

CLASSICAL GALTON-WATSON BRANCHING PROCESS
AND VACCINATION

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Abstract: Here we treat the transmission of disease through a population as a standard Galton-Watson branching process, modified to take the presence of vaccination into account. Vaccination reduces the number of secondary infections produced per infected individual. We show that introducing vaccination in a population therefore reduces the expected time to extinction of the infection. We also prove results relating the distribution of number of secondary infections with and without vaccinations.

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1. Introduction and Background

After the introduction of penicillin and mass vaccination campaigns of the 1950s, it was thought that infectious diseases would soon be a thing of the past. However, infectious diseases have turned out to be an intractable problem, as new infectious diseases continually emerge while previously existing diseases

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circumvent existing control measures through evolution. Accordingly, there is a continuing need to develop mathematically rigorous methods that can be applied to infectious disease epidemiology, in order to predict future spread of infections and assess the likely impacts of alternative control measures, including vaccination.

One such area of promise emerging from the field of probability is branching processes. Infectious disease transmission can be thought of as a branching process in which each infected individual in a given generation of infection produces some number of infected individuals in the next generation, as described by a probability density function. This picture is particularly apt in the early stages of an outbreak, when the proportion of infected individuals is small and the process is highly stochastic. Epidemiologists need to know whether a disease will die out, and how many individuals are likely to be infected before the extinction, given certain fundamental probability distributions such as the distribution of number of secondary infections produced per infected individual. They also need to know how these parameters will change once control measures such as vaccination are introduced.

Some work has started in applying branching process-type arguments successfully to the mathematical modelling of disease transmission in humans [15, 13] and in animals [21]. However much work remains to be done in developing a mathematically rigorous methodology to understand impact of vaccines. Branching processes have been applied to areas in biology such as the study of offspring distributions and the extinction of family surnames. However, there are issues that are particular to infectious disease epidemiology, such as the impact of vaccination on the branching processes. These peculiarities necessitate an extension of branching process methodologies to the case of infectious disease transmission and vaccination. Here, infectious disease transmission and vaccination are treated as a classic Galton-Watson branching process.

Let Z_n be the number of infected individuals in the n -th generation of disease transmission, where $n \geq 0$. Since we consider the early stages of disease transmission and the proportion of susceptibles is almost 1, infected individuals do not co-infect the same susceptible individuals. An ‘infected’ (resp. ‘susceptible’) here means an individual who is infected (resp. susceptible) in the present generation. Every infected individual has the same probability distribution of the number of individuals they infect, and these are distributed independently of one other. Assume each infected in the n -th generation generates N new individuals in the $(n + 1)$ -th generation. Here $N \in \mathbb{Z}^+$ is a measurable function (a r.v.) whose infected population distribution is $\{\theta_i\}_{i=0}^{\infty}$ i.e.

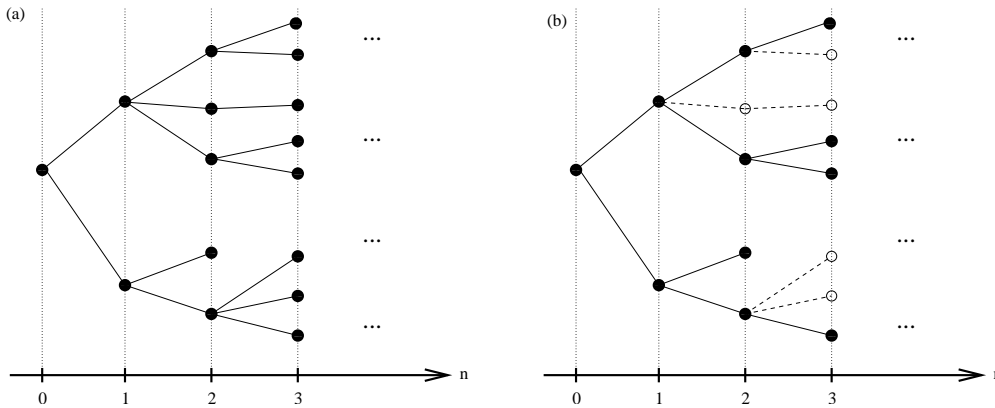


Figure 1: Probabilistic realization of branching process $\{Z_n\}_{n=0}^{\infty}$ without vaccination (a) and with vaccination (b)

$$\Pr[N = i] = \theta_i, \quad i \geq 0.$$

Let $N_r^{(n+1)}$ represents the number of infected by the r -th individual in n -th generation. These infected are account for the size of the population in the $(n + 1)$ -th generation. Then $Z_{n+1} = N_1^{(n+1)} + N_2^{(n+1)} + \dots + N_{Z_n}^{(n+1)}$. Assume that each $N_r^{(n)}$ is iid r.v.'s i.e. $\Pr[N_r^{(n)} = i] = \Pr[N = i] = \theta_i$. The size of the $(n + 1)$ -th generation Z_{n+1} depends on the number of infected individuals in the n -th generation, therefore Z_n satisfies the properties of a Markov chain. We assume that $Z_0 = 1$, guaranteeing that there is one infected individual from which the epidemic can start. After one disease generation (one discrete time interval), this individual has infected a further number of individuals as given by the probability distribution $\{\theta_i\}_{i=0}^{\infty}$. By this time, the original infected individual has also recovered (or died) from the infection. Thus the first generation constitutes Z_1 infecteds, which is the sum of the Z_0 random variables each with a probability θ_i . The second generation constitutes Z_2 infected and the process continues. We call this process an epidemic branching process (EBP).

In the next section we introduce probability generating function $I(x)$ for $\{\theta_i\}$ and study uniform convergence properties and related consequences of $I(x)$ for $x \in (-\mathbb{R}, \mathbb{R})$ and $x \in (-1, 1)$. The results on uniform convergence of $I(x)$ provided in this work are not new because $I(x)$ is a power series (introduced in the next section). We study extinction probabilities *with respect to* the mean number of infectious individuals generated by starting $Z_0 = 1$. This mean number is defined as $I'(1)$. In the mathematical epidemiology literature, $I'(1)$ would be referred to as the basic reproductive number. The process $\{Z_n\}$ is called

supercritical if $I'(1) > 1$ and the process is called sub critical if $I'(1) \leq 1$. We have not seen rigorous mathematical treatment of the branching process for the spread of virus and controlling the spread through vaccination in the population (except elementary branching process applications for understanding measles outbreaks [15], for virus HIV spread within the host cell dynamics [2] and renewing cell populations [24]). Extinction probability results in the pre-vaccination (i.e. without vaccination) scenario are derived from branching process studies available on offspring distribution, surnames and other general branching processes analysis (see for example, [6, 11, 12, 5, 10, 8, 14, 20, 1, 18, 19]) and fundamental results on uniform convergence can be seen in many classical analysis books). Hence some results in Section 2 do not bring new mathematics, but rather new applications. In some sense, Section 2 can be treated as a review of known results (without going into detailed proofs). In Section 3, we bring novelty through theoretical arguments on EBP when vaccination is introduced in the population. Studies such as [9] treated age-structured population, [22] incorporated migration into branching processes and [21, 16] studies processes with varying environments. However, we do not bring those issues while studying EBP. By vaccinating the individuals, the resultant probability density functions of infection densities shifts to the left and extinction of virus is quicker. We also explore some consequences of vaccination.

2. Elementary Results on Extinction Probability

We saw $\Pr[N_r = i] = \theta_i$ and N_r are independent discrete random variables. Suppose I_2 and J_r are probability generating functions of Z_2 and N_r for $r = 1, 2, 3 \dots$. Then we know $J_1 = I_1$ because $Z_1 = N_1$, $J_1 \cdot J_2 = I_2$. Suppose distribution of N_r are same (say some J), then $I_2 = [J]^2$, where $I_2 = I_2(x) = \sum_{i=0}^{\infty} \Pr[Z_2 = i] x^i$ is the probability generating function of Z_2 . In general let I_n is probability generating function of Z_n . Since $Z_2 = N_1 + N_2 + \dots + N_{Z_1}$, it follows that $\Pr[Z_2 = k + 1 / Z_1 = k] = \Pr\left[\sum_{i=1}^k N_i = k + 1\right]$. We can prove $I_2 = I_1(I_1)$ and $I_n = I_{n-1}(I_1)$, see [6]. Let $I(x) = \sum_{i=0}^{\infty} \Pr[N = i] x^i$ ($|x| < 1$) be the probability generating function for $\{\theta_i\}$. We prove convergence properties of $I(x)$ and hence bring elementary results on extinction of probability of the virus from the population.

Theorem 2.1. *Suppose $I(x)$ converges for $|x| < \mathbb{R}$, then for a $\delta > 0$, $I(x)$ converges uniformly on $[-\mathbb{R} + \delta, \mathbb{R} - \delta]$ and $I(x)$ is continuous and infinitely differentiable on any open interval $(-\mathbb{R}, \mathbb{R})$.*

Proof. It is enough to show existence of I' i.e. differentiability of I , then it follows continuity of I . This is because,

$$\lim_{x \rightarrow p} [I(x) - I(p)] = \lim_{x \rightarrow p} \frac{I(x) - I(p)}{x - p} [x - p] = I'(x) \cdot 0 = 0$$

Hence I is continuous. $I'(x) = \sum i\theta_i x^{i-1}$ ($|x| < \mathbb{R}$). Also, as $i \rightarrow \infty$, it follows that $\limsup \sqrt[i]{|\theta_i|} = \limsup \sqrt[i]{|\theta_i|}$. This is due to fact that $i \rightarrow \infty$, it follows that $\sqrt[i]{i} = 1$. Since $\limsup \sqrt[i]{|\theta_i|}$ as $n \rightarrow \infty$, it follows that $\sum \theta_i$ is convergent. Therefore, $\sum \theta_i x^i$ and $\sum i\theta_i x^i$ have interval of convergence in $(-\mathbb{R}, \mathbb{R})$. Since $I(x)$ is a power series, the required results is straight forward and can be seen in several classical analysis books. Suppose the series $\sum_{n=0}^{\infty} a_n x^n$ converges for $|x| < \mathbb{R}$, and define $g(x) = \sum_{n=0}^{\infty} a_n x^n$ ($|x| < \mathbb{R}$). Then g converges uniformly on $[-\mathbb{R} + \epsilon, \mathbb{R} - \epsilon]$, for every $\epsilon > 0$. Here g is continuous and differentiable in $(-\mathbb{R}, \mathbb{R})$ and $g'(x) = \sum_{n=1}^{\infty} n a_n x^{n-1}$.

The above theorem established that the probability generating function of the infected distribution is differentiable over the real line if $|x| < \mathbb{R}$ holds. However conventionally, we define $I(x)$ for $|x| < 1$. □

Theorem 2.2. For a given $\epsilon, \delta > 0$, let $\mathcal{B}_\epsilon(\sum \theta_i) = \{x \in \mathbb{R} : |x - \sum \theta_i| < \epsilon\}$ and $\mathcal{B}_\delta(1) = \{x \in \mathbb{R} : |x - 1| < \delta\}$ and $\theta_i < \theta_{i+1}$ for $\{i = 0, 1, 2 \dots\}$. Then for every $\mathcal{B}_\epsilon(\sum \theta_i)$, there exists a $\mathcal{B}_\delta(1)$ with the property that for all $x \in \mathcal{B}_\delta(1)$, $x \neq 1$, it follows that $I(x) \in \mathcal{B}_\epsilon(\sum \theta_i)$.

Proof. Let $T_i = \sum \theta_i$. Consider the sequence $\{T_i\}_{i=0,1,2,\dots}$. Here $T_0 = \theta_0$, $T_1 = \theta_0 + \theta_1$, $T_2 = \theta_0 + \theta_1 + \theta_2$ and so on. We assume $\theta_0 > 0$. Otherwise, if $\theta_0 = 0$ the branching process will terminate. Since $\theta_0 > 0$, and from the hypothesis we have, $\theta_1 > \theta_0 > 0$ and $\theta_2 > \theta_1$ and so on. Also, we know $\theta_i < 1$ because $\{\theta_i\}$ forms a complete probability distribution. Therefore $\{T_i\}$ is convergent. We have the very important result by Abel, which states that when $\sum \theta_n$ is convergent and as $x \rightarrow 1$, it follows that $\lim \sum \theta_n x^n = \sum \theta_n$ ($-1 < x < 1$). Hence from this result it follows that $x \in \mathcal{B}_\delta(1) \Rightarrow I(x) \in \mathcal{B}_\epsilon(T_i)$. □

Remark 2.3. The elementary Theorem 2.4 and the arguments in the proof given can also be found for studying extinction of surnames of families, extinction of particular offspring, particle extinction in a volume of gas and other biological applications. Otherwise, this theorem is very well known, but we state it here in the language of infectious disease extinction in the population. This will help readers to compare the above elementary result with the new results in the next section when a vaccine that prevents disease transmission is introduced into the population.

Theorem 2.4. Given $I(x)$ for $x \in [0, 1]$ and size of infected population in zeroth generation is one. If the process is sub critical or critical then $\lim \Pr [Z_n = 0] = 1$ as $n \rightarrow \infty$ and if the process is supercritical then there exists a $\pi (\neq 1) \in [0, 1]$ such that $I(\pi) = \pi$ and as $n \rightarrow \infty$ it follows that $\lim \Pr [Z_n = 0] = \pi$.

Proof. Consider the closed interval $[0, 1]$. We saw in Theorem 2.1 that $I(x)$ is continuous in $[0, 1]$ and also $I'(x) = \sum i\theta_i x^i > 0$. Therefore, $I'(x)$ is strictly increasing in $[0, 1]$. If the system is sub critical then $I'(1) \leq 1$. This means $I'(x) < 1$ for $x \in [0, 1)$. This implies, $\int_x^1 I'(x)dx < \int_x^1 dx \Rightarrow 1 - I(x) < 1 - x \Rightarrow I(x) > x$. $I(1) = \sum \theta_i = 1$. This means the curve of $I(x)$ never touches $I(x) = x$ in $[0, 1)$ and at 1 it will be 1. Therefore, $I(1) = 1$ has to be a unique fixed point for I in $[0, 1]$. Now it is left for us to show that $\lim \Pr [Z_n = 0] = 1$. We can easily prove that $\{\Pr [Z_n = 0]\}$ is convergent. Let π be the limit of this sequence, so that as $n \rightarrow \infty$, it follows that $\lim \Pr [Z_n = 0] = \pi$. Also, $\lim I(\Pr [Z_{n-1} = 0]) = I(\pi)$ and $I(\pi) = \pi$. But we saw above that, when $I'(1) \leq 1$, then $I(1) = 1$ is unique fixed point. Hence $\lim \Pr [Z_n = 0] = 1$.

Since $I'(x) = \sum i\theta_i x^{i-1} > 0$ for $x \in [0, 1]$, $I'(x)$ is strictly increasing, then there exists a $a \in (0, 1)$ such that for $b \in (a, 1)$ we will have

$$1 < I'(b) < I'(1) \quad (1)$$

$$\begin{aligned} \Rightarrow \int_b^1 dx &< \int_b^1 I'(x)dx \\ \Rightarrow 1 - b &< 1 - I(b) \Rightarrow b > I(b) \quad \text{for } b \in (a, 1). \end{aligned} \quad (2)$$

These kind of above arguments can be found in basic setting of branching process (see [6] Chapter 6, [11] Chapter 12, [5] Chapter 1, [23] Chapter 0, [1] Chapter 4). Equation 1 is a situation of supercritical process. When process obeys such property then our aim is to show that there exists two fixed points π and 1 in $[0, 1]$ such that $\pi \neq 1$. Every value of b between a and 1 (exclusive), the value of line $y = x$ is greater than the value of the curve $y = I(x)$ for $x \in (a, 1)$ on the XY - plane. Therefore, this situation is not conducive for us to find a π such that $I(\pi) = \pi$. If we bring a relation $I(x) - x = 0$ for some $x < 1$ then prove that x is unique, then we are ready to compute extinction probabilities. Consider $I(x) - x$. We have $I(0) - 0 = \theta_0 > 0$ and from equation 2 $I(b) < b$ for $b \in (a, 1)$. This means $I(x) - x < 0$ for $x = b$. Thus,

$$I(x) - x = \begin{cases} > 0 & \text{for } x = 0, \\ < 0 & \text{for } x = b. \end{cases}$$

The intermediate value theorem says if any continuous function on a given closed interval with values ranging from negative to positive, then this function

will be zero for some value in between the same closed interval in the domain. Therefore $I(x) - x = 0$ for some $x \in (0, b)$. Let $I(\pi) = \pi$ for $\pi \in (0, b)$. We are sure that in $(a, 1)$ there will be no fixed point. Suppose w is the another fixed point in $(0, 1)$ then either $w \in (0, \pi)$ or $w \in (\pi, 1)$. Since w is another fixed point, $I(w) - w = 0$, π is also a fixed point, so $I(\pi) - \pi = 0$ and $I(1) - 1 = 0$. $I(x) - x$ is differentiable and continuous in $(0, 1)$, so

$$\begin{cases} I(w_1) - w_1 = 0 & \text{for } 0 < w_1 < w, \\ I(w_2) - w_2 = 0 & \text{for } w < w_2 < \pi. \end{cases} \tag{3}$$

and

$$\begin{cases} I(w_1) - w_1 = 0 & \text{for } \pi < w_1 < w, \\ I(w_2) - w_2 = 0 & \text{for } w < w_2 < 1. \end{cases} \tag{4}$$

These equations (3) and (3) together contradict the fact that $I(x)$ is strictly increasing in $(0, 1)$. Therefore $w = \pi$. This means $\lim \Pr [Z_n = 0] = \pi$. Hence we have two fixed points π and 1 in $x \in [0, 1]$. □

Remark 2.5. If the mean number of infections exceed unity, then the virus from the population will go extinct in a finite number of generations with probability π . Suppose $Z_0 = N$ then each of these individuals process can be treated independently. Thus $\lim \Pr [Z_n = 0] = \pi^N$ and $\lim \Pr [Z_n = \infty] = 1 - \pi^N$. $\lim \Pr [Z_n = \infty] \rightarrow 0$ when $N \rightarrow \infty$ even if $\pi \gg 0$. This means virus will go extinct even if population at the zeroth stage has a large number of infected individuals.

3. Spreading is Restricted by Vaccination

Let the process $\{Z_n\}$ is controlled by introducing vaccination into the population, which protects susceptible individuals from infection and therefore reduces the number of secondary infections produced per infected individual. Vaccination of a proportion p of the population reduces the average number of secondary infections produced by each infected individual by a factor $1-p$, see [4]. Moreover, epidemiological evidence indicates that the number of secondary infections produced per infected individual can be well-described by a gamma distribution [17]. We model the probability density function of the number of secondary infections per infected person as a gamma function, so that it covers a wide range of epidemiologically-plausible scenarios. Vaccination will shift the peak of the probability density function to the left. Our aim here is to estimate the corresponding change in the time to extinction brought about by

vaccination.

Proposition 3.1. *Suppose the time to extinction without vaccination is τ_a and $P[N = w_a] = \Gamma_a [w_a, T_a, \alpha_a]$ and suppose the time to extinction with vaccination is τ_b and $P[N = w_b] = \Gamma_b [w_b, T_b, \alpha_b]$. If mean of Γ_b is less than the mean of Γ_a then $\tau_b < \tau_a$.*

Proof. Let $\overline{w}_a, \overline{w}_b$ means of Γ_a and Γ_b . We know that by vaccinating the population, the new number of infections generated by one infected is reduced and hence the sizes of $\{Z_n\}$ at each stage n is affected. We have $\overline{w}_b < \overline{w}_a \Rightarrow T_b \alpha_b < T_a \alpha_a$. Hence the time to extinct will be earlier with vaccine than that of without vaccination. \square

We discuss here some further consequences of vaccination. Suppose $\sum_{w_a=0}^{\infty} w_a \theta_{w_a} = \int_{-\infty}^{\infty} w_a d(\Gamma_a [w_a, T_a, \alpha_a]) = T_a \alpha_a$. Here $d(\Gamma[\cdot])$ is gamma distribution function. We have seen in the previous section that if $\sum w_a \theta_{w_a} \leq 1$ then the chance of extinction is one and if $\sum w_a \theta_{w_a} > 1$ then the chance is π for $\pi < 1$. This also means $\lim \Pr [Z_{n_a} = 0] = 1$ as $n_a \rightarrow \infty$. Suppose $\sum_{w_b=0}^{\infty} w_b \theta_{w_b} = \int_{-\infty}^{\infty} w_b d(\Gamma_b [w_b, T_b, \alpha_b]) = T_b \alpha_b$. Please note w_a and w_b denote infected individuals and θ_{w_a} and θ_{w_b} denote infected population distributions for pre and post vaccination. $\{w_j\}, j = 1, 2, 3, \dots$ are individuals in post vaccination scenario. Here $\lim \Pr [Z_{n_b} = 0] = 1$ as $n_b \rightarrow \infty$. Note that $Z_{n_b} < Z_{n_a}$ and $n_b < n_a$ (by Proposition 3.1). If we consider probability densities of these two scenarios on the XY -plane then the mean of the infection distribution with vaccination shifts to left of the mean of the infection distribution without vaccination, i.e. $T_b \alpha_b < T_a \alpha_a$. Suppose $\{T_j\}, \{\alpha_j\}$ for $j = 1, 2, \dots, n$ are set of parameters in the plausible range of post vaccine scenario. If $\mathbf{T} = \text{Min}\{T_1, \dots, T_n\}$ and $\alpha = \text{Min}\{\alpha_1, \dots, \alpha_n\}$ then post vaccination infection density will have one of these three parameters combinations: *I.* $\{\mathbf{T}, \alpha_j\}$ or *II.* $\{T_j, \alpha\}$ or *III.* $\{\mathbf{T}, \alpha\}$. In the cases of *I* and *II* the infection density could be realistic, but *III* is not certainly an expected density. To avoid situation *III*, we choose a set E_j consisting of all possible combinations of parameters $\{T_j, \alpha_j\}$ such that Γ -density is never a decreasing function.

The corresponding inequalities due to situations *I*, *II* and *III* are $\mathbf{T} \alpha_j < T_a \alpha_a$, $T_j \alpha < T_a \alpha_a$ and $\mathbf{T} \alpha < T_a \alpha_a$ for some j such that post vaccination parameter sets are in E_j . Since $\overline{w}_b < \overline{w}_a$ it can be viewed that $\tau_b < \tau_a$. However the mean of Γ_j for any j is less than the mean of Γ_a . This implies,

$$\Pr[Z_{n_a} = 0](\text{as } n_a \rightarrow \infty) < \Pr[Z_{n_b} = 0](\text{as } n_b \rightarrow \infty).$$

Also, $\Pr[Z_{n_a} = 0] < [Z_{n_j} = 0]$. Note that n_a, n_j are not associated with the same time axis because pre and post vaccination situations cannot occur

at the same time. In Section 2, Z_n, Z_{n+1}, \dots are associated to the same time axis. Consider the sequence $\{\Pr [Z_{n_a} = 0]\}_{n_a=0,1,2,\dots}$. Note that the suffix a is used here to indicate that size of the population in pre vaccine scenario. We have $I(0) = \Pr [Z_1 = 0] = \theta_0 > 0$ and also $\theta_0 < 1$. Then by the mathematical induction and monotonic property of I we can show that

$$\begin{aligned} I(\Pr [Z_{(n-1)_a} = 0]) &< I(\Pr [Z_{n_a} = 0]) < I(1), \\ \Rightarrow \Pr [Z_{n_a} = 0] &< \Pr [Z_{(n+1)_a} = 0] < 1. \end{aligned}$$

Similarly by considering the sequence $\{\Pr [Z_{n_j} = 0]\}_{n_j=0,1,2,\dots}$ we can show that

$$\begin{aligned} I(\Pr [Z_{(n-1)_j} = 0]) &< I(\Pr [Z_{n_j} = 0]) < I(1) \\ \Rightarrow \Pr [Z_{n_j} = 0] &< \Pr [Z_{(n+1)_j} = 0] < 1. \end{aligned}$$

Thus $\{\Pr [Z_{n_a} = 0]\}$ and $\{\Pr [Z_{n_j} = 0]\}$ are convergent sequences. Moreover $\{\Pr [Z_{n_j} = 0]\}$ converges earlier due to vaccination.

Proposition 3.2. *Suppose the mean distance between the peaks of the infection densities is $\bar{d}(P_j, P_a)$. Here $P_a(w_a, \Gamma_a(w_a))$ are $P_j(w_j, \Gamma_j(w_j))$ are the peak points for the pre and post vaccination densities. Then $\Gamma(\bar{w}_j) = \Gamma(w_a) \pm \left[\frac{1}{n^2} \left\{ \sum_j d(P_j, P_a) \right\}^2 - (w_a - \bar{w}_j)^2 \right]^{\frac{1}{2}}$.*

Proof. Let $P_j(w_j, \Gamma_j(w_j))$ be the point representing the peak of the density function after vaccination, in E_j . If $P_a(w_a, \Gamma_a(w_a))$ is the point representing the peak of the density function before vaccination, then Euclidean distance between these two points is $d(P_j, P_a)$ (see Figure 2). The mean ($\bar{d}(P_j, P_a)$) of this function over all possible j is

$$\bar{d}(P_j, P_a) = \frac{\sum_j d(P_j, P_a)}{n}.$$

For j possible types of post vaccine densities, let $\bar{P}_j(\bar{w}_j, \Gamma(\bar{w}_j))$ be the point corresponding to the mean peak. O is a point which is at a distance of $w_a - \bar{w}_j$ from \bar{P}_j to the right. Suppose $\bar{d}(P_a, \bar{P}_j)$ is the distance from P_a to \bar{P}_j . Then we know from Pythagoreen right triangle principle that $d(P_a, \bar{P}_j) = \sqrt{(OP_a)^2 + (O\bar{P}_j)^2}$. From general principles of means, we can easily verify the fact that $d(P_a, \bar{P}_j) = \bar{d}(P_j, P_a)$. Therefore,

$$\frac{1}{n^2} \left\{ \sum_j d(P_j, P_a) \right\}^2 = (w_a - \bar{w}_j)^2 + (\Gamma(w_a) - \Gamma(\bar{w}_j))^2$$

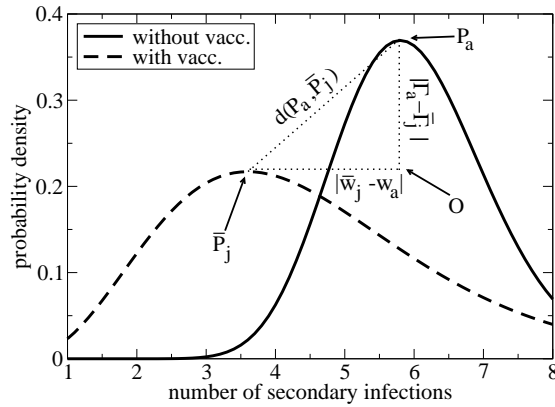


Figure 2: Examples of infection peaks with (P_j) and without (P_a) vaccination. For the with-vaccination scenario, the average peak over many possible types is shown (see text).

$$\Gamma(\bar{w}_j) = \Gamma(w_a) \pm \left[\frac{1}{n^2} \left\{ \sum_j d(P_j, P_a) \right\}^2 - (w_a - \bar{w}_j)^2 \right]^{\frac{1}{2}}.$$

This proposition relates the shape of the distribution of the number of secondary infections per infected individual before vaccination to the same after vaccination. This may be useful in situations where both distributions have small skew and w_a, w_j correspond to the expectation values of the distributions. □

Remark 3.3.

$$\begin{aligned} \sum n_a \Pr[Z_{n_a} = 0] \leq 1 &\Rightarrow \sum n_j \Pr[Z_{n_j} = 0] \leq 1 \\ &\Rightarrow \bar{d}(P_j, P_a) \leq v^2 \text{ for some } v \leq 1. \end{aligned}$$

Again,

$$\sum n_a \Pr[Z_{n_a} = 0] > 1 \Rightarrow \begin{cases} \sum n_j \Pr[Z_{n_j} = 0] > 1 \text{ (no impact of vaccination),} \\ \sum n_a \Pr[Z_{n_a} = 0] \leq 1 \text{ (impact of vaccination).} \end{cases}$$

Since vaccine has a positive role in reducing the infection process such that as $n_j > N$ (for some large N) it implies $\sum n_j \Pr[Z_{n_j} = 0] \leq 1$. When the process $\{Z_{n_a}\}$ is supercritical then initially the process $\{Z_{n_j}\}$ could also be supercritical and eventually $\{Z_{n_j}\}$ will attain sub criticality or criticality. Hence even if

$\sum n_a \Pr[Z_{n_a} = 0] > 1$, eventually $d > 1$. The larger the value of d the larger is the impact of vaccination and extinction occurs much earlier with probability $\pi_j(\pi_j < \pi)$.

4. Conclusions

Branching process analysis have provided a rigorous perspective on numerous physical problems in the past. Some important recent literature related to branching process applications to epidemiology can be found in [7] and [3] (Chapter 3). Here, we have analyzed application of branching processes for studying the early stages of epidemic spread in a population with vaccination. We modified the standard branching process to account for the effects of vaccination, showing how vaccination will decrease the time to extinction. There remains much work to be done in epidemic branching processes, particularly in the incorporation of other types of control measures (quarantine) and in the incorporation of realistic population structures such as age-structure.

References

- [1] J.S.A. Allen, *An Introduction to Stochastic Processes with Applications to Biology*, Prentice and Hall, New York (2002).
- [2] G. Alsmeyer, U. Rasler, Asexual versus promiscuous bisexual Galton-Watson processes: the extinction probability ratio, *Ann. Appl. Probab.*, **12**, No. 1 (2002), 125-142.
- [3] H. Andersson, T. Britton, *Stochastic Epidemic Models and their Statistical Analysis*, Lecture Notes in Statistics, **151**, Springer-Verlag, New York (2000).
- [4] R.M. Anderson, R.M. May, *Infectious Diseases of Humans: Dynamics and Control*, Oxford University Press (1991).
- [5] K.B. Athreya, P.E. Ney, *Branching Processes*, Springer-Verlag, New York-Heidelberg (1972).
- [6] N.T.J. Bailey, *The Elements of Stochastic Processes with Applications to the Natural Sciences*, John Wiley and Sons, Inc., New York-London-Sydney (1964).

- [7] F. Ball, P. Donnelly, Strong approximations for epidemic models. *Stochastic Process. Appl.*, **55**, No. 1 (1995), 1-21.
- [8] P. Broberg, A note on the extinction probability of branching populations, *Scand. J. Statist.*, **14**, No. 2 (1987), 125-129.
- [9] H. Cohn, Multitype finite mean supercritical age-dependent branching processes, *J. Appl. Probab.*, **26**, No. 2 (1989), 398-403.
- [10] M. Dwass, Branching processes in simple random walk, *Proc. Amer. Math. Soc.*, **51** (1975), 270-274.
- [11] W. Feller, *An Introduction to Probability theory and its Applications*, Volume I, John Wiley and Sons, Inc., New York-London-Sydney (1968).
- [12] D.R. Grey, On regular branching processes with infinite mean, *Stochastic Process. Appl.*, **8**, No. 3 (1978/79), 257-267.
- [13] C. Jacob, A.F. Viet, Epidemiological modeling in a branching population. Particular case of a general SIS model with two age classes, *Math. Biosci.*, **182**, No. 1 (2003), 93-111.
- [14] P. Jagers, Coupling and population dependence in branching processes, *Ann. Appl. Probab.*, **7**, No. 2 (1997), 281-298.
- [15] V.A.A. Jansen, N. Stollenwerk, H.J. Jensen, et al, Measles outbreaks in a population with declining vaccine uptake, *Science*, **301** (2003), 804-804.
- [16] O.D. Jones, On the convergence of multitype branching processes with varying environments, *Ann. Appl. Probab.*, **7**, No. 3 (1997), 772-801.
- [17] J.O. Lloyd-Smith, S.J. Schreiber, P.E. Kopp, W.M. Getz, Superspreading and the effect of individual variation on disease emergence, *Nature*, **438** (2005), 355-359.
- [18] P. Olofsson, C.A. Shaw, Exact sampling formulas for multi-type Galton-Watson processes, *J. Math. Biol.*, **45**, No. 4 (2002), 270-293.
- [19] L. Rass, Convergence results for contact branching processes, *Math. Biosci.*, **205**, No. 1 (2007), 59-76.
- [20] R.B. Schinazi, *Classical and Spatial Stochastic Processes*, Birkhäuser Boston, Inc., Boston, MA (1999).

- [21] P. Trapman, R. Meester, H.A. Heesterbeek, A branching model for the spread of infectious animal diseases in varying environments, *J. Math. Biol.*, **49**, No. 6 (2004), 553-576.
- [22] C.Z. Wei, J. Winnicki, Estimation of the means in the branching process with immigration, *Ann. Statist.*, **18**, No. 4 (1990), 1757-1773.
- [23] D. Williams, *Probability with Martingales*, Cambridge University Press, Cambridge (1991).
- [24] A. Yakovlev, N. Yanev, Branching stochastic processes with immigration in analysis of renewing cell populations, *Math. Biosci.*, **203**, No. 1 (2006), 37-63.

