

A Minimal Spatial Cellular Automata for Hierarchical Predator-Prey Simulation of Food Chains

K.A. Hawick and C.J. Scogings

Institute of Information and Mathematical Sciences

Massey University – Albany, North Shore 102-904, Auckland, New Zealand

Email: {k.a.hawick, c.scogings}@massey.ac.nz

Tel: +64 9 414 0800 Fax: +64 9 441 8181

Abstract

Models of complex spatial environmental and ecological systems are usually constructed using partial differential equations (PDEs), but cellular automata (CA's) can provide microscopically simple yet macroscopically rich alternatives. We develop a cellular automata model of a hierarchical predator-prey system and show that even a minimal automaton is able to capture the essential boom-bust and dynamical behaviour of real physical systems. A single probability rate of predator death is used to control predator behaviour. We describe the model in detail and explore the CA model for one- and two-predator food chains. We find a well delineated phase transition in the 2-predator system when the predator lifetime parameter is varied and present some system analysis and quantitative metrics. We discuss the CA model in comparison with PDE and more detailed event-driven agent-based models.

Keywords: cellular automata; spatial models; predator-prey; Lotka-Volterra; food chains; phase transition; stochastic rate equation.

1 Introduction

Cellular Automata (CA) [1] models often provide a simple yet insightful encapsulation of the key microscopic behaviours of a complex system [2]. CA's have been used to study: system dynamics, growth, emergence [3–5], chaos, randomness, complexity and other whole system properties such as the effect of diffusion [6]. CA's models can be explored through explicit enumeration of deterministic rules and behaviours and explicit starting conditions [7] or by using methods such as statistical mechanics [8], whereby computer generated random numbers provide different starting conditions,

or probabilistic pathways through different deterministic rule sets.

Environmental or ecological systems involving competing populations of organisms often involve specific predator-prey relationships and may in fact have hierarchical food-chains of some length. Such systems have traditionally been modelled using differential equations or systems of coupled differential equations such as the Lotka-Volterra model [9, 10]. This can be extended to spatial models with some considerable cost in computational cost. A partial differential equation (PDE) model system based upon the reaction-diffusion equation can be solved numerically for various starting conditions to map out the model phase space and potentially to yield statistical predictions about how a particular model system might evolve to stability or extinction.

Another approach is to develop a detailed event-driven agent model to capture essential system behaviours that can be explored through explicit simulation [11, 12]. A number of artificial life models [13] based upon animats [14, 15] (spatially-oriented agents) have been developed [16, 17] including [12, 18–21], including a model developed by the present authors [22, 23] for studying complexity in predator-prey ecological systems [24]. A similar animat model is described in [25] where a hierarchy of animats is established in which beetles need to eat worms and worms need to eat grass. These models typically involve a number of carefully chosen parameters and although they are computationally cheaper to operate than PDE based models, they still require quite considerable numbers of independent runs with different starting conditions to avoid bias effects.

CA's potentially provide a computationally cheaper alternative to both full PDE-based models and to detailed multi-parameter animat agent models. A spatial CA can be established on a simple mesh with each cell in the system following precise and deterministic au-

tomaton rules. The model can be enriched by imposing probabilistic behaviour whereby different deterministic rule pathways can be followed based on a random choice and controlled by a single rate parameter.

In this paper we describe a relatively simple CA based model that is both simpler and computationally cheaper to run than both a PDE-based approach and our animat-based detailed model. We describe the model in Section 2. We present some visual and quantitative results in Section 3. We explore the model macroscopic behaviour and discover phase transitional behaviour which we locate numerically and discuss in detail and offer some conclusions in Section 4.

We are primarily exploring predator-prey and predator-predator-prey behaviours as they might pertain to realistic spatially distributed participants in a food chain. To aid reader understanding, throughout this article we refer colloquially to predators and prey as bears, foxes and rabbits. This gives a memorable symbolism for equations and the simulation software. However our individual animats or cells are not necessarily representative of actual physical “rabbits” and “foxes” nor are they intended to be so. More realistically they might be bacteria, amoeba or plankton or some other ecological components of a food chain that has spatial extent and which therefore cannot be modelled by a simple differential equation.

2 Predator-Prey CA Model

Cellular automata can be constructed in two principle manners: either as fully synchronised update rules so that each cell is effectively updated exactly once per time step; or with Monte Carlo random updates so each cell is updated once on average, each time step. The former algorithm family requires a buffered set of cell memory locations or a data-parallel computer with exactly the same number of processing elements as there are cells. Otherwise sweeping artifacts of the algorithm can affect the results and introduce unrealistic correlations. More practically and now widely used, is the Monte Carlo random update whereby each of the N cells is selected at random and updated *in-situ*. This approach does not require extra memory and is generally easy to implement on both parallel and serial computers.

Our cellular automata rules for the 4-species predator-prey model are given in Algorithm 1.

Lines 5-10 can be omitted to revert to a three-species model (vacancy,rabbit,fox only). The model parameters are the system size N , the initialisation population

Algorithm 1 The spatial predator-prey Cellular Automata rules for 4 species (vacancy, rabbit, fox, bear). The if-clauses are controlled by probabilistic rates, so that should a clause in the algorithm rules fail due to the random probability test, the algorithm moves on to the next if-clause.

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1: for  $T$  steps do
2:   for  $N$  sites do
3:     choose a random site  $i$ 
4:     choose a random neighbour  $j$ 
5:     if  $i = \text{bear}$  and  $j = \text{fox}$  then
6:       bear eats fox and fox becomes bear with
       probability  $\sigma_b$ 
7:     else if  $i = \text{bear}$  then
8:       bear dies with probability  $p_b$ 
9:     else if  $i = \text{bear}$  and  $j = \text{vacancy}$  then
10:      bear moves to vacancy
11:    else if  $i = \text{fox}$  and  $j = \text{rabbit}$  then
12:      fox eats rabbit and rabbit becomes fox with
      probability  $\sigma_f$ 
13:    else if  $i = \text{fox}$  then
14:      fox dies with probability  $p_f$ 
15:    else if  $i = \text{fox}$  and  $j = \text{vacancy}$  then
16:      fox moves to vacancy
17:    else if  $i = \text{rabbit}$  and  $j = \text{vacancy}$  then
18:      rabbit reproduces into vacancy with prob-
      ability  $\mu$  or rabbit moves into vacancy
19:    end if
20:  end for
21: end for

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fractions and the control probability rate parameters. The model is dependent upon random numbers for initialisation and probability comparisons so it is not deterministic. Instead it is one of many stochastic cellular automata where we expect the statistical properties to converge to fixed values when averaged over a number of independent runs with the same parameters.

The model can be implemented on any cellular geometry, although we report on results for the square 4-nearest neighbour case only in this present paper. We also take the probability of predator death $p_b \equiv p_f \equiv p$ and $\sigma_b \equiv \sigma_f = \mu = 1$ for simplicity. We experiment with various p values on model systems of size 512×512 where the initial populations of the 3 or 4 species are equal and arranged randomly.

The algorithm is given for 4-species including 2 predators, and this can be extended to include a longer food chain in the obvious way or can be curtailed to a single predator species by simply omitting rules referencing “bears”

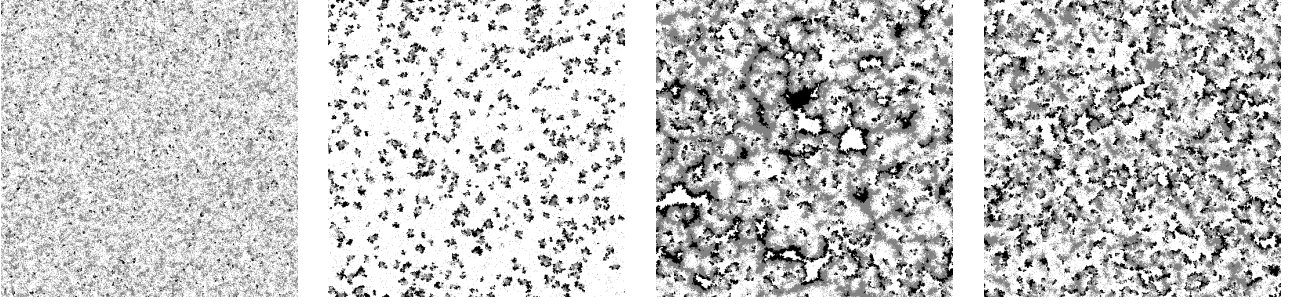


Figure 1: Screen shots of a 3-species model 512×512 configuration at times: 16, 32, 128, 511 steps with predators in gray, prey in black and vacancies in white.

3 Results

The CA model can best be explained by observing the spatial patterns of cells as the system evolves. In the experiments reported below, model CA systems on square periodic lattices of 512×512 cells are run for times of up to 2048 steps. Where appropriate, results presented have been averaged over ten independent runs with different random starting configurations.

Figure 1 shows some screen-shots of a 3-species model system evolved for up to 512 time steps from an initially random uniform mixture. The predators are shown in gray and the prey species in black against a white background of vacancies. The system rapidly evolves from the starting random mixture into clumps of individual species, often with predation occurring along the boundaries of a clump of prey. The particular regime we have chosen to explore in this present paper gives rise to relatively well mixed sets of small to medium sized clumps. If the death probability is set too high, predators die out and prey grow unbounded occupying the whole system. Likewise, if predation is too successful the prey population can crash, followed by a subsequent crash in the predator population too.

When we introduce a deeper food-chain with a second predator species that predaes upon another (4-species) the detailed microscopic pictures become harder to follow without dynamical colour animation. Instead we present some of the population time plots showing how the relative species population fractions change with simulation time. We first consider the 3-species (single predator) model, presenting data in this manner.

Figure 2 shows a linear time plot of population fractions where the initial transients that arise from the random uniform (and equal fractional) mix of 3-species is rapidly replaced by a set of oscillating boom-busts until on average the system reaches a sustainable dynamic equilibrium. This behaviour of the CA model is different from PDE models and detailed animat mod-

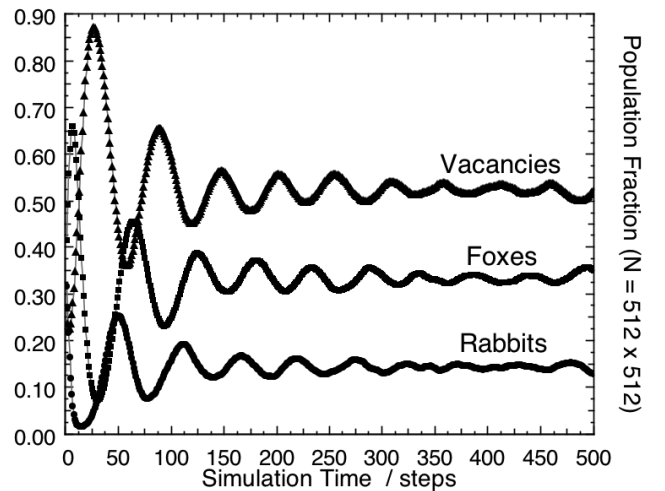


Figure 2: Linear population fractions for rabbits, foxes and vacancies for a 512×512 systems simulated using the CA model for 512 time steps, with $p = 0.2$; $\sigma \equiv \mu \equiv 1$ showing long-term dampening of periodic fluctuations in the system and long term steady state expectation values for population fractions.

els and is due to the relatively homogeneous population pressures across the model system. Although individual cells are dying, being eaten, diffusing and reproducing, the bulk behaviour settles down to a steady mean population albeit with periodic fluctuations still discernible. The plots shown are averaged over ten independent runs so that since the periodic oscillations are all at random phases, they combine to produce a flattish trace indicating the stable mean population fractions.

Figure 3 shows the same data as in Figure 2 but with time on a logarithmic scale. This emphasises the transient behaviour, which is remarkably repeatable within the error uncertainties obtained over averages over ten independent starting runs.

Figure 4 shows the traditional attractor plot for chaotic systems such as the population model. The rabbit-fox

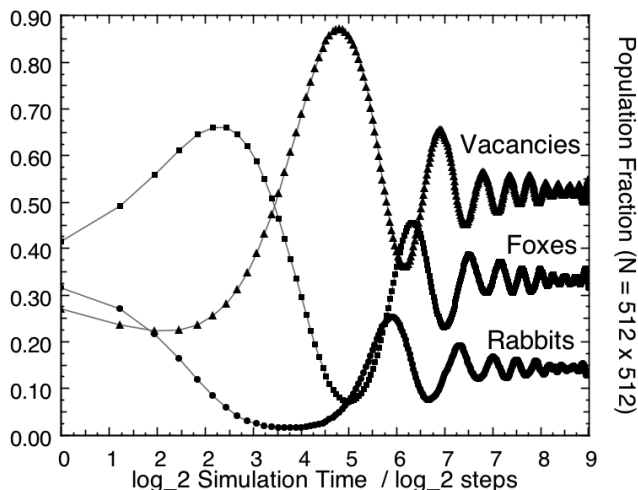


Figure 3: Log base 2 time plots for a 512×512 systems simulated using the CA model for 512 time steps, with $p = 0.2; \sigma \equiv \mu \equiv 1$ emphasising initial transient behaviour as the system settles down from random equal population mixture.

plot (lower left) shows a spiral decaying orbit going anti-clockwise, as the averages settle to long term values. The rabbit-vacancy trace (upper left) orbits clockwise, showing that vacancies are used up as rabbit numbers increase. Finally the fox-vacancy trace (right) also orbits clockwise showing vacancies are also diminished as fox numbers grow.

The three-dimensional trace plot shown in figure 5 illustrates the same information – average population frac-

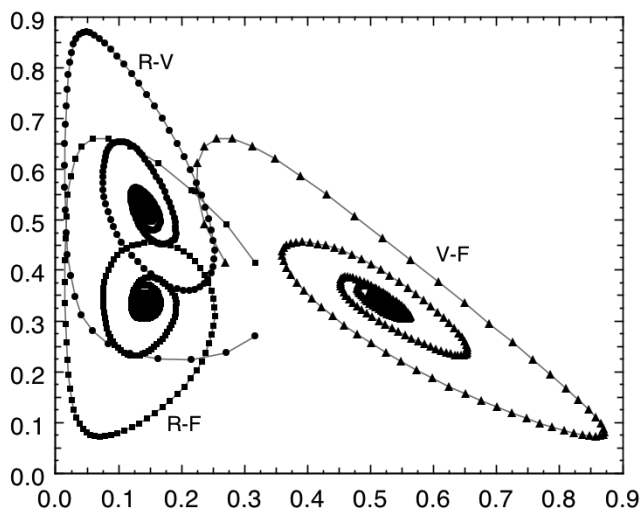


Figure 4: The experimental data attractors for foxes (F) and rabbits (R) and vacancies (V), for a 512×512 systems simulated using the CA model for 512 time steps, with $p = 0.2; \sigma \equiv \mu \equiv 1$.

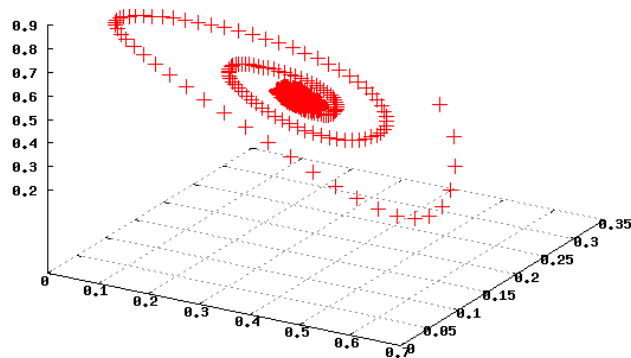


Figure 5: The 3-D attractor plotted for foxes (f) and rabbits (r) and vacancies (v), for a 512×512 systems simulated using the CA model for 512 time steps, with $p = 0.2; \sigma \equiv \mu \equiv 1$.

tions for rabbits, foxes and vacancies in a three-species model, over ten independent runs. The characteristic oscillation and their cross-dependence is shown in the phase orbital pattern. The averaged data converges to a small region of phase space, with fluctuations thereafter. An individual trace from a single experiment would form a characteristic orbital trace as the system goes through periodic boom-busts in the three (coupled) populations.

The error bars are not shown in this averaged data but are smaller than the plot symbols used.

In Figure 6 we see the steady state average population fractions after 2048 steps for different values of the predator death probability rate p . These experiments represent a scan in the p parameter and a measurement

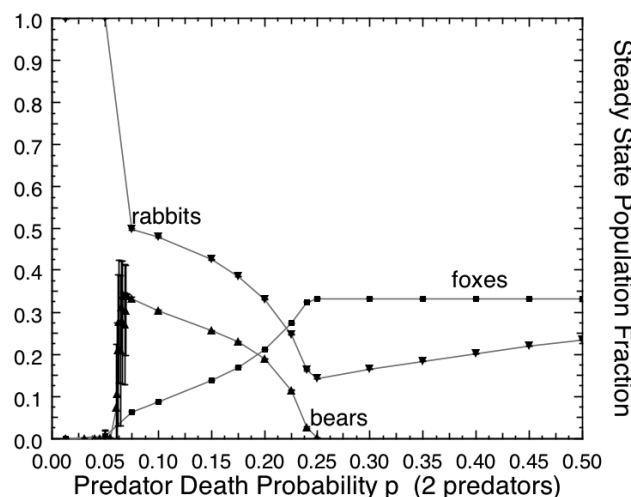


Figure 6: The steady state values of the predator populations in a 4-species model with two predators in the food chain (foxes and bears)

of the final values from an individual run of the type such as that shown in Figure 2.

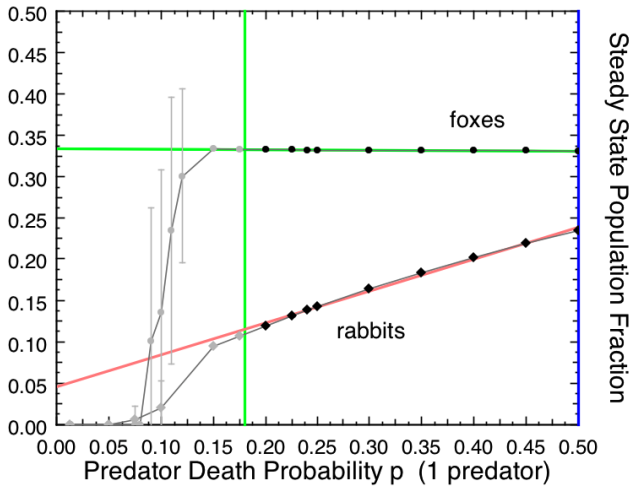


Figure 7: The steady state values of the predator populations in a 3-species model with a single predator in the food chain (foxes). Least squares fits are made to the limiting parts of the plots. The greyed-out low- p part is not fitted.

The data shows a phase transition in this parameter for both the four species (two-predator) model as well as the 3-species (single-predator) model in Figure 7. In the case of the four-species model (Figure 6) the transition is very sharply defined at $p \approx 0.05 \pm 0.001$, and the transition is still well defined but at around $p = 0.1 \pm 0.01$ for the three species model.

The linear sections of these steady state population fractions can be extrapolated and least-squares fits yield for the four-species, two predator model that the fox population = $-0.004p + 0.333$ and the rabbit population = $0.357p + 0.057$. Similarly for the three species (single predator) model, the model fox population = $-0.004p + 0.333$ and the rabbit population = $0.385p + 0.045$. In both cases fitted coefficients all have uncertainty estimates of around ± 0.001 . These results are consistent with observations from PDE models and suggest that the model area can only support a certain number of populated cells, and that furthermore there is a coexistence ratio limitation on the numbers of rabbits that can sustain a fox population and the number of foxes that can sustain a bear population.

Figure 8 shows the averaged number of like-like bonds or number of potential encounters between like-like species. The upper curve includes vacancies, the lower just rabbits, foxes and bears. The error bars or uncertainties associated with this data averaged over ten independent runs are smaller than the plot symbol sizes shown. The transient effects have settled out within

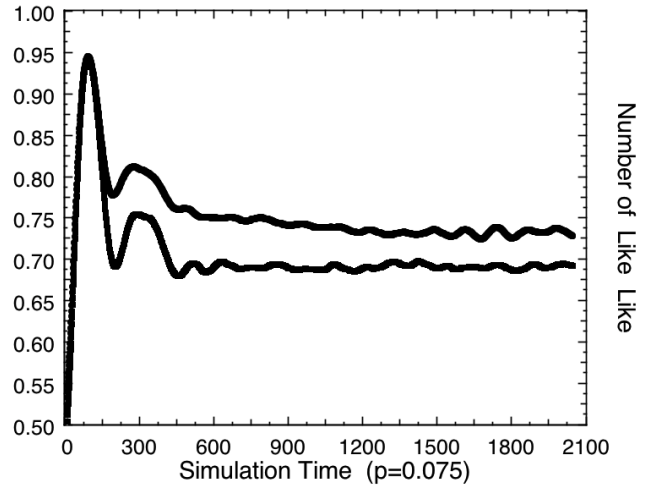


Figure 8: The averaged number of like-like bonds or encounters in a 512×512 model system with $p = 0.075$. The curve above includes vacancies, the curve below only rabbits, foxes and bears. Error bars are smaller than plot symbol sizes.

1000 simulation time steps and this suggests that the mean number of animal encounters is relatively stable on average. This is consistent with the configuration screen-shots - the clumps are not large percolated features but are small to medium sized population fluctuations that wave and wane and contribute to the overall model behaviour but do not individually dominate it. This is in contrast to other phase transitional models such as the Ising model [26] where the critical behaviour is attributed to the dominance of fluctuations on many different length scales.

4 Discussion and Conclusions

We have described a Cellular Automaton model that captures much of the essential periodic population behaviour of the Lotka-Volterra differential equations but yet is computationally cheaper to explore than a numerical solution of a spatial system of Lotka-Volterra equations would be. The Cellular Automaton model is considerably simpler than a detailed animal agent model and for the work reported here.

The vacancies are critical to the model working. Although they do not appear interesting *per se* they facilitate movement of the real cell species. We have used the slightly confusing notation that is common in the research literature and which refers to “3-species” and “4-species” models, treating the vacancies as a species.

We have shown phase transitional behaviour is just a

single adjustable parameter - the death probability of predator cells. The phase transition is quite sharp for the 4-species (2-predator) model. The error bars presented arise because a given model run with p in that short region will end up with “bears” extinct or surviving and the error bars represent an average. We anticipate that experiments with larger model system sizes would yield an even sharper transition region in p .

We have presented data on behaviour of the single predator and two predator variations of the model. We have investigated the attractors and fixed point steady state average behaviours of the model’s phase space. We believe the Cellular Automaton model is worthy of further exploration with different values of the rate equations for cell selection and reproduction. Models such as this have a useful role to play in exploring complexity in bulk systems, and could be further developed to incorporate more microscopic behavioural details. This sort of model has an important role to play in forming a computational bridge between PDE-based models and detailed experimental approaches.

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