GLOBAL STABILITY OF A CLASS OF DISCRETE
AGE-STRUCTURED SIS MODELS WITH IMMIGRATION

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Abstract. Immigration has an important influence on the growth of population and the transmission dynamics of infectious diseases. A discrete age-structured epidemic SIS model with immigration is formulated and its dynamical behavior is studied in this paper. It is found that population growth will be determined by the reproductive number and the immigration rate. In the simple case without infected immigration, the basic reproductive number is defined, and the global stability of equilibria is investigated. In the case with infected immigration, there is no disease-free equilibrium, and there always exists an endemic equilibrium, and the global stability conditions of the unique endemic equilibrium is obtained.

1. **Introduction.** The transmission of infectious disease is closely associated with migration at different levels. The demography of migration from higher prevalence nations to lower prevalence nations will increase infection. The movement of population among different areas in a country has impact on infectious disease. Travel may increase the possibility of transmission. Therefore, it is natural to integrate the immigration factor into epidemiological models and to investigate the influence of immigration on the transmission of an infectious disease.

Age is another important factor when we investigate the dynamics of infectious diseases, if the vital parameters (the transmission rate, the recovery rate) are related with age. Age-structured SIS models can provide better insight into the spread process of the infectious diseases. Some continuous age-structured epidemic models have been formulated and studied [7, 17, 3]. The dynamical behavior of age-structured epidemic models is more difficult to study, it is also not easy to collect enough data to estimate parameter functions in continuous age-structured models. Compared to the continuous ones, the well-posedness of discrete age-structured epidemic models is obvious; statistical data of discrete models are piled weekly, monthly, or yearly. Discrete models also exhibit richer dynamical behavior.

Discrete models in population dynamics have been extensively studied [5, 16, 14]. Formulations and analyses of discrete models in epidemiology are relatively few. Allen studied discrete SI, SIS, SIR epidemic models and found that SI and SIR models are similar in behavior to their continuous analogues under some natural restriction, and an SIS model can have more diverse behavior [1]. Castillo-Chavez and Yakubu studied a discrete SIS model which exhibits bistability over a wide range

of parameter values [4]. Mendez and Fort investigated the dynamical evolution of discrete epidemic models by taking into account an intermediate class of population [11]. Li and Wang constructed a discrete SIS epidemic model with stage structure. Two kinds of recruitment rates are used to show the complicated dynamics[10]. Zhang and Shi studied the oscillation and global asymptotic stability of a discrete epidemic model[15]. Sabatier et al. used a mathematical model to explore the phenomenology of the epidemic process in a sheep flock and the potential impact of an outbreak, according to several biological hypotheses and flock management practices[13]. Innocenzoa, Paladinia, and Renna analyzed discrete-time deterministic epidemic models numerically to determine their properties and evolutions. They found oscillations when a small fraction of individuals became not permanently immunised. The smaller the probability that a recovered becomes susceptible, the larger the period of the oscillations in the infected population[9]. Ramani et al. studied an epidemic model where the cured individuals are not permanently immunized; they found that the epidemic does not follow the usual pattern of growth and decay but rather oscillates towards a fixed point[12]. Allen and Thrasher formulated an age-dependent model for varicella and herpes zoster; the effects of various control strategies are investigated[2]. Zhou and Fergola formulated a general discrete age-structured SIS model and investigated the dynamical behavior of the model [18].

In this paper a general discrete age-structured SIS model with immigration is formulated. The dynamical behavior of the model is studied theoretically and numerically. The outline of the paper is organized as follows: the discrete age-structured population model with immigration is discussed in Section 2. The discrete age-structured SIS models without and with infected immigration are studied in Section 3 and Section 4, respectively. The comparison principle is used to prove the global stability of equilibria. Numerical simulation is given in Section 5, and concluding remarks are presented in Section 6.

2. **Discrete age-structured population model with immigration.** Since birth rate and death rate are closely age dependent, we assume that the individuals of the same age have the same probability of death and birth. And we divide the population into $m + 1$ subgroups according to their age. Let $N_j(t), j = 0, 1, 2, ...m$ denote the number of individuals whose age is between the interval $[jA/(m+1), (j+1)A/(m+1))$ at time t, where A is the maximal age that an individual can reach. The classical discrete age-structured population model is[8]

$$N_0(t + 1) = \sum_{k=0}^{m} b_k N_k(t), \quad N_{j+1}(t + 1) = p_j N_j(t), \tag{1}$$

where $p_j = 1 - d_j > 0$ is the survival rate of the individuals in group j, d_j is the death rate, $j = 0, 1, ..., m - 1$. b_j is the birth rate of the individuals in group j, and there exist m_1 and m_2, $0 < m_1 < m_2 < m$ such that $b_j > 0$ for $m_1 \le j \le m_2$. By using notations

$$\vec{N}(t) = \begin{pmatrix} N_0(t) \\ N_1(t) \\ N_2(t) \\ ... \\ N_m(t) \end{pmatrix} \quad \text{and} \quad L = \begin{pmatrix} b_0 & b_1 & b_2 & ... & b_{m-1} & b_m \\ p_0 & 0 & 0 & ... & 0 & 0 \\ 0 & p_1 & 0 & ... & 0 & 0 \\ ... & ... & ... & ... & ... & ... \\ 0 & 0 & 0 & ... & p_{m-1} & 0 \end{pmatrix}, \tag{2}$$

(1) is written as the classical Leslie model

$$\vec{N}(t+1) = L\vec{N}(t),$$

where L is called the Leslie matrix. In the rest part of the paper the Leslie matrix L refers to the definition given in (2).

The Leslie matrix L has a simple and dominant eigenvalue ρ_0, corresponding to a positive eigenvector $\vec{v}_0$. The net reproductive number of the Leslie model is defined to be

$$n = b_0 + b_1 p_0 + b_2 p_1 p_0 + ... + b_j p_{j-1} p_{j-2}...p_1 p_0 + ... + b_m p_{m-1} p_{m-2}...p_1 p_0.$$

The biological interpretation of n is the average number of offsprings produced by an individual over his whole life span[6]. n plays a crucial role in the dynamical behavior of the solutions. The population will go to extinction if $n < 1$. The population will tend to a stable age distribution if $n = 1$, and, the total number of the population will go to infinity if $n > 1$. In any case the age structured population model (1) has a stable age profile, i.e.,

$$\lim_{t \to \infty} \frac{\vec{N}(t)}{\rho_0^t} = c_0 \vec{v}_0.$$

The dynamical behavior of the classical age-structured population model (1) is simple since it is linear and does not have any immigration. Let us assume that the immigration to age group j is a_j, $j = 0, 1, ..., m$, then the age-structured population model with immigration is

$$N_0(t+1) = a_0 + \sum_{k=0}^{m} b_k N_k(t), \tag{3}$$
$$N_{j+1}(t+1) = a_{j+1} + p_j N_j(t), \quad j = 0, 1, ..., m-1,$$

where $a_j \geq 0$ is the input population in age group j. With the notation $\vec{a} = (a_0, a_1\, a_2, ..., a_m)^\tau$, the age-structured population model with immigration (3) can be written as

$$\vec{N}(t+1) = \vec{a} + L\vec{N}(t). \tag{4}$$

The recurrent calculation gives

$$\vec{N}(t+1) = (E + L + L^2 + ... + L^{t-1})\vec{a} + L^t\vec{N}(1), \tag{5}$$

where E is the identical $(m+1) \times (m+1)$ matrix. If the Leslie matrix L has no eigenvalue 1, model (5) can be written as

$$\vec{N}(t+1) = (E - L)^{-1}(E - L^t)\vec{a} + L^t\vec{N}(1). \tag{6}$$

If $\vec{v}$ is an eigenvector corresponding to the eigenvalue ρ of the matrix L, then $L^n\vec{v} = \rho^n\vec{v}$. If $\vec{v}$ is a generalized eigenvector corresponding to the eigenvalue ρ of the matrix L, satisfying $(L - \rho E)^2\vec{v} = \vec{0}$, then $L^n\vec{v} = n\rho^{n-1}L\vec{v} - (n-1)\rho^n\vec{v}$. If $\vec{v}$ is a generalized eigenvector corresponding to the eigenvalue ρ of the matrix L, satisfying $(L - \rho E)^k\vec{v} = \vec{0}$, then

$$L^k\vec{v} = \sum_{j=1}^{k} C_k^j (-1)^{j+1} \rho^j L^{k-j}\vec{v}.$$

By using this formula we have

$$L^{k+1}\vec{v} = \sum_{j=1}^{k} C_k^j (-1)^{j+1} \rho^j L^{k-j+1} \vec{v}$$

$$= k\rho L^k \vec{v} + \sum_{j=2}^{k} C_k^j (-1)^{j+1} \rho^j L^{k-j+1} \vec{v}$$

$$= k\rho \sum_{j=1}^{k} C_k^j (-1)^{j+1} \rho^j L^{k-j} \vec{v} + \sum_{j=2}^{k} C_k^j (-1)^{j+1} \rho^j L^{k-j+1} \vec{v}$$

$$= \sum_{j=1}^{k-1} C_k^j \frac{(k+1)j}{j+1} (-1)^{j+1} \rho^{j+1} L^{k-j} \vec{v} + k(-1)^{k+1} \rho^{k+1} \vec{v}$$

$$= \sum_{j=1}^{k} C_k^j \frac{(k+1)j}{j+1} (-1)^{j+1} \rho^{j+1} L^{k-j} \vec{v}.$$

Further calculation and mathematical induction yield

$$L^{k+n}\vec{v} = \sum_{j=1}^{k} C_k^j \frac{(k+1)(k+2)...(k+n)j}{n!(j+n)} (-1)^{j+1} \rho^{j+n} L^{k-j} \vec{v}. \tag{7}$$

In fact, if expression (7) holds for n, then

$$L^{k+n+1}\vec{v} = \sum_{j=1}^{k} C_k^j \frac{(k+1)(k+2)...(k+n)j}{n!(j+n)} (-1)^{j+1} \rho^{j+n} L^{k-j+1} \vec{v}$$

$$= \frac{k(k+1)...(k+n)}{(n+1)!} \rho^{n+1} L^k \vec{v}$$

$$+ \sum_{j=2}^{k} C_k^j \frac{(k+1)(k+2)...(k+n)j}{n!(j+n)} (-1)^{j+1} \rho^{j+n} L^{k-j+1} \vec{v}$$

$$= \sum_{j=1}^{k} C_k^j \frac{(k+1)(k+2)...(k+n+1)j}{(n+1)!(j+n+1)} (-1)^{j+1} \rho^{j+n+1} L^{k-j} \vec{v}.$$

From the theory of nonnegative matrix we know that the Leslie matrix L has a dominant eigenvalue ρ_0. ρ_0 is simple and positive. ρ_0 has a positive eigenvector $\vec{v}_0$. The module of other eigenvalues ρ_j of the matrix L is strictly less than ρ_0, i.e., $|\rho_j| < \rho_0$, $j = 1, 2, ..., m$. Let ρ_j be the eigenvalues of L, and $\vec{v}_j$, $j = 0, 1, ..., m$, be the eigenvectors or generalized vectors corresponding to the eigenvalue ρ_j. $\vec{v}_0$, $\vec{v}_1$, ..., $\vec{v}_m$ form the basis of the $m + 1$ dimensional Euclidian space R^{m+1}. The immigration vector $\vec{a}$ and the initial population vectors $\vec{N}(1)$ can be expressed to be the linear combination of those eigenvectors or generalized eigenvectors:

$$\vec{a} = \alpha_0 \vec{v}_0 + \alpha_1 \vec{v}_1 + ... + \alpha_m \vec{v}_m = \sum_{j=0}^{m} \alpha_j \vec{v}_j,$$

$$\vec{N}(1) = c_0 \vec{v}_0 + c_1 \vec{v}_1 + ... + c_m \vec{v}_m = \sum_{j=0}^{m} c_j \vec{v}_j.$$

Substituting expressions of $\vec{a}$ and $\vec{N}(1)$ into the expression of (5) we get

$$\vec{N}(t+1) = \sum_{i=0}^{t-1}\sum_{j=0}^{m}\alpha_j L^i \vec{v}_j + \sum_{j=0}^{m} c_j L^t \vec{v}_j.$$

If every eigenvalue of L is simple, and $\rho_0 > 1$ we have

$$\lim_{t\to\infty}\frac{\vec{N}(t+1)}{\rho_0^t} = \lim_{t\to\infty}\left(\sum_{i=0}^{t-1}\sum_{j=0}^{m}\alpha_j\frac{\rho_j^i}{\rho_0^t}\vec{v}_j + \sum_{j=0}^{m}c_j\frac{\rho_j^t}{\rho_0^t}\vec{v}_j\right)$$

$$= \lim_{t\to\infty}\left(\sum_{j=0}^{m}\alpha_j\frac{1/\rho_0^t - \rho_j^t/\rho_0^t}{1-\rho_j}\vec{v}_j + \sum_{j=0}^{m}c_j\frac{\rho_j^t}{\rho_0^t}\vec{v}_j\right)$$

$$= \frac{\alpha_0\vec{v}_0}{\rho_0-1} + c_0\vec{v}_0 = \left(\frac{\alpha_0}{\rho_0-1}+c_0\right)\vec{v}_0.$$

The inequality $C_k^j\dfrac{(k+1)(k+2)...(k+n+1)j}{(n+1)!(j+n+1)} = \dfrac{(n+2)(n+3)...(n+k+1)j}{j!(k-j)!(j+n+1)} \le$ $(n+k+1)^k$ implies that $\lim_{n\to\infty}\dfrac{(n+k+1)^k}{r^n} = 0$ for $r > 1$. If ρ_{j_0} is a multiple eigenvalue of L with a generalized eigenvector $\vec{v}_{j_0}$ such that $(L - \rho_{j_0}E)^k \vec{v}_{j_0} = \vec{0}$, we can have $|\rho_{j_0}/\rho_0| < 1$ and

$$\lim_{t\to\infty}\frac{L^{k+t}\vec{v}_{j_0}}{\rho_0^t} = \lim_{t\to\infty}\sum_{j=1}^{k}C_k^j\frac{(k+1)(k+2)...(k+t)j}{t!(j+t)}\left(\frac{\rho_{j_0}}{\rho_0}\right)^t(-1)^{j+1}\rho_{j_0}^j L^{k-j}\vec{v}_{j_0} = 0.$$

Therefore, we can obtain

$$\lim_{t\to\infty}\frac{\vec{N}(t+1)}{\rho_0^t} = \lim_{t\to\infty}\left(\alpha_0\sum_{i=0}^{t-1}\frac{1}{\rho_0^{t-i}}\vec{v}_0 + c_0\vec{v}_0 + \sum_{i=0}^{t-1}\sum_{j=1}^{m}\alpha_j\frac{L^i\vec{v}_j}{\rho_0^t} + \sum_{j=1}^{m}c_j\frac{L^t\vec{v}_j}{\rho_0^t}\right)$$

$$= \frac{\alpha_0\vec{v}_0}{\rho_0-1} + c_0\vec{v}_0 + \lim_{t\to\infty}\left((E-L)^{-1}\sum_{j=1}^{m}\alpha_j\frac{(E-L^t)\vec{v}_j}{\rho_0^t} + \sum_{j=1}^{m}c_j\frac{L^t\vec{v}_j}{\rho_0^t}\right)$$

$$= \left(\frac{\alpha_0}{\rho_0-1}+c_0\right)\vec{v}_0.$$

If $\rho_0 < 1$ we have

$$\lim_{t\to\infty}\vec{N}(t+1) = \lim_{t\to\infty}\left((E-L)^{-1}(E-L^t)\vec{a} + L^t\vec{N}(1)\right) = (E-L)^{-1}\vec{a}.$$

The expression of $(E-L)^{-1} = E + L + L^2 + ... + L^n + ...$ implies that $(E-L)^{-1}\vec{a} \ge 0$.

The dominant eigenvalue $\rho_0 = 1$ will lead to linear population increase. We can decompose the $\vec{a}$ and $\vec{N}(1)$ to be $\vec{a} = \alpha_0\vec{v}_0 + \vec{v}_a$, $\vec{N}(1) = c_0\vec{v}_0 + \vec{v}_N$, where $\vec{v}_a$ and $\vec{v}_N$ are in the complement space of the eigenvector $\vec{v}_0$:

$$\lim_{t\to\infty}\frac{\vec{N}(t+1)}{t} = \lim_{t\to\infty}\frac{1}{t}\left(\sum_{i=0}^{t-1}L^i(\alpha_0\vec{v}_0 + \vec{v}_a) + L^t(\vec{v}_0 + \vec{v}_N)\right)$$

$$= \lim_{t\to\infty}\frac{1}{t}\left(t\alpha_0\vec{v}_0 + \sum_{i=0}^{t-1}L^i\vec{v}_a + \vec{v}_0 + L^t\vec{v}_N\right) = \alpha_0\vec{v}_0.$$

We summarize our results in following theorem.

Theorem 2.1. *For the discrete age-structured population model with immigration,* (3), *the population will tend to a globally asymptotically stable equilibrium if $n < 1$, and it will tend to stable age distributions if $n \geq 1$. That is,*

$$
\begin{aligned}
\lim_{t \to \infty} \vec{N}(t+1) &= (E - L)^{-1}\vec{a}, && if \;\; n < 1, \\
\lim_{t \to \infty} \frac{\vec{N}(t+1)}{\rho_0^t} &= \left(\frac{\alpha_0}{\rho_0 - 1} + c_0 \right) \vec{v}_0, && if \;\; n > 1, \\
\lim_{t \to \infty} \frac{\vec{N}(t+1)}{t} &= \alpha_0 \vec{v}_0, && if \;\; n = 1.
\end{aligned}
\tag{8}
$$

In the rest of this paper we focus on the dynamics of the epidemiological models and assume that the total population reaches its equilibrium or stable age distribution, i.e., $N_j(t) = N_j^*$ if $\rho_0 < 1$, or $N_j(t) = \rho_0^t N_j^*$ if $\rho_0 > 1$, where N_j^* is defined by the right hand of (8), respectively.

3. **Age-structured SIS model with susceptible immigration.** Consider an infectious disease spreading in a population. We divide the population into susceptible and infectious subgroups, and assume that there is no infected immigration and all the immigrants are susceptibles. Let $S_j(t)$ and $I_j(t)$ denote the number of the susceptible and infected populations, respectively. We assume that all the newborns are in the susceptible group S_0. After one unit time the susceptibles in group S_j can live to become part of group S_{j+1}, or be infected to become part of group I_{j+1}, or die. The infected in group I_j can transfer to group I_{j+1}, or recover to group S_{j+1}, or die. The discrete age-structured SIS model with susceptible immigrants is

$$
\begin{aligned}
S_0(t+1) &= a_0 + \sum_{k=0}^{m} b_k N_k(t), && t = 0, 1, 2, 3, ..., \\
S_{j+1}(t+1) &= a_j + p_j S_j(t) - \lambda_j \sum_{k=0}^{m} \beta_k I_k(t) \frac{p_j S_j(t)}{N_j(t)} + \gamma_j p_j I_j(t), && j = 0, 1, ...m - 1, \\
I_0(t+1) &= 0, && \\
I_{j+1}(t+1) &= p_j I_j(t) + \lambda_j \sum_{k=0}^{m} \beta_k I_k(t) \frac{p_j S_j(t)}{N_j(t)} - \gamma_j p_j I_j(t), && j = 0, 1, ...m - 1, \\
S_j(0) &= S_{j0} \geq 0, \;\; I_j(0) = I_{j0} \geq 0, && j = 0, 1, ...m,
\end{aligned}
\tag{9}
$$

where $\beta_k \lambda_j$ is the transmission rate between an infected in group k and a susceptible in group j, γ_j is the recovery rate of infected individuals in group j. We assume that λ_j, β_j and γ_j are positive, $j = 0, 1, ..., m$. In order to make our notations and analysis simple, we combine λ_j and p_j (γ_j and p_j) to be one parameter. We still use λ_j (γ_j) to stand for the $\lambda_j p_j$ ($\gamma_j p_j$) in model (9). Model (9) has following simple

form:

$$S_0(t+1) = a_0 + \sum_{k=0}^{m} b_k N_k(t), \qquad\qquad\qquad t = 0, 1, 2, 3, ...,$$

$$S_{j+1}(t+1) = a_j + p_j S_j(t) - \lambda_j \sum_{k=0}^{m} \beta_k I_k(t) \frac{S_j(t)}{N_j(t)} + \gamma_j I_j(t), \qquad j = 0, 1, ... m-1,$$

$$I_0(t+1) = 0,$$

$$I_{j+1}(t+1) = p_j I_j(t) + \lambda_j \sum_{k=0}^{m} \beta_k I_k(t) \frac{S_j(t)}{N_j(t)} - \gamma_j I_j(t), \qquad j = 0, 1, ... m-1,$$

$$S_j(0) = S_{j0} \geq 0, \quad I_j(0) = I_{j0} \geq 0, \qquad\qquad j = 0, 1, ... m.$$
$$(10)$$

When the dominant eigenvalue of L is less than 1, the total population will tend to an equilibrium value. We study the asymptotical behavior of Model (10) in the case that the total population reaches the equilibrium value, i.e., $N_j(t) = N_j^*$, $j = 0, 1, 2, ..., m$. Using the fact that $S_j(t) + I_j(t) = N_j^*$ the SIS model (10) can be reduced to

$$I_0(t+1) = 0,$$

$$I_{j+1}(t+1) = (p_j - \gamma_j) I_j(t) + \lambda_j \sum_{k=1}^{m} \beta_k I_k(t) \left(1 - \frac{I_j(t)}{N_j^*}\right), \quad j = 0, 1, ... m-1,$$

$$I_j(0) = I_{j0}, \quad j = 0, 1, ... m.$$
$$(11)$$

The existence and uniqueness of the solution of the initial value problem (11) are obvious. The solution (11) is nonnegative if the following conditions hold [18]

$$(A) \quad \lambda_0 \sum_{k=1}^{m} \beta_k N_k^* \leq N_1^*, \quad d_j + \gamma_j + \frac{\lambda_j}{N_j^*} \sum_{k=1}^{m} \beta_k N_k^* \leq 1, \quad j = 1, 2, ..., m-1.$$

We can show that the domain

$$D = \{(I_1, I_2, ..., I_m) \mid 0 \leq I_j \leq N_j^*, \quad j = 1, 2, ..., m\}$$

is positively invariant for the model; that is, the solution of (11) with the initial value in D will keep being in D for all $t = 1, 2, ...$ In fact, if $0 \leq I_j(t) \leq N_j^*$, $j = 1, 2, ... m$, and condition (A) holds, then we have

$$I_{j+1}(t+1) = I_j(t) \left(1 - d_j - \gamma_j - \frac{\lambda_j}{N_j} \sum_{k=1}^{m} \beta_k I_k(t)\right) + \lambda_j \sum_{k=1}^{m} \beta_k I_k(t) \geq 0,$$

$$I_{j+1}(t+1) \leq (p_j - \gamma_j) I_j(t) + \lambda_j \sum_{k=1}^{m} \beta_k N_k^* \left(1 - \frac{I_j(t)}{N_j^*}\right)$$

$$\leq (p_j - \gamma_j) I_j(t) + (p_j - \gamma_j) N_j^* \left(1 - \frac{I_j(t)}{N_j^*}\right)$$

$$= (p_j - \gamma_j) N_j^* \leq p_j N_j^* = N_{j+1}^*, \quad j = 0, 1, ... m-1.$$

In [18] the basic reproductive number of (11) was defined; the global stability of the disease-free equilibrium was obtained if $R_0 < 1$. It was proved that the disease-free equilibrium is unstable if $R_0 > 1$. The existence and the local stability of the

endemic equilibrium were discussed when $0 < R_0 - 1 \ll 1$. Now, let us investigate the existence and global stability of the endemic equilibrium of (11) for $R_0 > 1$. The components $I_1^*, I_2^*, ..., I_m^*$ of the endemic equilibrium satisfy the following equations

$$I_1^* = \lambda_0 \sum_{k=1}^{m} \beta_k I_k^*,$$

$$I_{j+1}^* = (p_j - \gamma_j)I_j^* + \lambda_j \sum_{k=1}^{m} \beta_k I_k^* \left(1 - \frac{I_j^*}{N_j^*}\right), \quad j = 1, 2, ..., m-1. \tag{12}$$

We introduce the notations

$$\vec{I}^* = \begin{bmatrix} I_1^* \\ I_2^* \\ I_3^* \\ ... \\ I_m^* \end{bmatrix}, \quad B = \begin{bmatrix} 0 & 0 & ... & 0 & 0 \\ p_1 - \gamma_1 & 0 & ... & 0 & 0 \\ 0 & p_2 - \gamma_2 & ... & 0 & 0 \\ ... & ... & ... & ... & ... \\ 0 & 0 & ... & p_{m-1} - \gamma_{m-1} & 0 \end{bmatrix},$$

$$\vec{\lambda} = \begin{bmatrix} \lambda_0 \\ \lambda_1 \\ \lambda_2 \\ ... \\ \lambda_{m-1} \end{bmatrix}, \quad Q = \begin{bmatrix} 0 & 0 & ... & 0 & 0 \\ \lambda_1/N_1^* & 0 & ... & 0 & 0 \\ 0 & \lambda_2/N_2^* & ... & 0 & 0 \\ ... & ... & ... & ... & ... \\ 0 & 0 & ... & \lambda_{m-1}/N_{m-1}^* & 0 \end{bmatrix}.$$

The equilibrium equation for I_j^* can be written as

$$\vec{I}^* = \vec{\lambda}x + B\vec{I}^* - xQ\vec{I}^*, \tag{13}$$

where, $x = \beta_1 I_1^* + \beta_2 I_2^* + ... + \beta_m I_m^* = (\vec{\beta} \cdot \vec{I}^*)$, "$\cdot$" denotes the dot product of two vectors. $\vec{I}^*$ has the expression

$$\vec{I}^* = x(E - B)^{-1}(\vec{\lambda} - Q\vec{I}^*),$$

where E is the identity $m \times m$ matrix, and $(E - B)$ is invertible since $\det(E - B) = 1$. From the definition of B, we know that the inverse $(E - B)^{-1} = E + B + B^2 + ... + B^{m-1}$ is nonnegative. The definition of x implies $x = 0$, or

$$g(\vec{I}^*) = (\vec{\beta} \cdot (E - B)^{-1}(\vec{\lambda} - Q\vec{I}^*)) - 1 = 0. \tag{14}$$

The basic reproductive number of model (11) is defined to be $R_0 = \vec{\beta} \cdot (E - B)^{-1}\vec{\lambda}$. From the expression of $(E - B)^{-1}$ we see that

$$R_0 = \vec{\beta} \cdot E\vec{\lambda} + \vec{\beta} \cdot B\vec{\lambda} + \vec{\beta} \cdot B^2\vec{\lambda} + ... + \vec{\beta} \cdot B^{m-2}\vec{\lambda} + \vec{\beta} \cdot B^{m-1}\vec{\lambda}.$$

If we introduce one infected individual in every age group into the community with all individuals in the population susceptible, the secondary infection by those infected in the first year is $\vec{\beta} \cdot E\vec{\lambda}$, the secondary infected by those infected in the second year is $\vec{\beta} \cdot B\vec{\lambda}$, the secondary infection by those infected in the third year is $\vec{\beta} \cdot B^2\vec{\lambda}$, and the secondary infection by those infected in the mth year is $\vec{\beta} \cdot B^{m-1}\vec{\lambda}$. Subsequently, the biological interpretation of R_0 is the secondary infection if we introduce one infected individual in every age group to a whole susceptible pool. The discrete age-structured SIS model (11) has only the disease free equilibrium $\vec{I}^* = 0$ ($x = 0$) if $R_0 < 1$. When $R_0 > 1$, it is easy to see that $g(\vec{0}) = (\vec{\beta} \cdot (E - B)^{-1}\vec{\lambda}) - 1 = R_0 - 1 > 0$. When $\vec{I}^* = (N_1^*, N_2^*, ..., N_m^*)^\tau$, $x = \sum_{j=1}^{m} \beta_j N_j^*$, $\vec{\lambda} - Q\vec{I}^* = (\lambda_0, 0, 0, ..., 0)^\tau$, and $g(\vec{I}^*) = \lambda_0\beta_1 - 1 < 0$, since $\lambda_0 \sum_{k=1}^{m} \beta_k N_k^* \leq N_1^*$ in condition (A) implies $\lambda_0\beta_1 < 1$. Therefore, the existence of endemic equilibrium of (11) was established for $R_0 > 1$.

Theorem 3.1. *Assume condition (A) holds and $R_0 > 1$. Then model (11) has an endemic equilibrium $I^*(I_0^*, I_1^*, I_2^*, ..., I_m^*)$, which is globally asymptotically stable for positive initial value in D.*

Proof. The global attraction of the endemic equilibrium for the solutions with positive initial values can be proved by comparison principle. The derivative of $I_{j+1}(t+1)$ with respect to $I_k(t)$ is

$$\frac{\partial I_{j+1}(t+1)}{\partial I_k(t)} = \begin{cases} \lambda_j \beta_k \left(1 - \dfrac{I_j(t)}{N_j^*}\right), & k \neq j, \\[2mm] \lambda_j \beta_j \left(1 - \dfrac{I_j(t)}{N_j^*}\right) + 1 - d_j - \gamma_j - \dfrac{\lambda_j}{N_j^*} \sum_{k=1}^m \beta_k I_k(t), & k = j. \end{cases}$$

Under this assumption we see that $\dfrac{\partial I_{j+1}(t+1)}{\partial I_k(t)} \geq 0$; that is, the solution of model (11) is monotone with the initial conditions. For any solution of (11) with positive initial value $I_j(0)$, we can choose a small positive ε such that

$$\varepsilon I_j^* \leq I_j(0), \quad j = 1, 2, ..., m.$$

The comparison principle shows that

$$I_j^\varepsilon(t) \leq I_j(t), \quad j = 1, 2, ..., m, \quad t = 1, 2, ...,$$

where $I_j^\varepsilon(t)$ is the solution of (11) with the initial value $I_j^\varepsilon(0) = \varepsilon I_j^*$, and $I_j(t)$ is the solution of (11) with the initial value $I_j(0)$. For the solution $I_j^\varepsilon(t)$ we see that

$$\begin{aligned} I_{j+1}^\varepsilon(1) &= (p_j - \gamma_j)\varepsilon I_j^* + \varepsilon \lambda_j \sum_{k=1}^m \beta_k I_k^* \left(1 - \frac{\varepsilon I_j^*}{N_j^*}\right) \\ &= \varepsilon I_{j+1}^* + \varepsilon \lambda_j \sum_{k=1}^m \beta_k I_k^* \frac{(1-\varepsilon)I_j^*}{N_j^*} \\ &\geq \varepsilon I_{j+1}^* \left(1 + \lambda_j \beta_{j+1} \frac{(1-\varepsilon)I_j^*}{N_j^*}\right) \\ &\geq \varepsilon I_{j+1}^*(1 + (1-\varepsilon)\sigma), \end{aligned} \tag{15}$$

where $\sigma < \sigma_0$, and σ_0 is a positive number,

$$\sigma_0 = \min\left\{\frac{1}{10}, \ \lambda_1 \beta_2 \frac{I_1^*}{N_1^*}, \ \lambda_2 \beta_3 \frac{I_2^*}{N_2^*}, \ ..., \ \lambda_{m-1} \beta_m \frac{I_{m-1}^*}{N_{m-1}^*}\right\}.$$

The similar process shows this:

$$I_{j+1}^\varepsilon(2) \geq \varepsilon(1 + (1-\varepsilon)\sigma)I_{j+1}^*(1 + (1 - \varepsilon(1 + (1-\varepsilon)\sigma)\sigma).$$

The mathematical induction shows that

$$I_{j+1}(t) \geq \varepsilon_t I_{j+1}^*, \ t = 0, 1, 2, ...,$$

where ε_t is determined by following recurrent equation

$$\varepsilon_0 = \varepsilon, \ \varepsilon_{t+1} = \varepsilon_t\big(1 + (1 - \varepsilon_t)\sigma\big), \ t = 0, 1, 2, ...$$

It is easy to see that $\{\varepsilon_t\}_{t=0}^{+\infty}$ is a monotonically increasing sequence, satisfying $0 < \varepsilon_t < 1$ if $0 < \varepsilon_0 < 1$ and $0 < \sigma < \sigma_0 < 1/10$. Therefore, the limit $\lim_{t\to+\infty} \varepsilon_t$ exists and is greater than 0. The fact that

$$\lim_{t\to+\infty} \varepsilon_{t+1} = \lim_{t\to+\infty} \varepsilon_t\big(1 + (1 - \lim_{t\to+\infty} \varepsilon_t)\sigma\big)$$

implies that $\lim_{t \to +\infty} \varepsilon_t = 1$. Hence, for any given positive number η, $I_{j+1}(t) > (1 - \eta)I_{j+1}^*$ holds if t is large enough.

Now let us consider the solution of (11) with the initial value $I_j(0) = N_j^*$, $j = 1, 2, ..., m$. The solution of (11) satisfies

$$I_1(1) = \lambda_0 \sum_{k=1}^{m} \beta_k N_k^* < N_1^*,$$

$$I_{j+1}(1) = (p_j - \gamma_j)N_j^* < N_{j+1}^*, \quad j = 1, 2, ..., m-1,$$

If we use $I_j(1)$, $j = 1, 2, ..., m$ as the new initial value the comparison theorem implies $I_j(2) \leq I_j(1)$, $j = 1, 2, ..., m$. The mathematical induction shows that the solution of (11) with initial value $I_j(0) = N_j^*$ is a monotonically decreasing sequence $I_j(t + 1) \leq I_j(t)$, $j = 1, 2, ..., m$. The monotonicity of $I_j(t) \geq 0$ implies that the $\lim_{t \to +\infty} I_j(t) = I_j^{**}$, $j = 1, 2, ..., m$. The limit I_j^{**}, $j = 1, 2, ..., m$ satisfies the equation

$$I_{j+1}^{**} = (p_j - \gamma_j)I_j^{**} + \lambda_j \sum_{k=1}^{m} \beta_k I_k^{**} \left(1 - \frac{I_j^{**}}{N_j^*} \right), \quad j = 0, 1, ...m-1.$$

Therefore, $I_j = I_j^{**}$, $j = 1, 2, ..., m$ is also the equilibrium solution of model (11). The comparison theorem shows that $I_j^{**} \geq I_j^*$, $j = 1, 2, ..., m$. If there is one j_0 such that $I_{j_0}^{**} > I_{j_0}^*$, we can choose a sufficiently small ξ such that $\xi I_j^{**} < I_j^*$, $j = 1, 2, ..., m$ hold. Consider two solutions of model (11) with the initial values ξI_j^{**} and I_j^*, respectively. The similar procedure can show that the solution with initial value ξI_j^{**} satisfies $I_j^{\xi}(t) > (1 - \eta)I_j^{**}$ for sufficiently large t and any sufficiently small positive η. The comparison principle shows that $I_j^{\xi}(t) \leq I_j^*, j = 1, 2, ..., m, t = 1, 2, ...$, i.e., $(1 - \eta)I_j^{**} \leq I_j^*$, especially, $(1 - \eta)I_{j_0}^{**} \leq I_{j_0}^*$. That contradiction shows that $I_j^{**} = I_j^*, j = 1, 2, ..., m$.

For any given solution of (11) with nonnegative initial value $I_j(0) > 0$, we can choose a small positive number ε such that $\varepsilon I_j^* \leq I_j(0) \leq N_j^*$. We have proved that the two solutions of (11) with initial values εI_j^* and N_j^* tend to the endemic equilibrium $\vec{I}^*$. Then, the comparison theorem implies $\lim_{t \to \infty} I_j(t) = I_j^*, j = 1, 2, ..., m$. The proof of global attraction of the endemic equilibrium is completed.

For any give positive number ε, we can choose a positive number $\delta = \varepsilon/(2\|\vec{I}^*\|)$, where $\| \cdot \|$ is the usual norm in finite Euclidean space, i.e., $\|(I_1, I_2, ..., I_m)\| = \sqrt{I_1^2 + I_2^2 + ... + I_m^2}$. For any solution with initial value satisfying $\|\vec{I}(0) - \vec{I}^*\| < \delta$ we have $|I_j(0) - I_j^*| < \delta$ and $(1 - \delta)I_j^* < I_j(0) < (1 + \delta)I_j^*$. Then, the comparison principle implies that $I_j^{-\delta}(t) < I_j(t) < I_j^{+\delta}(t)$, where $I_j^{-\delta}(t)$ and $I_j^{+\delta}(t)$ are solutions of (11) with initial value $I_j^{-\delta}(0) = (1 - \delta)I_j^*$ and $I_j^{+\delta}(0) = (1 + \delta)I_j^*$, respectively. $I_j^{-\delta}(t)$ is monotonically increasing and $I_j^{-\delta}(t) \geq I_j^{-\delta}(0) = (1 - \delta)I_j^*$. $I_j^{+\delta}(t)$ is monotonically decreasing and $I_j^{+\delta}(t) \leq I_j^{+\delta}(0) = (1 + \delta)I_j^*$. Therefore, $\|\vec{I}(t) - \vec{I}^*\| < \varepsilon$ for any $t \geq 0$. The endemic equilibrium is stable. The global stability of the endemic equilibrium follows from the local stability and global attraction. $\square$

From Theorem 2.1 we see that the total population in each age group will increase to infinity and the age distribution will tend to a stable profile if the dominant eigenvalue ρ_0 of L is greater than the unit. Now, we assume that the age distribution of the total population reaches the stable value, i.e., $N_j(t) = \rho_0^t N_j^*$. Using the fact

that $S_j(t) + I_j(t) = \rho_0^t N_j^*$ the SIS model (10) can be reduced to

$$I_0(t+1) = 0,$$

$$I_{j+1}(t+1) = (p_j - \gamma_j)I_j(t) + \lambda_j \sum_{k=1}^{m} \beta_k I_k(t) \left(1 - \frac{I_j(t)}{\rho_0^t N_j^*}\right), \quad j = 0, 1, ...m-1,$$

$$I_j(0) = I_{j0}, \quad j = 0, 1, ...m.$$

$$(16)$$

By using the new variables $\tilde{I}_j(t) = I_j(t)/\rho_0^t$ and parameters $\tilde{\beta}_j = \beta_j/\rho_0$, $\tilde{p}_j = p_j/\rho_0 = 1/\rho_0 - d_j/\rho_0$, $\tilde{\gamma}_j = \gamma_j/\rho_0$, $\tilde{d}_j = d_j/\rho_0$, $j = 0, 1, ..., m$, we have the similar model as that $\rho_0 < 1$

$$\tilde{I}_0(t+1) = 0,$$

$$\tilde{I}_{j+1}(t+1) = (\tilde{p}_j - \tilde{\gamma}_j)\tilde{I}_j(t) + \lambda_j \sum_{k=1}^{m} \tilde{\beta}_k \tilde{I}_k(t) \left(1 - \frac{\tilde{I}_j(t)}{N_j^*}\right), \quad j = 0, 1, ...m-1,$$

$$\tilde{I}_j(0) = \tilde{I}_{j0}, \quad j = 0, 1, ...m.$$

$$(17)$$

We use the similar assumption

$$(B) \quad \lambda_0 \sum_{k=1}^{m} \tilde{\beta}_k N_k^* \le N_1^*, \quad \tilde{d}_j + \tilde{\gamma}_j + \frac{\lambda_j}{N_j^*} \sum_{k=1}^{m} \tilde{\beta}_k N_k^* \le 1, \quad j = 1, 2, ..., m-1.$$

The basic reproductive number $\tilde{R}_0$ of model (17) can be defined the same way. We can obtain the similar stability result.

Theorem 3.2. *Assume condition (B) holds. The endemic equilibrium of model* (17) *is globally asymptotically stable if* $\tilde{R}_0 > 1$.

The proof of Theorem 3.2 is similar to Theorem 3.1 since equations in (17) have the same form as those in (11). The epidemiological explanation of Theorem 3.2 is different from Theorem 3.1. Theorem 3.1 implies that the number of infected individuals in each age group will tend to a constant, i.e., $\lim_{t\to\infty} I_j(t) = I_j^*$. While Theorem 3.2 says that the age distribution of the infected individuals in each age group will tend to a constant, i.e., $\lim_{t\to\infty} I_j(t)/\rho^t = \tilde{I}_j^*$.

4. **Age-structured SIS model with infected immigration.** If there is immigration in both susceptible and infected populations, the analysis becomes more complicated. Let ϕ_j and ψ_j, $\phi_j + \psi_j = a_j$ $j = 0, 1, 2, ..., m$, denote the immigration number of susceptible and infected populations in age group j, respectively. We assume that the new borns are in susceptible groups and $\psi_0 = 0$, $\phi_0 = a_0$. The SIS

model (corresponding to (10)) with immigration is

$$S_0(t+1) = \phi_0 + \sum_{j=1}^{m} b_j N_j(t), \qquad\qquad t = 0, 1, 2, 3, ...,$$

$$S_{j+1}(t+1) = \phi_{j+1} + p_j S_j(t) - \lambda_j \sum_{k=0}^{m} \beta_k I_k(t) \frac{S_j(t)}{N_j(t)} + \gamma_j I_j(t), \quad j = 0, 1, ...m-1,$$

$$I_0(t+1) = 0,$$

$$I_{j+1}(t+1) = \psi_{j+1} + p_j I_j(t) + \lambda_j \sum_{k=0}^{m} \beta_k I_k(t) \frac{S_j(t)}{N_j(t)} - \gamma_j I_j(t), \quad j = 0, 1, ...m-1,$$

$$S_j(0) = S_{j0} \geq 0, \quad I_j(0) = I_{j0} \geq 0, \quad \phi_j + \psi_j = a_j, \qquad j = 0, 1, ...m. \tag{18}$$

When the dominant eigenvalue ρ_0 of matrix L is less than the unit, the total population in each age group will tend to its equilibrium state, i.e., $\lim_{t\to\infty} N_j(t) = N_j^*$. Using the fact that $S_j(t) + I_j(t) = N_j^*$, the SIS model with immigration (18) can be reduced to

$$I_1(t+1) = \psi_1 + \lambda_0 \sum_{k=1}^{m} \beta_k I_k(t),$$

$$I_{j+1}(t+1) = \psi_{j+1} + (p_j - \gamma_j)I_j(t) + \lambda_j \sum_{k=1}^{m} \beta_k I_k(t) \left(1 - \frac{I_j(t)}{N_j^*}\right), \tag{19}$$

$$j = 1, 2, ..., m-1,$$

$$I_j(0) = I_{j0} > 0, \quad j = 1, 2, ..., m.$$

There is no disease-free equilibrium for SIS model (19) due to the infected immigration. Let I_j^* be the *jth* component of the equilibrium (19), and $x = \sum_{j=1}^{m} \beta_j I_j^*$. We can have following equations

$$I_1^* = \psi_1 + \lambda_0 x,$$

$$I_2^* = \psi_2 + (p_1 - \gamma_1)I_1^* + \lambda_1 x \left(1 - \frac{I_1^*}{N_1^*}\right),$$

$$I_{j+1}^* = \psi_{j+1} + (p_j - \gamma_j)I_j^* + \lambda_j x \left(1 - \frac{I_j^*}{N_j^*}\right), \quad j = 2, 3, ..., m-1. \tag{20}$$

By introducing the notation $\vec{\psi} = (\psi_1, \psi_2, ..., \psi_m)^\tau$ the equilibrium equation for I_j^* can be written as

$$\vec{I^*} = \vec{\psi} + \vec{\lambda} x + B\vec{I^*} - xQ\vec{I^*}, \tag{21}$$

where $\vec{I^*}$, $\vec{\lambda}$, B, and Q are the same as those defined in section 3. The equilibrium $\vec{I^*}$ has the expression

$$\vec{I^*} = (E - B)^{-1}\vec{\psi} + x(E - B)^{-1}(\vec{\lambda} - Q\vec{I^*}),$$

where E is the identity matrix of dimension m. The definition of $x = (\vec{\beta} \cdot \vec{I^*})$ implies

$$(\vec{\beta} \cdot (E - B)^{-1}\vec{\psi}) + x(\vec{\beta} \cdot (E - B)^{-1}(\vec{\lambda} - Q\vec{I^*})) - x = 0, \tag{22}$$

When $\vec{I^*} = 0$ $(x = 0)$ the left side of (22) is $(\vec{\beta} \cdot (E - B)^{-1}\vec{\psi}) > 0$. When $\vec{I^*} = \vec{N^*} = (N_1^*, N_2^*, ..., N_m^*)^\tau$, $x = (\vec{\beta} \cdot \vec{N^*}) = \sum_{j=1}^{m} \beta_k N_j^* \triangleq x_N^*$, and $x(\vec{\beta} \cdot$

$(E - B)^{-1}(\vec{\lambda} - Q\vec{I^*})) = \beta_1 \lambda_0 x_N^*$. The left side of (22) is $(\vec{\beta} \cdot (E - B)^{-1}\vec{\psi}) - \beta_1 \lambda_0 x_N^*$. The existence of endemic equilibrium of (19) is stated in following theorem.

Theorem 4.1. *Assume that the dominant eigenvalue of the Leslie matrix L is less than one. Then, the discrete age-structured SIS model (19) has an endemic equilibrium $\vec{I^*} = (I_1^*, I_2^*, ..., I_m^*)$ if $(\vec{\beta} \cdot (E - B)^{-1}\vec{\psi}) - \beta_1 \lambda_0 x_N^* < 0$.*

The condition $(\vec{\beta} \cdot (E - B)^{-1}\vec{\psi}) - \beta_1 \lambda_0 x_N^* < 0$ may not be necessary for the existence of the endemic equilibrium of model (19). We hope that this condition can be canceled by further detailed analysis.

The difference of the equation in model (19) and (11) is the constant immigration ψ_j. The extra term ψ_j does not change the monotonicity of the model with respect to its initial value. The similar procedure as we have used in Section 3 can show global stability of (19).

Theorem 4.2. *Assume that the dominant eigenvalue of the Leslie matrix L is less than one and the condition (A) holds. Then, the solution of (19) is monotonically increasing with the initial value, and the endemic equilibrium $(I_1^*, I_2^*, ..., I_m^*)$ is globally asymptotically stable if it exists.*

When the dominant eigenvalue of the Leslie matrix is greater than the unit, the total population will not have the equilibrium state; we assume that the total population reaches the stable age profile, $S_j(t) + I_j(t) = N_j(t) = \rho_0^t N_j^*$, and we have

$$I_1(t + 1) = \psi_1 + \lambda_0 \sum_{k=1}^{m} \beta_k I_k(t),$$

$$I_{j+1}(t + 1) = \psi_{j+1} + (p_j - \gamma_j)I_j(t) + \lambda_j \sum_{k=1}^{m} \beta_k I_k(t) \left(1 - \frac{I_j(t)}{\rho_0^t N_j^*}\right), \qquad (23)$$

$$j = 1, 2, ..., m - 1,$$

$$I_j(0) = I_{j0} > 0, \quad j = 1, 2, ..., m.$$

The presence of the infected immigration makes it impossible to transform model (23) to a simple and time independent model by variable changes. We can study following linear model

$$I_1(t + 1) = \psi_1 + \lambda_0 \sum_{k=1}^{m} \beta_k I_k(t),$$

$$I_{j+1}(t + 1) = \psi_{j+1} + (p_j - \gamma_j)I_j(t) + \lambda_j \sum_{k=1}^{m} \beta_k I_k(t), \qquad j = 1, 2, ..., m - 1, \qquad (24)$$

$$I_j(0) = I_{j0} > 0, \quad j = 1, 2, ..., m.$$

For the same initial values, the comparison theory implies that the solution of model (23) is less than the solution of model (24). The basic reproductive number of the linear model (24) is $R_0 = \vec{\beta} \cdot (E - B)^{-1}\vec{\lambda}$. The linear model (24) has a globally asymptotical endemic equilibrium if $R_0 < 1$. And the solution of (24) will go to infinity if $R_0 > 1$. From the comparison theorem we know that the solution of model (23) will be bounded if $R_0 < 1$. The solution of model (23) may be bounded or keep increasing if $R_0 > 1$. We will use numerical simulation to investigate the dynamical behavior of model (23) in the next section.

5. **Numerical simulation.** In this section we present numerical simulation for different dominant eigenvalue ρ_0 of the Leslie matrix L and for different basic reproductive number R_0. We use equivalent model equations for the total population and for the infected individuals. m is chosen to be 17, and the model is

$$N_0(t+1) = a_0 + \sum_{k=0}^{m} b_k N_k(t),$$

$$N_{j+1}(t+1) = a_{j+1} + p_j N_j(t), \qquad\qquad j = 0, 1, ..., 16,$$

$$N_j(0) > 0, \qquad\qquad j = 0, 1, ..., 17,$$

$$I_0(t+1) = 0, \quad I_1(t+1) = \psi_1 + \lambda_0 \sum_{k=0}^{m} \beta_k I_k(t), \qquad\qquad (25)$$

$$I_{j+1}(t+1) = \psi_{j+1} + (p_j - \gamma_j) I_j(t) + \lambda_j \sum_{k=1}^{m} \beta_k I_k(t) \left(1 - \frac{I_j(t)}{N_j(t)} \right),$$

$$j = 1, 2, ..., 16,$$

$$I_0(0) = 0, \quad I_j(0) = I_{j0} \geq 0, \qquad\qquad j = 1, 2, ..., 17.$$

The equations in the model for the total population are independent of others, and two sets of parameters are used to show different cases: $\rho_0 < 1$ and $\rho_0 > 1$. The death rate in different age groups is $\vec{d}$=(6.17, 0.58, 0.41, 0.62, 0.98, 1.14, 1.31, 1.60, 2.46, 3.39, 5.29, 8.59, 14.55, 23.91, 40.27, 62.84, 101.81, 161.04)/1000. The immigration is $\vec{a}$=(3, 4, 5, 6, 7, 8, 9, 10, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2). The initial value is (180, 179, 179, 179, 179, 178, 178, 178, 178, 177, 177, 176, 174, 172, 168, 161, 151, 135). The birth rate in the first case is $\vec{b}$=(0, 0, 0, 10.5, 245.34, 204.88, 76.56, 17.3, 3.54, 1.02, 0, 0, 0, 0, 0, 0, 0, 0)/1000. The birth rate for the second case is $4\vec{b}$. In the first case, the dominant eigenvalue ρ_0 of the Leslie matrix L is 0.9032. The total population has the globally asymptotical equilibrium $\vec{N}^*$ =(42.21, 45.95, 50.92, 56.90, 63.86, 71.80, 80.72, 90.61, 101.47, 111.22, 119.84, 127.21, 133.11, 137.18, 138.90, 137.30, 131.68, 120.27)$^\tau$. In the second case, the dominant eigenvalue ρ_0 of the Leslie matrix L is 1.1501. The total population increases to infinity; the stable age profile is $\vec{N}^*$ =273.52, 236.35, 205.38, 178.50, 155.11, 134.73, 117.01, 101.60, 88.20, 76.50, 66.29, 57.33, 49.42, 42.34, 35.94, 29.99, 24.44, 19.08)$^\tau$.

For the disease transmission parameters, we take $\vec{\lambda}$ =(5.7, 2.3, 3.3, 3.4, 4.1, 2.9, 3.7, 4.7, 3.3, 2.4, 3.1, 2.9, 3.8, 4.5, 5.2, 5.7, 5.9, 6.2)/100, $\vec{\beta}$=(4.6, 6.6, 6.8, 8.2, 5.8, 7.4, 9.4, 6.6, 4.8, 6.2, 5.8, 7.6, 7.2, 6.4, 5.6, 5.1, 4.5)/100, $\vec{\gamma}$=(0.16, 0.17, 0.18, 0.19, 0.20, 0.21, 0.22, 0.23, 0.24, 0.25, 0.25, 0.24, 0.24, 0.23, 0.22, 0.15, 0.10), and $\vec{\psi}$=(1,2,3,3,4,4,5,5,5,4,4,4,3,2,2,1,1). Three sets of the initial conditions are used in the simulation. Those initial values for $(I_1, I_2, ..., I_{17})$ are (20, 25, 30, 35, 40, 45, 50, 55, 50, 45, 40, 35, 30, 25, 20, 15, 10), (80, 100, 120, 140, 160, 180, 200, 220, 200, 180, 160, 140, 120, 100, 80, 60, 40), and (4, 5, 6, 7, 8, 9, 10, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2), respectively. We increase the transmission rate β to 5β and 10β to see the influence of β to the infected equilibrium. The result is shown in Figure 1. The abscissa is time; the vertical coordinate is the total population or infected population. The top left figure is the total population; the top right is the infected with transmission rate β; the bottom left is the infected with transmission rate 5β; the bottom right is the infected with transmission rate 10β. The total population and the infected tend to their equilibrium states. The total value of the population and the infected at their equilibrium states are 1761, 223, 840, 1394, respectively.
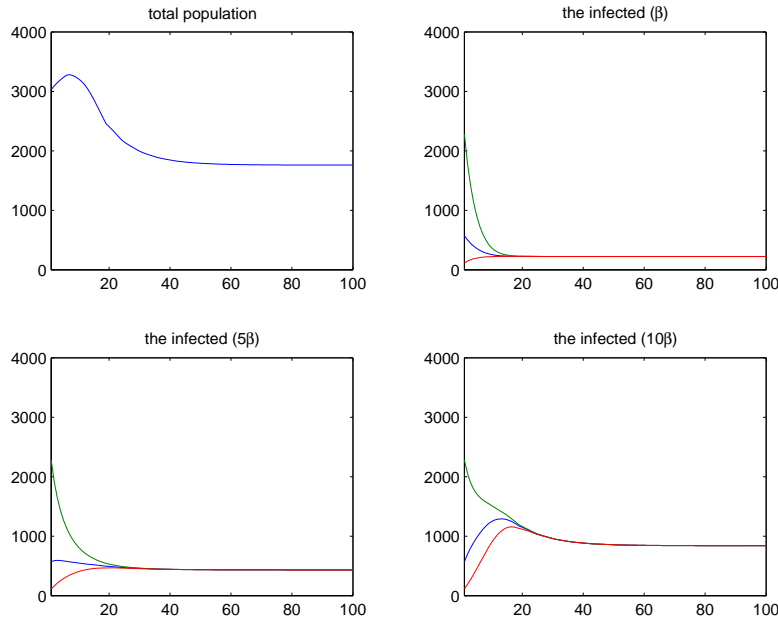
Figure 1.   The total population and total infected with different $\vec{\beta}$

Figure 2 shows the simulation results of model (25) with dominant eigenvalue $\rho_0 = 1.1501$. The birth rate of the population increases to $4\vec{b}$, and other parameters are kept the same as those in Figure 1. The total population keeps increasing very fast. While the infected numbers for the small and the middle $\vec{\beta}$ still tend to their equilibrium states. The total number of the infected for the given $\vec{\beta}$ is 227, only a little larger than that in Figure 1: 223. The total number of the infected for 5β is 674, even less than that in Figure 1: 840. The total number of the infected for the $10\vec{\beta}$ keeps increasing, and may go to infinity. Though the basic reproductive number defined in the previous section does not have the exact biological interpretation as the classical SIS or SIR model, the R_0 may still play an important role in the transmission of the spreading infectious disease.

6. **Concluding remarks.** The dynamics of the total population is important to the transmission of infectious disease. We have studied the dynamical behavior of the age-structured population model with immigration. The discussion is based on the classical Leslie matrix model. The net reproductive number n was defined and used as the threshold parameter to investigate the dynamical behavior. There exists a positive equilibrium and it is globally asymptotically stable if $n < 1$. There is no equilibrium and the number of the population will tend to infinity if $n > 1$. The population has a stable age profile even though the number of the population increases to infinity.

Under the assumption of fixed total population or stable age profile, the age-structured SIS model has been reduced to the model concerning equations of the infected and the total population. If there is no any infected immigration, the basic reproductive number R_0 determines the asymptotic behavior. The disease-free equilibrium is globally asymptotically stable if $R_0 < 1$. It is proved that there exists a globally asymptotically stable endemic equilibrium if $R_0 > 1$. The global stability
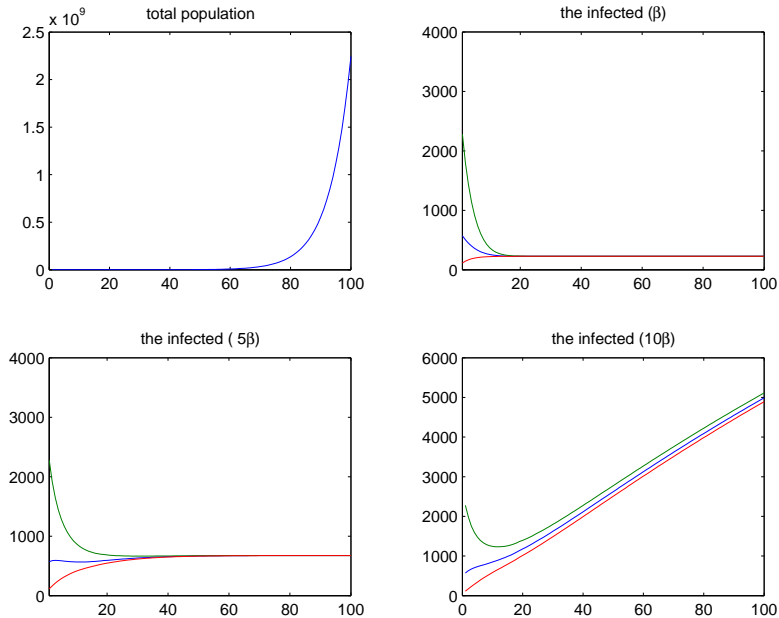
Figure 2. The total population and total infected with different $\vec{\beta}$

of endemic equilibrium is similar in both cases $n < 1$ and $n > 1$. Epidemiological interpretation is different: the number of infected individuals in every age group will tend to a positive constant if $n < 1$; the number of infected individuals will tend to a stable age profile, i.e., $\lim_{t \to +\infty} I_j(t)/\rho_0^t = \tilde{c}_j$, if $n > 1$. If there is immigration in both susceptible and infected populations, then there is no disease free-equilibrium. The endemic equilibrium is globally asymptotically stable for the equilibrium total population $(N_j(t) = N_j^*,\ n < 1)$. When $n > 1$ the SIS model with infected immigration becomes more complicated. The sufficient conditions for the boundedness of the infected population is obtained by comparison theory. The dynamical behavior of the model was investigated by numerical simulation.

Our discussion of the dynamical behavior of the age-structured SIS model is based on the natural condition (A) or (B). Condition (A) or (B) is biologically necessary since the solution of the model with positive initial values should be nonnegative. The condition is also sufficient to guarantee the monotonicity, which is crucial in mathematical analysis of the dynamics. Though the age-structured models of infectious diseases with immigration are more complicated, they are more realistic than models without age structure and immigration. There is very little research on discrete age-structured SIS models. The study in this paper improved and generalized our result in [18]. More data and detailed analysis on discrete age-structured epidemic models with immigration are the object of our current efforts.

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