Lecture 6 – Epidemics

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1 Continuous epidemics, "logistic model"

Pierre Francois Verhulst published in 1838 the equation,

$$\frac{dP}{dt} = rP(1 - \frac{P}{K})$$

when N(t) represents number of individuals at time t, r the intrinsic growth rate and K is the maximum number of individuals that the environment can support. In a paper published in 1845 he called the solution to this the logistic function, and the equation is now called the logistic equation.

Lemma 1. *If dynamic system y satisfies,*

$$\frac{dy}{dt} = \frac{c}{f(y)}$$

Then for any t, *we have* $F(y(t)) - F(y(0)) = $ ct *where F is a primitive function of f*

Proof. Let us assume function $h : t \longmapsto F(y(t))$. then we can get $h(t) - h(0) = c(t - 0)$. The derivative of the function h is then,

$$\frac{dy}{dt} \times F\prime(y(t)) = \frac{dy}{dt} f(y(t)) = c$$

$\square$

This lemma can be used to solve the equation above:

Assume for simplicity that $r = k = 1$ then we have $\frac{d}{dt}P(t) = P(t)(1 - P(t))$. So it means $\frac{dP}{dt} = P(1 - P) = \frac{1}{f(P)}$. And change the place between P(1-P) and f(P), it will be $f(P) = \frac{1}{P(1-P)} = \frac{1-P+P}{P(1-P)} = \frac{1}{P} + \frac{1}{1-P}$. Now we know P satisfied lemma with $f(y) = \frac{1}{y} + \frac{1}{1-y}$. And $F(P(t)) - F(P(0)) = t$ where F primitive of f, so that

$$F(P) = \int_1^P \frac{1}{x} + \frac{1}{1-x} dx = \ln(P) - \ln(1 - P) = \ln(\frac{P}{1-P})$$

From this equation, now we know $ln\frac{P(t)}{1-P(t)} - ln\frac{P(0)}{1-P(0)} = t$. Remove each log in the equation, then we get $\frac{P(t)}{(1-P(t))} / \frac{P(0)}{(1-P(0))} = exp(t)$. Move $\frac{P(0)}{1-P(0)}$ to the right and substitute $\frac{P}{1-P}$ to A then $P = \frac{A}{1+A}$. From this, we will get

$$P(t) = \frac{exp(t) \cdot \frac{P(0)}{1-P(0)}}{1 + exp(t) \cdot \frac{P(0)}{1-P(0)}} = \frac{P(0)}{P(0) + exp(-t) \cdot (1 - P(0))}$$

As it was mentioned before, this equation is called logistic function and it is a common sigmoid curve and it can model the "S-shaped" curve of growth of some population P.

1.1   Epidemic Model 1 : S → I

In this Epidemic Model 1, we can assume two kind of nodes. Some of them are not being infected which means susceptible. Others are infected. These infected nodes stay this infected state and will not be changed to uninfected state. And these nodes continue to infect everyone. In term of growth of infected population, reproduction rate is a function of the infection probability β and the size of the infected population (if there are twice more nodes infected, there are twice more chance for another remaining node to become infected). Resources mean that non-infected nodes in the model: when they become small then the growing rate of the infected population becomes smaller.

In other word, if we denote by $y(t)$ the number of infected nodes, and by n the total population, this epidemic follows the logistic equation:

$$\frac{dy}{dt} = \beta xy = \beta y(n - y), \text{ which leads to } y(t) = \frac{y(0)n}{y(0) + (n - y(0))exp(-\beta nt)}$$

1.2   Epidemic Model 2 : S ↔ I

In this Model, nodes which are infected before can be changed their state to the uninfected. It means we assume that infection is temporary and recurrent. So an infected node goes through an infectious period and it will be back to the previous state(susceptible) after certain time period.

With similar notation this Model 2 follows a differential equation that is similar except for an additional decrease term of the infected population y $(-\gamma y)$:

$$\frac{dy}{dt} = \beta y(n - y) - \gamma y$$

Hence, if β is greater than γ, endemics will be reach to $1 - \gamma/\beta$. However, if γ is greater than β, endemics will dies.

1.3   Epidemic Model 3 : S → I → R

This Model 3 is similar to 2 in that it stays in an infected state for some period time. What is different is that, after this period is over, infected nodes become again susceptible in Model 2, while in Model 3, nodes become vaccinated or dead which mean that they are removed from any future evolution.

Evolution follows again differential equations, similar to the above, with a couple of differences: First, since we have three possible states the number of susceptible nodes is exactly $n - y$. Let us hence denote by $x(t), y(t)$ and $z(t)$ respectively the number of nodes that are susceptible, infected and removed. If we assume that the follow a similar fluid flow evolution we have:

$$\frac{dx}{dt} = -\beta x \cdot y$$

$$\frac{dy}{dt} = \beta x \cdot y - \gamma y$$

$$\frac{dz}{dt} = \gamma y$$

In that case, the limit regime is characterize, first, by having all Infected individuals disappear (hence $\lim_{t \to \infty} y(t) = 0$. $x(t)$ and $z(t)$ converges each to a limit (whose sum is n). If we assume that initially we

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have $x(0)$ susceptible nodes and no removed nodes, then the limit satisfies

$$\lim_{t\to\infty} z = z_\infty \text{ where } n - z_\infty = x(0)\exp\left(-\frac{\beta}{\gamma}\cdot z_\infty\right)$$

1.4   Continuous epidemics: Summary

Type	Outcomes
S $\to$ I	Everyone infected
S $\leftrightarrow$ I	Depends on infection / recovery rate
S $\to$ I $\to$ R	No infectious node

First thing to remember is that each type of epidemics follows a differential equation. Initial conditions of this problems always have positive fraction already infected. This is because if a negligible fraction of nodes are initially infected, in this fluid flow limit probability of any infection becomes negligible and the system simply remain static.

The outcomes of epidemics depend on type of epidemic models. The speed of the epidemics is always given by the solution of the differential equation, it is typically exponential in the time t.

There is no topology in this continuous epidemics because anyone can infect to anyone in this model.

2   Discrete epidemics, "graph"

Discrete epidemics uses Graph, G = (V, E). It can be simply thought as a concrete graph by connecting everyone to everyone. However, generally we do not assume this case. In this graph, infection only spreads along edges of a given graph. Thus, some node infects its neighbor nodes and those nodes infect their neighbor nodes. But there is no arbitrary infection between nodes. There are challenges to Discrete epidemics. First, can a fraction be infected in a large graph? As graph size is increase, it should be considered that the limitation of the positive fraction of the graph infected or not. Second, What if some individuals are immune? Third, What is the speed of evolution of epidemics? It means that we saw everything is growing exponentially. But it can not be sure in the case of the graph. Fourth, How does it depend on the properties of the graph?

2.1   Epidemic Model 1 : S $\to$ I

As we know in the continuous epidemics, Model 1 is that anytime node gets infected then it stays infected. For example, we may think about the spread of news or innovation in the network. And there are two cases in this model: Broadcast and Gossip

Model 1 : Broadcast
Every time node become infected at time t infects all neighbors in $t+1$. Breath first search will be the one of the examples in this model. Thus, all nodes are infected within time D = diam(G) in the graph. And this is an extreme simple case in Epidemics.

Model 2 : Gossip
Broadcast has more constraints in the model and gossip is more general case. Node infects each neighbor with a given rate β. And each individuals will try to infect their neighbors continuously with a certain

rate β. Of course, at the certain time in the process, it can show all neighbor nodes are infected in some time. If there are large number of neighbors, it will take time but finally all neighbors will be infected. Eventually all nodes are infected within $O(D/\beta)$.

2.2 Epidemic Model 2 : S $\leftrightarrow$ I

Epidemic Model 2 has two cases. First one is neighbor contamination that node infects its neighbors. Second one is neighbor recovery. In this case, node become susceptible again which means it become non-infected status. Each of these nodes have a value X, we denote that $X_u = 1$ when node u is the infectious status and $X_u = 0$ when node u is the susceptible status. Node u follows the rate $\beta \cdot \sum_{v \in N(u)} X_v$ when u becomes infected. And node u recovers with rate $\gamma = 1$.

In a finite graph, after some period time, there will be time that all nodes eventually recover, it means that all nodes become susceptible. It happens because even if every node is infected, it is not a stable state and because $(X_u = 0 \ \forall u \in V)$ is the only absorbing state. It is a very small possibility to happen but it is possible when the model run in the infinite amount of time. On the other hand, it can different on infinite graphs such as lattices or trees. There is one question. Can we recover fast from an epidemic? For example, there is an epidemic virus going on the Internet then it is important to know how fast this virus going to remove.

Theorem 2. $P[X(t) \neq (0, ..., 0)] \leq C\sqrt{N} \exp(t \cdot (\beta\gamma - 1))$

where $\gamma(G)$ is largest eigenvalue of G's adjacency matrix and C is the square root of the number of initial infected population

The adjancency matrix of a graph with n nodes is a $n \times n$ matrix defined as $A_{u,v} = 1$ if and only if (u, v) is an edge in the graph (and 0 otherwise).

○ $\beta\gamma > 1$ then it does not say anything because $\beta\gamma > 1$ will be positive then exponential in the theorem goes to infinity as t grows and the inequality is trivial.

○ $\beta\gamma < 1$ then infection will be slow enough by given a value then the theorem going to zero extremely fast.

Some examples of value of $\gamma(G)$ for models of graphs are: - Complete graph : $\gamma(G) = n - 1$
- Hypercube : $\gamma(G) = log_2(n)$
- Uniform random graph : $\gamma(G) \approx (n - 1)p$, if we assume that $np = \omega(logn))$

2.3 Epidemic Model 3 : S $\rightarrow$ I $\rightarrow$ R

Model 1 : Single infection attempts
Whenever a node is infected, the node has one attempt to infect for every edges independently. After those attempts, the node will be removed. And it has the probability β for the infection. There are many names for this model. One of them is "Independent cascade model" and other one is Reed-Frost epidemics. Latter one is named so because those two people introduced this model.

Model 2 : Random infectious period (normalized)
This model is a natural generalization of what we have talked. There are many similarity between Model 1, 2 such as probability to spread is β but there is a significant difference in dependencies between fractions

of neighbors. It is difficult to apply independent assumption to this model because one infection can be co-related to the other nodes.

There is a common thing in these two model. There will be eventually no infectious nodes and fraction removed. The main problem of this model is the size of the removed fraction in the end.

Theorem 3. *Assuming $\beta\gamma < 1, E[|Y(\infty)|] \leq C\sqrt{\frac{N}{1-\beta\gamma}}$*

where $\gamma(G)$ is largest eigenvalue of G's adjacency matrix and C is the square root of the number of initial infected population

○ If $\beta\gamma < 1$ and $C = o(\sqrt{N})$, removal is only negligible fraction.

2.4 Discrete epidemics: Summary

Type	Outcomes
S → I	Everyone infected
S ↔ I	No infectious nodes
S → I → R	No infectious node

In this discrete epidemics, there are a collection of process between states. Initial condition is a small set of infected nodes that are a typically constant size. Outcomes are generally trivial because there are always everyone infected or no infectious nodes. However, important thing is speed or span depend on graph topology.

3 Epidemic algorithms

The key result of the research conducted in 1987 about epidemic algorithms, rumor spreading and gossip shows that these are not maintaining fixed communication topology and these contact a node uniformly and these spread if one node has a copy. Telephone network is the similar example of this situation. Someone call someone to tell a rumor. Then that person talk to someone. Then some point, many people receive the rumor. According to the same paper in 1987, the research shows the equation for the rumor spreads. $S_n = (1 + \frac{1}{ln2})log(n) + O(1)$ in probability.

Compare this gossip to the optimal case. In the case of binary tree, it takes $O(log(n))$ time by using $O(n)$ message. Thus, it seems to be optimal in both ways but it is prone to failure. In the case of gossip, it takes $O(log(n))$ time with $O(nlog(n))$ messages. And it is possible to improve $O(nlog(n))$ but not so much. In fact, uniform gossip requires at least $\omega(n)$ messages, and $\Omega(nloglong(n))$ if there are no addresses are kept.

Now let us restrict the condition that everyone can connect to everyone. In other words, what if the communication between nodes is constrained? As an example, let us draw a graph between gossiping nodes $G = (V, E)$ such that a node u can contact v only if (u, v) is an edge in E. Main question in here is which graph allows fast gossip dissemination. Also how does gossip dissemination compare to optimal?

3.1 Effect of network topology

Let us denote by $S(t)$ is the set of nodes in V that have received information at time t. The dynamics follows from $S(0) = v$ and at any time t, node u is contacting a single node v which is chosen according to a probability P_{uv}. When u contact v, if either $v \in S(t)$ or $u \in S(t)$, then $v \in S(t+1)$ and $u \in S(t+1)$.

Let us introduce:

$$T_{spr}^{one}(\varepsilon) = \sup_{v \in V} \left(\inf\{t : Pr(S(t) \neq V | S(0) = v) \leq \varepsilon\} \right)$$

We call it the one message dissemination time, and it is, for all starting point v an upper bound on the time needed for the event $S(t) = V$ to be "big" (at least with probability $1 - \varepsilon$).

Our main result is as follows: If P is irreducible and symmetric, then

$$T_{spr}^{one}(\varepsilon) = O(\frac{logn + log\varepsilon^{-1}}{\Phi(P)})$$

where

$$\Phi(P) = min_{S \subset : |S| \leq n/2} \frac{\sum_{i \in S; j \in S^c} P_{ij}}{|S|}$$

First term $log(n)$ is a slowly growing function of the size of network (so that large network can still disseminate information very fast to many nodes) and the second term $log(\varepsilon^{-1})$ is something that dependent on precision required before assuming that all nodes are reached.

The meaning of $\Phi(P)$ can be thought as follows. Considering the weighted graph where each edge (u, v) receives a weight $P_{u,v}$. Then $\Phi(P)$ is considering, for any subset S of V, the probability that a node in the subset contact a node that is not in the subset. This probability is divided by the size of the subset S. If S is very large, then this probability will be limited by the very small number of nodes not in S, so that we limit subset S to less than half of n.

Sketch of the proof For the full version, please see the next scribing.

There are two phases to proof it. First one is from $S(t) = \{v\}$ to $L - 1$. And second one is from $L = inf\{t | \#S(t) > n/2\}$ to $\#S(t) = n$. And ingredients of this proof are a. study evolution of conditional expectation $E[\#S(t + 1) - \#S(t) | S(t)]$, b. uses Markov inequality $(X \geq 0 \rightarrow P[X \geq a] \leq E[X]/a)$, and c. need to rewrite as super-martingale for phase 1. And proof is starting from c because of its simplicity. By considering $S(t)^c$, assume $t = 0, S(0)^c \leq n/2$. Showing any v that I choose, $time \leq cst \times \frac{logn + log(\frac{1}{\varepsilon})}{\phi(P)}$ with Probability, $1 - \frac{\varepsilon}{2n}$.

$$E[|S(t)|^c - |S(t+1)|^c | S(t)] \geq \sum_{j \in S(t)^c} \sum_{i \notin S(t)^c} P_{ji}$$

In this conditional expectation, we are looking for what happen to the next step.

$$E[|S(t+1)|^c S(t)] \leq |S(t)|^c [1 - \frac{\sum_{j \in S(t)^c} \sum_{i \notin S(t)^c} P_{ji}}{|S(t)^c|}] \leq |S(t)|^c (1 - \varphi)$$

If this equation is applied recursively,

$$E[|S(t)|^c | S(0)] \leq (1 - \varphi)^t \frac{n}{2} \leq \frac{n}{2} exp(-t\varphi)$$

We know the well known formula, $e^x \geq 1 + x$ and $e^{-x} \geq 1 - x$ and once we know,

$$E[S(t)^c] \leq \frac{n}{2} exp(-\varphi t)$$

Then it can be showed that, $P(S(t) \geq 1) \leq \frac{E[S(t)]}{2}$ This is also equal to, $P(S(t) \neq v) \leq \frac{n}{2} exp(-\varphi t)$
Thus, if choose t for a particular value, $\frac{ln(2)+2ln(n)+ln(1/\varepsilon)}{\varphi(P)}$. It can be showed that t is applied to previous fomular.