ON A PANDEMIC THRESHOLD THEOREM OF THE EARLY KERMACK–MCKENDRICK MODEL WITH INDIVIDUAL HETEROGENEITY

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ABSTRACT. In this paper, a pandemic threshold theorem of the Kermack–McKendrick epidemic system with individual heterogeneity is proved under the light of the definition of R_0 by Diekmann, Heesterbeek and Metz (1990). First I extend the early Kermack–McKendrick epidemic model to recognize individual heterogeneity, where the "state" variable does not only mean geographical distribution, but also any biological or social heterogeneity of individuals, and transmission of infectious agent occurs among individuals with different traits. Second, the basic reproduction number R_0 for the heterogeneous population is introduced. Subsequently we prove that the final size equation of the limit epidemic starting from a completely susceptible steady state at $t = -\infty$ has a unique positive solution if and only if $R_0 > 1$. Finally we prove that the positive solution of the final size equation gives the lower bound of any epidemic starting from a host population composed of susceptibles and infecteds, which is a new pandemic threshold result based on R_0 applied to non compact domain of heterogeneity variable.

1. THE BASIC MODEL AND R_0

First we extend the early Kermack–McKendrick model to take into account individual heterogeneity expressed by continuous variables. Let ξ be a (scaler or vector) parameter with domain $\Omega \subset \mathbf{R}^n$ which expresses any biological, epidemiological *state* of individuals. That is, ξ may indicate spatial distribution, genetical, physiological or behavioral characters (for example, the degree of infection risk) and so on. Although here we assume that the heterogeneity parameter of an individual does not change during the total period of the epidemic[1], it does not necessarily imply that the heterogeneity parameter is time-independent in a rigorous sense. For example, the chronological age of individuals is clearly time-dependent, but it can be approximately seen as a time-independent parameter to indicate a cohort of host population if the time scale of the epidemic is short enough in comparison with demographic time scale.

Let $S(t, \xi)$, $i(t, \tau, \xi)$ and $R(t, \xi)$ be the susceptible, infected and recovered population density with state ξ at time t respectively, where τ denotes the infection-age (time elapsed from the instant of infection). Then the early Kermack–McKendrick

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[1]Here we only deal with an epidemic which ends with eradication of infecteds, since there is no supplement of susceptibles.

model that recognizes individual heterogeneity is formulated as follows:

$$\frac{\partial S(t,\xi)}{\partial t} = -\lambda(t,\xi)S(t,\xi),$$

(1.1)
$$\frac{\partial i(t,\tau,\xi)}{\partial t} + \frac{\partial i(t,\tau,\xi)}{\partial \tau} = -\gamma(\tau,\xi)i(t,\tau,\xi),$$

$$i(t,0,\xi) = \lambda(t,\xi)S(t,\xi),$$

$$\frac{\partial R(t,\xi)}{\partial t} = \int_0^\infty \gamma(\tau,\xi)i(t,\tau,\xi)d\tau,$$

where the force of infection $\lambda(t,\xi)$ is given by

$$\lambda(t,\xi) = \int_0^\infty \int_\Omega \beta(\tau,\xi,\eta)i(t,\tau,\eta)d\eta d\tau,$$

and $\beta(\tau,\xi,\eta)$ denotes the transmission coefficient between infectives with infection-age τ and state η and susceptibles with state ξ and γ is the infection-age and state specific recovery rate. In particular, the separation of variable type transmission coefficient as $\beta(\tau,\xi,\eta) = \beta_1(\tau)\beta_2(\xi-\eta)$ is considered in [14].

Let $S(0,\xi) = S_0(\xi)$ and $i(0,\tau,\xi) = i_0(\tau,\xi)$ be initial data and let $N(\xi)$ be the density of total population at state ξ:

$$N(\xi) := S(t,\xi) + \int_0^\infty i(t,\tau,\xi)d\tau + R(t,\xi),$$

which is assumed to be time-independent. We assume that $S_0, N \in L_+^1(\Omega) \cap L_+^\infty(\Omega)$, $i_0 \in L_+^1(\mathbf{R}_+ \times \Omega)$ and $N(\xi) \geq S_0(\xi) > 0$ for almost all $\xi \in \Omega$. Then there exists a disease-free steady state composed of completely susceptible individuals $(N(\xi),0,0)$.

The linearized equation for infecteds at $(N,0,0)$ is given by

$$\frac{\partial y(t,\tau,\xi)}{\partial t} + \frac{\partial y(t,\tau,\xi)}{\partial \tau} = -\gamma(\tau,\xi)y(t,\tau,\xi),$$

(1.2)
$$y(t,0,\xi) = N(\xi)\int_0^\infty \int_\Omega \beta(\tau,\xi,\eta)y(t,\tau,\eta)d\eta d\tau,$$

where $y(t,\tau,\xi)$ denotes the density of infected population in the linear invasion phase.

Integrating the McKendrick equation in (1.2) along the characteristic line, we have

(1.3)
$$y(t,\tau,\xi) = \begin{cases} b(t-\tau,\xi)\Gamma(\tau,\xi), & t-\tau > 0, \\ \frac{\Gamma(\tau,\xi)}{\Gamma(\tau-t,\xi)}y(0,\tau-t,\xi), & \tau-t > 0, \end{cases}$$

where $b(t,\xi) := y(t,0,\xi)$ is the density of newly infected individuals in the initial invasion phase and

$$\Gamma(\tau,\xi) := \exp\left(-\int_0^\tau \gamma(x,\xi)dx\right),$$

is the survival rate at state ξ.

Inserting the expression (1.3) to the boundary condition of (1.2), we know that the newly infected population density $b(t,\xi)$ at the disease-free steady state without recovered individuals satisfies a renewal equation:

(1.4)
$$b(t,\xi) = N(\xi)G[y(0,\cdot)](t,\xi) + N(\xi)\int_0^t \int_\Omega \Psi(\tau,\xi,\eta)b(t-\tau,\eta)d\eta d\tau,$$

where

$$\Psi(\tau,\xi,\eta) := \beta(\tau,\xi,\eta)\Gamma(\tau,\eta),$$

$$G[y(0,\cdot)](t,\xi) := \int_t^\infty \int_\Omega \beta(\tau,\xi,\eta)\frac{\Gamma(\tau,\eta)}{\Gamma(\tau-t,\eta)}y(0,\tau-t,\eta)d\eta d\tau.$$

It is well-known since [3]) that the basic reproduction number R_0 of the renewal system (1.3) is given by the spectral radius of a linear positive operator (*next generation operator*) K on $L^1(\Omega)$ defined by

$$(1.5) \qquad (Ku)(\xi) := N(\xi)\int_0^\infty \int_\Omega \Psi(\tau,\xi,\eta)u(\eta)d\eta d\tau, \quad u \in L^1(\Omega).$$

That is, $R_0 = r(K)$ where $r(K)$ denotes the spectral radius of the positive operator K.

Here we introduce a technical assumptions for parameters:

Assumption 1.1.   (1) β and γ are uniformly bounded nonnegative measurable functions, and $\inf \gamma > 0$.

(2) β is comparable with a positive separable mixing function, that is, there exist functions $\beta_1 \in L_+^\infty(\Omega)$, $\beta_2 \in L_+^\infty(\mathbf{R}_+ \times \Omega)$ and a number $\alpha > 1$ such that

$$(1.6) \qquad \beta_1(\xi)\beta_2(\tau,\eta) \le \beta(\tau,\xi,\eta) \le \alpha\beta_1(\xi)\beta_2(\tau,\eta),$$

where $\inf_{\xi\in\Omega} \beta_1 > 0$ and $\beta_2(\tau,\eta) > 0$ for almost all $(\tau,\eta) \in \mathbf{R}_+ \times \Omega$.

(3) The following holds uniformly for $(\tau,\eta) \in \mathbf{R}_+ \times \Omega$,

$$(1.7) \qquad \lim_{h\to 0}\int_\Omega |\beta(\tau,\xi+h,\eta) - \beta(\tau,\xi,\eta)|\,d\xi = 0.$$

Although we omit the proof, it easily follows from the assumption 1 that G is a positive linear operator from $L_+^1(\mathbf{R}_+ \times \Omega)$ into itself and the following holds:

Proposition 1.2. *Under the Assumption 1.1, K is a nonsupporting and compact operator.*

From the theory of nonsupporting operators ([12]), it follows that the spectral radius $r(K)$ is the dominant positive eigenvalue of K associated with a positive eigenfunction. Moreover, we can state that the Malthusian parameter

$$(1.8) \qquad \lambda_0 := \lim_{t\to\infty}\frac{\log\|b(t,\cdot)\|_{L^1}}{t},$$

exists and the sign relation $\operatorname{sgn}(\lambda_0) = \operatorname{sgn}(R_0 - 1)$ holds ([7]). Then the epidemic outbreak occurs if $R_0 > 1$, while it does not if $R_0 < 1$.

2. The initial value problem and a result for compact domain

First let us consider an epidemic starting from time $t = 0$, that is, the initial data is given at $t = 0$. Integrating the McKendrick equation in (1.1) along the characteristic line, we have

$$i(t,\tau,\xi) = \begin{cases} B(t-\tau,\xi)\Gamma(\tau,\xi), & t-\tau > 0, \\ \frac{\Gamma(\tau,\xi)}{\Gamma(\tau-t,\xi)}i(0,\tau-t,\xi), & \tau-t > 0, \end{cases}$$

where $B(t,\xi) := i(t,0,\xi) = -\dot{S}(t,\xi)$ is the density of newly infected individuals. Then we obtain that

$$(2.1) \qquad \frac{\dot{S}(t,\xi)}{S(t,\xi)} = -\lambda(t,\xi) = \int_0^t \int_\Omega \Psi(\tau,\xi,\eta)\dot{S}(t-\tau,\eta)d\eta d\tau - G[i_0](t,\xi),$$

where $i_0 := i(0,\tau,\xi)$.

Define the *cumulative force of infection* as

$$\Lambda(t,\xi) := \int_0^t \lambda(x,\xi)dx = -\log\frac{S(t,\xi)}{S_0(\xi)},$$

where it is assumed that $S_0(\xi) = S(0,\xi) > 0$. By integrating both sides of (2.1) with respect to t from 0 to t, a nonlinear renewal equation is obtained:

$$(2.2) \qquad \Lambda(t,\xi) = g(t,\xi) + \int_0^t \int_\Omega \Psi(\tau,\xi,\eta)S_0(\eta)f(\Lambda(t-\tau,\eta))d\eta d\tau,$$

where

$$f(x) := 1 - e^{-x}, \quad g(t,\xi) := \int_0^t G[i_0](\sigma,\xi)d\sigma.$$

As is shown in [2], a convenient framework for the study of (2.2) is provided by the Banach space $C_T = C([0,T]; BC(\Omega))$ of continuous functions on $[0,T]$ with values in $BC(\Omega)$, which is the set of bounded continuous functions, equipped with the norm $\|\Lambda\|_{C_T} = \sup_{0\leq t\leq T} \|\Lambda(t,\cdot)\|_{BC(\Omega)}$. The reader may refer to [2] for precise assumptions for existence and uniqueness of solutions of (2.2).

From the basic assumption 1.1, it follows that

$$(2.3) \qquad \sup_{\xi\in\Omega} \int_\Omega \int_0^\infty \Psi(\tau,\xi,\eta)d\tau N(\eta)d\eta < \infty.$$

Then $\Lambda(t,\xi)$ is uniformly bounded, continuous and monotone increasing with respect to time t, so $\Lambda(\infty,\xi) := \lim_{t\to\infty}\Lambda(t,\xi)$ exists in the sense of uniform convergence in compact sets of Ω and it becomes the solution of the following limiting equation:

$$(2.4) \qquad \Lambda(\infty,\xi) = g(\infty,\xi) + \int_\Omega \int_0^\infty \Psi(\tau,\xi,\eta)d\tau S_0(\eta)f(\Lambda(\infty,\eta))d\eta.$$

The *intensity of epidemic* or the *final size of epidemic* at ξ is defined by

$$(2.5) \qquad p(\xi) := 1 - \frac{S(\infty,\xi)}{N(\xi)} = 1 - \frac{S_0(\xi)}{N(\xi)}e^{-\Lambda(\infty,\xi)}.$$

The intensity of epidemic (final size) was named by Bailey ([1]), although it was originally introduced by Kermack and McKendrick ([9]). The final size is the proportion of the total number of host individuals that finally contracts the disease provided that the initial population is composed of susceptibles and infecteds. It should be remarked that some authors have used a different definition of final size. Diekmann ([2]) called $\Lambda(\infty,\xi)$ the final size. In Rass and Radcliffe ([14]), the authors consider a model of *epidemics initiated from outside*, in which an epidemic in a totally susceptible host population is triggered by infected individuals introduced from outside who do not compose the total host population $N(\xi)$, so the final size is the proportion of the total number of the "initial susceptibles" that finally contracts the disease. In our notations, Rass and Radcliffe assume that $S_0(\xi) = N(\xi)$ and its final size is $1 - S(\infty,\xi)/S_0(\xi)$.

Based on the above limiting equation, Kendall's pandemic threshold theorem ([8]) has been extended to the infection-age structured Kermack–McKendrick model by Diekmann ([2]). Let

$$s_0 := \inf_{\xi \in \Omega} S_0(\xi), \quad \psi_0 := \inf_{\xi \in \Omega} \int_{\Omega} \int_0^{\infty} \Psi(\tau, \xi, \eta) d\tau d\eta.$$

In Theorem 4.1 of Diekmann (1978), it is proved that if (1) Ω is compact and connected; (2) $s_0 \psi_0 f(x) > x$ for $0 < x < q$; (3) for each $\xi \in \Omega$ there exists $\delta = \delta(\xi) > 0$ such that the set $\{x : |x - \xi| \le \delta\} \cap \Omega$ is contained in the support of $\int_0^{\infty} \Psi(\tau, \xi, \cdot) d\tau$, then $\Lambda(\infty, \xi) \ge q$ for all $\xi \in \Omega$, where q is the largest nonnegative root of $R_*(1 - e^{-x}) = x$ with $R_* := s_0 \psi_0$. Observe that

$$p(\xi) \ge 1 - e^{-\Lambda(\infty, \xi)} \ge 1 - e^{-q} = \frac{q}{R_*}.$$

Therefore if $R_* > 1$, a positive lower bound of $p(\xi)$ is given by the unique positive root $p = q/R_*$ of the intensity equation $1 - x = e^{-R_* x}$.

This threshold result tells us that if $R_* > 1$, the epidemic outbreak ultimately occurs everywhere in Ω no matter how small the initial infected population is (the *hair-trigger effect*). Although we omit the argument, Diekmann ([2])shows that the same kind of threshold result holds for non compact domain $\Omega = \mathbf{R}$ or $\Omega = \mathbf{R}^2$ when the transmission coefficient β is given by a separable function as $\beta(\tau, \xi, \eta) = \beta_1(\tau)\beta_2(\xi - \eta)$.

On the other hand, we should remark that Diekmann's pandemic threshold result is not based on the basic reproduction number R_0. Let us check the difference between the threshold number R_* and R_0. Now let us check the difference between R_* and R_0. Let f^* be the adjoint positive eigenfunctional of K associated with eigenvalue $R_0 = r(K)$. From the definition of the next generation operator K, we have $KS_0 \ge R_* N$. Then we have

$$\langle f^*, KS_0 \rangle = \langle K^* f^*, S_0 \rangle = R_0 \langle f^*, S_0 \rangle \ge R_* \langle f^*, N \rangle.$$

Therefore we obtain

$$R_0 \ge \frac{\langle f^*, N \rangle}{\langle f^*, S_0 \rangle} R_* \ge R_*,$$

which implies that the condition $R_* > 1$ is a stronger condition than the invasion condition $R_0 > 1$. Moreover, we can not calculate R_* without knowledge of the initial density of infecteds or susceptibles, although it is usually difficult to know the size of initial infecteds.

Thus we investigate an open problem for the model (1.1) whether there exists a positive lower bound of the intensity of epidemic given as a positive solution of the final size equation, which does not include the initial data, if $R_0 > 1$. Since R_0 can be calculated without data of initial infecteds, such a lower bound is useful to estimate the severity of epidemic in the real world.

3. THE FINAL SIZE OF THE LIMIT EPIDEMIC

In the following, let us consider the *limit epidemic* starting from a completely susceptible steady state at $t = -\infty$, that is, the size of initial infecteds is assumed to be infinitesimally small. In the real, an epidemic in a large scale population can start from few cases, the limit epidemic model is useful as the bench mark. In the following, although I formally introduce the limit epidemic model to formulate the

final size equation, the reader may refer to section 4.1 of [13] for more mathematically rigorous introduction of the limit epidemic model as a limiting equation of the initial problem (2.2) and its nonlinear renewal theorem[2].

Integrating the McKendrick equation in (1.1) along the characteristic line, we have

$$i(t, \tau, \xi) = B(t - \tau, \xi)\Gamma(\tau, \xi),$$

where

$$B(t, \xi) := i(t, 0, \xi) = \lambda(t, \xi)S(t, \xi) = -\dot{S}(t, \xi),$$

is the density of newly infected individuals. Then we obtain that

$$(3.1) \qquad \frac{\dot{S}(t, \xi)}{S(t, \xi)} = -\lambda(t, \xi) = \int_0^\infty \int_\Omega \Psi(\tau, \xi, \eta)\dot{S}(t - \tau, \eta)d\eta d\tau,$$

Define the cumulative force of infection as

$$\Lambda(t, \xi) := \int_{-\infty}^t \lambda(x, \xi)dx = -\log\frac{S(t, \xi)}{N(\xi)},$$

where we set as $S(-\infty, \xi) = N(\xi) > 0$ for all $\xi \in \Omega$.

By integrating both sides of (3.1) with respect to t from $-\infty$ to t, we obtain a nonlinear renewal equation:

$$(3.2) \qquad \Lambda(t, \xi) = \int_0^\infty \int_\Omega \Psi(\tau, \xi, \eta)N(\eta)f(\Lambda(t - \tau, \eta))d\eta d\tau.$$

Again $\Lambda(t, \xi)$ is uniformly bounded, continuous and monotone increasing with respect to time t, so $\Lambda(\infty, \xi) := \lim_{t \to \infty} \Lambda(t, \xi)$ exists and it becomes the solution of the following limiting equation:

$$(3.3) \qquad \Lambda(\infty, \xi) = \int_\Omega \int_0^\infty \Psi(\tau, \xi, \eta)d\tau N(\eta)f(\Lambda(\infty, \eta))d\eta.$$

Let us define the intensity of epidemic at state ξ for the limit epidemic by

$$(3.4) \qquad p_\infty(\xi) := 1 - \frac{S(\infty, \xi)}{N(\xi)} = 1 - \frac{S(\infty, \xi)}{S(-\infty, \xi)}.$$

Then $p_\infty(\xi)$ gives the ultimate proportion of recovered individuals at trait ξ, which is the final size of the limit epidemic at ξ. Using $p_\infty(\xi)$ and the fact that $S(\infty, \xi) = N(\xi)e^{-\Lambda(\infty, \xi)}$, we have

$$p_\infty(\xi) = 1 - e^{-\Lambda(\infty, \xi)},$$

then equation (3.3) can be written as

$$(3.5) \qquad -\log(1 - p_\infty(\xi)) = \int_\Omega \int_0^\infty \Psi(\tau, \xi, \eta)d\tau N(\eta)p_\infty(\eta)d\eta.$$

In the following, we seek a positive solution of (3.5) in L^∞. It is easy to see that L^∞-solution becomes a solution in $BC(\Omega)$ if we assume the continuity of the initial data and $\beta(\tau, \xi, \eta)$ with respect to ξ.

Equation (3.5) is rewritten as the final size *operator* equation as follows:

$$(3.6) \qquad 1 - \phi(\xi) = \exp(-(U^{-1}KU\phi)(\xi)), \quad \phi \in L_+^\infty(\Omega),$$

where $U : L^\infty \to L^1$ is a multiplication operator defined by

$$(U\phi)(\xi) := N(\xi)\phi(\xi).$$

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[2]The reader may also refer to section 8.4 of [4] for the spatial extension of the limit epidemic model, although its elaboration of Exercise 8.26 has something wrong.

Then we know that if the final size operator equation equation (3.6) has a positive solution, it gives the final size distribution of the limit epidemic satisfying (3.5).

To seek the positive solution, let us rewrite (3.5) as a fixed point equation $x = F(x)$ on $L^1(\Omega)$, where $x := U\phi$ and

$$(3.7) \qquad F(x) := U(1 - \exp(-(U^{-1}Kx))).$$

Then F is a positive operator from $L^1_+(\Omega)$ into a convex bounded set $\mathcal{D} := \{N\psi \in L^1_+(\Omega) : 0 \leq \psi \leq 1, \psi \in L^\infty(\Omega)\}$, and its Fréchet derivative at the origin, denoted by $F'[0]$, is the next generation operator K. If F has a positive fixed point $x \in \mathcal{D}$, $U^{-1}x$ gives a positive solution of the final size equation (3.6) in $L^\infty_+(\Omega)$.

Lemma 3.1. *Under the assumption 1.1, the positive operator F does not have two distinct non-zero fixed point in the cone.*

Proof. From Lemma 4.8 in [6], it is sufficient to show that under the assumption 1.1, the positive operator F is monotone and concave in $E_+ = L^1_+(\Omega)$ and there exists a $u_0 \in E_+ \setminus \{0\}$ such that for any $x \in E_+$ and any $0 < t < 1$, there exists a number $\eta = \eta(x,t) > 0$ satisfying

$$(3.8) \qquad F(tx) \geq tF(x) + \eta u_0.$$

Since the monotonicity of F is clear, we show that $F(x)$, $x \in E_+ \setminus \{0\}$ is comparable with N. Observe that $F(x) \leq N$ for any $x \in E_+$. On the other hand, we can observe that

$$(U^{-1}Kx)(\xi) \geq \langle z^*, x \rangle,$$

where $z^* := \inf \beta_1 x^*$ is a strictly positive functional on $L^1_+(\Omega)$, and x^* is a positive functional. Therefore we have for any $x \in L^1_+(\Omega) \setminus \{0\}$

$$0 < (1 - e^{-\langle z^*, x \rangle})N \leq F(x) \leq N.$$

Next observe that

$$F(tx) - tF(x) = U[1 - e^{-tU^{-1}Kx} - t(1 - e^{-U^{-1}Kx})],$$

where

$$1 - e^{-tU^{-1}Kx} - t(1 - e^{-U^{-1}Kx}) > 0,$$

if $U^{-1}Kx > 0$ for $t \in (0,1)$. Since $U^{-1}Kx \geq \langle z^*, x \rangle > 0$ for $x \in E_+ \setminus \{0\}$, inequality (3.8) holds when we choose $u_0 = N$ and a number

$$\eta(x,t) := 1 - e^{-t\langle z^*, x \rangle} - t(1 - e^{-\langle z^*, x \rangle}),$$

because $1 - e^{-tx} - t(1 - e^{-x})$ is a monotone function of x. Therefore F is a concave operator and satisfies the inequality (3.8). $\qquad \square$

Proposition 3.2. *Under the assumption 1.1, the final size operator equation (3.6) has a unique positive solution if $R_0 > 1$, while it has no positive solution if $R_0 \leq 1$.*

Proof. By using the same kind of argument as Proposition 4.6 in [6], it follows that F has at least one positive fixed point in $\mathcal{D}$ if $R_0 = r(K) = r(F'[0]) > 1$, and it follows from Lemma 3.1 that it is a unique positive solution. On the other hand, observe that the inequality $U^{-1}Kx > 1 - \exp(-U^{-1}Kx)$ holds for all $x \in L^1_+(\Omega) \setminus \{0\}$, which implies that $F'[0]x = Kx > F(x)$[3]. Suppose that there exists a

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[3]According to the convention of positive operator theory, here $x > y$ means that $x - y \in L^1_+(\Omega) \setminus \{0\}$.

positive fixed point $x = F(x)$. Then we have $Kx > x$. Let x^* be a strictly positive eigenfunctional of K^* associated with $r(K) = R_0$. Then it follows that

$$\langle x^*, Kx \rangle = \langle K^* x^*, x \rangle = r(K)\langle x^*, x \rangle > \langle x^*, x \rangle,$$

which implies that $r(K) > 1$, because $\langle x^*, x \rangle > 0$. Then there is no positive fixed point if $R_0 = r(K) \leq 1$. $\qquad\square$

4. A Pandemic Threshold Theorem

Next let us consider the initial value problem of (1.1) that an epidemic starts at $t = 0$ in a host population composed of susceptibles and infecteds. Suppose that $S(0, \xi) = S_0(\xi) \in L^1_+(\Omega)$ and $i(0, \tau, \xi) = i_0(\tau, \xi) \in L^1_+(\mathbb{R}_+ \times \Omega)$ are initial data such that

$$(4.1) \qquad N(\xi) = S_0(\xi) + \int_0^\infty i_0(\tau, \xi) d\tau.$$

Let ϵ be the size of initial infective population:

$$\epsilon := \int_0^\infty \int_\Omega i_0(\tau, \xi) d\xi d\tau,$$

and let $u_0(\tau, \xi)$ be the normalized initial distribution given by $i_0(\tau, \xi) = \epsilon u_0(\tau, \xi)$. Then we have

$$g(t, \xi) = \int_0^t G[i_0](\sigma, \xi) d\sigma = \epsilon g_0(t, \xi),$$

where

$$g_0(t, \xi) := \int_0^t G[u_0](\sigma, \xi) d\sigma.$$

From assumption 1.1, we have $g_0(\infty, \xi) < \infty$. In the following, $N(\xi)$ and $u_0(\tau, \xi)$ are assumed to be fixed functions, although ϵ (so S_0) can change.

Let $\Lambda(t, \xi; \epsilon)$ be the solution of the renewal equation:

$$(4.2) \qquad \Lambda(t, \xi; \epsilon) = \epsilon g_0(t, \xi) + \int_\Omega \int_0^\infty \Psi(\tau, \xi, \eta) d\tau S_0(\eta) f(\Lambda(t, \eta; \epsilon)) d\eta.$$

Then $\Lambda(\infty, \xi; \epsilon) := \lim_{t \to \infty} \Lambda(t, \xi; \epsilon)$ is a positive root of the limiting equation:

$$(4.3) \qquad \Lambda(\infty, \xi; \epsilon) = \epsilon g_0(\infty, \xi) + \int_\Omega \int_0^\infty \Psi(\tau, \xi, \eta) d\tau S_0(\eta) f(\Lambda(\infty, \eta; \epsilon)) d\eta.$$

Since the solution Λ is constructed by a positive iteration from the initial data ϵg_0 and f is monotone increasing, $\Lambda(\infty, \xi; \epsilon)$ is monotone increasing with respect to ϵ.

Let us define the intensity of epidemic at state ξ by

$$(4.4) \qquad p(\xi) := 1 - \frac{S(\infty, \xi)}{N(\xi)} = 1 - \frac{S_0(\xi)}{N(\xi)} e^{-\Lambda(\infty, \xi; \epsilon)}.$$

and the cumulative force of infection by

$$\Lambda(t, \xi; \epsilon) := \int_0^t \lambda(x, \xi) dx = -\log \frac{S(t, \xi)}{S_0(\xi)}.$$

Then $p(\xi)$ gives the ultimate proportion of recovered individuals at trait ξ, which is the final size of the epidemic at ξ with initial infecteds' distribution $i_0 = \epsilon u_0$.

Define a function $z \in L^1_+(\Omega)$ by

$$z(\xi; \epsilon) := N(\xi)(1 - \exp(-\Lambda(\infty, \xi; \epsilon))) = N(\xi)\left(1 - \frac{S(\infty, \xi)}{S_0(\xi)}\right).$$

Then $z(\xi;\epsilon)$ is a monotone increasing function of ϵ, since $\Lambda(\infty,\xi;\epsilon)$ is monotone increasing with respect to ϵ.

From equation (4.3), it follows that

(4.5) $$z \geq U(1 - \exp(-U^{-1}KI_\epsilon z)),$$

where $I_\epsilon : L^1 \to L^1$ is a multiplication operator defined by

$$(I_\epsilon\phi)(\xi) := \frac{S_0}{N}\phi = \left(1 - \frac{\epsilon}{N(\xi)}\int_0^\infty u_0(\tau,\xi)d\tau\right)\phi(\xi).$$

Let us consider an associated operator equation in $L^1_+(\Omega)$:

(4.6) $$y = U(1 - \exp(-U^{-1}KI_\epsilon y)) =: F_\epsilon(y).$$

Lemma 4.1. *Suppose that $R_0 > 1$. For sufficiently small $\epsilon > 0$, fixed point equation (4.6) has a unique positive solution $y(\xi;\epsilon)$ in $L^1_+(\Omega)$.*

Proof. Let $F'_\epsilon[0]$ be the Fréchet derivative of F_ϵ at the origin. Then $F'_\epsilon[0] \to F'[0]$ in the sense of operator norm when $\epsilon \downarrow 0$. Therefore it follows from $R_0 = r(F'[0]) > 1$ that for sufficiently small $\epsilon > 0$, we can assume that $r(F'_\epsilon[0]) > 1$. By repeating the same kind of argument as proof of Proposition 3.2, we conclude that fixed point equation (4.6) has a unique positive solution $y(\xi;\epsilon)$ in $L^1_+(\Omega)$. $\square$

Lemma 4.2. *If $R_0 > 1$, it holds that*

(4.7) $$\lim_{\epsilon\downarrow 0} z(\xi;\epsilon) = \lim_{\epsilon\downarrow 0} y(\xi;\epsilon) = N(\xi)p_\infty(\xi).$$

Proof. If we take a sufficiently small $\epsilon' > 0$ in advance, it follows from Lemma 4.1 that the positive solution y of (4.6) exists for all $\epsilon \in (0,\epsilon')$. Define a sequence $\{y_n\}_{n=0,1,2,..}$ by $y_n = F_\epsilon(y_{n-1})$ with $y_0 = z$. Then we have $y_0 = z \geq F_\epsilon(y_0) = y_1$. Since F_ϵ is a monotone operator, we have a positive monotone decreasing series $y_0 \geq y_1 \geq \cdots$. Since F_ϵ is a monotone concave operator such that it has a unique nonzero fixed point in the normal cone, then y_n converges to the unique nonzero fixed point $y = y(\xi;\epsilon)$ of F_ϵ (see Krasnoselskii 1964,Theorem 6.6). Then we have $z \geq \lim_{n\to\infty} y_n = y > 0$. Since $\lim_{\epsilon\downarrow 0} y = \lim_{\epsilon\downarrow 0} F_\epsilon(y) = F(\lim_{\epsilon\downarrow 0} y)$, we have $\lim_{\epsilon\downarrow 0} y = p_\infty N$. On the other hand, we can observe that

$$N(\xi)p_\infty(\xi) = N(\xi) - S(\infty,\xi) \geq \frac{N(\xi)}{S_0(\xi)}(S_0(\xi) - S(\infty,\xi)) = z(\xi;\epsilon),$$

so $\lim_{\epsilon\downarrow 0} z \geq \lim_{\epsilon\downarrow 0} y = p_\infty N \geq \lim_{\epsilon\downarrow 0} z$, which shows (4.7). $\square$

Proposition 4.3. *For the intensity of epidemic $p(\xi)$ given by (4.4), it holds that*

(4.8) $$\lim_{\epsilon\downarrow 0} p(\xi) \geq p_\infty(\xi),$$

where p_∞ is the final size of the limiting epidemic satisfying (3.5).

Proof. Suppose that $R_0 > 1$. Observe that

$$p(\xi) = 1 - \frac{S_0(\xi)}{N(\xi)}e^{-\Lambda(\infty,\xi;\epsilon)} \geq 1 - e^{-\Lambda(\infty,\xi;\epsilon)} = \frac{z(\xi,\epsilon)}{N(\xi)}.$$

Taking a limit $\epsilon \downarrow 0$, we obtain (4.8) from (4.7). On the other hand, $p(\xi) \geq p_\infty(\xi)$ trivially holds if $R_0 \leq 1$, because $p_\infty = 0$ when $R_0 \leq 1$. $\square$

5. Conclusions

From the above Proposition 4.3, we conclude that the well-known threshold theorem for the early Kermack–McKendrick model that the lower bound of the final size of an epidemic is given by the final size of the limit epidemic ([13], section 4.1) can be extended to recognize individual heterogeneity described by distributed parameters. Instead of assuming connectivity and compactness of the heterogeneity parameter domain, or separable mixing assumption for transmission kernel, we adopted conditions such that the next generation operator becomes a compact nonsupporting operator, which guarantees the existence of the basic reproduction number. Although it is advantage that our framework can be applied to non-compact domain of heterogeneity parameter, it does not yet cover cases such that the next generation operator is not compact and nonsupporting, or the transmission coefficient β is not comparable with a separable mixing function. However, even in such more general situations, we believe that the basic reproduction number R_0 in a general sense ([7]) will act as the threshold value.

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