Supplementary material 1

Model parameters

Table S1. Parameter distributions used in the model

Parameter	Description	Parameter in the Model*	Prior Distribution†	Median	Mode	95% range	References / Changes from national model
Population Structure							
Total population size	Baltimore	N	Fixed	242,185	NA	NA	
	San Francisco		Fixed	359,020	NA	NA	
Average time in model (y)		$1/\mu$	Fixed	25	NA	NA	
Proportion of population in each subpopulation	Baltimore, Black	pop_i	Fixed	0.57	NA	NA	
	Baltimore, Other		Fixed	0.37	NA	NA	
	Baltimore, Hispanic		Fixed	0.06	NA	NA	
	Baltimore, MSM			0.04	NA	NA	[1]
	San Francisco, Black		Fixed	0.045	NA	NA	
	San Francisco, Other		Fixed	0.793	NA	NA	
	San Francisco, Hispanic		Fixed	0.162	NA	NA	
	San Francisco, MSM			0.185	NA	NA	[1]
Proportion who are Sexually Active, 15-24 y males	Black	$p_{S,ijkl}$	Fixed	0.78	NA	NA	NSFG[2]
	Other		Fixed	0.64	NA	NA	"
	Hispanic		Fixed	0.68	NA	NA	"
	MSM		Fixed	0.67	NA	NA	(mean value assumed)
Proportion who are Sexually			Fixed	0.96	NA	NA	NSFG – no significant

Parameter	Description	Parameter in the Model*	Prior Distribution†	Median	Mode	95% range	References / Changes from national model
Active, 25-39 y males							difference between subpopulations [2]
Proportion who are Sexually Active, 15-24 y females			Fixed	0.66	NA	NA	″
Proportion of 25-39 y females			Fixed	0.98	NA	NA	″
Proportion of the Population in Each Sexual Activity Group	LowActivity (lower partner change rate)		Fixed	0.90	NA	NA	Assumption
	High Activity (higher partner change rate)		Fixed	0.10	NA	NA	″
Behavior							
Mixing with same sexual activity group	Stratified by race/ethnicity	$\varepsilon_{1,j}$	Beta (1.5, 1.5)	0.50	0.50	(0.06, 0.94)	Uninformative prior
Mixing with same age	Male 15-24 y and Female 25-39 y	$\varepsilon_{2,ijl}$	Beta (9,2.7)	0.78	0.82	(0.5, 0.95)	NSFG[2]
	Male 25-39 y and Female 15-24 y		Beta (6.1,2.3)	0.74	0.80	(0.4, 0.95)	″
	MSM		Beta (8,3.8)	0.69	0.71	(0.4, 0.9)	″
Mixing with same subpopulation	Black male	$\varepsilon_{3,ij}$	Beta (172.7,52.4)	0.77	0.77	(0.71, 0.82)	″
	Hispanic male		Beta (547.2,70.3)	0.89	0.89	(0.86, 0.91)	″
	Other male		Beta (183.7,72.6)	0.72	0.72	(0.66, 0.77)	″
	MSM		Beta (47.5,2.5)	0.96	0.97	(0.88, 0.99)	″
	Black female		Beta (217,28.8)	0.88	0.89	(0.84, 0.92)	″
	Hispanic Female		Beta (437.1,70.4)	0.86	0.86	(0.83, 0.89)	″
	Other female		Beta(99.1,59.1)	0.55	0.63	(0.70, 0.65)	″

Parameter	Description	Parameter in the Model*	Prior Distribution†	Median	Mode	95% range	References / Changes from national model
Minimum rate of partner acquisition	Stratified by race/ethnicity and age	$c_{min,jl}$	Gamma (5,5)	0.93	0.80	(0.32, 2.05)	NSFG[2]
Relative rate of partner acquisition, males 15-24 y		rp_{ijkl}					NSFG[2]
	Black, low activity		Gamma(2.2, 0.6)	3.13	2.00	(0.51, 9.86)	"
	Black, high activity		Normal(32.5, 8.9)	32.50	32.50	(15.06, 49.94)	"
	Hispanic, low activity		Fixed	1.0			"
	Hispanic, high activity		Gamma(4.3, 0.6)	6.62	5.50	(2.07, 15.36)	"
	Other, low activity		Gamma(2.2, 0.6)	3.13	2.00	(0.51, 9.86)	"
	Other, high activity		Normal(27.5, 11.5)	27.50	27.50	(4.96, 50.04)	"
	MSM, low activity		Fixed	1			"
	MSM, high activity		Normal(45, 15.3)	45.00	45.00	(15.01, 74.99)	"
Relative rate of partner acquisition, males 25-39 y		rp_{ijkl}					
	Black, low activity		Gamma(3.4, 1.6)	1.92	1.50	(0.5, 4.91)	"
	Black, high activity		Normal(45, 15.3)	45.00	45.00	(15.01, 74.99)	"
	Hispanic, low activity		Fixed	1			"
	Hispanic, high activity		Gamma(5.3,0.4)	12.43	10.75	(4.48, 26.68)	"
	Other, low activity		Gamma(3.4, 1.6)	1.92	1.50	(0.5, 4.91)	"
	Other, high activity		Normal(45, 15.3)	45.00	45.00	(15.01, 74.99)	"
	MSM, low activity		Fixed	1			"
	MSM, high activity		Normal(45.0, 15.3)	45.0 (15.0-75.0)			"

Parameter	Description	Parameter in the Model*	Prior Distribution†	Median	Mode	95% range	References / Changes from national model
Relative rate of partner acquisition, females 15-24 y		rp_{ijkl}					
	Black, low activity		Gamma(2.2, 0.6)	3.7 (0.5-10.0)			″
	Black, high activity		Gamma(1.9, 0.1)	17.7 (2.0-50.0)			″
	Hispanic, low activity		Fixed	1			″
	Hispanic, high activity		Gamma(4.3, 0.6)	7.0 (2.0, 15.0)			″
	Other, low activity		Gamma(2.2, 0.6)	3.7 (0.5-10.0)			″
	Other, high activity		Gamma(5.3, 0.4)	14.9 (5.0-30.0)			″
Relative rate of partner acquisition, females 25-39 y		rp_{ijkl}					″
	Black, low activity		Gamma(3.4, 1.6)	2.2 (0.5-5.0)			″
	Black, high activity		Gamma(8.5, 0.8)	11.3 (5.0-20.0)			″
	Hispanic, low activity		Fixed	1			″
	Hispanic, high activity		Gamma(5.3,0.4)	14.9 (5.0, 30.0)			″
	Other, low activity		Gamma(3.4,1.6)	2.2 (0.5-5.0)			″
	Other, high activity		Gamma(5.3,0.4)	14.9 (5.0-30.0)			″
Natural history							
Probability of Transmission	Male to Female	β_{ji}	Beta (10.8,21.4)	0.33	0.32	(0.19, 0.5)	Fit to national posterior distribution [3]
	Female to Male		Beta (41,13.8)	0.75	0.76	(0.63, 0.85)	″
	Male to Male		Beta (18.7,21.4)	0.47	0.46	(0.32, 0.62)	″
Average duration of symptomatic infection, d	Male	$1/\gamma_{ij}$	Gamma (5.48,0.416)	12.38	10.77	(4.56, 26.28)	Fit to national posterior distribution[3]
	MSM		Gamma (3.5276,0.2932)	10.92	8.62	(2.93, 27.45)	″
	Female		Gamma (3.026,0.3568)	7.57	5.68	(1.77, 20.36)	″

Parameter	Description	Parameter in the Model*	Prior Distribution†	Median	Mode	95% range	References / Changes from national model
Average duration of asymptomatic infection, d	Male	$1/\delta_{ij}$	Normal (244.5,54.6)	244.50	244.50	(137.49, 351.51)	"
	MSM		Normal (242.2,48.5)	242.20	242.20	(147.14, 337.26)	"
	Female		Normal (261.4,46.3)	261.40	261.40	(170.65, 352.15)	"
Probability of symptomatic infection	Male	σ_{ij}	Beta (74.2,26.6)	0.74	0.74	(0.65, 0.82)	Fit to national posterior distribution [3]
	Female		Beta (32.8,58.6)	0.36	0.36	(0.26, 0.46)	"
	MSM		Beta (17.9,10.9)	0.62	0.63	(0.44, 0.79)	"
Annual increase in transmission	MSM	$C_{1,rr}$	Beta (1,15)	0.0451584	0	(0, 0.22)	Assumption
Annual increase in transmission	MSW, F	$C_{2,rr}$	Beta (1,15)	0.0451584	0	(0, 0.22)	Addition to the model to allow for potential increases in heterosexual acquisition risk at urban centers
Screening and Reporting							
Probability asymptomatic case is reported if treated	Implemented as a Bezier curve with four control points (a-d) for the years from 2002 to end of calibration data. Here showing the start and end. Mid-points are Beta(1.1,1.1)	Π_a	Beta (90.1,25.5)	0.78	0.78	(0.7, 0.85)	[3]
		Π_d	Beta (116.1,12.1)	0.91	0.91	(0.85, 0.95)	"
Relative risk case is reported if symptomatic	Nonblack male	$rr_{symp,ij}$	Beta (12,3)	0.81	0.85	(0.57, 0.95)	More constrained prior than in the national model [3]

Parameter	Description	Parameter in the Model*	Prior Distribution†	Median	Mode	95% range	References / Changes from national model
							assuming reporting should be better at local level
	Black male		Beta (12,3)	0.81	0.85	(0.57, 0.95)	″
	Nonblack female		Beta (12,3)	0.81	0.85	(0.57, 0.95)	″
	Black female		Beta (12,3)	0.81	0.85	(0.57, 0.95)	″
Annual asymptomatic screen and treat rate, low sexual activity group	Implemented as a Bezier curve with four control points (a-d) for the years from 2002 to end of calibration data. Here showing the start and end. Mid-points are Beta(1.1,1.1).	ψ_{ijl}					3
	Other and Hispanic F 15-24		Start: Beta (12.6,24.3)	0.34	0.33	(0.2, 0.5)	″
			End: Beta (24.7,33.8)	0.42	0.42	(0.3, 0.55)	″
	Other and Hispanic F 25-39		Start: Beta (6.7,22)	0.23	0.21	(0.1, 0.4)	″
			End: Beta (7.9,17.4)	0.31	0.30	(0.15, 0.5)	″
	Other and Hispanic M 15-24		Start: Beta (2.6,22.3)	0.09	0.07	(0.02, 0.25)	″
			End: Beta (2.6,22.3)	0.09	0.07	(0.02, 0.25)	″
	Other and Hispanic M 24-39		Start: Beta (2.6,22.3)	0.09	0.07	(0.02, 0.25)	″
			End: Beta (2.6,22.3)	0.09	0.07	(0.02, 0.25)	″
	MSM 15-24		Start: Beta (5.7,10.2)	0.35	0.34	(0.15, 0.6)	″
			End: Beta (7,9.9)	0.41	0.40	(0.2, 0.65)	″
	MSM 25-39		Start: Beta (5.7,10.2)	0.35	0.34	(0.15, 0.6)	″
			End: Beta (7,9.9)	0.41	0.40	(0.2, 0.65)	″

Parameter	Description	Parameter in the Model*	Prior Distribution†	Median	Mode	95% range	References / Changes from national model
	Black F 15-24		Start: Beta (12.6,24.3)	0.34	0.33	(0.2, 0.5)	ʺ
			End: Beta (24.7,33.8)	0.42	0.42	(0.3, 0.55)	ʺ
	Black F 25-39		Start: Beta (6.7,22)	0.23	0.21	(0.1, 0.4)	ʺ
			End: Beta (7.9,17.4)	0.31	0.30	(0.15, 0.5)	ʺ
	Black M 15-24		Start: Beta (2.6,22.3)	0.09	0.07	(0.02, 0.25)	ʺ
			End: Beta (2.6,22.3)	0.09	0.07	(0.02, 0.25)	ʺ
	Black M 24-39		Start: Beta (2.6,22.3)	0.09	0.07	(0.02, 0.25)	ʺ
			End: Beta (2.6,22.3)	0.09	0.07	(0.02, 0.25)	ʺ
Relative Rate of Screening	Hispanic M vs. Other M	rr_pop_{ij}	Gamma (8.5,7.5)	1.09	1.00	(0.5, 2.01)	ʺ
	Hispanic F vs. Other F		Gamma (8.5,7.5)	1.09	1.00	(0.5, 2.01)	ʺ
	High Activity		Gamma (8.5,7.5)	1.09	1.00	(0.5, 2.01)	ʺ

*Subscripts i, j, k, and l indicate subpopulation, sex, sexual activity group, and age group, respectively. Model parameters correspond to the parameters described in Tuite *et al.* (2018).[3]

†Gamma distributions are described by shape (α) and rate (β) parameters; beta distributions are described by shape parameters (α and β).

Additional model detail

Use of NSFG data to reproduce sexual mixing by age and race/ethnicity

NSFG 2011-2013 data were used to characterize self-reported sexual mixing patterns by age and race/ethnicity by analyzing data from individuals who had reported ever having had sex and stratifying the results by respondents' race/ethnicity and the race/ethnicity of their most recent opposite-sex sex partner. Poster by Tuite *et al.* was presented at CDC STD 2016 conference (URL to poster: https://cdn2.sph.harvard.edu/wp-content/uploads/sites/54/2016/07/Tuite_mixing_CDC_STD.pdf), which describes the analysis and its results in more detail. Mixing was more assortative by race/ethnicity and age than we would expect if mixing was independent of race/ethnicity or age.

Sexual mixing in the model was defined by age and race/ethnicity using a mixing matrix where mixing by age and race/ethnicity was allowed to vary from fully assortative to proportionate. Given mixing by age did not differ by race/ethnicity in NSFG data, these two mixing patterns were modeled independently. Age mixing was accounted for in the model calibration stage (see calibration supplements, page 1, panel B), where distribution of partnerships in the model were calibrated to the respective data from NSFG. Use of NSFG assumes that national level patterns of sexual mixing among the heterosexual population are a good approximation of sexual mixing at local level. A further simplification we made was to calibrate to age-mixing only and not calibrate to race/ethnicity mixing. Instead, we compared the model outputs for race/ethnicity mixing to NSFG data. Further description of the modeling of sexual mixing can be found in the supplement of Tuite et al. 2018.[3]

Use of NHANES data to calibrate to gonorrhea prevalence

We pooled NHANES gonorrhea prevalence for 1999-2008 by race/ethnicity (Non-Hispanic White and Other, Non-Hispanic Black, Hispanic) and age (15-24, 25-39) to reflect plausible prevalence among women. Given the data are older, and prevalence at national-level may not be a good proxy for city-level prevalence, we calibrated to the data allowing for a larger variance to ensure that the prevalence data did not restrict the calibration to local-level data. The modeled calibrated prevalence estimates for women were higher than NHANES prevalence estimates in Baltimore and similar to NHANES in San Francisco (see supplements 2 and 3, page 1). The dominance of city-level gonorrhea diagnosis rates in guiding the calibration are demonstrated in Figure S1 in supplement 1, where the model-predicted incidence closely matches the diagnoses in each city.

Calibration of the model

We calibrated the model using a Bayesian framework. Calibrated parameter values were obtained using Markov chain Monte Carlo (MCMC) simulation, implemented with a Metropolis-Hastings algorithm.[4] Parameters governing the natural history of gonorrhea, sexual behaviors and treatment are varied in calibration. Because there are fewer data describing local-level gonorrhea epidemiology compared to the previous national-level analysis,[3] we made the following simplifications regarding model parameterization. i) Prior distributions for natural history parameters were defined based on posterior distributions estimated in the previous study, under the assumption that these parameters should be relatively invariant across locations. ii) For parameters determining reporting probabilities of symptomatic male infection, we defined informative prior distributions assuming better gonorrhea diagnosis reporting in the cities compared to the level estimated nationally. iii) The national-level analysis allowed increasing risk behavior for MSM. We accommodated potential increases in risk behavior in different population groups by allowing increasing transmission independently for the MSM and heterosexual populations. Parameters used in the model are presented in Supplementary Material 1, Table S1, along with further information on the assumptions and differences compared to the published national-level analysis.

Assuming posterior values from the national-level model as priors

In order to calibrate natural history parameters, which are informed by the national estimates,[3] we used the MASS library in R to fit beta distributions to a sample from the posterior distribution of the national-level model to estimate the probability of an incident infection being symptomatic, the probability of transmission, and gamma distributions to the duration of a symptomatic and asymptomatic case. These beta and gamma distributions were then taken as the prior in the regional model.

Increasing transmission probability

To facilitate the observed increasing prevalence trends, we allowed our model to assume a linearly increasing transmission probability during the calibration time period. Two separate rates of increase in transmission probability were calibrated for the heterosexual and MSM populations. The transmission probability at the beginning of the time period (Tr) is calibrated directly, while the transmission probability at the end of the time period is calibrated as a rate between 0 and 1 multiplied against (1-Tr). This rate of increase parameter is calibrated as a beta distribution.

Incidence estimate for MSM

To provide more information to the model for a reasonable estimate of the incidence rate among MSM, we estimated a 95% confidence interval of the incidence estimate to be between 2 and 20% based on two studies in Atlanta and San Francisco which provide incidence estimates among MSM. This was used in calibration as a gamma likelihood.

Morris et al. 2006[5]. Prospective cohort Study conducted in San Francisco 2001-2003. MSM were tested regardless of symptoms every 6 months. Study population of 603 men was 71% white and 6% black. The study identified a yearly incidence of rectal gonorrhea 3.5% (1.6-7.0%), urethral gonorrhea 1.5% (0.6-3.4%), and pharyngeal gonorrhea 11.7% (8.8-15.3%). Study by Kelley et al (2015)[6] and Sullivan et al (2014)[7] conducted a prospective cohort of 803 of whom 562 were followed up over 2011-2014. The prospective cohort was restricted to HIV-negative population. Incidence for rectal gonorrhea was 9.4 (6.3-13.4) among black men, and 3.7 (2.1-6.1) among white men. Urethral gonorrhea incidence was 2.2 (0.9-4.3) among black men and 0.2 (0.0-1.2) among white men.

Removing loss to follow-up

In the model, screening and treatment are operationalized simultaneously. The model-estimated screening rate represents *the effective screening rate* given a person was tested, not lost to follow-up and received treatment. $\mathrm{O}_{\mathrm{base}}$ is then the average duration from infection to testing and treatment initiation for asymptomatic women. In $\mathrm{O}_{\mathrm{base}} = \frac{\mathrm{T+D}}{(1-\mathrm{f})}$, T is the duration between screening tests, f is the proportion LTFU after screening and D is the average duration between testing and treatment start among those not LTFU. If we prevent LTFU (but do not alter average duration to treatment as in the analysis), we could reduce the duration of infection. Among those not lost to follow-up the mean time to treatment initiation is $\mathrm{O}_{treatall} = \mathrm{T} + \mathrm{D} = \mathrm{O}_{\mathrm{base}}(1 - \mathrm{f})$.

Implementing mobile outreach testing scenarios

The increase in screening via outreach screening was implemented as an average increase in screening across the population. We modified the rate of screening in the model so that there were an additional two screening tests per year among 14% of the population who were assumed to uptake the outreach screening. We also wanted to target high-activity and low-activity populations (HR and LR) differently with the assumption that the outreach screening is able to increase screening among high-activity population specifically. To obtain the different increase in screening between the high- and low-activity populations we calculated a weighted average, so that when 50% of the high-activity population (10% of the total population) are screened, there would be 10% of low-risk population screened to achieve overall 14% screening coverage. In the sensitivity analyses, we maintain the size of the target population at 14% and the increase in screening tests as 2 additional tests per year to assure that a similar number of additional tests are applied across the mobile outreach scenarios making them comparable. The percentage of high-activity individuals who are provided the additional two screening tests per year is adjusted from the 50% to 20% or 40%, and the size of the low-activity population is calculated accordingly.

Supplementary Results

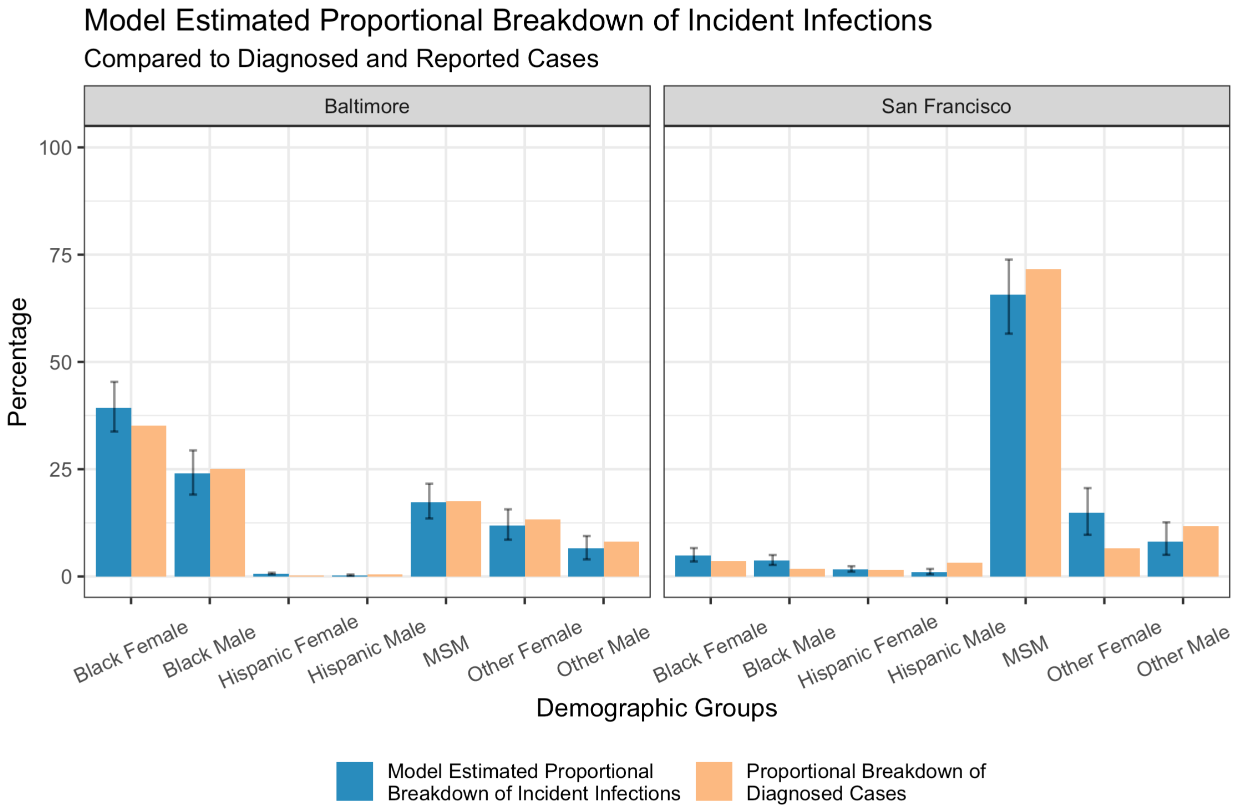


Figure S1. Percentage breakdown of new infections estimated to occur on the last calibration year (2017 and 2016 for Baltimore City and San Francisco, respectively).

The bar chart shows the proportion (%) of model-estimated incident infections occurring in each subpopulation (mean and 95% credible interval of the calibrated model). Black male (Non-Hispanic Black), Hispanic Male, and Other Male (non-Hispanic White and other race/ethnicity groups) refer to MSW populations only.

The breakdown of model-predicted incidence closely resembles the breakdown of gonorrhea diagnoses reflecting the influence of the surveillance data on the model calibration. To get the breakdown of diagnoses in men by race/ethnicity (as gonorrhea diagnoses are not reported by sexual orientation), we assumed that for a given MSW race/ethnicity group, their share of diagnoses was: (1-M)*R/T, where M is the fraction reported to be MSM of male cases (in SSuN), T is total diagnosed infections in men that year, and R is the total diagnoses in men of a given race/ethnicity.

Table S2. Model-estimated prevalence, cumulative infections averted and additional tests after 5 years in **Baltimore.**
HR: coverage among high-activity population, LR: coverage among low-activity population.

Intervention	**Prevalence (after 5 years)**	**Incident Infections Averted Relative to the Base Case**	**Additional Tests Relative to the Base Case**
Base Case	Mean: 1.4% Median: 1.4% 95%CrI: 1.1%, 1.9%	NA	NA
15-24 Annual Screening	Mean: 0.7% Median: 0.7% 95%CrI: 0.5%, 0.9%	Mean: 3.1% Median: 2.9% 95%CrI: 1.4%, 5.4%	Mean: 6.7% Median: 6.7% 95%CrI: 5.1%, 8.7%
15-24 Twice-Annual Screening	Mean: 0.3% Median: 0.3% 95%CrI: 0.2%, 0.5%	Mean: 5.4% Median: 5.2% 95%CrI: 3.1%, 8.2%	Mean: 16.6% Median: 16.6% 95%CrI: 12.9%, 20.9%
Female 15-24 Annual Screening	Mean: 1.2% Median: 1.2% 95%CrI: 1.0%, 1.5%	Mean: 0.5% Median: 0.4% 95%CrI: 0.0%, 1.9%	Mean: 2.4% Median: 2.4% 95%CrI: 1.8%, 3.2%
Female 15-24 Twice-Annual Screening	Mean: 0.7% Median: 0.7% 95%CrI: 0.5%, 0.9%	Mean: 2.8% Median: 2.6% 95%CrI: 1.5%, 4.8%	Mean: 7.2% Median: 7.2% 95%CrI: 5.5%, 9.0%
MSM Annual Screening	Mean: 1.4% Median: 1.4% 95%CrI: 1.1%, 1.9%	Mean: -0.0% Median: -0.0% 95%CrI: -0.1%, 0.0%	Mean: 0.3% Median: 0.3% 95%CrI: 0.2%, 0.4%
MSM Twice-Annual Screening	Mean: 1.4% Median: 1.4% 95%CrI: 1.0%, 1.9%	Mean: -0.1% Median: -0.1% 95%CrI: -0.5%, 0.3%	Mean: 0.9% Median: 0.9% 95%CrI: 0.7%, 1.1%
MSM Quarter-Annual Screening	Mean: 1.3% Median: 1.3% 95%CrI: 1.0%, 1.8%	Mean: 0.1% Median: 0.1% 95%CrI: -1.1%, 1.2%	Mean: 2.1% Median: 2.1% 95%CrI: 1.6%, 2.6%
Mobile Outreach Testing, 20% HR, 13.33%	Mean: 1.1% Median: 1.1% 95%CrI: 0.9%, 1.4%	Mean: 2.6% Median: 2.5% 95%CrI: 1.4%, 4.5%	Mean: 3.8% Median: 3.7% 95%CrI: 2.6%, 5.8%
Mobile Outreach Testing, 40% HR, 11.11% LR	Mean: 1.0% Median: 1.0% 95%CrI: 0.7%, 1.3%	Mean: 3.5% Median: 3.3% 95%CrI: 2.0%, 5.8%	Mean: 3.8% Median: 3.7% 95%CrI: 2.6%, 5.8%
Mobile Outreach Testing, 50% HR, 10% LR	Mean: 0.9% Median: 0.9% 95%CrI: 0.7%, 1.2%	Mean: 3.9% Median: 3.7% 95%CrI: 2.3%, 6.3%	Mean: 3.8% Median: 3.7% 95%CrI: 2.6%, 5.8%
Remove 10% LTFU, 20% MSW	Mean: 1.2% Median: 1.2% 95%CrI: 0.9%, 1.7%	Mean: 0.7% Median: 0.7% 95%CrI: 0.4%, 1.2%	NA
Remove 10% LTFU	Mean: 1.3% Median: 1.3% 95%CrI: 0.9%, 1.7%	Mean: 0.5% Median: 0.5% 95%CrI: 0.3%, 0.9%	NA
Remove 20% LTFU	Mean: 1.1% Median: 1.1% 95%CrI: 0.8%, 1.5%	Mean: 1.1% Median: 1.1% 95%CrI: 0.6%, 1.8%	NA

Table S3. Model-estimated prevalence, cumulative infections averted and additional tests after 5 years in San Francisco.
HR: coverage among high-activity population, LR: coverage among low-activity population.

Intervention	**Prevalence (after 5 years)**	**Incident Infections Averted Relative to the Base Case**	**Additional Tests Relative to the Base Case**
Base Case	Mean: 1.2% Median: 1.1% 95%CrI: 0.9%, 1.7%	NA	NA
15-24 Annual Screening	Mean: 1.0% Median: 1.0% 95%CrI: 0.8%, 1.5%	Mean: 0.7% Median: 0.6% 95%CrI: 0.2%, 1.9%	Mean: 4.3% Median: 4.1% 95%CrI: 3.0%, 6.1%
15-24 Twice-Annual Screening	Mean: 0.8% Median: 0.8% 95%CrI: 0.6%, 1.2%	Mean: 2.9% Median: 2.9% 95%CrI: 0.6%, 5.5%	Mean: 12.5% Median: 12.1% 95%CrI: 9.4%, 16.8%
Female 15-24 Annual Screening	Mean: 1.1% Median: 1.1% 95%CrI: 0.8%, 1.6%	Mean: 0.3% Median: 0.3% 95%CrI: 0.1%, 1.0%	Mean: 2.3% Median: 2.2% 95%CrI: 1.5%, 3.3%
Female 15-24 Twice-Annual Screening	Mean: 1.0% Median: 1.0% 95%CrI: 0.7%, 1.4%	Mean: 1.2% Median: 1.1% 95%CrI: 0.4%, 2.6%	Mean: 6.4% Median: 6.2% 95%CrI: 4.7%, 8.7%
MSM Annual Screening	Mean: 1.1% Median: 1.1% 95%CrI: 0.8%, 1.6%	Mean: 0.2% Median: 0.1% 95%CrI: 0.0%, 0.8%	Mean: 1.1% Median: 1.0% 95%CrI: 0.6%, 1.6%
MSM Twice-Annual Screening	Mean: 0.7% Median: 0.7% 95%CrI: 0.4%, 1.2%	Mean: 5.1% Median: 5.3% 95%CrI: -0.2%, 9.1%	Mean: 3.5% Median: 3.4% 95%CrI: 2.6%, 4.7%
MSM Quarter-Annual Screening	Mean: 0.5% Median: 0.4% 95%CrI: 0.2%, 1.0%	Mean: 10.8% Median: 11.1% 95%CrI: 1.2%, 17.8%	Mean: 8.3% Median: 8.2% 95%CrI: 6.4%, 11.1%
Mobile Outreach Testing, 20% HR, 13.33%	Mean: 1.0% Median: 1.0% 95%CrI: 0.8%, 1.3%	Mean: 2.7% Median: 2.5% 95%CrI: 0.6%, 6.0%	Mean: 3.8% Median: 3.7% 95%CrI: 2.4%, 5.7%
Mobile Outreach Testing, 40% HR, 11.11% LR	Mean: 0.9% Median: 0.9% 95%CrI: 0.7%, 1.2%	Mean: 3.8% Median: 3.6% 95%CrI: 0.8%, 7.9%	Mean: 3.8% Median: 3.7% 95%CrI: 2.4%, 5.8%
Mobile Outreach Testing, 50% HR, 10% LR	Mean: 0.9% Median: 0.9% 95%CrI: 0.7%, 1.2%	Mean: 4.3% Median: 4.1% 95%CrI: 0.9%, 8.7%	Mean: 3.8% Median: 3.7% 95%CrI: 2.4%, 5.8%
Remove 10% LTFU, 20% MSW	Mean: 1.0% Median: 1.0% 95%CrI: 0.7%, 1.4%	Mean: 1.3% Median: 1.2% 95%CrI: 0.2%, 2.4%	NA
Remove 10% LTFU	Mean: 1.0% Median: 1.0% 95%CrI: 0.8%, 1.5%	Mean: 1.0% Median: 1.0% 95%CrI: 0.1%, 1.7%	NA
Remove 20% LTFU	Mean: 0.9% Median: 0.9% 95%CrI: 0.7%, 1.3%	Mean: 2.1% Median: 2.1% 95%CrI: 0.2%, 3.8%	NA

Sensitivity analysis on the population-level impact of increasing screening for MSM

There is uncertainty in what impact screening of MSM has at population-level particularly given the limited data available. We aimed to better understand how screening at different levels impacted the transmission dynamics of the total model population.

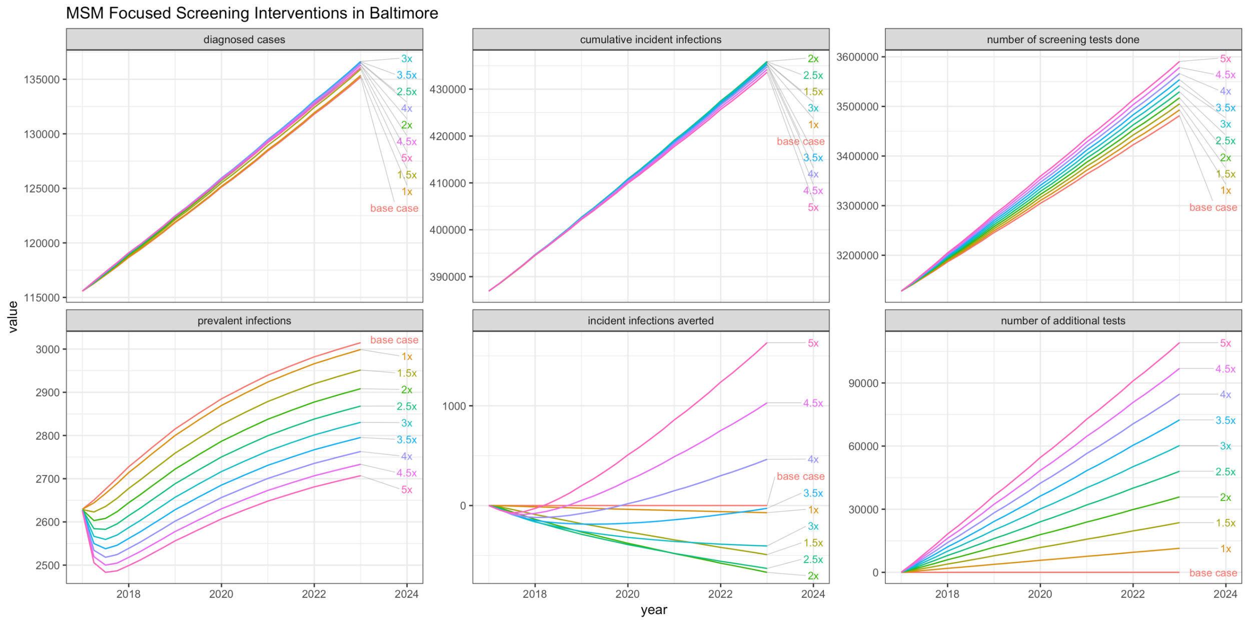
Figures S2 and S3 demonstrate the impact of increasing screening frequency in MSM from 1 per year to 5 times per year. When the rate of recovery is increased via screening in a population with high force of infection, the newly susceptible individuals get rapidly re-infected. Therefore, reducing duration of infection via screening can result in lower prevalence but more infections acquired, as presented for Baltimore in Figure S3.

In Baltimore, MSM are a small proportion (4%[1]) of the population with gonorrhea transmission still sustained in other populations when screening is increased only among MSM. Only when screening frequency is at very high intensity, do we estimate that there may be infections averted at population level (Figure S2), but even then there is substantive uncertainty in population-level outcomes with simulations spread between infections averted and infections acquired compared to the calibrated base case model.

Conversely, in San Francisco, MSM form a larger proportion of the total population (18.5%[1]), and they have the largest burden of incident gonococcal infections (Figure S1). When screening is increased in MSM in San Francisco, this targets majority of the population with gonorrhea infection, and population-level benefits are observed even when the screening frequency is only modestly above that estimated in the calibrated base case model.

Figure S2. Sensitivity analysis of the impact of screening MSM. Interventions vary screening from once-a-year (1x) to 5-times-a-year (5x). Outputs examined are cumulative infections averted (y-axis) and cumulative number of additional tests needed compared to base case (calibrated model) over the five-year intervention period. Each simulation is presented as a point on the scatter plot with mean of the scenarios presented as black circles.

A) Baltimore



B) San Francisco

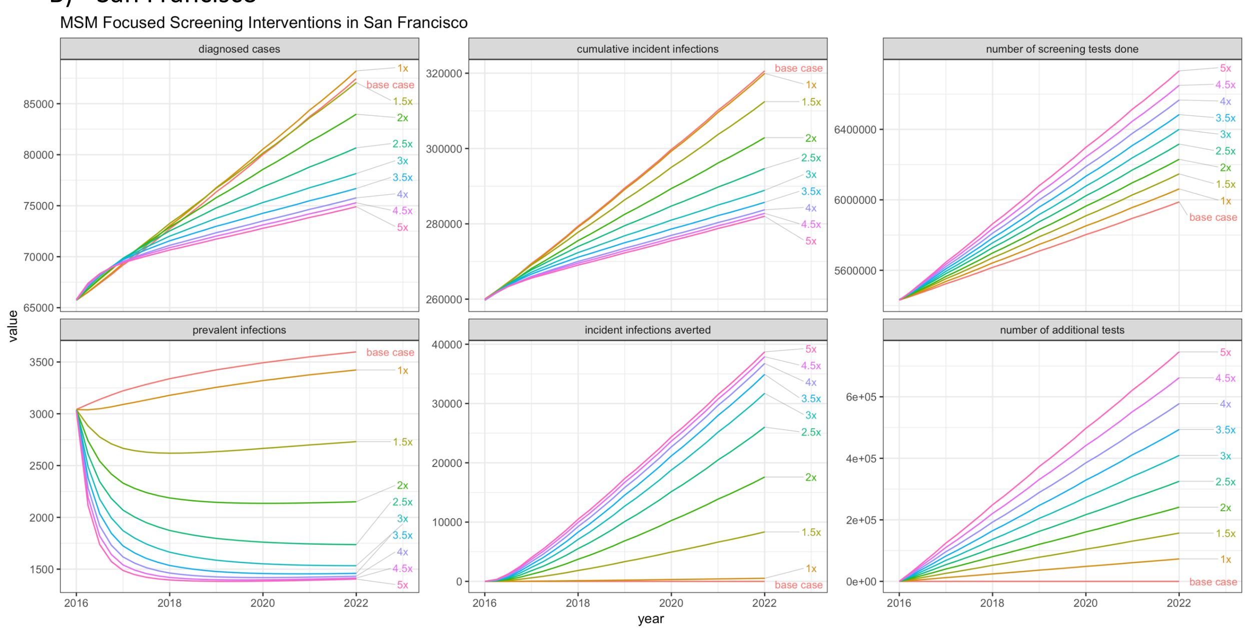


Figure S3. Sensitivity analysis of the impact of screening MSM among the total population. Interventions vary screening from once-a-year (1x) to 5-times-a-year (5x). Outputs examined are model-estimated mean of diagnosed infections, cumulative infections, number of screening tests done, prevalence, infections averted and number of additional tests needed compared to base case. The numbers presented as absolute, or absolute difference (where comparison to base case is made). Note that the y-axis does not start at zero in all the panels.

Sensitivity analysis for the mobile outreach testing

We examined the impact of lower uptake of screening among high-activity population (those with the highest partner change rate), while maintaining the overall additional number of tests similar across the analyses. Reduction in uptake among high-activity population screened reduces the overall impact of the intervention.

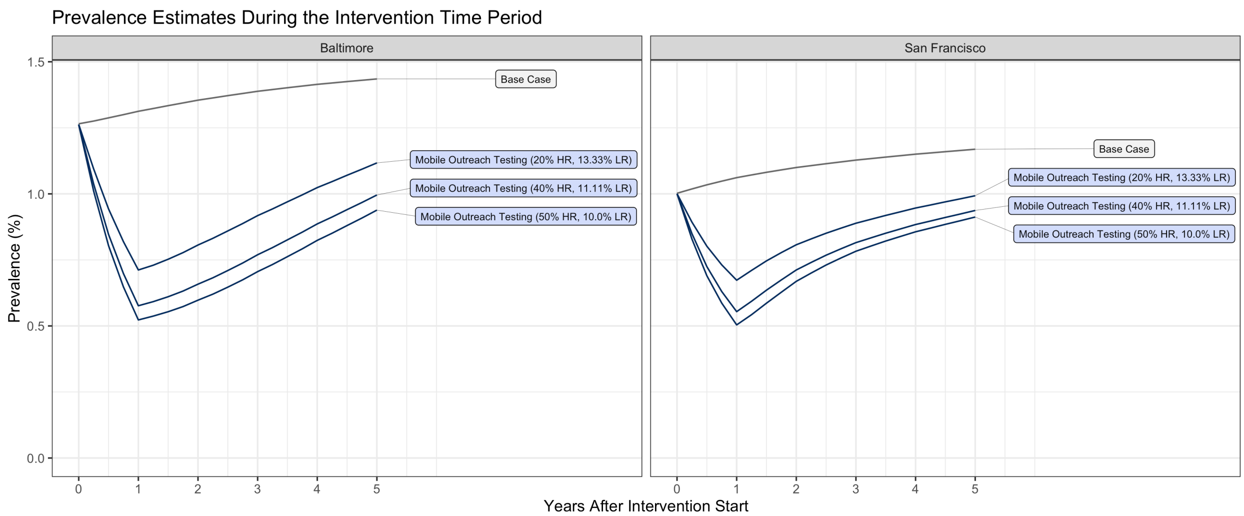


Figure S4. Population prevalence estimates per 100 persons during the intervention period, presented as the mean of the calibrated model (base case) and for the counterfactual mobile outreach interventions.

Footnote: HR: coverage among high-activity population, LR: coverage among low-activity population.

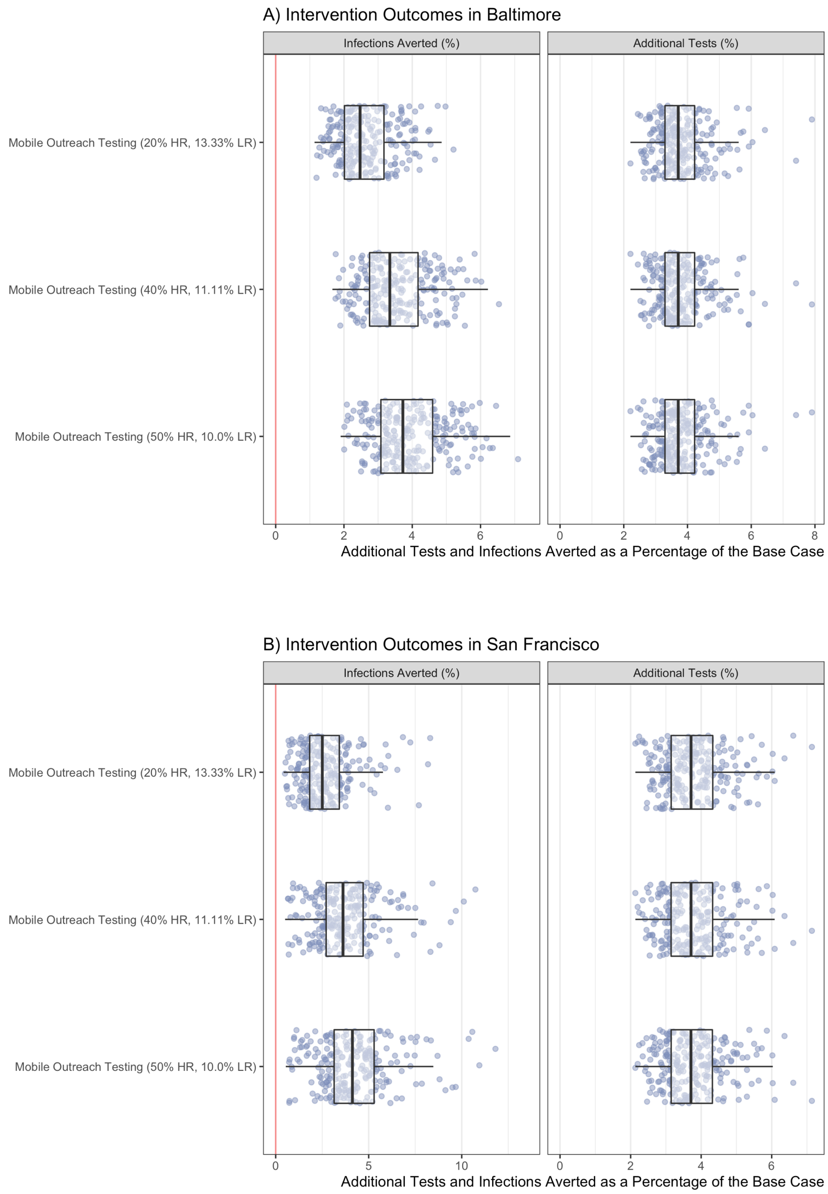


Figure S5. Cumulative infections averted and additional tests relative to the calibrated model (%) for the population in A) Baltimore City and B) San Francisco for the 5-year time period.

Footnote: Scatter plot presents a sample of 250 model simulations to display the underlying distribution. Boxplot use the full 1000 simulations.
HR: coverage among high-activity population, LR: coverage among low-activity population.

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