- Epidemics, SIR Model

1   Epidemics (Branching Processes) SIR Model

Susceptible, Infected, Recovered (SIR) model is an epidemiological model with applications. SIR is the model in which each individual proceeds through at most three states. First they are susceptible; then they may move to the infected state. After the infected state, they recover. If we have a contact network that captures how a disease or virus spreads, then one simple model is to assume that with probability p, an infected node infects a neighbor in a given time period (that relates to the time taken by the node to recover).

We study a highly idealized analysis of the SIR model. This approximation is often used in analysis of epidemics. The following notes are heavily based on the treatment of branching processes in the book by Easley and Kleinberg [EK10] (this treatment, in turn, is fairly standard and is similar to that in many books on branching processes and random graph dynamics).

We assume that the contact network is an infinite k-ary tree. Each infected individual attempts to infect k of its children, each with p probability. All attempts are conducted on distinct, new individuals. An infected person gets infected only once.

$R_0 = kp$ is the reproductive number of the epidemic. Infection is generally mapped as a tree, where first level has the first infected individual. Each node is connected to k distinct children, the individuals that they attempt to infect.

One of the main points of investigation is whether if the disease will die out: $P[\text{disease dies out}] = 1 - q*$. Following are the possibilities.

- $R_0 < 1$: disease dies out with probability 1.

- $R_0 = 1$: if $k = p = 1$, $q* = 1$. Otherwise, $q* = 0$.

- $R_0 > 1$: does not die out with probability $q*$.

To investigate these probabilities, consider as the following. Let X_i be the number of infected nodes. $E[X_i] = k^i p^i = R_0^i$. Total infected:

$$t[X] = \sum_i R_0^i =$$

$$= \frac{1}{1 - R_0} \qquad\qquad \text{if } R_0 < 1$$

$$= \infty \qquad\qquad \text{if } R_0 \geq 1$$

For all analyses, the graph is assumed to be tree-like, which is equivalent to the graph having a large girth (minimum cycle length). In real life, small cliques are prevalent. One way to apply these cases is to consider such cliques as atomic individuals.

One crucial point is that if $t[X] = \infty$ does not imply that $q* = 1$. Following is an analysis on $q*$.

$$q_i = Pr[\text{epidemic will not die out until level } i]$$
$$q* = \lim_{i \to \infty} q_i$$

$1 - q_i$, probability of the disease not surviving until the level i can be calculated as $1 - q_i = [(1-p) + p(1 - q_{i-1})]^k$, since for each k children of the node, disease may either not be contracted or the disease may die out in the $i - 1$ levels of the child.

$$1 - q_i = [1 - pq_{i-1}]^k$$
$$q_0 = 1$$

The applied function for this recurrence is $f(x) = 1 - (1 - px)^k$.

$$q_0 = 1 \qquad\qquad\qquad 1$$
$$q_1 = 1 - (1-p)^k \qquad\qquad\qquad f(1)$$
$$q_2 = 1 - (1 - p(...))^k \qquad\qquad\qquad f(f(1))$$

$$f'(x) = kp(1 - px)^{k-1}$$
$$f''(x) = -k(k-1)p^2(1 - px)^{k-2}$$

This shows that $f(x)$ is a concave and increasing graph if plotted for the interval $[0, 1]$ for X, since X is a probability. It will be seen from this plot that the limit of the expression is where the plot intersects with $x = y$ diagonal. For $R_0 > 1$, the plot of $f(x)$ will initially increase faster that $x = y$, hence the intersection will occur in the middle of the graph. For $R_0 < 1$, the plot will increase slower, hence the intersection will be 0. If $R_0 = 1$ and $k = p = 1$, then the plot will be $x = y$. Otherwise, the graph will initially increase with the rate equivalent to $x = y$, hence the limit will be 0.
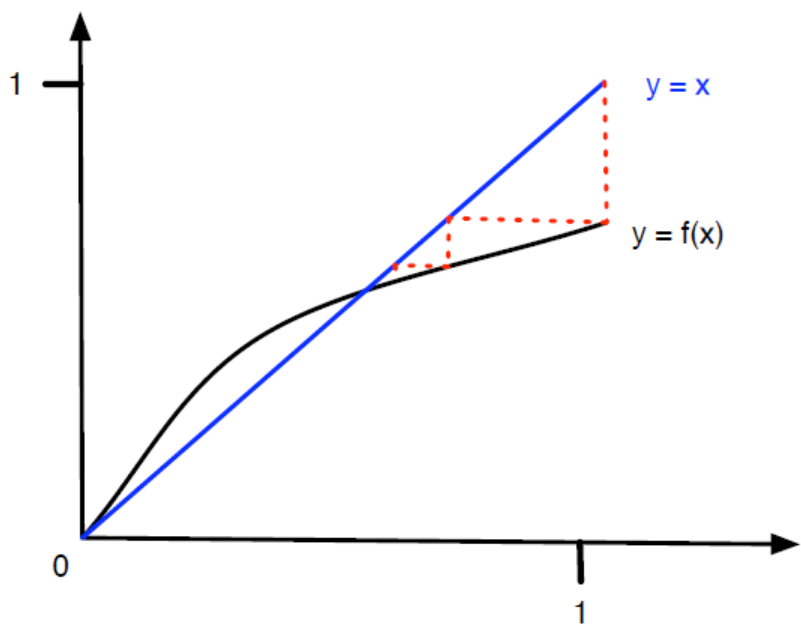
SIR model can be applied to general graphs. This application can be assumed as each infected node infecting its uninfected neighbors with p probability. This is equivalent to making a choice of probability p in the graph and assuming that these edges are carrier agents of the epidemic, hence finding the connected component from the initial node. This study, when conducted on infinite graphs, is *percolation theory*.

References

[EK10] D. Easley and J. Kleinberg. *Networks, Crowds, and Markets: Reasoning About a Highly Connected World*. Cambridge University Press, 2010.