

Estimating Individual and Household Reproduction Numbers in an Emerging Epidemic

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Appendix S1: Description of the simulations

Simulating Transmission in a Typical Household

To simulate transmission within a single household for numerical determination of $\beta^*(\tau^*)$ and R^* , a household size n was randomly drawn from the size biased household size distribution κ_n . Each individual was labelled $i = \{1, \dots, n\}$ and was allocated an infected-status indicator I_i and time-since-infection τ_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 $\tau^* = 0$, individual 1 is infected from outside the household.

At each time-step, individuals are infected with probability $\Lambda = \delta \sum_{i=1}^n I_i \beta_L(n, \tau_i)$ where δ is the time-step size. The infectiousness of the household is given by

$\beta^*(\tau^*) = \sum_{i=1}^n I_i \beta_G(\tau_i)$. After each time-step, time-since-infection is incremented by $\tau^* \rightarrow \tau^* + \delta$ 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_α were randomly drawn from the standard household size distribution k_n , where $\alpha = 1, \dots, M$ labels the households. Each individual was labelled (i, α) where $i = \{1, \dots, n_\alpha\}$ 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 α are infected with probability

$\Lambda_\alpha = \delta \left(\sum_{i=1}^{n_\alpha} I_{i,\alpha} \beta_L(n, \tau_{i,\alpha}) + (1/N) \sum_{\beta=1}^M \sum_{i=1}^{n_\beta} I_{i,\beta} \beta_G(\tau_{i,\beta}) \right)$ 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 δ 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.