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Concurrency of partnerships, consistency with data, and control of sexually transmitted infections

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ABSTRACT

Sexually transmitted infections (STIs) are a globally increasing public health problem. Mathematical models, carefully matched to available epidemiological and behavioural data, have an important role to play in predicting the action of control measures. Here, we explore the effect of concurrent sexual partnerships on the control of a generic STI with susceptible-infected-susceptible dynamics. Concurrency refers to being in more than one sexual partnership at the same time, and is difficult to measure accurately. We assess the impact of concurrency through the development of three nested pair-formation models: one where infection can only be transmitted via stable sexual partnerships, one where infection can also be transmitted via casual partnerships between single individuals, and one where those individuals in stable partnerships can also acquire infection from casual partnerships. For each model, we include the action of vaccination before sexual debut to inform about the ability to control. As expected, for a fixed transmission rate, concurrency increases both the endemic prevalence of infection and critical level of vaccination required to eliminate the disease significantly. However, when the transmission rate is scaled to maintain a fixed endemic prevalence across models, concurrency has a far smaller impact upon the critical level of vaccination required. Further, when we also constrain the models to have a fixed number of new partnerships over time (both long-term and casual), then increasing concurrency can slightly decrease the critical level of vaccination. These results highlight that accurate measures and models of concurrency may not always be needed for reliable forecasts when models are closely matched to prevalence data. We find that, while increases in concurrency within a population are likely to generate public-health problems, the inclusion of concurrency may be unnecessary when constructing models to determine the efficacy of the control of STIs by vaccination.

1. Introduction

Controlling the spread of sexually transmitted infections (STIs) remains an important public health challenge globally. Each year, there are an estimated 357 million new infections from four common STIs: chlamydia, gonorrhoea, trichomoniasis, and syphilis (Newman et al., 2015). Both chlamydia and gonorrhoea can lead to infertility and ectopic pregnancy (Cates et al., 1990; Ankum et al., 1996), while syphilis can be fatal if untreated (Kent and Romanelli, 2008). Further, these infections can increase the risk of transmission of another STI – the human immunodeficiency virus (HIV) (Gelmon and Piot, 1996; Cohen, 1998), which presently infects an estimated 36.7 million people globally (UNAIDS, 2017). These common STIs are usually treated with antibiotics. However, the increasing problem of antibiotic resistance (Cohen, 1992; Barry and Klausner, 2009) requires academics and public health professionals concerned with STIs to propose new and more effective control measures. As such, it has been suggested that the development of vaccines is required to abate the spread of many of the STIs where antibiotics are failing (Brunham and Rappuoli, 2013; Jerse et al., 2014; Cameron and Lukehart, 2014; Gottlieb et al., 2014). For HIV, which cannot be treated by antibiotics, incidence levels globally remain high (UNAIDS, 2017), and hence much research has focussed on developing an HIV vaccine (Burton et al., 2004; rgp120 HIV Vaccine Study Group et al., 2005), albeit with limited success (Sekaly, 2008).

For one STI, human papillomavirus (HPV), a vaccine has been successfully developed and deployed (Markowitz et al., 2007). HPV is the most common STI globally, with the majority of people being infected by the virus at some point in their lives (Koutsky, 1997). Though most will recover with no serious health consequences, in a small proportion of cases, HPV infection (especially with strains 16 and 18)

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can lead to cancer later in life: principally cervical cancer (Muñoz et al., 2003) but also oropharyngeal, vulvar, anal, penile and vaginal cancers; in addition HPV (strains 6 and 11) can cause genital warts (Ljubojevic and Skerlev, 2014). In many countries, including the UK (Jit et al., 2008) and the USA (Stokley et al., 2014), vaccination programmes targeted at young girls before the age of sexual debut have been implemented (Markowitz et al., 2012).

Due to its substantive public health impact, multiple predictive models have been developed to examine the effectiveness of vaccinating against HPV. These models range in complexity and sophistication, based on the questions they are attempting to address and the data that is available. The stochastic models developed by Kulasingam and Myers (2003), Goldie et al. (2004), and Canfell et al. (2012), while capturing individual-level behaviour in detail do not consider population-level changes in prevalence and therefore cannot capture the impact of herd immunity. In contrast, dynamic population-scale models capture this impact but require assumptions about partnership formation. For example, the model by Ribassin-Majed et al. (2013) assumed homogeneous random mixing throughout the population, while the models of Taira et al. (2004) and Barnabas et al. (2006) assumed sexual mixing patterns can be stratified between age-groups. The model by Jit et al. (2008), which provided health-economic policy advice to the UK, accounts for age, sex, risk-group and multiple strains of HPV. It has been observed previously that the differing assumptions between models for HPV control can lead to conflicting results (Van de Velde et al., 2010). However, all such models assume implicitly that individuals have serially monogamous relationships. While this is a reasonable first approximation, it is a simplification of real-world sexual networks. In the UK, where detailed data is available, it is estimated that around 20% of adults aged 16–24 years engage in a *concurrent partnership* in a year (Johnson et al., 2001), that is, temporally overlapping sexual partnerships with two or more people. Intuitively, concurrency breaks the protective nature of a partnership, allowing an STI to enter an otherwise uninfected pairing. It is thus an important question the extent to which the level of concurrent partnerships within a population impacts the success of vaccination efforts.

While concurrency is clearly an important feature of sexual transmission networks, and is epidemiologically important because it allows infection into otherwise closed partnerships, it is difficult to measure precisely. For example, the Natsal (National Survey of Sexual Attitudes and Lifestyles) questionnaires (Johnson et al., 2001) provide fine-scale details on sexual behaviour in the UK; for example capturing the number of sexual partners (and sexual behaviours) over multiple time scales. Such information allows for rich heterogeneous risk-structured models to be developed. In contrast, concurrency only features in limited number of questions; the third Natsal survey (Wellings and Johnson, 2013) only specifically asks about concurrency on three occasions: (i) a binary question about overlap between partners in last 5 years; (ii) a binary question about swinging couples; and (iii) an estimation of whether the respondents last three partners had overlapping sexual relationships. Other than these questions, concurrency is estimated from the dates of the last three sexual relationships. While this is likely to be the most detailed information on concurrency at the population scale, it is difficult to correlate this information with other risk factors and therefore difficult to robustly include concurrency in mathematical models. For these reasons, we test the sensitivity of predictive models for STI control by vaccination to the level of concurrency.

In this paper we develop three nested *pair-formation models* of STI spread. Pair-formation models, by explicitly modelling the formation and dissolution of partnerships, are particularly useful in modelling the spread of infections where the assumption of instantaneous contact is inappropriate. Such models are particularly applicable to the spread of STIs, given sexual partnerships are often long lasting. Kretzschmar and Heijne (2017) provide a useful review on this approach and previous applications to modelling STIs. We begin by developing a model with no concurrency; this is a deterministic ordinary differential equation (ODE) model, where an infection with susceptible-infected-susceptible (SIS) dynamics can only be transmitted through stable sexual partnerships. We then extend this model to include casual partnerships, where single individuals can acquire infection from other single individuals who are infected without having to enter into a stable partnership. Finally, to this model we add concurrent partnerships, where those in stable partnerships can acquire infection from both single infected individuals and infected individuals in other partnerships. For all these models we also consider the addition of a protected (vaccinated) subpopulation that is immune to infection. In agreement with HPV vaccination programmes, these individuals are assumed to have been immunised before sexual debut and are also assumed to obtain life-long protection (although the data on the duration of protection offered by the vaccine is limited (De Vincenzo et al., 2014)). We use the models developed to explore the effect of concurrency on the transmission of an STI and on the critical level of vaccination required to eliminate the infection from the population. We perform this analysis in two distinct scenarios: firstly, when the epidemiological and behavioural parameters are fixed and the level of concurrency is allowed to vary, mimicking changing patterns of sexual behaviour; and secondly, when models with and without concurrency are matched to available data, capturing the impact of model misspecification.

The effect of concurrent partnerships on the spread of STIs has been explored before: Watts and May (1992) develop a deterministic ODE model to explore the effects of concurrent partnerships on the dynamics of HIV; Kretzschmar and Morris (1996), Morris and Kretzschmar (1997) show that concurrent partnerships have a large impact upon the early growth rate of an epidemic through a stochastic simulation model; Bauch and Rand (2000) derive a moment closure approximation model of STI spread through a concurrent partnership network; Eames and Keeling (2004) compare their model of STI spread assuming serial monogamy against a model where individuals form short-term casual partnerships with others outside the relationship; and Leung et al. (2012) develop a dynamic partnership network model to explore the influence of concurrency. In particular, Xiridou et al. (2003, 2004) model concurrency in a similar approach to this paper to assess the contribution of stable and casual partnerships to the spread of HIV. While all these models highlight the implications of concurrency on transmission and endemic prevalence of infection, to our knowledge, the implications that concurrency has on the control of STIs when parameters are matched to data has not been fully explored.

The model we develop is deliberately simplified, described only by a few ODEs and ignores many levels of real-world structure. For example, the formulation of our model assumes that partnerships occur via random mixing. In reality, sexual networks are highly heterogeneous, with sexual behaviours depending upon a large number of factors such as age, sex, sexual orientation, and cultural norms (Adimora and Schoenbach, 2005; Garnett et al., 1992). Further, we do not specifically model any particular STI; rather, we model some generic STI with SIS-dynamics. We use this generic formulation to observe the effects of concurrency on transmission and control, and hence to inform future researchers whether modelling concurrent partnerships explicitly is necessary in more sophisticated models of STI control.

2. The model

2.1. A model without concurrency

We first develop a simple model of STI transmission across partnerships without concurrency; this introduces our methodology and provides simple predictions to compare with our later more realistic model. A large number of STIs follow SIS dynamics — that is, recovering from infection does not provide immunity to an individual, but rather returns them to the susceptible population. Chlamydia (Garnett and Anderson, 1996) and gonorrhoea (Hethcote and Yorke,

2014) are generally assumed to exhibit these dynamics, although not HIV due to the lack of recovery (Anderson et al., 1986). In addition, many of the models exploring the impact of vaccination against HPV also assume SIS-dynamics (Ribassin-Majed et al., 2013; Taira et al., 2004), although this may be an idealised view of the true behaviour (Beachler et al., 2015). In common with these studies, we focus on infections with SIS-dynamics throughout.

We develop a deterministic ODE-model focussing on the behavioural aspects (formation and breaking of partnerships) onto which we graft the spread of infection – we label individuals by their infectious state: S for susceptible and I for infected. Single individuals, not in a partnership and represented by S or I, are assumed to form partnerships at a rate f; while sexual partnerships, represented by $[SS]$, $[SI]$ and $[II]$ break at a rate $2b$ (as each partner breaks up the partnership at a rate b). Once in a partnership, an infected partner will transmit an infection to their susceptible partner at a rate τ. Infected individuals are assumed to recover at a rate γ, which could either represent natural recovery (as observed for HPV) or obtaining treatment. A table describing all terminology is provided in Appendix A. We set the time scale of all parameters to be yearly, though we omit the suffix yr^{-1} throughout. We also insist that $S + I + 2([SS] + [SI] + [II]) = 1$, such that the model refers to proportions of the population.

Our model makes a number of simplifying assumptions: we assume a closed population without demography (i.e. no births or deaths), the recovery of individuals back into the susceptible class is sufficient to maintain infection in the population; we assume homogeneous mixing within the population (i.e. partnerships are formed uniformly at random) ignoring the impact of gender and sexual preference (all partnerships within the population are equally likely). These assumptions are clearly unrealistic – for example the number and pattern of sexual partners is highly heterogeneous between individuals (Johnson et al., 2001; Anderson, 1988) – however, the effects of such heterogeneities is not the focus of this study, and indeed has been studied extensively elsewhere (Garnett et al., 1992; Eames and Keeling, 2002; Gupta et al., 1989). The simplifying assumptions we make are common to other studies exploring the effect of concurrency (Kretzschmar and Morris, 1996; Bauch and Rand, 2000) and allow us to highlight the likely impact of concurrency in a generic setting.

The model (Model 1) is described by the following ODEs:

Model 1:

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -2\mathrm{f}\,\mathrm{S} + \gamma I + 4b\,[\mathrm{SS}] + 2b\,[\mathrm{SI}] \tag{1.1}$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = -2\mathrm{fI} - \gamma I + 4b\,[\mathrm{II}] + 2b\,[\mathrm{SI}] \tag{1.2}$$

$$\frac{d\,[\mathrm{SS}]}{\mathrm{dt}} = \mathrm{fS}\frac{S}{S+I} - 2b\,[\mathrm{SS}] + \gamma\,[\mathrm{SI}] \tag{1.3}$$

$$\frac{d\,[\mathrm{SI}]}{\mathrm{dt}} = 2\mathrm{fS}\frac{I}{S+I} - 2b\,[\mathrm{SI}] - \tau\,[\mathrm{SI}] - \gamma\,[\mathrm{SI}] + 2\gamma\,[\mathrm{II}] \tag{1.4}$$

$$\frac{d\,[\mathrm{II}]}{\mathrm{dt}} = \mathrm{fI}\frac{I}{S+I} - 2b\,[\mathrm{II}] + \tau\,[\mathrm{SI}] - 2\gamma\,[\mathrm{II}] \tag{1.5}$$

A full justification of the model construction is given in Appendix B. We note that in this simple formulation transmission only occurs within an $[SI]$ partnership. We can consider the behavioural dynamics if we sum appropriate terms to obtain the proportion of individuals who are single or in a partnership. We set $F := S + I$, denoting the proportion of individuals free to form a partnership, and $P := 2([SS] + [SI] + [II])$, denoting the proportion of individuals currently in partnerships.

$$\frac{\mathrm{dF}}{\mathrm{dt}} = -\frac{\mathrm{dP}}{\mathrm{dt}} = -2\mathrm{f}\,\mathrm{F} + 4\mathrm{bP} \tag{1.6}$$

which has a non-trivial equilibrium at $F^* = \frac{b}{b+f}$, and $P^* = \frac{f}{b+f}$. The model developed here is similar to the deterministic model of Kretzschmar and Morris (1996), and yields the same equilibrium values for F and P. However, their model assumes a different disease dynamic – SI-dynamics as opposed to SIS-dynamics. This is primarily because their model was focussed upon the effect of concurrency on the early growth rate of an STI.

Using the equilibrium values found for F and P, we can find the fixed points of the full system, and hence the endemic prevalence of infection within the population. We denote the total prevalence as $I_{tot} := I + [SI] + 2[II]$. The fixed points of the system are given in full in Appendix B; the non-trivial equilibrium value of I_{tot}, when it exists, is given by:

$$\begin{aligned} I^*_{\mathrm{tot}} &= \frac{2b+2f+\gamma}{2b} I^* \\ &= \frac{(2b+2f+\gamma)(2b\,\mathrm{f}\tau - (2b\,\mathrm{f}\gamma + 3b\gamma^2 + 2b^2\gamma + b\gamma\tau + 2f\gamma^2 + \gamma^3))}{4b\,\mathrm{f}\tau(b+f)}. \end{aligned} \tag{1.7}$$

Hence we obtain conditions for the existence of the non-trivial equilibrium, which is stable, when $I^* > 0$:

$$2b\,\mathrm{f}\tau > 2b\,\mathrm{f}\gamma + 3b\gamma^2 + 2b^2\gamma + b\gamma\tau + 2f\gamma^2 + \gamma^3 \tag{1.8}$$

Further, in the case where transmission is rapid (instantaneous) within a partnership, such that $[SI]$ partnerships do not exist, the expression for the endemic prevalence simplifies to:

$$\lim_{\tau\to\infty} I^*_{\mathrm{tot}} = \frac{(2b+2f+\gamma)(2f-\gamma)}{4f(b+f)} \tag{1.9}$$

In this limit it is clear that, the formation of new partnerships must be sufficiently rapid compared to the recovery from infection to allow persistence; in particular $\gamma < 2f$ to maintain the infection which acts as a lower bound for the persistence of the full model (Eq. (1.1)). Fig. 1 highlights the effects of the main parameters (γ, τ, f and b) on the endemic prevalence. As expected I^*_{tot} is a monotonic increasing function of the infectious period, the within partnership transmission rate and the rate at which single individuals form partnerships. However, the effects of breaking partnerships is more complex with infection maximised at an intermediate value of b; this is because persistence of infection requires a turnover of partnerships in order to infect new individuals, but if this is too rapid there is insufficient chance of transmission within the partnership and most individuals spend the majority of their time single.

2.2. Including casual partnerships

Model 1 describes a situation where individuals must enter into a stable partnership before they engage in sexual activity that could lead to disease transmission. However, for real-world populations, especially those at greater risk of contracting STIs, some sexual partnerships will be over a much shorter time-period – where the pair engage in a single instance of sexual activity, but do not form a stable partnership. We refer to such partnerships as *casual partnerships* and can include them through small additions to Model 1. Let κ denote the rate that single individuals have a casual partnership with another single individual, and let p denote the probability of transmission by a casual partnership. The equations for individuals in partnerships remains unchanged from Model 1, whereas the equations for single individuals are modified to:

Model 2:

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -2\mathrm{fS} + \gamma I + 4b\,[\mathrm{SS}] + 2b\,[\mathrm{SI}] - \kappa\mathrm{p}\,\mathrm{S}\frac{I}{F} \tag{2.1}$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = -2\mathrm{fI} - \gamma I + 4b\,[\mathrm{II}] + 2b\,[\mathrm{SI}] + \kappa\mathrm{p}\,\mathrm{S}\frac{I}{F} \tag{2.2}$$

Although in this formulation it is only the product κp that influences the dynamics, it is useful to have a value for the probability of transmission across a casual partnership p. From Model 1 it is clear that the probability of transmission across the duration of a stable partnership is given by $\hat{p} = \frac{\tau}{2b+\gamma+\tau}$, and we assume that this should reasonably place an upper bound on the casual transmission probability p. The precise

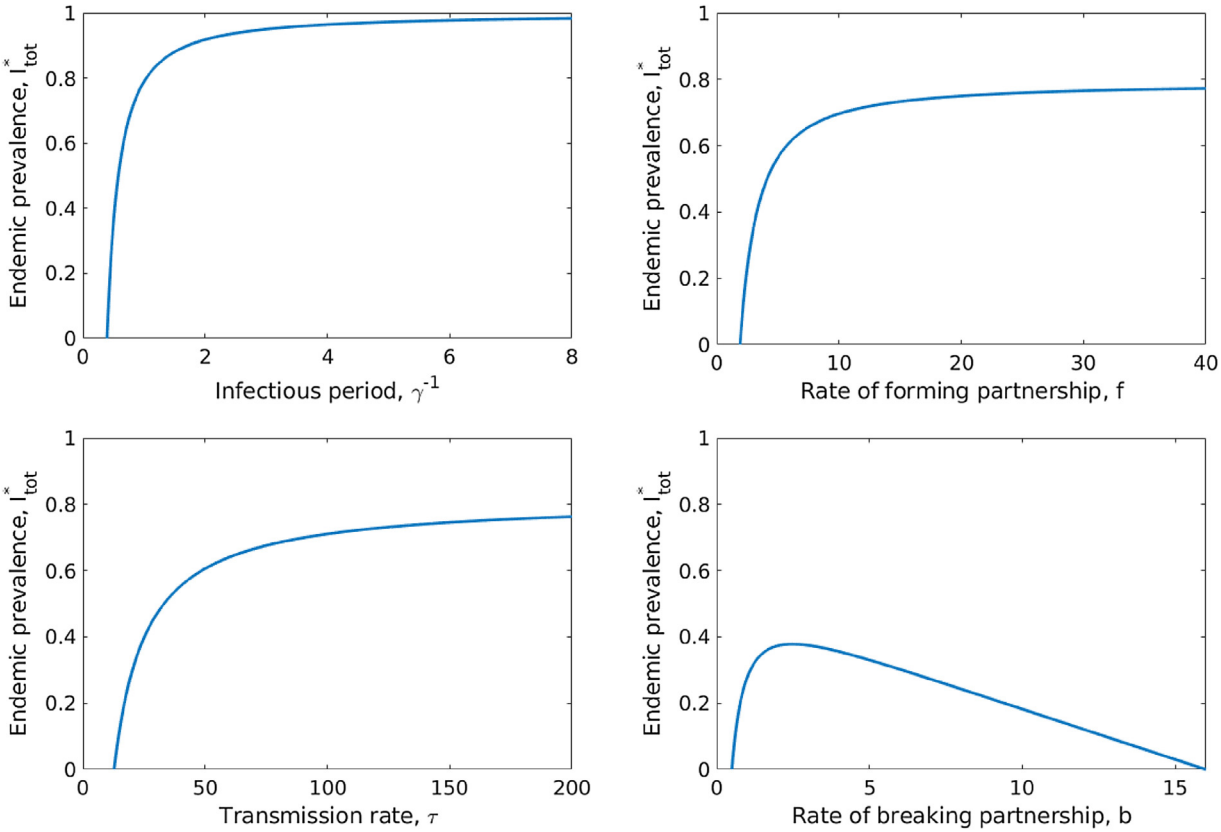

Fig. 1. The effect of varying parameters on endemic prevalence. We plot the effects of varying γ, τ, f, and b against I^*_{tot} respectively. Default parameter values are $\gamma = 2, \tau = 22.50, f = 3, b = 1.5$, while the key parameter is varied. As we increase the infectious period γ^{-1} the total level of infection asymptotes to one, whereas for τ and f the asymptote is lower. For b we find that I^*_{tot} is maximised at intermediate values.

relationship between p and $\hat{p}$ is complex and will depend on many factors including the number and type of sex acts involved. In addition, it has been observed that frequently an STI is transmitted early on in a partnership or not at all (Peterman et al., 1988; Kretzschmar and Dietz, 1998), suggesting that p should be close to $\hat{p}$. In the calculations that follow we assume that $p = \frac{1}{2}\hat{p}$, while acknowledging that this merely forms a scaling for the rate of casual partnerships κ.

Again we can determine the non-trivial endemic equilibrium of this system (given in full in Appendix C); the prevalence of infection, I_{tot}, is given by:

$$I^*_{\text{tot}} = \frac{f\tau(2b + 2f + \gamma) + \kappa p(2b^2 + 2b\,\mathrm{f} + 3b\gamma + b\tau + 2f\gamma + f\tau + \gamma^2)}{2b\,\mathrm{f}\tau + \kappa p(2b^2 + 3b\gamma + b\tau + \gamma^2)} I^* \tag{2.3}$$

where

$$I^* = \frac{b(2b\,\mathrm{f}\tau + \kappa p(2b^2 + \gamma^2 + 3b\gamma + b\tau) - (3b\gamma^2 + 2b^2\gamma + 2\gamma^2 f + \gamma^3 + 2b\,\mathrm{f}\gamma + b\gamma\tau))}{(b + f)(2b\,\mathrm{f}\tau + \kappa p(2b^2 + \gamma^2 + 3b\gamma + b\tau))} \tag{2.4}$$

Although not obvious from these equations, it is clear from the model formulation that the addition of these casual partnerships increases the prevalence of infection. The results of Model 1 are all regained by setting $\kappa = 0$.

2.3. Including concurrency

The models developed above (Models 1 and 2) describe populations where individuals are serially monogamous, and do not have overlapping partners: either they form a stable partnership, in which infection can be transmitted between partners, or they have a casual partnership – a one-time sexual partnership with another single individual. Here we develop two variations of the model that incorporate concurrent sexual partnerships – where an individual in a stable partnership can be involved in casual partnerships, with both single individuals and individuals in other stable partnerships. As such this breaks the protection of a partnership and can lead to greater transmission of infection. This approach is similar to that developed by Eames and Keeling (2004).

We now extend the model to allow both single individuals and those in stable partnerships to partake in casual sexual activity. We retain the parameter κ to be the rate at which any single individual takes part in a casual partnership, and include a new parameter K for the rate at which those in a stable partnership partake in an additional casual partnership. This leads to the following model:

Model 3:

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -2\mathrm{fS} + \gamma I + 4b[\mathrm{SS}] + 2b[\mathrm{SI}] - \kappa\mathrm{p}\,\mathrm{S}\hat{I} \tag{3.1}$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = -2\mathrm{fI} - \gamma I + 4b[\mathrm{II}] + 2b[\mathrm{SI}] + \kappa\mathrm{p}\,\mathrm{S}\hat{I} \tag{3.2}$$

$$\frac{d[\mathrm{SS}]}{\mathrm{dt}} = \mathrm{fS}\frac{S}{F} - 2b[\mathrm{SS}] + \gamma[\mathrm{SI}] - 2\mathrm{K}\,\mathrm{p}[\mathrm{SS}]\hat{I} \tag{3.3}$$

$$\frac{d[\mathrm{SI}]}{\mathrm{dt}} = 2\mathrm{fS}\frac{I}{F} - 2b[\mathrm{SI}] - \tau[\mathrm{SI}] - \gamma[\mathrm{SI}] + 2\gamma[\mathrm{II}] + 2\mathrm{K}\,\mathrm{p}[\mathrm{SS}]\hat{I} - \mathrm{K}\,\mathrm{p}[\mathrm{SI}]\hat{I} \tag{3.4}$$

$$\frac{d[\mathrm{II}]}{\mathrm{dt}} = \mathrm{fI}\frac{I}{F} - 2b[\mathrm{II}] + \tau[\mathrm{SI}] + -2\gamma[\mathrm{II}] + \mathrm{K}\,\mathrm{p}[\mathrm{SI}]\hat{I} \tag{3.5}$$

where $\hat{I}$ refers to the level of infection for individuals engaging in such casual relationship:

$$\hat{I} = \frac{\kappa I + K(2[\mathrm{II}] + [\mathrm{SI}])}{\kappa F + \mathrm{K\,P}}. \tag{3.6}$$

We define two variations of this model. In Model 3.1, we make the simplifying assumption that all individuals engage in casual relationships at an equal rate $K = \kappa$, which implies that $\hat{I} = I_{\mathrm{tot}}$. In Model 3.2, we let K and κ take different values, but in all figures we set $\kappa = 2K$ capturing the intuition that singles should be more likely to partake in casual sexual activity. We note that we can regain Model 2 by setting $K = 0$.

2.4. Including vaccination

Now, we extend our model to include a vaccinated and hence immunised class. We make the simplifying assumptions that these individuals are immunised before they enter the sexually active population and that the immunity is long-lived; hence individuals in this V-class play no active role in the epidemiological dynamics, but may limit the population spread on infection. Again, these assumptions are based on the natural history of HPV, where young girls (aged 12–13 years in the UK) are vaccinated. In Appendix E, we consider a model including waning immunity.

We let V denote the vaccinated individuals not in a partnership and $[VX]$ denote a stable partnership between a vaccinated individual and someone in state-X. Further, we let $S_P = [SI] + [SV] + 2[SS]$, $I_P = [SI] + [IV] + 2[II]$, and $V_P = [SV] + [IV] + 2[VV]$ – the susceptible, infected, and vaccinated individuals currently in a partnership. We amend Model 3 to include vaccination as follows:

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -2\mathrm{fS} + \gamma I + 2\mathrm{bS}_P - \kappa\mathrm{p\,S}\hat{I} \tag{4.1}$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = -2\mathrm{fI} - \gamma I + 2\mathrm{bI}_P + \kappa\mathrm{p\,S}\hat{I} \tag{4.2}$$

$$\frac{\mathrm{dV}}{\mathrm{dt}} = -2\mathrm{fV} + 2\mathrm{bV}_P \tag{4.3}$$

$$\frac{d[\mathrm{SS}]}{\mathrm{dt}} = \mathrm{fS}\frac{S}{F} - 2b[\mathrm{SS}] + \gamma[\mathrm{SI}] - 2\mathrm{K\,p}[\mathrm{SS}]\hat{I} \tag{4.4}$$

$$\frac{d[\mathrm{SI}]}{\mathrm{dt}} = 2\mathrm{fS}\frac{I}{F} - 2b[\mathrm{SI}] - \tau[\mathrm{SI}] - \gamma[\mathrm{SI}] + 2\gamma[\mathrm{II}] + \mathrm{K\,p}(2[\mathrm{SS}] - [\mathrm{SI}])\hat{I} \tag{4.5}$$

$$\frac{d[\mathrm{II}]}{\mathrm{dt}} = \mathrm{fI}\frac{I}{F} - 2b[\mathrm{II}] + \tau[\mathrm{SI}] - 2\gamma[\mathrm{II}] + \mathrm{K\,p}[\mathrm{SI}]\hat{I} \tag{4.6}$$

$$\frac{d[\mathrm{VV}]}{\mathrm{dt}} = \mathrm{fV}\frac{V}{F} - 2b[\mathrm{VV}] \tag{4.7}$$

$$\frac{d[\mathrm{SV}]}{\mathrm{dt}} = 2\mathrm{fS}\frac{V}{F} - 2b[\mathrm{SV}] + \gamma[\mathrm{IV}] - \mathrm{K\,p}[\mathrm{SV}]\hat{I} \tag{4.8}$$

$$\frac{d[\mathrm{IV}]}{\mathrm{dt}} = 2\mathrm{fI}\frac{V}{F} - 2b[\mathrm{IV}] - \gamma[\mathrm{IV}] + \mathrm{K\,p}[\mathrm{SV}]\hat{I} \tag{4.9}$$

where now $\hat{I} = \frac{\kappa I + KI_P}{\kappa F + \mathrm{K\,P}}$, $F = S + I + V$, and $P = 2([SS] + [SI] + [II] + [VV] + [SV] + [IV])$. We obtain the same differential equations for F and P as before. If we set $K = \kappa$, we obtain an analogue for Model 3.1 with vaccination, while analogues for Model 1 and Model 2 are recovered by setting $\kappa = K = 0$ or $K = 0$ respectively. With no vaccination, the infection remains endemic; when a large enough proportion of the population is vaccinated, the infection cannot persist - we refer to the smallest such proportion as the critical level of vaccination, denoted α_C. We explain how α_C is determined in Appendix C.

3. Results

3.1. Parameter inference

Our aim has been to develop a generic model of STI transmission and control by immunisation, rather than to model the specific details of any single infection. However, despite this generic approach, it is still important that we use parameters that reflect the general behavioural dynamics of human populations and the general epidemiology that is comparable with STIs. We do this by utilising data from surveys of sexual behaviour and estimates of HPV prevalence in England. We acknowledge that our simplified model cannot capture the complex heterogeneities of the true sexual network; for example, the rates of partnership, break-ups, and concurrent partnerships are not fixed, but rather are culturally situated social conventions (Adimora and Schoenbach, 2005), which change over time (Haavio-Mannila, 2001). However, we inform our default parameter choices from available real-world data.

The parameters determining partnership dynamics (f, b, κ and K) are estimated from data contained within the National Survey of Sexual Attitudes and Lifestyles conducted in 2000 (Natsal-2) (Johnson et al., 2001) and the US National Longitudinal Student of Adolescent Health (AddHealth) (Scott et al., 2011), focusing on the sexual behaviours of young adults (aged 16–24 years from Natsal-2, 18–25 years from AddHealth). We choose this group as they have, in general, a higher rate of sexual partnerships, are less likely to be in very long-term monogamous relationships, and report higher levels of concurrency (Johnson et al., 2001).

Men aged 16–24 years report an average of 1.45 new partnerships a year, while for women the average is 0.75. From this we assume an individual will average one new partnership a year. At equilibrium, the instantaneous rate of new partnership acquisition can be calculated: for Model 1 is given by $F^*f = \frac{\mathrm{fb}}{b+f}$, while for Model 3.2 this becomes $F^*f + F^*\kappa + (1 - F^*)K$.

From AddHealth, we find that 67% of 18–25 year olds are in an exclusive relationship. This gives us $F^* \approx 1/3 \Rightarrow f = 2b$. We use this US data source as no comparable question is asked in the Natsal-2 for the UK. For Model 1, this relationship data together with the partnership information allows us to make the approximation that $f = 3$ and $b = 1.5$, as $f = 2b$, $\frac{\mathrm{fb}}{b+f} = 1 \Rightarrow f = 3$, $b = 3/2$. We set these as our default values for f and b for all models.

From Natsal-2 we find that 20.8% of men and 15.2% of women aged 16–24 years report to be involved in at least one concurrent partnership within the previous year. From this we take our default level of concurrency to be 20%. We estimate our values of κ and K by reformulating our infection models to simply capture whether or not individual have been involved in a concurrent partnership, and assess the level of concurrency after 1 year (the full model is given in Appendix D). This gives us $K = 0.335$ for Models 3.1 and 3.2 (with $\kappa = K$ and $\kappa = 2K$ respectively). Given this definitive value for K we introduced two parameter variations for Model 2: in Model 2.1 we set $\kappa = 0.335$ as above, such that single individuals partake in the same level of casual partnerships in both Model 2.1 and Model 3.1; in Model 2.2 we set $\kappa = 0.335/F^* = 1.005$, which is three times as high, such that there are the same level of casual partnerships across the entire population in both Model 2.2 and Model 3.1. We note that keeping f and b constant, whilst adding in casual and concurrent partnerships, increases the overall rate of new partnerships: later we consider controlling for this.

We assume on average that within half a year of contracting the virus an individual will recover, i.e. we set $\gamma = 2$. We inform our default transmission rate τ by considering data on the prevalence of HPV in women aged 16–24 years in the UK prior to the introduction of the mass vaccination campaigns against the STI. Howell-Jones et al. (2012) report the prevalence of high-risk HPV substrains to be 35% for females of this age-group, which we set as our default endemic prevalence. For

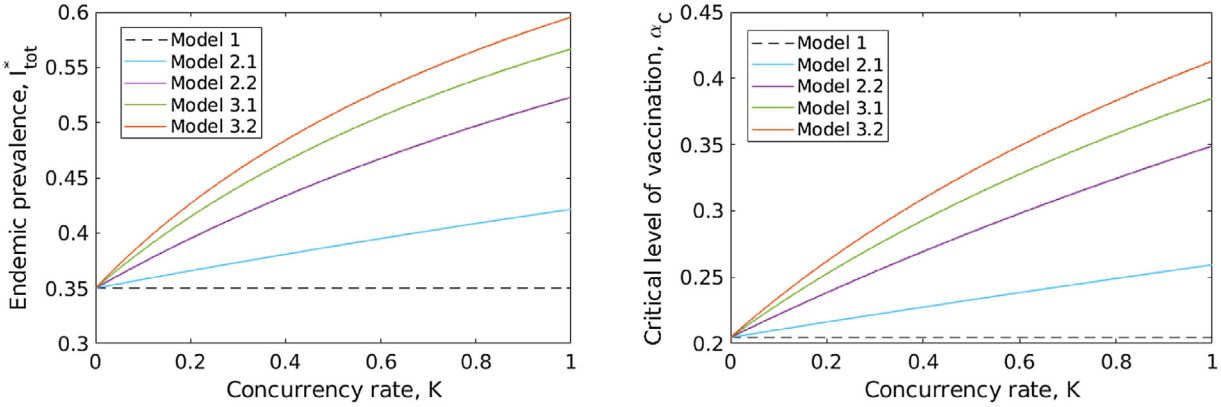

Fig. 2. Comparing endemic prevalence and critical levels of vaccination across models. In all models we maintain the same epidemiological and behavioural parameters while modifying the levels of concurrency (K). Model 1 does not allow for concurrency, so the endemic prevalence remains constant. In Model 2.1 (blue) and Model 3.1 (green), we insist that $\kappa = K$, while for Model 2.2 (purple) we set $\kappa = 3K$ and for Model 3.2 (orange) we set $\kappa = 2K$. In (A), we see the addition of casual partnerships increases endemic prevalence, and allowing individuals in stable partnerships to engage in casual sexual activity has a greater impact on endemic prevalence than allowing only individuals to engage in casual partnerships, even when the total rate of such partnerships remains equal (c.f. Model 2.2 and Model 3.1). In (B) we consider this translates into the critical level of vaccination α_C required to eradicate infection. ($f = 3$, $b = 1.5$, $\gamma = 2$, $\tau = 22.50$, $\Rightarrow p = 0.45$.) (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Models 1 and 2 we can derive a value of τ satisfying $I^*_{tot} = 0.35$ analytically - for Models 3.1 and 3.2 we obtain the appropriate value of τ via the bracket-and-bisection method.

3.2. Comparing models with fixed behavioural and epidemiological parameters

First, we compare models when behavioural and epidemiological parameters are fixed, and allow the rate of casual partnerships to vary. For models that include casual partnerships (all but Model 1) we find an increasing non-linear relationship between the rate of casual partnerships and the total prevalence of infection in the population; unsurprisingly increasing this rate also leads to increasing prevalence. Allowing those in stable partnerships to partake in casual partnerships, hence introducing concurrency to the population, has the greatest impact upon the prevalence of infection as it breaks the protection afforded by uninfected partnerships; we observe that, other things being equal, the introduction of concurrency increases endemic prevalence (c.f. Model 2.2 and Model 3.1, where the total level of casual partnerships is equal between models) (Fig. 2).

Accordingly, the critical level of vaccination, α_C, required to eliminate the disease from the population too has an increasing non-linear relationship between the rate of casual partnerships. With fixed parameters, the addition of concurrency can have a large impact upon α_C: in the absence of casual partnerships (Model 1) only 20.46% of the population need to be protected by the vaccine to eliminate the disease, while at $K = 1$ α_C is as high as 41.31% (Model 3.2).

3.3. Comparing models for a fixed endemic prevalence

In practice, we rarely have estimates of the transmission rate τ *a priori* which can be fed into our model. Rather, we generally need to estimate our value of τ to match the observed level of infection within the population. We can compare the models, and hence different levels of concurrency, by altering τ and fixing I^*_{tot} (Fig. 3). As expected, higher prevalences require higher levels of transmission, and this is non-linear due to the saturating nature of the dynamics. We also observe that the introduction of casual partnerships (going from Model 1 to Model 3.2) lowers slightly the transmission rate required to satisfy a given level of infection. Thus for a prevalence of 35%, which mimics reported levels of HPV, the fitted transmission rate drops from $\tau = 22.50$ to $\tau = 17.03$.

We can now use these fitted values of τ to determine for each model α_C, the critical level of vaccination required to eliminate infection. We find that when matching to the same endemic prevalence, the impact of model formulation is limited. We still find a ranked order of models (Model 1, Model 2.1, Model 2.2, Model 3.1, Model 3.2), with Model 3.2 needing a higher proportion of the population to be immunised in order to eliminate infection, but the differences between the models is minimal. At a prevalence of 35%, the critical proportions of the population that need to be protected by the vaccine range from 20.46% to 22.16%.

3.4. Controlling for the rate of new partnerships

As a further step to ensure agreement between models and data, we can aim to match both behavioural and demographic data. We therefore now insist that all models have both the same endemic prevalence of infection (I^*_{tot}) and the same rate of new partnerships (both long-term and casual) with the population (which we term, ρ). In Fig. 3, as we move from Model 1 to Model 3.2, the introduction of more casual partnerships inevitably leads to an increase in the expected number of sexual partners of each individual.

For Model 3.2 (which is the most general of the models with all other models nested within), we find that the rate of new partnerships, ρ, is:

$$\rho = F^*f + F^*\kappa + (1 - F^*)K \quad \Rightarrow \quad f = \frac{\rho - K}{F^*} - (\kappa - K) \tag{5}$$

Hence, we can determine the parameter f such that the expected number of new sexual partners per year agrees with reported values (here assumed to be approximately one per year). As previously described, to obtain $F^* = 1/3$ we require $f = 2b$. We then solve for the appropriate mix of K and κ (as prescribed by the model) and the parameter f, to obtain both 20% of individuals having a concurrent partnership within a year (Appendix D) and to achieve a given partnership rate from Eq. (5).

When we additionally control for the rate of new partnerships (ρ), a larger transmission rate is required to satisfy a given endemic prevalence for all versions of Models 2 and 3 (Fig. 4A). This is due to the corresponding lower rates of f and b for models with more casual partnerships, as these additional casual partnerships also contribute to ρ. In such models, individuals in [*SS*] partnerships are offered a longer duration of relative isolation (they can only be infected through casual partnerships) due to the lower rate of stable partnership break-up. Similarly, individuals in [*II*] partnerships are retained in the stable partnership for longer and hence are less infectious to the population.

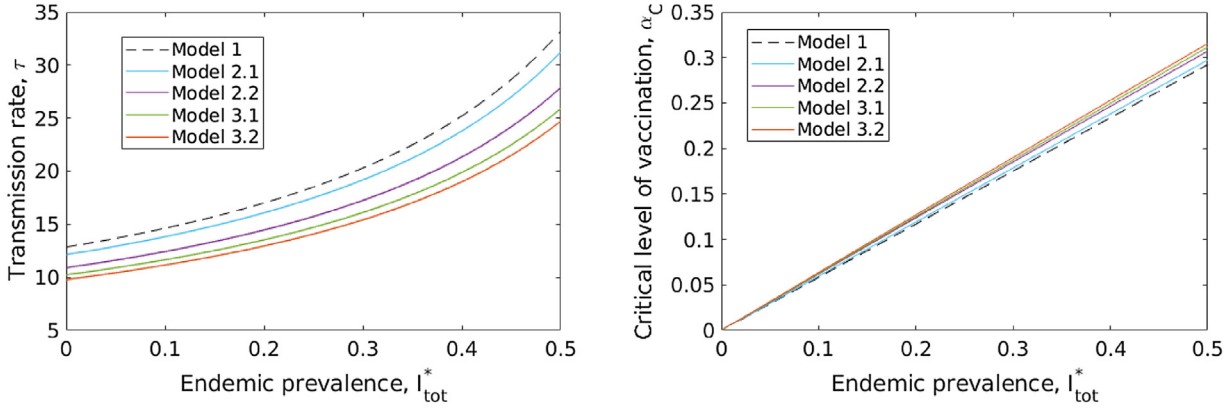

Fig. 3. Impact of constraining all models to have the same endemic prevalence. All models have their transmission rate τ set such that they reproduce the same prevalence of infection at equilibrium. In (A) we see that the models with less concurrency require a higher transmission rate to achieve the same endemic prevalence. In (B) we consider how this translates into the critical level of vaccination α_C required to eradicate infection. (For all models we set $f = 3$, $b = 3/2$ and $\gamma = 2$; Model 2.1 $\kappa = 0.335$, Model 2.2 $\kappa = 1.005$, Model 3.1 $\kappa = K = 0.335$; and Model 3.2 $\kappa = 2K = 0.670$.)

This effect is sufficiently strong to change the ordering of transmission rates compared to Fig. 3A; Model 1 now requires the lowest transmission rate, while the transmission rates needed for Model 2.2 and Model 3.2 are largest and comparable.

As we control for the rate of new partnerships, adding concurrency only has negligible impact upon the critical level of vaccination α_C; moreover for higher endemic prevalences, Model 1 requires the largest α_C while model 2.2 requires the lowest. If we instead fix the prevalence $I^*_{tot} = 35\%$, and vary the rate of new partnerships ρ, the differences between the five models is more clear, although the absolute differences in the required critical vaccination level are minimal. Larger partnership rates require slightly larger vaccination levels, but given that we are maintaining a constant infection prevalence even doubling the partnership rate invokes a relatively small change in α_C. We consistently find that Model 1 (without any casual partnerships) requires the greatest level of vaccination, while either Model 2.2 or 3.2 requires the least depending on parameter values.

4. Discussion

Models for the spread of STIs play a critical role in public-health planning, allowing policy-makers to assess the impact of control

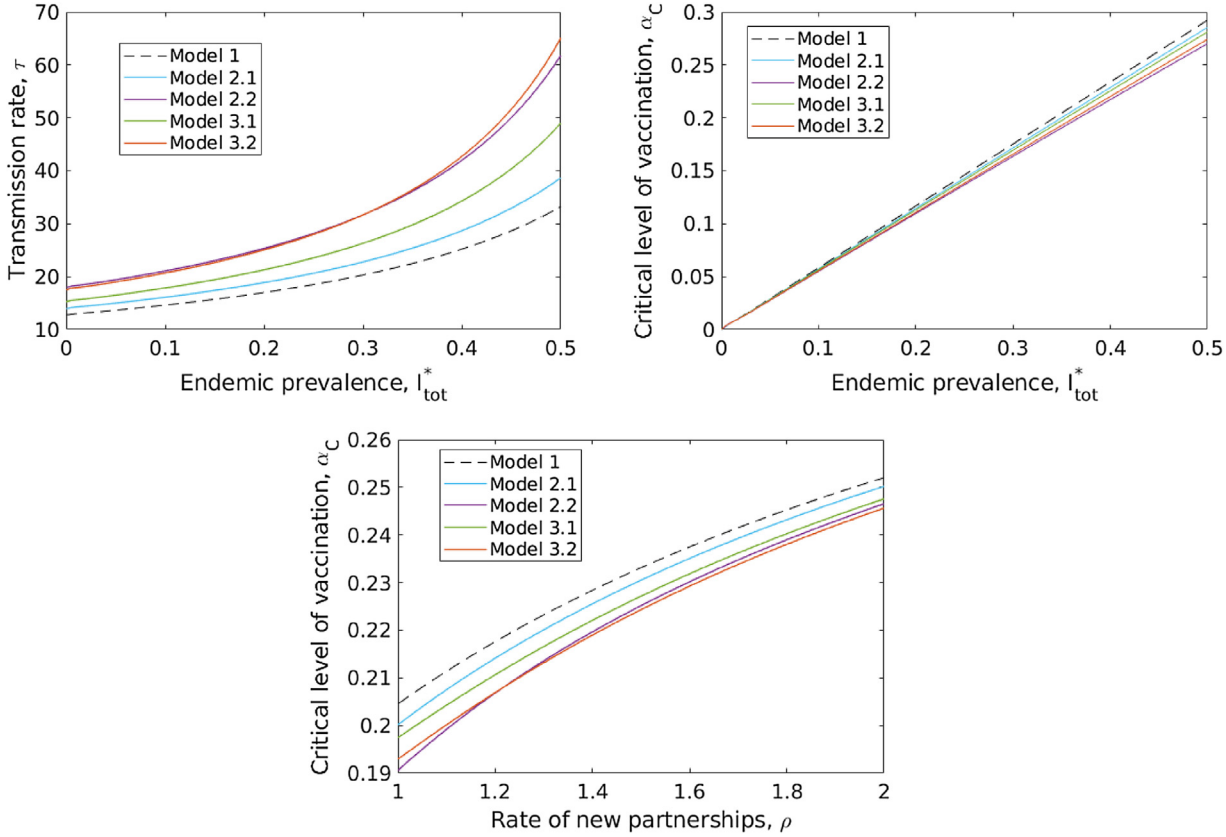

Fig. 4. Controlling τ for a fixed endemic prevalence and f to fix the rate of new partnerships. (A) and (B) For each model we choose values of f, b, K and κ such that $\rho = 1$, $F^* = 1/3$, and where appropriate 20% of the population will have a concurrent partnership in a year. We then find τ that satisfies the endemic prevalence, which is varied. (C) A similar approach is taken but I^*_{tot} is fixed at 35%, and the total rate of new partnerships per year ρ is varied.

measures. Of these, the control of HIV by increased behavioural awareness (Coates et al., 2008) or through anti-retroviral drugs (Granich et al., 2009), and HPV by vaccination, are amongst the most studied. One factor that arises from many of these models is that increases in concurrency (extra sexual partnerships in addition to stable sexual relationships), while all other factors remain constant, lead to greater prevalence of infection and more difficulty in controlling the infection. This is intuitive as an increase in concurrency both increases the number of sexual partnerships in the population and breaks the protection otherwise afforded to stable partnerships. This might suggest that models which include concurrency, compared to those that do not, will also predict greater prevalence and the need for greater control. However, this neglects the fact that these models should first be matched to available data, before the implications of control are assessed. Here we have developed a range of models that include various amounts of casual partnerships and consider the behaviour as we match the model to both epidemiological and behavioural data.

If we assume a fixed transmission rate, then our models echo previous findings that concurrent partnerships have a significant impact on the effectiveness and appropriateness of interventions; the addition of concurrency to such models increases markedly the endemic prevalence of infection, and hence the critical level of vaccination required to eliminate the infection. This captures what we would expect to happen if the level of concurrency (and the number of short casual relationships) increases in a population while all other aspects remains unperturbed.

To assess the importance of robustly measuring and capturing concurrency within a predictive model, we take an alternative approach. This is of public-health importance given the potential reluctance of individuals to disclose this behaviour and the difficulty of assessing how concurrency may correlate with other risk factors. To address this, we compared models with and without concurrency that are matched to the same endemic prevalence of infection. When we adjust the transmission rate τ to obtain the same endemic prevalence for each model (as would occur if we were matching models to observations), the inclusion of concurrent partnerships has a much more limited impact upon vaccination. Further, when we also control for the total rate of new partnerships (including stable and casual partnerships), the difference between estimates of the critical level of vaccination is further reduced and the rank-order of the models is reversed: the model without concurrency requires the greatest level of vaccination to control the infection. Given that models without concurrent partnerships are in general simpler – in our examples (Models 1 and 2) are analytically tractable – our predictions would question the need for the additional complexity of modelling concurrency to achieve accurate predictions for public-health policy.

This very weak dependence on the level of concurrency can be intuitively explained as follows. In the simple (one-dimensional) SIS model, that does not explicitly include partnerships, the critical vaccination level is equal to the endemic prevalence of infection. This precise relationship is only broken in models that capture partnerships due to the correlations that quickly develop between the status of individuals in partnerships due to transmission within the partnership. This simply introduces a linear scaling between prevalence and critical vaccination levels. The action of concurrent partnerships is effectively random across the population, so does not impact on the relationship between prevalence and critical vaccination levels.

Our models, and the data that underpin them, take a highly simplified form which is necessary to elucidate the behaviour. In our models we do not differentiate between genders – individuals are equally likely to form a partnership with any other. This simplification not only ignores the obvious point that most partnerships are heterosexual, but also ignores parameter differences between sexes. In the UK, reported rates of new partnership and rates of concurrency are higher amongst men (Johnson et al., 2001) (although this may represent reporting bias), while in cultures where polygyny is the prevailing social norm, this difference is even more pronounced (Reniers and Tfaily, 2012). Further, for a large number of STIs there can be asymmetric transmission between sexes (Hethcote and Yorke, 2014; Nicolosi et al., 1994; Nyitray et al., 2013). Such factors are important to consider in an applied context, given that vaccination campaigns such as those against HPV are generally targeted to young girls.

Our model describes a situation where there is a simple asymmetry between the types of partnerships. Individuals are either in long-term stable partnerships, or they are involved in casual one-time partnerships akin to a single sexual encounter with another individual. Hence for our model when there are concurrent partnerships they are always of the form one stable partnership and one casual partnership. Our models do not describe a situation where an individual can be engaged in multiple stable sexual partnerships; nor do they capture the spectrum of partnership durations. When considering the appropriateness of this model it is therefore important to consider the appropriateness of this assumption. This simple asymmetry may not hold across all cultures – in some sub-Saharan countries (a focal point of the global HIV-epidemic) the reported proportion of individuals engaged in multiple long-term partnerships is significant (reported to be as high as 55% in Lesotho, Southern Africa) (Carael, 1995). Thus our models may be a closer approximation to the behaviour in UK and western Europe, although we again expect a spectrum of behaviours. Other models of concurrency that allow for individuals in multiple stable partnerships have been developed: of note for their analytic tractability are the models created by Leung et al. (2012) and Miller et al. (2012). Our research could naturally be extended to such models, but carefully matching these models to data is paramount. When including multiple long-term partnerships, it may be important to consider the effect of *coital dilution* (as one engages in more sexual partnerships, they tend to have less frequent sexual contact with any one partner) on transmission parameters (Gaydosh et al., 2013).

Potentially the most substantial omission in our models is the lack of heterogeneity. Patterns of sexual partnerships are generally characterised by extreme levels of heterogeneity, such that some individuals have few lifetime partners while others have many (Anderson et al., 1986); in addition it is likely that the rate of new partners is correlated with other factors such as the propensity to be involved in concurrent partnerships, the likelihood of being involved in higher-risk sexual activities, or lower rates of vaccine uptake. It is well understood that heterogeneities in the rate of new sexual partnerships play an important role in STI transmission and control (May and Anderson, 1987). However, there is limited data, or theoretical studies, on the impact of the interaction between this heterogeneity and other elements of risk. Therefore, while we believe our findings are generic, the inclusion of heterogeneity across multiple risk factors is an important next step especially if greater realism is required; understanding how this risk heterogeneity and heterogeneity in concurrency interact is a key area of future work.

In summary, our simplified model highlights that the impact of casual partnerships (and hence concurrency) on the control of STIs by vaccination is limited, once the models are matched to infection prevalence and the rate of new partnerships. This strongly suggests that we should question the need of including the complexity of concurrent partnerships in more complex models. Obviously, complex models that include a multitude of heterogeneities are vital when addressing public health problems that require accurate answers, but we should continue to question the role of complexity in these models.

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Appendix A. Table of terminology

Term	Meaning
f	Rate at which individuals form a stable partnership
b	Rate at which individuals break up a stable partnership
τ	Transmission rate across a stable partnership
γ	Recovery rate
κ	Rate at which single individuals form casual partnerships
K	Rate at which individuals in partnerships form casual partnerships
p	Probability of transmission via a casual partnership
S	Susceptible individuals not in a partnership
I	Infected individuals not in a partnership
V	Vaccinated individuals not in a partnership
F	Totality of individuals not in a partnership
$[SS]$	Susceptible–susceptible partnerships
$[II]$	Infected–infected partnerships
$[VV]$	Vaccinated–vaccinated partnerships
$[SI]$	Susceptible–infected partnerships
$[SV]$	Susceptible–vaccinated partnerships
$[IV]$	Infected–vaccinated partnerships
P	Totality of partnerships
S_P	Susceptible individuals currently in a partnership
I_P	Infected individuals currently in a partnership
V_P	Vaccinated individuals currently in a partnership
I_{tot}	Totality of infected individuals
α	Proportion of population vaccinated
α_C	Critical level of vaccination required to eliminate the infection from the population
ρ	Rate of new partnerships (including casual partnerships)
Y	Individuals not in a partnership who have had a concurrent partnership
N	Individuals not in a partnerships who have not had a concurrent partnership
$[YY]$	Had concurrent partner – had concurrent partner partnerships
$[NN]$	No concurrent partner – no concurrent partner partnerships
$[YN]$	Had concurrent partner – no concurrent partner partnerships
r	Rate of vaccination
r_C	Critical rate of vaccination required to eliminate the infection from the population
ω	Rate of waning immunity

Appendix B. Justification of Model 1 formulation

Let f be the rate at which individuals form stable partnerships, b be the rate at which individuals break up partnerships, τ be the transmission rate across a stable partnership, and γ be the recovery rate. An individual leaves the class of susceptible individuals not in a partnership (S) if they form a partnership (which they do so at a rate f), or if any other individual not in a partnership forms a partnership with a susceptible individual (also at a rate f). Individuals enter the classes from the class of infected individuals at a rate γ. Individuals enter the class from the $[SI]$ class at a rate of $2b$, as the susceptible individual will enter the S class if they break up the partnership (which they do so at a rate b) or if their infected partner breaks up the partnership (also at a rate b). Individuals enter the class from the $[SS]$ class at a rate of $4b$, as either partner can break up the partnership, and both return to the susceptible class. Hence $\frac{dS}{dt}$ is given by

$$\begin{aligned}\frac{dS}{dt} &= -fS - fF\frac{S}{F} + \gamma I + 2b[SI] + 4b[SS] \\ &= -2fS + \gamma I + 2b[SI] + 4b[SS] \end{aligned} \tag{B.1}$$

Similar considerations give us the rest of the ODEs for Model 1, which are given in full in Section 2.1.

Appendix C. Finding the critical level of vaccination

To determine the critical level of vaccination, we consider the stability of the disease free equilibrium. At this equilibrium, there is random mixing between susceptible and vaccinated individuals, so if we vaccinate α of the population, the fixed points are given by $S^* = (1-\alpha)F^*$, $V^* = \alpha F^*$, $[SS]^* = (1-\alpha)^2P^*/2$, $[SV]^* = \alpha(1-\alpha)P^*$, $[VV]^* = \alpha^2P^*/2$, $I^* = [SI]^* = [II]^* = [IV]^* = 0$, where $F^* = \frac{b}{b+f}$, $P^* = \frac{f}{b+f}$. We then consider the Jacobian of the system evaluated at this equilibrium. The stability of the equilibrium is ensured given the real parts of all eigenvalues of the Jacobian are less than zero (Keeling and Rohani, 2011), thus varying α we numerically determine when the largest real part of the Jacobian's eigenvalues is 0 to find the critical level of vaccination.

Note, we do not have to consider the Jacobian of the full system, only of the states including an infected individual. If we let $f_I = \frac{dI}{dt}$, and so on, the Jacobian is given by:

$$J = \begin{pmatrix} \frac{\partial f_I}{\partial I} & \frac{\partial f_I}{\partial [\mathrm{SI}]} & \frac{\partial f_I}{\partial [\mathrm{II}]} & \frac{\partial f_I}{\partial [\mathrm{IV}]} \\ \frac{\partial f_{[\mathrm{SI}]}}{\partial I} & \frac{\partial f_{[\mathrm{SI}]}}{\partial [\mathrm{SI}]} & \frac{\partial f_{[\mathrm{SI}]}}{\partial [\mathrm{II}]} & \frac{\partial f_{[\mathrm{SI}]}}{\partial [\mathrm{IV}]} \\ \frac{\partial f_{[\mathrm{II}]}}{\partial I} & \frac{\partial f_{[\mathrm{II}]}}{\partial [\mathrm{SI}]} & \frac{\partial f_{[\mathrm{II}]}}{\partial [\mathrm{II}]} & \frac{\partial f_{[\mathrm{II}]}}{\partial [\mathrm{IV}]} \\ \frac{\partial f_{[\mathrm{IV}]}}{\partial I} & \frac{\partial f_{[\mathrm{IV}]}}{\partial [\mathrm{SI}]} & \frac{\partial f_{[\mathrm{IV}]}}{\partial [\mathrm{II}]} & \frac{\partial f_{[\mathrm{IV}]}}{\partial [\mathrm{IV}]} \end{pmatrix}$$

Evaluated at the disease-free equilibrium, and letting $c = \frac{p}{\kappa F + \mathrm{K\,P}}$, we obtain:

$$J = \begin{pmatrix} \kappa^2 c S^* - 2f - \gamma & \kappa \mathrm{K\,c} S^* + 2b & 2(\kappa \mathrm{K\,c} S^* + 2b) & \kappa \mathrm{K\,c} S^* + 2b \\ 2\kappa \mathrm{K\,c}[\mathrm{SS}]^* + 2f(1-\alpha) & 2K^2 c[\mathrm{SS}]^* - 2b - \tau - \gamma & 2(2K^2 c[\mathrm{SS}]^* + \gamma) & 2K^2 c[\mathrm{SS}]^* \\ 0 & \tau & -2(b+\gamma) & 0 \\ \kappa \mathrm{K\,c}[\mathrm{SV}]^* + 2f\alpha & K^2 c[\mathrm{SV}]^* & 2K^2 c[\mathrm{SV}]^* & K^2 c[\mathrm{SV}]^* - 2b - \gamma \end{pmatrix}$$

Appendix D. ODE model for estimating levels of concurrency

Let Y denote individuals not in a partnership who have had a concurrent partnership, N denote individuals not in a partnership who have not had a concurrent partnership, $[YY]$ partnerships between individuals who have both had concurrent partnerships, and so on. We rescale parameters f, b, and K so that they are over the time scale of a day – i.e. they are 1/365 of the corresponding parameters from the previous models. The model is described as follows:

$$\frac{\mathrm{dN}}{\mathrm{dt}} = -2\mathrm{fN} + 4b[\mathrm{NN}] + 2b[\mathrm{YN}] \tag{D.1}$$

$$\frac{\mathrm{dY}}{\mathrm{dt}} = -2\mathrm{fY} + 4b[\mathrm{YY}] + 2b[\mathrm{YN}] \tag{D.2}$$

$$\frac{d[\mathrm{NN}]}{\mathrm{dt}} = \mathrm{f\,N}\frac{N}{F} - 2b[\mathrm{NN}] - 2K[\mathrm{NN}] \tag{D.3}$$

$$\frac{d[\mathrm{YN}]}{\mathrm{dt}} = 2\mathrm{fY}\frac{N}{F} - 2b[\mathrm{YN}] + 2K[\mathrm{NN}] - K[\mathrm{YN}] \tag{D.4}$$

$$\frac{d[\mathrm{YY}]}{\mathrm{dt}} = \mathrm{fY}\frac{Y}{F} - 2b[\mathrm{YY}] + K[\mathrm{YN}] \tag{D.5}$$

We obtain our estimates for K by running the ODEs to equilibrium, and find the value of K that satisfies $Y + [YN] + 2[YY] = 0.2$ numerically. For Fig. 3, we set $f = 3/365\ day^{-1}$, $b = 3/730\ day^{-1}$, while for Fig. 4 we adjust values of f and b for the given K, such that $\rho = 1/365\ day^{-1}$. We then rescale our K value back to a timescale of years to use for our models in the main text.

Appendix E. Including waning immunity

In the main text, we consider the case of vaccination that confers lifelong immunity to an infection. In reality, protection against infection offered by vaccination often wanes over time. Previous HPV studies have shown that the duration of vaccine protection impacts the effectiveness of vaccination (Van de Velde et al., 2010). In this appendix we consider whether duration of vaccine protection impacts the results of the paper, i.e. whether for shorter durations of vaccine protection it still holds true that the addition concurrency has minimal impact upon the critical level of vaccination.

We now vaccinate susceptible individuals at a constant rate r, and allow the vaccine to wane at a constant rate ω. This amended model is given by:

$$\frac{\mathrm{dS}}{\mathrm{dt}} = -2\mathrm{fS} + \gamma I + 2\mathrm{bS}_P - \kappa \mathrm{p\,S}\hat{I} - \mathrm{rS} + \omega V \tag{E.1}$$

$$\frac{\mathrm{dI}}{\mathrm{dt}} = -2\mathrm{fI} - \gamma I + 2\mathrm{bI}_P + \kappa \mathrm{p\,S}\hat{I} \tag{E.2}$$

$$\frac{\mathrm{dV}}{\mathrm{dt}} = -2\mathrm{fV} + 2\mathrm{bV}_P + \mathrm{rS} - \omega V \tag{E.3}$$

$$\frac{d[\mathrm{SS}]}{\mathrm{dt}} = \mathrm{fS}\frac{S}{F} - 2b[\mathrm{SS}] + \gamma[\mathrm{SI}] - 2\mathrm{K\,p}[\mathrm{SS}]\hat{I} - 2r[\mathrm{SS}] + \omega[\mathrm{SV}] \tag{E.4}$$

$$\frac{d[\mathrm{SI}]}{\mathrm{dt}} = 2\mathrm{fS}\frac{I}{F} - 2b[\mathrm{SI}] - \tau[\mathrm{SI}] - \gamma[\mathrm{SI}] + 2\gamma[\mathrm{II}] + \mathrm{K\,p}(2[\mathrm{SS}] - [\mathrm{SI}])\hat{I} - r[\mathrm{SI}] + \omega[\mathrm{IV}] \tag{E.5}$$

$$\frac{d[\mathrm{II}]}{\mathrm{dt}} = \mathrm{fI}\frac{I}{F} - 2b[\mathrm{II}] + \tau[\mathrm{SI}] - 2\gamma[\mathrm{II}] + \mathrm{K\,p}[\mathrm{SI}]\hat{I} \tag{E.6}$$

$$\frac{d[\mathrm{VV}]}{\mathrm{dt}} = \mathrm{fV}\frac{V}{F} - 2b[\mathrm{VV}] + r[\mathrm{SV}] - 2\omega[\mathrm{VV}] \tag{E.7}$$

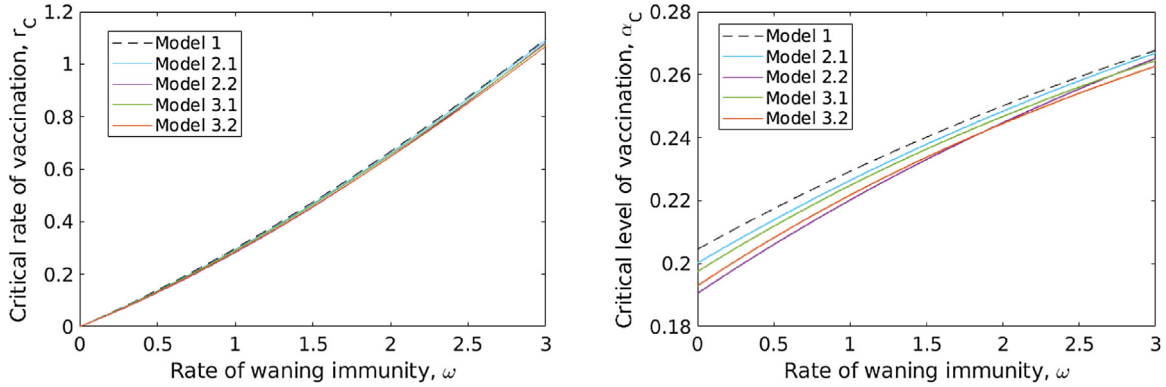

Fig. 5. Impact of including waning immunity. For each model we choose values of f, b, K and κ such that $\rho = 1$, $F^* = 1/3$, and where appropriate 20% of the population will have a concurrent partnership in a year. We set τ such that $I^*_{\text{tot}} = 0.35$ for each model, and vary the rate of waning. immunity ω. In (A) we consider the critical rate of vaccination, while in (B) we consider the critical level of vaccination, given by $\alpha_C = \frac{r_C}{r_C + \omega}$.

$$\frac{d[\mathrm{SV}]}{\mathrm{dt}} = 2\mathrm{fS}\frac{V}{F} - 2b[\mathrm{SV}] + \gamma[\mathrm{IV}] - \mathrm{K\,p}[\mathrm{SV}]\hat{I} + 2r[\mathrm{SS}] - \omega[\mathrm{SV}] - r[\mathrm{SV}] + 2\omega[\mathrm{VV}] \tag{E.8}$$

$$\frac{d[\mathrm{IV}]}{\mathrm{dt}} = 2\mathrm{fI}\frac{V}{F} - 2b[\mathrm{IV}] - \gamma[\mathrm{IV}] + \mathrm{K\,p}[\mathrm{SV}]\hat{I} + r[\mathrm{SI}] - \omega[\mathrm{IV}] \tag{E.9}$$

We then determine the value of r required to eliminate the infection by procedure outlined in Appendix C. The endemic proportion of the population vaccinated is given by $\frac{r}{r+\omega}$, and so the critical level of vaccination is given by $\alpha_C = \frac{r_C}{r_C+\omega}$ (Fig. 5).

As we increase the rate of waning ω, and hence decrease the duration of vaccine protection, the critical level of vaccination increases for all models. Importantly however, we see that for any given value of ω, the values of obtained for α_C remain within a small range between models; indeed, as we increase ω, this range decreases.

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