

Project 2

Modelling Complex Systems

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May 12, 2017

1 Network Epidemics

1.1 Simple Social Network

In Figure 1, a histogram of the distribution of linked individuals is presented for a total population of $N = 5000$ and link density, that is probability to link with another individual, $\delta = 0.0016$. The distribution tend to a binomial distribution.

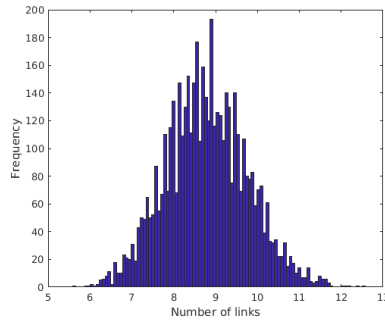


Figure 1: Histogram of number of links for link density $\delta = 0.0016$.

1.2 Infection

On each day, an individual connected to n other infected individuals becomes infected with probability

$$P_{inf}(n) = 1 - e^{-pn}, \quad (1)$$

where $p = 0.01$. An infected individual recovers each day with probability $r = 0.03$. In figure 2, the number of infected individuals is simulated for a total population of $N = 5000$ and initially 100 randomly infected individuals for 1000 days.

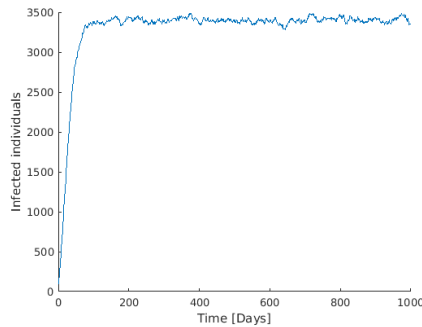


Figure 2: Number of infected individuals over time for an initial population of 5000 with $p = 0.01$.

1.3 Varying contagiousness

The simulation is repeated varying contagiousness of the infection in the range $p = \{0.001, 0.002, \dots, 0.01\}$. In Figure 3, the number of infected individuals as a function of time is presented.

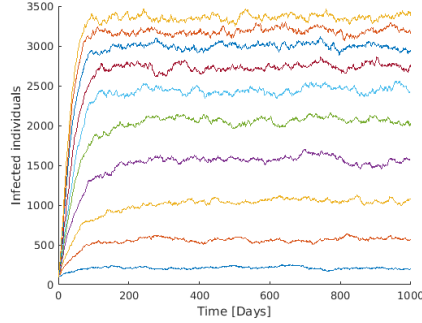


Figure 3: Number of infected individuals over time for an initial population of 5000 varying p .

The rate of recovery r over contagiousness p , $\frac{r}{p}$ is important when investigating the number of infected individuals at equilibrium. In Figure 4, the number of infected individuals as a function of $\frac{r}{p}$ is presented for $r = 0.03$ and $p = \{0.001, 0.002, \dots, 0.01\}$.

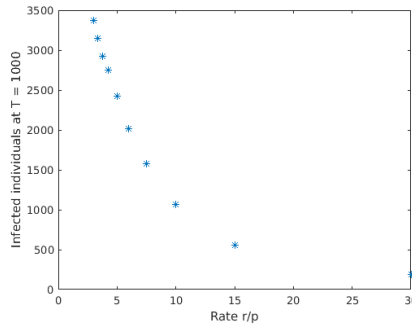


Figure 4: Number of infected individuals after 1000 days as a function of r/p .

1.4 Preferential Network

In the preferential network-model there is a higher probability that an individual with more links attached to it will get connected with a newly added one, that is,

$$P_{link}(i, t) = \frac{k_i(t-1)}{\sum_j k_j(t-1)}, \quad (2)$$

where k_i is the degree of the i :th individual at time $t-1$.

Since more links to an individual make the probability of another link to be added to that particular individual, most individuals will have few links attached, but few will have a lot. The resulting degree distribution seems to follow the Power Law-distribution and is presented in loglog-scale in Figure 5.

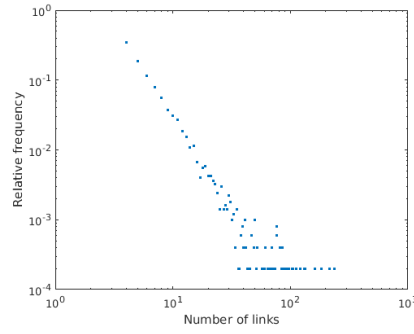


Figure 5: Degree distribution of 5000 individuals in log log scale.

Since few individuals with a large number of links were observed, the variance is higher. As proved in the lectures, the cumulative distribution is also power law distributed. In Figure 6 the cumulative distribution is presented in loglog-scale.

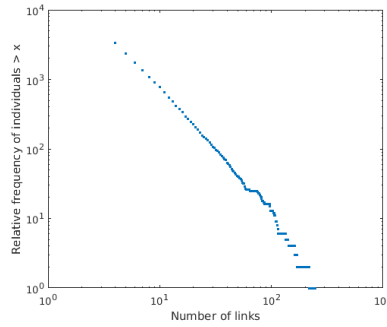


Figure 6: Cumulative degree distribution of 5000 individuals in log log scale.

1.5 Stationary

In accordance with Equation (2)

$$Q(k, t) = \frac{k}{2(t-1)} t P_{k,t}, \quad (3)$$

is the probability of a newly added node to link with a node of degree k . The master equation for the frequency of nodes with degree k for N parallel network is

$$N(t+1)P_{k,t+1} = NtP_{k,t} + 1 \cdot Q(k-1, t)N - 1 \cdot Q(k, t)N, \quad (4)$$

which gives

$$(t+1)P_{k,t+1} = \begin{cases} tP_{k,t} + \frac{k-1}{2(t-1)} tP_{k-1,t} & k > 1, \\ tP_{k,t} + 1 - \frac{k}{2(t-1)} tP_{k,t} & k = 1. \end{cases} \quad (5)$$

In equilibrium, when $t \rightarrow \infty$, the approximation

$$P_{k,t+1} \approx P_{k,t} := P_k \quad (6)$$

is adequate...

Due to excess of points from the first project, I will leave this exercise here.

1.6 Infection in preferential network

On each day an individual connected to n other individuals becomes infected according to Equation (1). In this network with preferential attachment however, few individuals with a large number of

links have high risk of getting infected, whereas the majority of the population has a rather limited chance of being infected. In Figure 7, the number of infected individuals over time is presented for the preferential network with $p = 0.01$ as in task 1.2.

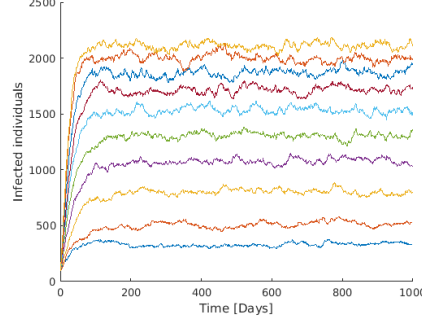


Figure 7: Degree distribution of 5000 individuals in log log scale.

The preferential network is less fragile to infections in random individuals than the undirected random network in exercise 1.1. However, if an infection spreads to a dense individual, that is an individual with a high number of links, it would cause severe damage. This is not modeled in this exercise but if a preferential network of connected routers would be attacked, and the attacker striked one of the dense nodes, the attacked is presumed to cause immense damage.

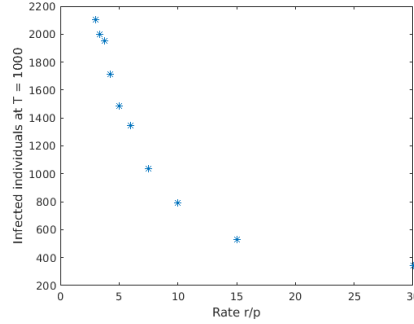


Figure 8: Number of infected individuals after 1000 days as a function of r/p for a preferential network.

2 Self-propelled Particle Model

2.1 Model setup

In this exercise a simulation of flocking is presented. If not else stated, the simulations are done in a $L \times L$ two dimensional world with periodic boundaries for 50 individuals with neighbour-radius $R = 2$. Care has been taken into assuring that two individuals on each side of the boundaries may be considered neighbours. Instead of using synchronized update with $\delta = 0.5$ of each particle the particles update by using a random $\hat{\delta} \sim \text{Exp}(\delta = 0.5)$ for each particle as it better describes different individual response time.

For the model setup, three different flocking behaviours are presented. In the first setting, the parameter tuning how prone the individuals are to face a random neighbour is set to $p = 0.3$, and the parameter tuning how prone the individuals are to follow a random neighbour is set to $q = 0.3$. Roughly it is one third chance that an individual will approach its neighbours, one third that an individual will follow the stream and one third that an individual will continue on its own path. In Figure 9 this behaviour of non-convergent form is presented.

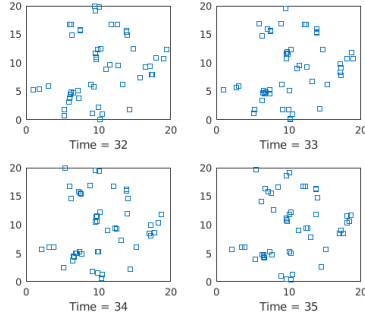


Figure 9: Simulation of flocking when $p = 0.3$ and $q = 0.3$ for 50 individuals.

If the parameters are altered as $p = 0$ and $q = 0.6$ as presented in Figure 10, a clear pattern is forming as the individuals tend to follow the same stream as their neighbours forming patterns of large flocks moving in the same direction (to the right), although sparsely as p is left zero.

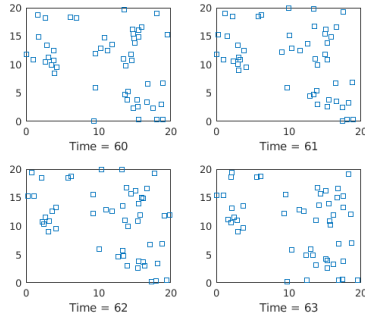


Figure 10: Simulation of flocking when $p = 0.3$ and $q = 0.3$ for 50 individuals.

If instead the parameters are set to $p = 0.6$ and $q = 0$ as presented in Figure 11, the directional behaviour is absent, instead the individuals cluster together in a more protective manner due to the high chance of facing a neighbour, but *zero* chance to follow the stream.

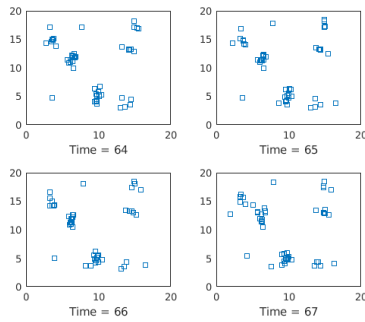


Figure 11: Simulation of flocking when $p = 0.3$ and $q = 0.3$ for 50 individuals.

2.2 Measure of alignment

With the number of individuals, $N = 50$, and the probability of an individual close in on a neighbour set to $p = 0.1$, the alignment is measured by using

$$\psi(t) = \frac{1}{N} \sqrt{\left(\sum_{i=1}^N \cos(\theta_i(t)) \right)^2 + \left(\sum_{i=1}^N \sin(\theta_i(t)) \right)^2}. \quad (7)$$

In Figure 12, a bifurcation diagram of $\psi(t)$ and parameter q , namely the probability that an individual will take one of its neighbours direction, is presented.

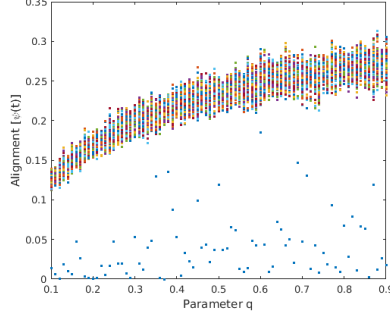


Figure 12: Bifurcation diagram describing alignment for q varying between 0.1 and 0.9. The colours, although scientifically disregarded, are merely for joyful purposes.

2.3 Measure of aggregation

The proposed measure of aggregation is the sum of deviations of each particle

$$\phi(t) = \frac{1}{N} \sqrt{\left(\sum_{i=1}^N (x_i(t) - \mu_x(t)) \right)^2 + \left(\sum_{i=1}^N (y_i(t) - \mu_y(t)) \right)^2}, \quad (8)$$

where $\mu_x(t)$ and $\mu_y(t)$ are the mean of each coordinate for all particles.

The mean examined for 100 simulations. In Figure 13, two bifurcation diagrams are presented for $N = 50$ and parameter (a) $p = 0.1$ and (b) $p = 0.3$. Clearly, a larger p suppresses the impact of q as p takes up more of the sample space.

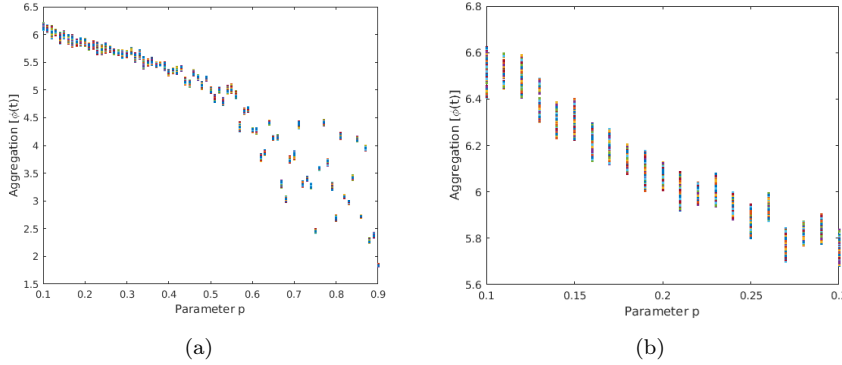


Figure 13: Bifurcation diagram describing aggregation for p with $N = 10$ and q fixed as (a) 0.1 and (b) 0.3.

In Figure 14, two bifurcation diagrams are presented for $N = 10$ and parameters (a) $p = 0.1$ and (b) $p = 0.3$. For large N , the aggregation spreads out for large q , as opposed to small N .

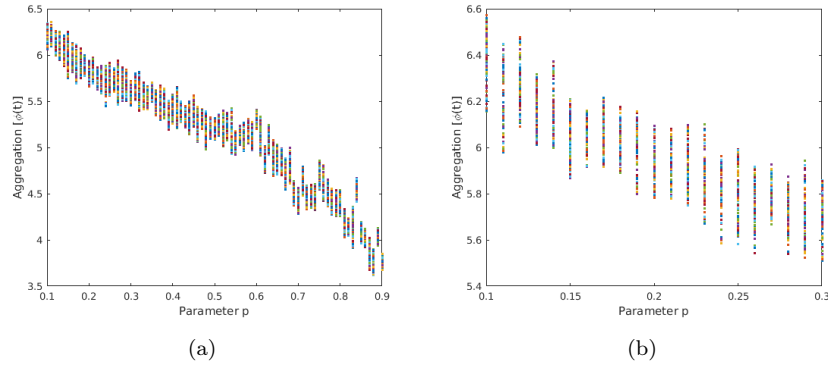


Figure 14: Bifurcation diagram describing aggregation for p with $N = 10$ and q fixed as (a) 0.1 and (b) 0.3.

3 Evolving Painter Robot

Contrarily to the instructions, to determine if the area on the tile under the robot, forward and the tiles to the left and right are signed by using variables 0 - empty, 1 - painted and 2 - wall. The actions coded in the chromosomes use variables 3 - walk forward, 4 - turn left, 5 - turn right, and 6 - walk randomly. This is due to facilitation of the implementation.

3.1 Random painter

In this exercise, four chromosomes with random behavior were tested in an empty room and their fitness were measured two of which scored particularly well. However, these are just simulated ones and for better estimates of their actual fitness, more simulations are needed. This is done in Exercise 3.3. In Figure 15 the four random chromosomes performance is shown.

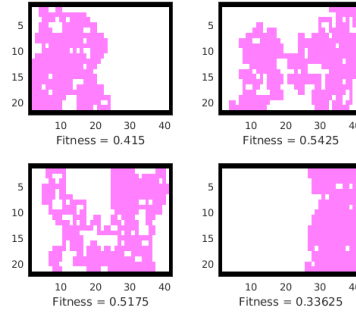


Figure 15: Bifurcation diagram describing alignment for q varying between 0.1 and 0.9

3.2 Simple strategy

Let F declare the tile in front of the painter, L declare the tile to the left of the painter and R declare the tile to the right of the painter. Consider the following strategy, combining some instructions into one multi-instruction to save space:

- If F is empty, move to F
- If F is a wall/colored and L is empty, move to L
- If F is a wall/colored and L is a wall/colored, move to R

This simple strategy will make the painter first go to the wall and then try to spiral counter clockwise. However, a bad initial position and direction may result in a large empty patch, and the third rule can in some basic cases cover that.

3.3 Evolution

In this exercise, 50 random chromosomes were tested 10 times in an empty room and their average fitness were measured as the average amount of painted tiles. Weighted by their average fitness, the chromosomes were evolved using single point cross-over and single gene mutation with 5 % mutation rate. After 200 generations, the chromosomes had evolved to paint a significant amount of the tiles in the room. In Figure 16, one particularly potent chromosome is presented.

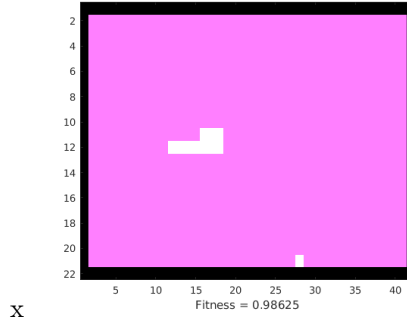


Figure 16: One particularly successful individual chromosome performing in an empty room.

3.4 Average fitness and gene diversity

In Figure 17 the average fitness of the chromosome population evolved is presented. As expected, some very crucially inefficient genes were avoided in the evolution at an early stage. These genes are supposedly genes that make the painter get stuck at walls and such.

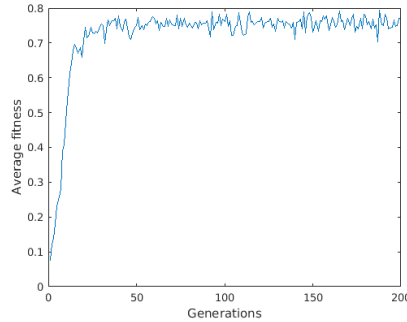


Figure 17: Simulation of one particular chromosome

In the final generation the chromosomes have several genes in common, with certain exceptions. These exceptions could be genes that are not very important to this problem.

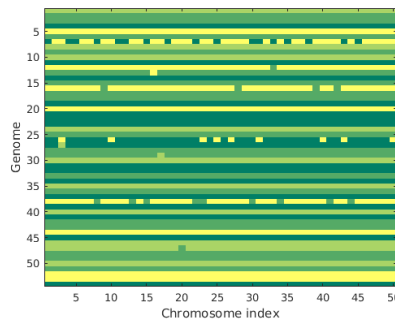


Figure 18: Chromosome deviance in the 200th generation.

3.5 Adding furnitures to the room

When adding furnitures to the room, the chromosomes trained in an empty room struggle to adapt to the new environment. While some easy traps like getting stuck in the wall disappear early in the evolution some combination of genes may be helpful to surpass more complicated traps. These combinations may be of less importance in a new environment. To really train a versatile chromosome, an idea could be to randomly perturb the environment in each generation, simulating the non-static environment in a real world setting. In Figure 19 a chromosome trained in an empty room performs in a room with furnitures and in Figure 20 a chromosome trained in the room with furnitures performs in the same setting. Notice that the one trained in the room with furnitures managed to enter into the centre of the room while the robot trained in an empty room falsely believed the centre to be inaccessible.

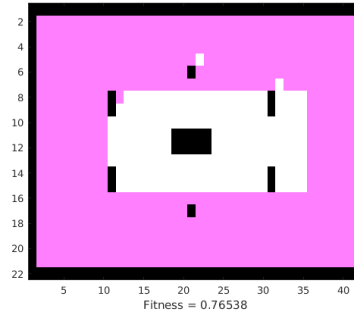


Figure 19: Simulation of one chromosome trained in an empty room.

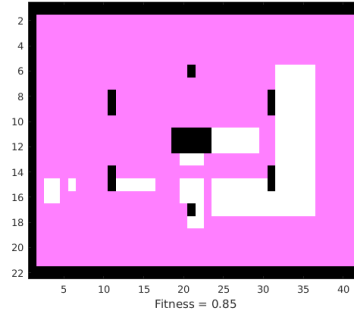


Figure 20: Simulation of one chromosome trained in the same room with furnitures.