New Algorithm for Potentials on Resistor Networks and Application to Dielectric Breakdown

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1 Introduction

In many problems one is confronted with the question of determining the electrostatic potential at the sites of some resistor network, under given boundary conditions. A standard approach is the "relaxation method", [1] where Kirchhoff's law is used in an iterative approximation scheme. Here we propose a new method for solving this problem in an exact way, and we present some applications to the Dielectric Breakdown Model (DBM). [2]

In this model, one considers a cell whose boundary is kept at a fixed potential, say $\Phi = 1$. An interior point, playing the role of seed for cluster growth, is kept at $\Phi = 0$. For points not belonging to the cluster, the potential satisfies the discrete Laplace equation, while for those of the cluster $\Phi = 0$. At each stage of growth one bond is chosen among those on the perimeter of the cluster with probability proportional to $\Delta\Phi_b^\eta$, where $\Delta\Phi_b$ is the potential drop across the boundary of the cluster, and η is a parameter of the model. Inside a region of size L , the average number of points in the cluster at the moment of breakdown is called $N(L)$, and it should scale as $L^{\bar{d}}$, where $\bar{d}$ is the fractal dimension.

2 The Resistivity Matrix

In order to obtain an accurate and efficient method for calculating the electrostatic potential Φ on the sites of a resistor network, we need to invert the method proposed by Derrida et al., [3] in which a matrix A is constructed relating the currents injected at lattice sites j to the resulting potentials at sites k by

$$I_j = \sum_k A_{jk} \Phi_k. \quad (1)$$

Such a matrix A in itself is not very useful for our purpose. What we need is an expression for Φ_j in terms of the I_k (most of which will in general be zero); we thus need the inverse of A .

Since a constant choice for Φ_k leads to zero currents, the matrix A is singular and does not have a straightforward inverse. This can be solved by choosing an arbitrary lattice site to be fixed at $\Phi = 0$. This site does not have to be included in our index set $\{j\}$; due to charge conservation its current will have to compensate

$\sum I_j$. A natural choice for this site in the DBM simulations is the central seed for the cluster growth.

For the remaining sites in our system, we can now try to construct the matrix B defined by

$$\Phi_j = \sum_{k \in \mathcal{I}} B_{jk} I_k. \quad (2)$$

The first problem is that we should never try to numerically calculate the matrix elements B_{ij} for sites belonging to disconnected parts of the lattice, since the corresponding B -values, will be infinite. The following prescription works only for a fully interconnected set of sites. Furthermore, we should include the site indices one by one into our index set, while adding to our matrix the first contribution of the resistances which link these sites to the rest of the system.

The algorithm for constructing the resistivity matrix B consists of three distinct parts, each to be repeated as many times as necessary:

1. The initial step is to include in the index set all sites directly connected through some resistances R_j to the seed (see Fig. 1). Since along these re-

Figure 1: Inclusion of first site

sistances we have a potential drop $\Phi_j = R_j I_j$ (if no other interconnecting resistances are present), we obviously have the starting rule for these sites:

$$B_{jj} = R_j. \quad (3)$$

2. The addition of a new site i to an already treated configuration of sites will have to occur through a resistance R between i and some site j of the configuration (see Fig. 2). This will change the matrix B into $\tilde{B}$: The current I_i

Figure 2: Addition of a new site

entering site i will flow into the system at site j , where it will be added to

the current I_j . Thus, for all k we may write

$$\tilde{B}_{ki} = B_{kj}. \quad (4)$$

Furthermore, since $\Phi_i = \Phi_j + I_i R$, we also have that

$$\tilde{B}_{ik} = B_{jk} \quad (5)$$

$$\tilde{B}_{ii} = B_{jj} + R. \quad (6)$$

3. The third operation that we must be able to describe is the addition of a resistance R between two sites i and j already belonging to the configuration. In order to keep the potentials Φ_k unchanged, the currents I_i and I_j should

Figure 3: Addition of a new resistance

be changed into $\tilde{I}_i$ and $\tilde{I}_j$ as follows (see Fig. 3):

$$\tilde{I}_i = I_i + \frac{1}{R}(\Phi_i - \Phi_j) \quad (7)$$

$$\tilde{I}_j = I_j + \frac{1}{R}(\Phi_j - \Phi_i) \quad (8)$$

and we need to know how B transforms into $\tilde{B}$, with

$$\Phi_k = \sum_m B_{km} I_m = \sum_m \tilde{B}_{km} \tilde{I}_m. \quad (9)$$

The result of a straightforward calculation is

$$\tilde{B}_{km} = B_{km} - \frac{(B_{ki} - B_{kj})(B_{mi} - B_{mj})}{R + B_{ii} + B_{jj} - 2B_{ij}}, \quad (10)$$

valid for all k and m (i and j included). This result is also valid for $R = 0$, i.e. for shortcircuiting i and j .

We should add the following remarks:

- The matrix is symmetric: $B_{ij} = B_{ji}$. This can be used to save computation time or memory capacity.

- If (as in the DBM model) the only constraint is that a given site a (the boundary, e.g.) is kept at unit potential, the only current will be I_a , and thus for the voltage at a : $\Phi_a = 1 = B_{aa}I_a$. The potential at all other sites is then obtained from

$$\Phi_i = \frac{B_{ai}}{B_{aa}}. \quad (11)$$

- The net resistivity between sites i and j is given by

$$R_{ij} = B_{ii} + B_{jj} - 2B_{ij}. \quad (12)$$

In combination with (10) this leads to the transformation rule

$$\tilde{R}_{km} = R_{km} - \frac{(R_{ki} - R_{kj} + R_{mi} - R_{mj})^2}{4(R + R_{ij})} \quad (13)$$

for the operation described in Figure 3.

- Equation (10) can in principle also be applied for $R < 0$. One might want to do this if an existing resistance R between i and j should be deleted, which can be achieved by adding a fictional resistance $(-R)$ in parallel between the same sites. This may, however, lead to infinite matrix elements when a site becomes in this way disconnected from the network.
- Whereas a complete control of the exactness of the result is the main advantage of this method, in comparison to the relaxation method, its big disadvantage is the necessary storage capacity for the $N \times N$ matrix, where N is the number of sites on the network.

3 Results for the DBM

The most simple method consists in a straightforward Monte Carlo generation of a large set of DBM realizations in each cell considered. $N(L)$ is then determined as the average number of sites in the growth cluster at breakdown. The Monte Carlo procedure consists in choosing at each step the next growth site at random between the many candidate sites, with relative probabilities given by their respective values of $\Delta\Phi_b^\eta$.

For cells that are not too large, this Monte Carlo method can be replaced by an exact enumeration of all possible growths up to the breakdown. This procedure is similar to that used in the enumeration of different kinds of walks on a lattice.[4] The value for $N(L)$ is then obtained by averaging N over all configurations at breakdown, with the product of the $\Delta\Phi_b^\eta$ at each step as weight factors.

When the cells become too large to allow an exact enumeration of all possible growth patterns, we have used a combined strategy. We have enumerated all possible growth patterns consisting of up to N_0 sites (where the maximum acceptable value for N_0 depends on the computational capacity), together with the weight factors of these patterns. If they break down before N_0 is reached, we calculate their contribution to $N(L)$. If the boundary of the cell has not been reached after N_0 steps, we continue from that configuration till breakdown with a Monte Carlo

sampling as described above. In order to increase the efficiency of the computation, the number of Monte Carlo runs for each configuration (and thus the accuracy of the estimate) can, e.g., be taken proportional to the weight of the configuration.

Whatever the strategy used, we calculate the potentials Φ at the lattice sites for each configuration through the algorithm sketched above. Each time a new site is added to the growth, this results in linking the two sites with a zero resistance (short circuiting these sites) and this translates into a readjustment of the matrix B through $n(n+1)/2$ simple calculations, where n is the number of sites that have to be monitored.

We have applied this method to square cells with site L , using cylindrical boundary conditions in one direction, and $\Phi = 0$ and $\Phi = 1$ on the boundaries in the other direction. In these calculations we used $N_0 = 4$, and we made sure that at least 100,000 Monte Carlo runs were performed for each cell. If we denote by $N(L; \eta)$ the average mass of the growth at breakdown within a square of side L , for a given η , we derive estimates for the fractal dimension of the growth $\bar{d}(\eta)$ from

$$\bar{d}(L', L; \eta) = \frac{\ln [N(L; \eta)/N(L'; \eta)]}{\ln(L/L')} \quad (14)$$

The results from our simulations are reproduced in Table I, both for $\eta = 0$ and $\eta = 1$. The values $N(3)$ and $N(4)$ are exact, coming from a complete enumeration. The extrapolations of $\bar{d}(1)$ in terms of $1/L$ are in agreement with known results from simulations on very large cells.

L'	L	$N(L; 0)$	$N(L; 1)$	$\bar{d}(L', L; 0)$	$\bar{d}(L', L; 1)$
	2	3.5	2.8922541		
2	3	7.6165	5.3723743	1.91768	1.52722
3	4	13.070(5)	8.370(3)	1.877(1)	1.541(1)
4	5	20.016(7)	11.863(5)	1.910(3)	1.563(3)
5	6	28.47(1)	15.99(5)	1.932(4)	1.572(4)
6	7	38.55(1)	20.198(7)	1.966(4)	1.594(5)
7	8	50.16(1)	25.04(1)	1.972(4)	1.608(6)
8	9	63.42(2)	30.30(1)	1.991(4)	1.62(1)
9	10	78.11(2)	35.99(1)	1.977(6)	1.63(1)
10	11	94.70(2)	42.08(2)	2.021(5)	1.64(1)
11	12	112.67(3)	48.58(5)	1.997(6)	1.65(2)
	∞			2.04(2)	1.72(4)

Table I: Values obtained for $N(L; \eta)$, the average mass of the growth at breakdown under cylindrical conditions within a square of side L , for $\eta = 0$ and 1, and corresponding estimates for the fractal dimension. The values mentioned for $L = \infty$ are linear extrapolations in $1/L$.

4 Conclusion

Our results prove that it is possible to obtain very good estimates on the fractal properties of the DBM through the finite size scaling method, without the need to perform Monte Carlo calculations on very large systems. Our relatively small systems give estimates for $\bar{d}$ that lie within the nowadays accepted range of values.

References

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