COT 6938 Network Science - Assignment 3

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Q1

With respect to epidemic spreading, what is the SIRS model?

The SIRS, or Susceptible-Infected-Recovered-Susceptible, epidemiological model describes an infection pattern where a disease infects a native population of susceptible individuals, they recover, and after an amount of time lose their immunity and become susceptible again. Rates of susceptible, infected, and recovered individuals are described by the following equations:

$$\frac{ds}{dt} = \delta r - \beta s x$$

$$\frac{dx}{dt} = \beta s x - \gamma x$$

$$\frac{dr}{dt} = \gamma x - \delta r$$

Q2

Give an example of a network (i.e., state or draw) where the Eigenvector centrality and Katz centrality are identical.

When $\beta = 0$ and $\alpha = \frac{1}{\lambda}$ the Katz centrality becomes the Eigenvector centrality.

Q3

Give an example of a network (i.e., state or draw) where the Eigenvector centrality and Katz centrality are not identical.

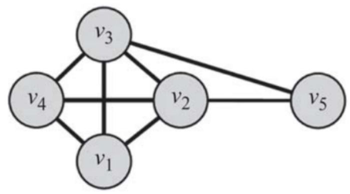

Figure 1: Network 2

$$A = \begin{bmatrix} 0 & 1 & 1 & 1 & 0 \\ 1 & 0 & 1 & 1 & 1 \\ 1 & 1 & 0 & 1 & 1 \\ 1 & 1 & 1 & 0 & 0 \\ 0 & 1 & 1 & 0 & 0 \end{bmatrix}$$ The Eigenvalues are (-1.68, -1.0, 0.35, 3.32)

Assume $\alpha = 0.25 < \frac{1}{\lambda}$ and $\beta = 0.2$.

$$KC = \begin{bmatrix} 1.14 \\ 1.31 \\ 1.31 \\ 1.14 \\ 0.85 \end{bmatrix}$$

Q4

What is Eigenvector Centrality (EC)? Why is it useful? Find the EC for all the nodes in a k-regular network (i.e, a network where all nodes have degree k).

Eigenvector Centrality (EC) is a method of evaluating importance where the influence of connections (e.g. the amount of connections each neighbor has) is considered in the importance of a node versus the mere number of a node's neighbors. It is useful in analyzing social networks where finding centrality can be tricky. For example in the Twittersphere a node can have many followers and look important, but examining the same node with EC will reveal those followers have no followers of their own and that node is not truly important.

Assume the following network where all nodes have a degree k=1:

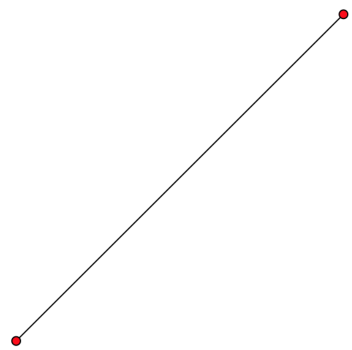

Figure 2: Both nodes have k=1

$$\lambda x = Ax$$

$$A = \begin{vmatrix} 0 & 1 \\ 1 & 0 \end{vmatrix}$$

$$det(\lambda I_u - A) = 0$$

$$det(\lambda I_u - A) = \begin{bmatrix} \lambda & 0 \\ 0 & \lambda \end{bmatrix} \text{-} \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix} = \begin{bmatrix} \lambda & -1 \\ -1 & \lambda \end{bmatrix} = 0$$

$$(\lambda^2 - 1) = 0$$
$$(\lambda + 1)(\lambda - 1) = 0 \rightarrow \lambda = \{-1, 1\}$$

The EC for all nodes is 1.

Q5

Consider a linear network with n nodes numbered 1, 2, 3, ... n. Find the Betweenness centrality nodes 1, 2, 3,....n. Give the general equation for the ith node.

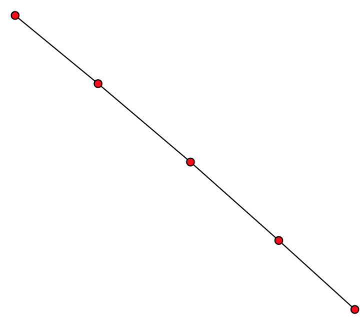

Figure 3: Linear network

Nodes at the edges of the linear network would get a Betweeness centrality (BC) of 0 as they aren't relied upon the connect other nodes in the network. From left to right down the network, Node 2 would have a BC of 1, Node 3 a BC of 2, Node 4 a BC of 3, Node n a BC of (n-1).

$$x_i = \sum_{st} (\eta_{st})^i = (i-1)(n-1) \tag{1}$$

Q6

Consider a 2-dimensional infinite discrete lattice. Let all lattice points be occupied with probability p. Draw a free-hand sketch of the average cluster size as p is increased from 0 to 1 considering i) all finite clusters, and ii) all clusters. Mark the point where phase transition occurs.

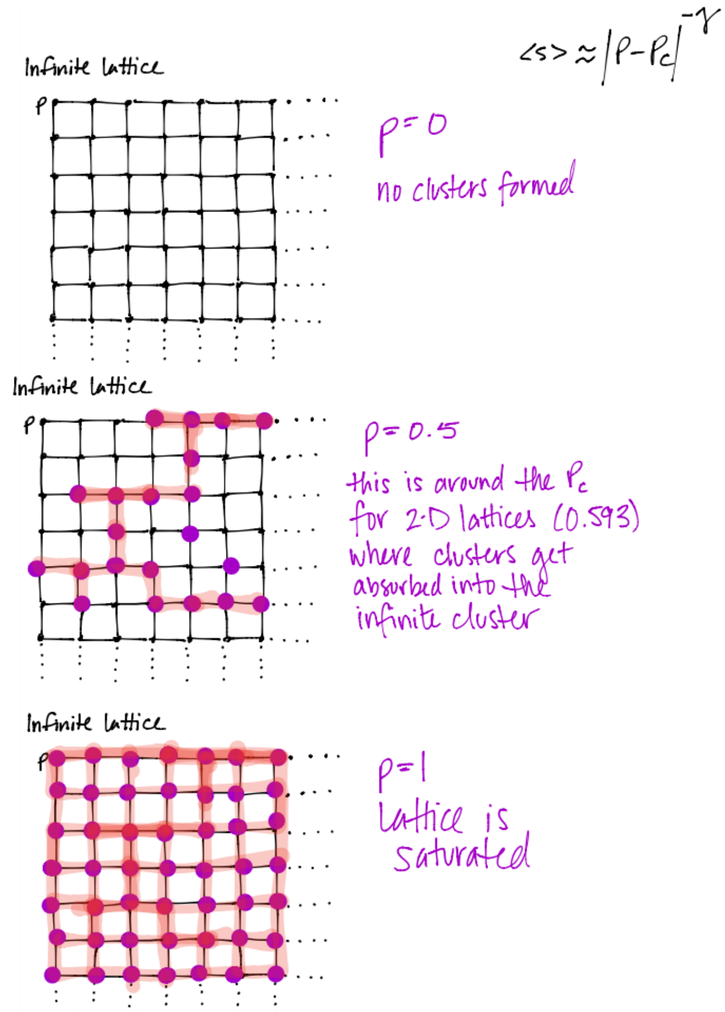

Figure 4: Infinite lattices

Q7

Discuss why scale-free networks, such as the Internet, are robust to random attacks but vulnerable to systematic attacks.

Scale free networks have a critical threshold (f_c) of nearly 1. That is, it would take the random removal of almost all nodes in order to fail. For any f $<$ f_c a giant component remains. Once f $>$ f_c, the giant component disappears. This is unlike lattice-type random structures where each node has a set number of edges. Scale-free networks, like the Internet, are very dense and thus have higher f_cs.

Q8

We assumed full mixing for all the epidemic models we studied in class. Such is not the case in reality as the infected ones might not be connected to (and therefore might not mix) to all others. How would the rate equations for the SI model change if full mixing is not assumed. Just write the modified equations for ds/dt and dx/dt. You do not have to solve them.

The SI Model is described using the following equations relating to the probability an individual will be susceptible/infected.

$$\frac{ds}{dt} = -\beta sx$$

$$\frac{dx}{dt} = \beta sx$$

In order to adjust for the fact an infected person will never fully mix with the rest of the population, $\frac{s}{n}$ must change to take into account the nodes an infected *does* come into contact with.

$$\frac{ds}{dt} = -\beta x \sum_j A_{ij}$$

$$\frac{dx}{dt} = \beta x \sum_j A_{ij}$$

Q9

Consider an undirected tree of n vertices. A particular edge in the tree joins vertices 1 and 2 and divides the tree into two disjoint regions of n1 and n2 vertices as sketched below. Show that the closeness centralities C1 and C2 of the two vertices are related by 1/C1 + n1/n = 1/C2 + n2/n. (n1 and n2 are generic – do not assume them to be 8 and 12 respectively as shown in the figure below.)

$$l_i = \frac{1}{n} \sum_j d_{ij}$$

$$C_i = \frac{1}{l_i} = \frac{n}{\sum_j d_{ij}}$$

$$C_1 = \frac{n}{n_2}$$

$$C_2 = \frac{n}{n_1}$$

$$C_1 - \frac{n}{n_2} = 0$$

$$C_2 - \frac{n}{n_1} = 0$$

$$C_1 - \frac{n}{n_2} = C_2 - \frac{n}{n_1}$$

$$C_1 + \frac{n}{n_1} = C_2 + \frac{n}{n_2}$$

$$\frac{1}{C_1} + \frac{n_1}{n} = \frac{1}{C_2} + \frac{n_2}{n}$$