# Resistivity Exponent of Two-Dimensional Lattice Animals 

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#### Abstract

We calculate the average resistance $R(L)$ of lattice animals spanning $L \times L$ cells on the square lattice using exact and Monte Carlo methods. The dynamical resistivity exponent, defined as $R(L) \sim L^{\xi}$, is found to be $\zeta=1.36 \pm 0.07$. This contradicts the Alexander-Orbach conjecture, which predicts $\zeta \approx 0.8$. Our value for $\zeta$ differs from earlier measurements of this quantity by other methods yielding $\zeta=1.17 \pm 0.05$ and $1.22 \pm 0.08$ by Havlin et al.


KEY WORDS: Lattice animal; resistivity exponent; fractal dimension; spectral dimension.

The Alexander-Orbach (AO) conjecture, ${ }^{(1)}$ originally proposed for percolation clusters, states that the spectral dimension of percolation clusters is $4 / 3$ for dimensions $d \geqslant 2$. This conjecture has stimulated much numerical calculations ${ }^{(2-4)}$ of the spectral dimension of percolation clusters in two and three dimensions at which the largest deviations from the $A O$ value are to be expected.

The extension of the AO conjecture to other random fractals, e.g., lattice animals, has also been examined. ${ }^{(5,6)}$ For lattice animals, numerical evidence has not been as extensive as in the case of percolation clusters, due to the difficulty in generating large lattice animals. ${ }^{(6)}$ Wilke et al. ${ }^{(5)}$ found in two dimensions the random walk dimension on lattice animals to be $z=2.6 \pm 0.3$. Using the relation $z=\zeta+d_{f}{ }^{(7)}$ where $\zeta$ is the resistivity exponent and $d_{f}$ is the fractal dimension, which is 1.5625 here, ${ }^{(8)}$ one obtains $\zeta \approx 1.0 \pm 0.3$. Havlin et al. ${ }^{(6)}$ obtained in two dimensions $z=$

[^0]$2.78 \pm 0.08$, which gives $\zeta=1.22 \pm 0.08$. Both of these studies were made by generating random walks on the lattice animals. Havlin et al. ${ }^{(6)}$ also measured $\zeta$ by relating it to the chemical distance exponent $d_{1}$ by the equation $\zeta=d_{f} / d_{1}$, a relation based on the assumption that the loop structure of the animals does not contribute to their resistance. Their determination of $d_{1}$ to be $1.33 \pm 0.05$ leads to $\zeta=1.17 \pm 0.05$. In the methods based on the diffusive properties on fractals using random walks as a probe, two sources of statistical error are involved, one coming from the generation of lattice animal configurations and the other from the random walk configurations.

In general, diffusion problems are related to conductivity problems through the Einstein relation, which gives a connection between the conductivity and the diffusion constant. ${ }^{(7)}$ Since the resistance of random networks can be calculated to arbitrary accuracy using relaxation methods such as the conjugate gradient method, ${ }^{(9)}$ one has a means of overcoming the second source of statistical error mentioned above.

Since the resistance $R(L)$ of a fractal with spatial extension $L$ goes as $R(L) \sim L^{\zeta}$, with a resistivity exponent $\zeta$, it is convenient to study lattice animals of a fixed spatial dimension $L$. Therefore we study lattice animals in an $L \times L$ cell and consider all animals that span the cell in a specified direction starting from one corner of the cell. In this specified direction, if we number by column 1 the column to which the starting corner of the animal belongs, then the animal spans columns 1 to $L$ of the cell. We calculate the resistance between all pairs of occupied sites of the animal in which one site of the pair is in column 1 and the other in column $L$ and then take the average.

For small $L$, this can be done exactly. ${ }^{(10)}$ We have done this up to $L=5$. This resistance is given by

$$
\begin{equation*}
R(L)=\sum_{n=L}^{L \times L} a_{n}(L) r_{n}(L) / \sum_{n=L}^{L \times L} a_{n}(L) \tag{1}
\end{equation*}
$$

where $a_{n}(L)$ is the number of $n$-site animals spanning an $L \times L$ cell in a specified direction, starting from one corner of the cell, and $r_{n}(L)$ is the average resistance of such animals. We give in Table I the values of $a_{n}(L)$ and $r_{n}(L)$. The values of $r_{n}(L)$ are calculated with the conjugate gradient method ${ }^{(9)}$ up to an accuracy of $10^{-6}$.

For larger $L$, since the computation time required for the exact enumeration increases exponentially, we resort to Monte Carlo methods. The Monte Carlo method used here is that of Dhar and Lam. ${ }^{(11)}$ This is a Monte Carlo version of the deterministic algorithm given in ref. 10. In the deterministic algorithm, the animal configurations are classified into a tree

Table 1. The Number of $n$-Site Animals $a_{n}(L)$ Spanning an $L \times L$ Cell in a Specified Direction Starting from One Corner of the Cell and Their Average Resistance $r_{n}(L)$

|  | $n$ | $a_{n}(L)$ | $r_{n}(L)$ |
| :---: | :---: | :---: | :---: |
| $L=3$ | 3 | 1 | 2.00000 |
|  | 4 | 5 | 2.50000 |
|  | 5 | 16 | 2.79948 |
|  | 6 | 27 | 2.68796 |
|  | 7 | 24 | 2.58600 |
|  | 8 | 8 | 1.77226 |
|  | 9 | 1 | 1.25926 |
| $L=4$ | 4 | 1 | 3.00000 |
|  | 5 | 7 | 3.50000 |
|  | 6 | 32 | 3.87630 |
|  | 7 | 118 | 4.13362 |
|  | 8 | 329 | 4.17990 |
|  | 9 | 688 | 4.15333 |
|  | 10 | 1062 | 4.07376 |
|  | 11 | 1171 | 3.90851 |
|  | 12 | 863 | 3.57332 |
|  | 13 | 388 | 2.99779 |
|  | 14 | 101 | 2.31641 |
|  | 15 | 15 | 1.83509 |
|  | 16 | 1 | 1.50446 |
| $L=5$ | 5 | 1 | 4.00000 |
|  | 6 | 9 | 4.50000 |
|  | 7 | 54 | 4.93133 |
|  | 8 | 247 | 5.21137 |
|  | 9 | 990 | 5.47641 |
|  | 10 | 3419 | 5.60581 |
|  | 11 | 10090 | 5.64545 |
|  | 12 | 25535 | 5.64483 |
|  | 13 | 55261 | 5.61837 |
|  | 14 | 101259 | 5.56326 |
|  | 15 | 154636 | 5.46895 |
|  | 16 | 192494 | 5.31715 |
|  | 17 | 189909 | 5.08211 |
|  | 18 | 143296 | 4.72718 |
|  | 19 | 79860 | 4.23997 |
|  | 20 | 32155 | 3.66142 |
|  | 21 | 9296 | 3.08188 |
|  | 22 | 1917 | 2.58879 |
|  | 23 | 272 | 2.20758 |
|  | 24 | 24 | 1.91239 |
|  | 25 | 1 | 1.68394 |

structure according to their lineage, with the one-site animal forming the root of the tree. The exhaustive enumeration of all animals having $n$ sites proceeds by a systematic exploration of the genealogical tree to height $n-1$. In the Monte Carlo version, when a particular $r$-site configuration is first generated, one chooses to ignore it and all its descendants in the enumeration with probability $1-p_{r}, r \geqslant 2$. The probability that a particular $r$-site animal will be enumerated in a given trial is

$$
\begin{equation*}
P_{r}=\prod_{i=2}^{r} p_{i} \tag{2}
\end{equation*}
$$

and is the same for all configurations with the same $r$. The algorithm generates an unbiased sample of configurations. If $M$ independent trials have been used in the enumeration of animal configurations in an $L \times L$ cell and $N_{n}(L)$ is the number of realizations of $n$-site animals spanning the cell, then the quantity $a_{n}(L)$ defined in (1) can be deduced from the relation

$$
\begin{equation*}
M a_{n}(L) \prod_{i=2}^{n} p_{i}=N_{n}(L) \tag{3}
\end{equation*}
$$



Fig. 1. Plot of $\log R(L)$ versus $\log L$. The crosses and the dots denote respectively exact and Monte Carlo results.

We have chosen $p_{i}=(1+i) /(4 i) .{ }^{(1)}$ Then (1) can be rewritten as

$$
\begin{equation*}
R(L)=\sum_{n} 4^{n-1}(1+n)^{-1} N_{n}(L) r_{n}(L) / \sum_{n} 4^{n-1}(1+n)^{-1} N_{n}(L) \tag{4}
\end{equation*}
$$

In Fig. 1 we plot $\log R(L)$ versus $\log L$ for $L$ up to 25 . For comparison the results obtained by exact enumeration are also shown. We see that the agreement is quite good. The data fall very much on a straight line. From the slope we find $\zeta=1.36 \pm 0.07$.

The spectral dimension $d_{s}$ is related to the resistivity exponent by ${ }^{(7)}$

$$
\begin{equation*}
d_{s}=2 d_{f} /\left(\zeta+d_{f}\right) \tag{5}
\end{equation*}
$$

where $d_{f}$ is the fractal dimension, which is known here to be $d_{f}=1.5625 .{ }^{(8)}$ The AO value $d_{s}=4 / 3$ would require $\zeta \approx 0.8$, which is very different from the value determined here. Actually, the calculations in ref. 6 are already violations of the AO conjecture of $20-30 \%$. The lattice animal problem therefore presents a much clearer violation of the AO conjecture than percolation clusters.

We find surprising the difference between our result and that of Havlin et al. ${ }^{(6)}$ which is too large to be attributed easily to statistical errors.

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