External bias in the model of isolation of communities

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Abstract

We extend a model of community isolation [1] in the d-dimensional lattice to a case with an imposed imbalance between the birth rates of competing communities. We provide analytical and numerical evidences that in the asymmetric two-species model there exists a well-defined value of the asymmetry parameter when the emergence of the isolated (blocked) subgroups is the fastest, i.e., the characteristic time t_c is minimal. A similar phenomenon is observed in the multi-species case with a geometric distribution of the birth rates.

Introduction

We are investigating the asymmetric case of the model [2]. Symmetry breaking is introduced as an external bias and is received by changing birth rates of different species occurring in the system, either by a simple imbalance in the two-species case or by setting a specific species probability distribution in the multi-species case. We shall consider the model of isolation of communities on a d-dimensional lattice where clusters of nodes sharing the same species will be isolated when neighbors (using von Neumann's sense of neighborhood [3]) of all the nodes in the cluster are connected with each other or with a different species.
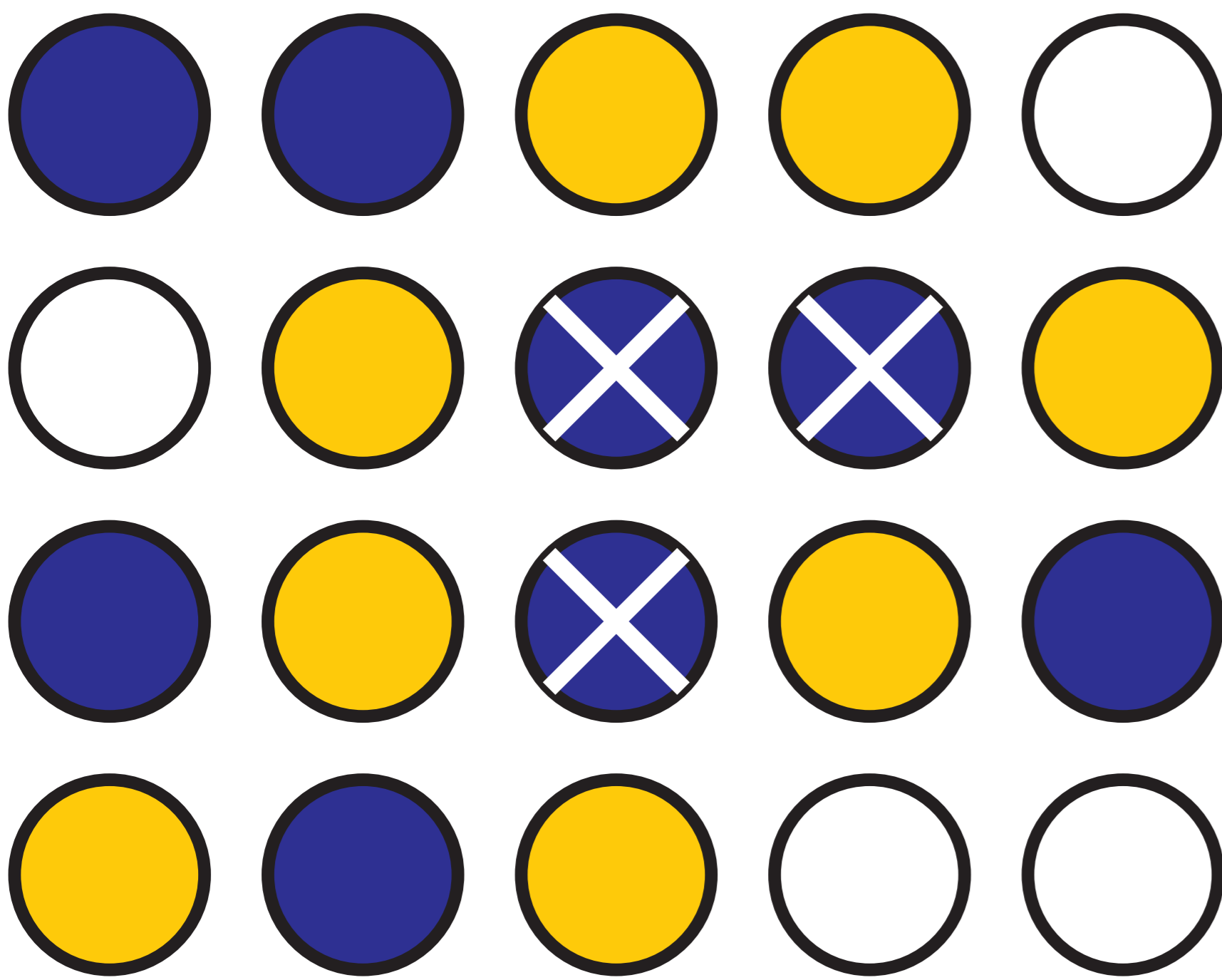

FIGURE 1: An example of cluster of size 3 on square lattice ($d = 2$) with $N = 20$ nodes and two different species (light and dark filled circles), after $t = 16$ time steps. Nodes marked with crosses are blocked.

Two species

First, we consider two species ($\uparrow$ and $\downarrow$) that we put into d-dimensional hypercubic lattice with a total number of sites $N = L^d$. Occurrence probabilities $p_\uparrow$ and $p_\downarrow$ of both species are non-equal and given by

$$p_\uparrow = 0.5 + \epsilon, \quad p_\downarrow = 0.5 - \epsilon, \tag{1}$$

where $\epsilon \in [0, 0.5]$ is the symmetry breaking parameter. These probabilities are microscopic parameters that describe model evolution. Starting from a lattice of empty nodes, after t timesteps the probabilities that a randomly picked node is occupied with the species ($\uparrow$) or ($\downarrow$) are $\text{Prob}(\uparrow) = p_\uparrow t/N$ and $\text{Prob}(\downarrow) = p_\downarrow t/N$.

Now, let us consider number of blocked nodes $Z^\uparrow$ and $Z^\downarrow$ of both species at time t. These numbers are well approximated by numbers of individual blocked nodes, i.e., by numbers of blocked clusters of size one of both species. When the total density of all blocked nodes is small ($Z^\uparrow + Z^\downarrow \ll t$) then:

$$Z^\uparrow \approx Z_1^\uparrow = (L-2)^d \text{Prob}^{2d}(\downarrow)\text{Prob}(\uparrow), \tag{2}$$

$$Z^\downarrow \approx Z_1^\downarrow = (L-2)^d \text{Prob}^{2d}(\uparrow)\text{Prob}(\downarrow), \tag{3}$$

Substituting the values $\text{Prob}(\uparrow)$ and $\text{Prob}(\downarrow)$ and taking into account the form of $p_\uparrow$ and $p_\downarrow$, the above relations for $L \gg 2$ may be expressed as

$$Z^{\uparrow,\downarrow} \approx \frac{t^{2d+1}}{N^{2d}}\left(\frac{1}{4} - \epsilon^2\right)\left(\frac{1}{2} \mp \epsilon\right)^{2d-1}, \tag{4}$$

where $Z^\uparrow$ corresponds to the "-" sign in the second bracket. The above equations allow us to calculate characteristic times $t_c^\uparrow$ and $t_c^\downarrow$ when the first representative of either species emerges. Putting $Z^\uparrow = 1$ (analogously for $\downarrow$), we obtain after a short algebra

$$t_c^{\uparrow,\downarrow} = \left[\frac{N^{2d}}{\left(\frac{1}{4} - \epsilon^2\right)\left(\frac{1}{2} \mp \epsilon\right)^{2d-1}}\right]^{\frac{1}{2d+1}}, \tag{5}$$

where $t_c^\uparrow$ corresponds to the "-" sign in the second bracket.
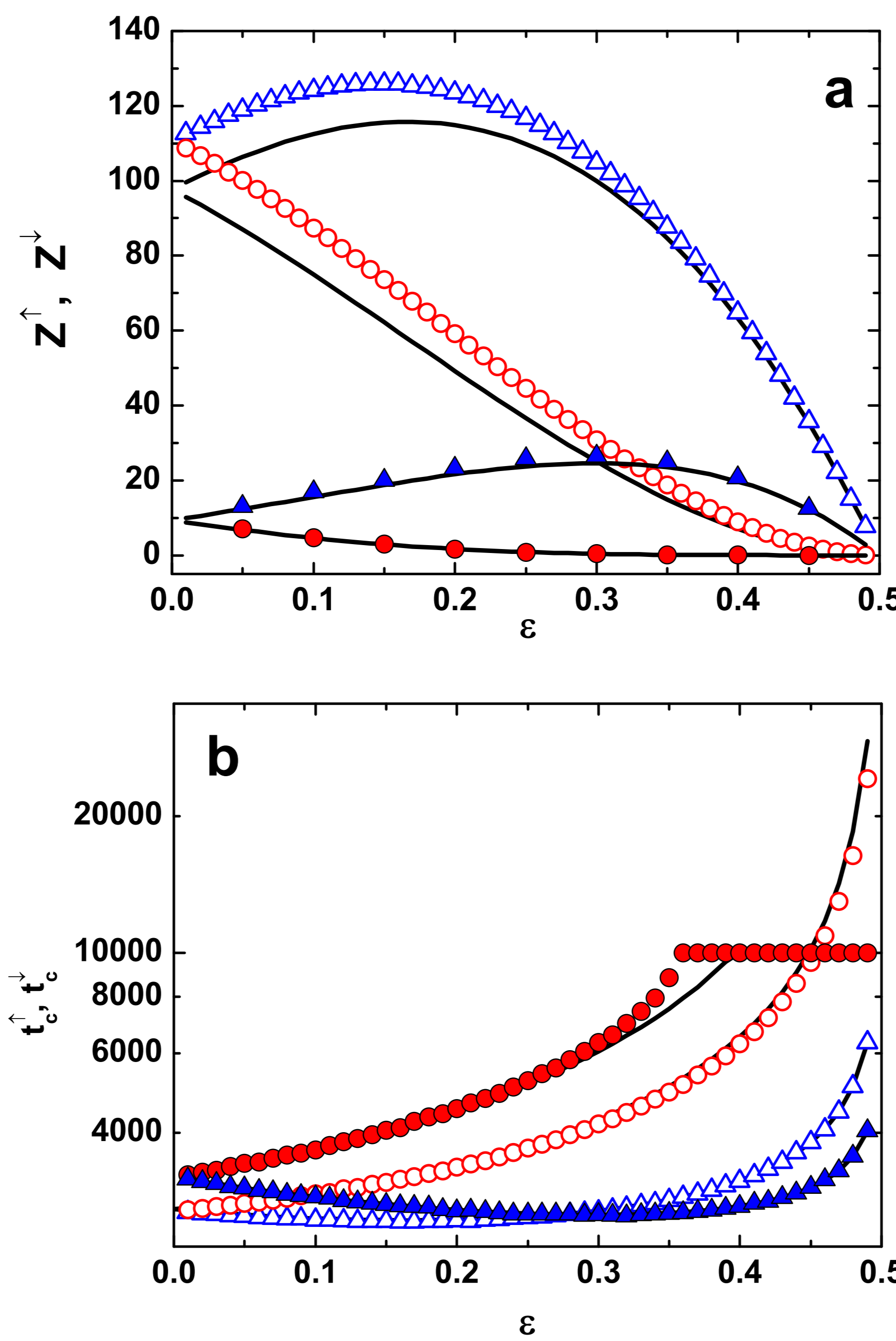

FIGURE 2: (a) Number of blocked nodes $Z_\uparrow$ and $Z_\downarrow$ versus symmetry breaking parameter ϵ on a chain (open symbols, simulations performed for $t = N/4$) and on a square lattice (filled symbols, simulations performed for $t = N/2$); circles ($Z_\uparrow$) and triangles ($Z_\downarrow$) correspond to simulation results and lines are calculated using Eq. (4). (b) Log-linear plots of the characteristic times $t_c^{(\uparrow)}$ (circles) and $t_c^{(\downarrow)}$ (squares) for $d = 1$ (filled symbols) and $d = 2$ (open symbols). Data points are taken from numerical simulations, while solid lines come from Eq. (5). For $d = 1$ simulations were performed for $N = 5 \times 10^4$ nodes, averaged over 10^5 runs, while for $d = 2$ it was $N = 10^4$ nodes, averaged over 10^3 runs.

There is difference between $Z^\uparrow$ and $Z^\downarrow$: $Z^\uparrow$ is monotonic while $Z^\downarrow$ first increases, reaches a prominent and well-defined maximum and then drops down. This observation is backed with a simple analysis of Eq. (4); in fact, the derivative $\partial Z_\uparrow/\partial \epsilon < 0$ for the whole range $\epsilon \in [0, 0.5]$ and in the case of $Z^\downarrow$ there is a maximum value for:

$$\epsilon^* = \frac{1}{2}\frac{2d-1}{2d+1}. \tag{6}$$

More than two species

If we consider more than two species, then we can use probability distribution $\text{Prob}(i)$, instead of the previously introduced probabilities $\text{Prob}(\uparrow)$ and $\text{Prob}(\downarrow)$. It requires changing microscopic probabilities $p_\uparrow$ and $p_\downarrow$ with the value of p_i. The connection between these two sets of variables is given by $\text{Prob}(i) = p_i t/N$, for $i = 1, 2, \ldots$ (the case p_i independent of i corresponds to the symmetric problem considered in [2]). Using the same approximation as is used in the two-species case we can obtain that:

$$Z^{(i)} \approx Z_1^{(i)} \approx N \sum_{k=1, k \neq i}^{\infty} \text{Prob}(k)^{2d}\text{Prob}(i), \tag{7}$$

for $i = 1, 2, \ldots$, which becomes:

$$Z^{(i)} = \frac{t^{2d+1}}{N^{2d}}p_i\left(\sum_{k=1}^{\infty} p_k^{2d} - p_i^{2d}\right). \tag{8}$$

Putting $Z^{(i)} = 1$, one obtains a set of characteristic times for each species i:

$$t_c^{(i)} = \left[\frac{N^{2d}}{p_i\left(\sum_{k=1}^{\infty} p_k^{2d} - p_i^{2d}\right)}\right]^{\frac{1}{2d+1}} \quad i = 1, 2, \ldots \tag{9}$$

For the numerical calculus, we used the geometric probability distribution $p_i = q^{i-1}(1 - q)$, $i = 1, 2, \ldots$. Characteristic times for this distributions are as follows

$$t_c^{(i)} = \left[\frac{N^{2d}(1 - q^{2d})q^{1-i}}{(1-q)^{2d+1}\left(1 - q^{2d(i-1)} + q^{2di}\right)}\right]^{\frac{1}{2d+1}}. \tag{10}$$

We can calculate global characteristic time as follows: total number of blocked species at time t is equal to $Z(t) = \sum_i Z^{(i)} = 1$. Thus, the global characteristic time can be expressed as:

$$t_c = \left[\frac{N^{2d}}{\frac{(1-q)^{2d}}{1-q^{2d}} - \frac{(1-q)^{2d+1}}{1-q^{2d+1}}}\right]^{\frac{1}{1+2d}}. \tag{11}$$

Fig. 3 suggests that there is some specific value of q for which the characteristic time is the lowest; assuming that $q^{2d} \ll 1$, one can estimate this value with

$$q^* = \frac{1}{2d+1}. \tag{12}$$

We stress that the value of q^* given by Eq. (12) is independent on the system size N, which is similar to the value of the ϵ^* parameter given by Eq. (6).
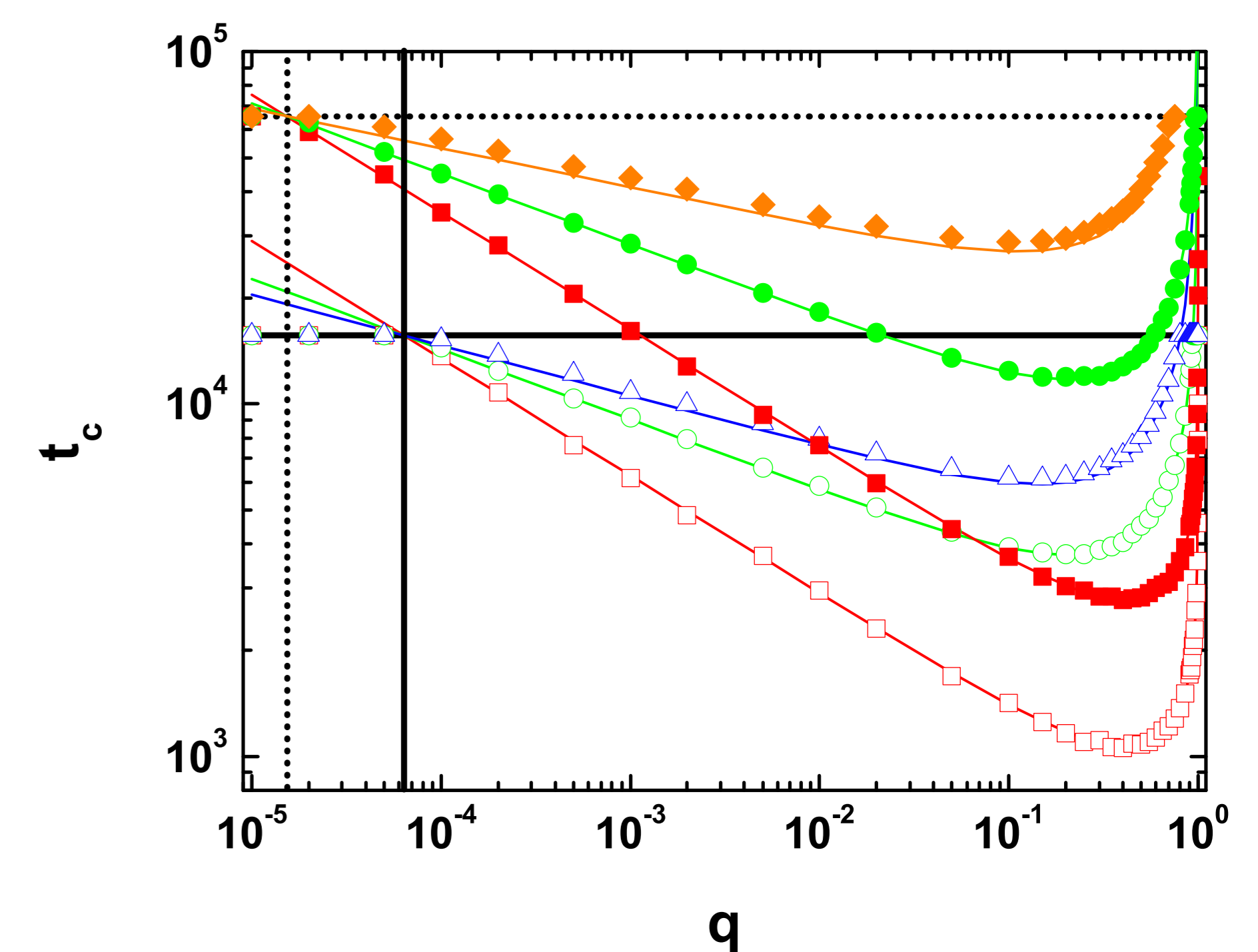

FIGURE 3: Log-log plot of the global characteristic times t_c versus parameter q of the geometric distribution for $N_1 = 15625$ (empty symbols) and $N_2 = 65536$ (filled symbols). Data points are taken from numerical simulations: squares are $d = 1$, circles are $d = 2$, triangles are $d = 3$ and diamonds are $d = 4$; all data points are averaged over 1000 runs. Solid lines come from Eq. (11) and the horizontal solid line is drawn for $t_c = N_1$, whereas the horizontal dotted one for $t_c = N_2$. The vertical solid line marks $q_{min} = 1/N_1$, while the vertical dotted line is drawn for $q_{min} = 1/N_2$

Conclusions

We have extended the simple model of community isolation to the case with the symmetry breaking. Our calculation and numerical simulations show that even a simple way of introducing the external bias between species can lead to interesting and non-trivial results. We have found that in both the two-species case where a parameter ϵ governs the symmetry breaking and in the multi-species case where the numbers of each entity are given by the geometric distribution, there exists some specific and well-defined value of the control parameter giving a minimum of the characteristic time t_c. The presented results can be easily further generalized to the cases of other topologies (e.g., complex networks) and other kinds of biases.

Acknowledgements

References

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