Heterogeneous Susceptibles–Infectives model: Mechanistic derivation of the power law transmission function

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Abstract

In many epidemiological models a nonlinear transmission function is used in the form of power law relationship. It is constantly argued that such form reflects population heterogeneities including differences in the mixing pattern, susceptibility, and spatial patchiness, although the function itself is considered phenomenological. Comparison with large-scale simulations show that models with this transmission function accurately approximate data from highly heterogeneous sources. In this note we provide a mechanistic derivation of the power law transmission function, starting with a simple heterogeneous susceptibles–infectives (SI) model, which is based on a standard mass action assumption. We also consider the simplest SI model with separable mixing and compare our results with known results from the literature.

Keywords: SI epidemiological model, heterogeneous populations, transmission function, power law, separable mixing

AMS (MOS) subject classification: 34C20, 34G20, 92D30

1 Introduction

It is customary to consider transmission function $T(S, I)$, which describes the incidence rate, i.e., the number of new cases per time unit, as a main component of any epidemiological model [4, 20]. Here we use usual notations for susceptible and infective individuals denoting them as $S$ and $I$ respectively. Assuming that there is no influx of susceptible hosts in our model, we can write that

$$\frac{d}{dt}S(t) = -T(S, I).$$

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Historically the earliest form of the transmission function was a simple bilinear form, i.e., $T(S, I) = \beta SI$, which follows from the assumptions of random contacts, host homogeneity, and application of the law of mass action, thereby implying that the contact rate of any individual is a linear function of the population size (see [5] for more details). Here $\beta > 0$ is the transmission coefficient. Under the proportional mixing assumption (the contact rate is fixed), the transmission function takes the form $T(S, I) = \beta SI/N$, $N$ is a population size. If the model includes an assumption of the constant population size these two transmission functions are virtually the same from any practical viewpoint, whereas variable population size can yield dramatically different behaviors (e.g., [2, 3, 22]).

It was early acknowledged that other than bilinear or proportional mixing transmission functions should be used in epidemiological models to provide better fit of the model solutions to empirical data (see [20] for a general account of different models for transmission functions).

One of the most widely used functions has the following form:

$$T(S, I) = \beta S^p I^q, \quad p, q > 0.$$  \hspace{1cm} (1)

We will term this transmission function as power law relationship. It was first used in [29, 30] in the form $T(S, I) = \beta S^p I$ “to investigate the consequences of various assumptions when the laws are not known”. Severo [25] considered general form (11) where both $p$ and $q$ are not equal to one, though he did not give a detailed analysis of the model. Liu et al. [18, 19] gave a thorough analysis of different compartmental epidemiological models with (11) and showed that incorporating power law transmission function yields various dynamical behaviors not observable in models with bilinear incidence rate, e.g., limit cycles and multiple equilibrium points. Additional analysis and details of such models can be found in [9, 10].

Since the first use of the power law transmission function its form was explained on a basis of “intrinsic heterogeneity in mixing pattern” of a population under question. The exponents $p$ and $q$ were dubbed as “heterogeneity parameters” [25], but the model itself is considered phenomenological and lacking mechanical derivation [20] in contract to, e.g., bilinear relationship, which is based on a dubious but well established law of mass action [8].

The link between phenomenological power law incidence rate and population heterogeneity was made explicit when it was shown that such mean-field models can provide an accurate approximation to network based simulations that include variation in the strength, duration, and number of contacts per person. In [26] the transmission function was used in the form $T(S, I) = \beta S^p I$, whereas full non-linear transmission function was implemented in [24]. In both cases it was shown that power law relationship improves the accuracy of mean-field model predictions when compared with models with bilinear transmission function (see also [11] for a review on comparison of homogeneous and heterogeneous models).

In this note we show that power law transmission function can be not only postulated but also derived, using a simple heterogeneous SI model. The paper organized as follows.
In the next section we formulate a mechanistic heterogeneous SI model from the first principles. Section 3 gives a brief exposition of necessary analytical tools. In Section 4 we present the main results of the study showing that our heterogeneous model is equivalent to a homogeneous one, but with a non-linear transmission function.

2 Model formulation

Heterogeneity profoundly affects the dynamics of infection. Differences in contact rates, spatial distributions of susceptible hosts, infectiousness and susceptibility of individuals have a direct effect on disease dynamics. Here, we specifically look into heterogeneity in disease parameters (such as susceptibility) do not touching an important topics of heterogeneity mediated by a structured variable, such as explicit space or age structure. Our approach is close to the one given in, e.g., [6, 7, 27] (see also [23] for more details).

Model I. We start with a generic assumption that the subpopulation of susceptible hosts is heterogeneous, and denote $s(t, \omega)$ the density of susceptibles at time $t$ having parameter value $\omega$, which determines susceptibility to a particular disease and varies from individual to individual. The total size of the susceptibles is given by $S(t) = \int_{\Omega} s(t, \omega) d\omega$, where $\Omega$ is the set of parameter values. Assuming that the subpopulation of the infectives is homogeneous (later we relax this assumption), the contact process is described with the law of mass action, and the rate of change in the susceptibles is determined by transmission parameter, which is a function of $\omega$, we obtain that

$$\frac{\partial}{\partial t} s(t, \omega) = -\beta(\omega) s(t, \omega) I(t).$$

Here $\beta(\omega)$ incorporates information on the contact rate and the probability of a successful contact.

The change in the infective class is given by

$$\frac{d}{dt} I(t) = I(t) \int_{\Omega} s(t, \omega) d\omega = \bar{\beta}(t) S(t) I(t),$$

where we denote

$$\bar{\beta}(t) \int_{\Omega} p_s(t, \omega) d\omega, \quad p_s(t, \omega) = \frac{s(t, \omega)}{S(t)}.$$

Therefore, $\bar{\beta}(t)$ is the mean value of the function $\beta(\omega)$ with respect to probability density function $p_s(t, \omega)$ for any time $t$. We need the initial conditions for the model (2), (3):

$$s(0, \omega) = s_0(\omega) = S_0 p_s(0, \omega), \quad I(0) = I_0.$$

Here $S_0, I_0$ are given numbers, and $p_s(0, \omega)$ is a given initial distribution of the susceptibility in the population.
We note that formally, after integrating equation (2) with respect to $\omega$, we obtain a homogeneous SI model with non-constant transmission parameter $\bar{\beta}(t)$ which, in its turn, depends on the current distribution of susceptibility in the population. If $\bar{\beta}(t)$ is known then the problem is solved. Interesting to remark that ad hoc approach to use time-dependent transmission coefficient $\beta(t)$ in an SIR model was used to approximate a heterogeneous epidemics with a mean-field model [16].

Model II. Let us assume now that not only the susceptibles are heterogeneous for some trait that influences the disease evolution, but also the infectives are heterogeneous, and consider the simplest possible SI model. Let $s(t, \omega_1)$ and $i(t, \omega_2)$ be the densities of the susceptibles and infectives respectively, here we assume that the traits of the two classes are independent, i.e., $\beta(\omega_1, \omega_2) = \beta_1(\omega_1)\beta_2(\omega_2)$. The number of susceptibles with the trait value $\omega_1$ infected by individuals with trait value $\omega_2$ is given by $\beta_1(\omega_1)s(t, \omega_1)\beta_2(\omega_2)i(t, \omega_2)$, and the total change in the infective class with trait value $\omega_2$ is $\beta_2(\omega_2)i(t, \omega_2)\int_{\Omega_1} \beta_1(\omega_1)s(t, \omega_1) d\omega_1$; an analogous expression applies to the change in the susceptible population. We emphasize that nothing else except for the standard law of mass action is supposed to formulate the terms for the change in susceptible and infective subpopulations. Combining the above assumptions we obtain the following model:

$$\frac{\partial}{\partial t} s(t, \omega_1) = -\beta_1(\omega_1)s(t, \omega_1)\int_{\Omega_2} \beta_2(\omega_2)i(t, \omega_2) d\omega_2$$
$$= -\beta_1(\omega_1)s(t, \omega_1)\bar{\beta}_2(t)I(t),$$

$$\frac{\partial}{\partial t} i(t, \omega_2) = \beta_2(\omega_2)i(t, \omega_2)\int_{\Omega_1} \beta_1(\omega_1)s(t, \omega_1) d\omega_1$$
$$= \beta_2(\omega_2)i(t, \omega_2)\bar{\beta}_1(t)S(t).$$

Model (5) is supplemented with the initial conditions $s(0, \omega_1) = S_0, s(0, \omega_1), i(0, \omega_2) = I_0, i(0, \omega_2)$. In (5) it is assumed that if an individual having trait value $\omega_1$ was infected by an individual with trait value $\omega_2$ he or she becomes an infective with trait value $\omega_2$. This is a restrictive assumptions which is necessary to apply the main theorem from the next section.

The global dynamics of (5), as well as of (2)-(4), is simple and is similar to the simplest homogeneous SI model.

Model III. Above we were talking about heterogeneity of the hosts: whether all susceptible individuals are of the same type with equal susceptibility, and whether all infectious individuals have equal ability to infect others. Another aspect of heterogeneity is the possible heterogeneous social contact network [1]. It is difficult to apply the general theory of heterogeneous populations (see below) to such models, however, there is a simple case, for which some results can be obtained.
Let us assume that \( n(t, \omega) \) denotes the density of individuals in the population, which are making \( \omega \) contacts on average. Every individual can be contacted by another individual, which differs in an average number of contact per individual. This situation is usually termed as \textit{separable mixing}. If we denote \( r \) the probability of transmission the disease given a contact, then, the simplest SI-model with separable mixing can be described by the following system:

\[
\frac{\partial}{\partial t} s(t, \omega) = -r \omega s(t, \omega) \frac{\int_{\Omega} \omega i(t, \omega) d\omega}{\int_{\Omega} \omega n_0(\omega) d\omega},
\]

\[
\frac{\partial}{\partial t} i(t, \omega) = -r \omega s(t, \omega) \frac{\int_{\Omega} \omega i(t, \omega) d\omega}{\int_{\Omega} \omega n_0(\omega) d\omega},
\]

where \( s(t, \omega) + i(t, \omega) = n_0(\omega) \) for any \( t \), and \( n_0(\omega) \) is a given density which specifies probability density function of contact distribution. Using the property that \( i(t, \omega) = n_0(\omega) - s(t, \omega) \), we obtain

\[
\frac{\partial}{\partial t} s(t, \omega) = -r \omega s(t, \omega) \left[ 1 - \frac{\int_{\Omega} \omega s(t, \omega) d\omega}{\int_{\Omega} \omega n_0(\omega) d\omega} \right].
\]

Models (2)-(4), (5), and (7) are infinite dimensional dynamical systems. The special form of the models, however, allows us to use well developed tools of the theory of heterogeneous populations, which are presented in the following section.

3 Some facts from the theory of heterogeneous populations

Here we present some results from the theory of heterogeneous populations in the form suitable for our goal noting that more general cases can be analyzed [13]. For the proofs we refer to [15], where similar models are considered.

Let us assume that there are two interacting populations whose dynamics depend on trait values \( \omega_1 \) and \( \omega_2 \) respectively. The densities are given by \( n_1(t, \omega_1) \) and \( n_2(t, \omega_2) \), and the total population sizes \( N_1(t) = \int_{\Omega_1} n_1(t, \omega_1) d\omega_1 \) and \( N_2(t) = \int_{\Omega_2} n_2(t, \omega_2) d\omega_2 \). Obviously, more than two populations can be considered, or some populations may be supposed to be homogeneous. Assume next that the net reproduction rates of the populations have the specific form which is presented below:

\[
\frac{\partial}{\partial t} n_1(t, \omega_1) = n_1(t, \omega_1) [f_1(v_1) + \varphi_1(\omega_1) g_1(v_1)],
\]

\[
\frac{\partial}{\partial t} n_2(t, \omega_2) = n_2(t, \omega_2) [f_2(v_2) + \varphi_2(\omega_2) g_2(v_2)],
\]

where \( v_1 = (N_1, N_2, \bar{\varphi}_2(t)) \), \( v_2 = (N_1, N_2, \bar{\varphi}_1(t)) \), \( \varphi_i(\omega_i) \) are given functions, \( \bar{\varphi}_i(t) = \int_{\Omega_i} \varphi_i(\omega_i) p_i(t, \omega_i) d\omega_i \) are the mean values of \( \varphi_i(\omega_i) \), and \( p_i(t, \omega_i) = n_i(t, \omega_i)/N_i(t) \) are the
corresponding pdfs, \( i = 1, 2 \). We also assume that \( \varphi_i(\omega_i) \), considered as random variables, are independent. The system (8) plus the initial conditions

\[
n_i(0, \omega_i) = N_i(0)p_i(0, \omega_i), \quad i = 1, 2,
\]

defines, in general, a complex transformation of densities \( n_i(t, \omega_i) \). An effective approach to analyze models in the form (8) was suggested in [11] (examples of model analysis are given in [12, 14, 15, 21]).

Let us denote

\[
M_i(t, \lambda) = \int_{\Omega_i} e^{\lambda \varphi_i(\omega_i)} p_i(t, \omega_i) d\omega_i, \quad i = 1, 2,
\]

the moment generating functions (mgfs) of the functions \( \varphi_i(\omega_i) \), \( M_i(0, \lambda) \) are the mgfs of the initial distributions, \( i = 1, 2 \), which are given.

Let us introduce auxiliary variables \( q_i(t) \) as the solutions of the differential equations

\[
dq_i(t)/dt = g_i(v_i), \quad q_i(0) = 0, \quad i = 1, 2.
\]

The following theorem holds

**Theorem 1.** Suppose that \( t \in [0, T] \), where \( T \) is the maximal value of \( t \) such that (8)-(9) has a unique solution. Then

(1) The current means of \( \varphi_i(\omega_i) \), \( i = 1, 2 \), are determined by the formulas

\[
\bar{\varphi}_i(t) = \left. \frac{dM_i(0, \lambda)}{d\lambda} \right|_{\lambda=q_i(t)} \frac{1}{M_i(0, q_i(t))},
\]

and satisfy the equations

\[
\frac{d}{dt} \bar{\varphi}_i(t) = g_i(v_i) \sigma_i^2(t),
\]

where \( \sigma_i^2(t) \) are the current variances of \( \varphi_i(t, \omega_i) \), \( i = 1, 2 \).

(ii) The current population sizes \( N_1(t) \) and \( N_2(t) \) satisfy the system

\[
\frac{d}{dt} N_i(t) = N_i(t)[f_i(v_i) + \varphi_i(t)g_i(v_i)], \quad i = 1, 2.
\]

From Theorem 1 follows that the analysis of model (8)-(9) is reduced to analysis of ODE system (10)-(11)-(13), the only thing we need to know is the mgfs of the initial distributions.

Concluding this sections we note that, with obvious notation changes, models (2)-(4) and (5) fall into the general framework of the master model (8).
4 Model analysis

We start with the model (2)-(4), which, according to Theorem 1, can be written in the form

\[
\begin{align*}
\frac{d}{dt} S(t) &= -\bar{\beta}(t)S(t)I(t), \quad S(0) = S_0, \\
\frac{d}{dt} I(t) &= \bar{\beta}(t)S(t)I(t), \quad I(0) = I_0, \\
\frac{d}{dt} q(t) &= -I(t), \quad q(0) = 0, \\
\bar{\beta}(t) &= \frac{dM(0, \lambda)}{d\lambda} \bigg|_{\lambda=q(t)} \frac{1}{M(0, q(t))}.
\end{align*}
\]

(14)

\(M(0, \lambda)\) is a given mgf of \(p_s(0, \omega)\).

**Proposition 1.** Model (14) is equivalent to the following model:

\[
\begin{align*}
\frac{d}{dt} S(t) &= -h(S(t))I(t), \quad S(0) = S_0, \\
\frac{d}{dt} I(t) &= h(S(t))I(t), \quad I(0) = I_0,
\end{align*}
\]

(15)

where

\[h(S) = S_0 \left[ \frac{dM^{-1}(0, \xi)}{d\xi} \bigg|_{\xi=S/S_0} \right]^{-1},\]

(16)

and \(M^{-1}(0, \xi)\) is the inverse function to mgf \(M(0, \lambda)\).

**Proof.** The first equation in (14) can be rewritten in the form

\[
\frac{1}{S(t)} \frac{d}{dt} S(t) = \bar{\beta}(t) \frac{d}{dt} q(t).
\]

\(\bar{\beta}(t)\) can be represented as \(\bar{\beta}(t) = \frac{d\ln M(0, \lambda)}{d\lambda} \bigg|_{\lambda=q(t)}\), which gives

\[
\frac{d}{dt} \ln S(t) = \frac{d}{dt} \ln M(0, q(t)),
\]

or, using the initial conditions \(S(0) = S_0, q(0) = 0\),

\[
S(t)/S_0 = M(0, q(t)),
\]

(17)

which is the first integral to system (14). Knowledge of a first integral allows to reduce the order of the system by one. Since \(M(0, \lambda)\) is an absolutely monotone function in the case of nonnegative \(\beta(\omega) \geq 0\), then it follows that

\[q(t) = M^{-1}(0, S(t)/S_0),\]

(18)
where \( M^{-1}(0, M(0, \lambda)) = \lambda \) for any \( \lambda \).

Putting (18) into (14) gives

\[
\frac{d}{dt} S(t) = \left. \frac{dM(0, \lambda)}{d\lambda} \right|_{\lambda = M^{-1}(0, S(t)/S_0)} S_0 I(t),
\]
or, by the inverse function theorem, (15) with (16).

Note that model (5) can be reduced to four-dimensional system of ODEs, which, in its turn, can be simplified to two-dimensional system. The proof is as in Proposition 1. Formally, we have

**Proposition 2.** The model (5) is equivalent to the model

\[
\frac{d}{dt} S(t) = -h_1(S) h_2(I), \\
\frac{d}{dt} I(t) = h_1(S) h_2(I),
\]

where \( h_i(x), i = 1, 2 \) are given by (16).

Combining together Propositions 1 and 2 we obtain the main result of the present note.

**Theorem 2.** A heterogeneous SI model in the form (2)-(4), or in the form (5), which both describe the contact process with the help of the law of mass action and model heterogeneities in disease parameters such as susceptibility to a disease or infectivity of an individual, are equivalent to a homogeneous SI model with a nonlinear transmission function.

An analogous conjecture was made in [27], where a substantially more complex model is analyzed. The strength of Theorem 2 is that it provides an explicit form for the nonlinear transmission function.

Consider a standard gamma distribution with parameters \( k \) and \( \nu \):

\[
p(0, \omega) = \frac{\nu^k}{\Gamma(k)} \omega^{k-1} e^{-\nu \omega}, \quad \omega \geq 0, \ k > 0, \ \nu > 0.
\]

Let us assume that \( \beta(\omega) = \omega \). The mgf of gamma-distribution is then

\[
M(0, \lambda) = (1 - \lambda/\nu)^{-k}.
\]

Using Proposition 1 we obtain that

\[
h(S) = \frac{kS}{\nu} \left[ \frac{S}{S_0} \right]^{1/k}.
\]

From (20) it immediately follows
Corollary 1. The power relationship \( q = 1 \), \( p = 1 + 1/k \) can be obtained as a consequence of the heterogenous SI model with distributed susceptibility when the initial distribution is a gamma-distribution with parameters \( k \) and \( \nu \).

Corollary 2. The power relationship \( q = 1 + 1/k_2 \), \( p = 1 + 1/k_1 \) can be obtained as a consequence of the heterogenous SI model with distributed susceptibility and infectivity when the initial susceptibility distribution is a gamma-distribution with parameters \( k_1 \) and \( \nu_1 \), and the initial infectivity distribution is a gamma-distribution with parameters \( k_2 \) and \( \nu_2 \).

Summarizing, we provided a mechanistic derivation of the power law transmission function, which was used phenomenologically in many epidemiological models, in the case when heterogeneity parameters \( p, q \) exceed one. Originally, these exponents were considered to be less than one (e.g., in \([25]\) they are put in the form \( p = 1 - a \), \( q = 1 - b \)), but no comparison with real world data was provided.

There is no universal agreement on the values of parameters \( p, q \) in \( [1] \). In \([24]\) these parameters were estimated when the incidence rate was inferred from epidemic simulations on random networks with different degree distributions. In all experiments values of \( p \) and \( q \) were estimated to be less than 1. In contrast to the last observation, in \([26]\), where the transmission function has the form \( T(S, I) = \beta S^p I \), it was argued that the exponent \( p \) should be greater than one. Fitting the solutions of the mean field model with nonlinear transmission function into the data obtained from large-scale simulations, it was found that \( p \) can range from 1.6 to 2.

In any respect, the question of deriving the power law transmission function on a solid mechanistic bases for the case \( p, q < 1 \) remains open, whereas the case \( p, q > 1 \) is fully covered by Corollaries 1 and 2.

5 Model III and separable mixing

We rewrite equation (17) in the form

\[
\frac{\partial}{\partial t} s(t, w) = -r\omega s(t, \omega) \left[ 1 - \frac{\bar{\omega}(t)S(t)}{K} \right],
\]

where \( K \) is the number of contacts, which are made by the total population, \( \bar{\omega}(t) \) is the average number of contacts made by one susceptible individual at time \( t \). We note that formally eq. (21) is not covered by Theorem \([1] \) because its growth coefficient depends on the average parameter value \( \bar{\omega}(t) \). However, it is possible to extend the theory presented in Section 3 to such cases with minor changes in notations (Karev, personal communication). In particular, it is possible to show that equation (21) is equivalent to the following ordinary differential equation:

\[
\frac{d}{dt} S(t) = -r h(S) \left[ 1 - \frac{h(S)}{K} \right],
\]

where \( h(S) \) is the infectivity function.
 where \( h(S) \) is given by (16).

It is interesting to note that we can compare solutions of (21) with solutions of the system of ODEs, obtained as a result of large mixing rates in the model on dynamic contact network [28]. For SI-model system (2.22)-(2.23) from the cited work reads

\[
\dot{\theta} = -r M_I \theta, \\
\dot{M}_I = \frac{r M_I}{g'(1)} (\theta g'(\theta) + \theta^2 g''(\theta)),
\]

(23)

where \( g(x) \) is the probability generation function for the distribution of the number of contacts in the population (this is PGF for pdf \( n_0(\omega)/\int_\Omega n_0(\omega) d\omega \); \( \theta(t) \) is the fraction of individuals that have only one contact and still susceptible by the time \( t \); \( r \) is the transmission rate; and \( M_I \) is the fraction of contacts made by infected individuals. The number of susceptible individuals is given by \( S(t) = g(\theta(t)) \).

To compare models (22) and (23) we need to specify the initial conditions. Since model (23) deals with PGF of the number of contacts of the total population, and eq. (22) incorporates mgf of the number of contacts of susceptible individuals it is reasonable to expect some discrepancy of the corresponding solutions if we use the same pdf for these purposes. See Fig. 1 for three solutions.

As can be seen from Fig. 1 the best agreement is found when we use \( \lambda = 1 \), i.e., the average number of contacts equals to 1. In this case two solutions coincide. In the cases \( \lambda > 1 \) or \( \lambda < 1 \) there is some divergence, although the limiting behavior of the models is the same.
Figure 1: Comparison of the solutions of system (23) (red line) with solution of eq. (22) (yellow bold line). Poisson distribution was used with parameters $\lambda = 1, 1.5, 0.5$ from top to bottom. $r = 2$. It was assumed that the population size is $N = 1000$. The initial conditions for problem (23) were chosen such that $\theta(0) = 1 - \varepsilon$, $M_I(0) = \varepsilon$, where $\varepsilon = 0.01$. $S(0)$ for (22) was found as $g(1 - \varepsilon)$. The dotted line shows $Np_0$, where $p_0$ is the proportion of individuals in the population who do not make the contacts.
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