Epidemic Spreading Models

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1 Introduction

The understanding of epidemic spreading can help us fight against health crises like COVID-19. In this paper, We use only mathematics to derive some meaningful epidemic spreading models. With different assumptions, we derive different models answer the same question: How does the infected population grow? First, we develop two continuous models and prove two threshold theorems. The first threshold theorem gives a criterion of the development of a epidemic. The second one indicates the eventual size of a epidemic. Then, using both intuitive and rigorous methods, we study a discrete time rumor spreading problem.

2 Continuous Models

The first model in this section is the simplest one we consider. The second one is more refined. Before giving the equations of models, we state the definitions and assumptions they share. The material of this section is summarized from p355 - p370 of [1].

At an arbitrary time t, we suppose that the population consist of the following four categories.

S(susceptibles): That subpopulation composed of individuals who are uninfected and susceptible to the infection.

E(exposed): That subpopulation composed of individuals who are infected but who are not yet capable of spreading the infection.

I(infectives): That subpopulation composed of individuals who are infected and actively spreading the disease.

R(removals): That subpopulation composed of individuals who are not susceptible or who have been infected and either subsequently cured or removed from possible contact with members of S.

At time t, the number of people in S, E, I and R is s(t), e(t), i(t) and r(t). Now, we state some basic assumptions.

1. s, e, i, t are differentiable functions. Although it is more reasonable to set them as integer value function, for large population, differentiable functions are good approximations.

2. The size of e is 0 which means that everyone who contracts the disease can immediately transmit it to others.

3. The total population is of fixed size.

4. R is the absorbing state. A person in S can stay in S or go to I. A person in I can stay in I or go to R.

5. The subpopulations S, I, R are pairwise disjoint and their union is the the entire population.

6. The population size is s(t) + i(t) + r(t) = n + 1. At t = 0, we have s(0) = n and i(0) = 1.

In our simplest model, we further assume:

7. No one is in R.

8. At time t, the rate of growth of I is proportional to $s(t) \cdot i(t)$. The product can be viewed as number of contacts per unit time between members in S and I.

With all assumptions above, we can write the following differential equation and initial condition.

$$\frac{ds}{dt} = -k \cdot s(t) \cdot i(t) = -k \cdot s(t) \cdot (n+1-s(t)) \tag{1}$$

$$s(0) = n \tag{2}$$

The constant k is called transmission rate. Equation (1) and (2) consist of our simplest model. The next goal is to solve s(t) and i(t). Then, we extract as much information from the solutions as we can.

Equation (1) can be written as

$$\frac{ds/dt}{s(n+1-s)} = -k$$

Using partial fractions, we get

$$\frac{ds/dt}{s(n+1)} + \frac{ds/dt}{(n+1-s)(n+1)} = -k \tag{3}$$

Integrating

$$\frac{1}{n+1}[\log(s) - \log(n+1-s)] = -kt + C$$

Then, we can write the expression for s(t)

$$s(t) = \frac{n+1}{1+Ce^{k(n+1)t}}$$
(4)

Using initial condition (2), we solve C = 1/n. The unique solution of the simplest model is

$$s(t) = \frac{n(n+1)}{n + e^{k(n+1)t}}, t \ge 0.$$
(5)

The uniqueness follows from the fact: "If x is another solution, write x = sy and the function y must be 1."[1] By i(t) = n + 1 - s(t) and (5), we have

$$i(t) = \frac{n+1}{1+ne^{-k(n+1)t}}, t \ge 0$$
(6)

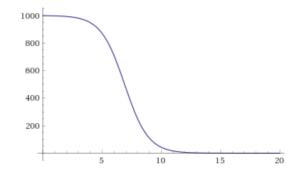


Figure 1: The graph of s(t) when k = 0.001, n = 1000.

To see how fast the disease spread, we analyze the epidemic curve which is the graph of (di/dt)(t). By equation (1),(5),(6), we have

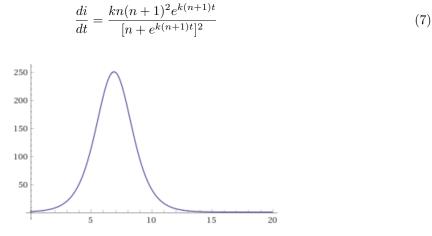


Figure 2: The graph of $\frac{di}{dt}$ when k = 0.001, n = 1000.

From Figure 2, we know the epidemic curve has only one global maximum. By solving $\frac{d^2i}{dt^2} = 0$, we find at $T_M = \frac{1}{k(n+1)} \log(n)$, population of I is increasing most rapidly. Notice T_M is a decreasing function of population size n+1. As k increase, T_M also becomes smaller. Thus, under the simplest model, if the population is large or disease is very contagious, we expect an early peak increasing rate (an early outbreak). At T_M , $s = \frac{n+1}{2}$ and $\frac{di}{dt} = \frac{k(n+1)^2}{4}$.

Our simplest model is based on too many constraints. So it has very limited applicability in the real world. Next, we extend the simplest model by introducing the removal subpopulations R. After we construct the extended model, we can find its solution and obtain two important threshold theorems. Let's start from the assumptions of the extended model.

In the extended model, besides the basic assumptions, we further assume: 8. At time t, the rate of growth of I is proportional to $s(t) \cdot i(t)$. 9. The removal rate is the rate of growth of the R subpopulation. It's proportional to the number of infected people at that time.

With these assumptions, we represent the extended model by a system of first-order nonlinear differential equations:

$$\frac{ds}{dt} = -k \cdot s(t) \cdot i(t), k > 0 \tag{8}$$

$$\frac{dr}{dt} = l \cdot i(t), l > 0 \tag{9}$$

$$\frac{di}{dt} = k \cdot s(t) \cdot i(t) - l \cdot i(t) \tag{10}$$

Although we can have an exact solution for s,t and i, an approximate solution is enough for us to derive some illuminating results. Before giving the solution, we can get the first threshold theorem from equation (10). We define an epidemic develops if di/dt is positive for some t. We define a constant $\rho = l/k$ to be the relative removal rate. Using this constant, we rewrite equation (10) as

$$\frac{di}{dt} = ki(t)[s(t) - \rho] \tag{11}$$

Theorem 1: A necessary condition for an epidemic to develop is that $s(0) - \rho > 0$, $\rho = l/k$.

Proof: s(t) is a decreasing function since people cannot move to state S from other state. If $s(0) - \rho \leq 0$, $ki(t)[s(t) - \rho] \leq 0$ for t > 0.

One way of interpreting this theorem is that given initial population of susceptibles s(0), an epidemic cannot develop if relative removal rate is greater or equal to s(0). Another way of interpreting this theorem is that given the removal rate, if s(0) is greater than the removal rate, an epidemic can develop. From the second interpretation, we can ask: Given ρ , if s(0) is slightly greater than ρ , how many people will be infected before the epidemic ends (no one is in I)? To answer the second question, we need to give an approximated solution to system of equation (8),(9) and (11).

Equation (9) can be written as

$$ki(t) = \frac{1}{\rho} \frac{dr}{dt} \tag{12}$$

Substitute ki(t) by $\frac{1}{\rho}\frac{dr}{dt}$ in equation (8), we have

$$\frac{1}{s}\frac{ds}{dt} = -\frac{1}{\rho}\frac{dr}{dt} \tag{13}$$

Integrate both side of equation (13) and use the initial condition r(0) = 0, we have

$$s(t) = s(0)e^{-r(t)/\rho}$$
(14)

By s(t) + i(t) + r(t) = n + 1 and equation (14), we have

$$i(t) = n + 1 - r(t) - s(0)e^{-r(t)/\rho}$$
(15)

Combining equation (15) and (9), we obtain an equation containing only r(t)

$$\frac{dr}{dt} = l[n+1-r(t)-s(0)e^{-r(t)/\rho}]$$
(16)

The exponential term increases the difficulty of solving equation (16). We expand the exponential term into Taylor series and keep the first few terms. The solution of the new equation obtained from cutting the tail of series can approximate the solution of equation (16).

$$e^{-r/\rho} = 1 - \frac{r}{\rho} + \frac{1}{2} \left(\frac{r}{\rho}\right)^2 - \frac{1}{3!} \left(\frac{r}{\rho}\right)^3 + \cdots$$
 (17)

Combining equation (17) and (16), we have

$$\frac{dr}{dt} = l \left[n + 1 - s(0) + \left(\frac{s(0)}{\rho} - 1 \right) r - \frac{s(0)}{2} \left(\frac{r}{\rho} \right)^2 + \dots \right]$$
(18)

We only keep the term of r and r^2 in equation (18) since it is the simplest approximation we can have to ensure the solution r is bounded. Thus, instead of solving equation (18), we solve for \hat{r} with initial condition $\hat{r}(0) = 0$ in the following equation.

$$\frac{d\hat{r}}{dt} = l \left[n + 1 - s(0) + \left(\frac{s(0)}{\rho} - 1 \right) \hat{r} - \frac{s(0)}{2} \left(\frac{\hat{r}}{\rho} \right)^2 \right]$$
(19)

Let a = l(n + 1 - s(0)), $b = l(\frac{s(0)}{\rho} - 1)$, $c = \frac{ls(0)}{2\rho^2}$. Observe that c is positive. Assume an epidemic develops. (We are not interested about the case of no epidemic development.) Then, we have b and c are positive by Theorem 1. Thus, $a + b\hat{r} - c\hat{r}^2 > 0$. We can rewrite equation (19) as

$$\frac{d\hat{r}/dt}{a+b\hat{r}-c\hat{r}^2} = 1 \tag{20}$$

Integrating

$$\hat{r}(t) = \frac{1}{2c} \left[b + q \frac{1 - e^{-qt + K}}{1 + e^{-qt + K}} \right]$$
(21)

where K is a integration constant which can be determined by $\hat{r} = 0$ and $q = (b^2 + 4ac)^{1/2}$.

In the end, every infected individual will go to state R. Thus, r(t) for t is large can estimate the total number of the infected during the epidemic. Next, by studying the asymptotic behavior of \hat{r} , we obtain a theorem about the eventual size of the epidemic.

Theorem 2: The total size of an epidemic resulting from the introduction of a trace infection into a population of susceptibles whose size s(0) is close to the threshold value ρ is approximately $2(s(0) - \rho)$.

proof:

$$\hat{r}_{\infty} := \lim_{t \to +\infty} \hat{r}(t) = \frac{b+q}{2c} = \frac{\rho(s(0)-\rho) + \rho[(s(0)-\rho)^2 + 2s(0)i(0)]^{1/2}}{s(0)}$$
(22)

Then, we view i(0) as a variable and consider the asymptotic size of $\hat{r}(i(0))$ as i(0) goes to 0.

$$\lim_{i(0)\to 0} \hat{r}(i(0)) = \frac{2\rho(s(0)-\rho)}{s(0)}$$
(23)

This limit represent the asymptotic size of an epidemic resulting from the introduction of a trace infection into a population of susceptibles.[1]

Since s(0) is close to the threshold value ρ , we can write $s(0) = \rho + \sigma$ where σ is small and positive. Thus

$$\lim_{i(0)\to 0} \hat{r}(i(0)) = \frac{2\sigma}{1 + (\sigma/\rho)} \cong 2\sigma$$
(24)

"Another way of stating this result is that in these circumstances the number of uninfected susceptibles remaining after the epidemic is just as far below the threshold value ρ as the initial population size was above ρ ."[1]

Caution: Theorem 2 is about an approximated function of r. It's not a conclusion about r. If the approximation is not accurate enough, theorem 2 is not useful to describe asymptotic behavior of r.[1]

3 Discrete-Time Models

In section 2, we gave two continuous models. Sometimes, we consider time as a discrete quantity and predict the number of the infected for $t \in T = \{t_1, t_2, \dots\}$. *T* is selected according to the structure of problem. The elements in *T* can not only be definite numbers but can also be random variables to accommodate the randomness in the problem. To illustrate the discrete-time modelling, we introduce the problem of rumor spreading. Rumor can be viewed as a "mental disease". It can be spread by communications. We will set up an intuitive and a rigorous model. Although different definitions are used in these two models, we show they share the same conclusion. Let's start from the basic assumptions of the rumor spreading problem. The material of this section is summarized from p378 - p387 of [1] and [2]

1. There are N + 1 villages. At time t_0 , one village know a rumor and is willing to spread it.

2. Villages can only communicate through a simple telephone system. This system is such that any two villages can call one another, but only two villages can use the system at a time. Each village has one telephone.

To state more assumptions about rumor spreading, we introduce following definitions.

S: The set of villages which have not yet heard the rumor but which would be interested in spreading it.

I: The set of villages which have heard the rumor and are interested in spreading it to other villages. *R*: The set of villages not in the set $S \cup I$.

The population vector is $\mathbf{p}(t) = (s(t), i(t), r(t))$ where s(t), i(t), r(t) denote the number of village in S, I, R at time t.

Both intuitive and rigorous model share the following assumptions.

3. Whenever a village makes a call, it is equally likely to call each of the other N villages.

4. If a village of type I calls a village of type S, then the latter becomes a village of type I and the former remains type I.

5. If a village of type I calls a village of type I or R, then the village originating the call becomes a village of type R while the village receiving the call does not change its type. And R is an absorbing state.

6. Telephone calls originating in villages of type S or R do not alter the types of any of the villages.

The assumption 5 needs a bit more explanation. It says that if a village in I tells rumor to a village which already knows the rumor or a village not interested in spreading the rumor, it will immediately loose interest in spreading the rumor. Next, we should find a meaningful time set T such that $\mathbf{p}(t)$ for $t \in T$ can show how rumor spread.

By assumption (4), (5), (6), we observe that only the calls from village of type I can change the population vector. We denote these calls as meaningful calls. Then, we select $T = \{t_0, t_1, t_2, \dots\}$ where t_0 is the initial time in the assumption, t_i is the time of i-th meaningful call for $i \ge 1$. In following discussion, we only consider $\mathbf{p}(t)$ for $t \in T$.

Our goal in this problem is to find how many villages are not infected when the rumor stop spreading (i = 0). Because of the randomness in our assumption, $\mathbf{p}(t)$ is a random vector. Thus, it's hard to directly compute the asymptotic behavior of $\mathbf{p}(t)$. One way to reach our goal is to define and analyze another quantity which has some relation with $\mathbf{p}(t)$. We hope that quantity give us useful information about $\mathbf{p}(t)$. This method is not rigorous but it worth mentioning. Although its computation is elementary, it provide a correct answer to our goal.

Definition: A vector $\hat{\mathbf{p}}$ is

$$\mathbf{p}_0 = (N, 1, 0)$$
$$\hat{\mathbf{p}}_1 = (N - 1, 2, 0)$$
$$\hat{\mathbf{p}}_2 = (s_2, i_2, r_2) = E[\mathbf{p}(t_2)]$$
$$\hat{\mathbf{p}}_k = (s_k, i_k, r_k) = E[\mathbf{p}(t_k)|\mathbf{p}(t_{k-1}) = \hat{p}_{k-1}], k \ge 3$$

 $(\mathbf{n}, \mathbf{n}, \mathbf{n})$

Assume $k \geq 3$, to compute $\hat{\mathbf{p}}_k$, it's enough to compute s_k and i_k .

$$s_{k} = (s_{k-1} - 1)P(\text{the k-th call dials to a village in S}|\mathbf{p}(t_{k-1}) = \hat{p}_{k-1}) + (s_{k-1})P(\text{the k-th call dial to a village in I or R}|\mathbf{p}(t_{k-1}) = \hat{p}_{k-1}) = (s_{k-1} - 1)\frac{s_{k-1}}{N} + (s_{k-1})\frac{N - s_{k-1}}{N}$$
$$s_{k} = \left(\frac{N-1}{N}\right)s_{k-1}$$
(25)

$$i_{k} = (i_{k-1} + 1)P(\text{the k-th call dials to a village in S}|\mathbf{p}(t_{k-1}) = \hat{p}_{k-1}) + (i_{k-1} - 1)P(\text{the k-th call dial to a village in I or R}|\mathbf{p}(t_{k-1}) = \hat{p}_{k-1}) = (i_{k-1} + 1)\frac{s_{k-1}}{N} + (i_{k-1} - 1)\frac{N - s_{k-1}}{N}$$
$$i_{k} = i_{k-1} + \frac{2}{N}s_{k-1} - 1$$
(26)

From the definition of \hat{p} and equation (25), we have

$$s_k = N\left(\frac{N-1}{N}\right)^k, k \ge 0 \tag{27}$$

From equation (26) and (27), we have a difference equation

$$i_k - i_{k-1} = 2\left(\frac{N-1}{N}\right)^{k-1} - 1, k \ge 2$$
(28)

With initial condition $i_1 - i_0 = 2 - 1$ and equation (28), we have

$$i_k = 2N\left[1 - \left(1 - \frac{1}{N}\right)^k\right] + 1 - k, k \ge 0$$
 (29)

Next, we want to find "the length of time the rumor is in circulation" [1]. By knowing it, we can "estimate the total number of villages which the rumor reaches" [1].

Definition: At time t, the rumor is in circulation if $i_t > 0$. At time t, the rumor is dead if $i_t = 0$.

We want to find k_0 such that $i_{k_0} \ge 0$ and $i_j < 0$ for $j > k_0$. Notice the k_0 -th call is the last meaningful call. Assuming the total number of villages N+1 is large, we solve the equation $i_{k_0} = 0$ with some approximations to get k_0 .

Approximation 1: As N large, $k_0 = \lambda N$ where λ is a constant independent of N.

Then, the equation $i_{k_0} = 0$ can be written as:

$$i_{k_0} = 2N \left[1 - \left(1 - \frac{1}{N} \right)^{\lambda N} \right] + 1 - \lambda N = 0$$

$$(30)$$

With algebraic manipulations, we have

$$\lambda = 2 - 2\left[\left(1 - \frac{1}{N}\right)^N\right]^\lambda + \frac{1}{N}$$
(31)

We notice that for large N, $\left[\left(1-\frac{1}{N}\right)^{N}\right]^{\lambda} \approx e^{-\lambda}$. Thus, we have our second approximation.

Approximation 2: λ satisfying equation (31) will be close to λ^* , where λ^* solves the following equation.

$$\lambda^* = 2 - 2e^{-\lambda^*} = g(\lambda^*) \tag{32}$$

This is an transcendental equation and we can solve it using a graphical method. On the x - y plane, we plot the line y = x and the curve $g(x) = 2 - 2e^{-x}$. Then, we find their intersection point. It turns out that there is only one intersection point. The figure below contains the plot.

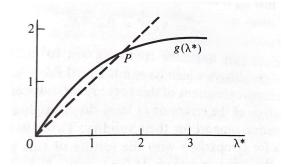


Figure 3: The graph of $y = \lambda_*$ and $g(\lambda_*).[2]$

By our graphical method, we find the solution of equation (32) is $\lambda^* = 1.594$. "If N is large enough, k_0 is approximately equal to 1.594N, and we conclude that the rumor dies after there have been 1.594N meaningful calls."[1]

Then, as N is large enough, s_{k_0} is approximately equal to s_{λ^*N}

$$s_{\lambda^*N} = N \left(\frac{N-1}{N}\right)^{\lambda^*N} \approx N e^{-\lambda^*} = 0.203N \tag{33}$$

We claim that for large N, $s(k_0)$ (a random variable) is approximately equal to 0.203N. Thus, when the rumor dies, there will be approximately 20% villages which have never heard the rumor.

The weakness of the intuitive model above is that the error between $s(k_0)$ and s_{λ^*N} is unknown. s_{λ^*N} is defined as a conditional expectation! Next, we develop a rigorous model and show that it generates the same result as the intuitive model.

We denote $s(t_k)$, $i(t_k)$, $r(t_k)$ as s_k , i_k and r_k for $k \ge 0$. In this model, they are random variables. Define $T = \inf\{t|i_t = 0\}$. T is a stopping time and it is similar to k_0 in the intuitive

model. "The main result we seek is s_T , the number of villages that never hear the rumor." [2] By assumptions of the rumor spreading problem, we have: for $i_k > 0$

$$P(s_{k+1} = s_k - 1, i_{k+1} = i_k + 1, r_{k+1} = r_k) = s/n$$
(34)

$$P(s_{k+1} = s_k, i_{k+1} = i_k - 1, r_{k+1} = r_k + 1) = 1 - s/n$$
(35)

We remind that $s_k + i_k + r_k = N + 1$.

Claim 1: T is a finite stopping time.

proof: Consider $P(i_k - i_{k-1} + 2(s_k - s_{k-1}) = -1)$ for $k \leq T$.

$$P(i_{k} - i_{k-1} + 2(s_{k} - s_{k-1}) = -1)$$

$$= P(i_{k} - i_{k-1} + 2(s_{k} - s_{k-1}) = -1, r_{k} = r_{k-1}) +$$

$$P(i_{k} - i_{k-1} + 2(s_{k} - s_{k-1}) = -1, r_{k} = r_{k-1} + 1)$$

$$= P(s_{k} = s_{k-1} - 1, i_{k} = i_{k-1} + 1, r_{k} = r_{k-1}) +$$

$$P(s_{k} = s_{k-1}, i_{k} = i_{k-1} - 1, r_{k} = r_{k-1} + 1)$$

$$= 1 \text{ by equation (34) and (35)}$$

Thus, $i_k - i_{k-1} + 2(s_k - s_{k-1}) = -1$. This is a difference equation. By induction,

$$i_k + 2s_k + k = i_0 + 2s_0 \tag{36}$$

Thus,

$$i_T + 2s_T + T = i_0 + 2s_0 \tag{37}$$

Since $i_T = 0$, $T = i_0 + 2s_0 - 2s_T \le 2N$ and

$$s_T = (i_0 + 2s_0 - T)/2 \tag{38}$$

We will show T/N converge to a constant in probability as $N \to \infty$. Then by equation (38), we conclude that s_T/N converge to a constant in probability as $N \to \infty$.

Claim 2: $\left(\frac{N}{N-1}\right)^k s_k$ is a martingale.

proof:

$$E\left[\left(\frac{N}{N-1}\right)^{k+1}s_{k+1}|F_k\right]$$
$$= \left(\frac{N}{N-1}\right)^{k+1}E[s_{k+1}|F_k]$$
$$= \left(\frac{N}{N-1}\right)^{k+1}\left[(s_k-1)\frac{s_k}{N} + s_k\left(1 - \frac{s_k}{N}\right)\right]$$
$$= \left(\frac{N}{N-1}\right)^k s_k$$

Since T is finite and $\left(\frac{N}{N-1}\right)^k s_k$ is a martingale, we have $E\left[\left(\frac{N}{N-1}\right)^T s_T\right] = s_0$ by optional stopping theorem. Since $T \leq 2N$ and $s_k \leq N$, we have $\left(\frac{N}{N-1}\right)^T s_T$ is bounded. Thus, the following claim is true.

Claim 3: $Var\left[\left(\frac{N}{N-1}\right)^T s_T\right] = K < \infty.$ By $E\left[\left(\frac{N}{N-1}\right)^T s_T\right] = s_0$, claim 3 and Chebychev's inequality, we have for any $\epsilon > 0$

$$P\left(\left|\left(\frac{N}{N-1}\right)^T \frac{s_T}{N} - \frac{s_0}{N}\right| \ge \epsilon\right) \le \frac{K}{N^2 \epsilon^2}$$
(39)

By equation (38), we obtain

$$P\left(\left|\left(\frac{N}{N-1}\right)^T \frac{i_0 + 2s_0 - T}{2N} - \frac{s_0}{N}\right| \ge \epsilon\right) \le \frac{K}{N^2 \epsilon^2}$$
(40)

Let $T = n\Lambda_n$. We have $s_0 = n + 1 - i_0$ by assumption. Equation (40) can be rewritten as

$$P(|f_N(\Lambda_N)| \ge \epsilon) \le \frac{K}{N^2 \epsilon^2}$$
(41)

where $f_N(x) = \left(\frac{N}{N-1}\right)^{Nx} \left(\frac{2-x}{x} + \frac{2-i_0}{2N}\right) - 1 + \frac{i_0-1}{N}.$

By equation (41), we have

$$P(\Lambda_N \in f_N^{-1}(-\epsilon,\epsilon)) \le 1 - \frac{K}{N^2 \epsilon^2}$$
(42)

We notice that for $x \in [0,2]$, $f_N \to f$ uniformly where $f(x) = e^x(2-x)/2 - 1$.

Claim 4: $P(|f_N(\Lambda_N)| < \epsilon) \to 1$ as $N \to \infty$ and $f_N \to f$ uniformly imply that $P(|f(\Lambda_N)| < 2\epsilon) \to 1$ as $N \to \infty$.

Proof: By law of total probability, we have

$$P(|f_N(\Lambda_N)| < \epsilon, |f_N(\Lambda_N) - f(\Lambda_N)| < \epsilon) = P(|f_N(\Lambda_N)| < \epsilon) - P(|f_N(\Lambda_N)| < \epsilon, |f_N(\Lambda_N) - f(\Lambda_N)| \ge \epsilon)$$

Since $|f_N(\Lambda_N)| < \epsilon$, $|f_N(\Lambda_N) - f(\Lambda_N)| < \epsilon$ implies $|f(\Lambda_N)| < |f_N(\Lambda_N)| + |f_N(\Lambda_N) - f(\Lambda_N)| < 2\epsilon$, we have

$$P(|f(\Lambda_N)| < 2\epsilon) \ge P(|f_N(\Lambda_N)| < \epsilon) - P(|f_N(\Lambda_N)| < \epsilon, |f_N(\Lambda_N) - f(\Lambda_N)| \ge \epsilon)$$

$$\ge P(|f_N(\Lambda_N)| < \epsilon) - P(|f_N(\Lambda_N) - f(\Lambda_N)| \ge \epsilon)$$

We have $P(|f_N(\Lambda_N)| < \epsilon) \to 1$. By uniform convergence, $P(|f_N(\Lambda_N) - f(\Lambda_N)| \ge \epsilon) \to 0$ as $N \to \infty$. Thus, as $N \to \infty$

$$P(|f(\Lambda_N)| < 2\epsilon) \to 1$$

By claim 4, we have $P(\Lambda_n \in f^{-1}(-\epsilon,\epsilon)) \to 1$ which means $\Lambda_n \to \{\text{zeros of } f(x) \text{ in } [0,2]\}$ in probability.

In [0,2], zeros of f(x) are 0 and 1.594. Λ_N won't converge to 0 in probability. As $N \to \infty$, the relative duration of the rumor has small probability decrease to 0 since there are a large number of susceptibles. Thus, we conclude that $\frac{T}{N} = \Lambda_N \to \lambda = 1.594$ in probability. By equation (38), we have

$$\frac{s_T}{N} \xrightarrow{p} \frac{2-\lambda}{2} = 0.203$$

The conclusions of two discrete models coincide.

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