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A stochastic model for the spread of a venereal disease and the mitigating effect of a vaccination scheme

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## A stochastic model for the spread of a venereal disease and the mitigating effect of a vaccination scheme

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**Abstract**

A multi-type stochastic epidemic model is defined as to analyze the spread of a venereal disease within a population, whose members are differentiated with respect to biological sex and sexual preference, with varying disease transmission probability with respect to the sexes of the pair engaged in the contact. The derivation of Ball (1986) for the final size distribution is presented, but simulations are used to determine it. A heuristic motivation for the branching process approximation is given, as well as definitions for the quantities defined in terms of it, i.e. the basic reproduction number and the probability for a major disease outbreak. Considering three cases of venereal diseases, we study the effect of a vaccination scheme as to determine whether certain groups of people should be targeted differently.

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# Contents

# 1 Introduction

One-Night Stand Land – population 10 000 – is not a real country in any sense of the word. Rather, it is either an utopian or nightmarish fiction, depending one's point of view: Is it a haven for the expression of free love, or is it a minefield of the obstacles preventing ever-lasting love? Perhaps, it is nothing more than an eye-catching title.

Actually, it is a consequence of a common simplification done when defining mathematical models for the study of the spread of infectious diseases – namely – that infectious contacts are instantaneous and that the population is homogeneously mixing. We will consider the spread of a venereal disease (or sexually transmitted disease, STD) in a population differentiated by biological sex and sexual preference in terms of biological sex, with which ensues a heterogeneous structure. We will not, however, include any social structure other than that resultant from sex and preference, thus refraining individuals to make longer-lasting bonds than instantaneous, one-night stands. (See section 2 for details.)

A particular venereal infection, the *human immunodeficiency virus*, commonly known by its abbreviated form *HIV*, has the property that the transmission probability is much higher for anal than for vaginal intercourse, where further oral intercourse has a negligible probability of resulting in infection. This affects people differently depending on their preferred type of intercourse, and, due to physical constraints, one's sex and the sex of one's preferred partner determine what type of intercourse one *can* engage in. As such, homo- and bisexual males are disproportionately afflicted by the HIV pandemic. We aim to study the effect of the differing transmission probabilities with the use of a stochastic epidemic model, where we determine the quantities

- **The final size**, $\boldsymbol{Z}$, which is defined as the number of initially susceptible individuals who ultimately become infected, in a closed population.
- **The basic reproduction number**, $R_0$, which is a threshold value determining whether the disease can evolve into a proper epidemic or not.
- **The probability for a major outbreak**, $p$, which is self-descriptive. Notably, if $R_0 \leq 1$ then $p = 0$, which illustrates the threshold property of $R_0$.

We will also study the effect of a proportion of the population being vaccinated, and whether different groups of individuals should be targeted differently. The second paragraph of section 1.1 gives reference as to where to find these quantities in the thesis.

Worthy of particular mention in this introduction are the lecture notes of Håkan Andersson and Tom Britton (2000), which have served as the main source of this thesis, not only with regard to its content, but also to its structure (for the theoretical sections 2-4).

## 1.1 Outline of thesis

The preamble of each section of this thesis aims to give a summary of the contents of that section, preliminaries necessary for the later subsections, or otherwise not subsection-worthy content. While the reader is assumed to have some knowledge on the subject of stochastic processes, particularly the Poisson process, concepts pertaining to the study of epidemic processes are presented in italics when they are defined (or referred to a later paragraph or subsection when they are not defined). Italics are also used for emphasis, although rarely.

A definition of the model is given in section 2, and a description of the consequent behaviour of this model is presented in section 3, where a system of equations to determine the final size distribution is also derived, but not implemented. In section 4 definitions for the basic reproduction number $R_0$ and the probability for a major outbreak $p$ are presented, as well as the branching process approximation from which they stem. A vaccination scheme, alternatively interpreted as the use of sexual protections (e.g. condoms), is presented in section 5. With the aid of simulation the final size distribution $\boldsymbol{Z}$ and the time-wise behaviour of the epidemic process is determined together with the aforementioned quantities $R_0$ and $p$ in section 6, where the result of the vaccination scheme is also presented.

We conclude this section with a note on notation, beginning with non-stochastic quantities. Scalars are denoted by lowercase letters $a$ (with the exception of the basic reproduction number $R_0$ (see section 4.2, due to its notation being standard in epidemiology). Non-stochastic vectors are denoted by bold lowercase letters $\boldsymbol{a} = (a_i)$, and matrices by bold uppercase letters $\boldsymbol{A} = (\boldsymbol{a_i}) = (a_{ij})$, where $\boldsymbol{a_i}$ is the $i$th column of $\boldsymbol{A}$ and $a_{ij}$ is the $i$th row and $j$th column element of $\boldsymbol{A}$. Univariate stochastic variables are denoted by uppercase letters $S$, and stochastic vectors by $\boldsymbol{S} = (S_i)$. All vectors, stochastic and non-stochastic, are column vectors. Note that uppercase bold letters may denote either a non-stochastic matrix $\boldsymbol{A}$ or a stochastic vector $\boldsymbol{S}$.

## 2 Definition of model

In order to analyse the spread of a venereal disease in a population, we define a stochastic multi-type *SIR* epidemic model. We follow Andersson and Britton (2000, *chs. 2, 6*), but the model predates their work by several decades, with the stochastic model of Kermack and McKendrick (1927) being almost a century old. There exist many variants of the SIR epidemic model; their common denominator being the *states* for which the abbreviation "SIR" stands. The states are defined as follows: At each point in time, each individual occupies either of the states $\mathcal{S}$, *susceptible*, i.e. the individual is susceptible for infection; $\mathcal{I}$, infectious; or $\mathcal{R}$, *removed*, i.e. the individual is neither susceptible nor infectious, and is thus removed from the epidemic. The latter state is commonly interpreted as recovered and thus immune, or simply dead. We will use the former interpretation.

Movement between states is unidirectional, as per

$$\mathcal{S} \longrightarrow \mathcal{I} \longrightarrow \mathcal{R}, \tag{1}$$

implying that a susceptible individual was never infectious. An alternative model, with circular movement between states, is the *SIS* model (again the abbreviation stands for the states of the model), which would be suitable for the analysis of venereal diseases such as gonorrhea or chlamydia. While this model is not of any focus in this thesis, it merits to be mentioned with respect to the study venereal disease, particularly due to the commonness of diseases such as gonnorrhea and chlamydia. (The *SIS* model is presented in further detail by Andersson and Britton (2000, *ch. 8.1*)).

The multi-type aspect of the model is what enables us to consider the spread of venereal diseases at all, as well as include both hetero- and homosexual contacts, where the probability of disease transmission may depend on the sexes of the individuals involved in the contact. In the simplified case, where all individuals are heterosexual, the *types* are simply males and females, and males may only engage with contact with females and vice versa. This would not be possible without some type-structure. A detailed description of the population and the types of individuals it consists of is given in section 2.1.

A full description of the model can be given with a few sentences: At time point $t = 0$ there exist $\boldsymbol{m}$ infectious individuals and $\boldsymbol{n}$ susceptible individuals. Infectious individuals make infectious contact to susceptible individuals according to a Poisson process with rate $\lambda_{ij}$ per pair, which depends on the respective types of the infectious and susceptible individuals and is independent of all other Poisson processes. When a susceptible individual is contacted by an infectious individual it immediately becomes infectious, and stays infectious for a period of time distributed according to a stochastic variable $I$ (which may be degenerate), after which it is removed.

Thus the model can be parametrized with the vectors $\boldsymbol{m}$, $\boldsymbol{n}$, the *initially infectious* and *susceptible* individuals respectively; the matrix of *infectious contact intensities*, $\mathbf{\Lambda} = (\lambda_{ij})$ and the *infectious period*, $I$. In the general stochastic multi-type SIR epidemic model, the distribution of $I$ may differ with respect to

type, but does not in our case. We will assume it to be exponentially distributed with mean $\gamma^{-1}$, solely due to the nice mathematical properties of the exponential distribution – particularly – the lack-of-memory property. Commonly the initially infectious are assumed to have contracted their infection precisely at time $t = 0$, as will we assume.

Whereas the definition of the stochastic multi-type SIR epidemic model could be given in full within one paragraph, the specific re-paramterization that will be used in this thesis craves three sections. In section 2.1 we define the types, such that we in section 2.2 can define a contact model, which in turn allows us to determine the matrix of infectious contact intensities. The re-parametrization thus only effects $\mathbf{\Lambda}$, and will be presented in section 2.3.

## 2.1 Population

As implicitly mentioned in the definition of the model, we consider a *closed* population. The properties of the individuals who make up the population are solely determined by their *type*. The types are defined such that individuals of bi-, hetero- and homosexual preference exist, or, explicitly, they are defined as every combination of biological *sex*, which can be male or female, and sexual *preference*, which can be either of the two sexes or both. Preference is an absolute concept in this thesis, i.e. individuals will not make contact with individuals who are not of their preferred sex. The types are denoted by the abbreviations of the set

$$\mathscr{T} = \{MM, MB, MF, FM, FB, FF\}, \tag{2}$$

where the first letter stands for sex and the latter for preference, with $B = \{M, F\}$ denoting both. The types are ordered as in (2) when ordered, i.e. in vectors and matrices, but when referring to a specific type the abbreviated form is used rather than its corresponding numerical order value. The number of individuals of each type is denoted by $\boldsymbol{\nu} = (\nu_i)$ and their proportion by $\boldsymbol{\pi} = (\pi_i)$. Naturally $\boldsymbol{\nu} = \boldsymbol{m} + \boldsymbol{n}$. We make use of the blunt simplification that individuals of bi- and homosexual preference are of equal proportion, and that the proportion of the two sexes are of equal proportion (although the latter simplification is anchored in reality). This allows us to parametrize $\boldsymbol{\nu}$ using the proportion of individuals of heterosexual preference $\pi_{He}$ and the total number of individuals in the population, which we denote by $\nu = \sum_{i \in \mathscr{T}} \nu_i$, such that the proportions can be given by

$$\pi_i = \begin{cases} \frac{(1-\pi_{He})}{4} & \text{if } i \in \{MM, MB, FB, FF\} \\ \frac{\pi_{He}}{2} & \text{if } i \in \{MF, FM\}, \end{cases} \tag{3}$$

and naturally $\nu_i = \nu\pi_i$. This simplification reduces the number of parameters, which allows us to illustrate the contact model (Figure 2) presented in the next section (sec. 2.2), but does not seem to provide us with any other convenient properties.

A pair of individuals of types $i, j$ are said to be *contactable* if the sex of the $i$-type individual is preferred by the $j$-type individual and the sex of the $j$-type

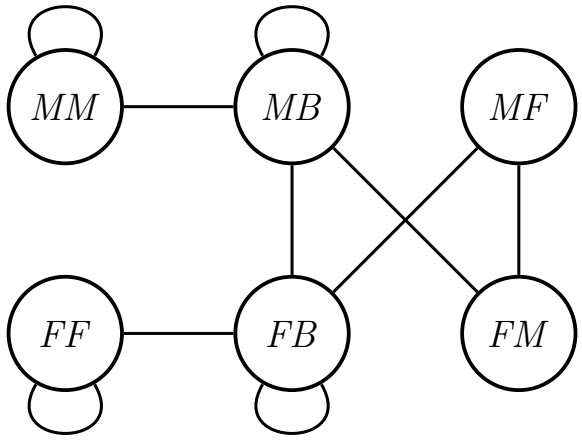



Figure 1: Contactable types connected with lines.

individual is preferred by the $i$-type individual. This is denoted by $c_{ij} = 1$ if they are contactable and $c_{ij} = 0$ if they are not. An illustration of contactable types is given in Figure 1. Contact is only made between contactable individuals.

## 2.2 Contact model

The type-structure defined in the previous section is the *only* structure we include with respect to how individuals make contact to one another. This is important to note when we make the following assumption: All individual share an *equal level of sexual activity*, i.e. in expectation they engage in the same number of sexual contacts for some fixed time period. This assumption is not reflective of reality, but it is natural when considering a type-structure that is not based on the level of sexual activity. In reality, the distribution for the number of sexual partners of individuals (without respect to the type-structure we have defined) is highly skewed, as is the subject of the empirical study of Freiesleben de Blasio, Svensson and Liljeros, who further give intuitive reasons for this, e.g. the simple fact that "people are not perceived as being equally attractive". Note also that the mean level of sexual activity is not necessarily equal in reality for the types we have defined.

Contact (possibly non-infectious) between a pair of individuals of types $i, j$ is made as per a Poisson processes with intensity $\kappa_{ij}$, independently of all other contact processes. Also, non-contactable individuals never make contact, hence $\kappa_{ij} = 0$ if $c_{ij} = 0$. In order to set a condition such that these intensities can be determined based on the number of individuals of each type, we consider the superpositioned Poisson processes of the number of contacts of a single individual, with intensity $\kappa$ independent of type. Since the intensity of the superpositioned process is equal to the sum of the underlying processes that constitute it, the equal level of sexual activity condition yields six equations (cf.

(4) below) – one for each type. However, there are ten unknown $\kappa_{ij}$ (cf. Figure 1), and as such this condition alone is insufficient to determine them.

To remedy this problem, we simply define the pair-wise contact intensities as a function of one-sided contact intensities – for an $i$-type individual denoted by $\kappa_i$, which reduces the number of contact intensity parameters to six. The, perhaps, simplest way to define this function is in terms of *perfectly successful one-sided contacts*, i.e. individuals of type $i$ "attempt" contact to others to which they are contactable with rate $\kappa_i$, and these attempts always result in a contact. This yields $\kappa_{ij} = \kappa_i + \kappa_j$, and the simplicity is apparent; It also allows us to consider contacts between a pair of individuals as the superposition of two one-sided contact processes, which is comfortable both from a mathematical and an intuitive standpoint.

We define the one-sided contact intensities $\kappa_i$ as the solution to the following system of equations:

$$\sum_{j \in \mathscr{T}} c_{ij}(\nu_j - \delta_{ij})(\kappa_i + \kappa_j) = \kappa \text{ for all } i \in \mathscr{T}, \tag{4}$$

where the Kronecker delta function ($\delta_{ij} = 1$ if $i = j$ and $\delta_{ij} = 0$ if $i \neq j$) may be omitted for an approximate condition for large $\nu_j$. Its inclusion is to avoid individuals to make self-contact, which, although it has a perfectly natural intuition, serves no purpose when modelling the spread of a disease between people, venereal or otherwise. The solution to this system of equations does not aid one's understanding of it, but rewriting it as

$$\kappa_i = \frac{\kappa - \sum_{j \in \mathscr{T}} c_{ij}\nu_j\kappa_j}{\sum_{j \in \mathscr{T}} c_{ij}\nu_j}$$

reveals that it has an intuitive, rather obvious, understanding: The one-sided contact intensities depend negatively to the number of individuals to which one is contactable. This also has a somewhat realistic interpretation: Individuals who are often approached in a seductive manner are less likely to approach others. An illustration of this is present in Figure 2, where we have used the simplified configuration of type-proportions in (3), showing that for realistic values of $\pi_{He}$ (i.e. closer to 1 than 0), the one-sided contact intensities differ immensely (note the logarithmic scale in Figure 2), which problematises the realistic interpretation. (As such, the condition (4) would certainly be more suitable for another type-configuration, where types are of more similar proportion.)

A non-trivial caveat to the method of determining the one-sided contact intensities by the condition (4) is that the system of equations does not generally yield a positive solution for all $\kappa_i$, i.e. there exist type-proportion configurations that yield negative $\kappa_i$. For the simplified type-proportion configuration (3), however, it does not (cf. Figure 2; assuming that the proportion of individuals with heterosexual preference, $\pi_{He}$, is chosen such that all $\nu_i$ are larger than 1, such that the inclusion of the Kronecker delta function in (4) does not yield negative values).

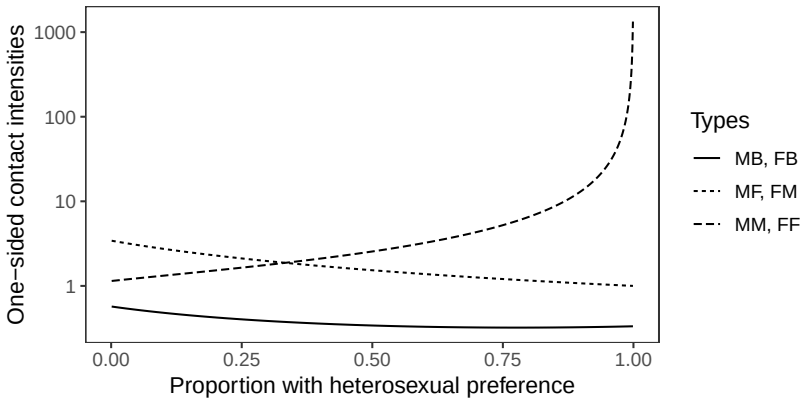



Figure 2: One-sided contact intensities as a function of the proportion with heterosexual preference, with simplified type-proportions as per (3) and a population of size 1, computed by omitting the Kronecker delta function in (4) and setting the level of sexual activity to 1.

## 2.3 Infectious contact and re-parametrization

Each contact between an infectious $i$-type individual and a susceptible $j$-type individual has a probability $\varpi_{\varsigma_i,\varsigma_j}$ of resulting it an infection for the $j$-type individual, where $\varsigma_i, \varsigma_j = \{♂, ♀\}$ only depend on the sexes of the individuals, not their respective preferences. (The symbolic notation ♂/♀ is used to avoid confusion with the type abbreviations.) Hence we distinguish between four (possibly) different transmission probabilities $\varpi_{\varsigma_i\varsigma_j}$. Infectious contact between an $i$-type individual and a $j$-type individual is hence made as per the thinned Poisson process with intensity $\lambda_{ij} = \varpi_{\varsigma_i\varsigma_j}\kappa_{ij}$. Recalling that $\kappa_{ij}$ is defined as a function of the level of sexual activity $\kappa$ and the number of individuals of each type $\boldsymbol{\nu}$ (which in turn may be parametrized by $\pi_{He}$ and $\nu$, cf. (3)), this concludes the parametrization of $\boldsymbol{\Lambda}$, and thus also the re-parametrization of the model.

# 3 Propagation of the epidemic

In this section, which is somewhat technical, we derive a system of equations for the *final size* distribution of the epidemic, annotated by $\boldsymbol{Z}$, in section 3.2. The specifics of doing so demands some elementary results to be presented from the subject of *renewal theory*, which will be done in section 3.1, where we also define an equivalent version of the model, to which renewal theory is applicable. (There are however methods not relying on renewal theory; See the last paragraph of this preamble.) Before delving into this, however, we present the epidemic *process* in some more detail.

We denote by $\big(\boldsymbol{X}(t), \boldsymbol{Y}(t)\big)$ the number of susceptible and infectious individuals in the population respectively at time $t \geq 0$, excluding the number of removed individuals $\boldsymbol{Z}(t)$, since this can be determined by the state of the epidemic process by $\boldsymbol{Z}(t) = \boldsymbol{\nu} - \boldsymbol{X}(t) - \boldsymbol{Y}(t)$, due to the population being closed with constant size $\boldsymbol{\nu}$. (Recall that all vectors and matrices have elements with respect to each type ordered as in (2).) Also, we let $(\boldsymbol{x}, \boldsymbol{y})$ generically denote a state of the epidemic process (not to be confused with the states of the epidemic in (1); the state space denoted by $(\boldsymbol{x}, \boldsymbol{y})$ simply correspond to the possible values of the epidemic process).

With $\boldsymbol{\lambda_i} = (\lambda_{ji})$ being the $i$th column of the matrix of infectious contact intensities, and $\boldsymbol{e_i}$ being the $i$th column of the identity matrix, the transition rates between states are given by, for $i = \{1, \ldots, 6\}$:

| from | to | at rate |
|---|---|---|
| $(\boldsymbol{x}, \boldsymbol{y})$ | $(\boldsymbol{x} - \boldsymbol{e_i}, \boldsymbol{y} + \boldsymbol{e_i})$ | $\boldsymbol{\lambda_i}^T \boldsymbol{y} x_i$ |
| $(\boldsymbol{x}, \boldsymbol{y})$ | $(\boldsymbol{x}, \boldsymbol{y} - \boldsymbol{e_i})$ | $\gamma y_i$ |

(5)

The first set of transitions, with rates $\boldsymbol{\lambda_i}^T \boldsymbol{y} x_i = \sum_{j \in \mathscr{T}} \lambda_{ji} y_j x_i$, correspond to individuals being infected, and the second, with rates $\gamma y_i$, to individuals being removed. While there exist no closed form expression for how the epidemic propagates through time (according to Britton (2010)), one may note that the rate at which individuals get infected is relative to the *product* of the number of infectious and susceptible individuals that are present in the population, which provides an intuitive sense of the time dynamics of the epidemic process.

As not to deceive the reader into thinking that there is only one way to determine the final size distribution, we must mention that, since the epidemic process $\big(\boldsymbol{X}(t), \boldsymbol{Y}(t)\big)$ is *Markovian*, there exist other methods to determine it other than the one presented below, that furthermore do not rely on renewal theory. For example, Ball (1986b) conduct a derivation for both the single-type and multi-type cases using coupling, as well as mention methods used by other authors – namely – the analytic argument by Daniels (1967) and the combinatorial one by Downton (1967); none of which yield closed form expressions for the final size distribution neither, however. The method used in section 3.2 is applicable for any finite-mean distribution for the infectious period. Given the preliminaries presented in the next section, however, the derivation of the system of equations that determine the final size distribution follows quite easily,

and elegantly (although a quick glance at the notation might lead one to think otherwise).

## 3.1 Preliminaries

From renewal theory we will make use of the concept of a stopping time, as well as Wald's equation. Ross (2014; *p. 420*) defines the former as follows (with slightly different notation):

> "The non-negative integer valued random variable $N$ is said to be a *stopping time* of a sequence of independent random variables $S_1, S_2, \ldots$ if the event that $\{N = n\}$ is independent on $S_{n+1}, S_{n+2}, \ldots$."

and the latter (in its simplest form) by (*thm. 7.2. p. 420*):

$$E\left(\sum_{k=1}^{N} S_k\right) = E(N)E(S),$$

where $S_k$ is equal in distribution to $S$ and further $E(N), E(S) < \infty$. The relationship between the definition of a stopping time and Wald's equation will become apparent in the derivation of equation (6) in section 3.2 below. Note that in the multi-variate case, to which our epidemic process belongs, the equivalent definition is that the event $\{\boldsymbol{N} = \boldsymbol{n}\}$ would have to be independent of $S_{i,n_i+1}, S_{i,n_i+2}, \ldots$.

To make this theory applicable to the epidemic model, we introduce the *Sellke* construction (eponymous to its originator, Sellke (1983)), as it appears in Andersson and Britton (2000, *pp. 52-53*), defined first by the *infection pressure* exerted on $j$-type individuals

$$A_j(t) = \sum_{i \in \mathscr{T}} \lambda_{ij} \int_{u=0}^{t} Y_i(u)\,\mathrm{d}u,$$

for $j \in \mathscr{T}$, where $Y_i(t)$ is the number of infectious $i$-type individuals in the population at time point $t$. Second, each individual has a threshold value, which, if superseded by their corresponding infection pressure, results in the individual becoming infectious. The threshold values are mutually independent and exponentially distributed with mean 1. We let $Q_{j,k}$ denote the threshold value of the $k$th $j$-type individual, where $k = 1, 2, \ldots, n_j$, and $Q_{j,(k)}$ denote the $k$th order statistic of $\{Q_{j,k}\}$, i.e. $Q_{j,(1)} < Q_{j,(2)} < \cdots < Q_{j,(n_j)}$. The subscript $(j, k)$ is the *label* of a given individual, where $(j, -(m_j - 1)), (j, -(m_j - 2)), \ldots, (j, 0)$ are the labels of the initially infectious individuals, although they naturally do not have a threshold value, since they are never susceptible.

This construction does indeed yield a model equivalent to the one described in section 2. We use Andersson and Britton's (2000, *p. 14*) motivation for why this is, noting that due to the lack-of-memory property of the exponential

distribution, we have that

$$P(Q_{j,1} > A(t+\Delta t) \,|\, Q_{j,1} > A(t)) = \exp(-(A_j(t+\Delta t) - A_j(t)))$$
$$= \exp\left\{-\sum_{i\in\mathscr{T}} \lambda_{ij} y_i \Delta t + o(\Delta t)\right\} = 1 - \sum_{i\in\mathscr{T}} \lambda_{ij} y_i \Delta t + o(\Delta t),$$

where the second equality is because no infection will occur in a small enough time interval $\Delta t$. Note that the above probability refers to that of individual $(j,1)$ *avoiding* infection from the $\boldsymbol{y}$ individuals currently infectious.

The Sellke construction will however only be used in its limit, where it denotes the total infection pressure exerted during the epidemic, where

$$A_j = \lim_{t\to\infty} A_j(t) = \sum_{i\in\mathscr{T}} \lambda_{ij} \sum_{\ell=-(m_i-1)}^{Z_j} I_{i,\ell},$$

such that the probability that a $j$-type individual *ultimately* avoids infection conditioned on $A_j = a_j$ is given by $e^{-a_j}$.

Finally, in order to make expressions fit within the width of the page, we use the following notation, for generic vectors $\boldsymbol{a} = (a_1, a_2, \ldots, a_k)^T$ and $\boldsymbol{b} = (b_1, b_2, \ldots, b_k)^T$, where $\boldsymbol{a} \le \boldsymbol{b}$ means that $a_i \le b_i$ and

$$\sum_{\boldsymbol{\ell}=\boldsymbol{a}}^{\boldsymbol{b}} = \sum_{\ell_1=a_1}^{b_1} \sum_{\ell_2=a_2}^{b_2} \cdots \sum_{\ell_k=a_k}^{b_k} \quad \text{and} \quad \binom{\boldsymbol{a}}{\boldsymbol{b}} = \binom{a_1}{b_1}\binom{a_2}{b_2}\cdots\binom{a_k}{b_k}.$$

## 3.2 Derivation of final size distribution

We follow Ball (1986) quite precisely, although with notation partly from Andersson and Britton (2000). The final size vector can be written in terms of the Sellke construction with

$$\boldsymbol{Z} = \min\left\{\boldsymbol{k} : Q_{j,(k_j+1)} > \sum_{i\in\mathscr{T}} \lambda_{ij} \sum_{\ell=-(m_i-1)}^{k_i} I_{i,\ell} \text{ for all } j \in \mathscr{T}\right\},$$

from which we note that $\boldsymbol{Z}$ is independent of $I_{i,\ell}$ for $\ell > Z_i$, which illustrates that the final size is a stopping time. To derive a Wald's identity for the model, we use a slightly different notation, as to be consistent with the notation of Ball (1986), where we reformulate the Sellke construction with

$$A_j = \sum_{i\in\mathscr{T}} \lambda_{ij} B_i \quad \text{and as such} \quad B_i = \sum_{\ell=-(m_i+1)}^{Z_i} I_{i,\ell},$$

where $B_i$ is simply the area under the trajectory of $i$-type individuals. With $\psi_i(s) = E(e^{sI_i})$ denoting the moment generating function of the infectious period of $i$-type individuals (which in our case, however, does not differ with

respect to type, i.e. $\psi_i(s) = \psi(s)$ for all $i \in \mathscr{T}$), we get through Wald's equation that

$$\begin{aligned}\prod_{i\in\mathscr{T}} \psi_i(s_i)^{m_i+n_i} =& E\left[\exp\left(-\sum_{i\in\mathscr{T}} s_i \sum_{\ell=-(m_i+1)}^{n_i} I_{i,\ell}\right)\right] \\ =& E\left[\exp\left(-\sum_{i\in\mathscr{T}} s_i \left(B_i + \sum_{\ell=Z_i+1}^{n_i} I_{i,\ell}\right)\right)\right] \\ =& E\left[\exp\left(-\sum_{i\in\mathscr{T}} s_i B_i\right) \prod_{i\in\mathscr{T}} \psi_i(s_i)^{n_i-Z_i}\right],\end{aligned}$$

where the last step is due the infectious period $I_{i,\ell}$ being independent of the final size $\boldsymbol{Z}$ and the total infection pressure $B_i$ for $\ell > Z_i$. Dividing both sides of the equation by the left hand side yields *Wald's identity for epidemics* in its multi-type form, corresponding to theorem 3.1. of Ball (1986):

$$E\left[\exp\left(-\sum_{i\in\mathscr{T}} s_i B_i\right) \Big/ \prod_{i\in\mathscr{T}} \psi_i(s_i)^{m_i+Z_i}\right] = 1. \tag{6}$$

From this, the derivation of the system of equations that determine the final size distribution follow neatly, by us making use of the symmetries of the epidemic process. First, we distinguish between the event that a certain number of individuals of each type ultimately become infected, and the event that a specific set of individuals do – the latter naturally being a subset event of the former. We denote the former by $\boldsymbol{\omega}$, where $\omega_j$ denotes the number of $j$-type individuals that ultimately become infected, and the latter by $\boldsymbol{\omega'}$, where $\omega'_i$ denotes that exactly the individuals labelled $(j,1),(j,2),\ldots,(j,\omega'_i)$ ultimately become infected. (At this point, one may note that the set of possible $\boldsymbol{\omega}$, i.e. $\{\boldsymbol{\omega} : \boldsymbol{0} \leq \boldsymbol{\omega} \leq \boldsymbol{n}\}$, may become very large even for a small number of types (e.g. six in our case). This will be discussed in the epilogue of this section.) Second, we denote the probabilities of these events by $P^{\boldsymbol{n}}_{\boldsymbol{\omega}}$ and $P^{\boldsymbol{n}}_{\boldsymbol{\omega'}}$ respectively. The superscript $\boldsymbol{n}$ will make sense shortly. Note that the choice of labelled individuals in $\boldsymbol{\omega'}$ is arbitrary with respect to $P^{\boldsymbol{n}}_{\boldsymbol{\omega'}}$; only the sizes of the sets for each type matters, since the probability that e.g. individuals $(j,2),(j,5)$ ultimately become infected is the same as the probability that $(j,1),(j,7)$ do. This is the *symmetry of the epidemic process*, and by use of this, we note that

$$P^{\boldsymbol{n}}_{\boldsymbol{\omega}} = \binom{\boldsymbol{n}}{\boldsymbol{\omega}} P^{\boldsymbol{n}}_{\boldsymbol{\omega'}}, \tag{7}$$

where the product of binomial coefficients $\binom{\boldsymbol{n}}{\boldsymbol{\omega}}$ simply count the number of sets of individuals with sizes $\{\omega_j\}$ there are, all of whom have the same probability $P^{\boldsymbol{n}}_{\boldsymbol{\omega'}}$ of occurring, and are subset events of $\boldsymbol{\omega}$. We retain the notation $\boldsymbol{S'}$ for a specific set of individuals of size $\boldsymbol{S} = \{S_i\}$ for the remainder of this section.

Next, we consider a "sub-epidemic" among a subset of the population $\boldsymbol{\ell'}$, where naturally $\boldsymbol{\omega} \leq \boldsymbol{\ell} \leq \boldsymbol{n}$, since the sub-epidemic must be contained within

$\boldsymbol{\ell'}$ to be useful. Also, let $\boldsymbol{Z^\ell}$ be the final size of the sub-epidemic. The event $\boldsymbol{\omega'}$ within $\boldsymbol{n'}$ corresponds to the event $\boldsymbol{\omega'}$ within $\boldsymbol{\ell'}$ together with the event that the at some point infectious individuals, $\boldsymbol{m'} \cup \boldsymbol{\omega'}$, fail to infect all individuals corresponding to the set difference $\boldsymbol{n'} \setminus \boldsymbol{\ell'}$, i.e.

$$P^{\boldsymbol{n}}_{\boldsymbol{\omega'}} = P^{\boldsymbol{\ell}}_{\boldsymbol{\omega'}} P(\boldsymbol{n'} \setminus \boldsymbol{\ell'} \text{ avoid infection from } \boldsymbol{m'} \cup \boldsymbol{\omega'} \mid \boldsymbol{Z^\ell} = \boldsymbol{\omega}),$$

which if we include the symmetry (7) of the epidemic process can be expressed in terms of $P^{\boldsymbol{n}}_{\boldsymbol{\omega}}$ and $P^{\boldsymbol{\ell}}_{\boldsymbol{\omega}}$, such that

$$\frac{\binom{\boldsymbol{\ell}}{\boldsymbol{\omega}}}{\binom{\boldsymbol{n}}{\boldsymbol{\omega}}} P^{\boldsymbol{n}}_{\boldsymbol{\omega}} = P^{\boldsymbol{\ell}}_{\boldsymbol{\omega}} P(\boldsymbol{n'} \setminus \boldsymbol{\ell'} \text{ avoid infection from } \boldsymbol{m'} \cup \boldsymbol{\omega'} \mid \boldsymbol{Z^\ell} = \boldsymbol{\omega}). \tag{8}$$

At this point, we make use of the Sellke construction for the latter probability. Since the probability that a certain $j$-type individual avoids infection conditioned on a total infection pressure (starting with $\boldsymbol{\ell}$ susceptible individuals) $A^{\boldsymbol{\ell}}_j = a_j$ is given by $P(Q_{j,1} > a_j) = e^{-a_j}$, the probability that $\boldsymbol{n'} \setminus \boldsymbol{\ell'}$ avoid infection is given by (since the individual thresholds are independent; note also that again we implicitly use the symmetry of the epidemic process)

$$\exp\left(-\sum_{j\in\mathscr{T}} (n_j - \ell_j) a_j\right),$$

and to remove the dependence on $A^{\boldsymbol{\ell}}_j$, we simply take the expectation over $A^{\boldsymbol{\ell}}_j$, such that the last probability in (8) becomes

$$\begin{aligned} &E\left[\exp\left(-\sum_{j\in\mathscr{T}} (n_j - \ell_j) A^{\boldsymbol{\ell}}_j\right) \middle| \boldsymbol{Z^\ell} = \boldsymbol{\omega}\right] \\ &= E\left[\exp\left(-\sum_{j\in\mathscr{T}} (n_j - \ell_j) \sum_{i\in\mathscr{T}} \lambda_{ij} B^{\boldsymbol{\ell}}_i\right) \middle| \boldsymbol{Z^\ell} = \boldsymbol{\omega}\right], \end{aligned} \tag{9}$$

where we write $A^{\boldsymbol{\ell}}_j$ in terms of $B^{\boldsymbol{\ell}}_j$ such that Wald's identity is applicable as it is defined in (6), where by putting $s_i = \sum_{j\in\mathscr{T}} (n_j - \ell_j)\lambda_{ij}$ we get that

$$E\left[\exp\left(-\sum_{i,j\in\mathscr{T}} (n_j - \ell_j)\lambda_{ij} B^{\boldsymbol{\ell}}_i\right) \Big/ \prod_{i\in\mathscr{T}} \psi_i\left(\sum_{j\in\mathscr{T}} (n_j - \ell_j)\lambda_{ij}\right)^{m_i + Z^{\boldsymbol{\ell}}_i}\right] = 1.$$

Noting that if we condition on $\boldsymbol{Z^\ell} = \boldsymbol{\omega}$ in the expectation above, the denominator becomes deterministic and can be moved outside of it. Using this,

as well as the law of total probability, we get that

$$\sum_{\boldsymbol{\omega}=\mathbf{0}}^{\boldsymbol{\ell}} \frac{P_{\boldsymbol{\omega}}^{\boldsymbol{\ell}} E\left[\exp\left(-\sum_{i,j\in\mathscr{T}}(n_j-\ell_j)\lambda_{ij}B_i^{\boldsymbol{\ell}}\right)\middle|\boldsymbol{Z}^{\boldsymbol{\ell}}=\boldsymbol{\omega}\right]}{\prod_{i\in\mathscr{T}}\psi_i\left(\sum_{j\in\mathscr{T}}(n_j-\ell_j)\lambda_{ij}\right)^{m_i+\omega_i}}=1,$$

where the numerator corresponds to the right hand side of (8) (cf. also (9) for the probability to avoid infection), which if replaced with the left hand side of (8) becomes

$$\sum_{\boldsymbol{\omega}=\mathbf{0}}^{\boldsymbol{\ell}} \binom{\boldsymbol{\ell}}{\boldsymbol{\omega}} P_{\boldsymbol{\omega}}^{\boldsymbol{n}} \Big/ \binom{\boldsymbol{n}}{\boldsymbol{\omega}} \prod_{i\in\mathscr{T}}\psi_i\left(\sum_{j\in\mathscr{T}}(n_j-\ell_j)\lambda_{ij}\right)^{m_i+\omega_i}=1.$$

By noting that $\binom{\boldsymbol{\ell}}{\boldsymbol{\omega}}/\binom{\boldsymbol{n}}{\boldsymbol{\omega}}=\binom{\boldsymbol{n}-\boldsymbol{\omega}}{\boldsymbol{\ell}-\boldsymbol{\omega}}/\binom{\boldsymbol{n}}{\boldsymbol{\ell}}$ we finally get the system of equations, corresponding to equation 3.4. of Ball (1986),

$$\sum_{\boldsymbol{\omega}=\mathbf{0}}^{\boldsymbol{\ell}} \binom{\boldsymbol{n}-\boldsymbol{\omega}}{\boldsymbol{\ell}-\boldsymbol{\omega}} P_{\boldsymbol{\omega}}^{\boldsymbol{n}} \Big/ \prod_{i\in\mathscr{T}}\psi_i\left(\sum_{j\in\mathscr{T}}(n_j-\ell_j)\lambda_{ij}\right)^{m_i+\omega_i}=\binom{\boldsymbol{n}}{\boldsymbol{\ell}},\ \mathbf{0}\le\boldsymbol{\ell}\le\boldsymbol{n}. \tag{10}$$

As previously mentioned, the number of possible scenarios quickly become very large even for a small number of types. For instance, consider a small population of 100 individuals with $\boldsymbol{n}=(2,2,46,46,2,2)$. With any number of initially infectious individuals, the number of possible scenarios $\{\boldsymbol{\omega}:\mathbf{0}\le\boldsymbol{\omega}\le\boldsymbol{n}\}$ is $3^4\cdot 47^2=178\,929$, which is an immensely large number, particularly with respect to how informative the computation of the final size distribution would be, since, for the types $k\in\{MM,MB,FB,FF\}$ with a small number of individuals, the number of possible $Z_k$ are far too few say anything *general* about the effect of the disease on those populations. Furthermore, Britton (2010) note that the single-type analogue of (10) may become numerically unstable for large population – a property magnified when considering multiple types (since the system of equations (10) is recursive). For these reasons, the above system of equations (10) will not be used to compute the final size distribution. (We will instead rely on simulations, see section 6.2.)

# 4 Branching process approximation

A tremendously useful tool when analyzing the initial stages of an epidemic process is the *branching process* approximation. The underlying idea behind this approximation is to let the number of initially susceptible individuals tend toward infinity, keeping the number of initially infectious individuals fixed, at which point the epidemic process converges to a continuous time branching process. A stringent proof of this convergence is given by Ball (1983) for both the single- and multi-type cases. The proof relies on *coupling* the epidemic process to a continuous time branching process, which shortly means that one constructs a probability space on which both processes can be defined. A definition of coupling is given by Andersson and Britton (2000, *ch. 3.2., p. 22*; the entire chapter (*ch. 3*) is devoted to coupling and its application to epidemics), but as they note in making their definition, it "is not very illuminating". In this thesis, we will let the inherent heuristics of the definition of the approximating branching process be enough for motivating its validity, referring the interested reader to the above sources. This definition is given in section 4.1.

Using the branching process we define the quantities of the basic reproduction number, $R_0$, in section 4.2, and the probability for a major disease outbreak, $p$, in section 4.3. The relation between these two quantities can shortly but comprehensively be summarized thusly: If $R_0 > 1$ a major disease outbreak (as opposed to a minor one) will occur with probability $p$, and if $R_0 \leq 1$ it will occur with probability 0, i.e. it will not occur. This conveys the importance of the basic reproduction number in the field of epidemiology, since it is a *singular* quantity which determines whether a major outbreak, i.e. an epidemic, *can* occur (cf. (10) in the previous section, which demands the computation of far more quantities than one (for any meaningful number of initially susceptible individuals)).

In the last paragraph of this preamble, we will make a definition of the matrix of infectious contact intensities, $\mathbf{\Lambda}$, such that is scales easily with the number of initially susceptible individuals, which we denote by $n$. Shortly we will define $\tilde{\mathbf{\Lambda}}$ such that $\mathbf{\Lambda} = \nu\tilde{\mathbf{\Lambda}} \approx n\tilde{\mathbf{\Lambda}}$, in a way that is perfectly consistent with our former definition (in fact, it could be construed as trivial). Hence, the reader will not lack in understanding the coming sections if they skip the next paragraph.

Recall from section 2.3 that the matrix of infectious contact intensities $\mathbf{\Lambda}$ is determined by a set of infection probabilities $\{\varpi_{\varsigma_i\varsigma_j}\}$ and a set of general contact intensites $\{\kappa_{ij}\}$, which in turn is determined by the one-sided contact intensities $\{\kappa_i\}$ with the function $\kappa_{ij} = \kappa_i + \kappa_j$. To define a version of the infectious contact intensities such that it easily scales with $\nu$ (which we later approximate with $n$), we only need to manipulate these one-sided contact intensities, since the infection probabilities do not depend on $\nu$. We denote by $\tilde{\kappa}_i = \nu\kappa_i$, which we use in stead of $\kappa_i$ in (4) (where we also omit the Kronecker delta function), from

which it follows that

$$\sum_{j\in\mathscr{T}} c_{ij}\nu_j\left(\frac{\tilde{\kappa}_i}{\nu}+\frac{\tilde{\kappa}_j}{\nu}\right)=\kappa \Longleftrightarrow \sum_{j\in\mathscr{T}} c_{ij}\pi_j(\tilde{\kappa}_i+\tilde{\kappa}_j)=\kappa,$$

which does not depend on $\nu$. We define $\tilde{\mathbf{\Lambda}}=(\tilde{\lambda}_{ij})$ by $\tilde{\lambda}_{ij}=\varpi_{\varsigma_i\varsigma_i}(\tilde{\kappa}_i+\tilde{\kappa}_j)$, and as such, the infectious contact intensity between a pair of individuals of types $i,j$, where the $i$-type individual is infectious, is $\tilde{\lambda}_{ij}\nu^{-1}$. Note that in e.g. Andersson and Britton (2000), the infectious contact intensities are always defined in this way (or rather, they are defined such that they scale easily with $n$, not $\nu$; nonetheless they are always defined such that they scale with the size of the population).

## 4.1 Definition of the branching process

As mentioned in the preamble of this section, we will attempt to define the approximating branching process such that it heuristically describes the asymptotic behaviour of the epidemic process as the number of initially infectious individuals tend toward infinity, although "intuitively" might be a better adverb to describe the level of stringency of this attempt. Our definition draws from the single-type definition of Andersson and Britton (2000, *ch. 3.3.*). The underlying idea behind the approximation is that one considers infectious contact to be made toward individuals occupying *all* states (which will make sense by the end of this subsection) – not only the susceptible one, i.e. an infectious $i$-type individual makes contact toward a certain $j$-type individual at rate $\tilde{\lambda}_{ij}\nu^{-1}$, implying that the superpositioned processes of their contact toward infectious, susceptible and removed individuals of type $j$ are $x_j\tilde{\lambda}_{ij}\nu^{-1}$, $y_j\tilde{\lambda}_{ij}\nu^{-1}$ and $z_j\tilde{\lambda}_{ij}\nu^{-1}$ respectively, which is in accordance with the definition of the epidemic process with respect to the contact toward susceptible individuals (cf. the table of transition intensities (5)). When the number of susceptible individuals is large with respect to the number of infectious and removed individuals, the probability that infectious contact is made between a pair of infectious individual or between an infectious individual and a removed individual is small. This is usually the case at the advent of the epidemic process (unless one is, for example, analyzing the effect of a sudden influx of a large number of infectious individuals, in which case one could argue that a major outbreak is already occurring, and as such the initial stage of the epidemic has already occurred). As the number of initially susceptible individuals tend toward infinity, the probability that infectious and removed individuals, who are of finite number, make contact to one another tend toward zero. In fact, Ball (1983) shows that the asymptotic behaviour of the epidemic process is that a continuous time branching process, which is defined in the coming paragraphs of this subsection, where the correspondence between its events and those of the epidemic process are also presented (with the typical terminology pertaining to branching processes in general is also presented for use in sections 4.2 and 4.3).

We denote by $\boldsymbol{Y}(t)$ the number of individuals in the continuous time branching process at time $t \geq 0$, where $\boldsymbol{Y}(0)$ is non-stochastic and set to the number of initially infectious individuals $\boldsymbol{m}$ when applied to the epidemic process. The vector $\boldsymbol{Y}(t)$ is differentiated by type, i.e. $\boldsymbol{Y}(t) = \big(Y_i(t)\big)$ for $i \in \mathscr{T}$, and its representation in notation is carefully chosen as to resemble the vector of infectious individuals in the epidemic process. Individuals are present in the branching process for a period of time distributed according to the variable $I$, corresponding to, and being equal in distribution to, the infectious period in the epidemic process, i.e. it is exponentially distributed with rate $\gamma$. The presence period of each individual is independent of all other events. When an individual's presence period terminates they are said to *die*, which corresponds to their recovery in the epidemic process. An $i$-type individual *gives birth* to $j$-type individuals according to a Poisson process with rate $\pi_j \tilde{\lambda}_{ij}$. The birthing $i$-type individual is said to be the *ancestor* of the birthed $j$-type individuals, who are said to be the *descendants* of the $i$-type individual. When an individual is born they immediately become a member of the branching process, and are capable to give birth themselves. The birth of individuals corresponds to infection events in the branching process, where an $i$-type individual makes contact to $j$-type individuals according to the superpositioned Poisson process with rate

$$X_j(t)\frac{\tilde{\lambda}_{ij}}{\nu} \approx n_j \frac{\tilde{\lambda}_{ij}}{n} \approx \pi_j \tilde{\lambda}_{ij}, \tag{11}$$

where both approximations are due to the number of initially infectious individuals being large. This approximation is illustrative of the fact that the branching process approximation is only valid for the initial stage of the epidemic process (noting that the right-hand side of (11) is equal to the rate at which $j$-type descendants are born from an $i$-type ancestor), since $\boldsymbol{X}(t)$ declines over time; thereby at some point making $\boldsymbol{n}$ unsuitable for approximation with it. Recall that infectious individuals were considered to make infectious contact toward individuals in all states; On the probability space defined by the coupling argument (again, see Ball (1983)), the difference between the branching process and the epidemic process is that an infectious contact between a pair of infectious individuals and or an infectious individual and a removed individual results in a birth in the former process, but does not result in an infection in the latter. For the duration of this section, we let $\boldsymbol{\lambda}'_{\boldsymbol{i}} = (\pi_j \tilde{\lambda}_{ij})$ for concise notation, realized as a column vector.

Descendants are born independently of one another (as per the definition of the Poisson process), as are their descendants (and their descendants etc.). This is what constitutes the *branching* behaviour of the branching process: Since all individuals give birth and die independently of one another, each individual constitutes the original ancestor of an independent branching process at their own right, which is referred to as a *branch*. Note that all branches of the branching process follow the same set of probability laws as the original branching process $\boldsymbol{Y}(t)$ (determined by $I$, $\tilde{\boldsymbol{\Lambda}}$ and $\boldsymbol{\pi}$).

We will give special attention to the generation-wise realization of the continuous time branching process $\boldsymbol{Y}(t)$, in that we consider the number of descen-

dants of individuals without respect to time. The number of descendants from an $i$-type ancestor is distributed according to the variable $\boldsymbol{D_i} = (D_{ij})$, whose distribution is not explicitly determined in this thesis, but whose expectation is determined in section 4.2 and whose probability generating function is determined in section 4.3. We denote by $\boldsymbol{B}(g)$ the $g$th generation of the *discrete time* branching process, where naturally $\boldsymbol{B}(0) = \boldsymbol{Y}(0)$.

## 4.2 Basic reproduction number

The *basic reproduction number*, denoted by $R_0$, is a (perhaps, *the*) central concept in the study of epidemic modelling, due to its threshold property. Its specific mathematical definition differs depending on the specific epidemic model studied (e.g. Pellis, Ball and Trapman (2011) present its form in the single- and multi-type cases as well as provide methods for computing it in more complex models), although its presence spans both deterministic and stochastic models (see Andersson and Britton (2000, *p. 7*) for a definition of a deterministic *SIR* model). Intuitively, it can be defined as the expected number of infections caused by an infectious individual, or the expected number of descendants from an ancestor, from which one can decipher that if this expected number is less than one, the expected number of infectious individuals will decline per each generation, and tend toward infinity if this expected number is more than one. For an exact definition in terms of our model, we follow Pellis et al (2011) to define it, although the same definition is provided by our main source, Andersson and Britton (2000, *p. 54*), albeit with less detail.

Consider the expected number of $j$-type descendants from an $i$-type ancestor, which we denote by $m_{ij} = E(D_{ij})$, and let the *reproduction matrix* $\boldsymbol{M} = (m_{ij})$ contain these values. The basic reproduction number, $R_0$, is defined as the largest eigenvalue of the matrix $\boldsymbol{M}$. To motivate that this definition implies a threshold property, we consider the expected number of individuals in some generation $g$ of the discrete time branching process $\boldsymbol{B}(g)$. With $\boldsymbol{D_{ik}}(g)$ denoting the number of descendants from the $k$th $i$-type ancestor in generation $g$, we get through Wald's equation and the independence branches that

$$E(\boldsymbol{B}(g)) = E\left(\sum_{i\in\mathscr{T}} \sum_{k=1}^{B_i(g-1)} \boldsymbol{D_{ik}}(g-1)\right) = \sum_{i\in\mathscr{T}} E(B_i(g-1))\boldsymbol{m_i},$$

where $\boldsymbol{m_i} = E(\boldsymbol{D_i})$ is the $i$th row of $\boldsymbol{M}$ (realized as a column vector). Writing the above equality solely in matrix notation and iterating over generations until we reach the original generation yields

$$E(\boldsymbol{B}(g))^T = E(\boldsymbol{B}(g-1))^T\boldsymbol{M} = E(\boldsymbol{B}(g-2))^T\boldsymbol{M}^2 = \cdots = (\boldsymbol{B}(0))^T\boldsymbol{M}^g,$$

since $\boldsymbol{B}(0)$ is non-stochastic (which is analogous to the single type case of Gut (2009, *thm. 3.7.2, p. 87*)). At this point we need to make an assumption on our matrix $\boldsymbol{M}$, which furthermore implies that we make an assumption on our model as a whole – namely – that there exists some $g$ such that all elements

of $\boldsymbol{M}^g$ are strictly positive. Consider the $(i,j)$th element of the matrix $\boldsymbol{M}^g$, which corresponds to the expected number of $j$-type individuals in the $g$th generation of a branching process originating with one $i$-type individual. There will exist a generation $g$ such that the matrix $\boldsymbol{M}^g$ is strictly positive *if* all types of individuals are expected to have descendants of all types for some $g$, i.e. there exists a "path" through which the disease can spread from an $i$-type individual to a $j$-type individual for all $i, j \in \mathscr{T}$ (cf. Figure 1) – a condition typically referred to as $\boldsymbol{M}$ being a *positively regular* matrix in the study of stochastic processes. (The condition is furthermore usually defined as there not being a partition of the type-set $\mathscr{T}$ into non-empty sets, say, $\mathscr{D}_1$ and $\mathscr{D}_2$ such that $m_{ij} = 0$ for all $i \in \mathscr{D}_1$ and all $j \in \mathscr{D}_2$, as it is in Andersson and Britton (2000, *p. 53*)). It is natural, and convenient, to assume that such a path exists, since if it were not to exist, one would be analyzing the spread of a disease in two or more (mutually) closed populations – an analysis that would certainly be easier if one considered these populations separately. It follows from Perron's theorem (Holst and Ufnarovski (2014, *thm. 10.15*, *p. 267*); Pellis et al (2011) refer to it as *Perron-Frobenius* theory) that the largest eigenvalue of $\boldsymbol{M}$ exists and is positive, and as such, $\boldsymbol{B}(0)^T\boldsymbol{M}^g$ will tend toward the zero vector if $R_0$ is strictly less than one, and toward the infinity vector if $R_0$ is strictly greater than one. The former convergence implies that $\boldsymbol{B}(g)$ also tends toward $\mathbf{0}$ in probability as $g$ tends toward infinity if $R_0$ is strictly less than one. (See e.g. Gut (2009, *eq. 6.3.5, p. 157*) for a proof of this implication; Intuitively, since $\boldsymbol{B}(g) \geq \mathbf{0}$, an expectation of $E(\boldsymbol{B}(g)) = \mathbf{0}$ implies that the entire probability mass is at $\mathbf{0}$.)

The elements of $\boldsymbol{M}$ are easily retrieved by using the law of total expectation, where

$$m_{ij} = E(D_{ij}) = E(E(D_{ij}|I)) = E(\lambda'_{ij}I) = \lambda'_{ij}\gamma^{-1},$$

but an expression for the largest eigenvalue of $\boldsymbol{M}$ will not be computed otherwise than numerically in this thesis. We will also consider the localized reproduction numbers $R_\star^{♂♂}$, $R_\star^{♂♀}$ and $R_\star^{♀♀}$, which denote the reproduction numbers among the type-subsets, respectively: $\{MM, MB\}$, i.e. male homosexual contacts; $\{MB, MF, FM, FB\}$, i.e. heterosexual contact; and $\{FB, FF\}$, i.e. female homosexual contacts. These are computed and defined by determining the eigenvalue of the corresponding sub-matrix of $\boldsymbol{M}$, and determine whether the disease is able to propagate into a major outbreak within the particular type-subset. In the case of the heterosexual reproduction number, the matrix elements $m_{ii}$ for self-contacting types $i \in \{MB, FB\}$ are further set to zero, reflecting the fact that these contacts are not heterosexual.

## 4.3 Probability for major outbreak

The second quantity we determine using the branching process approximation is the *probability for a major disease outbreak*, which we denote by $p$. As with the basic reproduction number, we only determine this quantity in terms of the approximating branching process, by conducting the very straight-forward

generalization of theorem 3.7.3 by Gut (2009, *pp. 88-89*), who derives the same probability in the single-type case (except the paragraph relating to the case specific distribution of the number of descendants).

Recall from section 4.1 that all "branches" of the branching process follow the same set of probability laws. This feature is central when determining the probability for the branching process to survive, although to determine this, we do the obverse and determine the complement event of the branching process ultimately going extinct. We denote this event by $\mathcal{E}$ and its probability conditioned on an initial population of one $i$-type individual by $q_i$, and let the vector $\boldsymbol{q} = (q_i)$ contain these probabilities. For an initial population of $\boldsymbol{k}$ individuals we thus have that

$$P(\mathcal{E} \mid \boldsymbol{B}(0) = \boldsymbol{k}) = \prod_{i \in \mathscr{T}} P(\mathcal{E} \mid B_i(0) = 1)^{k_i} = \boldsymbol{q}^{\boldsymbol{k}},$$

where we have invoked the notation $\boldsymbol{a}^{\boldsymbol{b}} = \prod_i a_i^{b_i}$, and used the fact that each initial branch is independent of all other initial branches. The probability for survival is thus given by $p = 1 - \boldsymbol{q}^{\boldsymbol{m}}$. Furthermore, since subsequent branches are also independent, the probability that a certain branch beginning with an $i$-type individual ultimately becomes extinct is still $q_i$. We let $\boldsymbol{D_i}$ generically (i.e not indexing by generation and ancestor) denote the number of descendants of an $i$-type individual, and let $h_i(\boldsymbol{s}) = E(\boldsymbol{s}^{\boldsymbol{D_i}})$ be its probability generating function. Then, by using the law of total probability and conditioning on the number of descendants, we have that $q_i$ must uphold the condition

$$q_i = \sum_{\boldsymbol{k}=\boldsymbol{0}}^{\infty} P(\mathcal{E} \mid \boldsymbol{D_i} = \boldsymbol{k}) P(\boldsymbol{D_i} = \boldsymbol{k}) = \sum_{\boldsymbol{k}=\boldsymbol{0}}^{\infty} \boldsymbol{q}^{\boldsymbol{k}} P(\boldsymbol{D_i} = \boldsymbol{k}) = E(\boldsymbol{q}^{\boldsymbol{D_i}}) = h_i(\boldsymbol{q}).$$

The distribution of the number of descendants of an $i$-type individual conditioned on an infectious period $I = l$ is Poisson distributed with parameter $l\boldsymbol{\lambda'_i}$, i.e. $\boldsymbol{D_i} \mid I = l \sim \mathrm{Po}(l\boldsymbol{\lambda'_i})$, as per the definition of the infectious contact process, and its probability generating function is given by $E(\boldsymbol{s}^{\boldsymbol{D_i}} \mid I = l) = e^{l\boldsymbol{\lambda'_i}^T(\boldsymbol{s}-\boldsymbol{1})}$. With this in mind, we use the law of total expectation and get that

$$h_i(\boldsymbol{q}) = E(\boldsymbol{q}^{\boldsymbol{D_i}}) = E\big(E(\boldsymbol{q}^{\boldsymbol{D_i}} \mid I)\big) = E(e^{I\boldsymbol{\lambda'_i}^T(\boldsymbol{q}-\boldsymbol{1})}) = \psi(\boldsymbol{\lambda'_i}^T(\boldsymbol{q}-\boldsymbol{1})),$$

where $\psi(s) = \frac{\gamma}{\gamma - s}$ is the moment generating function for the infectious period $I$ (which is analogous to the single-type case as presented by Andersson and Britton (2000, *p. 23*)). Hence we have that the extinction probability vector $\boldsymbol{q}$ must uphold the condition

$$q_i = h_i(\boldsymbol{q}) = \frac{\gamma}{\gamma - \boldsymbol{\lambda'_i}^T(\boldsymbol{q}-\boldsymbol{1})}. \tag{12}$$

The condition above does not, however, *uniquely* determine the probability of extinction. For example, since $\{h_i\}$ are probability generating functions, the trivial root $\boldsymbol{q} = \boldsymbol{1}$ will always exist, which would mean that it is impossible for

the branching process to survive. While this certainly would make sense intuitively, considering the fact that $\boldsymbol{Y}(0) = \boldsymbol{0}$ is an absorbing state, it is generally not so. In fact, the smallest non-negative root of the condition (12) constitutes the extinction probability vector. To show that this is indeed true, let the vector $\boldsymbol{h}(\boldsymbol{s}) = \big(h_i(\boldsymbol{s})\big) = \big(E(\boldsymbol{s}^{\boldsymbol{D_i}})\big)$ contain the probability generating functions for the number of descendants (each of which take the same argument, $\boldsymbol{s}$), and consider the probability generating function of the $g$th generation of a generic branching process, denoted by $H_g(\boldsymbol{s})$, for which through the law of total expectation we have that

$$H_g(\boldsymbol{s}) = E(\boldsymbol{s}^{\boldsymbol{B}(g)}) = E(E(\boldsymbol{s}^{\boldsymbol{B}(g)} \,|\, \boldsymbol{B}(g-1))) = E(\boldsymbol{h}(\boldsymbol{s})^{\boldsymbol{B}(g-1)}) = H_{g-1}(\boldsymbol{h}(\boldsymbol{s})), \tag{13}$$

which is analogous to theorem 3.6.1 of Gut (2009, *p. 80*; theorem 3.7.2, *p. 87*, previously mentioned in section 4.1 of this thesis makes reference to this theorem, and applies it to branching processes analogously to the above equation). The third equality stems from the fact that

$$\begin{aligned} E(\boldsymbol{s}^{\boldsymbol{B}(g)} \,|\, \boldsymbol{B}(g-1) = \boldsymbol{\ell}) &= E(\boldsymbol{s}^{\sum_{i\in\mathscr{T}} \sum_{k=1}^{\ell_i} \boldsymbol{D_i}_k(g-1)}) \\ &= E\left(\prod_{i\in\mathscr{T}} \prod_{k=1}^{\ell_i} \boldsymbol{s}^{\boldsymbol{D_i}_k(g-1)}\right) = \boldsymbol{h}(\boldsymbol{s})^{\boldsymbol{\ell}}, \end{aligned}$$

where the last equality is due to the independence of the number of descendants. Now, let $H_{gi}(\boldsymbol{s}) = E(\boldsymbol{s}^{\boldsymbol{B}(g)\,|\,\boldsymbol{B}(0)=\boldsymbol{e_i}})$ denote the probability generating function of the $g$th generation of a branching process originating with one $i$-type individual, and consider the first iteration of this function, for which

$$H_{1i}(\boldsymbol{s}) = E(\boldsymbol{s}^{\boldsymbol{B}(1)\,|\,\boldsymbol{B}(0)=\boldsymbol{e_i}}) = E(\boldsymbol{s}^{\boldsymbol{D_i}}) = h_i(\boldsymbol{s}).$$

From this and equation (13), we can construe that

$$H_{gi}(\boldsymbol{s}) = H_{g-1,i}(\boldsymbol{h}(\boldsymbol{s})) = H_{g-2,i}(\boldsymbol{h}(\boldsymbol{h}(\boldsymbol{s})) = \cdots = h_i(\underbrace{\boldsymbol{h}(\boldsymbol{h}(\ldots \boldsymbol{h}(\boldsymbol{s}) \ldots)}_{g-1 \text{ times}}). \tag{14}$$

Let $q_{gi} = P(\boldsymbol{B}(g) = 0 \,|\, \boldsymbol{B}(0) = \boldsymbol{e_i})$ denote the probability that a branching process originating with one $i$-type individual has gone extinct by the $g$th generation, let the vector $\boldsymbol{q_g} = (q_{gi})$ contain these probabilities, and let $\boldsymbol{q}^\star$ denote some non-negative root of the system of equations (12), which always exists due to the trivial solution $\boldsymbol{1} = \boldsymbol{h}(\boldsymbol{1})$. Obviously $\boldsymbol{q_g}$ is non-decreasing with $g$, since the event that the branching process has gone extinct by generation $g$ implies that it continues to be extinct for subsequent generations. To show that $\boldsymbol{q}$ constitutes the smallest root of equation (12), we will make use of two properties of the probability generating function. First, it has the eponymous property of generating probabilities, particularly, $P(\boldsymbol{B}(g) = \boldsymbol{0}) = H_g(\boldsymbol{0})$, and second, it is non-decreasing for $\boldsymbol{s} \geq \boldsymbol{0}$.

Since the zeroth generation of the branching process is non-stochastic, we have that

$$\boldsymbol{q_0} = \boldsymbol{0} \leq \boldsymbol{q}^\star = \boldsymbol{h}(\boldsymbol{q}^\star),$$

and for subsequent generations (using to the aforementioned properties of the probability generating function) that

$$\begin{aligned} \boldsymbol{q_1} &= \boldsymbol{h}(\boldsymbol{0}) \leq \boldsymbol{h}(\boldsymbol{q}^\star) = \boldsymbol{q}^\star \\ \boldsymbol{q_2} &= \boldsymbol{h}(\boldsymbol{h}(\boldsymbol{0})) \leq \boldsymbol{h}(\boldsymbol{h}(\boldsymbol{q}^\star)) = \boldsymbol{h}(\boldsymbol{q}^\star) = \boldsymbol{q}^\star \\ &\vdots \end{aligned}$$

and considering considering equation (14), we have that

$$\boldsymbol{q_g} = \underbrace{\boldsymbol{h}(\boldsymbol{h}(\ldots \boldsymbol{h}(\boldsymbol{0}) \ldots))}_{g \text{ times}} \leq \underbrace{\boldsymbol{h}(\boldsymbol{h}(\ldots \boldsymbol{h}(\boldsymbol{q}^\star) \ldots))}_{g \text{ times}} = \boldsymbol{q}^\star.$$

Since the event of ultimate extinction corresponds to the event that $\{\boldsymbol{B}(g) = \boldsymbol{0}\}$ for *some* $g$, it follows that $\boldsymbol{q_g}$ tends toward $\boldsymbol{q}$ as $g$ tends toward infinity, and since $\boldsymbol{q_g}$ is non-decreasing with $g$ and bounded from above by some non-negative root $\boldsymbol{q}^\star$, the extinction probability vector $\boldsymbol{q}$ must be the smallest non-negative root of $\boldsymbol{s} = \boldsymbol{h}(\boldsymbol{s})$.

# 5 Vaccination *or* Use of protections

In this section we present a method for mitigating the spread of the disease, to which, implied by the bititularity of this section, we apply two interpretations. The concept of vaccination should not be unheard-of by the reader, since it is a common practice in most industrialized societies (although recently its popularity has declined). Nevertheless, we make a definition for it: An individual who is vaccinated against a disease cannot contract that disease. A vaccine with this definition is referred to as a *perfect* vaccine, as opposed to an *imperfect* one, e.g. a *leaky* vaccine, which prevents the disease to evolve into a symptomatic illness in a vaccinated individual, but still allows that individual to infect others (although perhaps with a lower probability; This case is discussed in Pellis et al (2011)). We will not consider this particular imperfection, but another, which leads us to the second interpretation of vaccination, which (hopefully) should also not be unheard-of by the reader: The use of sexual protections, e.g. condoms, whose purpose is to prevent the exchange of the possibly disease carrying bodily fluids usually exchanged when one is engaged in sexual contact (with the additional purpose of preventing pregnancy caused by the vaginal intrusion of one of these fluids; Procreation is, however, typically not considered as an infectious disease, and as such, the case of it is excluded from this thesis; Cf. however the terminology of the branching process (sec. 4.1.)). Considering the idealized case of a perfect sexual protection, which is furthermore used perfectly and at every sexual contact by those using it, we note that an individual using this protection thusly cannot contract venereal diseases, which is identical to the definition of the perfect vaccine. The imperfect aspect of the protection-usage interpretation is that sexual protections generally are not perfect – there is a probability that they fail. While the latter interpretation is more realistic in the imperfect case – the author of this thesis does not know of any true vaccines with this particular imperfection – we will refer to this method of mitigating the disease as vaccination.

While vaccines are administered to individuals, who may consider it a personal protections against the disease, their effect can surpass the individual level and immunize the entire population – a condition referred to as *herd immunity*. This property of vaccination stems from the fact that if a certain proportion of the population is vaccinated, a proportion of births in the approximation branching process will be suppressed, and thereby decreasing the basic reproduction number, $R_0$. Herd immunity occurs when the proportion of the population vaccinated is sufficient as to decrease the basic reproduction number below its threshold value of one, in which case only a minor outbreak of the disease can occur (see section 4). We assume that with each individual vaccination incur a *cost* for e.g. the government (or whoever), and set the objective to minimize this cost under the condition that we achieve herd immunity. As has been the norm throughout this thesis, we do not determine analytical results for this objective, since these would rely on the previously undetermined expressions, instead simply defining the effect of vaccination on our model definition.

We redefine the type-structure of section 2.1 such that each type has two

sub-types – an unvaccinated one notated by $i^W \in \mathscr{T}^W$, and a vaccinated one notated by $i^V \in \mathscr{T}^V$ for $i \in \mathscr{T}$. Preference and level of sexual activity does not differ between sub-type $i$ and $i^V$. We order the vaccinated sub-type after all unvaccinated sub-types, with each set of sub-types ordered as in (2). A vaccinated individual has a reduced probability of both contracting and transmitting the disease; a property resultant from the protection-usage interpretation – individuals who use protections use them for all their sexual contacts. The reduction in probability is quantified by $p^V$, the *efficiency* of the vaccine, where an infectious $i$-type individual makes infectious contact to a susceptible $j$-type individual with probability $(1-p^V)\varpi_{\varsigma_i\varsigma_j}$ if either of them are vaccinated, i.e. if $i \in \mathscr{T}^V$ and or $j \in \mathscr{T}^V$. Since preference and level of sexual activity are left unchanged, this general contact intensities ($\kappa_{ij}$) are too, and as such, the matrix of infectious contact intensities can be expressed as

$$\mathbf{\Lambda}^V = \begin{pmatrix} \mathbf{\Lambda} & (1-p^V)\mathbf{\Lambda} \\ (1-p^V)\mathbf{\Lambda} & (1-p^V)\mathbf{\Lambda} \end{pmatrix}.$$

We let the proportion of vaccinated individuals differ between types, since the original probability for infection differs, where the proportion of $i$-type individuals who are vaccinated is denoted by $\pi_i^V$, i.e. such that $\pi_{i^V} = \pi_i^V \pi_i$. Note that previous sections, particularly the one relating the the basic reproduction number (sec. 4.2), are general enough to be applicable to this redefinition.

# 6 Results

In this section, we will present numerical computations of the basic reproduction number, $R_0$, in section 6.1 and the probability for major disease outbreak, $p$, as well as simulation results for the final size distribution in section 6.2, the temporal behaviour of the epidemic process in section 6.3, and the result of the vaccination scheme in section 6.4. The simulations have been done using the Sellke construction (see sec. 3.1) – more specifically – by drawing random Exp(1)-distributed and Exp($\gamma$)-distributed random variables in the programming language R, representing the individual thresholds and infectious period respectively. By using the slope of the infection pressure it is determined which individual threshold, if any, is next to be surpassed by the infection pressure, which is done iteratively until there are no infectious individuals remaining in the population.

Three cases are considered, identified by I, II and III. The first case considers the original motivation of this thesis – the spread of HIV – whereas the latter two are purely fictitious. We consider a population of $\nu = 10\,000$ individuals, where the heterosexual proportion is $\pi_{He} = 0.92$, such that

$$\nu_{MM} = \nu_{MB} = \nu_{FB} = \nu_{FF} = 200 \text{ and } \nu_{MF} = \nu_{FM} = 4\,600,$$

and only consider the case of one initial infectious individual of male sex and preference, i.e. $\boldsymbol{m} = (1, 0, 0, 0, 0, 0)^T$. The time step is set to 1 year, and the contact intensities ($\kappa_{ij}$) used in the simulations are determined by including the Kronecker delta function in (4), where we further set the level of sexual activity to $\kappa = 26$, i.e. individuals procure new partners biweekly, which is an exaggerated number if one compares to e.g. the most sexually active individuals from the empirical study of Freiesleben de Blasio et al (2007), who procured 30 new partners during a three-year period; It is, however, likely that some of these pairings resulted in relationships longer than the maximum of 1 sexual contact demanded by our model, and we consider $\kappa = 26$ to be a reasonable compromise (noting that it is essentially made-up).

## 6.1 Case parameters and $R_0$

We consider three cases, identified by I, II and III, with varying parametrizations – particularly – we vary the disease transmission probabilities $\{\varpi_{\varsigma_i\varsigma_j}\}$ and the mean of the infectious period $\gamma^{-1}$. The parametrizations of all cases originate with the property of HIV, that the transmission probability is higher for anal intercourse than for vaginal, which in turn is higher than for oral (which has a negligible transmission probability (Patel et al (2014)). In case I we use the per-act transmission probabilities empirically estimated by Patel et al (2014). Note, however, that the probability for contracting HIV from receptive anal intercourse with an infected individual is significantly higher than for insertive anal intercourse (estimated at 138 vs. 11 per 10 000 contacts); We have chosen the mean of these estimated probabilities to be the disease transmission probability between male individuals. Also, according to Patel et al (2014), the

difference in transmission probability for penile-vaginal intercourse is not significantly different if the male partaker is infectious as opposed to if the female partaker is. As such, we have assumed these two probabilities to be equal, and set to the higher estimate. Note that we are essentially assuming that male-male intercourse is always anal, that male-female intercourse is always vaginal, and that female-female intercourse is neither.

| Parameter/Case | I | II | III |
|---|---|---|---|
| $\kappa$ | 26 | 26 | 26 |
| $\gamma^{-1}$ | 10 | 5 | 2 |
| $\varpi_{♂♂}$ | 0.0075 | 0.0150 | 0.0375 |
| $\varpi_{♂♀}$ | 0.0008 | 0.0064 | 0.0215 |
| $\varpi_{♀♂}$ | 0.0008 | 0.0064 | 0.0215 |
| $\varpi_{♀♀}$ | 0 | 0 | 0 |
| Reproduction number | | | |
| $R_0$ | 1.5720 | 1.5735 | 1.5761 |
| $R_\star^{♂♂}$ | 1.5719 | 1.5719 | 1.5719 |
| $R_\star^{♂♀}$ | 0.2060 | 0.8240 | 1.1072 |
| $R_\star^{♀♀}$ | 0 | 0 | 0 |

Table 1: Parameters for cases I, II and III with corresponding reproduction numbers.

In Table 1 we see that for case I, the heterosexual reproduction number is very low, and one might reason that the heterosexual final size will also become very low. For that reason we define case II such that the heterosexual reproduction number is closer to, but below, one, as to answer the question whether a localized reproduction number below one can still produce a major outbreak among that localized type-subset (given that the basic reproduction number is above the threshold). For comparison, we define case III such that the heterosexual reproduction number is above one. Note that the infectious period has been varied, as to keep the duration of the epidemics of the three cases somewhat similar (see sec. 6.3), while keeping the male heterosexual reproduction number $R_\star^{♂♂}$ equal and $R_0$ approximately equal for all three cases.

The left plot of Figure 3 illustrates the effect the localized reproduction numbers have on the basic reproduction number, for a model otherwise parametrized as a case I epidemic. The basic reproduction number $R_0$ is close to being equal to the largest localized reproduction number, if the difference between localized reproduction numbers is large. Note that the heterosexual reproduction number is dominant even for heterosexual transmission probabilities less than that of the male-male transmission probability, and that the basic reproduction number $R_0$ is strictly greater than the localized reproduction numbers $R_\star^{♂♂}$ and $R_\star^{♂♀}$.

A motivation for considering the localized reproduction numbers is that they may entail some information on whether their corresponding type-subsets will be affected by the disease spread. In the left plot of Figure 3, we see that for small heterosexual reproduction numbers, the purely heterosexual population

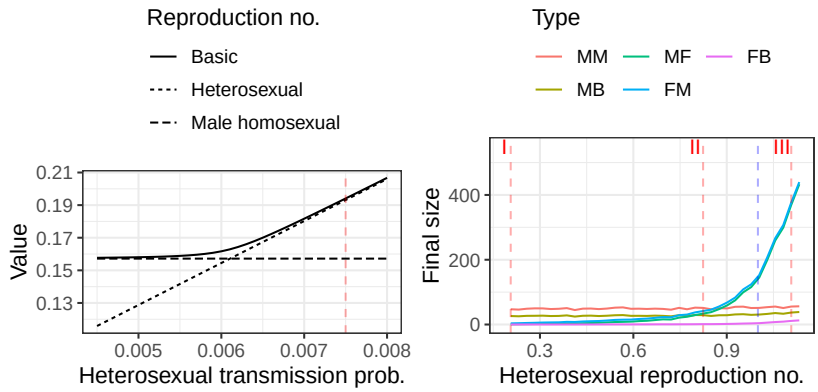



Figure 3: **Left:** Reproduction numbers as a function of the heterosexual disease transmission probability, $\varpi_{♂♀} = \varpi_{♀♂}$, for fixed male-male transmission probability, $\varpi_{♂♂} = 0.0075$, illustrated by the dashed red vertical line. (Further, $\kappa = 26$ and $\gamma^{-1} = 10$.) **Right:** Mean final size from 500 simulations each where the heterosexual transmission probability is varied from $\varpi_{♂♀} = 0.0008$ to $\varpi_{♂♀} = 0.0044$ with step 0.0001 as a function of $R_\star^{♂♀}$. Dashed red lines correspond to the heterosexual reproduction numbers $R_\star^{♂♀}$ for cases I, II and III, and the dashed blue line to $R_\star^{♂♀} = 1$. The basic and homosexual reproduction numbers are $R_0 \approx R_\star^{♂♂} = 1.5719$ for all values of $\varpi_{♂♀} \in (0.0008, 0.0044)$.

(i.e. excluding bisexual individuals) are almost unaffected by the disease spread for small $R_\star^{♂♀}$, but an increase in the final size is noticeable *before* the localized reproduction number increases above one.

## 6.2 Final size and $p$

In this section, we present final size distributions for the three cases, retrieved from simulations. (Note that while we have for all cases assumed female-female contact have zero probability of resulting in infection, histograms of the final sizes for female homosexuals, $Z_{FF}$, are present despite their triviality: $Z_{FF} = 0$ for all cases.) All simulations originate with one male individual of male preference, i.e. an $MM$-type individual, who is not represented in the histograms below.

A general note on the shape of the final size distributions is that they have two modes, which correspond to the events of a minor and a major outbreak, illustrating the importance of the basic reproduction number $R_0$; In section 6.4, Figure 9, histograms for final size distributions for epidemics with $R_0 < 1$ are illustrated, for which the "bumps" of the major outbreaks are not present. We also compute the probability for a major outbreak $p$ in all three cases, noting that since this probability is determined for an infinite population of susceptible individuals, the actual probability for major outbreak is less that that of $p$.

### 6.2.1 Case I

The final size distribution of the case I epidemic is unsurprising – individuals of types $MM$ and $MB$ represent almost all of the ultimately infected individuals, as is apparent from Figure 4. Also, $FM$-type individuals are worse affected than $MF$-type individuals, due to them being exposed to the disease through contacts with $MB$-type individuals. The probability for a major outbreak is $p = 0.3910$ and the extinction probability vector is

$$\boldsymbol{q} \approx (0.6090, 0.7918, 1.0000, 0.9988, 0.9994, 1)^T.$$

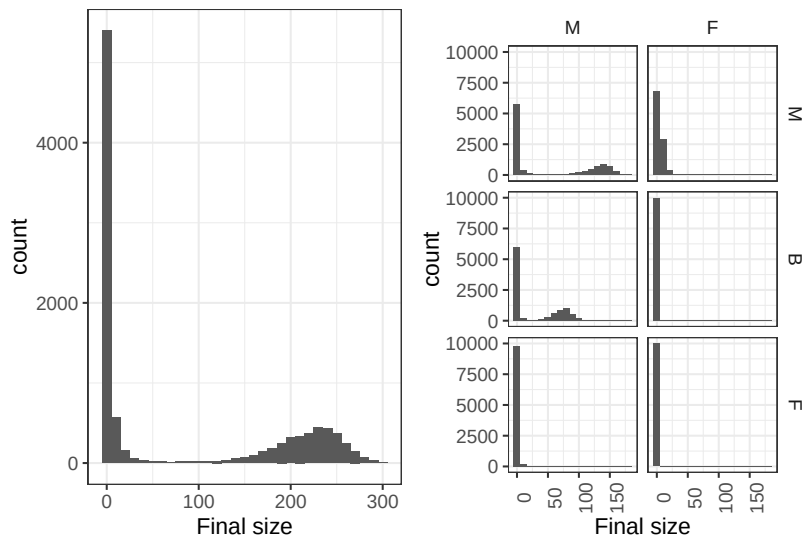



Figure 4: Final size from 10 000 simulations of a case I epidemic. The left plot shows the the total final size, whereas the right is differentiated with respect to type. Each bin represents 10 individuals.

### 6.2.2 Case II

The final size distribution of the case II epidemic, illustrated in Figure 5, is more surprising than the case I epidemic, since noticeable major outbreaks occur among individuals of types $MF$ and $FM$, despite the heterosexual reproduction number being lower than one. The probability for a major outbreak is $p = 0.3937$ and the extinction probability vector is

$$\boldsymbol{q} = (0.6063, 0.7861, 0.9888, 0.9862, 0.9918, 1)^T$$

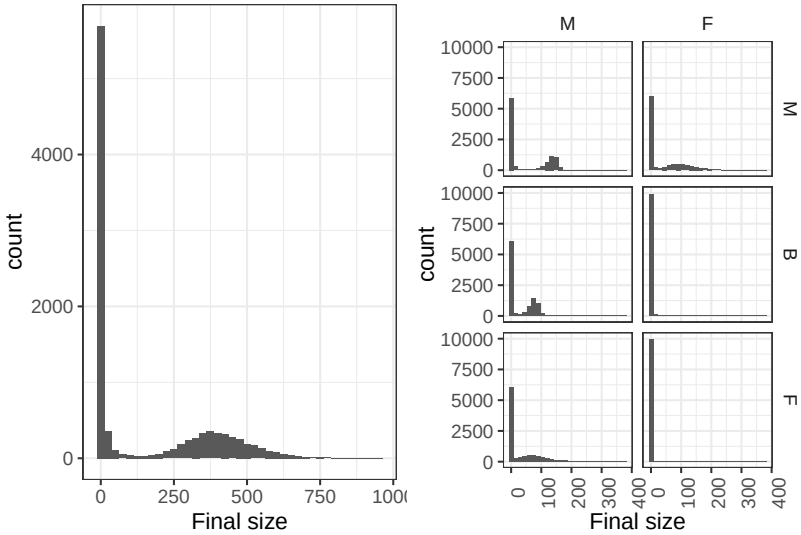



Figure 5: Final size from 10 000 simulations of a case II epidemic. The left plot shows the total final size, whereas the right is differentiated with respect to type. Each bin in the left plot represents 25 individuals, and in the right 15 individuals.

### 6.2.3 Case III

In Figure 6 the final size distribution of a case III epidemic is illustrated. Note that the final size *proportion* is used as to plot the different types on the same scale. Individuals of all types, except type $FF$, are affected by the spread of the epidemic, and the total final size for a major outbreak is much larger than for case I and II epidemics, mainly due to the numerosity of the types $MF$ and $FM$. The probability for a major disease outbreak is $p = 0.4373$, and the extinction probability vector is

$$\boldsymbol{q} = (0.5627, 0.6773, 0.7028, 0.7501, 0.8223, 1)^T.$$

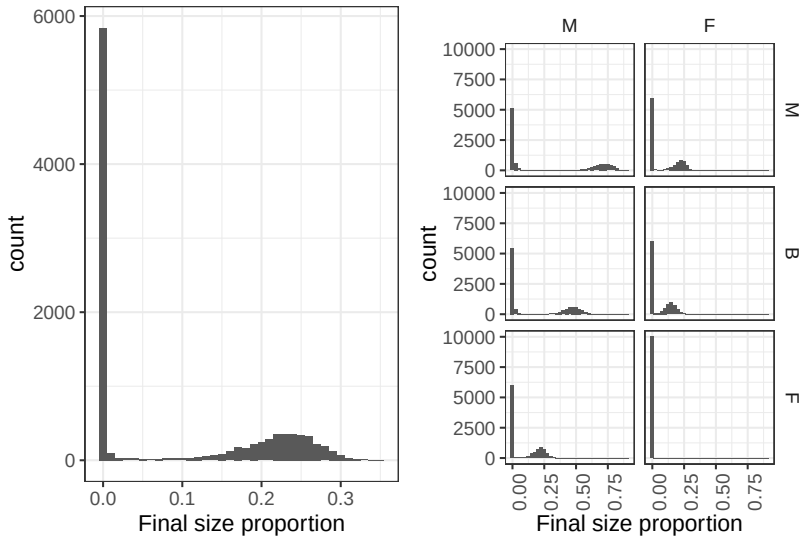



Figure 6: Final size proportion from 10 000 simulations of a case III epidemic. The left plot shows the total final size, whereas the right is differentiated with respect to type. Each bin in the left plot represents 2.5 per cent of the population, and in the right 1 per cent of individuals of each type.

## 6.3 Temporal behaviour

As mentioned in section 3, there exist no closed form expression for the temporal behaviour of the epidemic process, but with the aid of simulations, we can nevertheless make some statements about it. (This section is, however, more illustrative in nature, such that it may give the reader an idea of how the epidemic process propagates through time.) Figure 7 illustrates three (by eye) approximately typical realizations of disease outbreaks for the three cases. The trajectory of the case I epidemic is not very surprising, with individuals of types $MM$ and $MB$ representing almost all infectious individuals at all points in time. The case II simulation, however, reveals that the peak of the number of infectious $MM$- and $MB$-type individuals precede that of the $MF$- and $FM$-type individuals – a property that is exaggerated for the case III epidemic. While one could construe that the heterosexual peak supersedes the male homosexual one due to the fact that the number of heterosexual individuals is far greater, it is surprising that this occurs in the case II epidemic, since the localized heterosexual reproduction number is below its threshold. (Note, however, that the plots in Figure 7 are on continuous time – not generation-wise, for which an increasing number of infectious individuals would not be a typical trajectory for a reproduction number below one.) See Appendix A, Figure 11, Figure 12 and Figure 13, for the trajectories from several simulations of each case, and note that the peak for types $MF, FM$ seams to supersede that of types $MM, MB$ for most outbreak trajectories of the case II epidemic (and the case III epidemic).

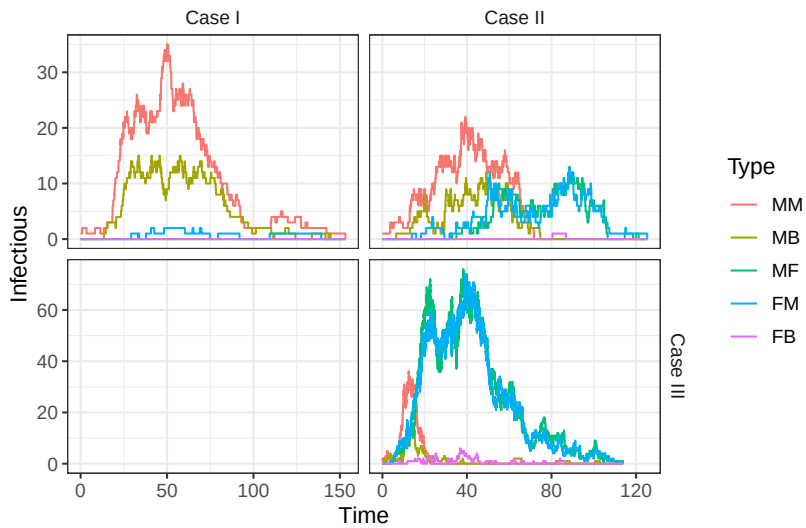



Figure 7: Trajectories of infectious individuals from simulations of case I, II and III epidemics.

The attentive reader may have noted that these outbreaks span over 100 time steps, which, since the time axis represents years, is embarrassingly unrealistic. In section 7 we mention that we could have (perhaps, should have) included a demographic process, allowing individuals to enter and exit the population at some rate. (Figure 11 in Appendix A reveals that one of the simulated case I epidemics spans over 300 time steps.) However, the time axis scales with the mean infectious period, $\gamma^{-1}$, and the level of sexual activity, $\kappa$, since these parameters do not differ with respect to type, and as such the shape of the above trajectories still entail information on the behaviour of epidemics with parametrizations of the transmission probabilities $\varpi_{\varsigma_i\varsigma_j}$ as in Table 1, but less (perhaps, not) so with the parametrization of $\kappa, \gamma^{-1}$.

## 6.4 Effect of vaccination

The general formulation of the vaccination scheme presented in section 5 allowed for the proportion of vaccinated individuals to vary with each type. In this section, we collapse this variability into three proportions based on whether individuals engage in certain contacts or not: one for males that make homosexual contact, one for males and females who make heterosexual contact but not male homosexual contact, and one for females who only make homosexual contact, denoted by

$$\pi^V_{♂♂} = \pi^V_{MM} = \pi^V_{MB} \ , \ \pi^V_{♂♀} = \pi^V_{MF} = \pi^V_{FM} = \pi^V_{FF} \ \text{ and } \ \pi^V_{♀♀} = \pi^V_{FF},$$

and referred to as the male homosexual, heterosexual and female homosexual vaccinated proportions respectively. We define the female homosexual vaccinated proportion to equal zero, since the female homosexual transmission probability is set to zero for all epidemic cases we consider. In the end of this section, we shortly discuss the case where the vaccinated proportions are not collapsed, with the example of allowing the proportions $\pi^V_{MM}$ and $\pi^V_{MB}$ to vary. The efficiency of the vaccine is assumed to be $p^V = 0.8$, and all simulated epidemic processes in this section originate with an unvaccinated type-$MM$ individual.

Recall that the objective of the vaccination scheme is to reduce the basic reproduction number below its threshold value of one as to obtain herd immunity, with the biobjective to minimize the proportion of the total population that is vaccinated. In Table 2 these proportions are presented, where $\pi^V$ denotes the proportion of the total population that is vaccinated. In cases I and II, the male homosexual proportion $\pi^V_{♂♂}$ necessary is equal to that necessary to reduce the localized male homosexual reproduction number $R_\star^{♂♂}$ below one (when rounding up to the nearest hundredth; this is *not* an exact equality, cf. Figure 3, neither is the equality between case I and II vaccinated male homosexual proportions). In the case III epidemic, the male homosexual vaccinated proportion necessary is above the necessary proportion to reduce the corresponding local reproduction number below one, while the heterosexual vaccinated proportion is below it (a proportion of 0.11 would be necessary), due to $MB$-type individuals being included in the male homosexual vaccinated proportion.

| Proportion / Case | I | II | III |
|---|---|---|---|
| $\pi^V_{♂♂}$ | 0.39 | 0.39 | 0.51 |
| $\pi^V_{♂♀}$ | 0 | 0 | 0.10 |
| $\pi^V_{♀♀}$ | 0 | 0 | 0 |
| $\pi^V$ | 0.0156 | 0.0156 | 0.114 |

Table 2: Minimized vaccinated proportions (rounded up to the nearest hundredth) to obtain herd immunity.

Figure 8 illustrates the basic reproduction number as a function of the male homosexual and heterosexual vaccinated proportions, where the minimized proportions of Table 2 are represented by black dots. This figure should be compared to the left plot of Figure 3, since the basic reproduction number is approximately equal to the dominating localized reproduction number (although only the contours of the localized reproduction numbers equalling one are included in Figure 8).

As for the effect that vaccination has on the final size distribution, Figure 9 illustrates the mean total final size for different vaccinated proportions (which is not very informative – obviously it decreases as the vaccinated proportion increases), as well as histograms of the final size distribution for vaccinated proportions equal to that of Table 2. The tail of these histograms are included without a scale to illustrate their shape, which is otherwise obscured by the

high prevalence of very small outbreaks. Note that a "major outbreak bump" akin to that of Figure 4, Figure 5 and Figure 6 is not present in either of the histograms in Figure 9, as is expected, since major outbreaks cannot occur for $R_0 < 1$.

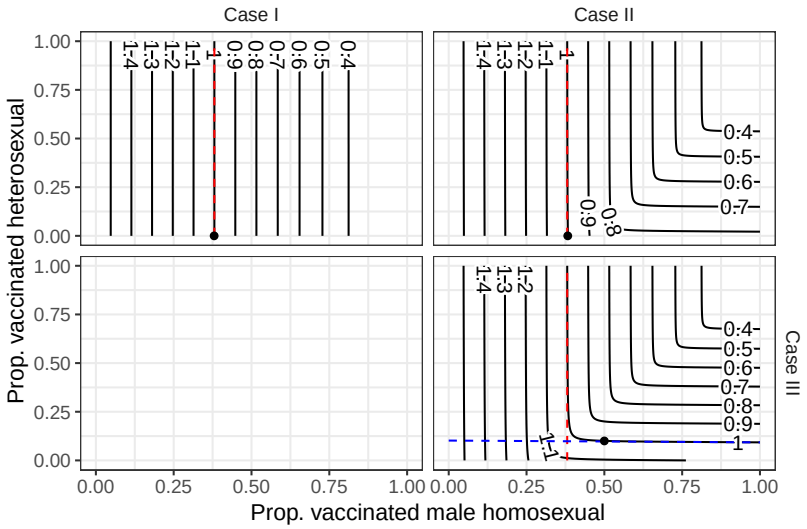



Figure 8: Basic reproduction number for varying proportions of vaccinated individuals, represented by contour lines. Red and blue dashed lines correspond to the proportions for which the male homosexual and heterosexual reproduction numbers respectively equal one. Black dots denote the minimal total proportion for which the basic reproduction number is less than one.

Finally, we mention that the proportion of the total population that is vaccinated could be minimized further, if we were to vary all vaccinated proportions $\pi_i^V$ for $i \in \mathscr{T}$. As an example, we consider varying $\pi_{MM}^V$ and $\pi_{MB}^V$ in a case I epidemic. In Figure 10 we see that it is sufficient only to vaccinate $MM$-type individuals to achieve herd immunity, which stems from the fact that $MB$-type individuals rarely make contact to other $MB$-type individuals. The necessary $MM$-type vaccinated proportion is $\pi_{MM}^V = 0.45$, which results in a vaccinated proportion of the total population of $\pi^V = 0.009$, which is almost half that necessary when not varying $\pi_{MM}^V$ and $\pi_{MB}^V$ (for which $\pi_{♂♂}^V = 0.39$ results in $\pi^V = 0.0154$). Also, due to the nature of heterosexual contact, it would be sufficient only to vaccinate one of the sexes to achieve herd immunity, if we were to vary these proportions in a case III epidemic.

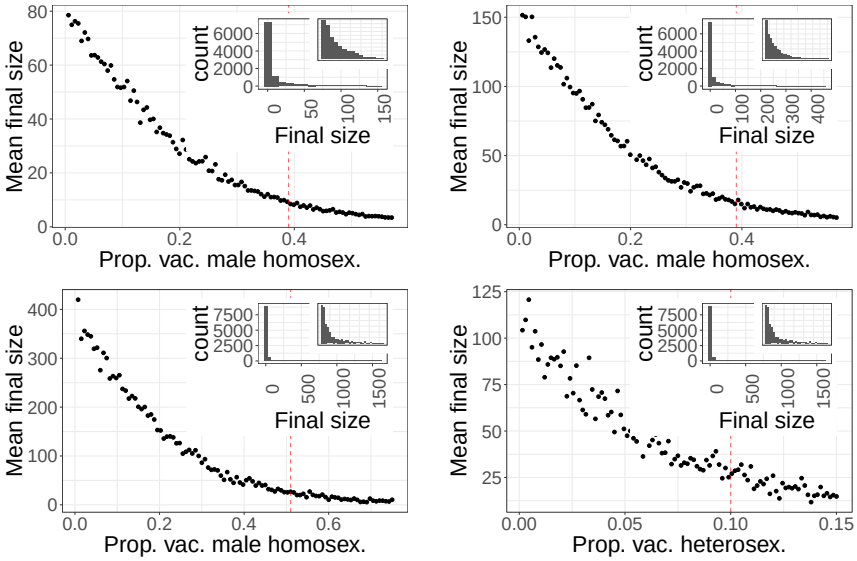
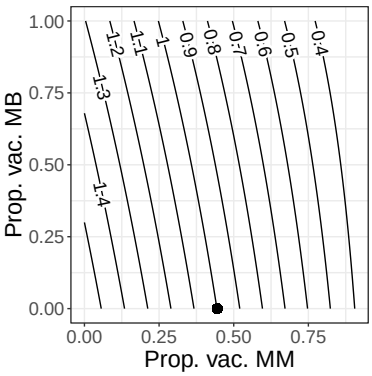



Figure 9: Mean total final size from 1 000 simulations each for varied proportions of vaccinated individuals with inset histograms of the final size from 10 000 simulations with vaccinated proportion corresponding to the dashed red line (for which $R_0 < 1$), and with additional inset histograms for the tail distribution. Clockwise from upper left: Case I epidemic with unvaccinated heterosexual population (histogram binwidth 10 individuals, tail histogram shows final sizes of 10 or more); Case II epidemic with unvaccinated heterosexual population (binwidth 15; tail shows 25 or more); Case III epidemic with vaccinated male homosexual proportion $\pi^V_{♂♂} = 0.51$ (binwidth 50; tail shows 50 or more); Case III epidemic with vaccinated heterosexual proportions $\pi^V_{♂♀} = 0.1$ (binwidth 50; tail shows 50 or more).

Figure 10: Basic reproduction number represented by contour lines for varying proportions of vaccinated *MM* and *MB*-type individuals for an otherwise unvaccinated population in a case I epidemic (or approximately a case II epidemic).



# 7 Discussion

In this section we will discuss the results of the previous section (sec. 6) in section 7.1 – momentarily ignoring the deficiencies of the model with respect to the realism of it, followed by a discussion on how these deficiencies could be mended in section 7.2, and to conclude this thesis, we make some suggestions for further study related to ours in section 7.3.

## 7.1 Conclusions

The aim of this thesis was, first, to study the effect that the differing disease transmission probabilities have on the final size distribution $\boldsymbol{Z}$, as well as to the basic reproduction number $R_0$ and the probability for a major outbreak $p$, although the latter two quantities are of interest mostly because they entail information on the final size distribution. The results (presented in section 6.1 and 6.2) are unsurprising for the case I epidemic, which is parametrized as to resemble HIV, the original motivation for this thesis. Noteworthy is however the magnitude of how disproportionately individuals of types $MB$ and, especially, $MM$ are represented in the major outbreak distributions – a majority of male homosexuals are eventually infected – while other types experience only minor affliction. The case II epidemic is more interesting, since individuals of types $MF$ and $FM$ experience noticeable major outbreaks (that is, noticeable in Figure 5), while their localized reproduction number is below one. While the localized reproduction numbers are not threshold values otherwise than for the purely imaginary localized epidemics among the type-subsets encompassed by them, it is noteworthy that the epidemic process may survive among these types despite, i.e. since $MF$-type individuals can not be infected from $MB$-type individuals, which $FM$-type individuals can, the epidemic process must have propagated among $MF$- and $FF$-type, i.e. heterosexual, individuals. The consideration of the localized reproduction numbers may therefore be unnecessary if they do not differ greatly. However, the final size distribution of both the case I and II epidemics motivate the consideration of the type structure of this thesis as opposed to a simplified type structure only considering heterosexual individuals. For the case III epidemic, where the lion's share of the total final size is constituted by $MF$- and $FF$-type individuals, it could perhaps have been prudent to consider such a simplified type structure, were one not interested in the final sizes of the specific types considered in this thesis.

The second aim of this thesis was to study the effect that a proportion of the population being vaccinated has on the final size distribution, and determining what is the least proportion necessary to achieve herd immunity. In this case, the localized reproduction numbers deemed useful, since in the case I and II epidemics it was sufficient to reduce the localized male homosexual reproduction number below one (again, when rounding up to the nearest hundredth), and in the case III epidemic, the necessary vaccinated heterosexual proportion was close to that necessary to reduce the corresponding localized reproduction number below one. Further, allowing the vaccinated proportion of individuals of different

types to differ proved to be an effective method to reduce the proportion of the total population that is vaccinated. This answers the question posed in the introduction of this thesis, whether different groups of individuals should be targeted differently.

## 7.2 Deficiencies of model

As was mentioned in section 6.3, the duration of the simulated epidemics are embarrassingly unrealistic, which stems from a deficiency in the original formulation of the model (although the size of the population used in the simulations naturally affect the duration of the epidemic). The model used in this thesis is more suitable for diseases having a higher transmission probability and shorter infectious period, thereby making the duration of the epidemic process short, which in turn makes the closed population an appropriate approximation of reality. In the case of venereal diseases, which has been the subject of this thesis, this is perhaps not an appropriate approximation at all, since individuals relatively rarely make new sexual contacts enabling the disease to spread. A remedy for this deficiency would be to introduce a *demographic process*, which allows individuals to enter and exit the population at some rate. Such a process is defined in the single-type in Andersson and Britton (2000, *ch. 8.1*).

As for the realism of our model with respect to HIV, we have not included any processes to model the spread via needle-sharing among drug users or child-birth (which would require some demographic process to be included, naturally), the latter having an estimated transmission probability of 0.226 in Patel et al (2014), which is a much higher transmission probability than those we have considered. Also, the probability of contracting HIV from an infectious individuals differs greatly depending on what stage of the HIV infection the infectious individual is in. Shortly, in the initial stage of HIV infection (acute HIV infection) the infectious individual is very infectious, which is followed by a latent period of low infectivity until the advent of AIDS, when the infectivity again increases. Also, as noted in section 2.2, the true level of sexual activity is not equal between individuals, and not necessarily between the types we have defined either.

## 7.3 Suggestions for further study

A theme throughout this thesis has been not to determine closed form expressions for the quantities considered. In the case of distribution of the final size $\boldsymbol{Z}$, it does not appear to exist such an expression as of the authorship of this thesis, but for the basic reproduction number $R_0$ and the probability for a major disease outbreak $p$ it would certainly be possible to determine such expressions, as would it for the localized reproduction numbers and the necessary vaccinated proportions to achieve herd immunity (since these are defined in terms of well-defined mathematical objects, i.e. the eigenvalue of a matrix for $R_0$ and the solution to a system of polynomial equations for $p$). It not certain, however, that such expressions would have an informative form, i.e. they might be quite complicated.

Originally, this thesis were also to include a contact tracing scheme, i.e. upon recovery, previously infectious individuals report (to some entity, e.g. health officials) their previous sexual contacts from some time period in the past, such that these individuals may undergo some procedure, e.g. a blood test, to determine whether they too are infected. The computational necessity of simulating all sexual contacts, even for a smaller population than the one considered, for the duration of the epidemic process deemed, however, unobtainable for the author of this thesis. On the note of contact tracing we must mention, however, that analytical results have been determined for a contact tracing scheme, namely that of Ball, Knock and O'Neill (2011). These results consider the initial behaviour of the epidemic process akin to that of the branching process approximation presented in section 4 in this thesis. However, the contact tracing scheme of Ball et al (2011) demands that individuals have knowledge on which of their contact were infectious, i.e. non-infectious contacts are not part of the scheme. In our case, this would be an ill approximation, since most contacts are non-infectious (due to the rather low transmission probabilities).

Finally, and naturally, a suggestion for improving the model would be to mitigate the unrealistic aspects of it presented in the previous section (sec. 7.2), particularly by including a demographic process.

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# A Temporal behaviour figures

This appendix consists of figures for the trajectories of the number of infectious individuals for case I, II and III epidemics from 1000, 500 and 200 simulations respectively.

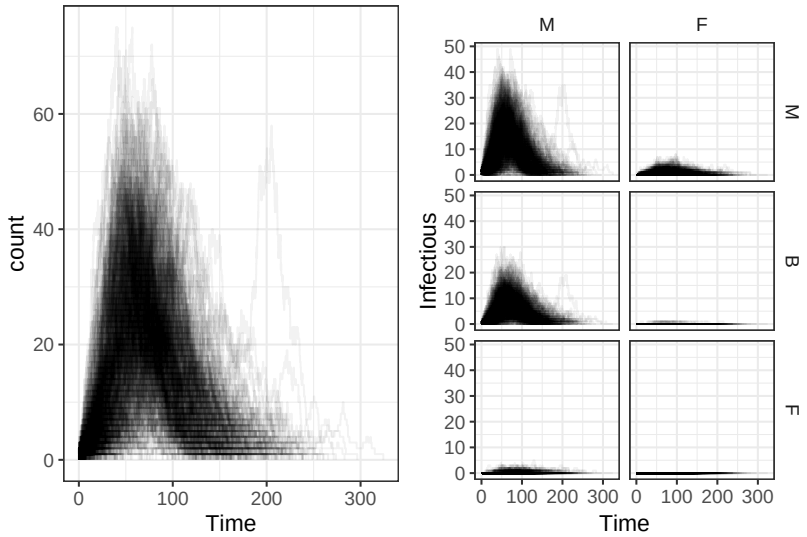


Figure 11: Trajectories of the number of infectious individuals from 1000 simulations of a case-I epidemic.

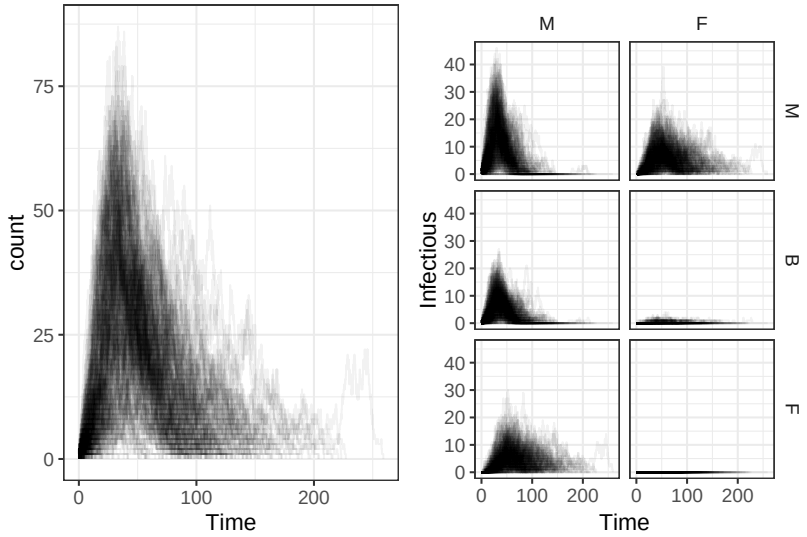


Figure 12: Trajectories of the number of infectious individuals of 500 simulations of a case-II epidemic.

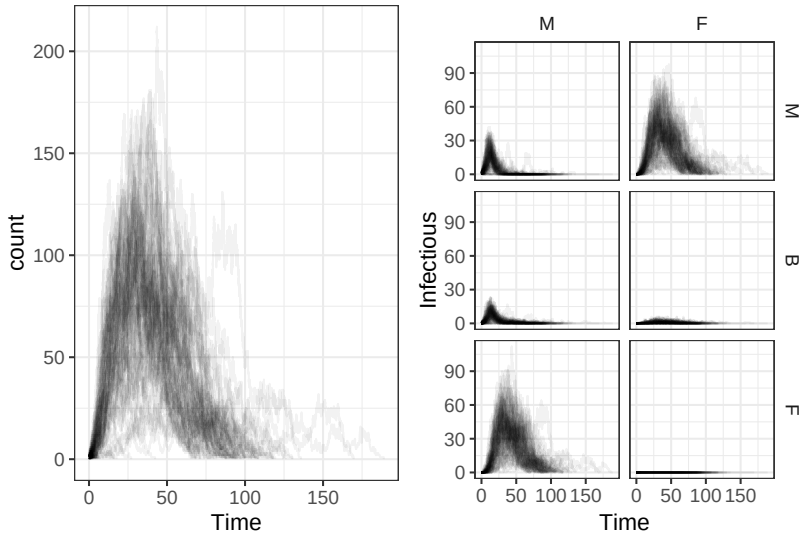


Figure 13: Trajectories of the number of infectious individuals of 200 simulations of a case-III epidemic.