Modelling Epidemics on Graphs

There are three primary parameter that are taken into consideration when modelling epidemics using graphs.

1. Contagion

   This takes into account how contagious a disease is.
   It can be measured by finding the probability that a person will get infected given that they came in contact with an infected person, or that they are neighbors with an infected node.
   It takes into account how many nodes a given node can infect at a time. Eg. A mosquito can infect only one person at a time, while a person carrying an airborne disease can infect many people at a time.
   It also takes into account how resistant susceptible nodes are to infection.

2. Strategy

   In a normal network, diffusion can be carried out in a strategic matter. However, in epidemics, a disease does not usually choose who to infect. Therefore it is random.

3. Topology

   This considers the shape of the network. It includes measuring some of the following:

   - Degree of vertices - a node with a higher degree can infect more people at a given time. Furthermore, a network that has a higher overall degree of connectivity, will have a diffusion. For example, in figure 1a, each node is connected to two or one other node, while in 1b, each node is connected to every other node. Therefore, the spread of disease will be fastest in figure 1b.

(a) Path Graph (5)

(b) Complete graph(5).

Figure 1: Complete versus path graph

   - Center of the graph - Diffusion occurs faster when it originates from the center of a network, rather than its periphery. For example, in figure 2, the spread of disease would be fastest if the disease originated from the central node, other than the nodes on the periphery. This is because the central node is connected to all other nodes, while the nodes on the periphery are each connected to one node.

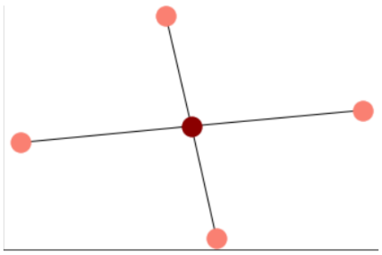

Figure 2: Star graph(5)

- Characteristic path length - this will tell us how many edges a disease will have to go through in order to infect the whole network. In figure 2, the node at the center needs only one edge to infect all the other nodes. However, if the disease originated from a peripheral node, it would take 2 edges to infect the rest of the system.
- Clustering coefficient - A disease is more likely to spread quickly within clusters, however, by blocking the link between clusters, we can prevent the disease from spreading between the two clusters. Eg. An airport is the link between clusters of people living in different countries.For example, if the two clusters in figure 3 represented two different communities, then by removing the node that bridges the two clusters together, the spread of disease would not pass between the two communities, but instead be contained within the community.

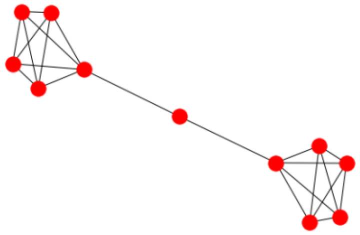

Figure 3: Two distinct clusters

Nice work! I would add hear a discussion on the SIR, SIS and the zombie model. We could describe the continuous model, and then introduce their graph versions. Here it would be a nice place to introduce the notion of small world network. You can also merge this file and the SIS model tex file