Model formulation

Our model is described schematically in Figure 1 of the main manuscript, but specifically it is formulated mathematically as a series of ordinary differential equations:

\[
\frac{dS_{i,j}}{dt} = (\mu P)_{i,j} \delta_{i,j} + \alpha_{j-1} S_{i,j-1} (1 - \delta_{i,j}) - \alpha_j S_{i,j} + \eta_S R_{S,i,j} + \eta_4 R_{T,i,j} + \eta_7 T_{S,i,j} - \lambda_{i,j}(t) S_{i,j} \tag{1}
\]

\[
\frac{dE_{i,j}}{dt} = \lambda_{i,j}(t) S_{i,j} + \alpha_{j-1} E_{i,j-1} (1 - \delta_{i,j}) - \alpha_j E_{i,j} - (\zeta_{j,i} + \zeta_{i,j}) E_{i,j} \tag{2}
\]

\[
\frac{dI_{A,i,j}}{dt} = \zeta_{A,i} E_{i,j} + \sigma_S I_{A,i,j} + \alpha_{j-1} I_{A,i,j-1} (1 - \delta_{i,j}) - (\alpha_j + \sigma_S + \gamma_{A,i,j} + \omega_{A,i}) I_{A,i,j} \tag{3}
\]

\[
\frac{dI_{S,i,j}}{dt} = \zeta_{S,i} E_{i,j} + \sigma_A I_{A,i,j} + \alpha_{j-1} I_{S,i,j-1} (1 - \delta_{i,j}) - (\alpha_j + \sigma_A + \gamma_{S,i,j} + \omega_{S,i}) I_{S,i,j} \tag{4}
\]

\[
\frac{dT_{A,i,j}}{dt} = \gamma_{A,i} I_{A,i,j} + \alpha_{j-1} T_{A,i,j-1} (1 - \delta_{i,j}) - (\alpha_j + \omega_{A,i}) T_{A,i,j} \tag{5}
\]

\[
\frac{dT_{S,i,j}}{dt} = \gamma_{S,i} I_{S,i,j} + \alpha_{j-1} T_{S,i,j-1} (1 - \delta_{i,j}) - (\alpha_j + \omega_{S,i}) T_{S,i,j} \tag{6}
\]

\[
\frac{dR_{A,i,j}}{dt} = \omega_A I_{A,i,j} + \alpha_{j-1} R_{A,i,j-1} (1 - \delta_{i,j}) - (\alpha_j + \eta_A) R_{A,i,j} \tag{7}
\]

\[
\frac{dR_{S,i,j}}{dt} = \omega_S I_{S,i,j} + \alpha_{j-1} R_{S,i,j-1} (1 - \delta_{i,j}) - (\alpha_j + \eta_S) R_{S,i,j} \tag{8}
\]

\[
\frac{dR_{A,i,j}^T}{dt} = \omega_A^T T_{A,i,j} + \alpha_{j-1} R_{A,i,j}^T (1 - \delta_{i,j}) - (\alpha_j + \eta_A^T) R_{A,i,j}^T \tag{9}
\]

\[
\frac{dR_{S,i,j}^T}{dt} = \omega_S^T T_{S,i,j} + \alpha_{j-1} R_{S,i,j}^T (1 - \delta_{i,j}) - (\alpha_j + \eta_S^T) R_{S,i,j}^T \tag{10}
\]

Each equation represents the rate of change in the number of people in one compartment. The compartments included in our model represent people that are susceptible to infection (S), exposed (E) (or latently infected), infected with either asymptomatic (I_A) or symptomatic (I_S) infection, undergoing treatment (T_A and T_S for asymptomatic and symptomatic infections, respectively), and people that have recovered from infection and are temporarily immune from infection (represented by R_A, R_S, R_{A,i,j}^T, or R_{S,i,j}^T depending on the progression of disease and recovery). For each of these equations, the subscript ‘i’ refers to the gender (male/female) and subscript ‘j’ refers to the age-group (i=1...7). Aging in and out of each age-
group is represented by the $\alpha_j$ parameters and initial entry into the sexually active population occurs into the first age-group of the susceptible compartment at constant rate $\mu P$; the Kronecker delta $\delta_{i,j}$ denotes that aging into infected compartments cannot occur for the first age group. The force of infection term, $\lambda_{i,j}(t)$, is described below but all other parameters are defined in Table 1 of the main manuscript.

The probability of transmission of infection per partnership is based on binomial probabilities of transmission per act [1] and determined from a combination of biological and behavioural factors (see below and Table 1 for parameter values). Although the intrinsic probability of infection per unprotected sexual act is not well known, we estimated it from available empirical studies [2] and used it to calibrate the model and calculate the average probability of infection per partnership per year. The per partnership transmission probability is age- and gender-specific, depending on the level of sexual activity (number of partnerships in a given time and the number of sexual acts per partnership in which transmission can occur) and condom usage. Risk groups were defined describing the number of new partners per year. Data from a national sexual behavior survey [3] was used to apportion the population to these groups according to age and gender, to estimate the average rates of partnership formation between males and females in each age-group, and to estimate the proportion of sexual acts in which condoms were used.

In our model, we denote the probability of transmission of Chlamydia from an infected individual to a susceptible individual during a single unprotected sexual act by $\beta$. If $\epsilon_c$ is the efficacy of condoms, referring to the proportion of acts in which transmission is prevented that could have resulted in transmission in the absence of condom use, then the transmission probability for protected acts is $(1-\epsilon_c)\beta$. We consider the average number of sex acts per partner per year $(n)$, which depends on the age-mixing of the partnership (see Table 1), and the
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proportion of sex acts in which condoms are used \((\phi)\) to calculate the probability of transmission of infection per partnership. The transmission probability per partnership is calculated as

\[
1 - (1 - \beta)^{(1 - \phi)} \left(1 - (1 - \epsilon_c) \beta\right)^{n^\phi},
\]

by using the binomial calculation [1]. If \(c_{jk}\) is the average number of new sexual partners that a person of gender ‘\(i\)’ and age-group ‘\(j\)’ will have with someone in age-group ‘\(k\)’ of the opposite gender per year, then the force of infection is given by

\[
\lambda_{j,k}(t) = \sum_k c_{jk} \left(1 - \beta \right)^{(1 - \phi)} \left(1 - (1 - \epsilon_c) \beta\right)^{n^\phi} \left(I_{A,j,k} + I_{S,j,k}\right) \frac{N_{j,k}}{N_{-j,k}} + \sum_k c_{jk} \left(1 - (1 - \rho) \beta \right)^{(1 - \phi)(1 - \zeta)} \left(1 - (1 - \epsilon_c)(1 - \rho) \beta\right)^{n^\phi(1 - \zeta)} \left(T_{A,j,k} + T_{S,j,k}\right) \frac{N_{j,k}}{N_{-j,k}}
\]

where

\[
N_{j,k} = S_{j,k} + E_{j,k} + I_{A,j,k} + I_{S,j,k} + T_{A,j,k} + T_{S,j,k} + R_{k,j,k} + R_{S,j,k} + R_{A,j,k} + R_{S,j,k}^	op + R_{S,j,k}^T.
\]

Here, the transmission probability per act decreases by a factor of \(\rho\) if the partner is currently on treatment and \(\zeta\) is the proportion of individuals on treatment that abstain from sex during the course of treatment.

**Sexual Mixing**

We must ensure that there is conservation of partnerships. That is, the total number of partnerships females of age A have with males of age B must be equivalent to the total number of partnerships males of age B have with females of age A [4, 5]. The average number of partners per person for females of age-group \(j\) with males of age-group \(k\) is \(c_{F,j} p_{F,j,k}\), where \(c_{F,j}\) is the total number of partners for females of age-group \(j\) and \(p_{F,j,k}\) is the proportion of their partnerships that are with males of age-group \(k\). Then the total number of partners females of age-group \(j\) have with males of age-group \(k\) is \(c_{F,j} p_{F,j,k} N_{F,j}(t)\), where \(N_{F,j}(t)\) is the number of females in age group \(j\). We must have

\[
c_{F,j} p_{F,j,k} N_{F,j}(t) = c_{M,k} p_{M,k,j} N_{M,k}(t),
\]

leading to:
which must be calculated dynamically (unless the number remaining in each age category for both genders is constant). This expression depends on the (unknown) \( c_{M_{k}}\)'s. But we also must ensure that the proportion of acts that men have, as distributed amongst the different female age-groups, sums to unity (for all male age-groups). That is, \( \sum_j P_{M_{k},j} = 1 \) implying that:

\[
c_{M_{k}} = \frac{1}{N_{M_{k}}(t)} \sum_j c_{F_{j},F_{j,k}} N_{F_{j}}(t).
\] (14)

**Supplementary Results**

Here we present the results of additional analyses and screening strategies that are not presented in the main manuscript. These are presented as box-and-whisker plots which illustrate the degree of uncertainty in the output from the model. As in the main paper, each individual (age- and gender-specific) strategy was simulated over 10,000 parameter sets and the inter-quartile range, mean (\(\mu\)), median (\(\tilde{\mu}\)) and 5th-95th percentile range (whiskers) are indicated in the standard way. The 1st-99th percentile range (\(\because\)) and minimum and maximum values (\(\times\)) are also indicated.

**Reduction in prevalence in men**

Figures S1a and S1b are analogous to Figures 3a and 3b in the paper but here the relative reductions in prevalence in men are shown. Fig S1a is for screening targeted at the under 30, under 25, and under 20 age-groups. Fig. S1b is for screening targeted at the 15-19, 20-24, and 25-29 age-groups.
Figure S1a

Figure S1b
**Mixed screening strategies**

Figure S2 shows the relative reduction in prevalence in females and males for screening strategies in which the female to male coverage ratio was 4:1.

![Figure S2](image1.png)

**Male only screening strategies**

Figure S3 shows the relative reduction in males and females for screening strategies in which males only (in the under 30, under 25, and under 20 age-groups) were screened at coverage ranging from 20% to 80% annually.

![Figure S3](image2.png)
References


