






Effects of Epidemiological Structure on the Transient Evolution of HIV Virulence


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
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Abstract

The evolutionary dynamics of parasite virulence over the course of an emerging epidemic have important implications both for our basic understanding of epidemiological dynamics and, potentially, for the outcomes of public health interventions. In general changes in fitness landscapes over the course of an epidemic will select for higher virulence during the early, exponential-growth phase of the epidemic, but quantitative outcomes can depend sensitively on biological details and the structure of mathematical models used to capture them. Fraser, Shirreff, and co-workers have proposed a series of models for eco-evolutionary dynamics of HIV that are relatively detailed in their portrayal of the tradeoffs between transmission and virulence (mediated by set-point viral load, SPVL) and their heritability between hosts. However, these models use very simple implicit representations of the transmission process that ignore the partnership dynamics that previous research has found to be critical in predicting epidemics of sexually transmitted diseases. We explore models that combine HIV virulence tradeoffs with a range of epidemiological structures, modeling partnership formation and dissolution and allowing for individuals to transmit disease outside of partnerships. We assess summary statistics such as the peak value of virulence (SPVL) and the time at which the peak occurs across all models and across a Latin hypercube sample that captures a realistic range of partnership dynamic parameters for sub-Saharan Africa. In order to account for the different interpretations of parameters across model structures, we scale all parameter sets to constrain the simulated epidemic growth rate to be identical, matching a realistic baseline value. Our primary result is that, for this particular model setting, the simplest random-mixing structure is actually the best approximation to the most realistic model; this surprising outcome occurs because the dominance of extra-pair contact in the realistic model tends to mask the effects of partnership structure.

Author Summary

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Introduction

The evolution of pathogen virulence is a fundamental process in evolutionary biology, of both theoretical and (potentially) practical importance. The trade-off theory [1] — which postulates that parasite virulence can be explained as the long-term evolutionary outcome of a saturating relationship between parasite clearance rate and transmission rate — has been criticized [2,3], but has also been successfully applied in a variety of host-pathogen systems [4–7]. One particularly interesting application of these ideas is the work by Fraser *et al.* showing that HIV appears to satisfy the prerequisites of the tradeoff theory: in a study of discordant couples (i.e. long-term sexual partnerships with one infected and one uninfected partner), HIV virulence as measured by the rate of progression to AIDS was both heritable and covaried with the set-point viral load (i.e., the characteristic virus load measured in blood during the intermediate stage of infection), which in turn predicted the probability of within-couple transmission [8,9]. Subsequent studies [10,11] used these data to parameterize mechanistic models of HIV virulence evolution, suggesting that HIV invading a novel population would initially evolve increased virulence, peaking after approximately [XXX] years and then declining slightly to a long-stable virulence level.

The work of Shirreff *et al.* [10], and particularly the predicted transient peak in HIV virulence midway through the epidemic, highlights the importance of interactions between epidemiological and evolutionary factors [12,13]. However, despite the attention to mechanistic detail at the individual or physiological level, the epidemiological structures used in these models are relatively simple.

As we discuss in detail below, the existing models of HIV eco-evolutionary dynamics either use implicit models that incorporate the average effects of within-couple sexual contact — without representing the explicit dynamics of pair formation and dissolution or accounting for extra-partnership contact — or use an agent-based formulation with parameters that effectively lead to random mixing among infected and uninfected individuals. Here we explore the effects of incorporating *explicit* epidemiological structure in eco-evolutionary models.

We add complexity to the epidemiological model following the general approach of Champredon *et al.* [14]; individuals join and leave partnerships at a specified rate, and can have sexual contact both within and outside of established partnerships. At the same time, our analysis somewhat simplifies the models of Shirreff *et al.* [10], for computational tractability; we check that our qualitative results are not sensitive to these simplifications. In order to explore how virulence evolution depends on epidemiological structure, we consider a series of models with increasing levels of complexity. In order to avoid dependence of the results on a particular set of parameters — as we explain below, finding matching sets of parameters across models with widely differing epidemiological structures is challenging — we evaluate our models across a wide range of parameters, again following Champredon *et al.* [14] in using a Latin hypercube design. For each model run, we compute a set of metrics (peak

virulence, timing of virulence peak, equilibrium virulence) that summarize the evolutionary trajectory of a simulated HIV epidemic.

Materials and Methods

As our primary goal is to explore how different epidemiological structures (i.e. partnership dynamics and contact structures) affect our conclusions about the evolution of virulence, our models use a simplified description of within-host dynamics and heritability derived from Shirreff *et al.*'s multi-strain evolutionary model [10]. Like Shirreff *et al.*, we use a simple susceptible-infected-susceptible demographic formulation; rather than modeling birth and death (or more specifically, recruitment into the sexually active population and death), we assume that whenever an individual dies from infection, another enters the susceptible compartment.

Infection dynamics

Like Shirreff *et al.* [10], we focus on the evolution of mean \log_{10} set-point viral load, SPVL (which we denote as α), rather than virulence (i.e. rate of progression to AIDS) itself. In contrast to Shirreff *et al.*, we use a single-stage disease model instead of accounting explicitly for progression through the three main stages of HIV infection (primary, asymptomatic, and disease), and we use a simple exponentially distributed infectious period instead of a more realistic Weibull-distributed infectious period. We account for varying transmission rates and durations of each disease stage by summing the durations of three stages (again based on Shirreff *et al.*'s model) and taking the duration-weighted average of transmission rates of three stages. Thus the within-couple transmission rate, β , for our models is given by:

$$\beta(\alpha) = \frac{D_P \beta_P + D_A(\alpha) \beta_A(\alpha) + D_D \beta_D}{D_P + D_A(\alpha) + D_D} \quad (1)$$

where the duration of infection (D_P and D_D) and rate of transmission (β_P and β_D) of the **P**imary and **D**isease stages of infection are independent of the host's SPVL. Following Shirreff *et al.*, the duration of infection (D_A) and rate of transmission (β_A) for the **A**symptomatic stage are Hill functions of the SPVL:

$$\begin{aligned} D_A(\alpha) &= \frac{D_{max} D_{50}^{D_k}}{V_\alpha^{D_k} + D_{50}^{D_k}}, \\ \beta_A(\alpha) &= \frac{\beta_{max} V_\alpha^{\beta_k}}{V_\alpha^{\beta_k} + \beta_{50}^{\beta_k}}, \end{aligned} \quad (2)$$

where $V_\alpha = 10^\alpha$. The **u**ncoupled and **e**xtra-couple transmission rates are scaled by multiplying the **w**ithin-couple transmission rate β by the contact ratios c_u/c_w and c_e/c_w .

Mutation

Like Shirreff *et al.* [10] we incorporate a between-host mutation process in the SPVL, but simplify Shirreff *et al.*'s evolutionary model slightly by using a one-to-one genotype-phenotype mapping. The mutational process in our model is directly taken from Shirreff *et al.*. Over the course of infection, mutation occurs within the host. However, it is assumed that SPVL of an infected individual is determined by the SPVL at the time of infection for simplicity (and is not further affected by within-host

mutation). Instead, the mutational effect takes place when an infected individual transmits the virus to a susceptible individual. First, the distribution of \log_{10} SPVL is discretized into a vector:

$$\alpha_i = (\alpha_{max} - \alpha_{min}) \frac{(i-1)}{n-1} + \alpha_{min} \quad i = 1, 2, 3, \dots n. \quad (3)$$

We have experimented with varying degrees of discretization in the strain distribution (i.e., values of n); in our model runs comparing results with Shirreff *et al.* [10] (Figure 1) we use $n = 51$ (i.e. a bin width of $0.05 \log_{10}$ SPVL for α), but we find only small differences when reducing n to 21 (bin width $0.25 \log_{10}$ SPVL), which we use for all other simulations.

Fig 1. Baseline dynamics. Time series of mean population virulence (\log_{10} SPVL). (a) Shirreff model, effects of varying r . (b) Effects of varying initial infectious density $I(0)$. (c) Effects of varying initial mean virulence $\alpha(0)$.

We construct an n by n mutational matrix, M — which is multiplied with the transmission term — so that M_{ij} is the probability that a newly infected individual will have \log_{10} SPVL of α_j given that the infector has \log_{10} SPVL of α_i . Finally, the probabilities are normalized so that each row sums to 1:

$$M_{ij} = \frac{\Phi(\alpha_j + d/2; i) - \Phi(\alpha_j - d/2; i)}{\Phi(\alpha_{max} + d/2; i) - \Phi(\alpha_{min} - d/2; i)}, \quad (4)$$

where $\Phi(x; i)$ is the Gaussian cumulative distribution function with mean α_i and variance of σ_M^2 , and $d = (\alpha_{max} - \alpha_{min})/(n-1)$. Transmission rate and disease induced mortality rates are discretized into a vector as well:

$$\beta_i = \beta(\alpha_i) \quad \lambda_i = \frac{1}{D_P + D_A(\alpha_i) + D_D} \quad (5)$$

Contact structure and partnership dynamics

We developed six multi-strain evolutionary models, designed to cover a gamut between Champredon *et al.*'s relatively realistic [14] and Shirreff *et al.*'s relatively simplistic [10] epidemiological structures, each of which is based on different assumptions regarding contact structure and partnership dynamics. Specifically, we focus on the effects of the assumptions of (1) instantaneous vs. non-instantaneous partnership formation and (2) zero vs. positive extra-partnership sexual contact and transmission on the evolution of mean \log_{10} SPVL.

Our first four models consider explicit partnership dynamics and are based on Champredon *et al.*'s model [14]. Models 1 and 2 assume non-instantaneous partnership formation (i.e. individuals spend some time uncoupled, outside of partnerships) and consist of five states that are classified by infection status and partnership status. S is the number of single (uncoupled) susceptible individuals, and I is the number of single infected individuals. SS is the number of susceptible-susceptible couples, SI is the number of serodiscordant (susceptible-infected) couples, and II is the number of concordant positive (infected-infected) couples. Model 1 includes extra-partnership contact (with both uncoupled individuals and individuals in other partnerships) whereas model 2 only considers within-couple transmission. Models 3 and 4 assume instantaneous partnership formation and thus consist of only the three partnered states: SS , SI , and II . Parallel to model 1 and 2, model 3 includes

extra-partnership contact (now only with individuals in other partnerships, since uncoupled individuals don't exist in this model) and model 4 only considers within-couple transmission.

In contrast, models 5 and 6 are not explicitly structured. Model 5 is an implicit serial monogamy model based on the epidemiological model used by Shirreff *et al.* [10]. It is actually a random mixing model that consist of only two states, S and I , and does not consider explicit partnership dynamics. However, to simulate the effect of instantaneous partnership formation, it uses an adjusted transmission rate that is derived from approximated basic reproduction number of a serial monogamy model [15]. Finally, model 6 is a simple random-mixing model.

The base model (i.e. model 1) for the first four models is an extension of Champredon *et al.*'s model [14]. Individuals in single compartment acquire a partner at a rate, ρ , and partnerships dissolve at a rate, c . Infected individuals in a discordant partnership infect susceptible partner at a rate β (within-couple transmission rate) and susceptible individuals outside the partnership at a rate c_e (extra-couple transmission rate). Likewise, a single infected individual can infect any susceptible individuals at a rate c_u through uncoupled mixing. Extra-couple and uncoupled transmission are modeled in a same way as Champredon *et al.*'s model. All the details have been adapted to a multi-strain scenario. Model 2, 3, and 4 are derived from the base model by removing epidemiological details (partnership formation and uncoupled/extra-couple contact). Model details are explained in the appendix.

Latin hypercube sampling

Despite considerable effort by many researchers [14, 15], the parameters determining the rate and structure of sexual partnership change and contact are still very uncertain; this led Champredon *et al.* [14] to adopt a Latin hypercube sampling (LHS) strategy [16] that evaluates model outcomes over a range of parameter values. In order to make sure that our comparisons among models apply across the entire space of reasonable parameter values, and in order to evaluate the differential sensitivity of different model structures to parameter values, we follow a similar protocol and perform LHS over a parameter set including both the transmission and duration parameters (β_P , D_P , β_D , D_D) and contact/partnership parameters (ρ , c , c_u/c_w , and c_e/c_w). We do not allow for uncertainties in parameters that are directly related to the evolutionary process (β_{max} , β_{50} , β_k , D_{max} , D_{50} , D_k , σ_M), using Shirreff *et al.*'s point estimates throughout [10].

Latin hypercube sampling is done as in Champredon *et al.* [14]. For each parameter, z , its range is divided into $N = 1000$ equal intervals on a log scale:

$$z_i = \exp \left(\log(z_{min}) + [\log(z_{max}) - \log(z_{min})] \frac{i-1}{N-1} \right) \quad i = 1, \dots, N. \quad (6)$$

For simplicity, we assume that all parameters are uniformly distributed on the log scale. Following the vectorization of a parameter range, a matrix is constructed so that each column contains a vector of a parameter series which it represents (z_1, \dots, z_N). Then, each column is replaced with a random permutation series of itself. Now, each row contains a different parameter set that is used for each simulation run.

Table ?? gives the ranges of the model parameters used for LHS. Parameter ranges regarding contact and partnership dynamics (ρ , c , and c_e/c_w) are taken from Champredon *et al.* [14], whereas those regarding infection (β_P , D_P , β_D , and D_D) are taken from Hollingsworth *et al.* [15]. The remaining parameters are taken from Shirreff *et al.* [10].

The one completely new parameter in our model, the ratio of uncoupled to within-couple transmission c_u/c_w , is needed to more flexibly contrast uncoupled and

extra-couple transmission dynamics within multi-strain models (Appendix); we need to pick a reasonable range for it. Champredon *et al.* [14] assume that the effective within-couple contact rate and effective uncoupled contact rate have the same range of 0.05 - 0.25. Given Champredon *et al.*'s parameter range, the possible maximum and minimum values of c_u/c_w are 5 and 1/5. Therefore, we use 1/5-5 as the range for the parameter c_u/c_w . Although this adds more uncertainty to the parameter c_u — Champredon *et al.*'s range implies a 5-fold difference whereas ours gives a 25-fold difference — as there is not much known about the uncoupled transmission rate, we consider the wider range appropriate.

Simulation runs

One of the most difficult parts of model comparison is finding parameter sets that are commensurate against many different model structures. For the most part, our models are too complex to easily derive analytical correspondences among them. Given a numerical criterion, such as r (initial exponential growth rate) or \mathcal{R}_0 (intrinsic reproductive number), we can adjust one or more parameters by brute force to ensure that all of the models match according to that criterion. While \mathcal{R}_0 is often considered the most fundamental property of an epidemic, and might thus seem to be a natural goal, here we focus on matching the initial growth rate r for several reasons. First, our primary interest is in the transient evolutionary dynamics of virulence, which are more strongly affected by r than \mathcal{R}_0 . Second, r is in general more directly observable in real epidemics; r can be estimated by simply fitting an exponential curve to the initial incidence or prevalence curves [17], while \mathcal{R}_0 typically requires either (1) knowledge of *all* epidemic parameters or (2) relatively sophisticated back-calculation based on r and knowledge of the serial interval or generation interval of the disease [18]. Thus, we scale a parameter so that every run has the same initial exponential growth rate in the incidence.

In order to allow for all models to have equal initial exponential growth rate, r , we need to pick a parameter, s , so that $\lim_{s \rightarrow 0} r(s) = 0$ and $\lim_{s \rightarrow \infty} r(s) = \infty$. As adjusting either partnership change rate (i.e. partnership formation and dissolution rate) or transmission rate does not fulfill this requirement for certain models, we decided to scale partnership change rate and dissolution rate by the same factor of γ : $\beta_{adj} = \gamma\beta_{base}$, $c_{adj} = \gamma c_{base}$, $\rho_{adj} = \gamma\rho_{base}$. Since transmission rate is adjusted by the scale of γ , uncoupled and extra-couple transmission rates are adjusted as well. For models 3, 4, and 5, all of which assume instantaneous partnership (and hence do not track single individuals), only the transmission rate and partnership dissolution rate (in this case equivalent to the partnership change rate) are adjusted.

We run each model for each of 1000 parameter sets chosen by Latin hypercube sampling, with fixed starting conditions of mean \log_{10} SPVL of 3 and epidemic size of 10^{-4} . After each run, initial exponential growth rate is calculated. Then, parameters are scaled so that the initial exponential growth rate is scaled to 0.04, which is approximately equal to that of Shirreff *et al.*'s model.

For each model we derive the following summary statistics: peak virulence, peak time, equilibrium virulence, and relative peak virulence. The transient phase of an epidemic is often characterized by high virulence, and we define peak virulence as the maximum virulence during this phase. It is simply calculated by taking the maximum value from the virulence trajectory, and peak time is the time at which the maximum value is reached. Once the epidemic enters the endemic phase, evolution of virulence stabilizes and reaches equilibrium. Equilibrium virulence is calculated by taking the mean virulence at 4000 years. Although most simulations reach equilibrium much earlier, we set our time horizon at a much later date as some simulation runs have slow rate of evolution depending on the parameter set and model assumptions.

We focus on these statistics for the following two reasons. First of all, knowing the possible ranges for the peak virulence allows us to estimate the worst-case scenario for the HIV and other sexually transmitted disease epidemics. Pathogens may already have evolved towards high virulence during the early stages of an epidemic, by the time it is observed by public health authorities. Understanding how virulent a pathogen can evolve before an epidemic begins can be helpful for controlling the disease. Furthermore, knowing the initial virulence, peak virulence, timing of the peak virulence, and equilibrium virulence provide sufficient detail to identify the shape of the virulence trajectory. During an epidemic outbreak, it is difficult to observe virulence evolution. Specifically, in the case of HIV and other sexually transmitted diseases, slow evolutionary time-scale makes observing changes in the mean virulence even more challenging. Knowing the ranges of these statistics can help real-time virulence evolution prediction during an epidemic less troublesome.

Results

Our simplifications of Shirreff *et al.*'s model [10] reproduce its qualitative behaviour — in particular, its predictions of virulence dynamics — reasonably well. As r decreases from 0.084 to 0.42 (the latter value matching the initial rate of increase in prevalence in Shirreff *et al.*'s full model) the initial trajectory of increasing virulence brackets the rate from the original model (Figure 1a). However, our model produces lower peak virulence (≈ 4.3 vs. $\approx 4.6 \log_{10}$ SPVL) and equilibrium virulence ≈ 4.25 vs. $\approx 4.5 \log_{10}$ SPVL) than Shirreff's, even for matching initial incidence trajectories (i.e., $r = 0.042 \text{ year}^{-1}$).

Changing the initial infectious density ($I(0)$), while it produces the expected changes in the initial epidemic trajectory (Supplementary material), has little effect on the virulence trajectory, making the virulence peaks slightly later and larger as $I(0)$ decreases. Decreasing $I(0)$ allows a longer epidemic phase before the transition to endemic dynamics (Figure 1b). Decreasing the initial virulence similarly but more strongly leads to progressively later, larger peaks in virulence (Figure 1c).

Across the entire range of parameters covered by the LHS analysis, all of the classes of models we considered produce qualitatively similar virulence trajectories (Figure 2). Although the speed of virulence evolution varies, leading to wide variation in the peak virulence (means ranging from approximately 3.75 to 4.5 \log_{10} SPVL), virulence peaks in all models between 200 and 300 years.

Fig 2. Envelopes of virulence trajectories under all models. All models were run until $t = 4000$ years; truncated series are shown here.

Our chosen summary statistics (peak time, peak virulence, equilibrium virulence, and relative peak virulence) all vary considerably across models 3. We first consider the models of intermediate realism (implicit, instantaneous-switching with and without extra-pair contact, and pair formation without extra-pair contact). Some parameter sets for these models lead to low equilibrium virulence ($\approx 2.5 \log_{10}$ SPVL); these same sets lead to correspondingly low peak virulence ($< 3.5 \log_{10}$ SPVL) and early peak times (before 200 years), but high relative peaks (> 1.3) (Figure 4, leftmost column) because the equilibrium virulence is low. At the opposite extreme, parameter sets that produce high equilibrium virulence also produce late peaks (> 200 years), high peak virulence, and low relative peaks (≈ 1.05). The pair-formation without extra-pair contact and implicit models occasionally have parameter sets that select for such low virulence across the board that they never exceed their initial virulence, leading to a tail of peak times near zero.

Fig 3. Univariate distributions of summary statistics. The distribution of equilibrium virulence for the random mixing model is very narrow, and has been replaced by a point in order to preserve the vertical axis scaling.

Fig 4. Pairs plot: bivariate relationships among summary statistics for each model structure. Dashed line in equilibrium vs. peak virulence plot shows 1:1 line.

The most striking aspect of the univariate comparisons in Figure 3, (and the bivariate comparisons in Figure 4) is the match between the output of the least (random mixing) and the most complex (pair formation with extra-pair contact) models. The random-mixing model has lower variability, because it is unaffected by uncertainty in pair formation and extra-pair contact parameters, but otherwise the virulence dynamics of these two extreme models are remarkably similar. This phenomenon is driven by the strength of extra-pair contact in the model with explicit pair formation and extra-pair contact (“pairform+epc” in Figures 2-5). When individuals spend time uncoupled between partnerships, and when these single individuals can transmit disease to coupled individuals, the resulting unstructured mixing overwhelms the effect of structured mixing within couples, leading to mixing that is effectively close to random.

Fig 5. Sensitivity plot. For each parameter in the Latin hypercube sample and each summary statistic, shows the distribution (points) and trend (smooth line) of the summary statistic as a function of the *unscaled* parameter value, i.e. prior to adjusting the parameters to achieve the standard initial epidemic growth rate.

Plotting the bivariate result distributions (Figure 4) shows that most of the relationships among the summary statistics are monotonic, except those involving the relative peak virulence (bottom row). Changes in parameters that increase the equilibrium virulence initially increase the peak virulence even more, so that the relative peak virulence increases as well, but beyond an equilibrium virulence of about 2.5 log₁₀ SPVL the peak virulence increases slower than the equilibrium virulence, leading to a decrease in the relative peak virulence.

The bivariate relationships also help distinguish the results of different models with similar univariate distributions. While the relationship between equilibrium virulence and peak time is similar for all model structures (top left panel), the other relationships are more separate. In particular, the implicit and pair-formation (without extra-pair contact) are very similar to each other, but distinct from the other models. We still do not have a convincing explanation for this distinction; we would have expected the implicit model to be most similar to the the instantaneous-switching model without extra-pair contact, which most closely matches its derivation. However, we note that the implicit model derivation is based on defining the force of infection to match a scaled version of \mathcal{R}_0 , and as such would be expected to match the equilibrium behaviour but not necessarily the epidemic-phase behaviour of a model with explicit partnership dynamics.

Finally, the sensitivity plots (Figure 5) show the effects of each parameter on the summary statistics. In almost every case the effects of the parameters are monotonic; note that the plot shows the effects of the *unscaled* parameters, i.e. before they have been adjusted to achieve a standard initial epidemic growth rate. Increases in the transmission rates (β_P , β_D) and durations (D_P , D_D) in the primary and disease stages generally decrease the equilibrium virulence, peak virulence, and peak time, although the random and pair-formation+extra-pair contact models have high, relatively constant values with respect to these parameters.

The base contact rate increases virulence and peak time in almost all cases, although

the pair-formation+extra-pair contact model is again relatively insensitive. The ratio of extra-pair to within-pair contact (c_e/c_w) affects virulence in the instantaneous-switching+epc model, but not the pair-formation+epc model (probably because the uncoupled individuals present in the pair-formation+epc model make extra-pair contact by coupled individuals less important). Surprisingly, neither of the pair-formation models is particularly sensitive to the rate of partnership formation (ρ); the rate of uncoupled contact increases virulence and peak time in the pair-formation+epc model, which is the only model to which it applies.

Discussion

All models must simplify the world. Many constraints — such as data availability, computation time, or code complexity — drive the need for parsimony, with different constraints applying in different contexts. The critical question that modelers must ask is whether the simplified model gives adequate answers, or whether the simplifications have led to qualitatively or quantitatively incorrect conclusions. This question is especially important for modelers who are hoping that their conclusions will guide management decisions.

In the particular example of HIV virulence eco-evolutionary dynamics and epidemiological, we reach the slightly ironic conclusion that the effort put into building a more realistic model essentially cancels out, leaving us in the same position as if we had ignored the problem of epidemiological complexity entirely and used a naive random-mixing contact model. Herbeck *et al.* [11] build a network model of partnerships, but they set the “partnership” duration to 1 day — very unrealistic in epidemic terms, but perhaps actually more true to real-world HIV epidemiological dynamics than a model with realistic partnership durations that neglects extra-pair contact [19]. Adding still further realism might push the results farther away from the random-mixing model. For example, our model forms partnerships randomly, and assumes that extra-pair contact is randomly mixing across the population; one could instead implement extra-pair contact as arising from multiple concurrent partnerships (some, such as contact with sex workers, of very short duration), or more structured partnership formation (by age, ethnicity, or behaviour group). The effects of other realistic complications such as explicit modeling of two sexes (both in contact structure and differential transmission probabilities), temporal and spatial variation in epidemic processes, or presence of genetic variation in hosts are harder to predict.

Parameterization is one of the biggest challenges of epidemiological modeling. In addition to following Champredon *et al.* [14] by doing Latin hypercube sampling across a wide range of epidemiological parameters, we calibrated each set of parameters to the same initial epidemic growth rate, chosen to match the results of previous models [10]. The previous models drew their parameters from previous cohort studies from the 1990s [15, 20] rather than doing any explicit calibration to epidemic curves, but they give reasonable order-of-magnitude growth rates ($\approx 0.04 \text{ year}^{-1}$) for the early stages of the HIV epidemic (although considerably lower than estimates of $\approx 0.07 - 0.1 \text{ year}^{-1}$ based on population genetic reconstructions [21]). However, our reason for calibrating was not to match any specific observed epidemic, but rather to make sure that we were making meaningful comparisons across a range of models with radically different epidemiological structures, and hence involving different interpretations of the same quantitative parameters. For example, in models with instantaneous switching the partnership dissolution rate c is identical to the partnership formation rate; in models with explicit partnership formation, the partnership formation rate is also c at equilibrium, but might vary over the course of an epidemic. It is not obvious whether models with equal parameters but different structures should be directly compared;

calibration solves this problem.

More generally, any model that wants to be taken seriously for management and forecasting purposes should be calibrated to *all* available data, using informative priors to incorporate both realistic distributions of uncertainty for all parameters from independent measurements [22] and calibration from population-level observations of epidemic trajectories. For practical (rather than exploratory) purposes, such a procedure would also be an improvement on the common — although not universal — practice of assessing uncertainty over uniform ranges, rather than distributions that allow more continuous variation in support over the range of a parameter.

Researchers have documented that HIV virulence and set-point viral load are changing, on time scales comparable to those portrayed here (e.g., compare Figure 2 to Herbeck et al's estimated rate of change of $1.3 \log_{10}$ SPVL per century [95% CI -0.1 to 3] [23]), and have begun to build relatively realistic models that attempt to describe how interventions such as mass antiretroviral therapy (ART) can be expected to change the trajectory of virulence evolution [19, 24]. While these efforts are well-intentioned, we caution that epidemiological and other structural details that are currently omitted from these models could significantly change their conclusions.

Conclusion

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Supporting Information

S1 Fig. Bold the title sentence. Add descriptive text after the title of the item (optional).

S2 Fig. Lorem Ipsum. Maecenas convallis mauris sit amet sem ultrices gravida. Etiam eget sapien nibh. Sed ac ipsum eget enim egestas ullamcorper nec euismod ligula. Curabitur fringilla pulvinar lectus consectetur pellentesque.

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Acknowledgments

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