Emergent Spatial Agent Segregation

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Abstract

Animat agents are usually formulated as spatially located agents that interact according to some microscopic behavioural rules. We use our predator-prey animat model to explore spatial segregation and other self-organising effects. We compare the emergent macroscopic behaviour with that of non-intelligence models such as those governed solely by microscopic statistical mechanics rules. We report on an emergent separation of sub-species amongst our prey animats when a very simple genetic marker is used and a microscopic breeding preference is introduced. We discuss some quantitative metrics such as the spatial density of animats and the density-density correlation function and how these can be used to categorize the different self-organisational regimes that emerge from the model.

Keywords: *animat; spatial agent; segregation; phase separation; self-organisation.*

1. Introduction

Self-organisation amongst agents is a fascinating topic with some interesting philosophical implications. It has been difficult to classify microscopic behaviours quantitatively in a way that is useful to interpret emergent macroscopic effects. Artificial life agents present an interesting special case, and our approach to studying self-organisation is to focus on the spatial patterns that arise from self-organising artificial life agents known as "animats" [20].

Artificial life simulations [1, 9, 13] have existed for some time and have been used extensively to demonstrate evolution and emergence. However many of these models have no spatial context and the "animats" that exist in them have no concept of neighbourhood or distance.

Our predator prey model has been refined over several years [17] during which we developed various techniques to optimise the use of time and space in this type of simulation [16]. This has enabled us to increase the number of animats in the model, leading to the formation of interesting emergent clusters discussed in [8]. Typical emergent formations can be seen in Figure 1.

In this paper we investigate the emergent effect of sub-species segregation when an elementary genetic marker is introduced. We construct the microscopic rules so that although prey agents are blind to this genetic marker, it affects the probabilities of offspring having a particular trait. We find that a remarkable spatial segregation of sub-species arises after some generations of animats. Since sub-species are relatively localised there is a multi-generational emergence of mating with the same sub-species simply because there are more of them in spatial proximity.

It has proved interesting in this paper to genetically mark prey at a microscopic level, and to explore the spatial segregation and domain growth [4] of sub-species of prey animats. Domain growth is often studied in terms of both cluster-oriented nucleation models [5] and once "droplets" or small clusters have established themselves, in terms of phase separation using field models [7]. These macroscopic effects are often attributable to well known growth classifications such as surface-tension driven effects or phase transitions that can be investigated quantifiably.

In section 2 we describe the basics of our model and the experiment is presented in section 3. In section 4 we explore some quantifiable metrics related to spatial self organisation [2, 11] and compare this behaviour with that found in some statistical mechanical models based solely on mi-
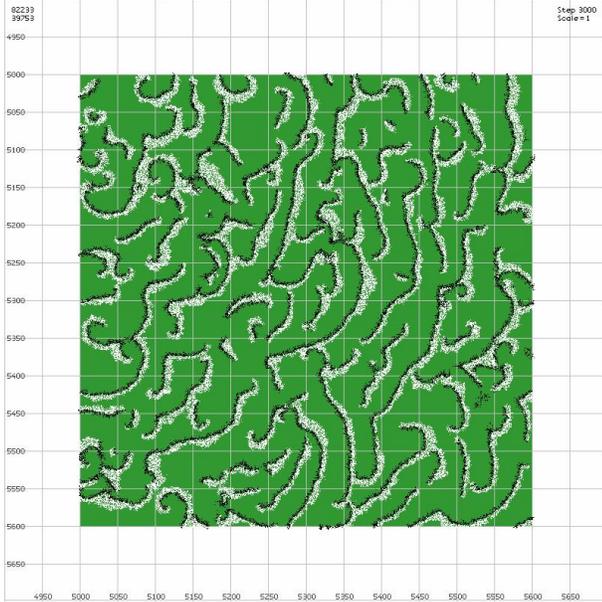
Figure 1. Over 120,000 animats on a square grassed area. Predators are black and prey are white. Various macro-clusters, including spirals, have emerged. Note how the animats stay almost exclusively on the grassed area.

croscopic physics rather than intelligent animat agents. We then present our results in section 5 and offer some conclusions in section 6.

2. The Model

The model contains two types of "animats" – predators that need to eat prey to survive and prey that need to eat "grass". Grass is placed only in certain areas of the map, thus effectively containing the animat populations. Previous work [14] has shown that animat behaviour is not affected by the edges of the grassed region.

At every time step, each animat executes a rule. Some rules (for example "hunting") are not always executed successfully. The effects of reducing the success rate of predators when hunting have been discussed in [15] and are also used in the experiments described below. Rules for predators are:
if well fed – breed with an adjacent predator
if hungry – hunt an adjacent prey animat
if well fed – move towards another predator
if hungry – move towards prey
move randomly

and the rules for prey are:

if well fed – breed with an adjacent prey animat
if hungry – eat grass (if available)
if well fed – move towards another prey animat
move away from an adjacent predator
move randomly

Each animat always executes the first rule in its list for which the conditions are satisfied. We have experimented with changing the order of priority of the rules [6] and thus produced different sub-groups of animats where each subgroup has the same set of rules but with a different priority order.

The interaction of the animats as they follow their rules has produced fascinating emergent features in the form of macro-clusters often containing many hundreds of animats. We have analysed and documented these emergent clusters in [8]. The most interesting cluster is a spiral and several spirals are visible in the figures in this article.

3. Genetic Markers

As an experiment we introduced "genetic markers" into the model. Prey animats were marked such that markers were evenly, and randomly, spread across the map. We were then able to use the markers to track different sub-species groups of prey animats. Predators were not marked and so remain unchanged as they are unable to detect the markers in the prey population. When two or more types of prey animats inter-breed, we require a probabilistic specification of the outcome. Following the complexities of a real biology we consider a probabilistic set of outcomes based on the properties of the parents.

For example, we might postulate that when two animats of the *same* type inter-breed, the offspring is also of that type. When two of a *different* type breed we might model the outcome offspring as being of the same type of *either* parent with exactly 50% probability. This seems sufficient for our model although a more sophisticated pseudo-genetics might consider recessive and suppressed genetic information - perhaps in the form of carrier genetic type information from the "grandparents" or even from further ancestors [18].

The offspring outcome rules are therefore:

$$A \oplus A \rightarrow \{A : p = 1\}$$
$$B \oplus B \rightarrow \{B : p = 1\}$$
$$A \oplus B \rightarrow \{A|B : p = 0.5\}$$
$$B \oplus A \rightarrow \{B|A : p = 0.5\} \tag{1}$$

We suppose for the present that our animats are unable to recognise markers and breeding pairing therefore occurs randomly subject to the vagaries of spatial distributions.

However there are interesting hidden consequences of the conditional probabilities in equation 1. Spatial regions that by spontaneous random chance have even a small predominance of pure-bred animats will grow that tendency. The emergent spatial behaviour is for spatial regions of a single group to emerge and to grow. Since these will by chance be intermingled with neighbouring regions where the other group dominates, the nature of the generational model is that inter-breeding will eventually only occur at the spatial boundaries. Individual animats are unprejudiced or unbiased, but the spatial fluctuations come to dominate since individual animats typically do not travel (diffuse) very far during their lifetimes.

Equation 1 can be generalised by making the scalar p into a tensor $P_{i,j,k}$ giving the probabilities of a given offspring type k from parents of types i, j. This approach allows us to investigate an arbitrary number n of groups. For the work reported in this present paper we restrict our attention to the simple case where $k \in i, j$. This is an interesting case of a phase separation effect due to the consequences of generational effects.

The group segregation effect can be explored by a simple extension to equation 1 to N_g different group types, with the simple extended rule that says same-group parents give rise to same-group offspring and a pair of any two differently typed parents give rise to an offspring of either type with equal probability. This effect is shown in Figure 2 for five groups of prey.

Regions separate into pure-breeds. In the limit of a large spatial area no one group will necessarily dominate in the long term, but with finite size and time effects it is possible for a group to die out. There is every reason to expect similar behaviour – subject to the usual graph/cell colouring limitations of 2-D geometry for an arbitrary number of groups.

However it appears that for finite sized world areas, fluctuations do occur. The data in Figure 3 shows that under the right circumstances one group ends up dominating by chance. Once a group has gained dominance it may require an unusual circumstance (fluctuation) for it to be displaced.

This metric is not easily averaged over different independent runs of the model. We expect all $n = 2, 3, 4, 5, ...$ sub-species groups to be equally advantaged in the situation $p \equiv 0.5$ and it is a matter of chance which group, if any, accidentally comes to dominate.

We have investigated this self-organizing segregation effect over a range of predator-prey regimes. We have already found that varying the predatory kill-success probability [15] changes the spatial structure of clumps of both predator and prey. We therefore use that parameter to set up
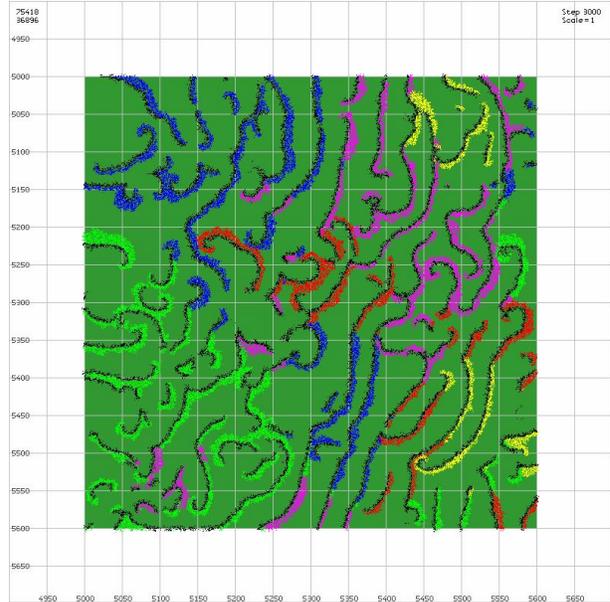

Figure 2. Animats on a square grassed area. Predators are black and the five prey subspecies groups have segregated into distinct regions. Overall animat behaviour remains unaffected.
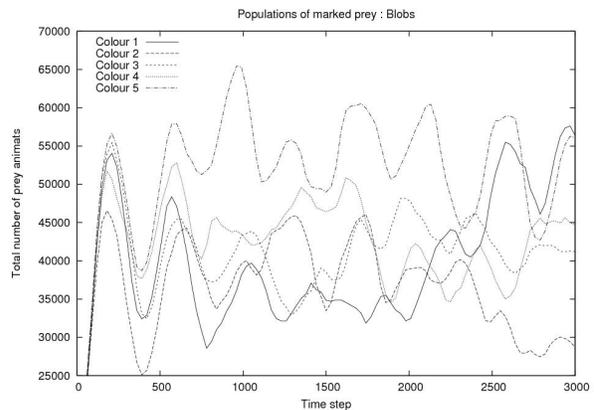

Figure 3. Populations of prey sub-species groups over time. A group can become dominant through slight fluctuations in the model.

situations where the prey group segregation effect can have a greater or less pronounced effect on the spatial structures formed.

In the case of low to medium predatory success, prey and predators intermingle in a sparse open sponge-like struc-
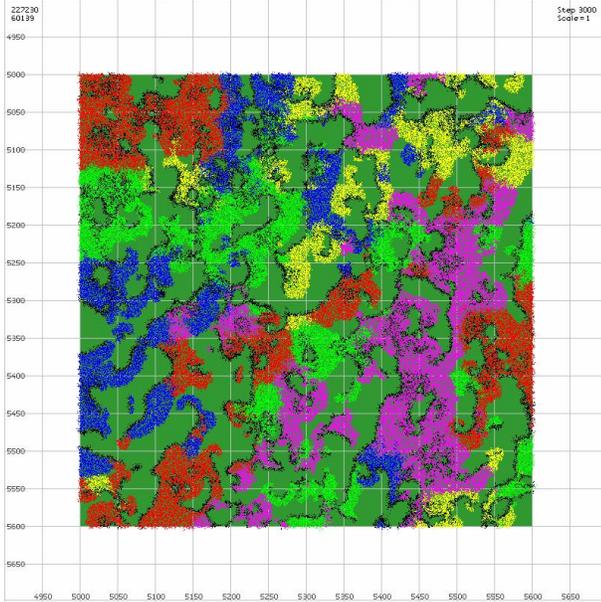
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Figure 4. Animats on a square grassed area. Predators are black and the five prey subspecies groups have again formed into clusters based on genetic markers. The prey are able to form larger, more diffuse clusters as the predators are not as successful at hunting as they were in Figure 2.

Figure 5. $Q = 3$ **state Potts Model on a** 128×128 **cell mesh after 592 time-steps following a random initialisation with** $\frac{1}{3} : \frac{1}{3} : \frac{1}{3}$ **of red, white and blue. A Kawasaki neighbour exchange dynamics (which conserves species number) has been applied around the critical temperature, resulting in first nucleation into separate domains, followed by coarsening into larger segregated regions.**

ture as shown in Figure 4. In this case, when multi-prey sub-species groups are used the different-coloured or genetically-marked groups separate into clumps as well. The spatial self-organisation is into large diffuse clumps with less distinct boundaries. The previous figures demonstrate the other extreme (when predators have a high kill-success rate) and the emergent structure is that of waves with a much more striated pattern.

4. Statistical Separation

It is interesting to compare our semi-intelligent animat model with a simpler physical system that is driven with straightforward statistical mechanical phenomena such as surface tension. The Q-State Potts model [12] can be formulated as an integer field variable on a 2D-grid, with a Hamiltonian or energy function that is specified by the interactions between each variable and its immediate neighbours on the grid.

The time-stepping dynamics is usually introduced in the form of a Monte-Carlo statistical mechanical scheme [3]
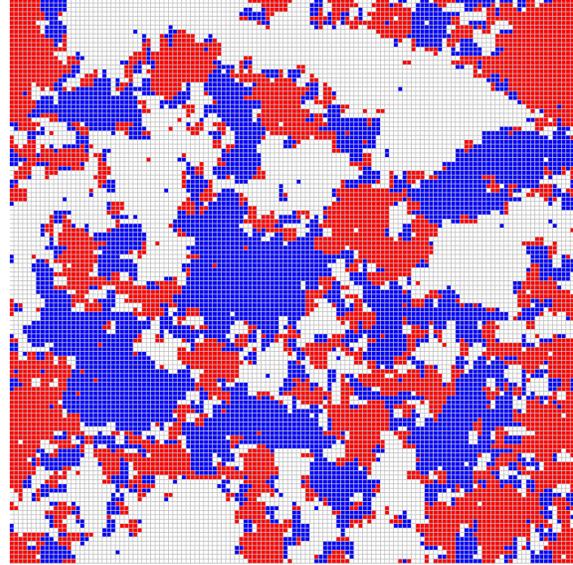
whereby a site is selected at random; a possible new state is chosen for it at random; the energy consequences are computed; and the change is accepted if a decrease in energy results, but can also be accepted with a Boltzmann-like probability that depends upon the temperature of the system. The global temperature parameter thus controls the overall regime the system is in and a "quenching experiment" can be set up whereby a random initial system with all the variables in any of the random Q-states can be chilled. This results in phase separation and domains are formed as shown in Figures 5 and 6.

Figure 5 shows a 128×128 cell Potts model configuration with approximately equal number of three (red, white and blue) microscopic states (or species) after a quench to just below the critical temperature T from a random completely mixed start. The snapshot is taken after 592 steps so that each microscopic component has had an opportunity to swap positions with a random neighbour 592 times, neighbour swaps being accepted if the overall energy of the system decreases, but still acceptable even if energy E increases according to to a random Boltzmann probability factor of $\exp -\Delta E/T$. This "Kawasaki" dynamics con-

serves the total number of each species, but allows them to "jump over one another" as they move around. Their energy is simple determined by the number of like-like nearest neighbour bonds. So an individual will tend to congregate with others of its own colour solely through the energy minimisation process of the dynamics.

Figure 6 shows a deeper quench experiment using species transmutation dynamics. Under these conditions, the system is again initialised with a random mixture of the three species but each cell can change to one of the other species if this will cause the system's overall energy to decrease, or if the random Boltzmann-based thermal probability allows it. As in the Kawasaki dynamics case, energy is solely determined by like-like nearest neighbour bonds on the square world mesh. In this case one species (red) is "winning" and the dynamics are driven by surface tension. At the low quench temperature, the only activity is along the phase boundaries and gradually small areas of a minority species will be taken over by the majority.
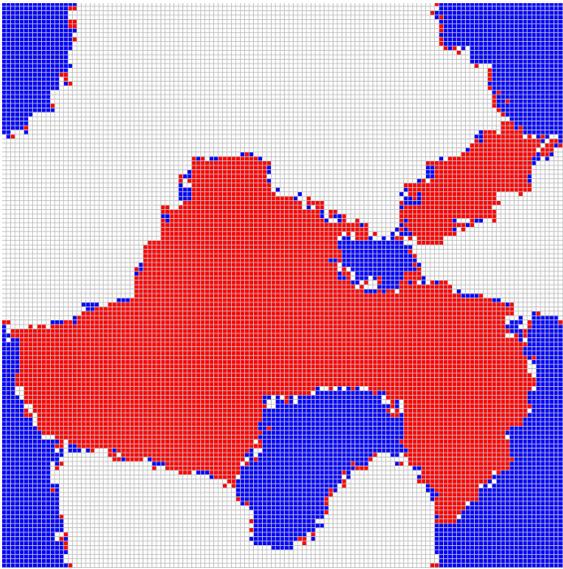

Figure 6. $Q = 3$ **state Potts Model with state transmutation dynamics, shown 935 steps after a deep quench. Surface tension is driving the domain dynamics and "red" is winning.**

Our animat model shows both similarities with, and differences from, these two statistical mechanical segregatory behaviours. Our model gives rise to phase separation in a rather different matter and without any global parameters such as temperature [14].

We hypothesize that the additional complexity introduced by the microscopic animat intelligent decision-making

causes this richer macroscopic behaviour.

5. Density and Correlations

The animats' world is effectively a bounded rectangle of known fixed area A which we subdivide into geometrically decomposed squares $A_{x,y}$ and over which we obtain mean and standard deviations for the individual species or subspecies groups and total animat densities $\rho_\mu, \rho_{\text{total}}$ with:

$$\langle \rho_\mu(t) \rangle_{\text{space}} = \frac{1}{N_{\text{cells}}} \sum_{x,y} N_\mu(x,y,t) A_{x,y} \quad (2)$$

$$\sigma_\mu^2(t) = \frac{1}{N_{\text{cells}}} \sum_{x,y} \left(\rho_\mu(x,y,t) - N_\mu(x,y,t) A_{x,y} \right)^2 \quad (3)$$

where the subscript μ is used to denote the species or subspecies being considered. Thus we can look at the density pattern for predators or prey or for a particular prey subspecies. The density of animats clearly fluctuates across the space of the model and also of course with time. Averaging over time, once the initial configuration has stabilised, will smear our the density, removing the periodic boom-bust cycles and give us an indication of how many animats (of each species) the model land is capable of supporting. The fluctuations themselves are captured by $\langle \sigma_\mu^2 \rangle_t$ and give us an indication of the depth of the boom-bust cycles.

Generally speaking "successful animats" will achieve an average level of coexistence amongst predators and prey that makes good use of the available world resources (grass) to achieve a high overall animat bearing capacity for the land. This is captured by the overall animat density.

It is also possible to measure the animat density-density correlation function. This indicates how closely together animats tend to live out their existence. The density-density pair correlation function is usually defined in terms of the density as:

$$C(r) = \langle \rho(r_0 \rho(r_0 + r) \rangle \quad (4)$$

where r_0 is a particular position at which the animat density can be measured and r is a vector to some other arbitrary position in the system. Our models are finite in spatial extent and the animat density can be defined as before for any of the sub-species labelled μ or for all animats as required.

For small systems a simple $O(n^2)$ algorithm to compute $C(r)$ is just:

```
radial bins ← 0
for all animats i do
    for all other animat j do
        compute r = r_{i,j}
        increment radial bin r by 1
```

end for
end for
$C(r) \leftarrow$ normalised radial bins

In this algorithm the loops only include animats of the species μ that we are interested in. This sums over space with the assumption that the density $\rho(r)$ takes simple values $0, 1$ and is only 1 where there is an animat, and zero universally elsewhere. In the two dimensional world we report on in this paper $r = (x, y)$ and it is in fact computationally faster to work with bins in the radius-squared and only to compute the square roots outside the two loops at the normalisation stage. There are other techniques for computing correlation functions that use Fast Fourier Transforms [4] but this simple algorithm suffices for the work reported here.

Generally speaking for an arbitrary model system $C(r)$ will fall off with r [11], but the manner in which it does so can give a clue to the classification of the sort of model dynamics and system involved. Plotting $\log C(r)$ vs $\log r$ will yield a straight line region with a negative slope that indicates a power-law relationship so that $C(r) \approx Ar^\alpha$. The exponent α varies depending upon the dimensionality of the system and sometimes also with the universality class of the model.

The density-density pair correlation function $C(r,t)$ can be tracked in time t for individual groups and all groups combined, and is shown in Figure 7 for the prey animats that appear in Figure 4. The system has been initialised at time $t \equiv 0$, the predators and prey spatially organise themselves into viable groupings and the overall system comes to a periodic equilibrium, whereby predators and prey oscillate according to the well known boom-bust behaviours [10, 19].

The model establishes a periodic equilibrium after an initial equilibration epoch of around 1000 steps. Running the model beyond 3000 steps yields a continued stable oscillation in overall population. So we have attained a stable macroscopic behaviour for our multi-agents based upon a set of microscopic rules. It remains however to understand the rich and highly varied spatial patterns that make up the mesoscopic model at spatial resolutions and scales in between.

As the model snapshots in Figures 1, 2 and 4 show, the individual animats will give rise to spatially complex patterns at the mesoscopic scale. These may include spirals; wavefronts at various angles; clumps of varying degrees of symmetry and local density. We have characterised the different model configurations by cataloging individual patterns [8]. This is time consuming and somewhat subjective since it is not always quantifiably precise what shape is what – particularly as they will change in time and transform from a clump into, for example, a spiral. An alternative and more
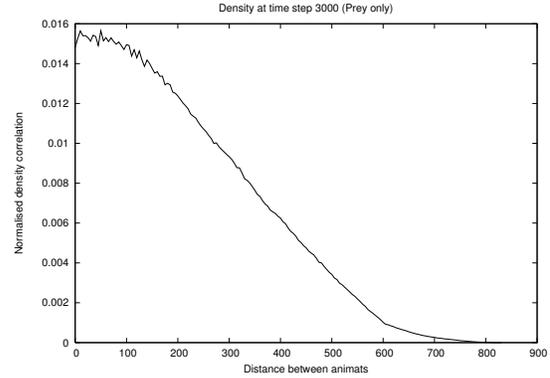

Figure 7. The pair correlation function $C(r)$ computed from the sample shown in Figure 4

easily quantifiable approach involves considering distributions of the animat density and the fluctuations in it and its moments.

Qualitatively this allows us to characterise a particular set of microscopic model parameters as giving rise to a high or low animat population average but also a high or low animat spatial density.
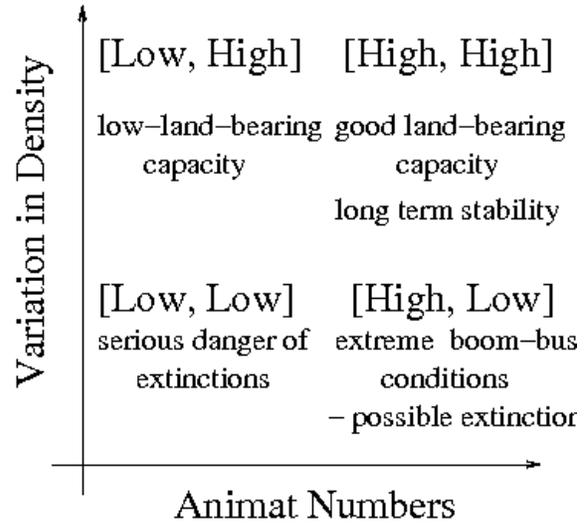

Figure 8. The animat density/number tableau

Figure 8 shows a tableau summarising these situations and some of the different "land capacity-bearing" possibilities for low and high numbers and densities of predators and prey.

6. Summary and Conclusions

We have presented our predator-prey animat model, with a set of "genetically-marked" prey sub-species that can be spatially tracked. We have shown how a model like this can be used to explore some of the emergent self-organising properties of semi-intelligent animat agents in a quantifiable manner. We have compared our model with simpler multi-species domain growth models driven entirely by physical mechanisms such as nucleation, thermal phase transitions and surface tension. An analysis of the density fluctuations and the density-density pair correlation function provides a useful tool to compare the somewhat richer spatial structures and patterns that emerge from our animat model with other models that are based on non-intelligent microscopic components.

In summary we find our animats can organise themselves into fractal structures with ragged domain edges or into near one-dimensional structures that straggle across their two-dimensional world in wave patterns. Which of these formations emerges depends upon a microscopic variation in the ways the predators succeed or fail when hunting. We have focused on a very simple genetic marker amongst our prey animats that directly manifests itself as pair-wise breeding progresses across generations. It would be interesting to expand the possible set of traits so marked and to consider sophisticated properties that are hidden or carried but which skip generations of direct manifestation.

It would also be possible to introduce some form of random mutation or long term hidden gene behaviour to protect against a sub-species dying out by chance. In the examples presented this would allow an animat of sub-species **A** to mate with another animat of sub-species **A** but still have a finite possibility of giving rise to offspring of other sub-species. We are also exploring how other behavioural traits could be linked to simple genetic markers.

We believe that this general approach of allowing animat agents to self-organise in a regular mesh space or at least on a graph or network of known topological properties might be a useful one for studying other agent behaviours.

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