Network and Random Processes Homework 2

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1. Birth-death process

   (a) Consider a continuous-time Markov chain $(X_t : t \geq 0)$, with state space $S = \mathbb{N}_0$ and jump rates α_x and β_x for increasing and decreasing by one from position x respectively. Hence, the generator is

$$G = \begin{pmatrix} -\alpha_0 & \alpha_0 & & & \\ \beta_1 & -(\beta_1 + \alpha_1) & \alpha_1 & & \\ & \beta_2 & -(\beta_2 + \alpha_2) & \alpha_2 & \\ & & \ddots & \ddots & \ddots \\ & & & & \end{pmatrix}$$

   or $G(x, y) = \beta_x \delta_{x-1,y} + \alpha_x \delta_{x+1,y} - (\beta_x + \alpha_x)\delta_{x,y}$, noting $(\beta_0 = 0)$.

   The master equation is

$$\frac{d\pi_t(x)}{dt} = \alpha_{x-1}\pi_t(x-1) + \beta_{x+1}\pi_t(x+1) - (\alpha_x + \beta_x)\pi_t(x)$$

   For X to be reducible, $p_t(x, y) > 0$, so $\alpha_i > 0 \ \forall i \in S$ and $\beta_i > 0 \ \forall i \in S \backslash \{0\}$.

   By detailed balance $\pi(x)g(x, x-1) = g(x-1, x)\pi(x-1)$,

$$\begin{aligned} \Rightarrow \pi(x) &= \frac{\alpha_{x-1}}{\beta_x}\pi(x-1) \\ &= \pi(0)\prod_{i=0}^{x-1}\frac{\alpha_i}{\beta_{i+1}} \end{aligned}$$

   (b) Assuming $\alpha_x = \alpha$ and $\beta_x = \beta$,

$$\pi(x) = \pi(0)\left(\frac{\alpha}{\beta}\right)^x$$

To be normalised the condition $\sum_{i=0}^{\infty} \pi(i) = 1$ must hold.

$$\begin{aligned}
&\Rightarrow \quad \sum_{i=0}^{\infty} \pi(0) \left(\frac{\alpha}{\beta}\right)^i = 1 \\
&\Rightarrow \quad \frac{\pi(0)}{1-\frac{\alpha}{\beta}} = 1 \text{ (for } \frac{\alpha}{\beta}<1) \\
&\Rightarrow \quad \pi(0) = 1 - \frac{\alpha}{\beta} \\
&\Rightarrow \quad \pi(x) = \left(1 - \frac{\alpha}{\beta}\right)\left(\frac{\alpha}{\beta}\right)^x
\end{aligned}$$

assuming $\alpha < \beta$, for which otherwise it is not possible to normalise the stationary distribution.

2. Contact process

   (a) Consider the contact process on the complete graph and let $N_t = \sum_{i\in\Lambda} \eta_t(i)$ be the number of infected individuals. The individual i changes infection status with rate $c(\eta, \eta^i) = \eta(i) + \lambda(1-\eta(i)) \sum_{j\neq i} \eta(j)$, so

$$\begin{aligned}
g(n, n+1) &= \lambda(L-n)n \\
g(n, n-1) &= n
\end{aligned}$$

since there are L possible individuals of which n are infected. This means

$$g(n,m) = \lambda(L-n)n\delta_{m-1,n} + n\delta_{m+1,n} - n(1+\lambda(L-n))\delta_{m,n}$$

Therefore, as the process shows that N_t can only increase or decrease by 1 at a particular time and the new transition rates will depend on the new value for N_t, independent of the state space, the process is a Markov chain as it only depends on the current value of N_t. $\mathbb{P}(N_{t+1} = n | N_0 = n_0, ..., N_t = n_t) = \mathbb{P}(N_{t+1} = n | N_t = n_t)$.

The master equation is

$$\frac{d\pi_t(n)}{dt} = \lambda(n-1)(L-n+1)\pi_t(n-1) + (n+1)\pi_t(n+1) - \lambda n(L-n)\pi_t(n) - n\pi_t(n)$$

Note this is valid $\forall n \in S$, as it gives

$$\frac{d\pi_t(0)}{dt} = \pi(1)$$

and

$$\frac{d\pi_t(L)}{dt} = \lambda(L-1)\pi(L-1) - L\pi(L)$$

as $\pi_t(x) = 0 \ \forall x \notin S$.

(b) The process is not irreducible as if $N_t = 0$ for some t, it will remain stationary as there are no infected individuals left to infect others ($p_t(0,n) = 0 \; \forall n$). This is an absorbing state.

Solving $\pi g = 0$, gives only the solution $\pi = (1, 0, ...)$, and so this is the only stationary distribution.

(c) Defining $\rho(t) = \frac{\mathbb{E}(N_t)}{L}$ and using the mean-field assumption.

$$\begin{aligned}
\frac{d\rho(t)}{dt} &= \frac{1}{L}\left(\sum_{i=0}^{L} n\frac{d\pi_t}{dt}\right) \\
&= \frac{1}{L}\Bigg(\sum_{i=0}^{L} n\Big(\lambda(n-1)(L-n+1)\pi(n-1) + \\
&\quad (n+1)\pi(n+1) - \lambda n(L-n)\pi(n) - n\pi(n)\Big)\Bigg) \\
&= \frac{1}{L}\Bigg(-\sum_{i=0}^{L} n\Big(\lambda n(L-n)+n\Big)\pi(n) + \\
&\quad \sum_{i=-1}^{L-1} \lambda\,(n+1)\,n\,(L-n)\,\pi(n) + \sum_{i=1}^{L+1}(n-1)\,n\pi(n)\Bigg) \\
&= \frac{1}{L}\Bigg(\sum_{i=0}^{L}\Big(-n\big(\lambda n(L-n)+n\big) + \lambda\,(n+1)\,n\,(L-n) + \\
&\quad (n-1)\,n\Big)\pi(n)\Bigg) \\
&= \frac{1}{L}\left(\sum_{i=0}^{L}\left(-n+\lambda nL-\lambda n^2\right)\pi(n)\right) \\
&= \frac{1}{L}\big(-\mathbb{E}(N_t) + \lambda L\mathbb{E}(N_t) - \lambda\mathbb{E}(N_t^2)\big) \\
&= -\frac{\mathbb{E}(N_t)}{L} + \lambda\mathbb{E}(N_t) - \frac{\lambda\mathbb{E}(N_t)^2}{L} \\
&= -\rho(t) + \lambda L\,(1-\rho(t))\,\rho(t)
\end{aligned}$$

(d) Considering $f(\rho(t)) = -\rho(t) + \lambda L\,(1-\rho(t))\,\rho(t) = 0 \Rightarrow \lambda L\rho(t)\big(\rho(t) - (1-\frac{1}{\lambda L})\big) = 0$ gives stationary points $\rho* = 0$ and $\rho* = 1 - \frac{1}{\lambda L}$.

$\frac{df(\rho)}{dt} = -1 + \lambda L - 2\lambda L\rho$, so $\frac{df(0)}{dt} = -1 + \lambda L$ and $\frac{df(1-\frac{1}{\lambda L})}{dt} = 1 - \lambda L$. Hence, $\rho* = 0$ is stable and $\rho* = 1 - \frac{1}{\lambda L}$ is unstable if $\lambda L < 1$ and $\rho* = 0$ is unstable and $\rho* = 1 - \frac{1}{\lambda L}$ is stable if $\lambda L > 1$.

If $\lambda L = 1$, then there is only one fixed point at $\rho* = 0$, which is unstable as $f(\rho + \epsilon) = 2\lambda L\epsilon\rho + O(\epsilon^2) > 0$ as $\epsilon \to 0$.

3. Simulation of contact process

   (a) Figure 1 shows a contact process simulation, averaged over 100 realisations, where there are 256 individuals, all originally infected, for different rates of infection, λ. The simulation shows that when λ

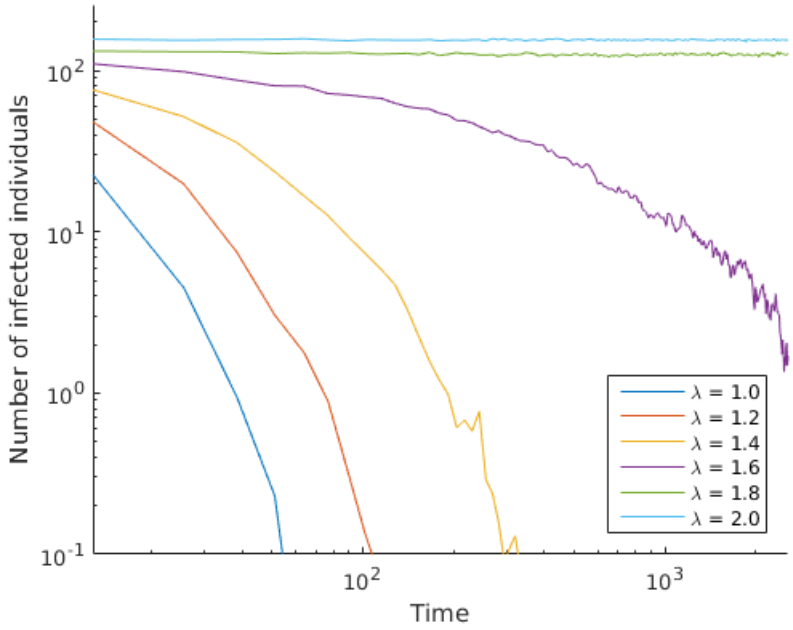


Figure 1: For number of individuals, $L = 256$, critical infection rate $\lambda_c \in [1.6, 1.8]$.

   is sufficiently small (certainly for $\lambda \leq 1.6$), the infection dies out ($N_t \to 0$ as $t \to \infty$), shown by the decay for large times, whereas if λ is larger, the infection persists in the population.

   (b) Now averaging over 500 realisations, the critical infection rate λ_c is found to two decimal places for different values of L, by judging by the ruler method whether N_t will curve upwards or downwards for increasingly smaller increments. Figure 2 shows that for $L = 128$, the critical infection rate lies between 1.69 and 1.70, so is approximately $\lambda_c = 1.695$ as the boundary between the behaviours occurs here. Similarly, for $L = 256$, the critical infection rate is between $\lambda_c = 1.66$ and 1.67 (Figure 3), for $L = 256$, between $\lambda_c = 1.65$ and 1.66 (Figure 4) and also for $L = 256$, between $\lambda_c = 1.65$ and 1.66 (Figure 5).

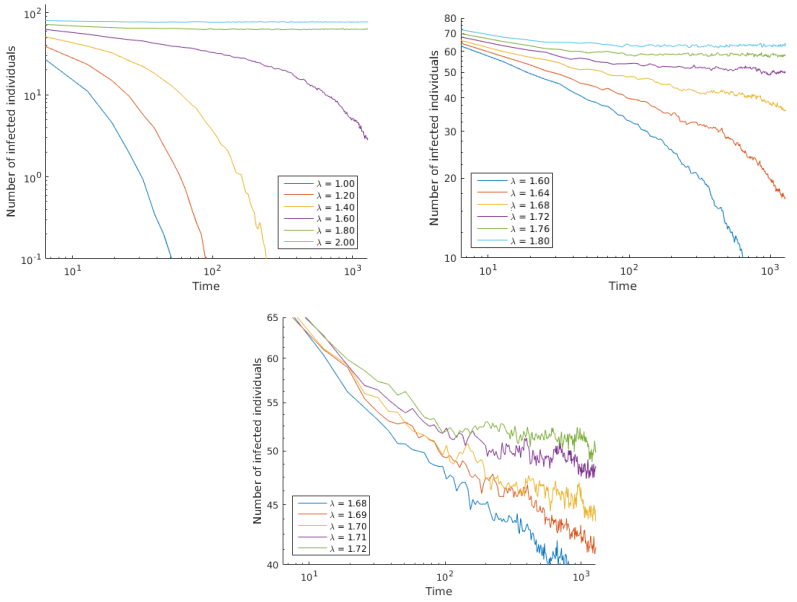


Figure 2: Simulating the contact process for $L = 128$.

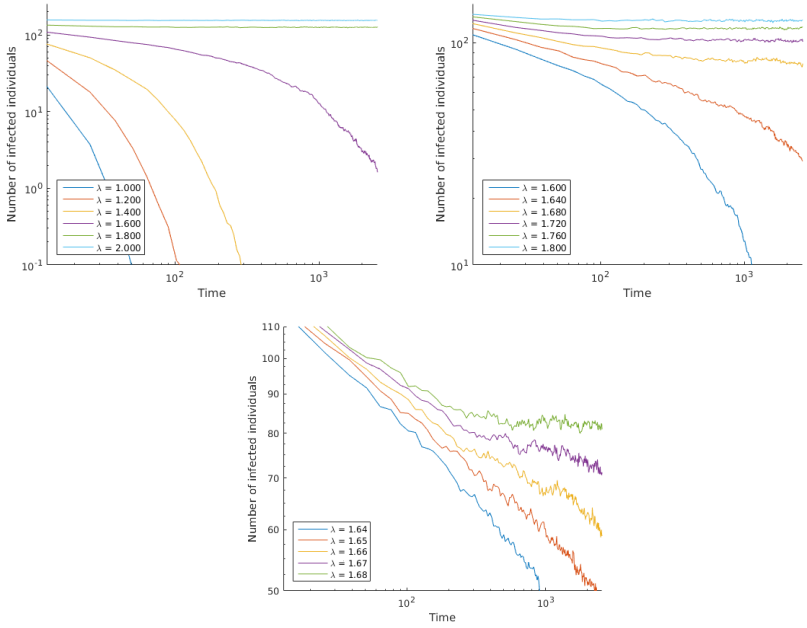


Figure 3: Simulating the contact process for $L = 256$.

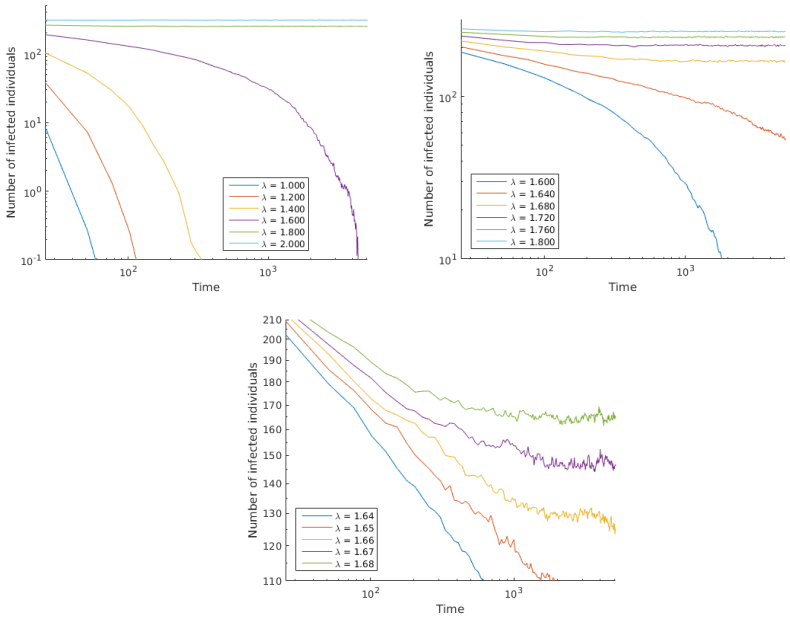


Figure 4: Simulating the contact process for $L = 512$.

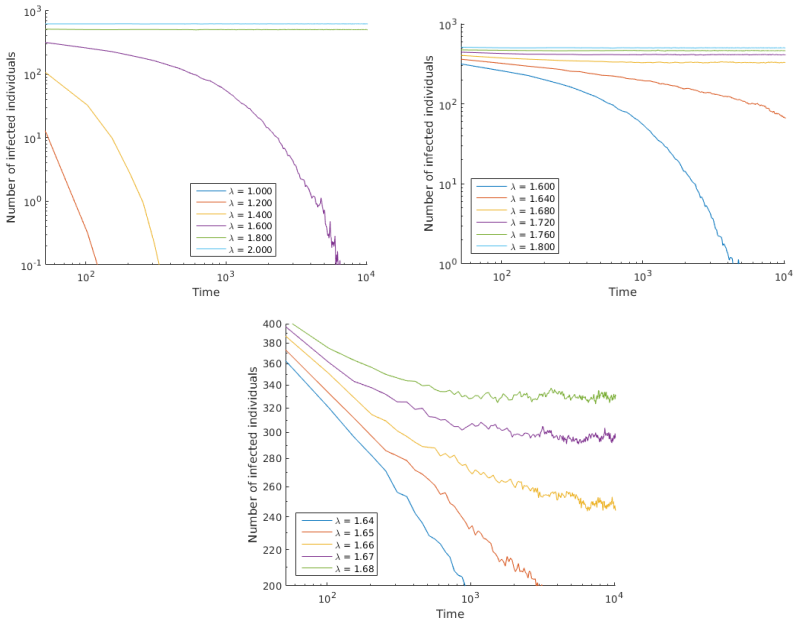


Figure 5: Simulating the contact process for $L = 1024$.

By plotting the error bars for $\frac{1}{L}$ against $\lambda_c(L)$ (Figure 6), the graph shows there is a linear fit and hence the value for λ_c as $\frac{1}{L} \to 0$ (i.e. $L \to 0$) is approximately 1.645.

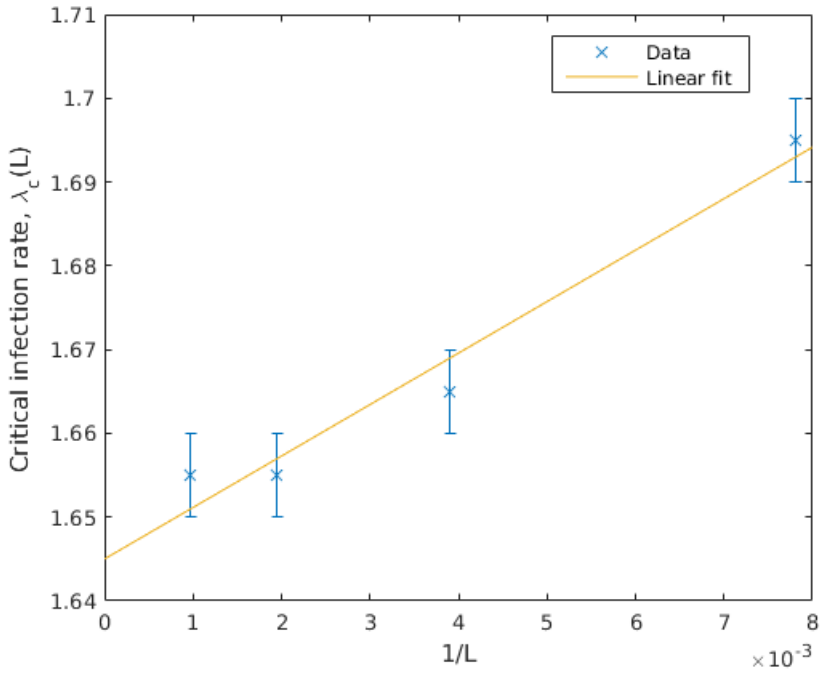


Figure 6: The critical infection rate, $\lambda_c \simeq 1.645$ for large L.

(c) In question 2, all individuals are able to infect all others, whereas in the first parts of question 3, only the two individuals adjacent can infect an individual. In deciding which individuals can infect others, a general undirected graph can establish the links of infection possible. Hence, given a graph $G = (V, E)$,the transition rate is

$$c(\eta, \eta^i) = \eta(i) + \lambda(1 - \eta(i)) \sum_{j:(i,j)\in E} \eta(j)$$

The contact process could then be simulated using this transition rate. However, if transition rates are heterogenous, since the random sequential update works by sampling at the maxium rate, there may be many instances where nothing changes after each step, which is a waste of computational time. Hence, the Gillespie algorithm may be more efficient as it takes the total rate at which events happen and so transitions occur at every step, which will be less computationally heavy for heterogenous networks.

4. Dorogovtsev-Mendes-Samukhin model

   (a) This model is a generalisation of the Barabasi-Albert model. In building a network with $N = 1000$ nodes, I start with an initial $m_0 = 5$ nodes in a complete graph and repeatedly add an additional node with $m = 5$ edges for each new node with probability of connecting to existing node i, $\frac{k_0+k_i}{\sum_{x \in V(t)}(k_i+k_0)}$ for constant $k_0 = 0, 2$ and 4. Figure 7 shows the degree distribution on a double logarithm plot for a single realisation and for an average over 100 realisations for all stated values of k_0. For all plots, for low k, the degree distribution tail is a straight line indicating that the distribution does follow a power law. For $k_0 = 0$, this is roughly parallel to a power law with exponent $-2 - \frac{k_0}{m}$ while for larger k_0 it is close to parallel, but deviates somewhat indicating a slightly different power law governs this distribution. Furthermore, for larger k, the degree distribution tail deviates from the power law, but this is explained as becuase the graphs are of finite size and so the power law cannot continue indefnitely and so it does not follow the expect pattern for large k. This could be corrected for a larger network, although would also fail for even larger k, due to these finite size effects.

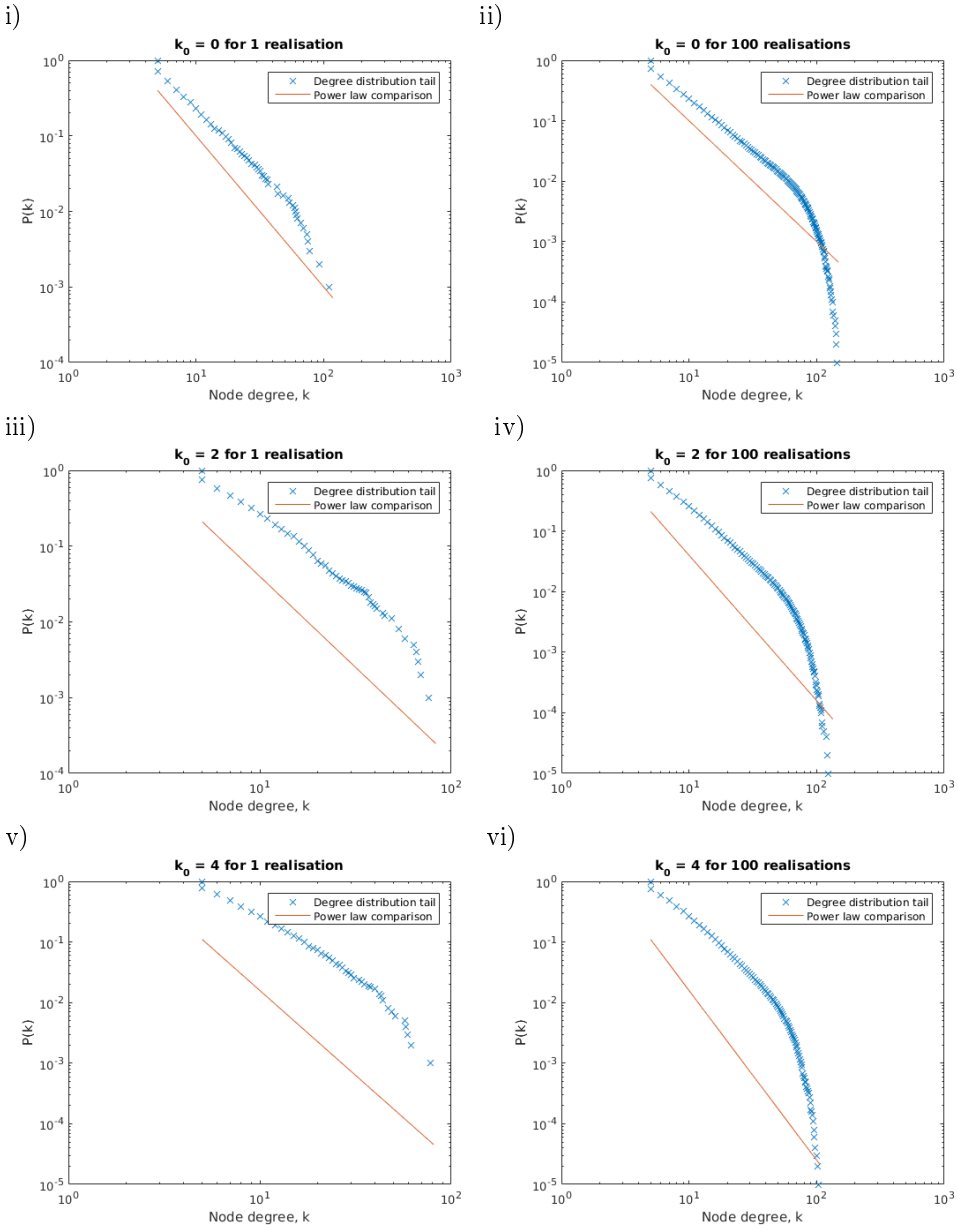


Figure 7: Degree distribution of nodes in the network

(b) The conditional degree distribution of graphs for different values of k_0 are calculated as $\mathbb{E}\Big[\sum_{i\in V} k_{nn,i}\delta_{k_i,i}/\sum_{i\in V}\delta_{k_i,k}\Big]$. Figure 8 shows that initially the graphs are disassortative, as the value of $k_{nn}(k)$ decreases with k before, in the case of $k_0 = 0$, becoming constant and

hence uncorrelated, or as for $k_0 = 2$ and $k_0 = 4$ increasing slightly for larger k, indicating the assortative property, due to he increased bias for nodes of lower degree for larger k_0. It should be noted that the larger values of k give poorer estimates as not all graphs have nodes of these degree and so there is less data on these nodes. Overall, it can be judged that the graphs are roughly constant as the absolute change in $k_{nn}(k)$ is minimal and so uncorrelated, although, in particular $k_0 = 0$ shows the disassortative property initially.

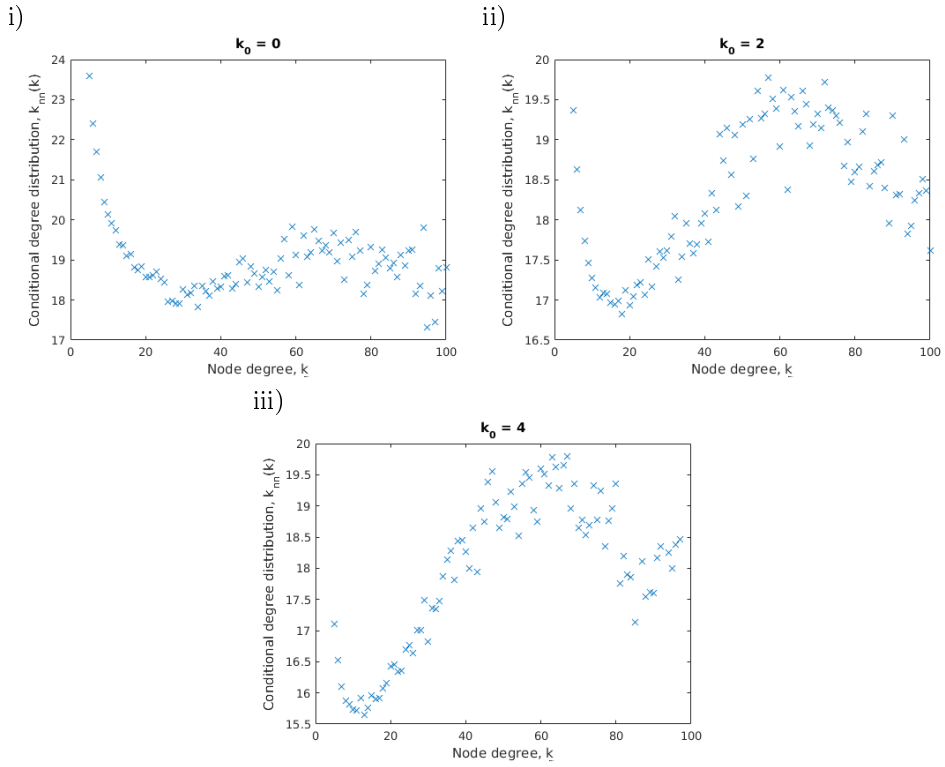
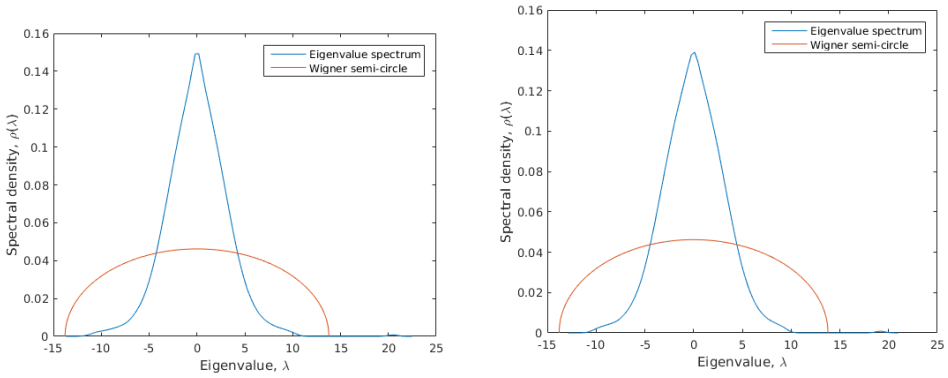


Figure 8: Conditional degree distribution of the node degree for values of $k_0 = 0, 2$ and 4.

(c) Figure 9 shows the eigenvalue spectrum of the adjacency matrices for different values of k_0 alongside the spectrum predicted by the Wigner semi-circle law. The spectrum is located in the same region as the Wigner semi-circle, but the semi-circle is a poor approximation. For larger k_0 it is slighlty improved, but not significantly. The approximation is poor because the adjacency matrices are not Wigner matrices and because in preferential networks choosing the edges is not independent, so this does not fulfill the criterion for Wigner's semi circle law.

i) ii)



iii)

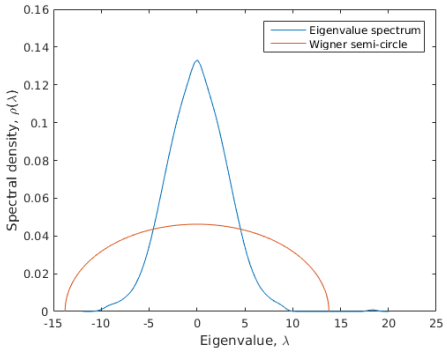


Figure 9: Wigner's semi-circle law is a poor approximation of the eigenvalue spectrum of the graphs. In i) $k_0 = 0$, ii) $k_0 = 2$, iii) $k_0 = 4$.

5. Erdos Renyi random graphs

   (a) I have generated 20 realisations of Erdos Renyi graphs $\mathcal{G}_{N,p}$, for $N = 100$ and $N = 1000$ with $p = \frac{z}{N}$, where $z = 0.1, 0.2, ..., 3.0$. The expected size of the largest two components for the graphs of differing N value are graphed against the different values of p (Figure 10) by taking the mean size of the two largest components. The plots show a similar pattern with the size of the largest compoinent increasing as edges are more likely to exist with greater p. The size of the second largest component initially increases too, but for larger p there is a decrease as the largest component begins to include almost all the nodes and so has a higher probability of linking to the second largest component. This transition occurs about $z = 1$ and and so allows percolation. The error bars are smaller for larger N as there is less variation in the larger network.

i) ii)

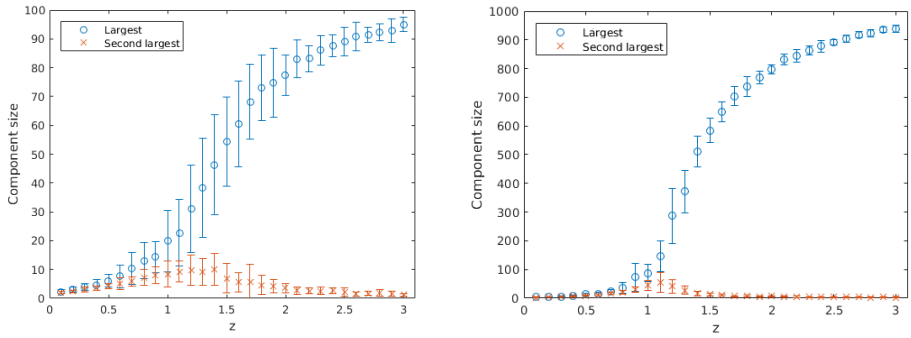


Figure 10: Size of the two largest components for i) $N = 100$ and ii) $N = 1000$.

(b) For $N = 1000$, the expected size of the average clustering coefficient for the graphs, $\mathbb{E}\big[\langle C_i \rangle\big]$, is calculated by taking the mean of the clustering coefficients for the different values of z (Figure 11). This value increases as the probability of edges increases as with more edges there will be more edges on each node.

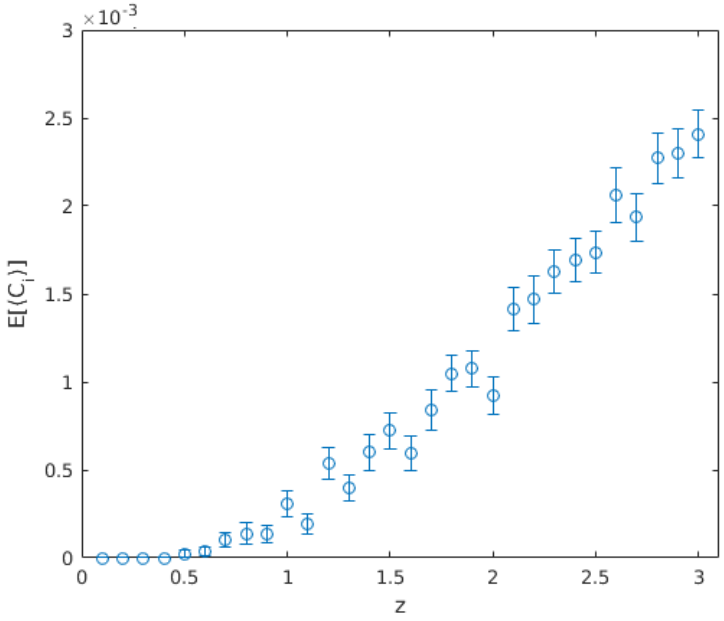


Figure 11: Expeccted value of the average clustering coefficient increases as the probability of edges increases.

(c) Now considering $z = 0.5, 1.5, 5, 10$ I have plotted the spectrum of these adajency matrices alongside the corresponding Wigner semi circles, which is suitable since the edges are chosen independently (Figure 12). In i) $p < \frac{1}{N}$ and so as expected, the spectral density deviates from the semi-circle, however, for all other values of z, $p > \frac{1}{N}$ and so the Wigner semi-circle rougly approximates the spectrum and would do in the limit $N \to \infty$. The approximation is better for larger values of z, since this will give greater values for p.

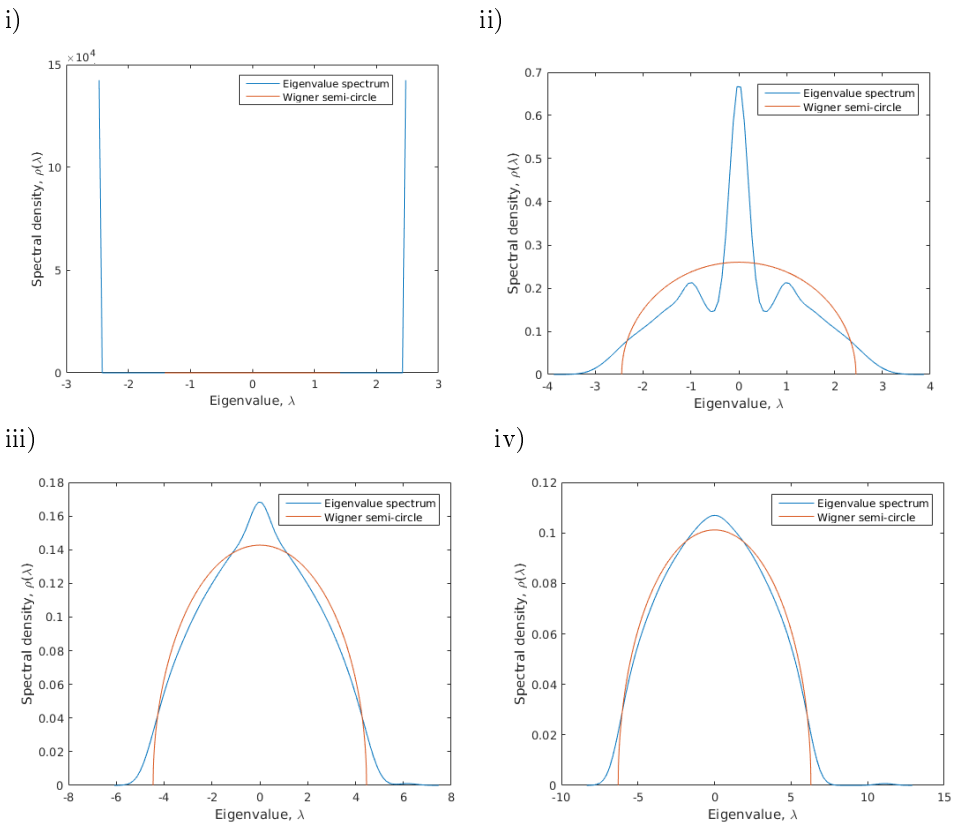


Figure 12: The eigenvalue spectrum of Erdos Renyi graphs approximates Wigner's semi-circle law for larger p. In i) $z = 0.5$, ii) $z = 1.5$, iii) $z = 5.0$, iv) $z = 10.0$.