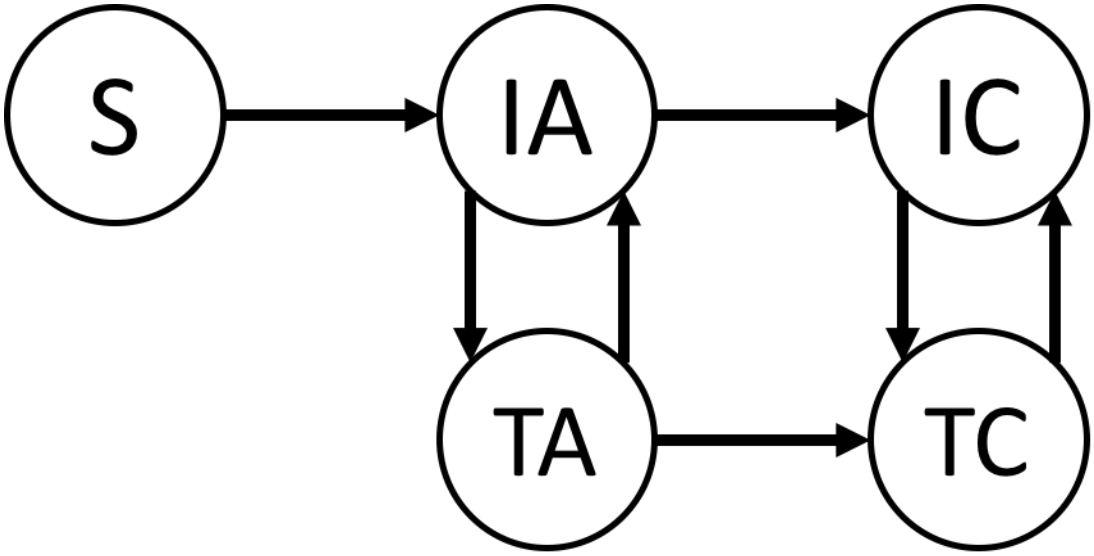
The impact of HIV infections introduced by individuals from outside the contact network was analyzed via a series of transmission network simulation experiments. In each simulation, a contact network is simulated under the Barabási–Albert (BA) model such that the resulting network would exhibit a power law (Albert & Barabási 2002). In order to represent the at-risk San Diego population, the model was parameterized with n = 100,000 individuals and edge parameter m = 2 so the median number of partners per individual is approximately 2 and the average number of partners per individual is approximately 4.

Then, n_s = 10,000 individuals split among k = 4 infection clusters are chosen to be infected at time 0 by edge-weighted randomly choosing k = 4 individuals and performing a random walk from each. In the random walk, a Bernoulli trial with p = 0.7 chance of success is performed to determine if the current uninfected node will be one of the initial infected nodes. The random walk ends when $\frac{n_s}{k} = \frac{10{,}000}{4} = 2{,}500$ are chosen to be initially infected in the current infection cluster.

With the initially infected individuals chosen, an HIV transmission network is simulated under a modified form of the epidemiological model proposed proposed by Granich et al. (Granich et al., 2009). We simplify the model by disallowing death and by using two stages of infection (to represent chronic and acute HIV infection) as opposed to the four stages in the original model. We further simplify the model by removing the Non-Susceptible state: all uninfected individuals are Susceptible (as opposed to needing to enter susceptibility at some rate).



Thus, the states of our model are Susceptible (S), Untreated Acute Infected (I_A), Untreated Chronic Infected (I_C), Acute Infected with ART (T_A), and Chronic Infected with ART (T_C). The edges in the above figure denote the possible state transitions of an individual in the contact network. The model is parameterized by the following Poisson rates:

- $\lambda_{S \to IA:IA}$: The rate of infection from an acute untreated individual
- $\lambda_{S \to IA:IC}$: The rate of infection from a chronic untreated individual
- $\lambda_{S \to IA:TA}$: The rate of infection from an acute individual with ART
- $\lambda_{S \to IA:TC}$: The rate of infection from a chronic individual with ART
- $\lambda_{S \to IA:O}$: The rate of infection from a source outside the contact network
- $\lambda_{IA \to IC}$: The rate at which acute untreated individuals transition to chronic infection
- $\lambda_{IA \to TA}$: The rate at which acute untreated individuals begin ART
- $\lambda_{IC \to TC}$: The rate at which chronic untreated individuals begin ART
- $\lambda_{TA \to TC}$: The rate at which acute individuals with ART transition to the equivalent of chronic infection with ART
- $\lambda_{TA \to IA}$: The rate at which acute individuals with ART stop ART

- $\lambda_{TC \rightarrow IC}$: The rate at which chronic individuals with ART stop ART

For a given susceptible individual v with N_{IA} partners in state I_A, N_{IC} partners in state I_C, N_{TA} partners in state T_A, and N_{TC} partners in state T_C, the transition from S to I_A is a Poisson process parameterized by the following rate:

$$\lambda_{S \rightarrow IA} = \lambda_{S \rightarrow IA:O} + \sum_{s \in \{IA, IC, TA, TC\}} N_s \lambda_{S \rightarrow IA:s}$$

To choose which partner was the source of the infection, a weighted die is rolled where the probability that the source of the infection was partner u (who is in state s_u) is the following:

$$P(U = u) = \frac{\lambda_{S \rightarrow IA:s_u}}{\lambda_{S \rightarrow IA}}$$

All other state transitions are Poisson processes parameterized by the corresponding rate as described above (e.g. the transition from I_A to I_C is a Poisson process parameterized by rate $\lambda_{IA \rightarrow IC}$).

We chose Poisson rates representative of the San Diego at-risk population by making the following series of assumptions:

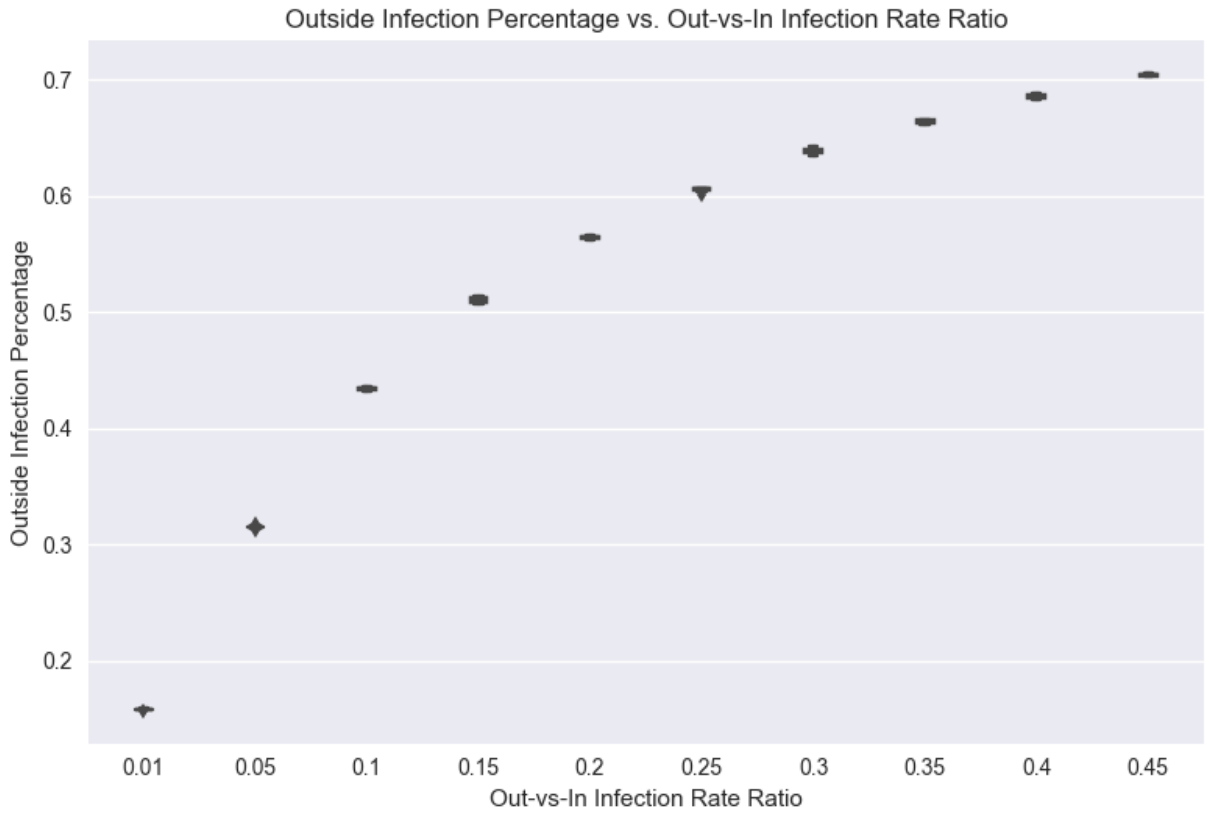
- $\lambda_{IA \rightarrow IC}$: The average time from initial infection to seroconversion is roughly 6 weeks (Bellan et al., 2015)
- $\lambda_{IA \rightarrow TA}$ and $\lambda_{IC \rightarrow TC}$: The average time to begin ART is roughly 77 days (Medland et al., 2017)
- $\lambda_{TA \rightarrow TC}$: Acute individuals who begin ART go to a risk of 0 in approximately 12 weeks
- $\lambda_{TA \rightarrow IA}$ and $\lambda_{TC \rightarrow IC}$: Individuals who stop treatment typically do so after approximately 25 months on average (Nosyk et al., 2015)

We then assumed the following magnitudes of infectiousness relative to the infectiousness of chronic untreated individuals ($\lambda_{S \rightarrow IA:IC}$):

- $\lambda_{S\rightarrow IA:IA}$: Roughly 5 fold infectiousness relative to chronic untreated individuals
- $\lambda_{S\rightarrow IA:TC}$: Negligible (0)
- $\lambda_{S\rightarrow IA:TA}$: Roughly ¼ the infectiousness of chronic untreated individuals

We then used the estimate of roughly 250 new HIV cases per year in order to learn absolute magnitudes for these four rates.

With all parameters except for $\lambda_{S\rightarrow IA:O}$ defined, we performed a series of simulations in which we varied $\lambda_{S\rightarrow IA:O}$. For each choice of $\lambda_{S\rightarrow IA:O}$, we performed 10 replicate simulations. Because all relative infection rates were with respect to a baseline of $\lambda_{S\rightarrow IA:IC}$, we varied $\lambda_{S\rightarrow IA:O}$ as a proportion of $\lambda_{S\rightarrow IA:IC}$. In the following figure, each value on the *x*-axis denotes a selection of $\lambda_{S\rightarrow IA:O} = x\lambda_{S\rightarrow IA:IC}$. We then computed the percentage of total infections that came from outside the contact network, which is depicted by the vertical axis in the following figure.



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