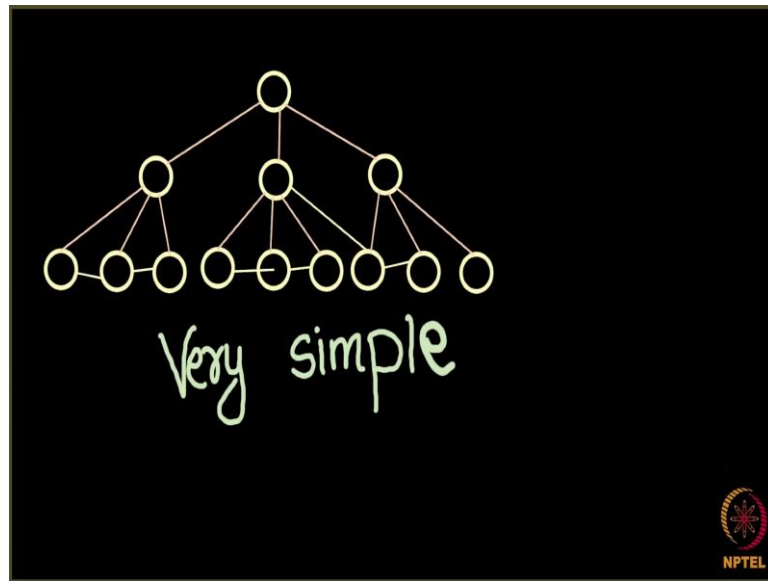


Social Networks
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Rich Get Richer Phenomenon – 2
Lecture - 133
Modeling epidemics on complex networks

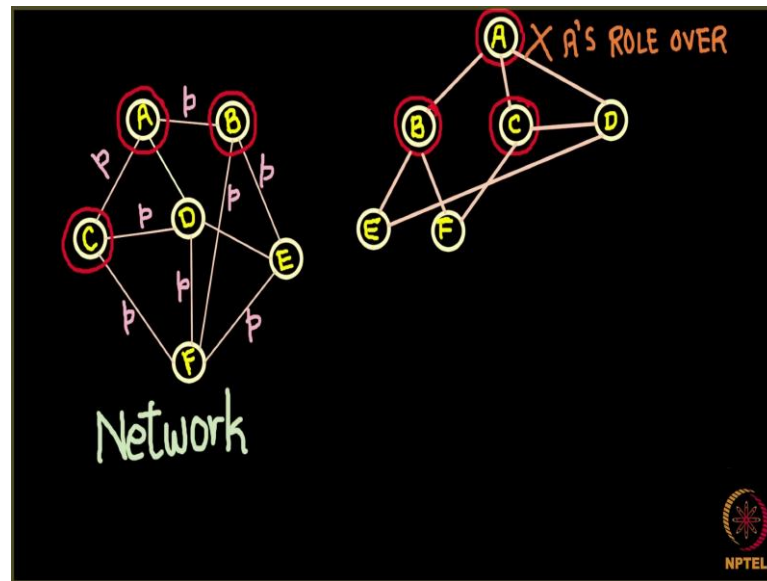
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Till now we have looked at the simplest epidemic model, we will be considered the simplest network and the network was in the form of a tree something like this simple. Now, we know that a real world network do not look like this, a real world networks they look complicated and rather if you do remember the lectures from the previous weeks you will say that a networking never look like this, there should be some triadic closure here right.

So, if this guy over here is a friend with both of these there is a good chance, that both of these are friends, both of these are friends and maybe the this person here can be a friend with this one So, networks actually look very complicated something like this. How can we modify a most simple branching process what we did before for a real-world networks which are not trees? That we are going to see in this chapter.

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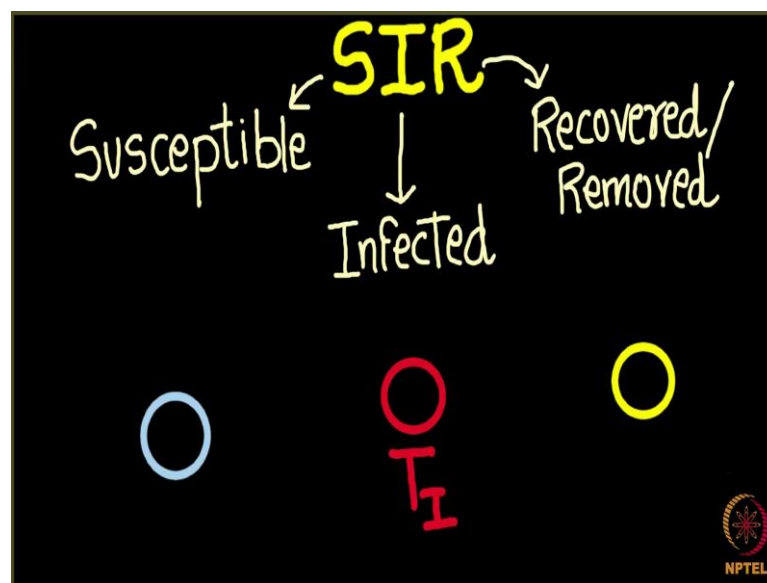
Let us say that we have a complicated network, not a tree. By complicate it what I mean is not a tree which looks something like this I have some nodes A, B, C, D, E, F here and every edge has a probability p of transmitting the infection as before. So, everything is same every edge is having a same probability. The only differences, in the layout of the network instead of the tree we have taken a proper network.

Let us say A is connected to D also here and the network look something like this. Now, I want to simulate the spreading of a contagion here how do we do that? Say initially A is infected and now A has three neighbors B, C and D and it tries to infect each of these again independently with the probability p . So, again here are three independent processes, we can flip coin for the edge A to C and if head comes, we infect C. Similarly, we can flip a coin for the edge A to D and if a head comes, we mark D as infect it and same thing we can repeat for B. So, maybe A is able to infect B and C.

How can I layout? Layout in the form of a tree, what is happening here? Let us see here is A, and A was having three neighbors B C and D and A was able to infect B and C. And now you see as role is over. I will discuss more about it. What I mean here in a branching model also at this step A's role was over A go to one chance to infect and A infected B and C. Now, it is B and C's turn now B and C will go ahead and see which of their neighbors they can infect; why so?

It should be so right because if A keeps getting a chance rather if every node keeps getting a chance to infect their neighbors at ever time period then this entire network will get infected. And that is not what happens in a real world also right you get infected from some disease and then you remain infected for some period of time. During this time you keep infecting other people and after that you might recover from the disease. So, we need a better model here let us make this picture clearer. So, what will be doing now is we will be looking at a very realistic diseases spreading model branching process was something very theoretical and very simple.

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Now, we are moving little bit more towards what happens in the real world and we are going to study a brand-new model not for the tree networks, but for any kind of networks and the model is SIR epidemic model. Why is it called SIR epidemic model is because it tells you, it talks about three life cycles of an infection.

So, whenever you get infected from a disease, you mainly pass through three phases. The first one is the susceptible, susceptible is the one where you are happy living your life you are not infected from any disease, you are not infected from the disease. And the second stage is infected, so you come in contact with somebody who is infected and you get infected and the last one is recovered or removed.

Recovered or removed is something that needs to be taken very seriously here, something which is very important. What do we mean by the recovered and removed

here is what makes this model the, what makes this model spatial this SIR model it is used for two kinds of diseases, first kind of disease is something which is the terminal illness. What happens in the case of a terminal illness is patient ultimately dies away. You are susceptible and then you get infected and finally, you will be killed by the disease and when you get killed by the disease you will be removed from the network.

Or a second case; second case is the diseases something like that which can occur to you only once in your lifetime. Something like measles, you are susceptible and then you get infected from measles. Now what will happen when you get infected from measles is your body will develop a lifetime immunity against this disease and you are never going to catch this disease again that time, we say that you are recovered. You are never going to go from infected back to the susceptible this disease is going to happen to you only once in your lifetime. So, either you will gain a permanent immunity, or you will be killed by this disease that is our SIR epidemic model.

In our next lecture we will see how can we simulate this model on an actual network; we are going to do that the forgoing. So, we are having. So, a node can here exist in three states as we saw and exactly one state at a time you cannot be susceptible and infected at the same time. And infected and recovered both at the same time you can be only in one phase at one time.

If you are susceptible I am going to show you by a blue circle, if you are infected I am going to show you by an infected circle I will tell you what this T_I is and if you are recovered or removed I am going to show you by yellow circle. So, yellow circles can be ignored from a network because they have recovered and removed, they have nothing to do with the spreading of the disease now.

What is this T_I here? T_I here is again something very logical what is T_I ? When you get infected there is some time period for which you remain infected it can be one day, two-day, one week, two weeks, during this time only you are going to infect other people. So, T_I define the time for which you are going to remain infected. So, maybe for the flu this time can be let us say three days. So, during these three days you will be infected with flu and you will keep infecting other people.

If you look at this figure here, where I said that here is A, and then A infected these two people B and C. And then we said that as role is over and these are B and C were going

to further infect other people. Can you tell me what is the value of T_1 here? So, T_1 the time for which you are infecting here is 1 right because it was 2, after A infected B and C A will again get a chance to infect once more, we will look at it in detail just wanted to tell you the use of T_1 . So, this is it this is an SIR model and in our next lecture we will see that how we can simulate this SIR model on a given network.