, the lower border, upper border or both borders have been touched. In this way we can be sure to count only those animals which span a given rectangle in the vertical direction. That all animals span the horizontal direction is ensured by the set updating rules detailed below.

The total configuration of occupied sites and the touching of the borders can be encoded by a pair of integers (S, k) , where k indicates which borders have been touched, and S is the integer whose binary representation is obtained by assigning 3 bits to each σ_i in the configuration of occupied sites, $S = \sum_{i=0}^{W-1} \sigma_i 8^i$. We shall call such a (S, k) -pair a *signature*, and in practise represent it by an integer $\hat{S} = S + k * 8^W$. For $W \leq 20$ a signature can thus conveniently be stored in the computer as a 64-bit integer, while for $W > 20$ we need to switch to a more complicated representation, say, in terms of several 16-bit integers. Often we shall explicitly write out the configuration $\{\sigma_i\}$ instead of S and use the notation $\{S_1 S_2\}$ to indicate a configuration obtained by concatenating the strings S_1 and S_2 .

The major improvement of the method used to enumerate animals in this paper is that we require animals to span the rectangle in *both* directions. In the original approach [12] animals were only required to span in the lengthwise direction and animals of width less than W were generated many times. It is however easy to obtain the animals of width exactly W and length exactly L from this enumeration [17]. The only drawback of the new approach is that for most configurations we have to use four distinct generating functions. The major advantage is that the memory requirement of the algorithm is exponentially smaller.

Realizing the full savings in memory usage comes from two enhancements to the original algorithm. Firstly, for each configuration we keep track of the current minimum number of occupied sites N_{cur} which have been inserted to the left of the intersection in order to build up that particular configuration. Secondly, we calculate the minimum number of additional sites N_{add} required to produce a valid animal. There are three contributions, namely the number of sites required to connect all the separate pieces of the partially completed animal, the number of sites needed to ensure that the animal touches both the lower and upper boundary, and finally the number of sites needed to extend at least W columns in the length-wise direction. If the sum $N_{\text{cur}} + N_{\text{add}} > 2W_{\text{max}}$ we can discard the partial generating function for that configuration because it won't make a contribution to the animal count up to the size we are trying to obtain. Furthermore, for any W we know that contributions will start at $2W - 1$ since the smallest animals have to span a $W \times W$ rectangle. So for each configuration we need only retain $2(W_{\text{max}} - W) + 1$ terms of the generating functions. With the original algorithm contributions started at W because the animals were required to span only in the length-wise direction.

2.1.1 Derivation of updating rules

In Table I we have listed the possible local 'input' states and the 'output' states which arise as the kink in the boundary is propagated by one step. The most important boundary site is the 'lower' one situated at the bottom of the kink (the site marked with the second '2')

Table I: The various ‘input’ states and the ‘output’ states which arise as the boundary line is moved in order to include one more site of the lattice. Each panel contains two ‘output’ states where the left (right) most is the configuration in which the new site is empty (occupied).

Lower \ Upper	0	1	2	3	4
0	00 10	01 24	02 23	03 33	04 34
1	add 10	-- 24	-- 23	-- 33	
2	$\overline{00}$ 20	$\overline{01}$ 23	$\overline{02}$ $\widehat{23}$	02 23	01 24
3	00 30	01 33	02 $\widehat{33}$	03 33	04 34
4	$\overline{00}$ 40	$\overline{01}$ 34	$\overline{02}$ 33	$\overline{03}$ $\widehat{33}$	

in figure 1). This is the position in which the lattice is being extended and obviously the new site can be either empty or occupied. The second most important boundary site is the ‘upper’ one at the top of the kink (the site marked ‘3’ in figure 1). The state of the upper site is very important in determining the state of the lower site when occupied. The state of the upper site is likely to be changed as a result of the move. In addition the state of a site further afield may have to be changed if a branch of a partially completed animal terminates at the new site or if two independent components of a partially completed animal join at the new site. In the following we give the details of how some of these updating rules are derived. We shall refer to the signature before the the move as the ‘source’ and a signature produced as a result of the move as a ‘target’.

- 00: The lower and upper sites are empty. If the new site is empty the signature is unchanged. If the new site is occupied it isn’t connected to other sites in the boundary and is in state 1. From the source configuration $\{S_1 00 S_2\}$ we get the targets $\{S_1 00 S_2\}$ and $\{S_1 10 S_2\}$.
- 01: The lower site is empty and the upper site is isolated. If the new site is empty the signature is unchanged. If the new site is occupied it is connected to the upper site and is in state 2 while the state of the upper site is changed to state 4.
- 02: When the new site is occupied it is connected to the upper site. The state of the lower site becomes 2 (the new first site in the set) while the state of the upper site is changed to 3 (it is now an intermediate site).
- 10: The lower site was an isolated occupied site so if the new site is empty we have created a separate graph. This is only allowed if there are no other occupied sites on the boundary line (otherwise we generate graphs with separate components) and if both the lower and upper borders have been touched. The result are valid lattice animals. The generating function is accumulated into the final animal generating function. If the new site is occupied it isn’t connected to other sites in the boundary and is therefore still in state 1.
- 11: The new site has to be occupied and it is connected to the upper site. The new site is in state 2 while the state of the upper site is changed to state 4.

- 14: This situation never occur. The upper site is the last among a set of occupied sites. This implies that the site immediately to the left of the upper site is occupied, this in turn is connected to the lower site, which therefore cannot be an isolated occupied site.
- 20: The lower site is the first among a set of occupied sites, so if the new site is empty, another site in this set changes its state. Either the *first* intermediate site becomes the new first site, and its state is changed from 3 to 2, or, if there are no intermediate sites, the last site becomes an isolated occupied site, and its state is changed from 4 to 1. Note that there could be connected parts of the animal interspersed between the first site and the matching intermediate or last site, so locating the site which has to be changed requires a little computation. This is illustrated in figure 1 where the first 2 is connected to the last 4, and a piece of the animal is placed in between these two sites. In this example if the first 2 became a 0 the last 4 becomes a 1, while if the second 2 becomes a 0 the 3 above it becomes a 2. In general the nesting can be quite complicated and the general rule for updating the configuration is as follows: Start from the 2, which we are changing to a 0, and move upwards in the configuration. Count the number of 2's and 4's as we pass them. If an equal number has been passed and we encounter a 3 or 4 this is the matching site we are looking for and it is changed either to 2 or 1. This change of a matching site is indicated in Table I by over-lining. When the new site is occupied the configuration is unchanged. So from the source $\{S_120S_2\}$ we get the targets $\{S_100\overline{S_2}\}$ and $\{S_120S_2\}$.
- 22: The updating when the new site is empty is as before. When the new site is occupied the connectivity is altered since we are joining two separate pieces of the animal. The new site remains the first site in the joined piece while the upper site becomes an intermediate site. The last site in the set of connected sites starting at the upper site also becomes an intermediate site in the joined piece. Locating this site is similar to the operation indicated by over-lining. However, in this case we ignore sites in state 3 and the matching site in state 4 becomes a 3. We indicate this type of transformation by putting a hat over the string. The source $\{S_122S_2\}$ gives rise to the targets $\{S_102\overline{S_2}\}$ and $\{S_123\widehat{S_2}\}$.
- 40: When the new site is empty we must change a matching site, either an intermediate site to a last site or a first site to an isolated occupied site. The transformation is similar to the case 20, but we have to search downwards in the configuration.
- 43: When the new site is occupied we change the connectivity. The first site, from the set of sites connected to the lower site, is changed to an intermediate site. This transformation is similar to the 'hat' transformation described at case 22, but we now have to search downwards in the configuration.
- 44: This can't happen for the same reason that 14 is impossible.

2.1.2 The algorithm

As a new site is added to the lattice we construct a new set of partial generating functions from the existing set. This can be done by running through all members of the existing set. Using bit-masking we can extract the states of the lower and upper sites and then apply the relevant updating rules, which generate at most 2 target signatures. First we check if the signature already exists, if so the generating functions of the source and target are added (with an addition weight factor u on the source if the new site is occupied). If the signature doesn't exist already, we check whether or not it makes a contribution, that is, we see if $N_{\text{cur}} + N_{\text{add}} \leq 2W_{\text{max}}$ (N_{cur} of the target is N_{cur} of the source if the new site is empty and $N_{\text{cur}} + 1$ otherwise). If the target makes a contribution it is assigned a storage position and its generating function is the generating function of the source (again with an extra factor of u if the new site is occupied). When the target generating functions have been created the storage position of the source generating function is released since it is no longer required and thus can be recycled.

The algorithm for the enumeration of animals spanning a $W \times L$ strip is:

1. Start by inserting an isolated occupied site in the top left corner. This configuration has the signature $(8^{W-1}, 2)$, which enters with a count of 1.
2. For j from 2 to $W - 1$ add a site to the lattice in the first column. Run through all existing signatures using the updating rules described above (note that as this is the first column the lower site is always empty). Add an additional configuration with a single occupied site at position $W - j$ with a count of 1. These configurations have the signature $(8^{W-j}, 0)$, since none of the borders have been touched.
3. Put in the last site in the first column. Again we run through all existing signatures. If the new site occupied we have to mark the signature as having touched the lower border. Add an additional configuration with a single occupied site in the lower left corner with a count of 1, the signature is $(1, 1)$.
4. Put in the top site in the next column. Run through all existing signatures. Since we are at the top border we only use the updating rules in Table I with the upper site in state 0 (obviously the lower site cannot be in states 2 or 3). If the new site is occupied make sure that the signature is marked as having touched the upper border. In this generic case we do *not* put in the additional configuration of a single isolated occupied site since it would not touch the left-most border.
5. For j from 2 to $W - 1$ add a site to the lattice in row $W - j$. Run through all existing signatures using the updating rules. Again no isolated occupied should be inserted.
6. Put in the last site in the column. If the new site is occupied make sure that the signature is marked as having touched the lower border.
7. If the number of completed columns is less than L go to 4.

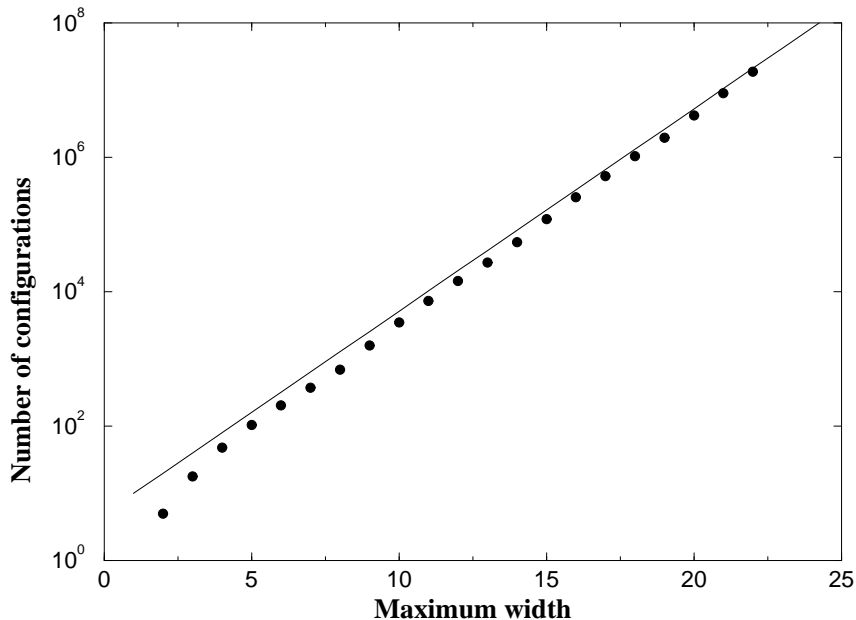


Figure 2: The number of configurations required in order to count the number of lattice animals correct up to twice the maximum width. The solid line is drawn as a guide to the eye and would correspond to a growth rate of exactly 2.

2.1.3 Computational complexity

The algorithm has exponential complexity, that is the time required to obtain the animals up to size n grows exponentially with n . Time and memory requirements are basically proportional to the maximum number of distinct configuration generated during a calculation. This in turn depends on the maximum number of terms we wish to calculate and thus on W_{\max} . In figure 2 we have shown how the maximal number of configurations, N_{Conf} , grows with W_{\max} . From this it is clear $N_{\text{Conf}} \propto a^{W_{\max}}$, and from the figure we estimate that a is a little larger than 2. Since we obtain $2W_{\max}$ terms the computational complexity grows exponentially with growth constant \sqrt{a} . Note that this is much better than a direct enumeration in which time requirements are proportional to the number of animals and therefore has the growth constant, $\lambda \simeq 4.06\dots$, of lattice animals. The price we have to pay for a faster algorithm is that the memory requirement also grows exponentially like N_{Conf} , whereas in direct enumerations the memory requirement typically grows like a polynomial in the number of terms.

2.1.4 Further particulars

Finally a few remarks of a more technical nature. The number of contributing configurations becomes very sparse in the total set of possible states along the boundary line and as is standard in such cases one uses a hash-addressing scheme [19]. Since the integer coefficients occurring in the expansion become very large, the calculation was performed using modular arithmetic [20]. This involves performing the calculation modulo various prime numbers p_i and then reconstructing the full integer coefficients at the end. In order to save memory

we used primes of the form $p_i = 2^{15} - r_i$ so that the residues of the coefficients in the polynomials could be stored using 16 bit integers. The Chinese remainder theorem ensures that any integer has a unique representation in terms of residues. If the largest integer occurring in the final expansion is m , then we have to use a number of primes k such that $p_1 p_2 \cdots p_k > m$. Up to 6 primes were needed to represent the coefficients correctly.

2.2 Calculation of the radius of gyration

In the following we show how the definition of the radius of gyration can be expressed in a form suitable for a transfer matrix calculation. As is well-known the radius of gyration of n points at positions \mathbf{r}_i is

$$n^2 R_n^2 = \sum_{i>j} (\mathbf{r}_i - \mathbf{r}_j)^2 = (n-1) \sum_i (x_i^2 + y_i^2) - 2 \sum_{i>j} (x_i x_j + y_i y_j). \quad (3)$$

This last expression is suitable for a transfer matrix calculation. As usual we actually calculate the generating function, $\mathcal{R}_g^2(u) = \sum_n a_n \langle R^2 \rangle_n n^2 u^n$, since this ensures that the coefficients are integers. In order to do this we have to maintain five partial generating functions for each signature, namely

- $A(u)$, the number of (partially completed) animals.
- $R^2(u)$, the sum over animals of the squared components of the distance vectors.
- $X(u)$, the sum of the x -component of the distance vectors.
- $Y(u)$, the sum of the y -component of the distance vectors.
- $XY(u)$, the sum of the ‘cross’ product of the components of the distance vectors, e.g., $\sum_{i>j} (x_i x_j + y_i y_j)$.

As the boundary line is moved to a new position each configuration S might be generated from several configurations S' in the previous boundary position. The partial generation functions are updated as follows

$$\begin{aligned} A(u, S) &= \sum_{S'} u^{n(S')} A(u, S'), \\ R^2(u, S) &= \sum_{S'} u^{n(S')} [R^2(u, S') + n(S')(x^2 + y^2)A(u, S')], \\ X(u, S) &= \sum_{S'} u^{n(S')} [X(u, S') + xn(S')A(u, S')], \\ Y(u, S) &= \sum_{S'} u^{n(S')} [Y(u, S') + yn(S')A(u, S')], \\ XY(u, S) &= \sum_{S'} u^{n(S')} [XY(u, S') + xn(S')X(u, S') + yn(S')Y(u, S')] \end{aligned} \quad (4)$$

where $n(S')$ is the number of occupied site added to the animal.

2.3 Enumeration of lattice trees

Lattice trees can be enumerated in essentially the same manner as animals. We merely get some further restrictions on the rules listed in Table I. The necessary restriction is that the new site cannot be occupied if the lower and upper sites already are connected, since this would obviously result in the formation of a circuit. So in the cases ‘23’, ‘24’, ‘33’, and ‘34’ the new site cannot be occupied, otherwise the updating rules are identical to those for animals.

3 Analysis of the series

The series listed in Table II have coefficients which grow exponentially, with sub-dominant term given by a critical exponent. The generic behaviour is $g_n \sim \mu^n n^{\xi-1}$, and hence the generating function has the behaviour, $G(u) = \sum_n g_n u^n \sim (1 - u/u_c)^{-\xi}$, where $u_c = 1/\mu$. From (1) we get the following predictions for the animal generating functions:

$$\mathcal{A}(u) = \sum_n a_n u^n = A(u)(1 - u\lambda)^{1-\tau}, \quad (5)$$

$$\mathcal{R}_g^2(u) = \sum_n a_n \langle R^2 \rangle_n n^2 u^n = \sum_n r_n u^n \sim R(u)(1 - u\lambda)^{-(\tau+2\nu+1)}. \quad (6)$$

Similar expressions hold for the corresponding tree generating functions though with a different growth constant λ_0 . So the animal and tree generating functions are expected to have a logarithmic singularity, while the radius of gyration series are expected to diverge with an exponent $2 + 2\nu$, where we assumed the conjecture $\tau = 1$ to be correct.

In the first stage of the analysis, we used the method of differential approximants [22]. Estimates of the critical point and critical exponent were obtained by averaging values obtained from second order inhomogeneous differential approximants. In Table III we have listed the estimates obtained from this analysis. The error quoted for these estimates reflects the spread (basically one standard deviation) among the approximants. Note that these error bounds should *not* be viewed as a measure of the true error as they cannot include possible systematic sources of error. From this we see that the animal generating function has a singularity at $u_c = 0.246150(1)$, and thus we obtain the estimate, $\lambda = 4.06256(2)$, for the growth constant. The exponent estimates are consistent with the expected logarithmic divergence, thus confirming the conjecture $\tau = 1$. The central estimates of u_c obtained from the radius of gyration series are a little larger than, but nonetheless consistent with the animal generating function. From this analysis we see that the series has a divergence at u_c with an exponent $2 + 2\nu = 3.2840(8)$, and thus $\nu = 0.6420(4)$.

The tree generating function has a singularity at $u_c = 0.2634870(5)$, and thus $\lambda_0 = 3.795254(8)$, with the expected logarithmic divergence. In this case estimates from the radius of gyration series yield $2 + 2\nu = 3.2823(1)$, and thus $\nu = 0.64115(5)$. Since the u_c estimates from the two tree series are in excellent agreement we claim that the best estimate for ν is the one obtained from the tree series. This estimate is consistent with, but much more accurate than, the recent estimate $\nu = 0.642(2)$ obtained from Monte Carlo simulations

Table II: The number of lattice animals, a_n , lattice trees, t_n , and the coefficients in the respective generating functions for their radius of radius.

n	a_n	$n^2 a_n (R^2)_n$	t_n	$n^2 t_n (R^2)_n$
1	1	1	1	1
2	2	2	2	2
3	6	28	6	28
4	19	252	18	244
5	63	1840	55	1680
6	216	11924	174	10214
7	760	71476	570	57476
8	2725	405204	1908	305476
9	9910	2202724	6473	1553632
10	36446	11590162	22202	7641218
11	135268	59417180	76886	36608932
12	505861	298186524	268352	171666468
13	1903890	1470151308	942651	790650724
14	7204874	7140410208	3329608	3586822020
15	27394666	34237750548	11817582	16062938368
16	104592937	162350915772	42120340	71135451440
17	400795844	762391407024	150682450	311964025352
18	1540820542	3549556185044	540832274	1356392904818
19	5940738676	16400558514664	1946892842	5852609697844
20	22964779660	75263022053196	7027047848	25081266854732
21	88983512783	343273594201564	25424079339	106827845665800
22	345532572678	1557003525653380	92185846608	452491861285360
23	1344372335524	7026663432447428	334925007128	1906994132045328
24	5239988770268	31565321263960648	1219054432490	8000039128666316
25	20457802016011	141201716724567204	4444545298879	33420021839691568
26	79992676367108	629195375725422292	16229462702152	139072296450104904
27	313224032098244	2793681657766773944	59347661054364	576665646646645628
28	1228088671826973	12363167055143142440	217310732774774	2383267493411599452
29	4820975409710116	54544020640717162468	796703824808133	9819513412114987172
30	18946775782611174	239950473304391505440	2924252282840112	40342989684066501360
31	74541651404935148	1052776828941036051656	10744903452821876	165306633582934256304
32	293560133910477776	4607511085613062500648	39521236485358584	675665329410485731504
33	1157186142148293638	20117772038497717315976	145503056229823138	2755244324874079014600
34	456553929115769162	87647322688578954475976	536170499427125956	11210822859036572606668
35	18027932215016128134	381065022045089903130608	1977427804277385532	45521864027574363668480
36	71242712815411950635	1653532426475382203248376	7298688919041663694	184484204103594541676168
37	281746550485032531911	7161875592952535220704656	26959808299736689704	746280442016872847892140
38	1115021869572604692100	30965967036768698515049964	99655022360008737496	3013643917345287146830452
39	4415695134978868448596	133667644427251173600540220	368617606804069356072	12149786877969635612633264
40	17498111172838312982542	576087681668533750775182764	1364371688078200595674	48906771633330499596166064
41	69381900728932743048483	2479166130662936965224977368	5053070869464350119408	196574389975234157470737780
42	275265412856343074274146	10653909826486480285867012570	18225415026570087447460	788994500989152614915884776
43	1092687308874612006972082		69430306096976372288324	
44	4339784013643393384603906		257571182441471056810356	
45	17244800728846724289191074			
46	68557762666345165410168738			

Table III: Estimates for the critical point u_c and exponents $1 - \tau$ and $1 + \tau + 2\nu$ obtained from second order inhomogeneous differential approximants to the series for the generating functions of lattice animals, lattice trees and their radius of gyration. L is the order of the inhomogeneous polynomial.

Square lattice site animals				
L	u_c	$1 - \tau$	u_c	$1 + \tau + 2\nu$
0	0.246149987(43)	-0.000523(46)	0.246150539(87)	3.28413(11)
2	0.24614992(14)	-0.00043(14)	0.24615046(10)	3.28402(28)
4	0.24615007(15)	-0.00055(16)	0.24615037(22)	3.28394(30)
6	0.24614999(24)	-0.00046(25)	0.24615068(16)	3.28426(22)
8	0.24615001(15)	-0.00052(13)	0.24615067(25)	3.28432(44)
10	0.24614997(22)	-0.00044(28)	0.24615055(31)	3.28417(56)
Square lattice site trees				
L	u_c	$1 - \tau$	u_c	$1 + \tau + 2\nu$
0	0.26348751(73)	-0.00039(55)	0.263487100(52)	3.282325(42)
2	0.26348716(21)	-0.00014(13)	0.263487033(57)	3.282276(35)
4	0.26348698(32)	0.00002(27)	0.263487029(58)	3.282276(35)
6	0.26348693(20)	0.00000(12)	0.263487079(17)	3.282308(12)
8	0.263486943(70)	0.000009(58)	0.263487061(32)	3.282297(20)
10	0.26348700(17)	-0.00001(10)	0.263487059(19)	3.282296(13)

of lattice trees [23]. It is also consistent with the estimate $\nu = 0.6408(3)$ obtained using phenomenological renormalization to lattice animals [18].

A more detailed analysis of the animal series was performed in [21]. It showed that in a plot of exponent vs u_c estimates, as $1 - \tau$ approach 0, u_c approach 0.2461497. From the spread among the approximants we obtained the final estimate $u_c = 0.2461496(5)$, and thus the growth constant $\lambda = 4.062570(8)$. A similar analysis of the radius of gyration series yielded estimates of ν consistent with those obtained for lattice trees.

Finally we use the series to derive improved rigorous lower bounds for the growth constants of lattice animals and trees. Using concatenation arguments Rands and Welsh [24] showed that if we define a sequence p_n such that

$$a_{n+1} = p_{n+1} + p_n a_2 + \dots + p_3 a_{n-1} + p_2 a_n, \quad (7)$$

and construct the generating functions

$$\mathcal{A}^*(u) = 1 + \sum_{n=1}^{\infty} a_{n+1} u^n \quad (8)$$

and

$$\mathcal{P}(u) = \sum_{n=1}^{\infty} p_{n+1} u^n \quad (9)$$

then

$$\mathcal{A}^*(u) = 1 + \mathcal{A}^*(u)\mathcal{P}(u) \quad (10)$$

and $\mathcal{A}^*(u)$ is singular when $\mathcal{P}(u) = 1$. The coefficients in $\mathcal{P}(u)$ are obviously known correctly to the same order $N = 2W_{\max} - 1$ as $\mathcal{A}^*(u)$. If we look at the polynomial P_N obtained by truncating $\mathcal{P}(u)$ at order N then the unique positive zero, $1/\lambda_N$, of $P_N - 1 = 0$ is a lower bound for λ . Using our extended series we find that $\lambda \geq 3.903184\dots$

For site trees the best lower bound appears to arise from a different concatenation procedure [25], which leads to the equation

$$\mathcal{T}(u) = \frac{1 - \mathcal{Q}(u)}{1 - 2\mathcal{Q}(u)} \quad (11)$$

and $\mathcal{T}(u)$ is singular when $\mathcal{Q}(u) = 1/2$. This approach yields a lower bound for site trees, $\lambda_0 \geq 3.613957\dots$

4 Conclusion

We have presented an improved algorithm for the enumeration of site animals on the square lattice. The computational complexity of the algorithm is exponential with time (and memory) growing as $a^{n/2}$, where a appears to be a little larger than 2. Implementing this algorithm

has allowed us to count the number of site animals up size 46. Our extended series enables us to give an improved estimate for the growth constant and confirm to a very high degree of certainty that the associated generating function has a logarithmic divergence. The algorithm was also modified to enumerate lattice trees up to size 44, and a generalised version was used to calculate the radius of gyration of animals and trees up to size 42. Analysis of the series confirmed that animals and trees belong to the same universality class and an accurate estimate was obtained for the size exponent ν .

E-mail or WWW retrieval of series

The series for the generating functions studied in this paper can be obtained via e-mail by sending a request to I.Jensen@ms.unimelb.edu.au or via the world wide web on the URL <http://www.ms.unimelb.edu.au/~iwan/> by following the instructions.

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