COMP6026: Assignment 2

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January 8, 2013

1 Introduction

Powers, Penn, and Watson [2007] show that environmental conditions need not be externally imposed in order to promote the evolution of cooperative traits. They present a model which permits suitable conditions to arise via individual selection, and show that even in environments that initially select for selfish behaviour, a niche construction process can allow for cooperative behaviours to be ultimately successful. This paper reimplements the algorithm described, and exends the model to show not only that the process is accelerated by the introduction of mutation to the model, but also that a side-effect of the niche construction process then favours selecting against individuals that are able to mutate, resulting in a more stable niche.

2 Reimplementation

In Powers et al. [2007], an algorithm is presented which demonstrates that under the right circumstances, individuals can select for environments that promote cooperation. Using the trait-group aggregation and dispersal model presented in Wilson [1975], individuals are permitted to select for control both over individual strategy and initial group size. Groups are formed according to individual size preferences, and with a random but globally proportionate composition of strategies. Individuals in groups are then reproduced over a number of generations, with shares of the group's resources (r_i) allocated according to the proportion of individuals with a particular genotype within that group (equations 1 and 2). This results in an environment where the cooperative trait can have greater individual fitness, as between-group variation ultimately globally favours the growth of groups with a higher proportion of cooperative individuals.

$$r_i = \frac{n_i G_i C_i}{\sum\limits_{j}(n_j G_j C_j)} R \tag{1}$$

$$n_i(t+1) = n_i(t) + \frac{r_i}{C_i} - K n_i(t) \tag{2}$$

In the reimplementation, individuals are represented as aggregate populations by genotype. Each individual can specify two genes: one for size, and one for strategy, and each gene can take one of two values, large/small and cooperative/selfish, respectively. This results in four possible genotypes, and so a migrant pool is maintained of the total count of each of the four types. Each group also maintains only the total count of each genotype within it, and aggregation, reproduction, dispersal and scaling operations are all carried out by population rather than individually.

The algorithm has no explicit fitness function - rather, an individual's fitness may be approximated by the total resource share of its genotype within the population as a whole. There is no crossover, but the algorithm could be said to be generational, as after each aggregation/dispersal round the whole population is rescaled back to a nominal 'carrying capacity' (N).

After initialising the migrant pool with N individuals, Powers et al. [2007] presents the following algorithm as an implementation of the trait-aggregation model. The steps represent a single cycle, and should be repeated for T generations.

1. **Aggregation:** Assign individuals in the migrant pool randomly to groups according to their size preference - each group will have a random composition of strategies, but the average should be proportionate to the global ratios. Surplus individuals may be discarded.
2. **Reproduction:** Perform reproduction within groups - equation 1 gives the resource share that each genotype population recieves, and equation 2 gives the resulting change in population size. Repeat for t generations.
3. **Dispersal:** Return the progeny of each group to the migrant pool.
4. **Scaling:** Rescale the migrant pool back to size N, retaining the proportion of individuals with each genotype.

Behaviour parameters	Cooperative	Selfish
Growth rate, G_i	0.018	0.02
Consumption rate, C_i	0.1	0.2

Size parameters	Large	Small
Group size, S_i	40	4
Resource influx, R_i	50	4

Global parameters	Value
Population size, N	4000
Generations, T	120
Reproductions, t	4
Death rate, K	0.1

Table 1: Parameters from Powers et al. [2007], used throughout.

2.1 Results
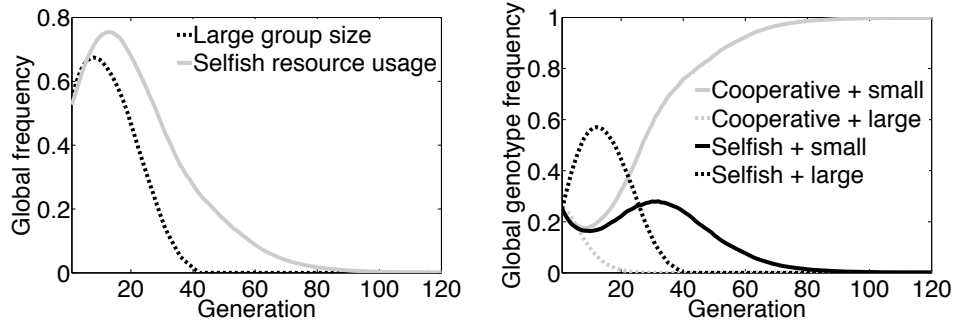
Figure 1: Left: average environment and strategy through time.
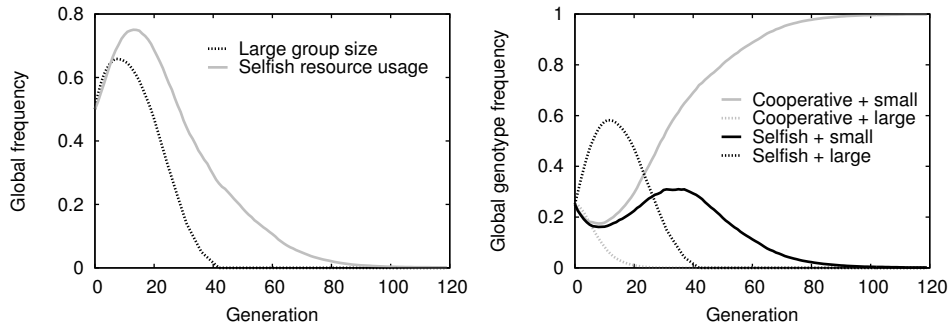Right: change in genotype frequencies over time. [Powers et al., 2007]

Figure 2: Results provided by reimplemented algorithm, as above. The plots match to a high degree of accuracy, showing accurate reimplementation.

3 Extension

The original result can be shown to be quite robust: even in the case of severe imbalance in the inital genotype distribution, it is generally seen that the cooperative + small genotype successfully forms a niche and eventually fixes (Appendix A, figure 5). However, this is only possible when there exists a critical minimum population of cooperative + small individuals to survive long enough that between-groups variation begins to select in favour of that genotype. In the model as presented, if a particular genotype dies out or does not exist in the initial distribution, then it is never possible for it to (re)enter the gene pool. In certain situations, this can be seen as disvantageous - for example, in the original model, if the cooperative + small individuals were able to form larger groups again once the selfish allele had been eradicated, then they could reap the resource bonus without exploitation by selfish individuals (as in Appendix A, figure 6).

As an extension to the original model, this paper then presents analysis of cases where individuals are allowed to change size preference, behaviour and their own mutation rate, in a manner similar to a low rate of mutation across the whole population [Smith and Fogarty, 1996].

3.1 Representation

Once again, individuals are represented by genotype as populations of identical clones. As there are three distinct genes, there are now eight separate combinations of alleles representing populations in the migrant pool and in each group. The reproduction code has been modified to respect the possibility of newly mutated individuals existing in a group size different to that specified by their genotype. Mutation potentially occurs after each within-group reproduction cycle.

Ochoa et al. [2000] notes that 'optimal per-locus mutation rates depend mainly on $1/L$ (the reciprocal of the genotype length)'. In this model, the length of each individual's genotype is only 3, and a mutation rate of $1/3$ is high enough to cause no significant solution to arise. However, the original reasoning behind the heuristic leads to a more effective value for mutation within the model. The use of a mutation rate of $1/L$ is intended to result in an average of one change to one gene in the individual per reproduction - in the model presented, the desired mutation rate is on the order of one change of one group per cycle of reproduction, and so a value of $1/num\_groups$ is more appropriate. Though the actual number of groups fluctuates based on prevailing group size preference, 550 groups may be

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taken as a reasonable approximation[1]. A mutation rate M of $\frac{1}{550} \approx 0.002$ is therefore used throughout the rest of the paper.
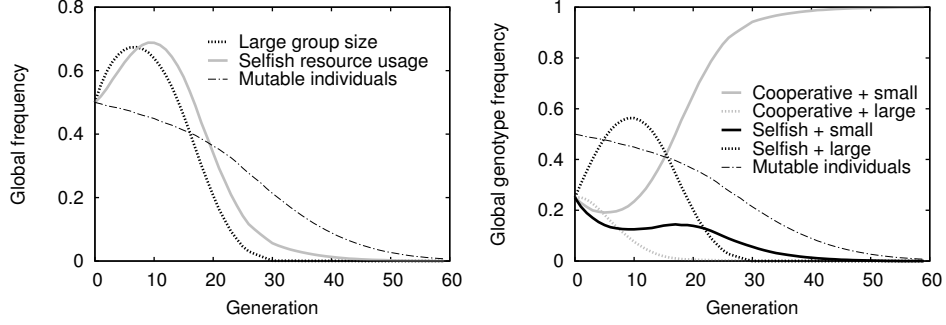
3.2 Results

Figure 3: In many cases, the addition of mutable individuals leads to the same outcome more quickly. The increase or decrease in proportion of mutable individuals is highly self-reinforcing, and though the ultimate outcome is largely stochatsic, exhibits a generally non-mutable bias.
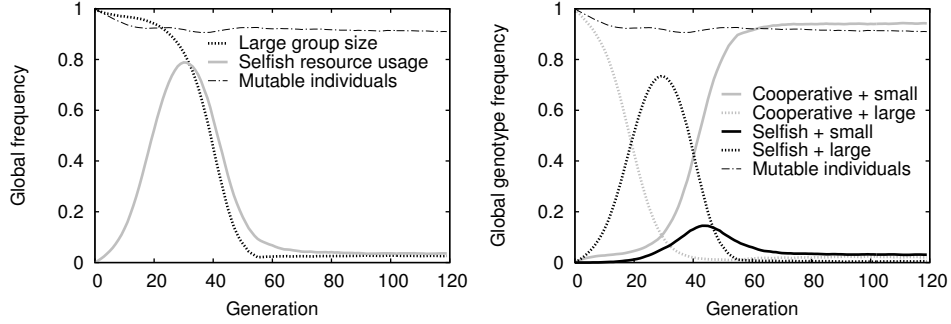

Figure 4: With the addition of mutability, the niche-creation process can occur even in initial distributions that contain no small + cooperative individuals.

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[1] using the parameters in table 1 with equal distribution of genotypes: $\frac{2000}{40} + \frac{2000}{4} = 550$

4   Conclusion

The addition of mutable individuals increases stochasticity - particularly for the ultimate proportion of mutable individuals. As it has no inherent effect on fitness, it is self reinforcing. Often the algorithm will select towards non-mutability as there is bias in that direction.

References

G. Ochoa, I. Harvey, and H. Buxton. Optimal mutation rates and selection pressure in genetic algorithms. In *Proceedings of the Genetic and Evolutionary Computation Conference*, volume 1, pages 315–322. Citeseer, 2000.

S. Powers, A. Penn, and R. Watson. Individual selection for cooperative group formation. *Advances in Artificial Life*, pages 585–594, 2007.

J. Smith and T.C. Fogarty. Self adaptation of mutation rates in a steady state genetic algorithm. In *Evolutionary Computation, 1996., Proceedings of IEEE International Conference on*, pages 318–323. IEEE, 1996.

D.S. Wilson. A theory of group selection. *Proceedings of the National Academy of Sciences*, 72(1):143–146, 1975.
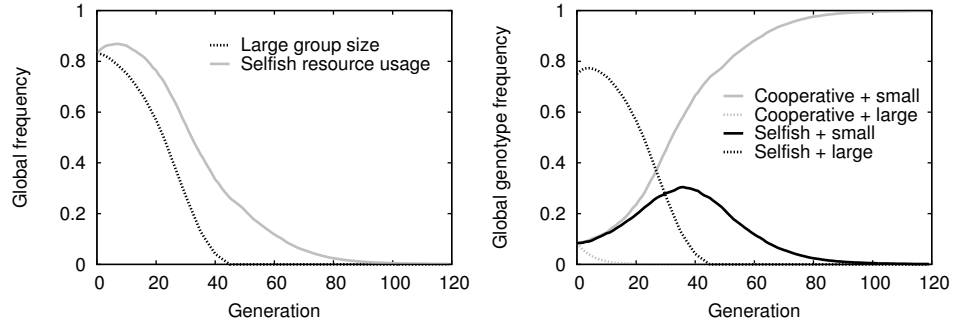
A   Additional graphs

Figure 5: The presented model is robust even in the face of severe imbalance in the initial genotype distribution.
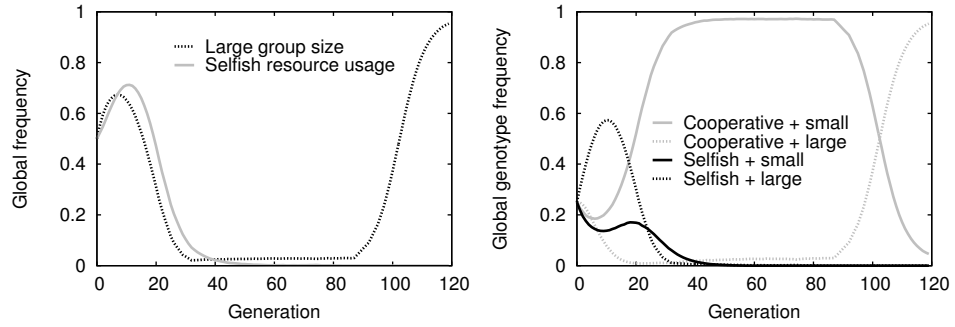

Figure 6: Mutation on size only allows the cooperative + large genotype to reappear and then eventually flourish once the selfish allele has died out.