Technical appendix

1 Model overview

We developed a dynamic compartmental model that describes gonorrhea transmission in a single sex population stratified by sexual risk. This model represented a population of men who have sex with men (MSM), who experience a significant burden of gonorrhea in the United States and in whom emergence of resistance is of concern [1, 2]. A model schematic is presented in the main text (**Figure 1**).

2 Sexual mixing

The model population was divided into groups with three levels of sexual activity (k, low, intermediate, and high), that were characterized by annual rates of partner change. We assumed that individuals remained in a given activity group for the duration of their sexual lifespan, with the size of each group equal to N_k. The total population size was assumed to remain constant. The relative rate of partner change (rp) in the different risk groups was estimated using data from the National HIV Behavioral Surveillance System [3] and the rate of partner change (c_{min}) in the low activity group was estimated by model fitting. The rate of partner change for each activity group was therefore:

$$c_k = rp * c_{min}$$

We used the approach of Garnett et al. [4] to derive the probability of contact within and between groups, with the parameter ϵ describing mixing between groups. ϵ could range from 0 (proportionate or random mixing between groups) to 1 (assortative mixing, with individuals partnering exclusively with individuals of the same risk group). The probability that a person of sexual activity class k formed a partnership with a person of activity class k' was calculated as:

$$p_{kk'} = \epsilon\delta_{kk'} + (1-\epsilon)\frac{c_{k'}N_{k'}}{\sum_{k'=1}^{3} c_{k'}N_{k'}}$$

where $\delta_{kk'} = 1$ if $k = k'$ and 0 otherwise. The rate at which susceptible individuals are infected from partners of class k' depends on the partner change rate (c_k), the transmission probability per partnership (b), and the proportion of sexual partnerships occurring between sexual activity groups k and k' ($p_{kk'}$):

$$\beta_{kk'} = bc_k p_{kk'}$$

3 Force of infection

The overall force of infection was calculated as:

$$\lambda_k = \sum_{x=1}^{8} \sum_{k'=1}^{3} \frac{\beta_{kk'} f_x (Y_{x_{k'}} + Z_{x_{k'}})}{N_{k'}}$$

Here, x represents 1 of 8 possible antibiotic susceptibility profiles: susceptible, single resistance to antibiotic A, B, or C, dual resistance (AB, AC, or BC resistance), or resistance to all three antibiotics. Y_x and Z_x represent the number the number of symptomatic and asymptomatic infections with a given antibiotic susceptibility profile, and f_x is the fitness of a gonococcal isolate with a particular antibiotic susceptibility profile.

The rate at which susceptible individuals were infected with an isolate having a particular resistance profile was calculated as:

$$\lambda_{x_k} = \sum_{k'=1}^{3} \frac{\beta_{kk'} f_x (Y_{x_{k'}} + Z_{x_{k'}})}{N_{k'}}$$

4 Model equations

The natural history of gonorrhea infection was described by the following model states: susceptible (S), symptomatic infection (Y), and asymptomatic infection (Z). Each of the infectious states was further subdivided to represent the resistance profile of the infecting strain to three antibiotics (A, B, and C). A detailed description of how treatment was modeled is in the following section. We did not model different anatomical sites of infection, but assumed a probability of symptomatic infection that was intermediate between commonly cited probabilities for urethral and rectal/pharyngeal infections. Model parameters are defined in the table below the equations and values for the model parameters are presented in the main text (**Tables 1 and 2**). For an individual of a given sexual activity group (k), the model is described by the following system of differential equations, where N_k represents the total sexually active population in a given group:

$$
\begin{aligned}
\frac{dS_k}{dt} = & -\lambda_k S_k + (1-\omega_A(\xi_{A|0}+\xi_{AB|0}+\xi_{AC|0}) \\
& -\omega_B(\xi_{B|0}+\xi_{AB|0}+\xi_{BC|0})-\omega_C(\xi_{C|0}+\xi_{AC|0}+\xi_{BC|0}))(\tau_s Y_{0_k}+\tau_m Z_{0_k}) \\
& +(1-\xi_{A|A})(1-\omega_B(\xi_{B|A}+\xi_{AB|A}+\xi_{BC|A}) \\
& -\omega_C(\xi_{C|A}+\xi_{AC|A}+\xi_{BC|A}))(\tau_s Y_{A_k}+\tau_m Z_{A_k}) \\
& +(1-\xi_{B|B})(1-\omega_A(\xi_{A|B}+\xi_{AB|B}+\xi_{AC|B}) \\
& -\omega_C(\xi_{C|B}+\xi_{AC|B}+\xi_{BC|B}))(\tau_s Y_{B_k}+\tau_m Z_{B_k}) \\
& +(1-\xi_{C|C})(\xi_{all}-\omega_A(\xi_{A|C}+\xi_{AB|C}+\xi_{AC|C}) \\
& -\omega_B(\xi_{B|C}+\xi_{AB|C}+\xi_{BC|C}))(\tau_s Y_{C_k}+\tau_m Z_{C_k}) \\
& +(1-\xi_{A|AB}-\xi_{B|AB}-\xi_{AB|AB})(1-\omega_C(\xi_{C|AB}+\xi_{AC|AB}+\xi_{BC|AB}))(\tau_s Y_{AB_k}+\tau_m Z_{AB_k}) \\
& +(1-\xi_{A|AC}-\xi_{C|AC}-\xi_{AC|AC})(1-\omega_B(\xi_{B|AC}+\xi_{AB|AC}+\xi_{BC|AC}))(\tau_s Y_{AC_k}+\tau_m Z_{AC_k}) \\
& +(1-\xi_{B|BC}-\xi_{C|BC}-\xi_{BC|BC})(1-\omega_A(\xi_{A|BC}+\xi_{AB|BC}+\xi_{AC|BC}))(\tau_s Y_{BC_k}+\tau_m Z_{BC_k}) \\
& +(\xi_{ABC|ABC}(\tau_s Y_{ABC_k}+\tau_m Z_{ABC_k}) \\
& +\xi_{A|A}(\pi_s\tau_{sr}Y_{A_k}\pi_m\tau_{mr}Z_{A_k})+\xi_{B|B}(\pi_s\tau_{sr}Y_{B_k}+\pi_m\tau_{mr}Z_{B_k})+\xi_{C|C}(\pi_s\tau_{sr}Y_{C_k}+\pi_m\tau_{mr}Z_{C_k}) \\
& +(\xi_{A|AB}+\xi_{B|AB}+\xi_{AB|AB})(\pi_s\tau_{sr}Y_{AB_k}+\pi_m\tau_{mr}Z_{AB_k}) \\
& +(\xi_{A|AC}+\xi_{C|AC}+\xi_{AC|AC})(\pi_s\tau_{sr}Y_{AC_k}+\pi_m\tau_{mr}Z_{AC_k}) \\
& +(\xi_{B|BC}+\xi_{C|BC}+\xi_{BC|BC})(\pi_s\tau_{sr}Y_{BC_k}+\pi_m\tau_{mr}Z_{BC_k}) \\
& +(1-\xi_{ABC|ABC})(\pi_s\tau_{sr}Y_{ABC_k}+\pi_m\tau_{mr}Z_{ABC_k}) \\
& +\delta(Y_{0_k}+Y_{A_k}+Y_{B_k}+Y_{C_k}+Y_{AB_k}+Y_{AC_k}+Y_{BC_k}+Y_{ABC_k} \\
& +Z_{0_k}+Z_{A_k}+Z_{B_k}+Z_{C_k}+Z_{AB_k}+Z_{AC_k}+Z_{BC_k}+Z_{ABC_k}) \\
& +\rho N_k-\rho S_k \\
\frac{dY_{0_k}}{dt} = & \sigma\lambda_{0_k}S_k-\tau_s Y_{0_k}-\delta Y_{0_k}-\rho Y_{0_k} \\
\frac{dY_{A_k}}{dt} = & \sigma\lambda_{A_k}S_k+\omega_A(\xi_{A|0}+\xi_{AB|0}+\xi_{AC|0})\tau_s Y_{0_k} \\
& -(1-\xi_{A|A})\tau_s Y_{A_k}-\xi_{A|A}\pi_s\tau_{sr}Y_{A_k}-\delta Y_{A_k}-\rho Y_{A_k}
\end{aligned}
$$

$$
\begin{aligned}
\frac{dY_{B_k}}{dt} &= \sigma\lambda_{B_k}S_k + \omega_B(\xi_{B|0} + \xi_{AB|0} + \xi_{BC|0})\tau_s Y_{0_k} \\
&\quad - (1-\xi_{B|B})\tau_s Y_{B_k} - \xi_{B|B}\pi_s\tau_{sr}Y_{B_k} - \delta Y_{B_k} - \rho Y_{B_k} \\
\frac{dY_{C_k}}{dt} &= \sigma\lambda_{C_k}S_k + \omega_C(\xi_{C|0} + \xi_{AC|0} + \xi_{BC|0})\tau_s Y_{0_k} \\
&\quad - (1-\xi_{C|C})\tau_s Y_{C_k} - \xi_{C|C}\pi_s\tau_{sr}Y_{C_k} - \delta Y_{C_k} - \rho Y_{C_k} \\
\frac{dY_{AB_k}}{dt} &= \sigma\lambda_{AB_k}S_k + \omega_A(\xi_{A|B} + \xi_{AB|B} + \xi_{AC|B})\tau_s Y_{B_k} \\
&\quad + \omega_B(\xi_{B|A} + \xi_{AB|A} + \xi_{BC|A})\tau_s Y_{A_k} \\
&\quad - (1-\xi_{A|AB} - \xi_{B|AB} - \xi_{AB|AB})\tau_s Y_{AB_k} \\
&\quad - (\xi_{A|AB} + \xi_{B|AB} + \xi_{AB|AB})\pi_s\tau_{sr}Y_{AB_k} - \delta Y_{AB_k} - \rho Y_{AB_k} \\
\frac{dY_{AC_k}}{dt} &= \sigma\lambda_{AC_k}S_k + \omega_A(\xi_{A|C} + \xi_{AB|C} + \xi_{AC|C})\tau_s Y_{C_k} \\
&\quad + \omega_C(\xi_{C|A} + \xi_{AC|A} + \xi_{BC|A})\tau_s Y_{A_k} \\
&\quad - (1-\xi_{A|AC} - \xi_{C|AC} - \xi_{AC|AC})\tau_s Y_{AC_k} \\
&\quad - (\xi_{A|AC} + \xi_{C|AC} + \xi_{AC|AC})\pi_s\tau_{sr}Y_{AC_k} - \delta Y_{AC_k} - \rho Y_{AC_k} \\
\frac{dY_{BC_k}}{dt} &= \sigma\lambda_{BC_k}S_k + \omega_B(\xi_{B|C} + \xi_{AB|C} + \xi_{BC|C})\tau_s Y_{C_k} \\
&\quad + \omega_C(\xi_{C|B} + \xi_{AC|B} + \xi_{BC|B})\tau_s Y_{B_k} \\
&\quad - (1-\xi_{B|BC} - \xi_{C|BC} - \xi_{BC|BC})\tau_s Y_{BC_k} \\
&\quad - (\xi_{B|BC} + \xi_{C|BC} + \xi_{BC|BC})\pi_S\tau_{sr}Y_{BC_k} - \delta Y_{BC_k} - \rho Y_{BC_k} \\
\frac{dY_{ABC_k}}{dt} &= \sigma\lambda_{ABC_k}S_k + \omega_A(\xi_{A|BC} + \xi_{AB|BC} + \xi_{AC|BC})\tau_s Y_{BC_k} \\
&\quad + \omega_B(\xi_{B|AC} + \xi_{AB|AC} + \xi_{BC|AC})\tau_s Y_{AC_k} \\
&\quad + \omega_C(\xi_{C|AB} + \xi_{AC|AB} + \xi_{BC|AB})\tau_s Y_{AB_k} \\
&\quad - \xi_{ABC|ABC}\tau_s Y_{ABC_k} - (1-\xi_{ABC|ABC})\pi_s\tau_{sr}Y_{ABC_k} \\
&\quad - \delta Y_{ABC_k} - \rho Y_{ABC_k} \\
\frac{dZ_{0_k}}{dt} &= (1-\sigma)\lambda_{0_k}S_k - \tau_m Z_{0_k} - \delta Z_{0_k} - \rho Z_{0_k} \\
\frac{dZ_{A_k}}{dt} &= (1-\sigma)\lambda_{A_k}S_k + \omega_A(\xi_{A|0} + \xi_{AB|0} + \xi_{AC|0})\tau_m Z_{0_k} \\
&\quad - (1-\xi_{A|A})\tau_m Z_{A_k} - \xi_{A|A}\pi_m\tau_{mr}Z_{A_k} - \delta Z_{A_k} - \rho Z_{A_k} \\
\frac{dZ_{B_k}}{dt} &= (1-\sigma)\lambda_{B_k}S_k + \omega_B(\xi_{B|0} + \xi_{AB|0} + \xi_{BC|0})\tau_m Z_{0_k} \\
&\quad - (1-\xi_{B|B})\tau_m Z_{B_k} - \xi_{B|B}\pi_m\tau_{mr}Z_{B_k} - \delta Z_{B_k} - \rho Z_{B_k} \\
\frac{dZ_{C_k}}{dt} &= (1-\sigma)\lambda_{C_k}S_k + \omega_C(\xi_{C|0} + \xi_{AC|0} + \xi_{BC|0})\tau_m Z_{0_k} \\
&\quad - (1-\xi_{C|C})\tau_m Z_{C_k} - \xi_{C|C}\pi_m\tau_{mr}Z_{C_k} - \delta Z_{C_k} - \rho Z_{C_k}
\end{aligned}
$$

$$
\begin{aligned}
\frac{dZ_{AB_k}}{dt} &= (1-\sigma)\lambda_{AB_k}S_k + \omega_A(\xi_{A|B}+\xi_{AB|B}+\xi_{AC|B})\tau_m Z_{B_k} \\
&\quad + \omega_B(\xi_{B|A}+\xi_{AB|A}+\xi_{BC|A})\tau_m Z_{A_k} \\
&\quad - (1-\xi_{A|AB}-\xi_{B|AB}-\xi_{AB|AB})\tau_m Z_{AB_k} \\
&\quad - (\xi_{A|AB}+\xi_{B|AB}+\xi_{AB|AB})\pi_m\tau_{mr}Z_{AB_k} - \delta Z_{AB_k} - \rho Z_{AB_k} \\
\frac{dZ_{AC_k}}{dt} &= (1-\sigma)\lambda_{AC_k}S_k + \omega_A(\xi_{A|C}+\xi_{AB|C}+\xi_{AC|C})\tau_m Z_{C_k} \\
&\quad + \omega_C(\xi_{C|A}+\xi_{AC|A}+\xi_{BC|A})\tau_m Z_{A_k} \\
&\quad - (1-\xi_{A|AC}-\xi_{C|AC}-\xi_{AC|AC})\tau_m Z_{AC_k} \\
&\quad - (\xi_{A|AC}+\xi_{C|AC}+\xi_{AC|AC})\pi_m\tau_{mr}Z_{AC_k} - \delta Z_{AC_k} - \rho Z_{AC_k} \\
\frac{dZ_{BC_k}}{dt} &= (1-\sigma)\lambda_{BC_k}S_k + \omega_B(\xi_{B|C}+\xi_{AB|C}+\xi_{BC|C})\tau_m Z_{C_k} \\
&\quad + \omega_C(\xi_{C|B}+\xi_{AC|B}+\xi_{BC|B})\tau_m Z_{B_k} \\
&\quad - (1-\xi_{B|BC}-\xi_{C|BC}-\xi_{BC|BC})\tau_m Z_{BC_k} \\
&\quad - (\xi_{B|BC}+\xi_{C|BC}+\xi_{BC|BC})\pi_m\tau_{mr}Z_{BC_k} - \delta Z_{BC_k} - \rho Z_{BC_k} \\
\frac{dZ_{ABC_k}}{dt} &= (1-\sigma)\lambda_{ABC_k}S_k + \omega_A(\xi_{A|BC}+\xi_{AB|BC}+\xi_{AC|BC})\tau_m Z_{BC_k} \\
&\quad + \omega_B(\xi_{B|AC}+\xi_{AB|AC}+\xi_{BC|AC})\tau_m Z_{AC_k} \\
&\quad + \omega_C(\xi_{C|AB}+\xi_{AC|AB}+\xi_{BC|AB})\tau_m Z_{AB_k} \\
&\quad - \xi_{ABC|ABC}\tau_m Z_{ABC_k} - (1-\xi_{ABC|ABC})\pi_m\tau_{mr}Z_{ABC_k} \\
&\quad - \delta Z_{ABC_k} - \rho Z_{ABC_k}
\end{aligned}
$$

4.1 Model parameters

Table 1: Parameter symbols and definitions.

Symbol	Definition
k	Sexual activity group
x	Antibiotic susceptibility profile
abx	Antibiotic treatment regimen
N_k	Number of individuals in given sexual activity group
ρ	Rate of model entry/exit
λ_k	Force of infection
ω_x	Probability of developing resistance to antibiotic x on treatment
$\xi_{abx\|x}$	Probability of treatment with given antibiotic(s), given susceptibility profile
σ	Proportion of infections that are symptomatic
τ_s	Treatment rate, symptomatic infection
τ_{sr}	Re-treatment rate if treatment failure, symptomatic infection
τ_m	Treatment rate, asymptomatic infection
τ_{mr}	Re-treatment rate if initial treatment failure, asymptomatic infection
δ	Natural recovery rate
π_s	Probability treatment failure recognized, symptomatic infection
π_m	Probability treatment failure recognized, asymptomatic infection

5 Modeling of treatment

We modeled treatment with three antibiotics, which could be used individually or in combination. Resistance could emerge during treatment, or an individual could be infected with a resistant strain. Each antibiotic had a probability of resistance emergence on treatment (ω_{abx}) and a fitness cost ($1 - f_{abx}$) associated with resistance (reflecting the transmissibility relative to the susceptible strain).

We used genomic data to estimate the properties of antibiotic resistant N. gonorrhoeae strains [5]. These data suggest that resistance to fluoroquinolones (ciprofloxacin) emerges relatively frequently, and that there is a minimal fitness cost associated with resistance acquisition. Resistance to macrolides (azithromycin) also occurs relatively frequently, but there appears to be a high associated fitness cost, such that these mutant strains do not transmit widely in the population. Resistance to ESCs (ceftriaxone) appears to emerge at a lower frequency than for the other two antimicrobials, with resistant strains displaying an intermediate fitness cost. To map these qualitative measures of the relative likelihood of emergence and transmission of resistant strains to model parameters, we selected base case values for initial analysis and explored a range of parameter values in sensitivity analyses. Base case fitness costs were selected such that BC resistance emerged over a time frame consistent with what has been observed for other anti-gonococcal agents [6].

For doubly or triply resistant strains, we conservatively assumed that the fitness was equal to the product of the individual strain fitness (e.g., fitness of AB resistant (f_{AB}) = $f_A * f_B$). The properties of each of the antibiotics were selected to mirror the classes of antibiotics used to treat gonorrhea infection: fluorquinolones (A), macrolides (B), and extended spectrum cephalosporins (C). We assumed that acquisition of antibiotic resistance was sequential (i.e., an individual did not simultaneously acquire resistance to multiple antibiotics during a single course of treatment).

Men with symptomatic infection were assumed to seek medical care and receive treatment, while men with asymptomatic infection could be identified via screening. Current guidelines recommend at least annual screening of MSM at sites of contact, with more frequent screening in men at increased risk [7]. Screening was implemented as an annual rate and estimated by model fitting, as described in Section 6. Men could be treated with a drug to which the infecting strain was susceptible or resistant, with different approaches to treatment choice described below. For simplicity, we did not model antibiotic efficacy. If treated with an effective antibiotic (i.e., one to which the infecting strain was susceptible), an individual returned to the susceptible state. If treated with an ineffective antibiotic (i.e., one to which the infecting strain was resistant), an individual remained in the infected state. Among men treated initially with an ineffective antibiotic, there was a probability that they could be re-treated with an effective antibiotic, with some delay. The probability of having treatment failure recognized depended on whether an infection was symptomatic or asymptomatic. In the case of no treatment or unrecognized treatment failure, men returned to the susceptible state via natural clearance of infection. Men treated with an initially effective antibiotic but who acquired *de novo* resistance during treatment transitioned to the appropriate new infectious state, where they could have their infection recognized and treated, dependent on their symptom status and probability of screening. For all strategies, we assumed that all treated cases

received one of the antibiotics/antibiotic combinations described in the model, such that all detected cases received treatment (i.e., the sum of all treatment probabilities for a case with a given susceptibility profile = 1).

5.1 No point-of-care test

In the absence of a POC test, all diagnosed cases (either due to seeking medical care for symptoms or identified via screening) were treated with antibiotics B and C, consistent with U.S. treatment guidelines which currently recommend combination therapy with azithromycin and ceftriaxone [7] such that:

$$\xi_{BC|x} = 1$$

where $\xi_{abx|x}$ represents probability of treatment with a given antibiotic or antibiotic combination (abx) given the resistance profile (x) of the infection (8 possible states). Treatment with all other antibiotics was assumed to be 0.

5.2 Point-of-care test for antibiotic A only

When a rapid diagnostic test was available for detecting resistance to antibiotic A only, A susceptible cases were treated with antibiotic A, with all other cases treated with a combination of antibiotics B and C:

$$\begin{aligned}
\xi_{A|(0,B,C,BC)} &= p_{test} * \psi_A \\
\xi_{BC|(0,B,C,BC)} &= p_{test} * (1 - \psi_A) + (1 - p_{test}) \\
\xi_{A|(A,AB,AC,ABC)} &= p_{test} * (1 - \kappa_A) \\
\xi_{BC|(A,AB,AC,ABC)} &= p_{test} * \kappa_A + (1 - p_{test})
\end{aligned}$$

Treatment with all other antibiotics or antibiotic combinations was assumed to be 0. Here, κ_{abx} and ψ_{abx} represent test sensitivity and specificity for detecting resistance to a given antibiotic and p_{test} represents the proportion of identified cases in which the test is used.

5.3 Point-of-care test for all three antibiotics

When a rapid diagnostic test was available for detecting resistance to all three antibiotics, treatment probability (ξ), given underlying resistance profile and test characteristics, was determined as described below. In our base case analysis, we assumed that when multiple antibiotic could treat an infection, the antibiotic with the highest fitness cost associated with resistance was chosen, such that B was preferred over C, which was preferred over A. The treatment

probabilities presented below include this preferential rank ordering:

$$
\begin{aligned}
\xi_{A|0} &= p_{test} * FP_{BC|0} \\
\xi_{B|0} &= p_{test} * (\psi_A * \psi_B * \psi_C + FP_{A|0} + FP_{C|0} + FP_{AC|0}) \\
\xi_{C|0} &= p_{test} * (FP_{B|0} + FP_{AB|0}) \\
\xi_{BC|0} &= 1 - p_{test} \\
\xi_{ABC|0} &= p_{test} * FP_{ABC|0}
\end{aligned}
$$

$$
\begin{aligned}
\xi_{A|A} &= p_{test} * ((1 - \kappa_A) * FP_{BC|A}) \\
\xi_{B|A} &= p_{test} * (\kappa_A * \psi_B * \psi_C + FP_{C|A} + (1 - \kappa_A) * \psi_B * \psi_C) \\
\xi_{C|A} &= p_{test} * FP_{B|A} \\
\xi_{BC|A} &= 1 - p_{test} \\
\xi_{ABC|A} &= p_{test} * \kappa_A * FP_{BC|A}
\end{aligned}
$$

$$
\begin{aligned}
\xi_{A|B} &= p_{test} * (\kappa_B * FP_{C|B}) \\
\xi_{B|B} &= p_{test} * ((1 - \kappa_B) * \psi_A * \psi_C + (1 - \kappa_B) * FP_{AC|B} \\
&\quad + (1 - \kappa_B) * FP_{C|B} + (1 - \kappa_B) * FP_{A|B}) \\
\xi_{C|B} &= p_{test} * (\kappa_B * \psi_A * \psi_C + \kappa_B * FP_{A|B}) \\
\xi_{BC|B} &= 1 - p_{test} \\
\xi_{ABC|B} &= p_{test} * \kappa_B * FP_{AC|B}
\end{aligned}
$$

$$
\begin{aligned}
\xi_{A|C} &= p_{test} * (\kappa_C * FP_{B|C}) \\
\xi_{B|C} &= p_{test} * (sens_C * \psi_A * \psi_B + \kappa_C * FP_{A|C} + (1 - \kappa_C) * \psi_A * \psi_B \\
&\quad + (1 - \kappa_C) * FP_{A|C}) \\
\xi_{C|C} &= p_{test} * ((1 - \kappa_C) * FP_{AB|C} + (1 - \kappa_C) * FP_{B|C}) \\
\xi_{BC|C} &= 1 - p_{test} \\
\xi_{ABC|C} &= p_{test} * \kappa_C * FP_{AB|C}
\end{aligned}
$$

$$
\begin{aligned}
\xi_{A|AB} &= p_{test} * (FN_{A|AB} * (1 - \psi_C)) \\
\xi_{B|AB} &= p_{test} * (FN_{AB|AB} * \psi_C + FN_{AB|AB} * (1 - \psi_C) + FN_{B|AB} * (1 - \psi_C) \\
&\quad + FN_{B|AB} * \psi_C) \\
\xi_{C|AB} &= p_{test} * (\kappa_A * \kappa_B * \psi_C + FN_{A|AB} * \psi_C) \\
\xi_{BC|AB} &= 1 - p_{test} \\
\xi_{ABC|AB} &= p_{test} * \kappa_A * \kappa_B * (1 - \psi_C)
\end{aligned}
$$

$$
\begin{aligned}
\xi_{A|AC} &= p_{test} * FN_{A|AC} * (1 - \psi_B) \\
\xi_{B|AC} &= p_{test} * (\kappa_A * \kappa_C * \psi_B + FN_{AC|AC} * \psi_B + FN_{A|AC} * \psi_B \\
&\quad + FN_{C|AC} * \psi_B) \\
\xi_{C|AC} &= p_{test} * (FN_{AC|AC} * (1 - \psi_B) + FN_{C|AC} * (1 - \psi_B)) \\
\xi_{BC|AC} &= 1 - p_{test} \\
\xi_{ABC|AC} &= p_{test} * \kappa_A * \kappa_C * (1 - \psi_B)
\end{aligned}
$$

$$
\begin{aligned}
\xi_{A|BC} &= p_{test} * \kappa_B * \kappa_C * \psi_A \\
\xi_{B|BC} &= p_{test} * (FN_{BC|BC} + FN_{B|BC}) \\
\xi_{C|BC} &= p_{test} * FN_{C|BC} \\
\xi_{BC|BC} &= 1 - p_{test} \\
\xi_{ABC|BC} &= p_{test} * \kappa_B * \kappa_C * (1 - \psi_A)
\end{aligned}
$$

$$
\begin{aligned}
\xi_{A|ABC} &= p_{test} * FN_{A|ABC} \\
\xi_{B|ABC} &= p_{test} * (FN_{B|ABC} + FN_{ABC|ABC} + FN_{AB|ABC} + FN_{BC|ABC}) \\
\xi_{C|ABC} &= p_{test} * (FN_{C|ABC} + FN_{AC|ABC}) \\
\xi_{BC|ABC} &= 1 - p_{test} \\
\xi_{ABC|ABC} &= p_{test} * \kappa_A * \kappa_C * \kappa_C
\end{aligned}
$$

Treatment with all other antibiotics or combinations of antibiotics was assumed to be 0. $FP_{abx|x}$ and $FN_{abx|x}$ represent the false positive and false negative values for the multiple resistance test, with calculations shown below.

5.4 Test characteristics for the triple resistance POC test

Based on assumed test sensitivity and specificity for detecting resistance to each of the three antibiotics, we calculated false positive and false negative probabilities for the combination test as follows, under the assumption that the

test properties for detecting resistance to each antibiotic were independent:

$$
\begin{aligned}
FP_{ABC|0} &= (1-\psi_A)*(1-\psi_B)*(1-\psi_C) \\
FP_{AB|0} &= (1-\psi_A)*(1-\psi_B) - FP_{ABC|0} \\
FP_{AC|0} &= (1-\psi_A)*(1-\psi_C) - FP_{ABC|0} \\
FP_{BC|0} &= (1-\psi_B)*(1-\psi_C) - FP_{ABC|0} \\
FP_{A|0} &= (1-\psi_A) - FP_{AB|0} - FP_{AC|0} - FP_{ABC|0} \\
FP_{B|0} &= (1-\psi_B) - FP_{AB|0} - FP_{BC|0} - FP_{ABC|0} \\
FP_{C|0} &= (1-\psi_C) - FP_{AC|0} - FP_{BC|0} - FP_{ABC|0}
\end{aligned}
$$

$$
\begin{aligned}
FP_{BC|A} &= (1-\psi_B)*(1-\psi_C) \\
FP_{B|A} &= (1-\psi_B) - FP_{BC|A} \\
FP_{C|A} &= (1-\psi_C) - FP_{BC|A}
\end{aligned}
$$

$$
\begin{aligned}
FP_{AC|B} &= (1-\psi_A)*(1-\psi_C) \\
FP_{A|B} &= (1-\psi_A) - FP_{AC|A} \\
FP_{C|B} &= (1-\psi_C) - FP_{AC|A}
\end{aligned}
$$

$$
\begin{aligned}
FP_{AB|C} &= (1-\psi_A)*(1-\psi_B) \\
FP_{A|C} &= (1-\psi_A) - FP_{AB|C} \\
FP_{B|C} &= (1-\psi_B) - FP_{AB|C}
\end{aligned}
$$

$$
\begin{aligned}
FN_{A|AB} &= (1-\kappa_A)*\kappa_B \\
FN_{B|AB} &= \kappa_A*(1-\kappa_B) \\
FN_{AB|AB} &= (1-\kappa_A)*(1-\kappa.B)
\end{aligned}
$$

$$
\begin{aligned}
FN_{A|AC} &= (1-\kappa_A)*\kappa_C \\
FN_{C|AC} &= \kappa_A*(1-\kappa_C) \\
FN_{AC|AC} &= (1-\kappa_A)*(1-\kappa.C)
\end{aligned}
$$

$$
\begin{aligned}
FN_{B|BC} &= (1-\kappa_B)*\kappa_C \\
FN_{C|BC} &= \kappa_B*(1-\kappa_C) \\
FN_{BC|BC} &= (1-\kappa_B)*(1-\kappa.C)
\end{aligned}
$$

$$
\begin{aligned}
FN_{A|ABC} &= (1-\kappa_A)*\kappa_B*\kappa_C \\
FN_{B|ABC} &= \kappa_A*(1-\kappa_B)*\kappa_C \\
FN_{C|ABC} &= \kappa_A*\kappa_B*(1-\kappa_C) \\
FN_{AB|ABC} &= (1-\kappa_A)*(1-\kappa_B)*\kappa_C \\
FN_{AC|ABC} &= (1-\kappa_A)*\kappa_B*(1-\kappa_C) \\
FN_{BC|ABC} &= \kappa_A*(1-\kappa_B)*(1-\kappa_C) \\
FN_{ABC|ABC} &= (1-\kappa_A)*(1-\kappa_B)*(1-\kappa_C)
\end{aligned}
$$

6 Model fitting

We calibrated model parameters describing gonorrhea natural history and sexual behavior using maximum likelihood estimation. Model estimates of overall gonorrhea prevalence at equilibrium (in the absence of any resistant strains) were compared to available prevalence data in MSM [8, 9, 10]. We assumed that prevalence followed a beta distribution, with variance estimated from the lower and upper bounds of the available point estimates. Initial parameter estimates drew on the best estimates from the biomedical literature or by assumption. Parameters were either log transformed to ensure positivity or logit transformed to ensure probabilities were bounded between 0 and 1.

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