Exam Modelling and Simulation

Question 1 (20 points)

a) Explain the distinction between a system, a model and a simulation. How are they related?

b) A one-dimensional cellular automata can be defined in terms of k number of states and r the range of the neighbourhood. Given k = 3 and r = 2, calculate the size of the rule table (number of inputs) and the number of possible configurations of the rule table.

c) The Wolfram encoding is a way to describe a particular rule for a CA. Define this rule encoding.

d) The Langton Parameter λ is a way to describe the behaviour of a cellular automata.
(i) Define how to calculate λ for a given CA with rule table Δ.
(ii) Given a specified λ value, Langton describes two ways in which to generate a CA for the given value of λ. Describe these two methods.

Question 2 (20 points)

a) John Conway's Game of Life is a 2-dimensional cellular automata.
Answer the following questions regarding game of life.
(i) Define the four rules of game of life.
(ii) Draw two examples of still life patterns (stable) in the game of life.

b) Game of Life (GOL) has been shown to emulate a Universal Turing Machine (UTM).
(i) If Game of Life is a Universal Turing Machine, what algorithms can it calculate?
(ii)Demonstrate that the Game of Life is a Universal Turing Machine (which three components are needed, which Boolean functions are required, how can this be done just with NAND?)

Question 3 (20 points)

Consider the genetic network shown in Fig. 1.

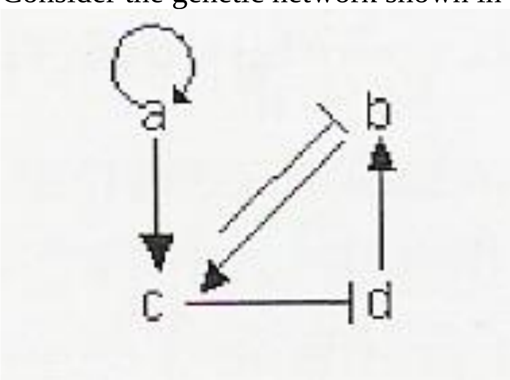

Fig 1. Genetic network with 4 genes, an arrow indicates activation, a blocked arrow indicates inhibition

a) Which type of graph is the network shown in Fig 1?
b) Give the adjacency matrix for the network shown in Fig. 1.
c) Give the Boolean rules for a Boolean model of this network. When you have constructed the Boolean rules, what kind of information can you extract from the

successive states in the Boolean network? Show the development in time of the initial state a=0,b=0, c=0, d=0, what can you conclude from this trajectory?

d) In the Boolean model of the gene network you have to do a binarization step, explain how to do this and if there potential problems here?

Question 4 (20 points)

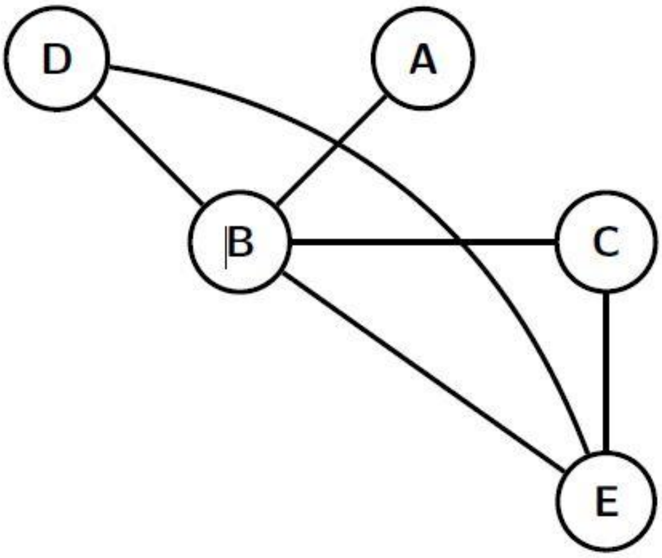

Fig 2. Network

(a) Define the adjacency matrix, network diameter and average clustering coefficient for the network shown in Fig 2.

(b) Random networks can be described in the form G(p;N), where p is the probability of two nodes connecting and N is the total number of nodes. Answer the following in the context of random networks.
(i) What is the probability to get a particular realization of a graph G(p,N) with L links

(ii) Given N = 4 and p = 0:4, what is the probability of creating any network with exactly 3 links

(b) Consider an Erdos-Renyi random network *N*(N;L) and its largest connected subgraph G(N_G;L_G). We will investigate the fraction of nodes in $G, S = N_g / N$. Consider two nodes of N, n_i and n_j, with $i \neq j$
(i) What are the ways in which a node n_i is not connected to the giant component through some other node n_j?
(ii) What is the probability that n_i is not connected to G through nj
(iii) Show that $S = 1 - e^{-<k>S}$

Question 5 (20 points)

a) Describe the algorithm to construct networks with the Watts Strogatz Model

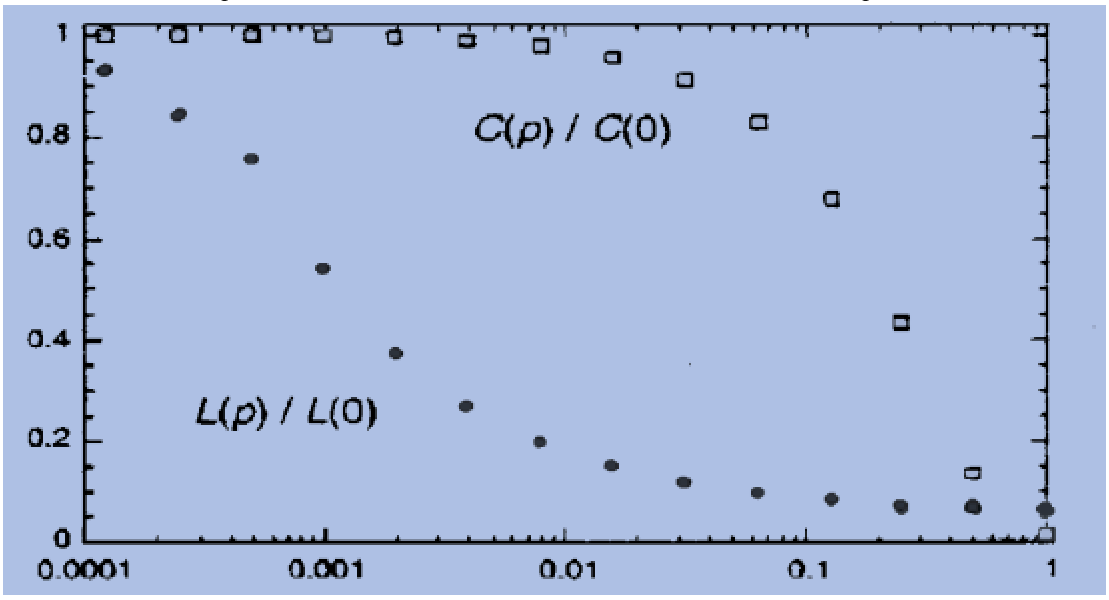

Fig 3. Plot of the clustering coefficient C(p) (top curve) and path length L(p) (bottom curve), for probability p (also indicated as β in the Watts Strogatz model) at the x-axis

b) Explain what you can conclude from Fig. 3.

c) What is a scale free network? Can you model scale free networks with the random networks or Watts Strogatz model (explain your answer)

Good luck!