Improved Majority Identification by the Coarsened Majority Automaton

David Peak
Charles G. Torre
Jenny R. Whiteley

Physics Department, Utah State University
Logan, Utah 84322

The initial majority identification task is a fundamental test problem in cellular automaton research. To pass the test, a two-state automaton has to attain a uniform configuration consisting of only the state that was initially in the majority. It does so solely through its local, internal dynamics—i.e., success in the task is an example of emergent computation. Finding new, better-performing automata continues to be of interest for what additional clues they might reveal about this form of computation. Here we describe a novel, coarsened version of one of the standard majority identifiers. We show that this coarsened system outperforms its parent automaton while significantly reducing the number of computations required to accomplish the task.

Keywords: cellular automata; majority identification; coarsened dynamics

1. Introduction

An experiment conducted with fish(!) [1] motivates the work reported here. The experiment mixes together minnows initially trained to school toward yellow and blue targets. The two subpopulations continue to school toward the target each was trained to prefer if there is only a small majority of one over the other. On the other hand, adding a large number of untrained fish with no net target preference often causes the entire new population to school toward the target favored by the initial small majority. This counterintuitive result has produced much discussion in the literature in terms of potential implications for the biological and social sciences. The paper we consider here, however, focuses narrowly on the minimal ingredients needed for the fish to come to consensus without a leader [2]. In it, the authors propose that the minnows are essentially solving the cellular automaton initial majority identification task. The authors of [2] argue that using a model they call the directed majority automaton (DMA) naturally explains several of the unexpected observations reported in [1].

The model results of [2] are interesting and might potentially provide an alternative interpretation to the observations in [1, 3]. Exactly how the DMA performs majority identification and how to improve it, however, are unexplored in [2]. We address both of these issues here. To do so, we adopt the view that majority identification is similar to aspects of collective behavior in physical systems. With this perspective, we find that renormalization and universality arguments from thermal physics yield important insight into how the DMA works. In particular, we show that majority identification by the DMA is equivalent to a directed percolation phase transition. Using these arguments, we develop a coarsened version of the DMA that performs the majority identification task substantially better and also much more rapidly.

2. Definition and Performance of the Directed Majority Automaton

The space of the DMA we study is an $N \times N$ square grid of cells with toroidal boundary conditions. Each cell can be in one of two states—for example, $+/-1$. In each time step, each cell simultaneously executes the "NE/SW" rule: if at time t the cell's state is $+1$, then at time $t+1$ the cell's state is the current majority of itself and its nearest neighbors to the north and east; if the state is -1, then the state is the majority of itself and its nearest neighbors to the south and west. (The rules for the ES/WN, SW/NE and WN/ES directions perform identically.) The DMA successfully identifies the majority if (a) there is a majority of one of the states over the other at $t=0$; and (b) after repeated iterations, it produces a uniform configuration consisting only of the initial majority state. (Note that [4] and [5] also analyze some aspects of the DMA of [2], and the focus of interest here, but call it the "2dGKL automaton.")

Figure 1 shows the DMA's successful identification rates as functions of the fractions of the initial majority states and for different space sizes (with $N = 8, 16, 32, 64$ and 128). Each data point shown is the average of 10^4 simulations for randomly chosen initial configurations.

As is the case for all two-state cellular automata [6, 7], the DMA does not successfully identify the majority for all initial configurations. When the DMA fails to identify the initial majority state, the final configurations are either all of the wrong state or unresolving mixtures of $+1$ and -1.
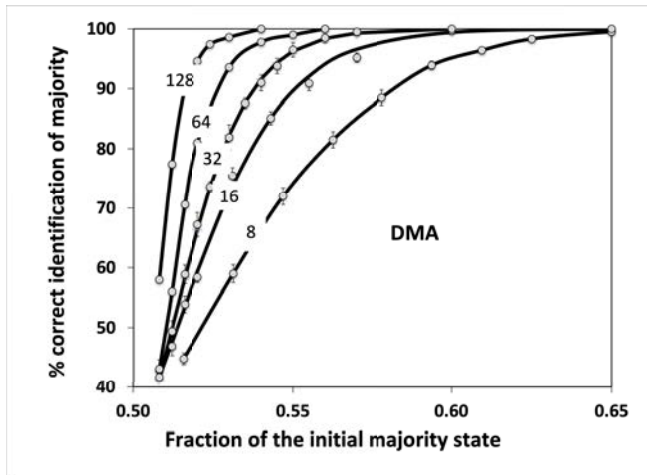
Figure 1. Average fraction of times the DMA correctly converges to a uniform configuration of the state initially in the majority in a random configuration. Space sizes $2^n \times 2^n$, with $n = 3, 4, 5, 6, 7$.

3. The Directed Majority Automaton Renormalization Flow

The successful majority-identification curves in Figure 1 are observed to be well fit by the form

$$\sigma(N, f) = 100 / (1 + \exp[\{AN + B\}\{2f - 1\} + \ln\{CN + D\}]). \tag{1}$$

Here, $\sigma(N, f)$ is the percentage of the cases in which the DMA successfully identifies the majority initially present with fraction f, in a space of size $N \times N$. In equation (1), for the data in Figure 1, $A = -1.006$, $B = -9.532$, $C = 0.042$ and $D = 1.433$. The uncertainty in these values is about $\pm 3\%$. The form of equation (1) is also suggested by the observation (discussed below) that the results of the DMA dynamics are analogous to a classical thermal system evolving to an equilibrium condition from an unstable initial configuration. In this analogy, the denominator in equation (1) can be interpreted as a grand canonical partition function, with $2f - 1$ playing the role of an inverse temperature, $-(AN + B)$ the energy level of the system of size $N \times N$, and $\ln(CN + D)$ the analog of (a temperature-dependent) chemical potential.

The $2^n \times 2^n$ spaces referred to in Figure 1 have no majority when $f = 0.5$. For this case, the final configurations are either all $+1$, or equally all -1, or periodically varying configurations of fixed numbers of $+1$ and -1. The value $\sigma(N, 0.5)$ is the percent of the time a

50-50 configuration converges to all $+1$ (or, equally, to all -1). The fractions of the time each of these $+1$, -1 and mixed configurations appear are determined by the size of the space—with the fraction of the mixed configuration increasing as N increases (ranging from 28% for $N = 8$ to 74% for $N = 128$). When f is greater than 0.5 by even a small amount, however, the DMA converges to the majority identification values shown in Figure 1. Thus, for the DMA, $f = 0.5$ produces a critical condition of the dynamics.

A complex dynamical system can sometimes be transformed into a simpler equivalent form guided by the system's "beta function." For the DMA it is useful to define such a function, $\tilde{\beta}(N, f)$, as

$$\tilde{\beta}(N, f) \equiv \frac{\partial \sigma}{\partial [\ln (f)]} = -2f\sigma(AN + B)(1 - \sigma / 100). \tag{2}$$

Substituting the (negative) values for A and B from above shows that, for the DMA, $\tilde{\beta}(N, f) \geq 0$. At the critical value, $f = 0.5$, $\tilde{\beta}$ is not only positive but also increases as N increases; for example, $\tilde{\beta}(128, 0.5) = 10.7 \tilde{\beta}(8, 0.5)$. Configurations with $f = 0.5$ are unstable and increasingly more so (as signaled by the increasing value of $\tilde{\beta}$) as the automaton space size increases. On the other hand, for all N, as f approaches 1, σ approaches 100, and therefore $\tilde{\beta}$ approaches 0. Thus, for all space sizes, the DMA dynamics "flow" away from the $f = 0.5$ configurations toward configurations of increasing f. As shown in Figure 1, the DMA dynamics is essentially scale invariant for f greater than about 0.65. When this is the case, the dynamics can be renormalized—that is, converted into another dynamical system with similar results, operating at coarser length scales [8].

4. The Directed Majority Automaton Universality Class

To investigate consequences of the renormalization of the DMA, we first examined the DMA's critical exponents. As noted, small increases in f above 0.5 lead to increased successful majority identification via the DMA. The initial majority fraction f is therefore a control parameter for the dynamics and the successful majority identification fraction σ is the related order parameter. In the study of universal phenomena, the critical exponent β (not the value of the system's beta function) is defined through the relation

$$\frac{\sigma - \sigma_C}{\sigma_C} = A\left(\frac{f - f_C}{f_C}\right)^{\beta}, \text{ as } f \to f_C, \tag{3}$$

with approximately the same value for β for each space size. To evaluate the average β for the DMA, we approximated the limit in equation (3) using $f_c = 0.5$ and the values $f_1 > 0.5$, corresponding to mixed configurations with one more $+1$ than 50-50 for each $N \times N$ space. (For 8×8, for example, $f_1 = 33/64 = 0.5156$, and so on for the other N.) For each value of N, we averaged 10^4 simulations for random initial configurations with the same $f_C = 0.5$ and the same smallest f_1. The results are the black data points on the log–log plot shown in Figure 2.
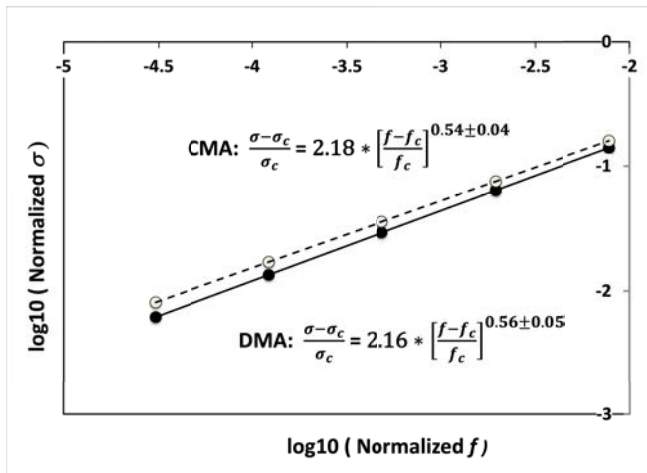
Figure 2. Successful majority identification as a function of initial majority near the critical fraction $1/2$ for different space sizes.

As each data point (each N) is supposed to have the same β value, the slope of the best fit to the log–log data yields an estimate of this parameter for all space sizes. From the data in Figure 2, we find $\beta = 0.56 \pm 0.05$, for the DMA. This result indicates that the DMA is (probably) a member of the universality class of directed percolation in two spatial dimensions—that is, for which $\beta = 0.583 \pm 0.003$ [9].

5. Coarsening the Directed Majority Automaton

Dynamical systems that exhibit critical behavior typically contain self-similar configurations of states. In such cases, assigning a new effective state to blocks of multiple cells of the original configuration and

applying a new dynamical rule to the evolution of the blocks yields quantitatively similar results to the original dynamics while reducing the associated computational requirements. We applied such a coarsening strategy—which we designate as the coarsened majority automaton, the CMA—to the DMA dynamics.

Because the DMA always converges to one of three generic configurations—that is, all $+1$, all -1 or mixed $+1$s and -1s—we allowed our coarsening algorithm to also incorporate three possible values: $+1$, -1 or 0. The coarsening rule we used is: replace every 2×2 block with a single block and assign to it the state that was in the majority in the 2×2; if there was no majority, assign the state 0 to the block. Following that, we apply the dynamical rule: (a) if the block state at time t is $+1$, set the state at $t+1$ to the majority of the block, the block to its north and the block to its east; if there is no majority, however, set the new state to 0; (b) if the block state is -1, set the new state to the majority of the block, the block to its south and the block to its west; if there is no majority, set the new state to 0; (c) if the block state is 0, set the new state to the majority of the block plus its four nearest neighbors. The blocks in the CMA are toroidally wrapped in the same manner as the cells in the DMA spaces. As the DMA in this study is defined on $2^n \times 2^n$ spaces, n repetitions of this coarsening plus dynamics process lead to a single block. The CMA successfully performs the majority task, then, when the state of its final single block is $+1$ (or -1), whenever $+1$ (or -1) was in the majority in the initial configuration.

## 6. Majority Identification by the Coarsened Algorithm

It is not obvious that the CMA defined here has any relation to the original DMA. The CMA, after all, is a different automaton. As a first check to see if they might be related, we ran the CMA for 10^4 random initial configurations with the same space sizes and values of f as we did for the DMA. The results for the CMA, shown in Figure 3, are qualitatively much like those for the DMA in Figure 1.

Fitting the data in Figure 3 by the same functional form as equation (1) yields coefficient values similar to those for the DMA: $A = -1.700$, $B = -6.623$, $C = 0.003$ and $D = 1.414$, the uncertainties of which are about $\pm 8\%$.

To further examine the degree to which the DMA and the CMA are related, we followed the same procedure as previously for finding the CMA's critical exponent β. The results are shown in the log–log plot of Figure 2 as the open circle data points. The best fit to the CMA data yields a slope equal to $\beta = 0.54 \pm 0.04$, which is essentially

indistinguishable from the result for the DMA. Thus, like the DMA, the CMA also (probably) belongs to the universality class of two-dimensional directed percolation.

It is natural to wonder if the DMA and CMA perform the initial majority identification task identically, or if one does so better than the other. To investigate this question, we reran the CMA dynamics using each of the initial configurations as in Figure 1. Again, for each space size and for each value of the initial majority we ran and averaged the results of 10^4 simulations. We found that the CMA actually outperforms the DMA using exactly the same initial configurations.
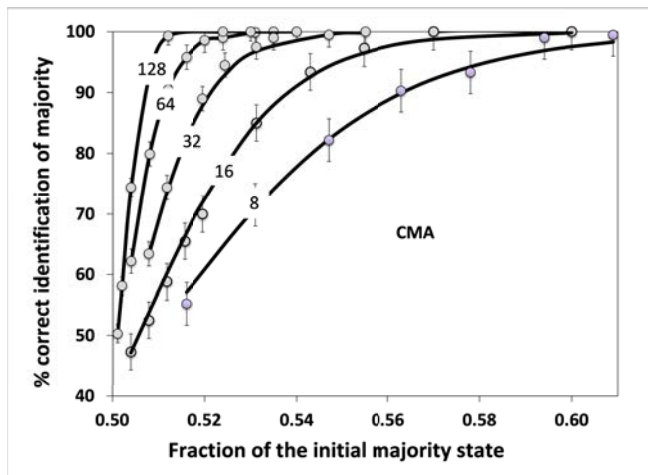

Figure 3. Average fraction of times the CMA (see text) correctly converges to a uniform configuration of the state initially in the majority in a random configuration. Space sizes $2^n \times 2^n$, with $n = 3, 4, 5, 6, 7$.

Figure 4 summarizes the results. The identification rate of the CMA is about 20% higher than that of the DMA when averaged over the same initial majority fractions for the same space sizes we used. Moreover, the CMA performs the task much more economically. For example, for 128×128 spaces, we observe that the DMA typically requires about 350 complete updates of all 16384 cell states to achieve a fixed or periodic end configuration—that is, nearly 6×10^6 updates. For the same initial conditions, the CMA always achieves its end state in seven iterations—involving a total of 5397 complete state updates, a factor of about 1000 fewer computations.

Also shown in Figure 4 are results reported in [5]. In that study, the authors employed a genetic algorithm search for alternative rules to the DMA to improve majority identification. The CMA's improvement over the DMA is at least equivalent to, and—for the data

available in [5] and reported here—possibly better than that obtained from the genetic algorithm search. And again, the CMA does so while very significantly reducing the associated computational cost compared to the best genetic algorithm found rule.
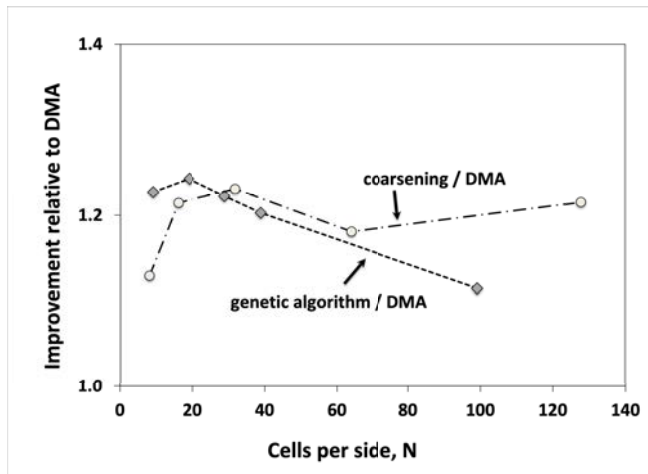
Figure 4. Comparison of the improvement of initial majority identification over the DMA for the coarsening algorithm in the text and for a method produced by a genetic algorithm search.

7. Undecidability and Predictive Features in the Directed Majority Automaton

Figure 5 shows three 16×16 initial configurations with the same initial fraction of $+1$ (black) (52.3%) and -1 (white) (47.7%) cells. In the column immediately to the right of the initial configurations are single blocks representing the respective final 16×16 configurations produced by the DMA dynamics. In the top row, the final 16×16 configuration is 100% black. (According to Figure 1, all black is produced about 60% of the time for this setup.) In the middle row, the final configuration is 100% white. At the bottom, the final configuration—represented as gray—is an unresolving mixture of black (59.8%) and white (40.2%). If the DMA were a perfect majority identifier, all three of these final configurations would be 100% black.

To the eye, the initial configurations shown in Figure 5 appear qualitatively identical, yet the final configurations are clearly different. In other words, the exact spatial relation of all of the states to each other is important for the DMA's output. This fussy dependence on the initial placement of states is referred to as "undecidability." In general, if an automaton is undecidable, the only way—almost—to

determine what it will produce for each initial configuration requires running the dynamics nearly to completion (see, e.g., [10]).
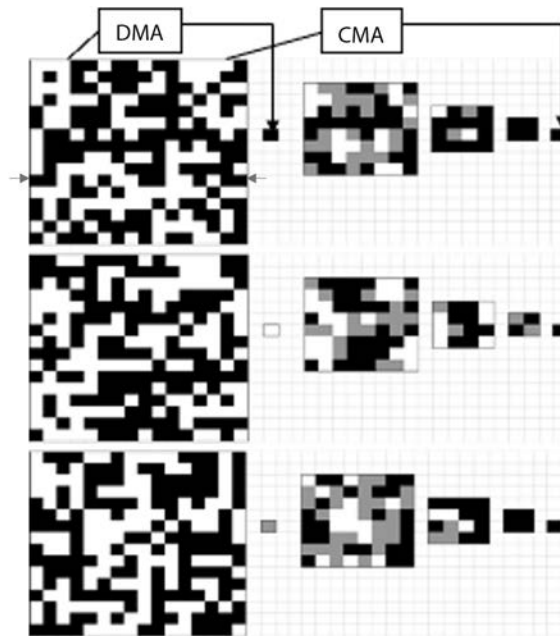
Figure 5. Three different configurations of 134 black and 122 white cells on a 16×16 space. The DMA converges to all black (top), all white (middle) and a 153-black and 103-white mixture (bottom). Also shown are the respective CMA block configurations (8×8, 4×4, 2×2 and 1×1). In each case, the final—correct—block is black.

The DMA is almost undecidable because its final configuration is almost always preceded by the formation of one or more percolation paths. A percolation path on a torus is a single state, nearest-neighbor connected path that spans the torus. It is closed, in the sense that a cell on it in the upper row is in the same column as a cell on it in the lower row (or in the same row as cells in the first and last columns). When the final configuration of a DMA run consists of all the same state, the percolation paths that form early on consist only of that final state. Such percolation paths "fatten" in succeeding iterations, leading eventually to a systemwide collective state change. Consistent with our provisional identification of the DMA universality class, we propose that successful identification of the initial majority by the DMA is equivalent to a directed percolation phase transition.

When the DMA evolves to a mixed configuration, there will either be two nonintersecting percolation paths of opposite state forming

during the intermediate dynamics, or, more rarely, no percolation paths at all. Typically, such predictive precursor structures—one or more paths of the same state or nonintersecting paths of both states—emerge in only a few time steps. (The rare no-percolation-paths case typically takes much longer to develop and is consequently not a useful predictor.) Thus, the DMA is almost undecidable.

While it is still generally impossible to infer the outcome of a DMA process by just examining its initial configuration (unless there is already a percolation path present, such as the black "horizontal" path in the top initial configuration in Figure 5—the ends of which are identified by the two gray arrows), the formation of percolation paths after only a small number of iterations of the dynamics provides useful clues. For 16×16 spaces with 50-50 initial configurations, for example, each of the three final configuration types appears (after 30 to 40 iterations) roughly equally. Random guessing after a few iterations gets the right answer about a third of the time. Using percolation path clues, however, allows the final configuration to be successfully predicted about 60% of the time after just three iterations.

8. Why Does the Coarsened Majority Automaton Outperform the Directed Majority Automaton in the Majority Identification Task?

Figure 5 also shows the results of the CMA dynamics evolving the same initial configurations as applied to the DMA. Starting with 16×16 states, there are in each case successively 8×8, 4×4 and 2×2 states and finally, one single state. The CMA states can be black (+1), white (−1) or gray (0). In each of the cases shown, the final all-black configuration, in contrast to the DMA results for the same initial configurations, correctly identifies the initial majority.

In each of the cases shown, the successively coarser configurations contain increasing fractions of the initial majority state. For the purpose of calculating the black content fraction, gray can be usefully interpreted as half black, half white. Thus, in the top trial depicted in Figure 5, the black content fraction for the CMA increases from 52% (for 16×16) to 59% (for 8×8) to 81% (for 4×4) to 100% (for 2×2). In the middle trial, the black fractions are 55%, 56% and 75%. In the bottom trial, the fractions are 58%, 75% and 100%. This sequential majority amplification appears to be a general result. For example, an average of 1000 experiments starting each time with random configurations, but with the same initial black fraction (52.3%) as in Figure 5 and where the CMA converges to one black cell (which occurs 78% of the time), yields the increasing sequence 58.5 ± 0.4 (for 8×8), 74.3 ± 1.0 (for 4×4) and 95.7 ± 1.4 (for 2×2). In other words, whenever the coarsening algorithm successfully identifies the initial

majority, it essentially always amplifies the initial state fraction in each coarsening.

In addition to state amplification, whenever the coarsening algorithm correctly identifies the initial majority, at least one percolation path consisting of all the majority states emerges in the coarsened configurations before the final configuration. In the examples in Figure 5, after each first coarsening (i.e., the 8×8 configurations) there are already multiple black percolation paths—counting gray as 50% black—but no white one.

Therefore, the reason the CMA outperforms the DMA is because when the coarsening algorithm eventually identifies the initial majority, it increasingly amplifies the initial state fraction in each coarsening step while at the same time sequentially involving fewer and fewer cells. It is more likely, therefore, that the CMA will produce closed percolation paths of the correct state—the progenitors of correct identification—than the DMA.

9. Summary

The directed majority automaton (DMA) is a two-dimensional, two-state cellular automaton that competently, though not perfectly, performs the initial majority task over a wide range of initial majority fractions. This feat is accomplished autonomously by the automaton's collective dynamics. Here, we demonstrate that the DMA's dynamics reside in the universality class of directed percolation. We observe that successful majority identification is always preceded by the appearance of a closed percolation path, consisting solely of the initial majority state, traversing the automaton space. Such paths subsequently initiate a phase transition in which all of the cells of the automaton take on the initial majority state. Exploiting the possibility that the collective dynamics of the DMA might be renormalizable, we developed a coarsened version of the DMA—the CMA—which resides in the same universality class as the DMA. The CMA performs the majority identification task with higher success rates and considerably fewer computations than the DMA. It does so by also developing percolation paths in the coarsened state spaces.

References

[1] I. D. Couzin, C. C. Ioannou, G. Demirel, T. Gross, C. J. Torney, A. Hartnett, L. Conradt, S. A. Levin and N. E. Leonard, "Uninformed Individuals Promote Democratic Consensus in Animal Groups," *Science*, **334**(6062), 2011 pp. 1578–1580. doi:10.1126/science.1210280.

[2] J. D. Christensen, D. B. Griffin and D. Peak, "Undecided Cliques Promote Consensus in the Directed Majority Automaton," *International Journal of Unconventional Computing*, **13**(4), 2018 pp. 359–375.

[3] Y. Katz, K. Tunstrøm, C. C. Ioannou, C. Huepe and I. D. Couzin, "Inferring the Structure and Dynamics of Interactions in Schooling Fish," *Proceedings of the National Academy of Science*, **108**(46), 2011 pp. 18720–18725. doi:10.1073/pnas.1107583108.

[4] S. M. Messinger, K. A. Mott and D. Peak, "Task-Performing Dynamics in Irregular, Biomimetic Networks," *Complexity*, **12**(6), 2007 pp. 14–21. doi:10.1002/cplx.20181.

[5] M. Cenek and M. Mitchell, "Evolving Cellular Automata," *Encyclopedia of Complexity and Systems Science* (R. A. Meyers, ed.), New York: Springer, 2009 pp. 3233–3242. doi:10.1007/978-0-387-30440-3_191.

[6] M. Land and R. K. Belew, "No Perfect Two-State Cellular Automata for Density Classification Exists," *Physical Review Letters*, **74**(25), 1995 pp. 1548–1550. doi:10.1103/PhysRevLett.74.5148.

[7] A. Bušić, N. Fatès, J. Mairesse and I. Marcovic, "Density Classification on Infinite Lattices and Trees," *Electronic Journal of Probability*, **18**, 2013 pp. 1–22. doi:10.1214/EJP.v18-2325.

[8] K. G. Wilson, "The Renormalization Group: Critical Phenomena and the Kondo Problem," *Reviews of Modern Physics*, **47**(4), 1975 pp. 773–840. doi:10.1103/RevModPhys.47.773.

[9] J. Wang, Z. Zhou, Q. Liu, T. M. Garoni and Y. Deng, "High-Precision Monte Carlo Study of Directed Percolation in $(d + 1)$ Dimensions," *Physical Review E*, **88**(4), 2013 042102. doi:10.1103/PhysRevE.88.042102.

[10] S. Wolfram, *A New Kind of Science*, Champaign, IL: Wolfram Media, Inc., 2002 pp. 753–755.