

screening, which can be used by commissioners to evaluate and plan their local service provision. The model and an analysis of national data have been recently published in *BMJ*. Increasingly, financial constraints will mean that tools such as ours will be vital to provide value for money in healthcare.

Method We will give a live demonstration of our spreadsheet model using the example from our recent study. We invite delegates to input their own data in real time to a laptop for comparison and testing against the national and international picture. We plan to promote this before the meeting.

Main outcome measures Cost effectiveness of screening (as cost per individual tested, cost per positive diagnosis, total cost of screening, number screened, number infected, sex ratio of those tested and treated). We will show how to compare current programmes with a planned change eg, in screening coverage or partner notification efficacy.

Results In 2008–2009 screening was estimated to cost £46.3 m and £506 per infection treated. The model results suggest that increasing male screening coverage from 8% to 24% (to match female coverage) would cost an extra £22.9 m and increase the cost per infection treated to £528. Increasing partner notification efficacy from 0.4 to 0.8 partners per index case would cost an extra £3.3 m and reduce the cost per infection diagnosed to £449.

Conclusions The results are broadly representative of the national picture, but further evaluation of the cost effectiveness of partner notification and screening is urgently needed. We encourage practitioners who want to test this tool in their own setting to contact us (katy.turner@bristol.ac.uk). *BMJ* 2011; 342:c7250 10.1136/bmj.c7250.

P1-S4.18

USING MATHEMATICAL MODELLING TO INVESTIGATE THE ROLE OF THE HIDDEN "POPULATION OF MEN WHO HAVE SEX WITH MEN (MSM) ON THE HIV EPIDEMIC IN SOUTHERN INDIA"

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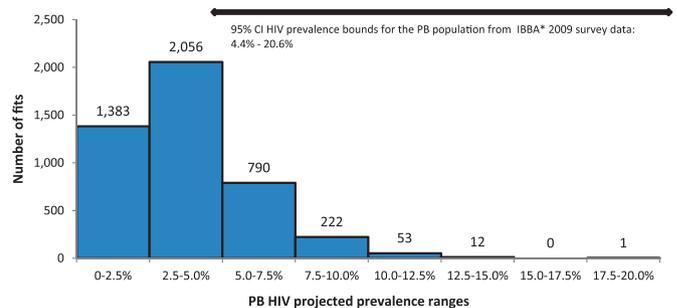
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Background Biological and behavioural data for men who have sex with men (MSM) in Bangalore, Karnataka, India, have mainly been collected from sites where commercial sex is prevalent. Consequently, the survey data may fail to capture the behaviour of a larger lower-risk "hidden" MSM population. Mathematical modelling is used to explore the potential bias in the survey data and better quantify the characteristics of this hidden population.

Methods A dynamic model of HIV transmission among MSM was developed and parameterised using detailed data* from high risk MSM in urban Bangalore. The MSM were categorised into three subgroups: Kothi and Hijra (KH): who mostly take the receptive role in anal sex, Panthis and Bisexuals (PB) who are predominantly insertive partners and Double Deckers (DD) who take both roles. Due to the sampling methods used, it was thought the MSM survey data were more representative of KH and DD than PB, although the extent of this bias is unknown. Therefore, no fitting constraint was applied to the PB HIV prevalence and instead the model was used to explore what PB HIV prevalence values are projected if the model was only fit to the 95% CIs of the prevalence data for KH and DD. One million randomly sampled model simulations were undertaken to find model fits.

Results Abstract P1-S4.18 figure 1 shows that, although the model can produce HIV prevalence estimates consistent with the survey estimates, overall the model projections suggest a lower PB HIV

prevalence is more consistent with the survey estimates for KH and DD. In addition, 80% of the model fits to the KH and DD HIV prevalence data had a sampled frequency of sex acts for PB in the lower half of the uncertainty interval suggesting PB's sexual activity may be lower than the median reported in the MSM survey. As expected, an inverse relationship occurs between PB population size and their level of sexual activity, with the median PB population size being 55 400 (2.7% of the total urban male population) and varying between 28 000 and 73 000 (1.5 to 3.9% of the total urban male population) for the IQR of the model fits. Conclusions: Survey data imply MSM are a small, highly active group, many of whom regularly sell sex, have very high numbers of partners and typically take the receptive role. As demonstrated here, modelling can be used to provide insights into the likely HIV prevalence, population size and sexual activity of hidden "MSM not reached in surveys."



Abstract P1-S4.18 Figure 1 Number and range of projected HIV prevalence estimates for the PB population (from the model fits to KH and DD data. *Integrated biological and behavioural assessment (IBBA) 2009, collected within the monitoring and evaluation of Avahan, the India AIDS initiative.

P1-S4.19

STOCHASTIC NETWORK MODELS

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Background We present a general modelling scheme particularly adapted for the epidemiology of sexually transmitted infections. Emphasis is placed on the complex interaction structure of the population and on the probabilistic nature of the dynamics.

Methods We represent the interaction structure of the population with complex network models. Markov Stochastic Processes are used to consider the probabilistic time evolution of both the network structure and the epidemiological state of the population. Idealised epidemiological problems are considered: they are qualitatively inspired by real-world systems but no actual real-world data is fed to the models. All analytical results are systematically validated through Monte Carlo numerical simulations.

Results By dedicating compartments to individuals with both similar epidemiological states and similar contact patterns, we observe great agreement between analytical results and Monte Carlo simulations see Abstract P1-S4.19 Figure 1. This is a special case of the general observation that compartmental models perform better when individuals within each compartment are very similar among themselves. Explicit examples are given for contact patterns changing through time as well as for the interactions of different infections in the same population.

Conclusions By specifying the structure of the population through its local features, we successfully model the probabilistic evolution of complex epidemiological systems. Infection stages and/or behavioural groups are considered the same way they are in "classical" compartmental models. The generality of the approach facilitates its application to a vast array of epidemiological phenomena.