

COMP6202: Evolution of Complexity

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1 Introduction

Paper re-implemented: *Individual Selection for Cooperative Group Formation* (paper 4)

1.1 The Experiment

The experiment involves creating a ‘pool’ of individuals. These individuals can either display selfish or cooperative traits. This trait determines the amount of resources they receive and the growth rate of the individual’s population. The individuals are sorted into two groups, each consisting of sub-groups of fixed sizes. The first group has large sub-groups, whereas the second has small sub-groups. An individual “picks” the group size they are willing to join. Therefore, an individual has 2 defining features: whether or not it is cooperative and if it joins small or large groups.

The individuals are then reproduced, which involves finding their new populations based on received resource and growth rate. This occurs for T generations. What the experiment shows is that the overall ‘pool’ converges towards one type of individual; selfish + small. It is an example of niche construction and shows how cooperative behaviour can arise through individual selection.

1.2 Individual Representation

In the re-implementation, each individual in the migrant pool is represented with a 2-bit bit-string. This bit-string correlates to a genotype in accordance to the table below:

11	Cooperative + Large
10	Cooperative + Small
01	Selfish + Large
00	Selfish + Small

The advantage of representing individuals in such a way is that it allows extensions to be implemented effortlessly. If, for example, the genotypes were represented statistically, meaning the proportions of each genotype was stored instead of actual individuals, then it would have been difficult to experiment with aspects such as mutation and crossover.

One disadvantage of using actual individuals was that during reproduction, often the increase in population of a genotype, particularly in small groups, was very small and a fraction of an individual could not be represented. This issue was solved by storing the population of genotypes as a float during the t time steps of reproduction, and then re-populating the groups with the new population rounded to the nearest integer.

2 Re-implemented Results

The initial experiment aimed to recreate Figure 2 from the original paper. Here it is shown as Figure 1. The recreated figures are 2 and 3.

The parameters used in the experiment can be found in the appendix.

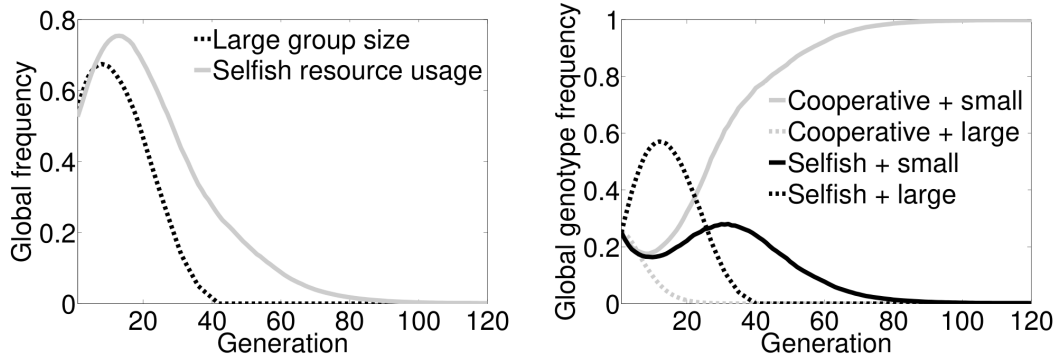


Figure 1: Figures from the paper which were to be re-implemented

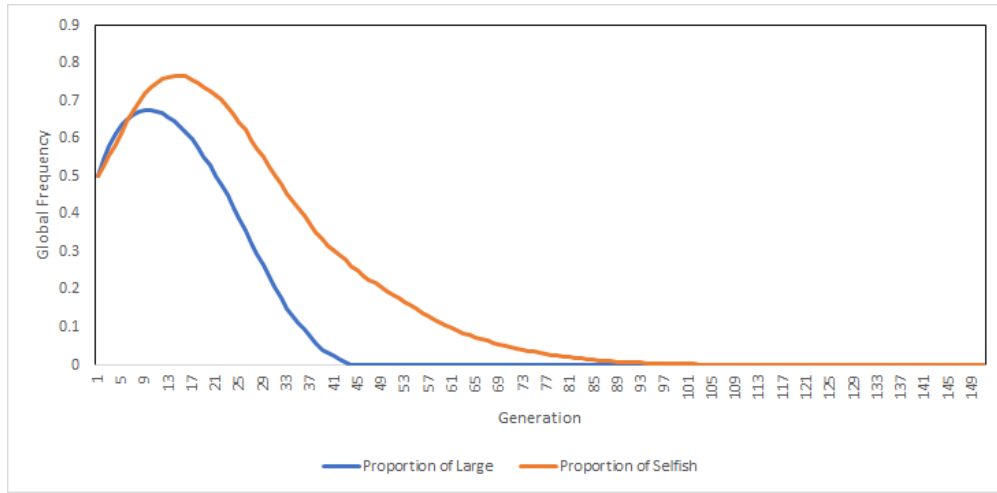


Figure 2: Proportions of selfish and large genotypes in the migrant pool

Figure 2, which is a recreation of the left-hand side of figure 1 shows the proportion of the large and selfish trait over generations. Both traits increase in frequency at first but then suffer a decrease. The reason for this is clear when looking at figure 3, which is a recreation of the right-hand side of figure 1.

In figure 3, a dramatic increase in the ‘selfish + large’ genotype can be seen for the first 20 generations, followed by a decrease to extinction in the next 25. On the other hand, ‘cooperative + small’ individuals suffer a small decrease followed by an increase in frequency, and over time become the dominant genotype. ‘Cooperative + large’ individuals become extinct almost immediately, whereas ‘selfish + small’ show a small increase after the extinction of ‘selfish + large’ but also slowly reduce to 0.

The reason behind the increase in the proportion of large and selfish genotypes in the beginning is due to their advantage when it comes to getting resources for growth. In large groups, the selfish trait beats the cooperative one hence allows for faster population growth. However, this unsustainable strategy means that over time these individuals are not able to survive. In small groups, the cooperative strategy is preferred. Hence, when the migrant pool mainly consists of small genotypes, (approx. generation 35) the cooperative strategy beats the selfish one.

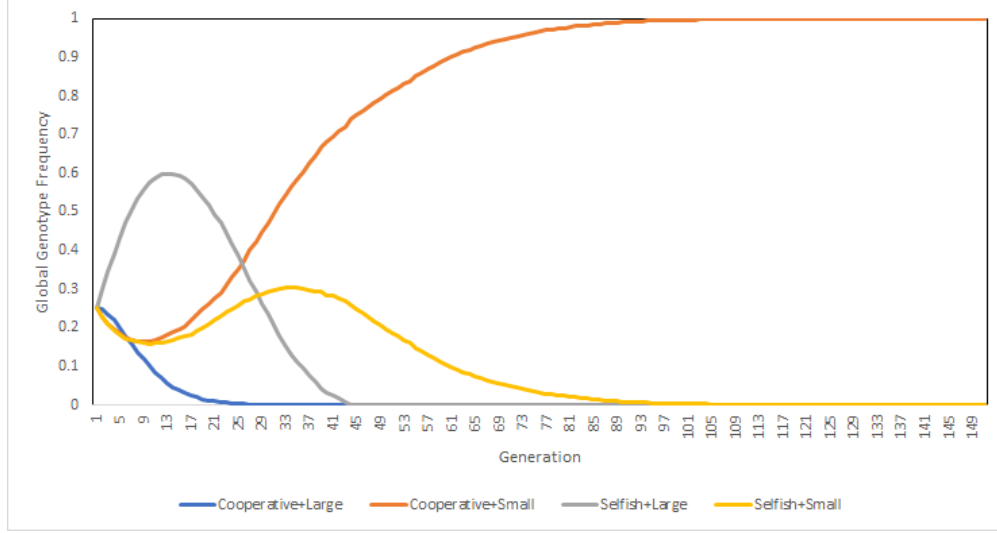


Figure 3: Population of each genotype over generations

3 Extension

The title of the extension is:

“Studying the effects of a diverse population on the frequency of cooperative behaviour”

3.1 Hypothesis

Hypothesis: in a population where the “level” of cooperative behaviour of an individual varies between individuals, the population should converge towards an ideal level of cooperation.

The expected results are similar to that of the original paper, where the cooperative and small individuals slowly become the majority, however there may be some changes. For example, the most common individual by the end of the simulation may be slightly more selfish than the most cooperative individual. This is because they may have the advantages of being cooperative in small groups but the slightly higher selfish trait may mean they perform better than a completely cooperative individual. Obviously, this advantage will be lost when the other individuals ‘die’ out.

On the other hand, a different scenario would be that the upper-hand of cooperative behaviour in small groups may be lost when there is a large diversity in the population. That is to say, “when everyone is at least a little selfish; the most selfish will win”. If this scenario is correct, then one would expect to see the selfish trait become the majority.

3.2 Implementation

The experiment could be implemented in a similar way to that of the original paper with some important changes; regarding how individuals are represented and how one’s level of cooperative behaviour is calculated.

The individual is represented as a bit-string of n length, (for the experiment $n=8$). On top of this, there is a character appended to the end of each individual representing the group size the individual belongs to. This can either be L or S , for large and small respectively. Although the size parameter could have also been a bit, there would have been no programmatical advantage and this method is more human-readable.

An example of an individual is “1111111S”.

The number of 1s on the individual signifies how cooperative it is. If an individual has 8 1s then it has the base ‘growth rate’ (G) and ‘consumption rate’ (C) values, meaning it is the most cooperative it can be.

An individual with 8 0s has the maximum G and C values, making it the most selfish. Individuals with a number of 1s and 0s in-between 8 will have G and C relative to the number of each. For example, an individual “00001111S” will have a G and C which is the half-way point between base and max. The formula for calculating G is given below:

$$G_i = G_b + (Z_i * (G_m - G_b)/n)$$

Here, G_b is base G , Z_i is the number of 0s in the individual, G_m is max G and n is the length of an individual’s bit-string. The formula for calculating C is similar.

The migrant pool is initialised with an equal number of each genotype. After this they are sorted into their retrospective groups and reproduced for t steps (similar to the original paper). Their resource allocation is calculated based on the number of each genotype in the group. Since each genotype is sorted to put the 0s in front of the 1s, there is no issue of a incorrect counting, i.e. ‘10101010S’ and ‘00001111S’ are exactly the same. This can be done as only the number of 1s and 0s matter rather than their order. Finally, the individuals are returned to the migrant pool and the pool re-proportioned. This is repeated for T generations.

3.3 Results

Since the extension contained such a large number of different genotypes, the data has been split into two graphs. One shows the frequency of genotypes with the large trait, while the other shows ones with the small trait. It must be kept into consideration that populations shown in both graphs are from the same pool. Once again, the parameters used are available in the appendix.

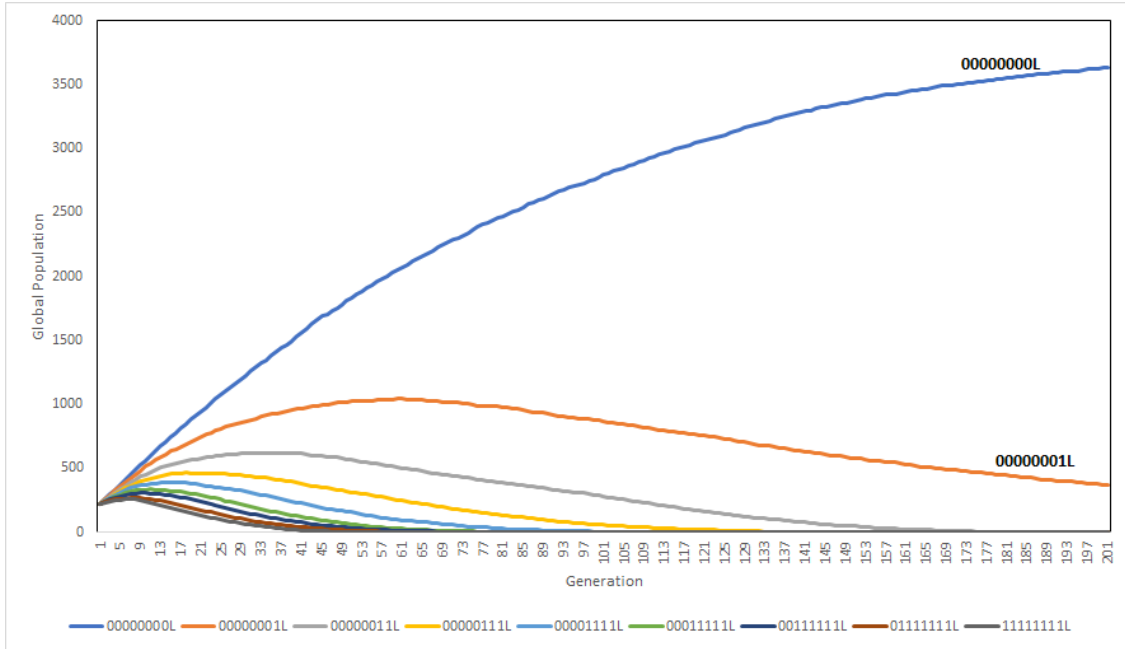


Figure 4: Global population of large genotypes over generations

Figure 4 shows the change in the population of large genotypes. The genotype at the end of 200 generations which is most frequent is ‘00000000L’. This is the most selfish genotype in this group. The second most frequent genotype is the second most selfish and so on. Figure 5 shows the change in the population of small genotypes. What it shows is that all small genotypes suffer a decrease in population at around the same rate until they all become extinct. Their level of cooperative behaviour does not seem to affect this decline.

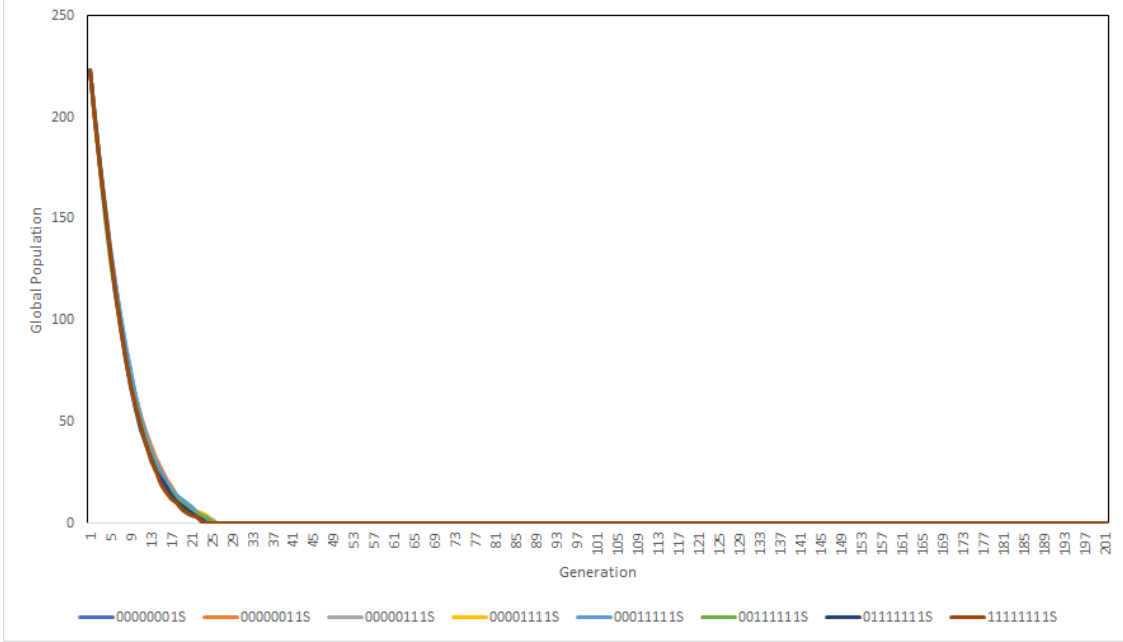


Figure 5: Global population of small genotypes over generations

These results do not support the hypothesis, where it was proposed that the end population will have some level of cooperation. In fact, the results show the opposite is true, where cooperative behaviour is a hindrance to growth and selfish traits win. However, this is not entirely true. From figure 5 we can see that all small groups suffer a similar decline. Therefore, what the results actually show is that being in small groups is detrimental to growth and being in large groups is favourable.

A proposed justification for the results is as follows. The decline in small groups at a constant rate is due to the lack of similar genotypes. Since small groups only had 4 individuals, when calculating an individuals growth it was very unlikely that a group had many identical genotypes. This meant that these genotypes did not grow much.

On the other hand, large groups had 40 individuals, hence it was more probable for there to be more identical genotypes and therefore larger growth. This also meant that selfish genotypes beat the cooperative ones as in large groups selfish trait has always been favoured.

3.4 Further Tests

An aspect to test in this extension was the affect of G and C values on the results. Therefore, further experiments were conducted where difference between the base and maximum values where altered. Figure 6 shows the results when the maximum and base G and C were changed in accordance to the table below:

	Halved	Doubled
G_b	0.019	0.009
G_m	0.02	0.04
C_b	0.15	0.05
C_m	0.2	0.4

What this experiment showed was that the only effect of G and C values was the rate at which the most selfish large individual became dominant. When the maximum G and C values were larger, the rate was faster. All genotypes are not shown in figure 6 since graphing the dominant individual was adequate to understand the trend. For the same reason only the first 50 generations are shown.

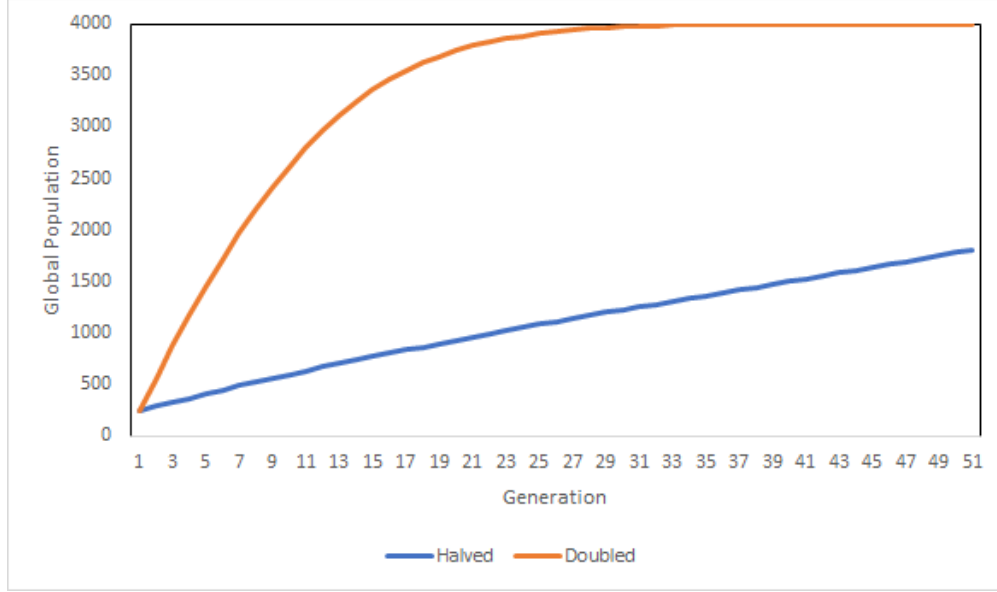


Figure 6: Effect of G and C on the population of the '00000000L' genotype

4 Conclusion

To conclude, the extension showed that in a diverse population, small groups are at a disadvantage due to the smaller growth rate that comes from the inability to find identical individuals. Large groups do not have this disadvantage and hence flourish. Since, in large groups, selfish individuals grow faster than cooperatives ones, overall the most selfish individual becomes the dominant genotype.

4.1 Evaluation

The advantage of implementing the individuals as bit-strings became clear when creating a diverse range of individuals. The length of the bit-string could be changed to represent new genotypes and the code logic needed little modification. However, an improvement would be to improve the efficiency of the code as some functions were slow and convoluted.

To ensure the correctness of the extension, the code was modified to simulate the original experiment. This could be done very easily by changing the 'allele_size' parameter to 1. Doing this gave similar results to the original experiment, hence it was clear that the extension was implemented correctly and the results for diverse individuals could be accepted.

4.2 Future Work

Originally the plan was to investigate the effect of mutation on a diverse population. This was due to the rather premature acceptance of the hypothesis. Given the unexpected results, which required further investigation, this could not be achieved in the scope of this assignment. Thus, an appropriate extension would be to investigate the effect of mutation on the frequency of cooperative individuals in a diverse population.

Other areas which could be explored are the effects of changing the group size, the resource amount and the number reproduction cycles.

5 Appendix