Lecture - 31

Thursday, 26 October 2016 (15:20- 16:10)

Epidemic Modeling (Using Random Variables)

There has been a large number of contagious diseases attacking our world from time to time. Black death in late 1340s have killed more than one third of the Europe's population. Bubonic plague, cholera, Malaria like diseases turned epidemic many number of times. More recently, Ebola in 2014 raised a worldwide alarm. Currently, Chickengunya has become a severe problem in the national capital. It is the worst outbreak in the last 6 years. Scientists are increasingly being concerned about the prediction of epidemics. This prediction requires one to understand the spreading pattern of the contagious diseases. In this lecture, we apply our knowledge of probability, random variables and expectations to develop the most basic model of epidemic spreading.

1 Model For Epidemic Spreading

The two most important factors which determine the course of an epidemic are

- Contagiousness of epidemic. A disease like HIV which requires a close proximity may be less contagious than a disease like common cold whose virus can even transmit to you from a person who is sitting next to you in a plane. We represent this probability as p. Given two connected individuals, if one is infected, the probability of other getting infected is p.

- The network structure. A city where people rarely meet each other has less chance of inviting an epidemic than a city where people frequently communicate with each other.

2 The Framework for the Problem

In our analysis, we consider the most basic network structure. We consider the network in the form of a tree, where every node except the leaf nodes have k children. As specified before, the probability of infection transmission across every edge is p. This has been shown in Figure 1.

Given the network and the probability of the disease transmission, our aim is to determine whether the disease will convert into an epidemic or not. We define two terms for that. Let q_n be the probability that the disease persists till n levels i.e. there is at least one infected individual at the level n. $q^* = q_n(n \rightarrow \infty)$.

We show that

$$If \ pk < 1, \ then \ q^* = 0 \ and \ If \ pk > 1, \ then \ q^* > 0$$

3 Recursive formulation

We divide an event $*$ as : Root node infects first of its child and the infection reaches to level n with the help of this child.
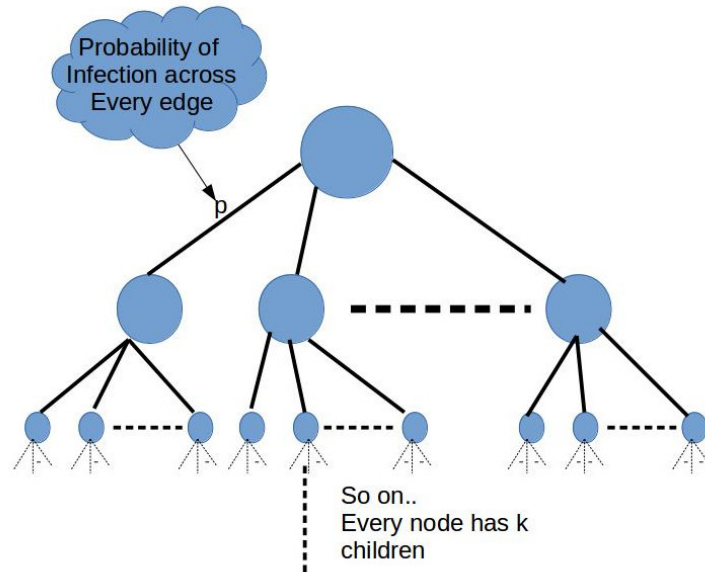
Fig. 1: The network is considered as a tree

$$Pr(*) = p \times q_{n-1}$$

The root passes the disease to its first child with a probability p. Now this child can be visualised as a new root, and the disease reaches n levels down if it reaches $n-1$ levels down from this child.

Please note that there are k such $*$ events. The disease fails to reach the level n is all of these events fail.

Hence, $1 - q_n = (1 - p \times q_{n-1})^k$

$q_n = 1 - (1 - p \times q_{n-1})^k$

$q_0 = 1$, our aim is to find $q_1, q_2, ..., q_n, ...q^*$

Consider the function $f(x) = 1 - (1 - p \times x)^k$

One can observe that to find the value of $q_1, q_2, ...,$ one should figure out the values of $f(1), f(f(1)), f(f(f(1))), ...$

Let us investigate function $f(x) = 1 - (1 - p \times x)^k$.

 – The derivative of the function is positive which shows that the function is monotonically increasing.

– The derivative of the function at $(0,0) = pk = R0$, the reproductive number.

– $f(1) = 1 - (1-p)^k$, which is less than 1.

3.1 Case 1: $R0 > 1$

Please note that when $R0 > 1$, the slope of the function $f(x)$ is greater than 1. Hence, the curve for this function moves above the line $y = x$. We also know that the value of $f(1)$ is less than one. So, there exists a point where the two curves $f(x)$ and $y = x$ intersect. This has been shown in Figure 2.
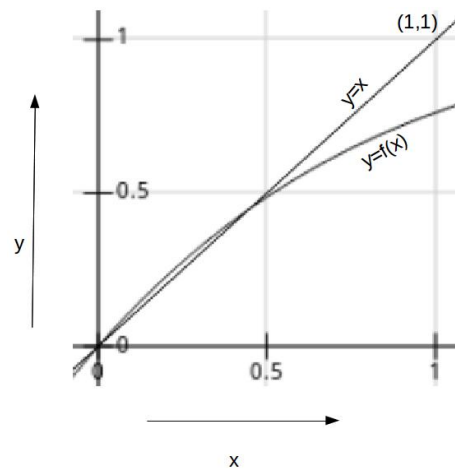

Fig. 2: $f(x) = 1 - (1 - 0.25x)^5$

To find the value of $f(f(f(.....f(1))))$, we start from the point $(1,1)$. Moving vertically downwards, we get the point $1, f(1)$. Moving horizontally left we get $f(1), f(1)$. Moving down, we get $f(1), f(f(1))$. Moving right we get $f(f(1)), f(f(1))$. This has been shown in Figure 3. We keep moving down and right in the same way. Finally, we see that the process converges at the intersection point, which has value greater than zero. This shows that when $R0 > 1$, q^* is positive.

3.2 Case 2: $R0 < 1$

Please note that when $R0 < 1$, the slope of the function $f(x)$ is less than one. Hence, the curve for this function moves below the line $y = x$. We also know that the value of $f(1)$ is less than one. So, there is no point where the two curves $f(x)$ and $y = x$ intersect. This has been shown in Figure 4.

To find the value of $f(f(f(.....f(1))))$, we start from the point $(1,1)$. Moving vertically downwards, we get the point $1, f(1)$. Moving horizontally left we get $f(1), f(1)$. Moving down, we get $f(1), f(f(1))$. Moving right we get $f(f(1)), f(f(1))$. This has been shown in Figure 5. We keep moving down and right in the same way. Finally, we see that the process converges at the origin. This shows that when $R0 < 1$, q^* is zero.
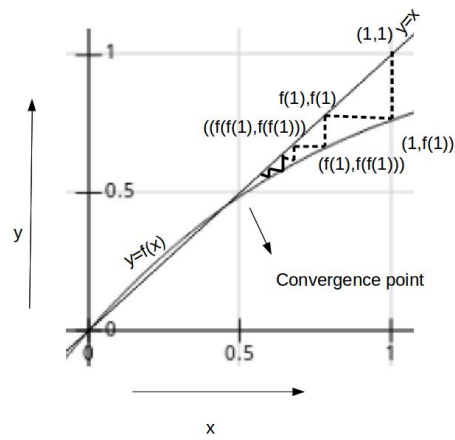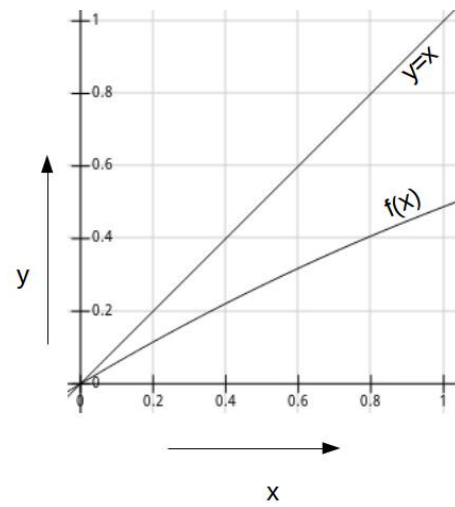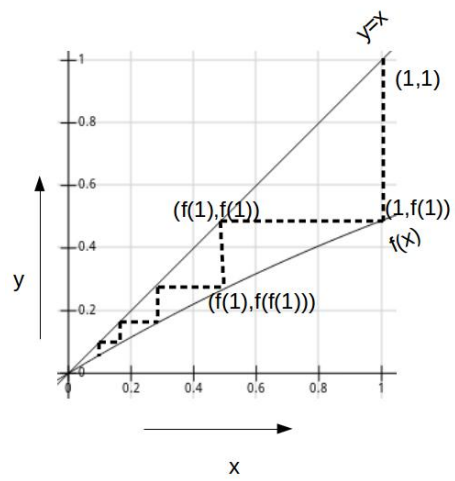
Fig. 3: Finding $f(f(...f(1)))$

Fig. 4: $f(x) = 1 - (1 - 0.2x)^3$

Fig. 5: Finding $f(f(...f(1)))$