

# Simulation of epidemic dynamics based on the effective contact process

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## 1 Introduction

The stochastic model described hereunder aims at representing the epidemic dynamic of an infectious disease that spread within a population. In particular, the model focus on the description of the infectiousness over the course of the infectious period, accounting for features that can affect and modify the realization of infection events.

Infectious diseases are spread through interactions between hosts, called transmission routes or contacts, which are pathogen-specific and depend on the considered host population. Not all of these interactions lead to observe infection events, that can depend on the couple of hosts having the contact and on the time at which the contact occurs since the time of infection. In addition, the contact rates can vary over the course of the infectious period: the onset of symptoms can cause infectives to change their normal behavior reducing the number of social interaction (e.g., staying at home)[1].

The infectiousness measure, independently from the contact rate, can be affected by several features. When susceptible perceive the risk of being infected, they can act more carefully when in contact with an infective, reducing the probability of an infection event. Furthermore, the administration of antivirals can reduce the infectivity (e.g. Oseltamivir), decreasing the probability of the infection event, given a contact.

The present model aims at establishing a framework in which components that could affect either the infectiousness, or the contact rate, can be included. It is flexible, allowing to track changes at the individual level and it can easily be adapted to include the desired components. The stochastic nature makes the model suitable to investigate the aforementioned effects in small populations. Complexity makes the code computationally intense and requires a careful implementation to represent correctly the desired dynamic.

## 2 Theoretical description of the model

Consider a specific pathogen and the underlying contact network in a closed population of size  $n$ . Let  $i, j$  be distinct individuals in this population that have contact between themselves. We assume that the contact process among  $i$  and  $j$  is described by a Poisson Process of rate  $r_{i,j}$ . When one of the two, say  $i$ , becomes infectious, at time  $t_i$ , he or she can spread the infection to  $j$ , as well as to all the other individuals is in contact with. Contacts, are accepted, i.e. lead to an infection event, according to a probability value that is the product of the infectiousness measure  $\nu_{i,j}(t)$ , i.e. which quantifies the level of infectiousness over the infectious period, and

the total infectivity  $q_{i,j}$ , i.e. the total number of infection events over the contact rate [2]. The former quantity is a positive measure with unitary mass along the infectiousness period while the latter is assumed to be a constant value. If individual  $j$ , at the time of the contact, is not susceptible, this probability has value zero. In this terms, the effective contact between  $i$  and  $j$  results to be described by a non-homogeneous Poisson process of rate  $r_{i,j}q_{i,j}\nu_{i,j}(t)$ . The mean number of effective contact between  $i$  and  $j$  is thus given by:

$$\bar{\mathcal{R}}_0 = \int_0^{\mu_i} r_{i,j}q_{i,j}\nu_{i,j}(t)dt = r_{i,j}q_{i,j}$$

where  $\mu_i$  is the length of the infectious period of individual  $i$ . For a fixed value of the contact rate, the implementation is correct as long as  $q_{i,j}\nu_{i,j}(t) \leq 1$  for every time  $t$ . This mathematical description is also known as thinning of a Poisson Process. We assume that the effective contact processes among  $i$  and the other members of the population are independent. Therefore, the rate at which  $i$  makes effective contacts is:

$$\sum_{j \neq i} r_{i,j}q_{i,j}\nu_{i,j}(t)$$

Note that this framework allows to define different contact rates between different individuals as well as different acceptance probability functions. The mean number of effective contact individual  $i$  makes during the infectious period is given by:

$$\bar{\mathcal{R}}_0 = r_{i,j}q_{i,j} \tag{1}$$

We remark here that the number of effective contacts is an approximation of the basic reproduction number. In fact, in the former cases effective contacts could be realized with the same person. The two quantities coincide when the population is infinite and individuals are contacted with the same probability. In this case, the probability of contacting two time the same individual is zero.

## 2.1 Mass-action model

In a mass-action model the population is assumed to be homogeneous and the contact processes to be independent. The contact rate is scaled by the population size, i.e.

$$r_{i,j} = \frac{\bar{r}}{n-1}$$

According to this formulation, the expected number of effective contacts an infectious individual makes is given by:

$$\bar{\mathcal{R}}_0 = rq \tag{2}$$

We remark here that this formulation is valid for every distribution of the infectious period length, since the infectiousness measure has unitary mass along the infectious period of each individual.

## 2.2 Infectiousness measure as viral load function

With this model we describe the epidemic dynamic of infectious diseases. At first, we assume that the infectiousness measure  $\nu(t)$  resembles the shape of the viral load curve. This assumption is motivated by the fact that a virus, before establishing in a host individual, has to overcome the external immune system. The higher is the viral load, the higher is the amount of virus spread in a contact with a consequent higher probability of successfully infecting the host. However, as mentioned before, perceive risk by susceptibles or antiviral can affect the infectiousness measure. This is model substituting the original infectiousness measure  $\nu(t)$  that represents the viral load, with another infectiousness measure  $\bar{\nu}(t)$  that describes the decrease thereof. If the change in the infectiousness measure happens at time  $t^*$  for all individuals independently from the length of the infectious period, the mean number of effective contact is given by

$$\bar{\mathcal{R}}_0 = \int_0^\infty \left[ \int_0^{t^*} r q \nu(t) dt + \int_{t^*}^s r q \bar{\nu}(t) dt \right] f(s) ds$$

where  $f(s)$  is the infectious length density function.

An example of a change in the infectiousness measure is given in the simulation scripts in that account for the effect of an antiviral.

## 2.3 Decrease of contact rate due to control measures

Next to a decrease in the infectiousness measure, a decrease in the contact rate reduces also the number of infection events. When isolation or quarantine are included, the contact rate decreases accordingly to the efficacy of the control measure. Assume that a change in the contact rate, from  $r$  to  $\bar{r}$  happens at time  $t^*$  for all the individuals, and the infectiousness measure is always the same. In this case the mean number of effective contacts results to be:

$$\bar{\mathcal{R}}_0 = \int_0^\infty \left[ \int_0^{t^*} r q \nu(t) dt + \int_{t^*}^s \bar{r} q \nu(t) dt \right] f(s) ds$$

where  $f(s)$  is the distribution of the infectious period length. An example of the reduction in contact rate is given in the scripts that account for isolation and quarantine measures.

## References

- [1] P. H. Rhodes, M. E. Halloran, and I. M. Longini Jr. Counting process models for infectious disease data: distinguishing exposure to infection from susceptibility. *Journal of the Royal Statistical Society: Series B (Methodological)*, 58(4):751–762, 1996.
- [2] Å. Svensson. A note on generation times in epidemic models. *Mathematical biosciences*, 208(1):300–311, 2007.