

Stochastic Simulation of Inherited Kinship-Driven Altruism

Heather Turner and Dimitar Kazakov

Department of Computer Science, University of York
Heslington, York, UK

hrt103@cs.york.ac.uk ; kazakov@cs.york.ac.uk

Abstract

The aim of this research is to assess the rôle of a hypothetical inherited feature (gene) promoting altruism between relatives as a factor for survival in the context of a multi-agent system simulating natural selection. Classical Darwinism and Neo-Darwinism are compared, and the principles of the latter are implemented in the system. The experiments study the factors that influence the successful propagation of altruistic behaviour in the population. The results show that the natural phenomenon of kinship-driven altruism has been successfully replicated in a multi-agent system, which implements a model of natural selection different from the one commonly used in genetic algorithms and multi-agent systems, and closer to nature.

1 Introduction

The aim of this research is to assess the rôle of a hypothetical inherited feature (gene) promoting altruism between relatives as a factor for survival. The two main goals are, firstly, to replicate the phenomenon of altruism, which has been observed in nature, and show that the proposed mechanism leads to altruistic individuals being selected by evolution. Secondly, the research aims to provide an implementation of a Multi-Agent System (MAS) employing a model of natural selection, which is different from the one commonly used in Computer Science (Goldberg, 1989), and, hopefully, closer to the one existing in nature.

Altruism can be defined as selfless behaviour, action that will provide benefit to another at no gain to the actor himself, and possibly even to his detriment. In *kinship-driven altruism*, this behaviour is directed between individuals who are related. Hamilton (1964a) introduces an analytical model, in which altruistic behaviour towards relatives is favoured by evolution, provided that the amount of help that an individual bestows on relatives of a given distance is appropriately measured.

Both MASs (Wooldridge and Jennings, 1995) and Genetic Algorithms (GAs) (Goldberg, 1989) can be used effectively to simulate the interaction of a population that evolves over a period of time. A MAS allows study of the interactions at the level of the individual, while a GA is a better tool for generalisation over an entire population. In a GA, no distinction is made between individuals with the same *genotype* (i.e., inherited features), whereas in a MAS these are represented by different *phenotypes*, or set of observable characteristics resulting from the interaction of each genotype with the environment

Table 1: MAS vs. GA simulation of natural selection

Feature	MAS	GA
Representation of individuals	genotype + phenotype	genotype only
Survival of individuals	deterministic, based on the lifetime interaction with environment	probabilistic, based on genotype's fitness
Population size	unlimited	fixed
Environment resources	limited capacity	use bounded by maximum population size
Preservation of energy	enforced	not considered

(Thompson, 1996). The use of MAS with large populations is limited by the requirement for extra resources to represent individual phenotypes. In a GA, the individual is anonymous, so there is no capacity to “zoom-in” on its behaviour, but in contrast, there is the possibility of scaling up to consider a much larger population, which may be statistically more relevant.

The GA uses a fitness function to estimate how well each individual will fare in the future and uses this to influence the likelihood that they survive to subsequent generations. A MAS uses information about the current position of an individual in the environment, and taking into account its internal state, considered to be the cumulative result of its actions and experiences in the past, determines its actions. In a GA, the population size is fixed, and during each system cycle, individuals may be selected to mate (and be replaced by their descendants) or they pass to the next generation. The anonymity of each individual is suited to the probabilistic selection afforded to this algorithm, and the resulting possibility that clones of an individual be produced in future generations. Without this anonymity, in a system that ‘tracks’ the behaviour of individuals through the generations, complications could arise on cloning. Attachment of energy values becomes difficult if the probabilistic freedom is to be maintained without producing a system that can produce and destroy energy at will. In a MAS, the population size is not explicitly constrained, and the internal state of an individual determines its lifespan. A system cycle will not generally represent an entire generation, as individuals may survive for many cycles. Table 1 summarises the main differences between the GA and MAS models of natural selection.

We combine features of each approach to produce a more scalable, personality-driven system without a modelled spatial dimension. The probabilistic nature of all events and the high level of abstraction typical for the GA are preserved. However, the description of each individual consists of a set of inherited features (genome) along with a—very abstract—description of the actual organism (phenotype). The internal state of each individual is changed by the interaction with a very simple, abstract, environment, in which both the selection of an individual’s action and its outcome are modelled as probabilistic functions. This permits us to avoid the use of an explicit fitness function, and instead describe the survival of an individual directly as a probabilistic function of its internal state (e.g., current energy levels).

Our system is designed to simulate a population in which some of the individuals are carriers of a gene forcing them to share their energy with the individuals they meet in proportion to the degree of kinship (i.e., number of shared genes). The exact sharing policy

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is subjected to selection and studied. Food consumption results in increased individual energy level. Falling below a certain energy level means death. An encounter of two individuals of the same species could result in the creation of offspring if their energy levels are sufficient. The initial energy level of the offspring is subtracted from that of the parents.

This research uses the hybrid platform described above to study from a different angle an extended version of some of the experiments with kinship-driven altruism performed by Barton (2001).

2 Altruism and Darwinian Theory

The possible evolution of a selfless gene is an interesting area of study as it does not necessarily seem intuitive that an individual should value the survival of another to the extent of causing detriment to itself (perhaps by decreasing its own chance of mating or survival) in order to help the other. It would be in contrast to the classic Darwinian theory of natural selection, according to which selfish individuals would always take the upper hand, and eliminate altruists, as the behaviour of the latter would by definition hinder their reproductive success. There is evidence however, as Hamilton (1964b) illustrates, that many species in nature exhibit this altruistic trait. Neo-Darwinian theory (Watson, 1995) attempts to provide an explanation with the idea of 'inclusive fitness', and the hypothesis that natural selection works not at the level of an individual, but on each individual gene. Many individuals can carry copies of the same gene, and if these individuals could identify one another, it would be possible for them to aid in the process of natural selection over that gene by attempting to secure reproductive success and the passing of this gene to the next generation. The evidence provided by Hamilton suggests that nature has evolved to recognise that it is likely for close relatives to have similar genetic makeup. In Hamilton's model, the degree of kinship is quantified, and it can then be used to determine how much help an individual can bestow on a relative, at detriment to itself and yet still be likely to benefit the inclusive fitness, the 'fitness' of the gene.

Barton (2001) used a MAS to model a population of individuals who behaved altruistically competing in an environment with a population of the same size that was not altruistic. His MAS used GA principles by associating genes with each individual in an attempt to find optimum solutions for variables used in his simulations. In some of his experiments, it was the sharing population that prevailed, in others, the non-sharing population over-ran the environment. He quotes 'Gause's Competitive Exclusion Principle', stating 'no two species can coexist if they occupy the same niche', and hypothesises that given the limitations of his simulated system, his competing populations are likely to 'end up having the same, or very similar, niches'.

In the MAS he uses, there are agents to represent food and the individuals of each population. The environment is represented on a grid with varying terrain that could restrict movement, or provide water as sustenance to fulfil 'thirst,' one of the 'drives' that describe the internal state of an agent in a given cycle. Each agent uses the values of its drives, its immediate surroundings and some deterministic rules to make life choices in each cycle.

3 Design

The system we have implemented to investigate altruistic behaviour combines features used in a MAS and those used in a GA. Rather than providing co-ordinates for the position of each individual in the system, we model encounters with food (energy) and other individuals probabilistically, reflecting the likelihood that these would occur in a given cycle. We do not constrain the population size, thus permitting easier comparisons with Barton’s work (Barton, 2001). We stem the growth of our population by increasing the probability of random death as the individual ages. The individuals in our implementation retain a portion of genetic material, encoding their behaviour, and sharing policy, and thus allowing evolution of optimum policies. The diagram provides the proposed environmental interaction module for our system. Each individual stores as its phenotype the value of its sex drive, its hunger (or energy level), age and the probability of survival. These values are updated in each system cycle. Figure 1 contains an outline of the proposed simulation, where individual boxes have the following functions:

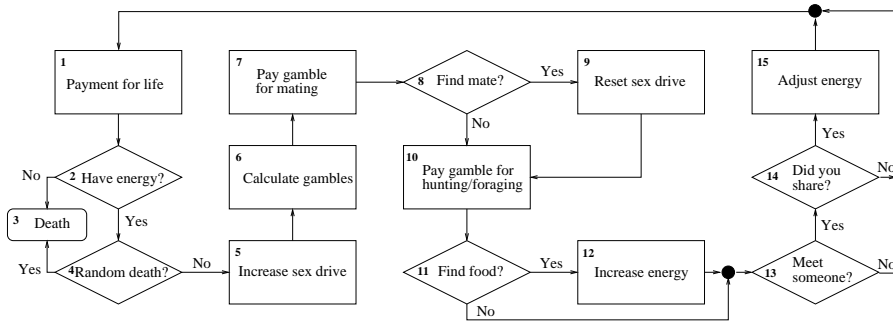


Figure 1: Simulation outline

1. Make a payment of energy to the environment (energy expended to survive generation).
2. If all energy is used up, the individual dies.
3. Individual has ‘died’ and is therefore removed from the population.
4. Random death occurs with some probability for each individual (this probability increases exponentially with age).
5. Increase sex drive, and thus priority of reproduction.
6. Genetic material encodes a function to determine behaviour based on the values of the drives. This function produces “gambles” dictating how much, if any of the available energy to expend in search of a mate or food.
7. The gamble for mating is ‘paid’ to the system.
8. Pairs selected at random from the mating pool are deemed to have ‘met’ with some probability. Each must satisfy certain energy requirements, and the pair must not be related as parent and child. The probability that they mate is set in proportion to their mating gambles and determines whether or not they actually produce offspring. On mating, new individuals are created from clones of the genetic material,

and by resetting non-genetic parameters. Each parent contributes energy for sharing equally amongst the offspring. The clones undergo crossover producing two children to be included in the population for the next cycle.

9. The sex drive of the individuals who mated successfully is reset.
10. The gamble for hunting/foraging (or *food* gamble) is ‘paid’ to the system.
11. A probability distribution based on the gamble determines how much energy an individual receives. For a gamble of zero, the probability that an individual receive any energy should be very low.
12. Energy level is increased by the amount of food found.
13. Pairs are further selected from the population, and with some probability are deemed to meet.
14. If the better fed of the pair is an altruist, they decide to share as per his genetically encoded sharing policy.
15. The energy of each individual is then adjusted as appropriate.

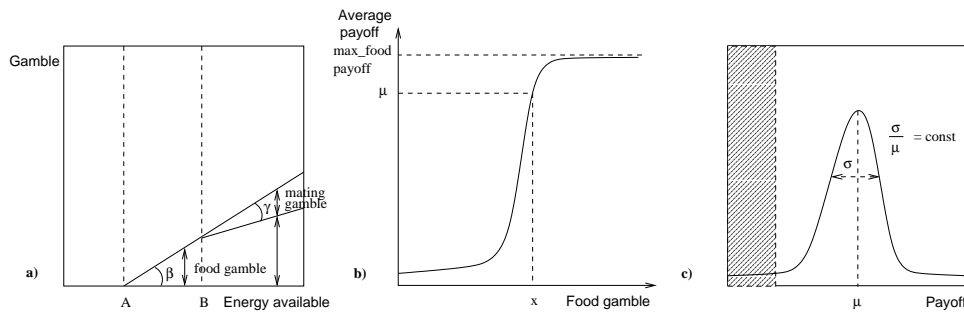


Figure 2: (a) Computing the food and mating gambles from the available energy. (b) Mapping food gambles to average food obtained. (c) Distribution of the amount of food received for a given average payoff μ .

Gambling policies The searches for a mate and food are modelled as stochastic processes, in which an individual spends (or “gambles”) a certain amount of its energy, and receives a payoff from the environment (finds a mate or a given amount of food) with a certain probability. The functions described in Table 2 and displayed in Figure 2a are used to compute the food and mating gambles. The mating gamble is used as described above. The actual amount of food received from the environment is determined from the food gamble in the following way. Firstly, the sigmoid function from Equation 1 is used to compute the average number of units of food/energy μ that the effort represented by the food gamble will produce (see Figure 2b).

$$\mu = \frac{\text{max_food_payoff}}{1 + e^{-0.025 * (\text{gamble} - 200)}} \quad (1)$$

The actual amount of food is then generated at random according to a Gaussian distribution $G(\mu, \sigma)$ (Figure 2c) where the ratio σ/μ is kept constant for all μ to ensure that

Table 2: Computing gambles from the energy available

if Energy \leq A
Food Gamble := 0
Mating Gamble := 0
if A < Energy \leq B
Food Gamble := $tg \beta * (\text{Energy} - A)$
Mating Gamble := 0
if Energy > B
Food Gamble := $tg \beta * (B - A) + tg (\beta - \gamma) * (\text{Energy} - B) =$ $tg \beta * (\text{Energy} - A) - tg \gamma * (\text{Energy} - B)$
Mating Gamble := $[tg \beta - tg (\beta - \gamma)] * (\text{Energy} - B) = tg \gamma * (\text{Energy} - B)$

only a very small, fixed proportion of the payoffs are negative; these, when generated, were reset to zero.

The parameters of the gambling function, that is, A , B , $tg \beta$ and $tg \gamma$, are encoded in the genes of the individuals, and, therefore, are subject to natural selection.

The above discussion shows that in this simulation spatial phenomena (food discovery, encounter with another individual) are represented as random processes with a certain probability. It is worth noting that physical distance between individuals is ignored, and the encounter of each pair is equally probable. Similarly, the probability of finding food does not depend on the past actions of the agent, as it would be the case if its co-ordinates were taken into account.

4 Experiments and Evaluation

The tool specified in the previous section was implemented in C++, and used to study the influence of several factors on the evolution of altruistic behaviour. In all cases, the evaluation assesses whether the hypothetical altruistic gene is selected by evolution, and studies the circumstances in which this happens.

Degree of kinship Individuals may (1) have a complete knowledge of their genealogy (*Royalty* model), (2) estimate the degree of kinship according to the presence of some inherited visible indicators (*Prediction*), or (3) not have this information available (*Unknown*).

The Royalty kinship recognition policy assumes one knows its relatives and the degree to which they are related. Each individual keeps a record of their relatives up to two levels up and down the genealogical tree (see Figure 3). Instead of recording the actual relationship, relatives are grouped in two sets, according to whether on average they share 50% or 25% of their genes with the individual in question. The first group consists of parents and children, the second of grandparents, grandchildren, and siblings. Treating siblings in this way can be explained by the fact that individuals change partners in every generation, and, therefore, the vast majority of siblings are actually half-sibs, which is the case displayed in Figure 3. One peculiarity of our implementation is that when two individuals mate, they produce exactly two children, the chromosomes of which are produced from the parents' by crossover. This means that if one child inherits a copy of a gene

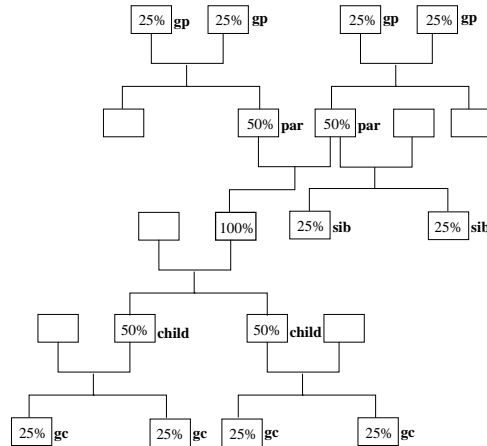


Figure 3: Average expected percentage of shared genes between relatives.

from one parent, the other child will *not* have that gene, unless the other parent carried it. In any case, the likelihood of two individuals mating together on more than one occasion is negligible in larger populations and the case of full-sibs is therefore discounted for simplicity in this implementation. Individuals who do not appear in either of the above groups of relatives are treated as being no relation at all.

The Prediction kinship recognition policy assumes that all genes but one (coincidentally, the one identifying altruistic individuals) are visible in the phenotype. A simple linear metric is then used to measure the similarity between the visible parts of genotype of the two individuals.

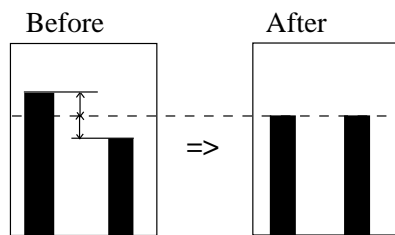


Figure 4: Sharing between identical twins: Communism

Type of sharing function Three social models are considered. *Communism* equalises the energy levels of two individuals with the same genome (see Figure 4). *Progressive Taxation with a non-taxable allowance* is a simple linear function with a threshold: $y = \alpha(x - \theta)$ for $x > \theta$; $y = 0$ otherwise. *Poll Tax* defines an altruistic act between two individuals as an exchange of a fixed amount of energy pt set in the genes of the donor, which does not depend on the energy level of either individual. The above descriptions correspond to the case of sharing between two individuals with the same set of genes. In all other cases, the actual amount given is reduced in proportion to the difference between the two individuals' genomes, as derived from the perceived degree of kinship.

All combinations of the above two factors have been studied by running each of the nine possible experiments three times (see Table 3). All parameters of the sharing func-

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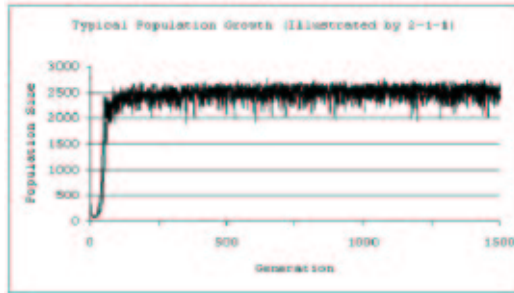
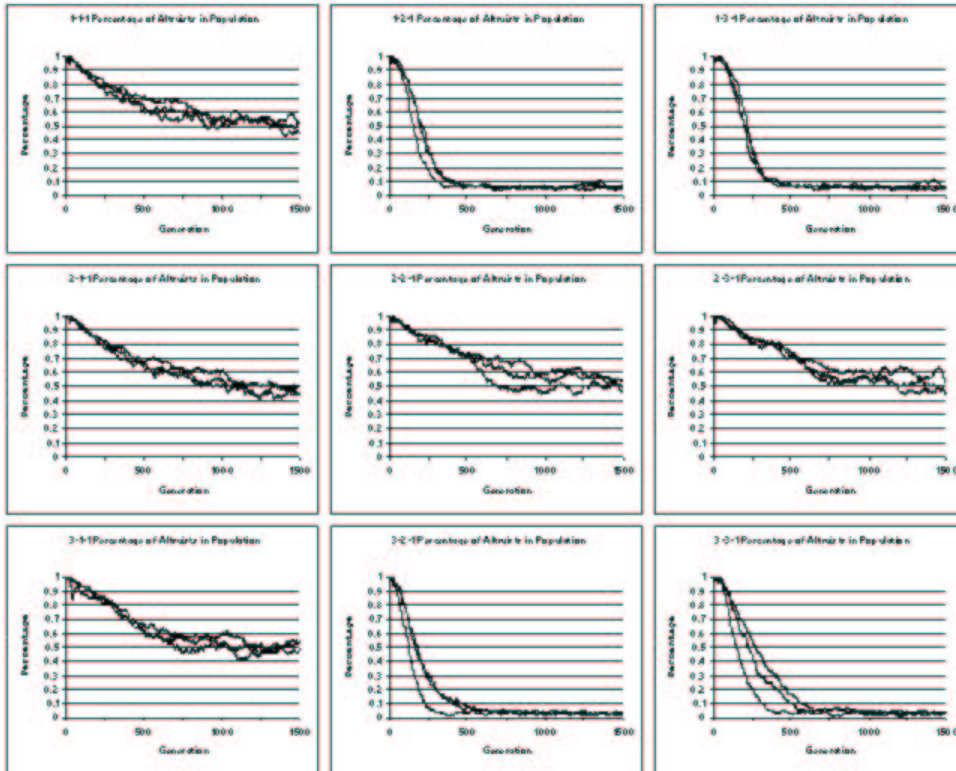


Figure 5: Evolution of population size

Table 3: Percentage of altruistic individuals in the population (1=100%). (Columns, from left to right: Royalty, Prediction and Unknown models of kinship recognition. Rows, top to bottom: Communism, Progressive Taxation and Poll Tax sharing functions.)



tions (α, θ) , resp. pt were initially set at random, and left to evolve. When employing the Unknown model of kinship, a rather optimistic assumption was made, under which the donor treated the aid receiver as a parent or child.

The graphs in Table 3 are self-explanatory. In brief, the use of either perfect knowledge of the degree of kinship or a sharing function based on progressive taxation ensures that a substantial level of altruism is selected and maintained in the population. The population size remains the same in all cases, and is given by the amount of food supplied. A representative example of the way in which the population size evolved is shown in Figure 5 on the case of Royalty with Progressive Taxation.

Degree of altruism and availability of resources In the experiments, all individuals carry a gene defining them as either selfish or altruistic. Simply counting the individuals carrying either gene is a good measure of the altruism in the population only in a communist society. In the other two cases, individuals, which are nominally altruistic, can have their sharing parameters set in a way, which reduces the effects of altruism to an arbitrary low level, e.g., α or $pt \rightarrow 0, \theta \rightarrow \infty$. In these cases, the ratio of what is given to what is actually owned by the individual, integrated over the whole energy range, is considered a more appropriate measure. The idea in the case of progressive taxation is shown in Figure 6 where a nominally altruistic individual is assigned a degree of altruism given by the ratio of the filled triangle and the square made of the ranges of energy owned and exchanged.

Changes in the level of resources available in the system will by definition have an effect on the carrying capacity (maximum population size) of the environment, and could be expected to cause variations in the system dynamics, and possibly the ability of the environment to support altruism. We ran several experiments to see how the degree of altruism in the system varies for the different sharing policies (note that this level does not change, and is considered equal to 100% for the Communist sharing policy, so the graphs are omitted) with different amounts of energy (resources) available. The graphs in Table 4 indicate that altruism tends to converge faster to a single stable level when more energy is provided by the environment.

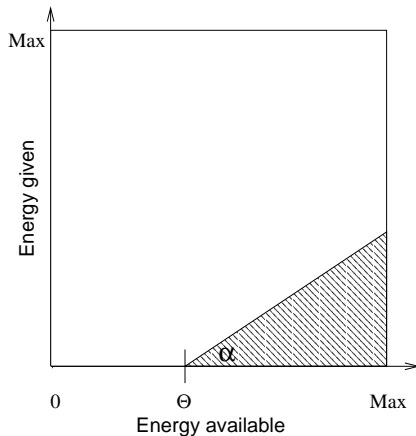
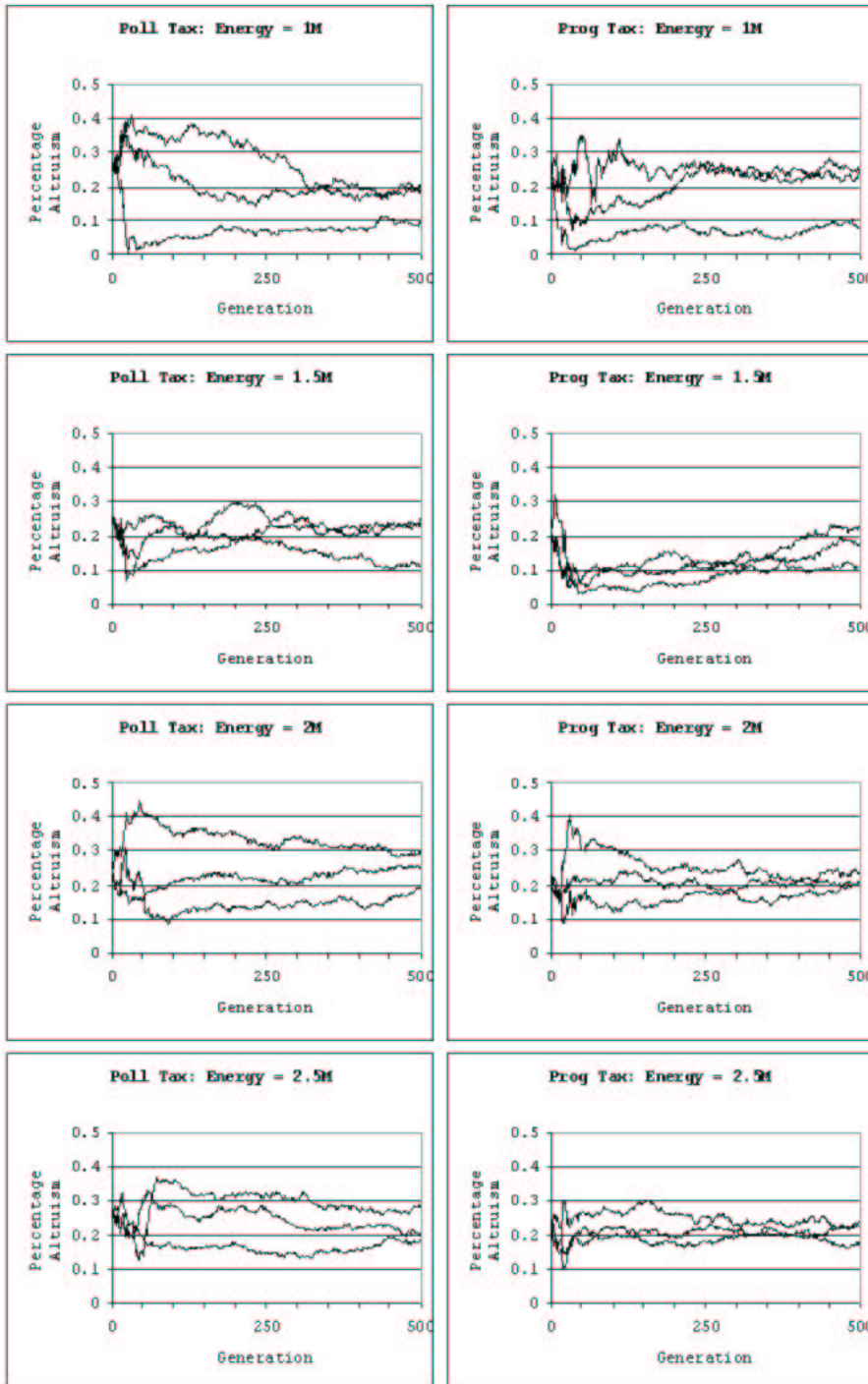


Figure 6: Measure of altruism

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Table 4: Percentage of altruism (1=100%) evolving in the population as the sharing strategy and level of energy (resources) available are varied.



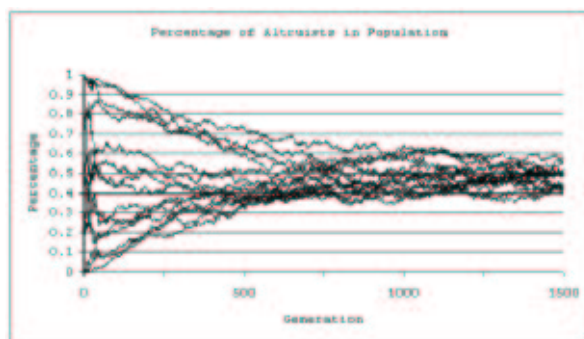


Figure 7: Percentage of altruists in the population with respect to initial levels (1=100%)

Initial ratio between altruistic and selfish individuals To study the influence that the initial proportion of altruistic to selfish individuals has on the levels of altruism selected by evolution, the Royalty with Progressive Taxation experiment was run with several initial values for this ratio. The results in Figure 7 show that the system reaches a dynamic equilibrium which, in the cases shown, does not depend on the initial ratio.

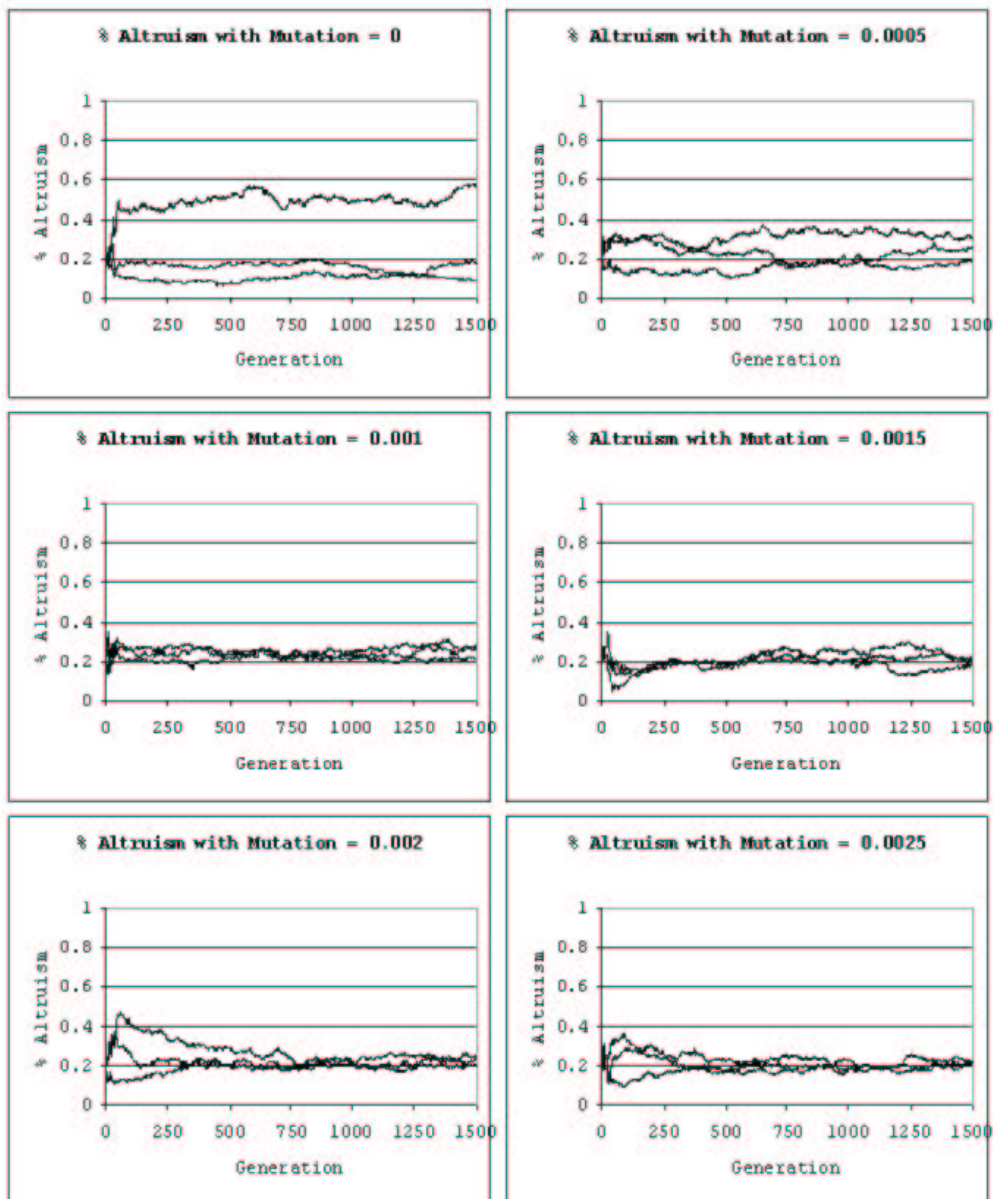
Mutation We conducted some experiments where the rate of mutation in the system was varied. Although it was maintained at relatively low levels, variation was seen in the speed of convergence to a stable level of altruism and the eventual level. The mutation rates were set at: 0; 0.0005; 0.001; 0.0015; 0.002 and 0.0025, with other variables fixed as follows: sharing function = Progressive Taxation, kinship-recognition policy = Royalty and Energy = 2.5M (see Table 5). At the lowest rates of mutation, there appears to be a greater variation in the evolved levels of altruism between runs of the experiment, making it difficult to draw conclusions about the rate of convergence. As the mutation rate increases, a more definite level of altruism is evolved, and the experimental populations converge faster to this level. It is unlikely that this trend would continue as the mutation rate increases much higher, since, at some point, the high level of mutation is likely to override the effects of natural selection. (For the third chart, where the level of mutation is at 0.001, note that it is just an extension of chart eight in Table 4: Progressive Taxation with 2.5M energy units, the same experimental setup, but run for three times as long.)

5 Discussion

Both goals of this research, as stated in Section 1, are successfully met. The proposed algorithm has been implemented, and altruism has, indeed, been shown to be selected and maintained by evolution in a number of cases. No direct comparison with Barton's work could be made as his detailed results were not available in a suitable form. However, a few major points can be made. Firstly, it has been confirmed that the policy of Progressive Taxation produces more altruists than Communism. An additional policy (Poll Tax) was studied in this research, which also introduced the new dimension of 'knowledge of the degree of kinship' in the experimental setup. Unlike Barton's, these experiments produced populations of virtually the same size. Barton treats altruists and non-altruists as two different species, which in turn results in one species completely taking over the other

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Table 5: Effect of varying mutation rate on the percentage of altruism in the population (1=100%).



one. In our results, there are several cases in which a balance between altruists and selfish individuals is maintained.

Altruism is a demonstration of the mechanisms on which natural selection is based. Note that this work does not aim to imply the existence of such gene in reality, and indeed nothing of that said above would change if one assumed altruistic behaviour being inherited not as a gene, but through upbringing.

There is interest in the use of natural selection in artificial societies. This research should bring the implementation of natural selection in artificial societies a step closer to the original mechanism that is copied. The authors' expectations are that the natural selection incorporating altruism would be suitable in cases, when the task is to produce an optimal population of agents rather than a single best individual, in situations when the knowledge about the performance of the population is incomplete and local.

The software described here may also represent a useful tool for the simulation of natural societies and give an interesting insight in their inner making, although this would be up to experts in the relevant fields to judge.

The two main characteristics of the model of altruism discussed here, namely, 'inherited' and 'kinship-driven', also mark the limits of its reach.

Firstly, the model does not allow changes in the altruistic behaviour of an individual within its lifespan. In fact, natural selection and individual learning are not perceived here as mutually exclusive. It is expected that, in many cases, combination of the two could be a successful strategy, where natural selection provides the starting point for the individual behaviour, which is modified according to the agent's personal experience. The actual technique employed at this second stage could be, for instance, based on game theory, where natural selection provides a suitable initial strategy. If individual behaviour is to be modified by a machine learning technique, natural selection could also provide it with a suitable bias. Research in this direction should be helped by the York MAS, currently under development, which supports natural selection among agents, as well as logic-based programming of behaviour and individual learning (Kazakov and Kudenko, 2001).

The second limitation of the model of altruism discussed here is that it does not discuss the case when agents can at will opt in and out of a society promoting altruism among its members. Since the names of many such societies draw analogies with kinship, e.g. 'fraternities' or 'sororities', in order to evoke the corresponding spirit of altruism (or 'brotherhood') in its members, the authors believe that also in this case the findings described in the paper would not be without relevance.

In comparison with logic-based approaches, this research makes one simple initial assumption, and attempts to see if altruism can be worked out from first principles. The actual behaviour of agents can be deterministic (and described in logic) or stochastic, that should not be of principle importance. On the other hand, no further background knowledge is assumed here—the agent's rules of behaviour are left to evolve, and not set in advance. In the future, comparisons with Hamilton's analytical model, and the evolutionary game theory point of view would also be worth exploring.

6 Future Work

It would be interesting to extend the platform developed to implement different mating policies, so that pairs of individuals could be selected from a single mating pool or from separate mating pools into which individuals have previously been grouped according to their internal state: rich meet (mostly) rich, poor meet poor, individuals with high sexual drive are grouped together, etc.

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In addition to the impact of resource availability and rates of mutation, studied in this paper, another environmental parameter, the probability of meeting another individual, should be taken into account, and used to test the effectiveness of altruistic *vs.* selfish policy in various, and changing, environments.

An important and, potentially, non-trivial issue is the analysis of the content of the individuals' sets of genes and their evolution in time. In the case when the propagation of all genes is subject to simultaneous selection, one would have to study data sets, which are multidimensional—one dimension per locus plus an extra dimension representing time—hence difficult to visualise. One could expect that there would be a correlation between the genes selected in each locus, and that certain combinations might show a trend of dominating the population, which would form clusters around those points. Methods and tools for multivariate data visualisation with a minimal loss of information, such as those described by Schröder and Noy (2001), would be considered for the above task.

Acknowledgements

The second author wishes to express his gratitude to his wife María Elena and daughter Maia for being such a wonderful source of inspiration.

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