Modeling the Impact of Post-Diagnosis Behavior Change on HIV Prevalence in Southern California Men who have Sex with Men (MSM)

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Running Head

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Abstract

Our objective is to demonstrate the population level effects of individual-level post-diagnosis behavior change (PDBC) in Southern Californian men who have sex with men (MSM) recently diagnosed with HIV. While PDBC has been empirically documented, the population-level effects of such behavior change are largely unknown. We use behavioral data from the Southern California Acute Infection and Early Disease Research Program (AIEDRP) and biological data from a number of published sources. We create network models derived from the exponential random graph model (ERGM) family. Our models incorporate vital processes of birth, death, and aging, and other related epidemiological processes, namely, circumcision-status, testing behavior, treatment, methamphetamine use, diagnosis status, partnership types, viral load, and sexual role. We find that without PDBC HIV prevalence among MSM would be significantly higher at any reasonable frequency of testing. We also demonstrate that cross-sectional data cannot capture the effects of PDBC and longitudinal data are needed.

Keywords: Post-Diagnosis Behavior Change, Men who have Sex with Men (MSM), HIV Modeling, Exponential Random Graph Models (ERGMs)

Introduction

Men who have sex with men (MSM) form one of the highest risk groups for HIV in the United States [1, 2], with roughly half of new infections occurring in this population [3] . The CDC estimated the prevalence of HIV in the MSM community in 2008 was 19% [3].

Recent longitudinal studies have found that MSM reduce risky sexual activity [4, 5, 6] upon HIV diagnosis. It seems likely that such post-diagnosis behavior change (PDBC) occurs on account of a desire in the MSM community to protect one's partners [7]. Such "community-initiated" [7] strategies may have much potential for prevention of new infections. However, a review of cross-sectional studies found that MSM diagnosed as HIV-infected practice a high level of risky sexual activity [8]. Another cross-sectional study found an increase in condom use and/or abstinence among MSM, but that a high proportion of those who reported anal intercourse still reported no condom use [9]. Given the cross-sectional nature of the studies in this review, it is difficult to assess the change in level of risky sexual activity upon diagnosis.

The timing, extent and heterogeneity in reduction of risky sex on account of behavior change are questions that are still being investigated by the scientific community. However, even short-term reductions among recently HIV diagnosed individuals can be highly effective in reducing onward transmission events especially since recently diagnosed individuals may be in (or not far removed from) the stage of acute infection when viral loads are very high and patients are likely to be highly infectious [10]. If behavior change to reduce risk of onward transmission occurs when individuals are most infectious, its preventive potential may be maximized. However, other papers in the literature question the effectiveness of risk-reduction approaches that men undertake and emphasize the "urgent" importance of public health messages around the effectiveness of such strategies [11].

In this paper we use mathematical models to demonstrate the impact of PDBC (of recently diagnosed MSM) on overall HIV prevalence in Southern Californian MSM when the natural history of HIV infection and behavior-change of recently diagnosed MSM are taken

into account. We also demonstrate that while levels of risky sexual behavior (defined in this work as unprotected anal intercourse, henceforth UAI) in diagnosed people may be higher than in undiagnosed people, PDBC is a temporal phenomenon that shows individual-level *change* in behavior following diagnosis. This finding suggests that cross-sectional data cannot capture the effects of PDBC and longitudinal data are needed. We end with a discussion on using PDBC as a preventive tool. We thus employ novel modeling tools in this paper to address questions of immediate public health relevance.

Background

Southern California is a populous and racially diverse area of the United States. The cities of Los Angeles (LA) and San Diego (SD), and their respective counties, are major population centers of this region. The HIV epidemic here is large – Los Angeles County (LAC) is home to 29% of the population of California [12], but is estimated to contain 41% of new HIV cases, and 76% of all AIDS cases in the state [13].

Sexual contact in MSM is estimated to account for 71.4% of the cumulative HIV cases in California males between 1983 and 2005 [2]. Of the 40,000 persons living with HIV and AIDS (PLWHA) in LA County at the end of 2009, 88% were male [14] and 72% of PLWHA were MSM [14]. We see similar trends of high prevalence among MSM in San Diego County; from 1985-2004 non-IDU MSM accounted for 79% of the HIV transmission events [15].

MSM have been shown to modify sexual behavior in the time following diagnosis, presumably with the goal of reducing risk of transmission to partners who are HIV-uninfected [5]. These modifications include reducing the number of sexual partners, especially casual ones [4, 5], reducing unprotected anal sex within partnerships [4, 5], and choosing partners with the same HIV status (serosorting) [4, 5]. Since transmission of HIV is more probable when the infected partner is insertive, rather than receptive [16], modifying sexual role in partnerships (sero-positioning) is another behavioral strategy MSM adopt to reduce transmission events [4, 5].

The use of methamphetamines – "meth" – has been relatively common among MSM since

at least the 1990's [17], and is especially common on the west coast of the United States [18]. Meth use is associated with behavioral disinhibition, multiple sexual partners, low rates of condom use, prolonged sexual activity, encounters with casual/anonymous partners [19] and low rates of adherence to HIV treatment regimens [20]. Thus MSM who use meth tend to have higher rates of risky sexual behavior than non-users, and meth use is an important covariate to consider in estimating population-level impacts of PDBC in this population.

MSM have multiple types of sexual contacts, ranging from stable main partnerships to casual, one-time contacts [4, 21]. Levels and patterns of PDBC appear to vary by partnership type [6], as may be expected, since the desire to protect one's partner would reasonably vary with levels of emotional intimacy.

In this work, we demonstrate the impact of PDBC on overall HIV prevalence in the population when the natural history of HIV infection and behavior of MSM are taken in to account. We explicitly model both main partnerships and casual contacts, and disaggregate behavioral patterns between meth users and non-users.

Methods

Overview

We create a dynamic, stochastic network simulation based in the exponential random graph modeling (ERGM) framework, parameterized using biological, behavioral and demographic data. The model structure closely follows that developed for the Prevention Umbrella for MSM in the Americas (PUMA) project, as do many of the biological parameters [22]. (We will refer to this modeling study as PUMA henceforth in this manuscript). Our model incorporates births, deaths, aging, treatment, circumcision status, testing behavior, meth use, diagnosis status and post-diagnosis behavior, change, partnership types, temporal overlap in partnerships, viral load, and sexual role.

Extensive detail on each component is included in the online appendix; summary data are below. The behavioral data are primarily from the behavioral sub-study of the Southern California Acute Infection and Early Disease Research Program (AIEDRP) study. Com-

plete details on the AIEDRP sub-study are elsewhere [4, 6]. Since treatment is an important component of HIV epidemiology in United States MSM, we adopted a basic model of treatment that accounts for race differentials as measured by the waiting time between onset of infection and commencement of treatment in accordance with clinical data from the University of Nebraska Medical Center [23] and as presented in PUMA [22]. In summary, newly diagnosed HIV positive men completed AIEDRP questionnaires at baseline. Follow-up information was collected by offering interviews every 3 months after initial enrollment. 193 respondents completed at least one follow-up survey. At baseline, respondents provided detailed information on their three most recent partners, and at follow-up, on the most recent partner, yielding a total of 1011 partner reports. Although multiple types of partnerships were stressed, for simplicity, we dichotomize these partnerships as "main" and "non-main"; the former category includes partners reported as main, the latter category includes all other partners (unknown, one-time, acquaintance, friend, regular, trade).

We use these data to create network models constructed using exponential random graph model framework (ERGMs, also called p^* in the literature). In their most basic form, ERGMs allow us to simulate cross-sectional networks (within stochastic variation) of a number of network features. These features are described in the form of statistics that may include various forms of dependence in the ties in the network. This capability is a major strength of the applicability of the ERGM framework to modeling the sexual partnerships since it allows us to capture temporal overlap in partnerships that classical compartmental methods for modeling HIV transmission cannot [24]. As in classical compartmental models, we are also able to account for various selection forces such as assortative mixing based on age, race and knowledge of HIV status. Separable Temporal ERGMs (known as STERGMS) [25] are an extension that allow us to model the network structure in a stochastically evolving dynamic network in a statistically principled fashion.

The ERGM framework is implemented using the **statnet** suite of packages [26] programmed in the **R** programming language.

Non Main Networks: Specification and Estimation

We model UAI contacts in non-main partnerships in our population as a series of cross-sectional networks. This network contains no duration information and consists only of statistics estimated from egocentric data (that provide detailed reports on the last three partners) that describe the network structure. We therefore model non-main partnerships using cross-sectional ERGMs.

The specific features of the network structure that we capture are the mean number of partnerships per person, levels of sexual activity, assortative mixing by age and race, and differential levels of activity of meth users and non-users. In this network, PDBC is modeled by considering two network features: a reduction in total UAI with non-main partners of diagnosed individuals and selective mixing by diagnosis status so that the number of ties between individuals of the same diagnosis status is greater than would be expected by chance.

Data for all of these features (except race mixing and meth use) are obtained from the AIEDRP study. While the AIEDRP study reports data on race mixing in MSM, these data were too sparse to adequately parameterize our models and therefore we use a study of MSM from a different city in California, namely San Francisco [27]. Note that we are not assuming that the race composition of San Francisco and LAC are the same, but rather, that the patterns of within and across-race mixing in the two settings is the same, conditional on the local composition.

The proportion of meth users in the AIEDRP sample is extremely high presumably because this is a sample of recent seroconverters. To use estimates more reflective of meth use in the population we are interested in (MSM in Southern California), we use data from a separate study that reports 11% of MSM recently diagnosed with AIDS in Los Angeles County have used meth in the past 12 months [28]. Our modeled population of 5000 men therefore has 550 meth users. These race composition of the set of these 550 meth users is identical to the the composition in AIEDRP.

Main Network: Specification and Estimation

The main network incorporates duration information in addition to information on network statistics measurable from egocentric cross-sectional data. Therefore, we use the STERGM class of models [25]. This approach preserves the following features (stochastically): the proportion of individuals who report 0, 1, or 2 ongoing main partnerships at a given time; the mean difference in the square roots of the ages of main partners; race mixing (as described above for non-main networks). As in the case of non-main networks, all statistics except race mixing are from AIEDRP, and race mixing is from the same study of MSM in San Francisco [27].

We model transmission of infection in the main network through UAI acts that occur on a given day (more details below). PDBC in the main network is modeled by considering a reduction in the daily probability of UAI in main partnerships that are discordant by diagnosis status. The daily probability of UAI in non-main partnerships is obtained through AIEDRP, but the daily probability of UAI in main partnerships discordant by diagnosis status is obtained from PUMA [22]. For main partnerships, the daily probability of UAI was not directly estimable from AIEDRP, therefore, we used this estimate as given in PUMA [22].

Components of Simulation

We create an initial population of 5000 MSM using a simulated annealing algorithm that approximates the network structural statistics estimated from our behavioral data sources. We randomly infect 19% of our population in accordance with recent estimates of HIV prevalence in United States MSM [3]. We then simulate our model forward in daily time steps, with each of the following steps:

1. Arrivals: Men enter our population at age 18, when they are untested for HIV, and are HIV-negative. We set the number of arrivals to have a population that grows slightly given a stable HIV epidemic.

2. Deaths/Departures: Non-HIV deaths follow US age-specific mortality rates derived from CDC life-tables [22]. AIDS-related deaths occur as a function of time since infec-

tion, treatment, and suppression history (see below). Individuals leave the population of interest at 65 years of age (the general upper limit for available behavioral data).

3. UAI in main partnerships: UAI events occur with a given probability on a particular day in accordance with parameters used in PUMA since these parameters are not directly estimable from AIEDRP (more details in the discussion). This daily probability is based on the relative sero-statuses of the two partners. In the non-main network, partnerships are UAI contacts on a particular day.

4. Transmission in main and non-main partnerships: Transmission of HIV occurs probabilistically in partnerships on days containing UAI events. This probability is a function of the viral load and circumcision status of the infected partner. We consider transmission only due to UAI, and ignore transmission due to other events such as oral intercourse, or needle sharing.

5. Update network: We then update the network by considering changes in population size due to births, deaths, and aging, formation and dissolution of main partnerships, formation of new non-main partnerships, and changes in other attributes of the nodes (viral load, infectivity, treatment status). Viral load is a function of time since infection and treatment status. Treatment initiation and patterns of suppression are set to match observed data for MSM populations in the United States. We also match epidemiological data on the proportion of HIV-infected and diagnosed individuals on treatment at any given point of time as presented in PUMA [22]. Details are in the appendix. We then repeat steps 4 and 5 over a 50 year period to allow the epidemic trajectory sufficient time to equilibrate.

Other biological and demographic processes that we model are explained in detail in the Online Appendix.

Modeling Post Diagnosis Behavior Change (PDBC)

To recap, we model the following mechanisms of PDBC:

1. Reduction in total number of non-main partnerships: We model a 25.6% reduction in mean degree of non-main partnerships upon diagnosis in accordance with AIEDRP data (as seen in Figure 1 of Gorbach et al.[6]) where the mean number of non-main partners is 8.37 in the three months prior to diagnosis, and 6.23 post-diagnosis, taking the mean over the four follow-up periods.

2. Selection of non-main partners by diagnosis status:

   AIEDRP data classify the HIV status of partners as positive, negative or unknown. We reclassify the unknown parters as positive or negative according to the proportion of HIV positives in the population nationally.

   Then, to account for selective mixing by diagnosis status, we model an approximate reduction of 40% (with stochastic variation) in the proportion of discordant non-main ties compared to the number expected if there was proportional mixing by diagnosis status. The precise extent of this reduction depends on the precise number that are infected at the start of any given simulation (drawn from a binomial distribution) and this number varies slightly due to the stochasticity of the process. A given proportion of these infecteds are then classified as diagnosed, which itself is a Bernoulli process (and the precise number is again stochastically variable).

3. UAI in Main Partnerships: Within main partnerships, we model a reduction in daily probability of UAI from 0.156 to 0.109. As explained above, the former is obtained from AIEDRP data and the latter is from PUMA [22].

In this work, we do not model sero-positioning as a risk reduction strategy.

Counter-Factual Models

We explore counter-factual models that vary from the baseline models by modeling no reduction in total number of non-main partners upon diagnosis, proportional mixing by diagnosis status in non-main partnerships, and the same daily probability of UAI within negatively concordant and discordant (by diagnosis status) main partnerships.

Parameters from the AIEDRP follow-up data represent the behavior of diagnosed men. Therefore, our base scenario that models PDBC includes parameters from both baseline and follow-up data-sets. The counterfactual that does not incorporate PDBC includes information only collected at baseline to capture the behavior of undiagnosed men.

Sensitivity Analysis

Our base model parameterized testing frequency using studies containing self-reports of the time since last test for negative men from a study of MSM in clinics in four major US Cities [29]. The study reports a median inter-test interval of 243 days [29]. If we assume a simple exponential waiting time distribution for the time till test, this statistic corresponds to median inter-test interval of 351 days. Our models indicate that at this level of testing, about 95% of infected MSM are aware of their status (at steady state).

Other studies have reported different summary metrics on testing and awareness, e.g. the proportion of HIV-positive men in a given setting who are aware of their status. For instance, based on NHBS data, the CDC reported that about 44% of infected MSM nationally are not aware of their status [3]. Our models indicate that to obtain this level of awareness of infection, the testing rate has to be extremely low (slightly less than an average of one test per year).

These different summary metrics may generate very different pictures of testing and awareness, even when they come from the same study. Indeed, our dynamic models suggest that these two figures are incompatible with one another; it is not possible for testing frequencies to be that high and status awareness to be that low. Multiple explanations for this discrepancy exists (see the discussion). Since we cannot ascertain which is correct, we instead conducted a sensitivity analysis in which we varied the mean testing frequency, which in turn led to different proportions of the HIV+ population being aware of their status in the long run. We experimented with two main scenarios:

1. "Testing Frequency" (Baseline Models): In this setting we assume that men test once every 351 days on average in accordance with clinical data from Helms et al.[29].

2. "Level of Awareness": Here we assume that the proportion of HIV-positive MSM who are aware of their status as reported by the CDC (56%) is correct [3]. We experimented with scenarios iteratively in order to obtain the mean testing frequency that results in about 55-60% awareness of infection at equilibrium.

We repeated each experiment ten times. We then ran additional simulations in between these values, and varied the average testing rate between two times every ten years and ten times every years (at increments of two tests per ten years) to compare the difference in prevalence in counterfactuals that exclude and include PDBC, relative to the case that includes PDBC.

Results

Figure 1 shows a comparison of prevalences in the baseline testing frequency models with and without PDBC. We see that final equilibrium prevalence when PDBC is accounted for is 31.9% (averaged over 10 repetitions) and 41.7% when there is no PDBC. Thus, prevalences would be higher by close to a third (30.6%) without PDBC given our baseline models. With testing at this frequency, our model suggests that approximately 94.8% of HIV-positive men would be aware of their status at the steady-state.

In contrast, under the level of awareness model (Figure 2), the effects of PDBC are much smaller: the mean equilibrium prevalence (over 10 repetitions of the experiment) with and without PDBC is 44.5% and 45.3% respectively. Recall that to reduce the level of awareness, we had to assume that the average testing frequency in this model is slightly less than once every 10 years (one test every 4000 days, or 10.9 years). The mean proportions of those infected who are aware of their infection-status in the cases with and without PDBC are 62.3% and 62.9% respectively.

Since these two models yield strongly different results, and have such different assumptions, we investigated various scenarios with average rates of testing in between the two extremes of the testing frequency and level of awareness cases. In Figure 3 we see that even at an average of two tests every ten years, the equilibrium prevalence without PDBC is

15.2% higher than when PDBC is accounted for.

Note that the prevalences we see in this paper are higher than national estimates for MSM, since our baseline model is parameterized by the behavior of men just before seroconversion. We discuss implications below.

We compare the mean number of non-main partners per person (mean degree) of diagnosed and undiagnosed (includes true negatives and undiagnosed positives) in Figure 4. We see that both "testing frequency" and "level of awareness" models show diagnosed individuals have greater number of non-main partners per individual than undiagnosed individuals.

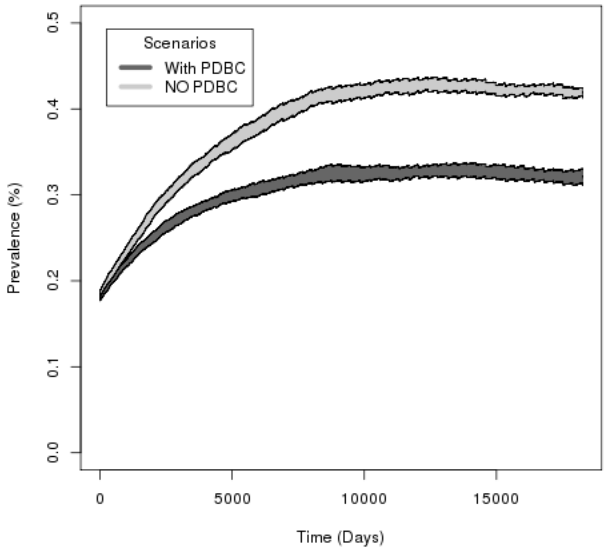

Figure 1: HIV Prevalence in two different scenarios with and without post-diagnosis behavior change (PDBC) in the baseline "testing-frequency" models. The shaded areas corresponds to 95% confidence regions.

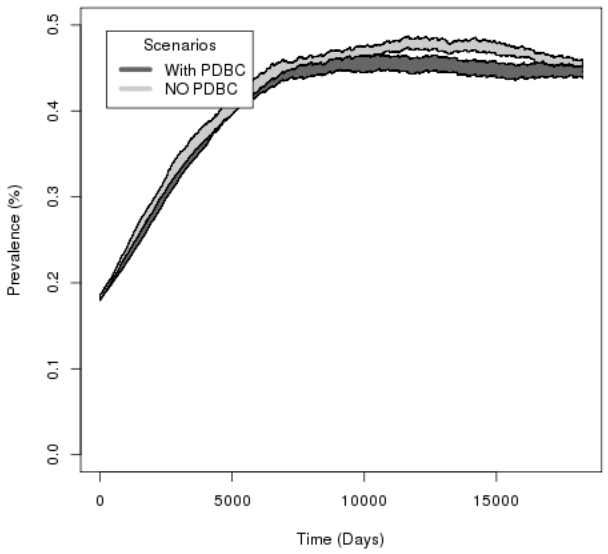

Figure 2: HIV Prevalence in two different scenarios with and without post-diagnosis behavior change (PDBC) in the "level of awareness" Models. The shaded area corresponds to 95% confidence regions.

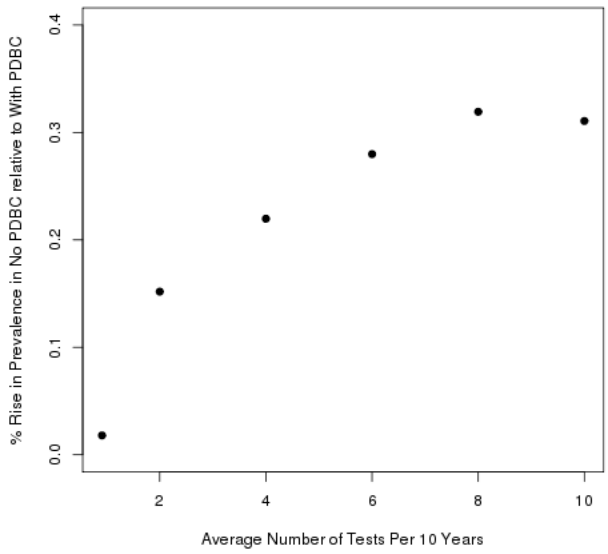

Figure 3: Ratio of difference in equilibrium prevalence between the "No PDBC" and "With PDBC" cases to the equilibrium prevalence in the "With PDBC" case.

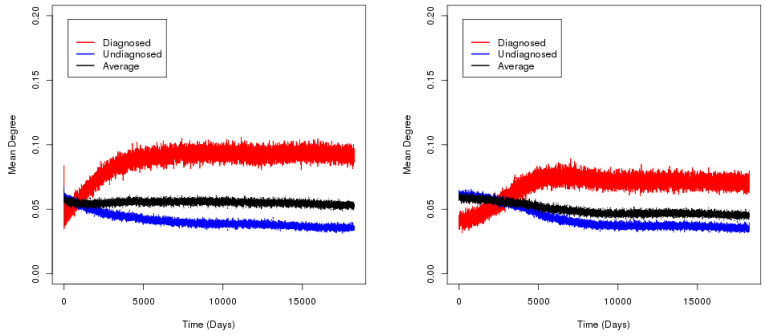

Figure 4: Mean degrees of diagnosed and undiagnosed men, and average mean degrees in the "testing frequency" (left figure) and "level of awareness" (right figure) cases when we account for PDBC. Mean Degree is the mean number of non-main partners per individual. Undiagnosed includes true negatives and positive but undiagnosed. Results presented are averaged over 10 experimental repetitions.

Table 1: Proportion of infected individuals who are diagnosed early for the intermediate cases shown in Figure 3 with and without PDBC. The column on the left gives the average number of tests every 10 years, and the "With PDBC" and "No PDBC" columns show the outcome of interest in each case.

Average Rate of Testing (10 years)	With PDBC	No PDBC
2	6.9%	7.3%
4	13.7%	13.6%
6	18.3%	19.4%
8	24.1%	24.3%

In the testing frequency scenario, we also found that the mean proportion of infected individuals who were diagnosed within the first 180 days ("early diagnosis") is 31.6% and 30.5% with and without PDBC. In the level of awareness models, the mean proportion of individuals diagnosed early is 3.7% and 3.3% with and without PDBC. We present the proportion of infected individuals who are diagnosed early for the various intermediate cases shown in Figure 3 and Table 1.

Discussion

In this paper, we demonstrate the population-level effect of the individual-level change in behavior of recently diagnosed HIV positive men. Our baseline ("testing frequency") models – that are based on testing behavior as reported in clinical data from four major metropolitan centers in the United States [29] – show that without PDBC, HIV prevalence in the MSM community would be higher by about 30.6% relative to current estimates. Our second set of models ("level of awareness") that match CDC data that show approximately 56% of infected MSM are aware of their status [3] are based on an average testing frequency of one test every 4000 days (or 10.9 years). These models show that without PDBC, equilibrium prevalence would be higher by only about 1.8% relative to models that incorporate PDBC. However, our analyses indicate that even under very low rates of testing (twice every ten years on average) without PDBC prevalence would be higher by about 15%.

We have seen the large difference in the proportion of infected who are aware of their status in the testing frequency and level-of-awareness scenarios. Another method to demon-

strate this incompatibility is to assume that both of the defining conditions of the two scenarios (approximately yearly testing on average, and about 50% awareness of infection) are true. Then, if we consider HIV prevalence in MSM to be 20% [30], assume half of these infected individuals are unaware (in accordance with NHBS 2008 and the level-of-awareness scenario), and about 60% tested in the past year, [6] then we conclude that approximately 6% of MSM nationally tested negative at the last test and sero-converted in the past year (or some HIV positive MSM mis-reported results). However, it is established that about 1-2% of MSM become HIV positive in a given year [31]. Thus the testing frequency and level of awareness scenarios are incompatible with each other. On the other hand, if we assume only about 5% of positive MSM are unaware of their status – consistent with our modeling results in the testing frequency case – then we estimate about 1.2% of all MSM sero-converted in the past year, which is much closer to the accepted number.

As we saw earlier, the testing frequency data come from a clinical study in four major urban centers in the US and the level of awareness numbers come from 2008 NHBS data. These datasets use different sampling methods – the clinical studies report data on MSM testing at clinics, and the NHBS reports data on MSM frequenting venues popular in the community. Some of the incompatibility between these data might therefore be attributed to the sampling mechanisms; it is likely that men regularly attending an HIV clinic test more frequently than the average member of the population while younger MSM sampled in the community are more likely to be unaware of their infection status. However, it is unlikely that the extent of this incompatibility is entirely due to sampling.

It is believed that knowledge of HIV status is not as low as the NHBS data suggest (Sullivan, personal communication). Stigma against HIV and the resulting social-desirability bias may be factors why men tend to under-report knowledge of positive HIV status. Moreover, venues where NHBS data are collected (bars, clubs) [3] tend to have an over-representation

[6] We arrive at the estimate that about 60% of negative or undiagnosed MSM tested in the past year by assuming that testing is a memoryless process with a constant daily probability p. Then under yearly testing (as per the testing frequency scenario and [29]), this daily testing probability p is $1/365$ and the proportion of men who tested within the past year is $1 - (1 - p^{365}) = 63.4\%$. We approximate this estimate as 60%.

of young MSM, who are particularly likely to not be diagnosed. Thus the low infection awareness in the NHBS data, and in our "level of awareness" models is likely an artifact of the interplay of various factors, and less representative of the real infection awareness in MSM.

We saw that at any reasonable level of testing, even as low as an average of twice every 10 years per individual, a lack of PDBC results in an increase in equilibrium prevalence by about 15.2%. Thus HIV prevalence in MSM would be substantially higher were PDBC not a real phenomenon.

Given the importance of treatment in the HIV epidemiology of MSM in the United States, we adopted a basic model of treatment that accounts for race differentials as measured by the waiting time between onset of infection and commencement of treatment in accordance with a clinical study [23], as reported in PUMA [22]. However, the landscape of treatment is constantly evolving, and future work on the subject should account for changes in such treatment patterns. It is also important to remember that the focus here is on the effectiveness of PDBC, and not on treatment as a prevention approach.

The prevalences we see in this paper are somewhat higher than the national estimates of 20-25% in MSM because the baseline component of these data come from a group of recently HIV-diagnosed individuals. Since our sample consists of recent sero-converters, on average, the behavior of these men with regards to HIV acquisition is potentially more risky than a typical member of the MSM population. It is also likely that the follow-up data show more reduction in behaviors directly related to HIV acquisition than typically occur because these men are participants in the follow-up components of the study and are therefore likely more conscious of their behavior upon diagnosis than a typical member of the population. However, our work shows the extent to which PDBC potentially mitigates the epidemic – under the assumption that diagnosed individuals reduce their sexual activity with regards to the 3 mechanisms we model.

This study is not an attempt to model the historical trajectory of the epidemic. Therefore

readers should not interpret Figures 1 and 2 as a prediction of HIV prevalence over the next 50 years. Rather, the purpose of this paper is to model HIV prevalence trajectories given current data on the sexual behavior of Southern California MSM and demonstrate how much higher prevalence could be if PDBC was not present, and the potential for behavior change to impact the course of the epidemic.

Figure 4 shows that even when we account for PDBC in the population, diagnosed individuals have more partners (per person) than undiagnosed individuals cross-sectionally. More longitudinal studies are needed to capture the true extent of PDBC; cross-sectional measures of levels of sexual activity among diagnosed and undiagnosed individuals are not suggestive of the extent to which PDBC exists in a population.

Our level of awareness scenario is based on an average test every 4000 days. A number of possible techniques to match the report of 55-60% awareness are possible. One reasonable method to match this report might be to build in an attribute that decides the potential for the men in every race to mis-report their test result. Data on mis-reporting of HIV test results were presented at the 2012 Conference on Retroviruses and Opportunistic Infections and further studies on this subject are in progress (Patrick Sullivan, personal communication). The models we have developed during the course of this work allow for easy extension to addition of an indicator function for individuals that mis-report their status (and this individual-level attribute can be easily made dependent on race too). The broader implication of mis-reporting of test results suggests the extent to which HIV stigma is present even today, particularly among Black MSM. HIV prevention efforts should consider the prevalence of such stigma when reaching out to communities that are especially at risk.

Gorbach et al. [6] found evidence for behavioral rebound towards more potentially transmitting sex acts around month 12 after diagnosis; their metric of interest was the proportion of partners of unknown HIV status with whom the respondents had recent UAI. Our model was parameterized in terms of temporal frequency of UAI with main and casual partners of different perceived serostatuses, a metric that includes that of Gorbach et al [6] plus ad-

ditional information about overall coital frequency and numbers of partners by perceived serostatus. In this combined metric, the appearance of rebound at month 12 was less clear, and we thus did not include such an effect on our model. Rebound effects would clearly reduce the degree to which PDBC has lowered HIV burden in this population relative to the counterfactual of no PDBC. The degree to which this would change our results is unclear, although we note that all rebound would occur long after the end of the acute phase, when infectiousness has declined. More information on the situations under which rebound does or does not occur, as well as its magnitude and duarability, is needed. Our research team is currently running a longitudinal prospective cohort study of newly diagnosed men, which should help clarify many of these issues, and we hope that future modeling work will revisit this question with these data. Additional modeling work, also in progress, considers the potential impact of various approaches to instituting tests capable of detecting HIV earlier than those currently in wide use, and/or increasing testing frequency among MSM.

Our findings sucggest that PDBC retains a significant role in altering the future course of HIV epidemics among MSM. This role is in addition to benefits that may come from diagnosis, in terms of earlier treatment and subsequent prevention of transmission through reduced viral load. As other studies [32, 33] have pointed out, and has been highlighted in the international financial press [34], even with the introduction of new biomedical methods of HIV prevention, and has been highlighted in the international press it is recognized that the HIV epidemic cannot be fully contained without significant behavioral changes alongwith the adoption of (and adherence to) biomedical interventions that reduce overall transmission rates.

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Online Appendix: Model Formulation, Parameter Estimation, Simulation, and Comprehensive Listing of Data Sources

In this Appendix, we describe several technical details that are not in the main body of the manuscript. We start with an exposition of the non-main network, parameters used to model this partnership network, followed by the estimation procedure for the statistics for these parameters. We repeat the same process for the network model for the main network. We follow with the derivation of statistics for the no post-diagnosis behavior change (no PDBC) model. We describe the various biological and demographic processes that are used in the simulation to model disease transmission and evolution of the network over time (while keeping the statistics of the main and non-main networks within stochastic variation of the mean). Finally, we list our sources for the various behavioral, biological and demographic parameters.

Any item marked "AIEDRP" represents data from the Southern California Acute Infection and Early Disease (AIEDRP) study [4, 6]. A number of biological and demographic parameters are selected from recent modeling work on HIV in MSM called the Prevention Umbrella for MSM in the Americas (henceforth PUMA) [22] and the sources for those parameters are marked "PUMA."

Model for Non-Main Partnership Network

The network for non-main partnerships in our network is cross-sectional. We estimate this network once at the start, and then simulate a cross-sectional network from it at each timestep using exponential random graph models in the *statnet* package [26].

Model and Paramaterers

This non-main network is

$$\begin{aligned}\text{logit}(p(y_{ij}=1|Y_{ij}^c)) &= \theta\delta(e)+\theta_a\delta_a e(|\sqrt{a_i}-\sqrt{a_j}|)+ \\ &\sum_{c=0,c\neq 3}^{5}\theta_c\delta_c(e(c))+\sum_{r_1,r_2}\theta_{r_1,r_2}\delta_{r_1,r_2}m(r_1,r_2)+\sum_{d_1,d_2}\theta_{m,d_1,d_2}\delta_{d_1,d_2}m(d_1,d_2)+ \\ &\theta_{I,R}\delta_{I,R}m(I,R)+\theta_A\delta_A e(A) \qquad (1)\end{aligned}$$

where $\delta(e)$ is the total number of non-main ties, $e(|\sqrt{a_i}-\sqrt{a_j}|)$ is the mean difference in the square root of ages of all partners multiplied by the number of edges, $m(r_1,r_2)$ is the mean number of ties between all combinations of races (one is left out to avoid collinearity with edges), $m(d_1,d_2)$ is the mean number of ties between men of the same diagnosis status (discordant is left out to avoid collinearity with edges), $m(I,R)$ is the average number of ties between strictly insertive and receptives (should be 0 but set to 1 for model to converge, though the coefficient corresponding to this statistic is set to $-\infty$.), $e(A)$ is the number of ties of men who have progressed to AIDS. The δ terms corresponding to each of these statistics are the changes in their values associated with a toggle of a dyad (i.e. switching the value of any dyad) [25]. This list describes the parameters in our model, the θ terms are the coefficients associated with each of these parameters.

Parameter Estimation

1. From AIEDRP data, we know the number of non-main partners reported over the past three months. We divide this number by 90 days to get the mean number of non-main partners per day as 0.10. However, this number is not limited to unprotected intercourse, therefore, we divide this mean by the proportion of times unprotected sex occurred (from the computation for main network above) to obtain a mean number of non-main partners of 0.075.

   However, this number is restricted to negative/undiagnosed men. From AIEDRP, we

know that the number of non-main partners reported over the past three months at baseline and follow-up differ by about 25.6%. We also know from NHBS [3] that about half of MSM nationally are unaware of their status, and about 25% of MSM are positive. Therefore, we roughly estimate about 13% of MSM nationally to be unaware of their status. The weighted mean degree for MSM, accounting for both positively diagnosed and negative/undiagnosed men, therefore, is

$$0.075 - (0.256 \times 0.075) = 0.056.$$

It follows that the expected number of non-main ties for our network of 5000 men is

$$\frac{0.075(0.87)(5000) + 0.056 \times (0.13)(5000)}{2} = 181.3$$

2. Casual Activity Classes: To compute the activity levels of each class, we divide the rates on UAI in non-main partnerships in to five groups by percentile. Then we compute the mean for each of these groups. However, this rate of non-main UAI applies to an entirely negative/undiagnosed population. To make these means compatible with a population of positively diagnosed individuals, we reduce the means for each of the groups by 25.6%. We then obtain the means for the five groups as 0.00017, 0.0119, 0.028, 0.0623, 0.1705.

3. Age: The difference in square roots of ages for the non-main partners is 0.75 years. Therefore the mean statistic is $0.075 \times 181.3 = 135.9$.

4. Mixing Matrix for Race: The AIEDRP data set was too sparse to reliably estimate race mixing in the population. Therefore, we used a study of MSM in San Francisco from 2009 [27] to estimate the "degree of mixing" between any two races (There are slight inconsistencies in the number of partnerships between X and Y as reported by X and Y; these are resolved by taking the mean of the two reports.). We do not assume

the the race distribution in LA County and San Francisco is the same; our data on the the number of individuals in each race for our population of 5000 men come from LA County [35].

We use the number of individuals in each race to compute the total number of possible "dyads" between all combinations of races (i.e. the maximum number of ties between two race groups). The San Francisco data [27] give us the proportion of partnerships in any combination of races that are actually realized (relative to the maximum possible number of dyads). We do assume that the mean proportion of possible ties between any two races that are realized in the two locations is the same.

Given the number of individuals in each race in our hypothetical population we know the number of possible dyads for each combination of races, and the proportion of possible ties between any two races that are realized. We also have an estimate for the total number of non-main ties in our population (from AIEDRP), and the distribution of these ties across the four races from [27]. Thus we constrain the total number of non-main ties in our mixing matrix to equal our estimate on non-main ties in the model from AIEDRP.

Thus we obtain the mixing matrix for the non-main network in Table 2.

Table 2: Race Mixing Matrix for the Non-Main Network. The rows represent respondents, and the columns represent the partners.

Race Groups					Total Degree	Mean Degree
	W	B	L	O		
W	24.4	8.2	51.7	20.0	128.6	0.0715
B		4.0	10.8	2.0	29.0	0.0724
L			38.2	16.6	155.5	0.0723
O				4.2	47.1	0.0725

5. Diagnosis Status: From our AIEDRP data set we know that of all the ties that belong

to diagnosed individuals, 35.6% are between positively concordant partners who are aware of their statuses (averaging the proportion of partners non-main partners who are positive at each of the four follow-up visits). Since the total degree for positively diagnosed individuals is 36.4, the number of positively concordant ties is

$$\frac{36.4 \times 0.356}{2} = 6.5.$$

6. Meth Use: Meth-users in our AIEDRP sample (defined as respondents who have used meth with at least one of the last three partners at baseline) have a mean rate of UAI of 0.101. Of the 194 respondents, 62/194 = 31.9% have used meth. Therefore, the total number of degrees for meth users is

$$5000 \times 0.319 \times 0.101 = 161.3.$$

7. Sexual Role: We set the number of ties between strictly insertive and strictly receptive partners as 1 but then set the coefficient for the estimate to $-\infty$ to not have any possible ties between strictly versatile groups. We had to set the number to 1 initially for the models to converge.

8. Reduction in UAI with non-main partners on transition to AIDS: 40%.

Model for Main Partnership Network

The network of main partnerships is estimated using separable temporal ERGMs [25] also impemented in *statnet* [26]. The variable $y_{ij,t}$ (i.e. the value of the dyad y_{ij} at time t) takes on the value 1 if nodes i and j have a main partnership at time t, and it is 0 otherwise. The variable $Y^c_{ij,t}$ is the rest of the network excluding the tie information of i and j. The variable u is the total number of ties of a particular type, and m represents mixing between two types. The variable v represents nodes with at least two main partnerships.

Model and Paramaterers

The model is

$$\begin{aligned}\text{logit}(p(y_{ij,t}=1|y_{ij,t-1}=0,Y^c_{ij,t})) &= \theta\delta(e)+\theta_a\delta_a(e(|\sqrt{a_i}-\sqrt{a_j}|))+\sum_{d=0}^{2}\theta_d\delta_d(\eta(d))+\\ &\quad \sum_r \theta_r\delta_r(e(r))+\sum_r \theta_{M,r}\delta_{M,r}(M(r)) \qquad (2)\end{aligned}$$

where e is the number of edges in the network, $e(|\sqrt{a_i}-\sqrt{a_j}|)$ is the difference in the square roots of the ages of all main partners, times the number of edges, $\eta(d)$ is the total number of nodes with degree 0, 1 and 2 in the network, $e(r)$ is the mean number of ties for each of the four races, $M(r)$ is the mean number of ties between partners belonging to the same race. All the above statistics are measured at time t. The δ functions are "change statistics" defined as the change in the statistics associated with a toggle of a dyad (i.e. switching the value of any dyad) [25]. The θ terms are the coefficients for each of these statistics. The network $Y^c_{ij,t-1}$ is the network at the time step $t-1$ without the dyad between the particular pair of actors i and j.

The dissolution models is a Bernoulli model of the form

$$\text{logit}(p(y_{ij,t}=0|y_{ij,t-1}=1))=\theta_{\text{diss}} \qquad (3)$$

where θ_{diss} is the coefficient associated with the dissolution of one tie (which corresponds to a change statistic of 1, in absolute value).

Statistics for Network of Main Partnerships

1. Momentary Degree Distributions: From the AIEDRP questionnaire, we have information on the number of ongoing main partnerships in a sample of 194 men at baseline. This information is scaled to a set of 5000 men in Table 2.

Table 3: Degree Distributions for Main Partnerships for network of size 5000.

Number of Partners	0	1	2	3	Not Reported
Number of Actors	3351	1546	52	51	0

We define the last category as "2+" and constrain the maximum number of partnerships in our main network (2) to 2.

2. Total Number of Partnerships: From Table we estimate a mean degree of 0.36. Therefore, the total number of partnerships in our population is $5000 \times 0.36/2 = 900$.

3. Mean Difference in Ages: We compute the mean difference in the square roots of the ages of main partners in the AIEDRP data set. This difference is 0.61. Since the modeled population has 900 main edges on average the mean statistic for difference in ages is $0.61 \times 900 = 549$.

4. Mixing Matrices by Race: As in non-main partnerships, we again use the data from San Francisco [27] in conjunction with the race distributions from LA County [13] to estimate mixing by race. This estimated mixing matrix for tha main network is in Table 4.

Table 4: Race Mixing Matrix for the Main Network. The rows represent respondents, and the columns represent the partners.

Race Groups					Total Degree	Mean Degree
	W	B	L	O		
W	121.0	40.5	259.5	99.1	641.1	0.36
B		19.8	54.2	10.0	144.3	0.36
L			194.0	82.6	784.9	0.36
O				20.9	233.6	0.36

5. Mean Partnership Duration: In the AIEDRP data set, the mean partnership durations are 906.7 days at baseline and 921 days at follow-up. Since the follow-up data set consists mostly of last partner information, we assume that each of the main partnerships in the follow-up data set are existent. Therefore the mean partnership duration in the follow-up data set is

$$(906.7 \times 0.87 + 921 \times 0.13) = 908.6$$

days assuming that our population consists of 87% individuals who are aware of their diagnosis status and 13% who are unaware. We estimate durations from the extant ties because our assumption is that the time for which a tie exists is geometrically distributed, and given this assumption, the mean of extant partnerships at any given time gives an unbiased estimate of the duration. Complete mathematical details are in [36].

6. Probability for UAI in Main Partnerships: From the baseline information in AIEDRP we know the number of sex acts in main partnerships, the length of main partnerships, and the proportion of times unprotected intercourse occurred. From this information, we compute the mean probability of UAI in main partnerships for negative/undiagnosed individuals as 0.156 (almost identical to the estimate found in PUMA through other studies).

   We also need the mean probability of UAI for positive and diagnosed individuals with negative/undiagnosed individuals. A similar method applied to follow-up information in AIEDRP yields a mean probability of 0.311. However, in the follow-up information in AIEDRP it is impossible to distinguish between unprotected oral and anal acts. It is very likely that upon diagnosis individuals switch from oral to anal intercourse. However, we only model transmission via UAI; therefore, this mean probability cannot be used. We therefore use the mean probability 0.109 of UAI for negative/undiagnosed individuals with positive individuals from [22].

7. Sexual Role: We set the number of ties between strictly insertive and strictly receptive partners as 1. Theoretically, this number should be zero, but we specified it as 1 for our models to converge, but as explained above, the coefficient is set to $-\infty$.

8. Reduction in UAI with Main Partners on transition to AIDS: 40% from the Rakai Study of discordant heterosexuals [37]. [7]

Statistics to Model Counter-Factual with No PDBC

1. Non-Main Network: The mean degree is only based on the behavior of negative/undiagnosed men. This mean degree is 0.075, translating to an average of 188 ties in the non-main network. Correspondingly, the casual activity classes change to 0.0023, 0.01595, 0.03798, 0.08415 and 0.2292. The mean statistic for the difference in ages is therefore $0.075 \times 188 = 141$. The cells in the race mixing matrix now sum to 188. This matrix is in Table 5.

2. Main Network: We keep the probabilities for UAI in discordant partnerships the same as that in negatively concordant partnerships.

Table 5: Race Mixing Matrix for the Non-Main Network in the counter-factual that does not include PDBC. The rows represent respondents, and the columns represent the partners.

Race Groups					Total Degree	Mean Degree
	W	B	L	O		
W	25.2	8.4	54.6	20.3	133.7	0.0743
B		4.1	11.3	2.0	29.9	0.0748
L			41.3	17.0	165.5	0.077
O				4.2	47.7	0.0734

[7] While we assume an equivalent reduction in daily probability of UAI after transistion to AIDS in non-main and main networks, the modeling method itself is different. In the non-main network, daily UAI defines the network so this 40% reduction is modeled as a reduced propensity to form ties. In the main network, daily UAI (and consequent possible disease transmission) are modeled as events distinct from the network; therefore, upon transition to AIDS we model a 40% reduction in daily probability of UAI that does not affect the partnership network itself.

The statistic corresponding to average number of non-main ties for meth users increases by 4% consistent with the per cent increase in the total number of non-main ties.

We do not consider mixing by diagnosis status since there is no diagnosis induced behavior change in this scenario and therefore mixing by diagnosis status is contingent simply upon the proportions of the two diagnosis states that are present in the population.

Other Biological and Demographic Processes

1. Infection Transmission: In accordance with Model 2 in [22], we model transmission events and their probabilities broken down by roles of the two partners, and their circumcision states. These relative transmission probabilities in UAI are from [38] – a study of heterosexuals. We used data from a cohort of heterosexuals because it presented time varying risk of UAI (as opposed to other widely cited studies on the topic [37, 39, 40, 41]).

2. Viral Load in absence of treatment: We model the viral load trajectory in each man as a six-parameter curve in the following manner [22]:

   (a) Days 0-21: rises linearly from 0 to 6.886

   (b) Days 21-40: declines linearly from 6.886 to 4.5 Days 40-3650: assumes a set point of 4.5 [42] that lasts until the onset of AIDS 10 years post-infection [43]

   (c) Days 3650-4380: linear rise from 4.5 to 7.0

   (d) Day 4380: death

3. Treatment Trajectories: We follow the basic structure of PUMA. We assume that treatment results in either no suppression, partially effective suppression and full suppression. For each race, we assume that for 15.0 % men there is no suppression, for 29.8% men there is partial suppression, and for 55.3% men there is no suppression [22].

4. As per [22], we assume a 40% reduction in UAI once AIDS stage is reached. This reduction is modeled in the form of a reduction of 40% reduction in daily probability of UAI in main partnerships and a 40% reduction in men number of non-main partners per day.

5. Treatment Initiation: In accordance with PUMA, we model treatment initiation as 4.1 years for Blacks, 5.0 years for Latinos, and 3.6 years for Whites and Others, measured since time of of infection [22].

6. Reduction in UAI upon transition to AIDS stage: We model a 40% reduction in probability of UAI with main partners and a 40% reduction in mean number of daily UAI events with non-main partners [22].

7. Circumcision: Circumcision rates are parametrized in accordance with PUMA [22]. Xu (2007) reports the rates of circumcision in various racial groups in the National Health and Nutrition Examination Surveys (NHANES) as 88% in non-Hispanic whites, 73% in non-Hispanic blacks, 42% in Mexican-Americans, and 50% in others [44]. We use these rates for Whites, Blacks, Latinos and Others in our population respectively. We assume that for a fully recovered circumcised individual infectivity reduces to 40% of the level initially. If full recovery from the surgery has not occurred, infectivity rises to 130%. Both these changes in infectivity are in accordance with PUMA.

8. Role: As per PUMA we assume that 7% of Other, 13% of Black, and 9% of Latino MSM are strictly insertive and strictly receptive. PUMA does not report the proportion of Whites who are strictly insertive and strictly receptive; but the "Other" category in PUMA includes Whites. We assume that the proportion of strictly insertive or strictly receptive MSM for Whites is the same as the proportion of Other in this work.

9. Testing: We based our baseline testing models on PUMA. A clinical study in four major US metropolitan centers [29] reports a median inter-test interval of 243 days. If

we assume a simple exponential distribution for time until testing, this median measure corresponds to a mean inter-test interval of 351 days. As we discussed this mean rate of testing corresponds to a mean of 95% of men who have ever tested. Another study [45] that presents NHBS data (from June 2004 to April 2005) reports that 92% of men have ever tested. Thus our baseline testing models are consistent with NHBS data from 2004 to 2005, though not so with NHBS data from 2008 (as we discussed in the main body of the paper).

Itemized List for Data Sources

1. Initial prevalence: NHBS (2008) [3]
2. Age-specific non-AIDS mortality rates: National Vital Statistics Reports [46]
3. Race distributions: LA County Department of Health Services [35]
4. Circumcision rates by race: National Health and Nutrition Examination Surveys (1999–2004) [44]
5. Prevalence of role exclusivity: PUMA
6. Proportion of positive men who never receive treatment: PUMA
7. Proportion of Treated Men who Achieve Full Suppression: PUMA
8. Role versatility in non-main partnerships: PUMA
9. Daily probability of HIV testing: Clinical study from 4 major US urban centers (Seattle-King County, San Francisco, Denver and District of Columbia) [29]
10. HIV Test Window Period: 22 days, and treated as a sensitivity parameter [22]. A detection window of 22 days is reasonable four fourth generation and RNA tests [47].
11. Initial age distribution: Uniformly distributed between 18 and 65 years for every man in the population.

12. Non-Main Partnerships

    (a) Race Mixing matrix: Study of MSM in San Francisco [27] in combination with race distribution from LA County Department of Health Services [35]

    (b) Mean age difference of main partners: AIEDRP

    (c) Quintiles for activity classes in Non-Main Partnerships: AIEDRP

    (d) Number of Partnerships for meth users and non-users: AIEDRP

    (e) Mixing by diagnosis status: AIEDRP

13. Main Partnerships:

    (a) Baseline daily probability of UAI: AIEDRP for negatively concordant partnerships, PUMA for partnerships discordant by diagnosis status

    (b) Momentary (cross-sectional) degree distributions for main partnerships: AIEDRP

    (c) Race mixing matrix: Study of MSM in San Francisco [27] in combination with race distribution from LA County Department of Health Services [35]

    (d) Age mixing in the main partnerships: Mean difference in ages of main partners in AIEDRP

    (e) Distribution for number of partnerships at cross-section: AIEDRP

    (f) Average Partnership Duration: AIEDRP

    (g) Reduction in UAI with Main Partners in AIDS stage: Study of HIV discordant couples in Uganda [37]

Biological Data: Estimates for all of the following parameters are from PUMA.

1. Time until peak of acute viremia

2. Time from peak viremia until set point

3. Set point viral load

4. Time from onset of set point until AIDS-related viral increase
5. Time from onset of AIDS-related viral increase until death
6. Slope of viral load during AIDS
7. Viral load at full suppression
8. Mean viral load for those partially suppressed
9. Time from initiation of treatment until partial suppression
10. Time until partial suppression escape
11. Partial escape slope
12. Probability of transmission by act

References

[1] Department of Health and Human Services, Centers for Disease Control and Prevention. Vital Signs: HIV Testing and Diagnosis Among Adults - United States, 2001-2009. Morbidity and Mortality Weekly Report. 2010 December 3;59(47):1550–1555.

[2] Office of AIDS, Center for Infectious Diseases, California Department of Public Health. Integrated Epidemiologic Profile of HIV/AIDS in California, 2001-2005 with 2007 Update; 2010. Retrieved April 27, 2010 from the World Wide Web: `www.cdph.ca.gov/programs/aids/Documents/EPIProfile.pdf`.

[3] Department of Health and Human Services, Centers for Disease Control and Prevention. Prevalence and Awareness of HIV Infection Among Men Who Have Sex With Men - 21 cities, United States, 2008. Morbidity and Mortality Weekly Report. 2010 September 24;59(37):1201–1207.

[4] Gorbach PM, Drumright LN, Daar ES, Little SJ. Transmission behaviors of recently HIV-infected men who have sex with men. Journal of Acquired Immune Deficiency Syndromes. 2006 May;42(1):80–85.

[5] Steward WT, Remien RH, Higgins JA, Dubrow R, Pinkerton SD, Sikkema KJ, et al. Behavior Change Following Diagnosis with Acute/Early HIV Infection – A Move to Serosorting with Other HIV-Infected Individuals. The NIMH Multisite Acute HIV Infection Study: III. AIDS and Behavior. 2009 Dec;13(6):1054–1060.

[6] Gorbach PM, Weiss RE, Jeffries R, Javanbakht M, Drumright LN, Daar ES, et al. Behaviors of Recently HIV-Infected Men Who Have Sex With Men in the Year Postdiagnosis: Effects of Drug Use and Partner Types. Journal of Acquired Immune Deficiency Syndromes. 2011 Feb;56:176 – 182.

[7] Sullivan PS, Carballo-Dieguez A, Coates T, Goodreau SM, McGowan I, Sanders EJ, et al. Successes and challenges of HIV prevention in men who have sex with men. Lancet. 2012 Jul;.

[8] van Kesteren NM, Hospers HJ, Kok G. Sexual risk behavior among HIV-positive men who have sex with men: A literature review. Patient Education and Counseling. 2007 Jan;65(1):5–20.

[9] van Kesteren NM, Hospers HJ, van Empelen P, van Breukelen G, Kok G. Sexual decision-making in HIV-positive men who have sex with men: How moral concerns and sexual motives guide intended condom use with steady and casual sex partners. Archives of Sexual Behavior. 2007 Jun;36(3):437–449.

[10] Fox J, White PJ, Macdonald N, Weber J, McClure M, Fidler S, et al. Reductions in HIV transmission risk behaviour following diagnosis of primary HIV infection: a cohort of high-risk men who have sex with men. HIV Med. 2009 Aug;10(7):432–438.

[11] Kurtz SP, Buttram ME, Surratt HL, Stall RD. Resilience, syndemic factors, and serosorting behaviors among HIV-positive and HIV-negative substance-using MSM. AIDS Educ Prev. 2012 Jun;24(3):193–205.

[12] Chen JL, Kodagoda D, Lawrence AM, Kerndt PR. Rapid public health interventions in response to an outbreak of syphilis in Los Angeles. Sexually Transmitted Diseases. 2002 May;29(5):277–284.

[13] HIV Epidemiology Program, Los Angeles County Department of Health Services. HIV/AIDS Semi-Annual Surveillance Summary – Cases Reported as of June 2005; 2005. Los Angeles: Los Angeles County Department of Health Services.

[14] County of Los Angeles Public Health: HIV Epi. An Epidemiologic Profile of HIV and AIDS in Los Angeles County 2009; 2009.

[15] of San Diego Health C, Unit HSAHE. AIDS in Men who have Sex with Men (MSM). County of San Diego, 2004; 2004. Retrieved June 10, 2012 from the World Wide Web: `http://www.sdcounty.ca.gov/hhsa/programs/phs/documents/AIDS_in_MSM.pdf`.

[16] Vittinghoff E, Douglas J, Judson F, McKirnan D, MacQueen K, Buchbinder SP. Per-contact risk of human immunodeficiency virus transmission between male sexual partners. American Journal Of Epidemiology. 1999 Aug;150(3):306–311.

[17] Molitor F, Truax SR, Ruiz JD, Sun RK. Association of methamphetamine use during sex with risky sexual behaviors and HIV infection among non-injection drug users. West J Med. 1998 Feb;168(2):93–97.

[18] Rajasingham R, Mimiaga MJ, White JM, Pinkston MM, Baden RP, Mitty JA. A systematic review of behavioral and treatment outcome studies among HIV-infected men who have sex with men who abuse crystal methamphetamine. AIDS Patient Care STDS. 2012 Jan;26(1):36–52.

[19] Semple SJ, Patterson TL, Grant I. Motivations associated with methamphetamine use among HIV plus men who have sex with men. Journal of Substance Abuse Treatment. 2002 Apr;22(3):149–156.

[20] Shoptaw S, Reback CJ. Associations between methamphetamine use and HIV among men who have sex with men: A model for guiding public policy. Journal Of Urban Health-Bulletin Of The New York Academy Of Medicine. 2006 Nov;83(6):1151–1157.

[21] Gorbach PM, Holmes KK. Transmission of STIs/HIV at the partnership level: beyond individual-level analyses. J Urban Health. 2003 Dec;80(4 Suppl 3):15–25.

[22] Goodreau SM, Carnegie NB, Vittinghoff E, Lama JR, Sanchez J, Grinsztejn B, et al. What Drives the US and Peruvian HIV Epidemics in Men Who Have Sex with Men (MSM)? PLoS ONE. 2012 11;7(11):e50522. Available from: http://dx.doi.org/10.1371%2Fjournal.pone.0050522.

[23] Swindells S, Cobos DG, Lee N, Lien EA, Fitzgerald AP, Pauls JS, et al. Racial/ethnic differences in CD4 T cell count and viral load at presentation for medical care and in follow-up after HIV-1 infection. AIDS. 2002 Sep;16(13):1832–1834.

[24] Morris M, Kurth AE, Hamilton DT, Moody J, Wakefield S. Concurrent Partnerships and HIV Prevalence Disparities by Race: Linking Science and Public Health Practice. American Journal of Public Health. 2009 Jun;99(6):1023–1031.

[25] Krivitsky PN, Handcock MS, Morris M. Adjusting for network size and composition effects in exponential-family random graph models. Statistical Methodology. 2011;8(4):319339.

[26] Handcock MS, Hunter DR, Butts CT, Goodreau SM, Morris M. statnet: Software tools for the Statistical Modeling of Network Data. Seattle, WA; 2003. Version 2.0. Available from: http://statnetproject.org.

[27] Raymond HF, McFarland W. Racial Mixing and HIV Risk Among Men Who Have Sex with Men. AIDS and Behavior. 2009 Aug;13(4):630–637.

[28] Wohl AR, Frye DM, Johnson DF. Demographic characteristics and sexual behaviors associated with methamphetamine use among MSM and Non-MSM diagnosed with AIDS in Loa Angeles county. AIDS and Behavior. 2008 Sep;12(5):705–712.

[29] Helms DJ, Weinstock HS, Mahle KC, Bernstein KT, Furness BW, Kent CK, et al. HIV Testing Frequency Among Men Who Have Sex With Men Attending Sexually Transmitted Disease Clinics: Implications for HIV Prevention and Surveillance. Journal Of Acquired Immune Deficiency Syndromes. 2009;50(3):320–326.

[30] Centers for Disease Control and Prevention. HIV Among Gay, Bisexual and other Men who have sex with Men (MSM); 2010. Retrieved December 6, 2010 from the World Wide Web: `http://www.cdc.gov/hiv/topics/msm/index.htm`.

[31] Department of Health and Human Services, Centers for Disease Control and Prevention. HIV and AIDS among Gay and Bisexual Men; 2010. Retrieved December 6, 2010 from the World Wide Web: `http://www.cdc.gov/nchhstp/newsroom/docs/FastFacts-MSM-FINAL508COMP.pdf`.

[32] Friedland GH. HIV medication adherence. The intersection of biomedical, behavioral, and social science research and clinical practice. J Acquir Immune Defic Syndr. 2006 Dec;43 Suppl 1:3–9.

[33] Rotheram-Borus MJ, Swendeman D, Chovnick G. The past, present, and future of HIV prevention: integrating behavioral, biomedical, and structural intervention strategies for the next generation of HIV prevention. Annu Rev Clin Psychol. 2009;5:143–167.

[34] Financial Times Special Report. Biggest Obstacle is Human Behavior; 2012. Retrieved January 15, 2013 from the World Wide Web: `http://www.ft.com/intl/reports/hiv-nov2012`.

[35] of Los Angeles Department of Health Services Office of AIDS Programs C, Policy. County of Los Angeles HIV Prevention Plan 2004 - 2008;. Retrieved From the World WIde Web.

[36] Krivitsky P. Statistical Models for Social Network Data and Processes. University of Washington; 2009.

[37] Wawer MJ, Gray RH, Sewankambo NK, Serwadda D, Li XB, Laeyendecker O, et al. Rates of HIV-1 transmission per coital act, by stage of HIV-1 infection, in Rakai, Uganda. Journal Of Infectious Diseases. 2005 May;191(9):1403–1409.

[38] Leynaert B FAU Downs AM, Downs AM FAU de Vincenzi I, de Vincenzi I. Heterosexual transmission of human immunodeficiency virus: variability of infectivity throughout the course of infection. European Study Group on Heterosexual Transmission of HIV. American Journal of Epidemiology. 1998;148(1):88–96.

[39] Hollingsworth TD, Anderson RM, Fraser C. HIV-1 transmission, by stage of infection. Journal Of Infectious Diseases. 2008 Sep;198(5):687–693.

[40] Abu-Raddad LJ, Longini IM. No HIV stage is dominant in driving the HIV epidemic in sub-Saharan Africa. AIDS. 2008 May;22(9):1055–1061.

[41] Pinkerton SD. Probability of HIV transmission during acute infection in Rakai, Uganda. AIDS And Behavior. 2008 Sep;12(5):677–684.

[42] Little SJ, McLean AR, Spina CA, Richman DD, Havlir DV. Viral dynamics of acute HIV-1 infection. Journal Of Experimental Medicine. 1999 Sep;190(6):841–850.

[43] Buchbinder SP, Katz MH, Hessol NA, O'Malley PM, Holmberg SD. Long-term HIV-1 infection without immunologic progression. AIDS. 1994 Aug;8(8):1123–1128.

[44] Xu F, Markowitz LE, Sternberg MR, Aral SO. Prevalence of circumcision and herpes simplex virus type 2 infection in men in the United States: The national health and

nutrition examination survey (NHANES), 1999-2004. Sexually Transmitted Diseases. 2007 Jul;34(7):479–484.

[45] Department of Health and Human Services, Centers for Disease Control and Prevention. HIV Prevalence, Unrecognized Infection, and HIV Testing Among Men Who Have Sex with Men - Five U.S. Cities, June 24-April 2005. Morbidity and Mortality Weekly Report. 2005 June 24;54(24):597–600.

[46] Arias E. United States Life Tables, 2004; 2007. Atlanta: US Centers for Disease Control and Prevention, Division of Vital Statistics.

[47] Branson BM, Stekler JD. Detection of acute HIV infection: We can't close the window. Journal of Infectioius Diseases. 2012 Feb;205(4):521–524.