Appendix S1: Description of the simulations

Simulating Transmission in a Typical Household

To simulate transmission within a single household for numerical determination of $\beta^\ast(\tau^\ast)$ and $R^\ast$, a household size $n$ was randomly drawn from the size biased household size distribution $\kappa_n$. Each individual was labelled $i = \{1, \ldots, n\}$ and was allocated an infected-status indicator $I_i$ and time-since-infection $\tau_i$. Uninfected susceptible individuals have $I_i = 0$ while infected individuals have $I_i = 1$. Time-since infection is frozen to $\tau_i = 0$ for all uninfected individuals.

At time $\tau^\ast = 0$, individual 1 is infected from outside the household.

At each time-step, individuals are infected with probability $\Lambda = \delta \sum_{i=1}^{n} I_i \beta_{\delta} (n, \tau_i)$ where $\delta$ is the time-step size. The infectiousness of the household is given by $\beta^\ast(\tau^\ast) = \sum_{i=1}^{n} I_i \beta_{\delta} (\tau_i)$. After each time-step, time-since-infection is incremented by $\tau^\ast \rightarrow \tau^\ast + \delta$ and $\tau_i \rightarrow \tau_i + \delta$ for all $i$ such that $I_i = 1$.

10,000 simulations were carried out for Figures 2 and 3 with time-step 0.02 for influenza and 0.05 for measles.
Simulating Transmission in a Community of Households

To simulate transmission within a community of \( M \) households, \( M \) household sizes \( n_\alpha \) were randomly drawn from the standard household size distribution \( k_\alpha \), where \( \alpha = 1, \ldots, M \) labels the households. Each individual was labelled \((i, \alpha)\) where \( i = \{1, \ldots, n_\alpha\} \) and was allocated an infected-status indicator \( I_{i,\alpha} \) and time-since-infection \( \tau_{i,\alpha} \).

At time \( t = 0 \), individual \((1,1)\) is infected from outside the community.

At each time-step, individuals within each household \( \alpha \) are infected with probability

\[
A_\alpha = \delta \left( \sum_{i=1}^{n_\alpha} I_{i,\alpha} \beta L(n_i, \tau_{i,\alpha}) + \frac{1}{N} \sum_{\beta=1}^{M} \sum_{i=1}^{n_\beta} I_{i,\beta} \beta G(\tau_{i,\beta}) \right)
\]

where the first term represents transmission within households and the second represents random mixing,

\( N = \sum_{\alpha=1}^{M} n_\alpha \) is the total population size and \( \delta \) is the time-step size. After each time-step, time is incremented by \( t \rightarrow t + \delta \) and time-since-infection is incremented by \( \tau_{i,\alpha} \rightarrow \tau_{i,\alpha} + \delta \) for all \( i - \alpha \) such that \( I_{i,\alpha} = 1 \).

10 simulations in populations of \( M = 2,000 \) households were carried out for Figure 4 with time-step 0.02 for influenza and 0.05 for measles.