An Agent-Based Model to Study the Effects of Non-Pharmaceutical Interventions on the Spread of Sexually Transmitted Infections among Youth

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Abstract. Due to their flexibility and efficiency, agent-based simulations are becoming one of the main approaches for epidemiological modelling, as they allow to deal more naturally with the high variability of human behaviours and interactions. In this paper, an agent-based model developed in NetLogo is presented. This model can be used to simulate and investigate the effectiveness of non-pharmaceutical interventions respectively to the spread of sexually transmitted infections among a sexually-active heterosexual population of youth, as it involves pair formation mechanisms and takes into account the individual choices by means of random variables with given distributions. Finally, in order to evaluate the accuracy of the model, a case study regarding the spread of chlamydia is presented. From that, it is concluded that the most important interventions to contain this infection are: (1) the ability to notify a great number of past sexual partners, especially casual ones; (2) the level of awareness of the individuals, expressed in terms of use of barrier methods and frequency of spontaneous screenings.

1 Introduction

Sexually transmitted infections (STIs) are responsible for various diseases as well as short-term and long-term complications, including pelvic inflammatory disease, ectopic pregnancy, infertility, chronic pelvic pain and arthritis. Furthermore, STIs can be transmitted from mother to child during pregnancy, and they are likely to increase the risk of human immunodeficiency virus (HIV) acquisition and transmission [1–3].

The majority of newly reported sexually transmitted infections occur among youth aged from 15 to 24 years. This is primarily due to behavioural factors such as a higher number of sexual partners, a lower condom usage and a tendency to avoid regular tests [1–5]. In order to trace and contain the spread of these infections among the youth population, a number of control programs have been promoted by the EU, and the UK chlamydia screening program for sexually active adolescents and young adults established in 2008 was particularly effective [3]. However, as in most cases STIs remain asymptomatic, it is vital to increase the level of awareness about the diseases and to enhance screening programs.

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Unfortunately, this is often not enough. The said practices, indeed, must be sustained by an efficient and effective contact-tracing framework, also known as *partner notification*, which aims to prevent reinfection of the index case, minimise complications, and reduce the population prevalence of STIs in the community.

Although STIs can be either cured with antibiotics or treated to prevent further transmission [6, 7], it is evident that non-pharmaceutical interventions (NPIs) are essential for their containment. A plethora of research and reports investigated the level of success of this type of interventions, along with other studies which targeted the correct trade-off between costs and contributions [5]. By studying the evolution of the endemic disease using a simulated model, the present work aims at identifying to which extent these interventions can effectively reduce the incidence of STIs – particularly chlamydia – among youth, as well as setting bounds within which each intervention should work in order to avoid unexpected outbreak.

2 Epidemiological Modelling for STIs

The origins of epidemiological modelling can be traced back to the early 20th century, when Kermack and McKendrick developed the SIR compartmental model to study the effects of endemic diseases on a population [8]. Since then, many of its variations have been proposed with the aim of taking into consideration the peculiar aspects of each disease, population, and environment. For example, the spread of airborne viruses is certainly different from vector-borne ones; for some infections, an everlasting immunity can be acquired either naturally or through a vaccine, while for some others it is possible to catch the infection more than once; finally, in some cases it is desirable to model the presence of symptomatic and asymptomatic cases, or even the presence of quarantined and hospitalised individuals, in order to see how they can impact on the progression of the infection.

When it comes to STIs, the general approach is to use either the SIR (Susceptible - Infected - Recovered), SIS (Susceptible - Infected - Susceptible), or SIRS (Susceptible - Infected - Recovered - Susceptible) model depending on the type of infection [5, 9–11]. Indeed, while some infections, such as chlamydia, gonorrhoea, trichomoniasis and syphilis have a limited recovery period during which the infection can be cured with a dose of antibiotics, for others, such as herpes, there is no known cure but only a series of treatments to prevent their spread, which leaves the individuals in a "recovered" state forever [6, 7].

A distinctive aspect in STIs modelling is the necessity of including some kind of pair-formation mechanisms. Among all, Kretzschmar [12] pointed out that this mechanisms can indeed bring several realistic effects to the model, e.g., that two susceptible individuals involved in a stable relationship are effectively protected from the infection, or that two infected individuals in a stable relationship "waste" contacts without infecting others. As a result, in a situation with pair formation, the rise of the prevalence towards endemic equilibrium is

much slower, and the eventual endemic prevalence is lower than estimated by a model that ignores partnership duration [12, 13].

However, being based upon ordinary differential equations, mathematical modelling for the spread of epidemics has two main disadvantages. Firstly, the complexity of the models does not scale very well, as any extension generally introduces a massive number of parameters which soon become unmanageable, and this gets particularly worse for STIs, where both individuals and pairs have to be modelled. Secondly, as explained by Garnett [14], much of our initial understanding of the epidemiological consequences of the natural history of STIs has been drawn from studies which considered population averages, which by definition suppress the variability of each individual and thus prevent from a more detailed understanding of the phenomena. In order to overcome these limits, agent-based models – i.e., bottom-up techniques in which the system is modelled from the perspective of constituent parts – started to be developed both to confirm the correctness of the mathematical models and to test more complex environments.

3 Model Definition and Development

The agent-based model presented was developed leveraging Uri Wilensky's NetLogo simulator [15], and it can be used to illustrate how certain behavioural factors and non-pharmaceutical interventions affect the development of the infection among a sexually-active heterosexual population of youth. A deeper explanation of the model's structure and parameters is provided in the next subsections; however, the implementation is publicly available and can be consulted at `www.github.com/giuluck/STI-Spread-Simulator`.

3.1 Population and Network Structure

Three different networks are maintained in the simulation, each of which controls a different aspect of the individuals' relationships.

First of all, a network of opposite-sex close contacts is used to choose individuals' partners for stable relationships. The idea of establishing pairs over a layer of close contacts has been effectively used in a number of prior studies [16, 17], and it reflects the tendency of individuals to consume relationships among their neighbourhood of friends, co-workers, or any other kind of frequent contact. Additionally, as friendship networks have been proven to possess small-world properties, with nodes' degree following a Gaussian distribution [18, 19], this network is built using the Watts-Strogatz formulation [20] with an average degree of 20 opposite-sex contacts and rewiring probability $p = 0.25$.

Secondly, a network of current partners is maintained to provide a snapshot of the ongoing relationships among individuals. Relationships can be either stable or casual, and while the former are required to be consumed among one's neighbourhood, the latter ones can be formed between any two opposite-sex individuals, as they tend to involve in never before acquainted partners or casual friends [21].

Finally, a network of past partners, containing links between any two people who have been sexual partners at least once, is used for two main reasons. Firstly, it enables to show the degree distribution of sexual encounters; and then, more importantly, it allows to keep track of the list of people who must be notified during the contact tracing phase. To do so, three different kinds of links are used – namely, `Already Traced`, `Traced Casual`, and `Traced Stable` –, representing past relationships between already-tested, casual and non-tested, and stable and non-tested partners, respectively.

3.2 Individual's Status and Relationships Formation

In this model, five sexual statuses are allowed: `Single`, `Seeking Casual`, `Seeking Stable`, `Casual`, and `Stable`. The way individuals change their status is governed by four parameters, which regulate different aspects of the population sexual behaviours.
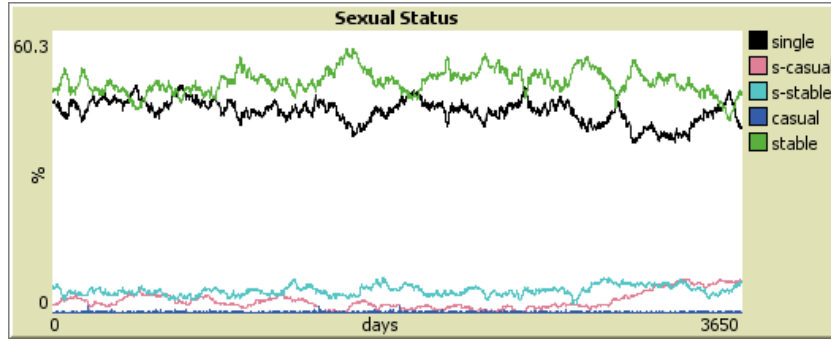

Fig. 1. Sexual statuses distribution among a simulation.

First of all, a `Breakup Probability` accounts for the frequency at which stable couples break-up. Since both Meier et al. [22] and Manning et al. [23] report that stable relationships among youth last on average between 12 and 14 months, a probability $p = \frac{1}{370 \text{ days}}$ was chosen. Additionally, a `Single Probability` accounts for the frequency at which a `Single` individual decides to start seeking a new relationship. From a statistical point of view, this means that both the intra-relationship and the inter-relationship time for each stable couple is sampled from a geometric random variable with mean $\lambda = 370$ days and $\lambda = 230$ days, respectively. This last estimation was carried out by taking into consideration that between 50% and 70% of youth are engaged in some kind of relationship [22, 23], a trend that, as shown in Fig. 1, was accurately mimicked through the use of this value.

Secondly, a `Casual Probability` is used to represent individuals' binary decisions to seek either a casual or a stable relationship. This probability is set to $p = 0.25$, according to data reported in [21] and [23], where it is estimated that

the number of stable partners is on average between 5 and 6, with 2 additional partners from casual encounters. Moreover, an `Intercourse Probability` is used to decide whether or not a stable couple will have a sexual intercourse – for casual couples, this happens with 100% probability as the relationship lasts one time only. This parameter can affect the probability of the spread of the infection among stable couples, and is also regulates the rate at which core members of the population decide to seek casual sex[1]. However, as no relevant data could be found for this parameter, the distribution was modelled as a geometric one, with mean λ fixed to 7 in order to indicate an average of one sexual intercourse per week.

3.3 STIs and NPIs-related Parameters

Together with sexual status, individuals have an infection status, which can be either: `Susceptible`, `Incubating`, `Asymptomatic`, `Tracing`, or `Recovered`. In particular, `Incubating`, `Asymptomatic`, and `Tracing` individuals are those infected, so they are to be considered as different instances of the `I` class in SI* models. In particular, `Tracing` individuals are those – infected only, for simplicity – who have been listed for notification by a positive past partner but have not been contacted yet. A clearer overview of how statuses evolve is shown in Fig. 2.
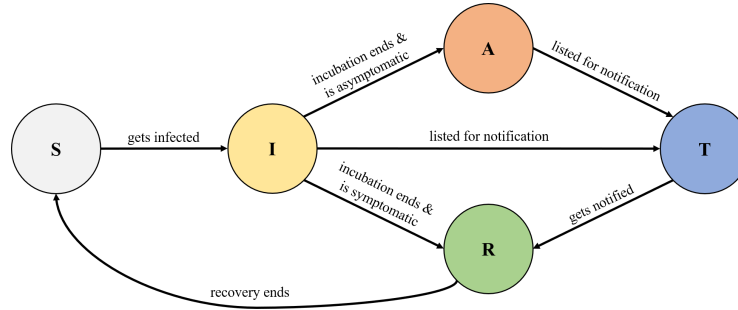

Fig. 2. Infection statuses evolution – **S**usceptible, **I**ncubating, **A**symptomatic, **T**racing, and **R**ecovered.

Furthermore, some additional parameters are involved. They are not fixed in the code, but they rather can be changed by the users depending on the simulation. Some of them control the characteristics of the infection itself, namely the `Initial Infected Percentage`, the `Symptomatic Probability`, and the `Incubation` and `Recovery Time`[2]. Along these, the compartmental model itself can be chosen as well. Indeed, even though the default option is SIRS, it is

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[1] More on core vs. non-core members is added in subsection 3.3.
[2] This last one accounts for both the time to get tested and the time to get cured.

possible to switch either to a SIS or a SIR scenario by setting the recovery time to zero or "infinite", respectively. A detailed explanation of how these parameters were chosen for the chlamydia case study is presented in Sect. 4.
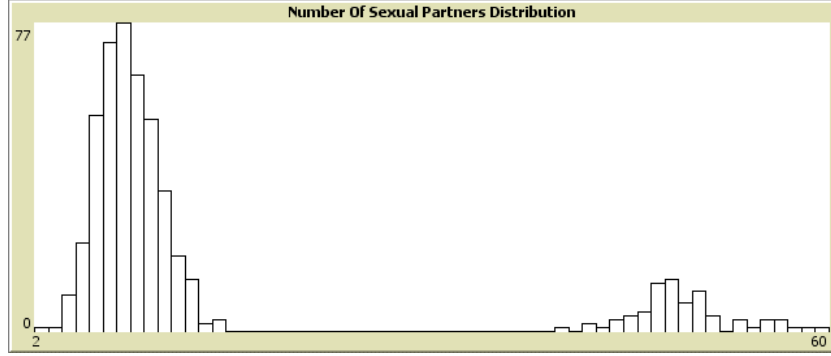

Fig. 3. Distribution of the number of sexual partners. The distribution is bimodal due to the presence of core members – on the right – and non-core members – on the left.

Together with STIs-related parameters, six others are used to configure the effectiveness of NPIs. Firstly, a `Core Group Percentage` is used to decide how many core individuals will be part of the population. The idea of dividing the population into a group of core members, having certain "extreme" behaviours, and non-core members, having more common behaviours, was introduced by Moghadas [24] and it has been used by various epidemiological simulations regarding STIs [5, 25]. In this context, core members are defined as those seeking casual relationships only, something that results in a much higher number of sexual partners, as shown in Fig. 3.

Secondly, an `Infection Spread Probability`, accounting for both the actual load of the infection and the correct use of condoms or other barrier methods, is used to represent the probability that an infected individual will infect a susceptible one during an intercourse. Moreover, both a `Casual` and a `Stable Tracing Probability` can be set to decide the chance that a past casual or stable partner, respectively, gets notified and does undergo a screening[3]. Finally, an `Average Notification Delay` accounts for the time passed – due to ex-partners uncertainty, lack of memory and other difficulties encountered when contacting the individuals – between the moment an individual's past partner has tested positive and the individual is notified, while an `Average Screening Time` represents the average number of years passing between two spontaneous screenings for each individual. Mathematically speaking, both of these are to be thought as geometric random variables with mean $\lambda = \frac{1}{p}$.

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[3] Current stable partners, instead, are always notified.

3.4 Simulation Evolution

Once the parameters are fixed, the simulation proceeds as follows. At the beginning, each individual is initialised as `Single` and `Susceptible`, and the potential partners network is generated, while the past and current partners networks are empty. Thus, in order to have a realistic picture of the social environment, as done in other works [17, 26], the simulation is warmed-up for a year to make it form pairs before the introduction of the infection. Then, once the given percentage of the individuals is infected, another year of warm-up is performed, in order to let the infection reach an endemic state. At this point, the actual simulation begins and continues for a given number of years. At each clock step, which is set to one day, the simulation algorithm performs these tasks:

1. Relationships are put to test. `Stable` ones can break-up according to the predefined probability, while `Casual` ones always do. In any case, whenever there is a break-up, individuals' status is set to `Single` again and the link between them is removed from the current partners network.
2. The status of `Single` individuals is then changed. Core members can decide to remain `Single` or to start to seek a casual relationships, while non-core members can decide to remain `Single` or to seek a relationship, and if they do, they have to choose its kind as well. In any case, each of these decisions is regulated by the respective probability.
3. Pairs are formed among those having the same `Seeking` status. `Casual` pairs do not consider their neighbourhoods, while `Stable` ones do. In any case, current and past links are initialised – or changed, if already present – according to the chosen type of relationship. Potential links are removed in the case of stable relationships to prevent two individuals to fall back together due to a lack of availability in their neighbourhood. In fact, while churning phenomena are reported to be common in adolescents [23], they happened to be clearly over-represented in the model without this alteration. Still, casual relationships between two ex-partners are possible.
4. Once the pairs are formed, the infection is spread with the given probability every time there is a sexual intercourse between a susceptible and an infected individual. When infected, susceptible individuals become `Incubating` and will have to wait a certain amount of time before symptoms may or may not appear.
5. Then, the infection evolves depending on the status of each individual. `Incubating` ones may have to wait for some more time, or they can switch to the `Recovered` or `Asymptomatic` state depending on whether or not they show symptoms[4]. Similarly, `Recovered` individuals may have to wait more, or they can become `Susceptible` again.
6. Finally, screenings are performed. Any individual can undergo a spontaneous screening depending on the chosen probability. Then, if they test positive, a given percentage of their past casual and stable partners is listed for no-

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[4] For simplicity, those who show symptoms get immediately tested and cured.

tification, i.e., they get in the `Tracing` state[5]. At this point, individuals in the `Tracing` state have a certain probability to be actually notified in that particular time step and, if that is the case, they will undergo the screening and eventually notify some of their past partners.

At the end of the simulation, it is possible to inspect both the three networks and some plots regarding the progress of both sexual and infection status of the individuals. Then, by changing the parameters and running other simulations, the effectiveness of NPIs can be measured in terms of the difference between the number of infected individuals in the scenarios.

4 A Case Study: Chlamydia

According to the 2016 bulletin of the World Health Organization [1], chlamydia is the most frequently reported sexually transmitted infection. Almost two-thirds of new chlamydia cases occur among youth aged 15-24 years [4], with the infection remaining asymptomatic in nearly 70% of the cases [5]. In order to trace and contain the spread of these infections among the youth population, the EU started to promote a control program, which gave major results in the UK, where a screening program for sexually active adolescents and young adults was established in 2008 [3]. Since then, many studies reported how contact tracing plays a crucial role in the solution of the issue, especially when it comes to identify infected males, who are less likely to present for chlamydia screening [27].

In order to run this experiment, most of the STIs-related parameters were chosen according to a previous study by Armbruster and Brandeau [5], which turns out to be consistent when compared to what is being reported on major fact sheets from governments and institutes [1–3,28–30]. The population size was set to 500, with a percentage of initially infected of 5%. Symptoms are shown in 30% of the cases, with an incubation period of 14 days. The recovery time was set to 14 days to account for both the average 7-days delay to get the test result and for 7 more days of antibiotic treatment.

A baseline scenario with default NPIs-related parameter was run in order to compare its results with other configurations. After the two-years warm-up, the simulation went on for ten more years, according to the fact that adolescents, as reported by Meier and Allen [22], have an average of ten to twelve years of romantic experience prior to marriage. The number of core members was set to one out of ten, with a 40% probability for the infection to be spread during sexual intercourse. Contact tracing effectiveness was set to work for an average of three casual and eight stable partners out of ten. Finally, the average notification delay was set to seven days, recalling the average delay to get the results for the test, while the average inter-screening time for spontaneous screenings was set to five years.

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[5] For simplicity, non-infected individuals who are to be notified do not pass in the `Tracing` state, as their screening will not have any consequence.
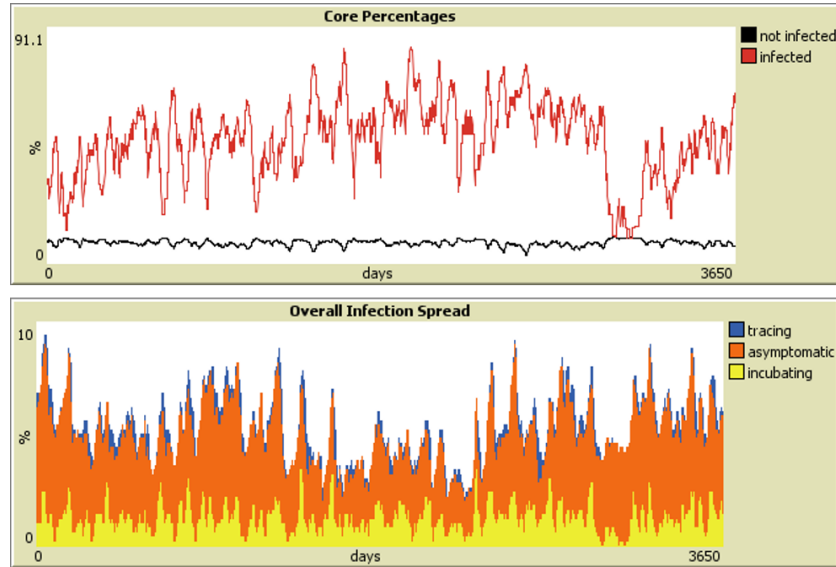
Fig. 4. Endemic behaviour in a simulation with default parameters.

As shown in Fig. 4, this configuration led to an endemic situation in which the number of infected people fluctuates between 4% and 8%, with peaks up to 10%. Periodical outbreaks were effectively contained via contact tracing, as made clear by the increasing number of `Tracing` individuals soon after the outbreak itself, and they were also clearly correlated to a massive spread in the core group as the trends of the two plots are similar. Moreover, since the percentage of infected core members with respect to the total number of infected individuals is kept around 60%, with peaks up to 90%, it is possible to conclude that, as expected, core members do act as hubs, and thus they should be motivated to undergo spontaneous screenings more frequently than non-core ones.

Afterwards, some more configurations were tried out in order to understand how each single parameter can affect the outcomes of the simulation.

4.1 Core Group Percentage

Three simulations were performed using default parameters setting the number of core members to none, half, and everyone, respectively. Each of these simulations led to a different scenario that demonstrated how the number of infected individuals increases with the percentage of core members. Indeed, while in the first case the infection was effectively eradicated after some years, in the second case the endemic behaviour ranged between 10% and 20%, going up to 20%-30% in the third scenario. Similarly, in the second scenario the number of infected core members with respect to the total of infected individuals was kept almost constant and around nine out of ten, which is way higher than the 60% reported

in the default simulation. This is also the reason why a higher and more constant number of individuals in the `Tracing` state was reported.

Moreover, even with a maximal spread probability, the infection could still be eradicated when no core members were included, while when having just one core member out of ten as in the default configuration lead to up to 20% of the population being infected. In the latter scenario, in particular, core group infection peaked at 60% of the total, while the same value was 90% in the default simulation, meaning that, when barrier methods are not used, the infection is more likely to spread and persist in stable couples as well.

However, the outcomes of these and other tests, show that, in general, whenever the infected percentage of core members with respect to the whole infected population reaches zero, there is a high probability that the infection will be eradicated in a short amount of time. This has to be regarded as another proof that core members do act as hubs, and thus performing screenings on these individuals is way more effective than performing random screenings.

4.2 Infection Spread

Regarding the spread probability, two tipping points for the infection eradication were found in two different scenarios. When using the default parameters, this value is 25%, meaning that if barrier methods are effectively used in at least three intercourse out of four, chlamydia could be fully eradicated within a short period of time. Instead, in a simulation with core members only, this value is lowered to 10%, meaning that to eradicate the infection, it should spread in maximum one intercourse out of ten. These findings show how condoms, and barrier methods in general, are of great importance for the containment of chlamydia, and that their relevance is even greater when dealing with polygamy.

4.3 Stable & Casual Tracing

Other simulations, aimed at investigating the effects of both stable and casual contact tracing, reported that the latter is of much greater importance in the containment of the infection. On the one hand, when effectively notifying an average of 40% of the ex casual partners, the infection could be fully eradicated after a few years. This value is a tipping point which remains constant even when the number of ex stable partners who are effectively notified is decreased, as well as when the parameter decreasing is the percentage of core members. On the other hand, when the number of core members is increased to half of the population, the tipping point is a bit higher, but it still remains resilient with respect to changes to the stable tracing probability. As casual intercourse are more prominent in core members, this is, once again, a proof that they could act as vectors for the infection, and thus it is fundamental for them to keep track of their past partners with some sort of diary-based technique. In fact, with default parameters for both the infection spread and the screening time, 65% of casual tracing probability was found to be enough in order to eradicate the infection in a population of core members only.

4.4 Notification Delay

Simulations regarding the average number of days needed to notify previous partners has shown that, as expected, this value directly correlates with the percentage of infected individuals. However, this measure seems not to influence the outcomes in a particular way. Indeed, while the only way to eradicate the infection was to use a one-day delay – which is somehow infeasible due to the fact that tests need to be processed before giving a result, and that contacting past partners may require some time –, when an average of 14 days was set, the results did show a significant change if compared with the ones in the default simulation. Additionally, increasing that delay period to 30 days made the number of infected individuals increase up to 15%, while with 90 days this value reached 22%. Thus, as reported by these results, what comes out is that it is way more important to contact a higher number of previous partners, even after some time, than to contact a few of them but immediately. There are two main reasons for this behaviour: one is that, as stable couples are more frequent than casual ones and last longer than the average delay, these individuals often do not pass the infection to more than one person during the waiting time; another reason, instead, is related to the model itself, according to which this delay is sampled from a geometric random variable so that, even with a higher average delay, there is still some non-negligible probability that some individuals will get notified within a much shorter amount of time.

4.5 Average Screening Time

Finally, from an analysis of the inter-screening time, it came out that combining a two-year average time with a 30% infection spread could effectively eradicate chlamydia among the population within a few years, while this is not always the case if the infection spread is increased to 40% – but still, the average percentage of infected people is way lower than in the default simulation. This means not only that increasing the awareness on spontaneous testing is very important – in particular if taking in mind the limitation of the model, where people test independently from their sexual status, while in a real-life scenario people are encouraged to get tested whenever they change sexual partner or when they have a non-protected intercourse –, but also that it is important to link this awareness with that of having protected sex, as the two things are clearly correlated. Indeed, if the spread probability reaches higher values, such as 70%, the impact of a two-years inter-screening time with respect to a five-years one is practically insignificant. Moreover, even in a scenario with a totally polygamous population, combining an average of one screening per year with a 10% spread probability for the infection is enough to eradicate chlamydia by effectively notifying just one partner out of four on average, meaning that behavioural changes obtained by a rising of STIs awareness might be sufficient to contain the infection, even without a massive infrastructure for contact tracing.

5 Conclusions

In this work, an agent-based model aimed at studying the effects of non-pharmaceutical interventions on the spread of sexually-transmitted infections among a sexually-active heterosexual population of youth was presented. The model, which uses pair formation mechanisms to account for the presence of both stable relationships and casual encounters, can be customised thanks to the presence of various adjustable parameters regarding both the properties of the infection, the percentage of core members, and the effectiveness of behavioural and structural non-pharmaceutical interventions.

The model was proven to be accurate enough to reproduce the endemic nature of chlamydia in a population of 500 individuals – 50 of them being core. Then, starting from a default configuration of parameters, the incidence of each one was investigated by looking at the outcomes of ad hoc simulations. What emerged is that, as foreseeable, core members have great impact on the total number of infected people, as they act as hubs and spread the infection among both core and non-core individuals. Similarly, the effectiveness of contact tracing, primarily regarding casual encounters, resulted to be of vital importance, as it acts mainly on core members, who indeed have a higher number of sexual partners than non-core ones.

However, these results are not to be used as proof that polygamy is the cause of the spread of chlamydia – and other STIs –, but rather that polygamy should be sustained by both behavioural and structural interventions in order to rise the awareness on sexually-transmitted infections. Indeed, even with population of core members only, if the infected individuals effectively notify at least two previous partners out of three, the infection can be easily eradicated within just a few years. This number can be even lowered to one out of four if individuals undergo spontaneous screenings once per year and use barrier methods during intercourse to reduce the spreading probability down to 10%, showing how there would be no need for a massive contact tracing infrastructure if adolescents were made aware of the risks of unprotected sex via sex education programs.

5.1 Future Works and Improvements

Even though it is able to accurately reproduce the endemicity of chlamydia, this model does have some main limitations, particularly regarding the behavioural aspects of individuals, which are somehow difficult to reproduce as they involve various factors such as personal experiences and opinions, social environment and psychological status. For instance, as already said in subsection 3.4, churning phenomena were not considered in the model for simplicity reasons. The same holds for other phenomena such as cheating and non-exclusive relationships, even though they are reported to appear for about 30% of teenagers [23]. In addition to this, behavioural factors can influence the choice of undergoing spontaneous screenings. Institutions and governments recommend people to get tested for STIs every time they change sexual partner or have had a non-protected intercourse, and the screening must be carried out not too early, otherwise the

infection may not be detected [28–30]. Moreover, it is highly recommended to test again three months after recovering from the infection, as in many cases there is a strong probability of reinfection. This final aspect was not modelled for simplicity, but it is evident that it brings poor effects to the simulation, as many core members are likely to get infected repeatedly by other core members during casual encounters.

Additionally, as stated multiple times, this model accounts for heterosexual relationships and encounters only. Though, extending the model with regard to this aspect could be very complex as different sex practices, each one involving certain risk levels, are typical within individuals of certain sexual orientations. Nevertheless, studying these behaviours is very important not only to understand the development of sexually-transmitted infections among these social groups, but also to provide ways to tackle the stigmas that the homosexual and bisexual communities are compelled to face when it comes to STIs.

In conclusion, a major aspect which was somehow neglected is that the distribution of sexual partners was reported not to be bimodal, as shown in Fig. 3, but rather a power-law one, with the majority of individuals having just a few partners and a minority having a lot [19, 25, 31]. Liljeros suggests that the mechanisms that could account for this behaviour are related to an increased skill in getting new partners as the number of previous partners grows, different levels of attractiveness, and the need to have many new partners to maintain self-image; however, as he explains, this means that, even though it is useful during modelling to understand different social behaviours, the concept of the "core group" considered in epidemiological studies is somewhat arbitrary as there is no well-defined threshold or boundary separating the core group from other individuals. One way to model this power-law trend would be to create the sexual partners graph over a layer of potential partners which has both small-world and scale-free properties. The Klemm-Eguíluz formulation [32, 33] allows to do that, but for this particular scenario it must be improved in order to consider individuals' gender and status and therefore guarantee a correct pair formation mechanism that will, eventually, reflect the scale-free properties even in the partners network.

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