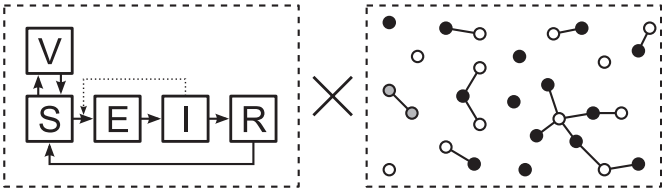

Abstract P1-S4.19 Figure 1 Epidemiology on networks.

P1-S4.20 MATHEMATICAL MODELLING OF HIV TRANSMISSION AND CONTROL AMONG MEN WHO HAVE SEX WITH MEN: A REVIEW OF 25 YEARS OF LITERATURE

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Background For a quarter of century, mathematical models have been used to study the spread and control of HIV among men who have sex with men (MSM). We reviewed this literature to summarise the methodologies used, key model developments, and recommended strategies for HIV control among MSM.
Methods Review of the literature on dynamic compartmental models of HIV transmission among MSM was conducted. MEDLINE/EMBASE were searched from earliest date to end 2010.
Results Of 742 studies identified, 127 studies met the inclusion criteria and were selected for review. Most studies employed deterministic methods (80%), and potentially as a result of this, as the complexity of models increased over time with respect to antiretroviral therapy (ART), there was a marked decline in the complexity of models with respect to sexual activity. Only a small proportion of models were fitted to data (22%) and even fewer were validated (17%), somewhat reducing confidence in the findings from these studies. That said, a number of common findings emerged, including (1) the importance of assumed changes in infectivity and sexual contact rates on the impact of ART on HIV incidence, and that this led to follow-up empirical studies to gather these data, and (2) the recommendation that multiple strategies would be required for effective HIV control among MSM.
Conclusions Mathematical models have been useful in indentifying key empirical studies and for showing that multiple prevention strategies would be required for effective control of HIV epidemics in MSM. The lack of model fitting and validation emphasise that this area should be targeted for developments in the future. An improved methodology for parameter estimation will help generate predictions that more fully express uncertainty, allowing more informed public heath decision making.

P1-S4.21 CALIBRATION OF AN INDIVIDUAL-BASED MODEL OF STI TRANSMISSION IN UGANDA: A NOVEL ABC-BAYESIAN EMULATION HYBRID APPROACH

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Introduction The complexity of dynamic epidemic systems has led to the use of large-scale stochastic models for prediction purposes. However, methods for robustly calibrating and analysing these models can be prohibitively inefficient. We propose an algorithm for fitting complex models that incorporates elements of both Approximate Bayesian Computation (ABC) and Bayesian Emulation. ABC enables inference about model parameters without needing to calculate a likelihood function, by generating approximations from repeated model runs. However, each model run might take hours. Emulation methods are being developed in the fields of cosmology and meteorological modelling. The complex model function is summarised as an "emulator": a stochastic function that represents global behaviour of the function as a linear regression model and local deviations from this behaviour as Gaussian processes. The emulator acts as a cheap proxy for the complex model, allowing both calibration and sensitivity analysis to be conducted in a fraction of the time.
Methods We report the initial application of an emulation-based calibration algorithm to an individual-based stochastic model of STI transmission in Uganda. Starting with uninformative priors for 19 behavioural and biological input parameters, we "trained" an emulator with 200 sampled parameter sets and their corresponding model output (point estimates of HIV prevalence). Sampling a further 10 000 parameter sets from the priors, we used the emulator to make output predictions over a large area of input parameter space. Weighting each parameter set by goodness of fit to observed data, we identified promising areas of parameter space for complex model evaluation. A more accurate emulator was then trained, incorporating this additional complex model output. The process was repeated as in sequential ABC methods.
Results The use of emulators allowed evaluation of large areas of parameter space due to increased computational efficiency. Processing time for one prevalence point estimate was reduced from over 15 min on an HPC cluster to less than 0.1 s on a PC. Even the first two waves of such an algorithm provided helpful insight into the most influential parameters.
Conclusions The development of an ABC—Bayesian Emulation hybrid approach to complex model calibration is promising. Emulators offer large advantages in computational efficiency. However, further research is needed regarding weighting, tolerance levels and covariance.

P1-S4.22 IMPACT OF A HYPOTHETICAL CHLAMYDIA VACCINE ON POPULATION PREVALENCE: A MATHEMATICAL MODELLING STUDY

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Background It has not yet been possible to develop a *Chlamydia trachomatis* (chlamydia) vaccine but research to achieve this continues. It is therefore important to evaluate the potential impact of different chlamydia vaccine strategies on population prevalence. The optimal strategy might differ depending on whether a vaccine prevents chlamydia infection, or prevents ascending infection to reduce the risk of long term complications. Here, we used a mathematical model to focus on vaccination strategies that aim to reduce population prevalence.
Methods We developed a deterministic pair model of heterosexuals aged 15–39 years that incorporates the formation and dissolution of sexual partnerships. We used sexual behavioural data from UK population-based studies to inform the model. The model has a baseline chlamydia prevalence of 3%. In all strategies examined, vaccination was introduced before sexual debut. We investigated the impact on population prevalence of different types of vaccine coverage, vaccine efficacy and duration of protection. We also assumed different types of protection after vaccination. We started with full protection, but since animal models have shown that sterilising immunity is difficult to achieve we also investigated partial protection of the vaccine by assuming a decreased susceptibility to infection after vaccination or, when infected, a shorter duration of infection or a reduced transmission probability.

Results The impact of different vaccination strategies on chlamydia population prevalence depends on the characteristics of the vaccine. In the best case scenario, where the vaccine coverage and efficacy is 100% and duration of protection lifelong, it takes about 7 years to half the prevalence. With an average duration of protection of 10 years, a vaccine coverage or vaccine efficacy of around 70% or higher per year was needed to half the chlamydia prevalence in 10 years. For high vaccine coverage levels, the impact of vaccinating women alone on population prevalence was greater than vaccinating both men and women. The potential impact of a vaccine on chlamydia population prevalence was sensitive to the duration of protection of the vaccine and the vaccine efficacy.
Conclusion The model suggests that the impact of vaccination strategies on chlamydia prevalence highly depends on characteristics of future vaccines. Current efforts in vaccine development should be accompanied by mathematical models to investigate the optimal strategies.

P1-S4.23 DESCRIBING THE PROGRESSION FROM *CHLAMYDIA TRACHOMATIS* TO PELVIC INFLAMMATORY DISEASE: SYSTEMATIC REVIEW OF MATHEMATICAL MODELS

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Background *Chlamydia trachomatis* (chlamydia) is an important cause of pelvic inflammatory disease (PID). Preventing PID is a main objective of chlamydia screening. There are many uncertainties about how and when bacteria spread from lower to upper genital tract. The potential impact of screening and treatment, which could interrupt ascending infection, might be affected by the timing of development of PID. Models are often used to investigate the potential impact of screening strategies on PID and should therefore include information about the timing of progression. We conducted a systematic review to determine how the progression from chlamydia to PID is described in mathematical models.
Methods We searched four electronic databases using search terms related to mathematical models and PID from the earliest date to 19 October 2009 without language restrictions. Eligible publications included progression from chlamydia to PID either using a decision tree or a mathematical model. We extracted information about how authors conceptualised the dynamics of chlamydia infection and the development of PID, and assumptions about rates of progression.
Results We identified 41 unique publications about chlamydia infection; 28 of these included PID in a static decision tree. The average percentage of women developing PID in decision analyses was 22.9% (range 10–35%, n=26). For five publications it was not clear how the described model worked. The other eight publications described progression from chlamydia infection to PID dynamically. Of these, two models incorporated PID as a state in a Markov-chain model, four used compartmental models and two used individual-based models. Explicit statements about model structure included the possibility that PID can occur uniformly during a woman's infection, that tubal damage occurs in the second half of the chlamydia infection, and that the model had the ability to vary PID development time. Twenty-eight publications did not mention the stage during a chlamydia infection that progression to PID happens.
Conclusion Most modelling studies do not consider dynamic aspects of *C trachomatis* transmission and the timing of progression to PID. The mechanisms proposed in studies that made explicit statements could be compared to examine the impact of screening. We suggest that explicit statements about the timing and rates of progression would help improve understanding of the pathogenesis of chlamydial complications and the potential effects of screening.

P1-S4.24 BALANCING THE "SUPPLY AND DEMAND" OF SEX ACTS: IMPLICATIONS FOR MODELLING THE HIV EPIDEMIC AMONG MEN WHO HAVE SEX WITH MEN IN SOUTHERN INDIA

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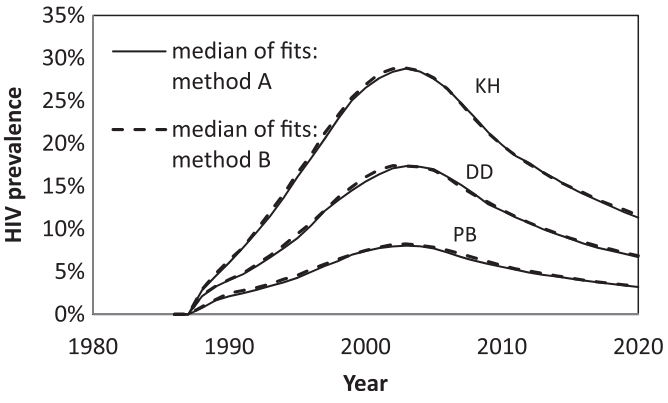
Background In India, men who have sex with men (MSM) have distinct identities related to the role taken in anal sex (Panthi/Bisexual (PB): mostly insertive, Kothi/Hijra (KH): mostly receptive, Double Deckers: both). Wide discrepancies are found between the supply and demand for sex acts estimated for each group using data on reported frequency of anal sex, role taken and estimated group population sizes.
Methods Two methods for balancing the number and type of sex acts between different groups were compared. They were used in a deterministic HIV transmission model to estimate mixing patterns and HIV prevalence over the first 20 years of the epidemic (including reported condom use trends) and a subsequent 10-year intervention (10% absolute increase in condom use). Data collected from Bangalore for the evaluation of Avahan (the India AIDS initiative) on the mean reported frequency of sex acts per individual, role taken in anal sex and population sizes for each group were used to construct a mixing matrix. In method A, the PB group size was set to balance the total number of insertive and receptive acts, and receptive acts for each group were distributed among the three groups in proportion to the number of insertive acts offered. In method B, the proportion of receptive acts KH had with other KH was an additional input parameter, with remaining receptive acts distributed as in method A. The number and type of contacts for all groups were adjusted to achieve balancing. The model was run using 300 000 randomly sampled parameter sets drawn from the data and multiple fits were found to group-specific HIV prevalence data.
Results Model fits for method B had more assortative (like-with-like) mixing than method A, particularly for PB (median number of acts PB have with other PB: 48.5% (IQR 33.3–63.3%) in A, 63.3% (IQR 47.3–74.1%) in B), related to larger PB group sizes and PB taking the insertive role less often in B. Despite these differences, the fitted epidemic curves were very similar for all three groups across the two methods (Absrtact P1-S4.24 figure 1), as was the predicted



Abstract P1-S4.24 Figure 1 MSM.