

## SPATIAL EMERGENCE OF GENOTYPICAL TRIBES IN AN ANIMAT SIMULATION MODEL

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### ABSTRACT

We observe the spontaneous emergence of spatial tribes in an animat agent model where simple genetic inheritance is supported. Our predator-prey model simulates a flat-world of animat agents which breed, move, eat and predate according to priorities encoded in their genotype. Initialising a random mixture of all possible priority list genotypes, we find not only that only a small fraction of possible genotypes are favoured for survival, but that distinct spatial patterns of different tribes emerge. We report on the emergent macroscopic features in our model and discuss their correspondent mapping to microscopic animat rules and genotypes. Even a simple gene-reordering mechanism gives rise to complex emergent behaviour.

### 1 INTRODUCTION

Model simulations play an important role in understanding emergent behaviours (Ronald, Sipper, and Capcarrère 1999) in complex systems of collective individuals (Levy 1992). There is continued interest in the interplay between individually advantageous strategies and those that benefit the collective, both from applications in business and organisation theory and in society at large (Santa Fe Institute 2007). Although spatial game theory (Nowak, Bonhoeffer, and May 1994) provides a powerful set of tools to analyse and reason about cooperative behaviour, numerical experiments of simulation models that can be precisely controlled and repeated at a microscopic level, provide a valuable link between theory and experiments on real physical or societal systems.

We have developed an agent-based collective model in which various individual behaviours can be prescribed microscopically and the emergent macroscopic behaviours and patterns observed in simulation experiments (Hawick, James, and Scogings 2005).

A number of excellent model systems such as Tierra (Ray 1991), Avida (Adami 1998, California Institute of Technology 2007) and Echo (Holland 2007) have provided experimental systems for studying evolutionary behaviour in cellular model systems. We have however found it difficult to make any headway in relating the sheer combinatorial complexity of microscopic properties of such models to the bulk emergent behaviours observed. Our model is consequently deliberately designed to have a much smaller number of microscopic behaviours. Our animal agents (animats, Wilson 1991) eat, breed, seek or avoid other sorts of animats, or move randomly about their world.

In previous work we have reported the spatial emergence of macroscopic patterns (Hawick, Scogings, and James 2004) such as spirals, symmetrical clumps and wavefronts of animats. That work was limited to just two specific species of animats interacting – predators (“foxes”) and prey (“rabbits”). We had engineered specific behaviours for those two animat types at a microscopic level. We have also carried out a very simple search of the animat fitness space that results by considering all possible combinations of the rules for our animats (Scogings, Hawick, and James 2006). That work indicated that simply starting the simulated system with an even mixture of all possible animats rapidly favoured a very limited set of the possible animats.

In this paper we explore the predator or “Fox” rules in more detail and in particular the spatial structure that emerges from an interplay of mixed animat species in the starting configuration. It turns out that a very small number of “fox subspecies” dominates the model and comes to dominate a very large part of the model world as territory. In section 2 we explain the detailed workings of our model. We outline the simulation architecture in 3. In section 4 we describe a series of experiments we have carried out to explore the fox rule space and present some results in section 5. We discuss these and draw some conclusions about the Fox rule

phase space in section 6. Our main finding in this paper is that our scheme of re-ordering a fixed set of genes, while very simple, does lead to noteworthy emergent behaviour.

## 2 RULE-BASED MODEL

Our model is based on animat “machines” which have a fixed strategy in the form of a set of rule priorities that they follow.

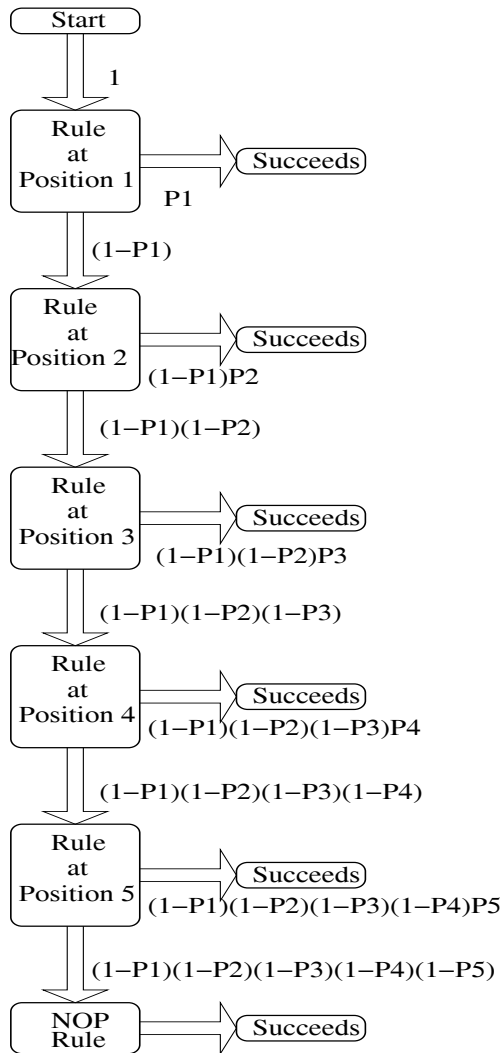


Figure 1: The stochastic animat machine model. The animat tries to execute its list of possible genetic instructions until one succeeds or it hits the terminating NOP instruction.

Figure 1 illustrates how individual animats in our model process their genetic instructions in accordance with information from their environment. Each animat has a fixed length “genotype” and attempts to process each instruction in turn from head to tail, until one succeeds. The no-operation (“NOP”) instruction at the tail always succeeds. The indi-

vidual probabilities  $P_i$  of success for each attempted instruction depend on the animat’s circumstances and environment. They can be measured empirically from a particular simulation run. The stochastic machine model works to explore an animat’s entire gene sequence of length  $n$  providing there is a finite probability  $P_{\text{final}} = (1 - P_1)(1 - P_2)\dots(1 - P_n)$ .

The model is initialised with a random pattern of animats of different types and is evolved with each animat applying its stochastic machine model to move forward one discrete time step. The order of update of animats in a time step is randomized to avoid spatial bias or sweeping effects.

Figure 2: A typical animat “rabbit” gene – denoting a particular rule priority list for use in the model. In the work reported in this paper all rabbits have this same gene.

The microscopic rules driving animat behaviour in the model are:

Predator (“Fox”) rules:

1. Eat prey if hungry and prey is adjacent
2. Move towards prey if hungry
3. Breed if not hungry and adjacent to another predator
4. Move towards another predator if not hungry
5. Move randomly 50% of the time
6. Do nothing (NOP)

Prey (“Rabbit”) rules:

1. Move away from an adjacent predator
2. Move away from adjacent prey if hungry (to relieve overcrowding)
3. Breed if not too hungry and adjacent to another prey
4. Move towards another breeding partner if not too hungry
5. Move randomly 50% of the time
6. Do nothing (NOP)

In the work reported in this paper, all our prey (“rabbit”) animats have the one standard gene that we derived from various previous experiments. This is shown in Figure 2, which denotes the gene head, tail and terminating-NOP.

These behavioural rules interact with an individual animat’s environment and circumstances. Predators must eat prey to survive. The model rules place an emphasis on hunger (for both prey and predators). For example: a predator only eats if hungry (without this, the model would become dangerously unstable as prey numbers could become rapidly depleted under certain conditions); animats only breed if not hungry. Each animat has a simple integer counter to specify its hunger. Other properties such as location of nearest mate, prey, and the overcrowding factor

are computed from the environment at each discrete time step.

The prey do not have to actively seek food (like the predators do) but are assumed to have food permanently within reach (grass). However, if prey become overcrowded then they will be unable to feed, will become progressively more hungry, and will starve to death unless the overcrowding can be relieved. Thus prey have an explicit rule to attempt to move away from crowded areas if they are hungry. Rabbits do not have an explicit “eat” command; they are assumed to always be eating unless they are overcrowded when they will start to become hungry. This is modeled by the rabbit avoid-overcrowding rule 2.

We look at the emergence of rule priorities, not at the emergence of rules. By retaining the same individual rules, but changing the priority of the rules within the set for particular animats, allows us to focus on a more manageable combinatoric space and attempt to relate microscopic genes to emergent macroscopic properties. The priority of the rules is very important. An animat will always execute the first rule in the list for which the conditions are true. If the conditions for a rule are not satisfied, then the next rule in the sequence will be checked. For example, assume a predator that is not hungry and is not adjacent to any other animats. It will execute predator rule 4 in the above list and move towards the nearest potential breeding partner.

There are in principle  $5! = 120$  rule list permutations for a fixed gene length of five, since the final terminating NOP is not really free. We do not investigate animats that always “do nothing”, thus reducing our space of interesting animats from  $6! = 720$  to a more manageable scale.

### 3 SIMULATION ARCHITECTURE

Our animat simulation code is written in C++ and uses two principle data structures:

- a list of currently live animats
- a 2D spatial grid of cells

Using these two data structures together allows for the efficient formulation of code that can iterate over all animats **or** over space. Unlike the common approach to such models which employ a fixed grid with periodic boundary conditions, we employ an open boundary spatial system, so that a small initialised configuration can grow unbounded (until we run out of memory). This allows us to avoid reflections and other distortions that are solely artifacts of the boundary conditions. In practice, our model is CPU-bound due to the processing time required for animat updates rather than memory bound.

The simulation architecture is outlined in Algorithm 1. Our second series of experiments used a single fox gene and uniform random rabbit genes. The simulation code

uses various parity summation checks to ensure animats are correctly counted, and various other assertions and pre- and post-conditions to ensure integrity. In total the simulation code requires around 1,500 lines of highly optimised C++ code, and the post analysis suite an additional 2,000 lines of code.

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#### Algorithm 1 Simulation pseudocode for experiment 1.

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**Require:** Choose random number seed  
 Initialise Animat Configuration  
 Set up spatial fox pattern: **uniform random genes**  
 Set up spatial rabbit pattern: **single standard gene**  
**for** each time step **do**  
   **if** total animat extinction **then**  
     break  
**end if**  
 List current live animats  
**for** each animat in a random order **do**  
   update animat according to its rules  
**end for**  
 Add new births to live list  
 Garbage collect dead animats  
 Record time step statistics  
**end for**

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In addition to the main simulation, there are also various ancillary programs that support post-analysis options, as outlined in Algorithm 2. The simulation architecture allows these to be run interactively on individual experiments or as batch jobs averaging the results over several different seeded random runs.

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#### Algorithm 2 Simulation post-analysis

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Make visualisable still image of entire model world  
 Make movie frames of a sequence of stills  
 Plot time evolution of animat or rule utilisation metrics  
 Histogram animat populations  
 Identify spatial animat clusters (spirals, waves, clumps)

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### 4 EXPERIMENTAL METHOD

Generally our experimental approach is to identify emergent features of the model that are statistically preserved across different randomly seeded simulation runs. We then aim to relate these to the controlling microscopic input rules.

We have carried out a number of model runs with different random starting conditions to investigate the relative utilisation probabilities for each fox rule. The initialisation procedure is described in section 4.1. In addition we tried two simple mechanisms for breeding (section 4.2). A number of metrics can be garnered from the runs and are used to identify emergent properties of the model system as a whole (section 4.3).

#### 4.1 Model Initialisation

We initialise the model state with 120 rule priority sets (or genes) for predators and 120 rule priority sets for prey. These different rule sets are applied randomly throughout the starting population. Thus approximately 0.8 percent (each) of the initial starting population of 820 predators and 2240 prey have the same rule set. The starting populations are spread over a uniformly distributed random spatial area of the model world.

The model is remarkably insensitive to the exact starting pattern of animats, with statistically similar long term behaviour always observed. We note that previous versions of the model started with much smaller numbers of animats scattered randomly across the world. Due to these random and unstable starting positions the population was much more precarious and prone to wild fluctuations and often died out before stabilizing which normally occurred around step 400 (Hawick, James, and Scogings 2005). The current version of our model can use a starting arrangement derived from the state of a typical previous run at step 400 and thus provides a far more stable point of origin for the population.

The model spatial grid is centred around an origin but can grow arbitrarily on all four sides. The initial starting pattern is located around the centre and generally the model grows remarkably steadily in all directions with no particular observable bias.

#### 4.2 Breeding Mechanisms

An important aspect of our model is the animat breeding mechanism. In our current work, by using very high level instruction rules to reduce the size of the combinatoric space, we are able to apply a brute force approach and sample all possible rule list combinations. Thus we are not using a genetic algorithm to explore an enormous fitness landscape, but instead are trying to relate microscopic properties to emergent macroscopic patterns and behaviours.

In section 5 below we present results from two different simple breeding mechanisms. The breed rule involves an animat checking to see if it is in proximity to a potential breeding partner (of the same species) and if so, it successfully creates a new animat of some gene type. In the case of all members of a species having the same exact genetic code there is no point in elaborating a sexual mechanism in the simulation and in effect breeding pseudo asexually. Our rules require two partners in proximity to allow a new animat to be created, but the offspring is identical to both parents anyway.

An alternative mechanism is to support simple exact cloning of either of the two partners with a 50% probability of either gene being copied. We have also implemented this simple **either-or** cloning reproduction mechanism and

are presently working on alternative genetic combination operations.

In the former case, the constraint that an animal is always an exact clone of its initiating parent (“mother”) has the advantage of ensuring that the number of rule priority sets will always decrease, as certain sets become dominant and others disappear. This enables us to study the reasons why certain rule sets become dominant over time without adding the confusion of new sets appearing at unpredictable moments in time. The second case 50/50 “either-or” cloning rule allows one species to proliferate much more rapidly.

#### 4.3 Metrics

Our simulation code supports a number of bulk measurement metrics and we are able to post-analyse a run to examine properties of successful animats and spatial patterns.

The simulation model is run and managed as a set of time slices. We are generally able to run models of up to around 10,000 discrete time steps with around 100,000-250,000 animats of both predator and prey species. The initial configuration of animats might occupy only around a region of  $100 \times 100$  grid cells but this can expand to a spatial territory of over  $1000 \times 1000$  cells in this time.

Animat properties such as: average age at death; average hunger; average health score; and typical cause of death can all be histogrammed. In the case of work reported in this paper it is also possible to histogram the relative proportions of different genotypical subspecies of predator.

We are presently working on a spatial grid density metric that will allow comparisons between our discrete model and a field theoretical model based on partial differential equations.

Figure 7 shows an example of how the rule utilisation probabilities can be tracked in time empirically from a model run.

### 5 RESULTANT EMERGENT BEHAVIOURS

Our first experiment series reported here concerns the asexual breeding mechanism using a simple direct clone of initiating parent.

As the model progresses, new animats are born and are exact clones of their initiating parent (“mother”). Thus certain “tribes” of animats emerge where all members of the tribe have the same set of rule priorities. We can then analyse which rule sets become dominant and which become extinct. It is important to note that the difference between tribes consists of the different order in which the rules are presented (the rule priority). Every animat of a single species uses the same five individual rules – it is only the order that is changed, so that a particular tribe effectively has a different stochastic machine due to the different order of trial of rules.

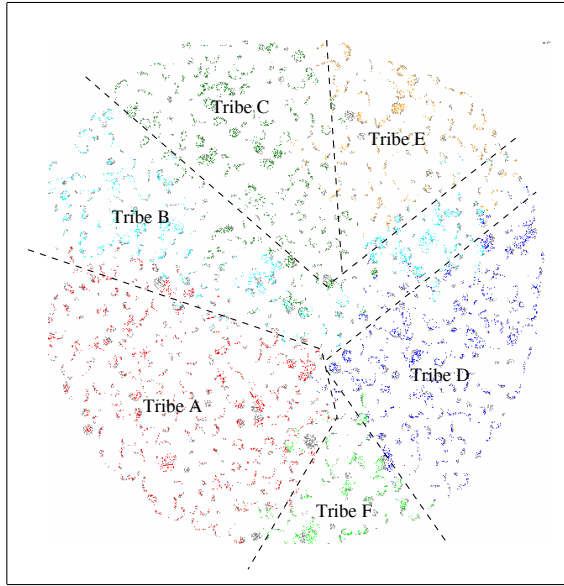


Figure 3: Balanced animat tribes at step 7000 in a typical model run with asexual behaviour.

Figure 3 shows a circularly symmetric world that has evolved from a standard initial mix of 120 different sorts of asexual foxes. The snapshot is shown after 300 model time steps. The model has grown uniformly in space and a relatively small number of tribes coexist, with definite exclusion zones between them. This spontaneous “apartheid” appears to be an emergent consequence of the microscopic rules. The emergent tribes have roughly similar proliferation success rates and the model generally converges to support around five to eight.

Figure 4 shows how the standard mix of 120 different fox types evolves if reproduction is “sexual” using the 50/50 cloning rule from both parents. Note the marked success of one particular tribe of foxes - denoted as tribe “A” (red). This snapshot is after 300 model steps. Figure 5 shows the continued success of this tribe in achieving widespread proliferation but also a steady state (on average) with the rabbit population.

Note the characteristic size and shape of the spatial structures that emerge in Figures 3, 4 and 5. These shapes and their typical size ratios are consistent with our findings from monogenetic populations. Individual clumps and spirals rise and fall under the typical boom-bust behaviour of a predator-prey model. However, these fluctuations become damped out overall as the world population grow, and expand to fill more spatial territory. This is an interesting feature of our open boundary condition model and allows exploration of parameter regimes that would not remain stable in a closed world with the more typical periodic boundaries.

Figure 6 lists the rule list priorities (or “genes”) of the four most successful fox tribes that emerged from the experiment shown in Figures 4 and 5. Repeating the exper-

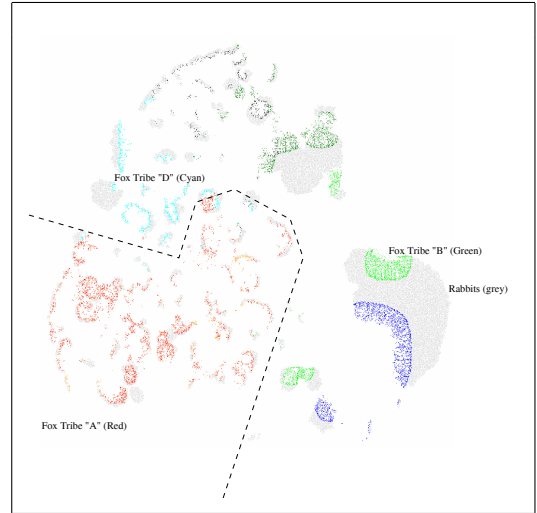


Figure 4: Animat tribes in step 3000 with sexual behaviour. Note the success of Tribe “A” (red) in terms of territory dominated. Rabbits are denoted by grey and the other tribes present are “B” (Green), “C” (Blue) and “D” (Cyan).

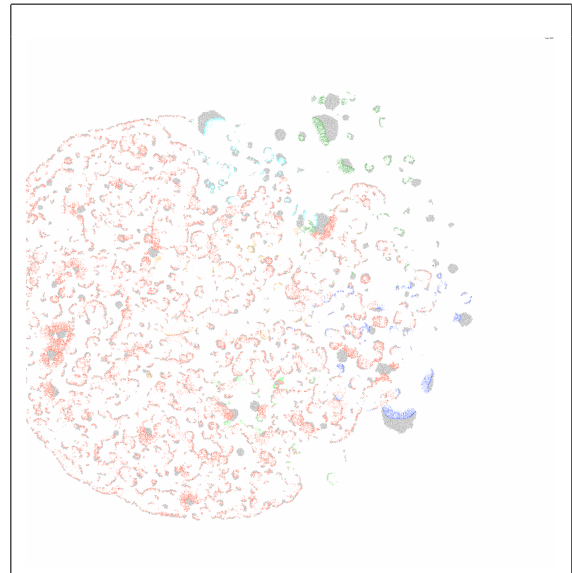


Figure 5: The continued runaway success of tribe A (red) foxes, which are breeding with a 50/50% chance of offspring being an exact clone of either parent.

iment with different random number seeds yields broadly similar results in that a large number of the 120 possible tribes rapidly die out, leaving a relatively small number between three and twelve. Depending upon the breeding behaviour – sexual (or asexual), this number of tribes becomes eventually dominated by one (or not), although there is no direct competition or interaction amongst tribes. A small number of rule priority lists (genes) are favoured by the fitness landscape and eventually demonstrate a much greater success at proliferation than their siblings.

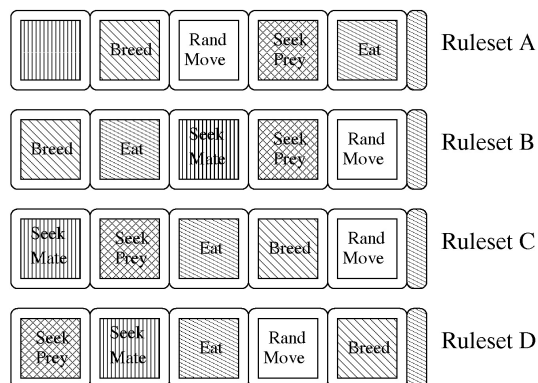


Figure 6: Four predator (“fox”) rule sets: “A” (red); “B” (green); “C” (blue) and “D” (cyan) as discussed in the text.

Figure 7 shows how the rule utilisation percentages do change with model evolution. An early noisy phase shows the influence of the boom-bust predator-prey interaction, followed by a long term stability for the red tribe A as it settles down to dominate the world.

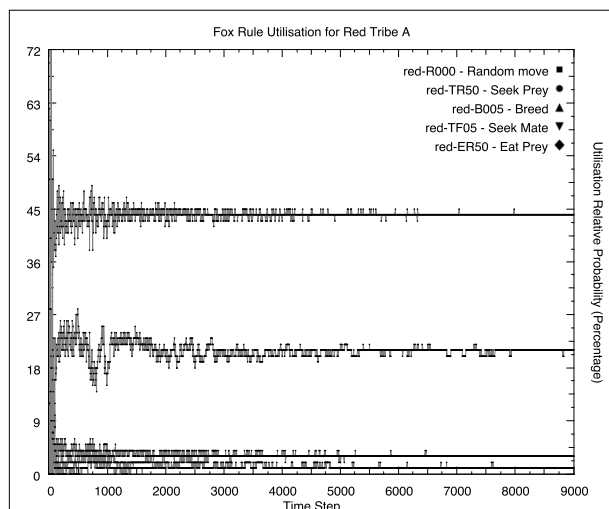


Figure 7: Relative utilisation probabilities of the rules use by the red tribe A of foxes. Initial fluctuations due to the usual boom-bust of a predator-prey model are damped out as the red tribe achieves a large and stable proliferation in balance with available prey.

Table 1 shows the relative rule utilisations as measured experimentally from the model run discussed above where tribe are ranked – A is the most successful and tribe D the least prolific. Note that in general, success is correlated with activity as measured by avoidance of the terminating “NOP” do-nothing instruction. Tribe A shows a significant reversal of the seek-prey and random-move that the remaining runners-up display.

In general the pattern of tribe A has evolved to allow a sustainable population of prey to survive. Eating is much less

Table 1: Relative rule utilisation probabilities as percentages for each fox tribe (ranked in order of success as determined by proliferation).

Rule	A (Red)	B (Green)	C (Blue)	D (Cyan)
Breed	3	3	3	2
Eat Prey	1	2	3	4
Seek Mate	3	3	3	4
Seek Prey	<b>21</b>	40	36	31
Rand Move	<b>44</b>	23	25	28
NOP	28	29	30	31

important than seeking potential prey. Seeking a (sexual) mate and breeding are only marginally more important than eating. Moving randomly is better than doing nothing as it at least explores the local landscape.

The pattern of the expanding world of occupied territory tends towards a circularly symmetric pattern, located by the centre of mass of the most successful breeding tribe. In the case of asexual breeding, all tribes still present after the initial extinctions are more or less equally successful so the Figure 3 is very symmetric. As tribe A comes to dominate, the initially distorted growth pattern of Figure 4 stabilises to a more symmetric pattern but now centred on the dominating tribe A.

## 6 DISCUSSION AND CONCLUSIONS

We have described our simulation model, its architecture and the core idea of stochastic machine based animat agents.

We have found a remarkable set of statistically stable and reliable emergent phenomena that are independent of the particular random starting conditions. These include the emergence of spatial clusters such as spirals, clumps and wavefronts; the spatial separation of different subspecies of predator; and the spatial symmetry of the growing world model under open boundary conditions.

It appears that the local behaviour of model is relatively insensitive to particular rule priorities, but that bulk behaviour can be changed considerably by reordering the rules within a single species gene. It is particularly interesting that under the subtly different breeding mechanisms studied (clone of initiating parent or 50/50 clone of both parents) very different tribal growth occurs. The 50/50 clone mechanism allows a single species to proliferate and gain significantly more territory than other tribes.

The relative utilisation probabilities as empirically measured give a particular signature that characterises the way a particular tribe is responding to its environment. It is particularly noteworthy that those rules that directly support proliferation (breeding; seeking a partner and moving to explore territory) tend to appear at the beginning of a successful predator’s gene, whereas eating prey and seeking

prey tend to be towards the end. This indicates successful emergence of a successful species rather than selfishly successful individuals (which would favour eating and personal survival).

There are several other aspects of the model that we plan to study, including alternative genetic mixing mechanisms; the lengthening of the genotype; and the role of genetic instructions within the prey species.

We believe our simulation architecture may also be of some interest to researchers investigating other spatial aspects of game theory.

## ACKNOWLEDGMENTS

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