**SUPPLEMENTARY MATERIAL**

**Supplementary Table S1.** Infectious disease states used in the simulation.

|  |  |  |  |
| --- | --- | --- | --- |
| **Disease state** | **Infectious** | **Circulating** | **Description** |
| Susceptible |  | • | The person is susceptible to infection |
| Latent |  | • | The person has been infected but has not begun to shed virus |
| InfIncubation | • | • | The person has started to shed virus, but it is still too early to experience symptoms |
| InfSympCirc | • | • | The person is infectious, symptomatic, and circulating in the community |
| InfSympNotCirc | • |  | The person is infected and symptomatic, but not circulating in the community (i.e., retreated to the household) |
| InfAsympCirc | • | • | The person is infected but asymptomatic (i.e., unaware of the infection) |
| Recovered |  |  | The person has recovered from the infection |
| Removed |  |  | The infection was fatal and the person has been removed from the simulation |

**Supplementary Table S2.** Community-level mixing groups.

|  |  |
| --- | --- |
| **Mixing group** | **Description** |
| Neighborhood | The purpose of the neighborhood mixing groups is to model transmission among people living in the same area. Typically, a neighborhood consists of 500 individuals |
| Community | The community mixing group models the probability of transmission among any individual. For example, anyone might randomly meet anyone in public spaces, such as streets and shopping centers |

**Supplementary Table S3.** Transmission probabilities at household and community levels by age. The probabilities are computed as the product of the contact probability and the likelihood of transmission when contact occurs (values from [1]). The tabulated values in [1] denote contact probabilities and were multiplied by 0,12 (the average per-contact transmission probability suggested in [1]). The computed transmission probabilities were also marginally adjusted to account for the Swedish setting, e.g. the community-level contact probabilities for the elderly are slightly decreased.

|  |  |  |
| --- | --- | --- |
| **Mixing group** | **Age (years)** | **Age (years)** |
| 0–5 | 6–18 | 19–64 | 65– |
| Household | 0–5 | 0.08 | 0.08 | 0.03 | 0.03 |
| 6–18 | 0.08 | 0.08 | 0.03 | 0.03 |
| 19–64 | 0.03 | 0.03 | 0.04 | 0.04 |
| 65– | 0.03 | 0.03 | 0.04 | 0.04 |
| Neighborhood | 0–5 | 0.00004 | 0.00004 | 0.00004 | 0.00004 |
| 6–18 | 0.00004 | 0.00012 | 0.00012 | 0.00012 |
| 19–64 | 0.00004 | 0.00012 | 0.00016 | 0.00016 |
| 65– | 0.00004 | 0.00012 | 0.00016 | 0.00016 |
| Community | 0–5 | 0.00001 | 0.00001 | 0.00001 | 0.00001 |
| 6–18 | 0.00001 | 0.00003 | 0.00003 | 0.00003 |
| 19–64 | 0.00001 | 0.00003 | 0.00004 | 0.00004 |
| 65– | 0.00001 | 0.00003 | 0.00004 | 0.00004 |

**Supplementary Table S4.** Transmission probabilities for mixing groups related to childcare and schools [adjusted from 1].

|  |  |  |
| --- | --- | --- |
| **Mixing group** | **Age** | **Transmission probability** |
| Playgroup | 0–5 | 0.0400 |
| Daycare | 0–5 | 0.0150 |
| Elementary school | 6–12 | 0.0145 |
| Middle school | 13–15 | 0.0125 |
| High school | 16–18 | 0.0105 |

**Supplementary Table S5.** Transmission probabilities at workplaces (basic transmission probability for the Industrial-administrative workplace culture adjusted from [1]).

|  |  |  |
| --- | --- | --- |
| **Workplace culture** | **Workgroup size (*n*)** | **Transmission probability within the workgroup** |
| 1. Industrial-administrative | 20 | 0.00575 |
| 2. Academic-creative | 40 | 0.00575 |
| 3. Academic-creative, restricted | 40 | 0.002875 |
| 4. Self-employed | 1 | 0 |

**Supplementary Table S6.** Probability distribution for disease stage durations [2].

|  |  |  |
| --- | --- | --- |
| **Type** | **Age (years)** | **Day no.** |
| 0 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 |
| Incubation period | 0–12 | 0.25 | 0.75 |  |  |  |  |  |  |  |  |  |  |  |  |
| 13– |  | 0.25 | 0.75 |  |  |  |  |  |  |  |  |  |  |  |
| Latent period | 0–12 |  | 0.5 | 0.5 |  |  |  |  |  |  |  |  |  |  |  |
| 13– |  |  | 0.75 | 0.25 |  |  |  |  |  |  |  |  |  |  |
| Infectious period | 0–12 |  |  |  |  |  |  |  | 0.5 | 0.25 | 0.2 | 0.05 |  |  |  |
| 13– |  |  |  |  |  |  |  | 0.5 | 0.4 | 0.02 | 0.02 | 0.02 | 0.02 | 0.02 |

# Supplementary text S1

## Details of the community model

Of the nine mixing group types in the model, four (household, neighborhood, community, and society) can be visited by every person. Neighborhoods with 500 people and communities are generated based on geographical data in sufficient numbers to cover the simulated population (Table S2). Households are assigned randomly to a neighborhood, and all members of a household are assigned to the same neighborhood.

The model assumes that the probability of a preschool child (age <6 years) being in daycare is 0.75. Children considered to be in daycare are assigned to the daycare center closest to the household location (based on geographical coordinates). Preschool children who are not in daycare are assigned to a playgroup mixing group associated with their neighborhood. Each playgroup consists of at most 4 children. Children in elementary and middle school (age 6–15 years) are assigned to the school closest to their household location (based on geographical coordinates). Since the model assumes that children of the same age mix while in school, it uses one mixing group for each year in each of the schools. In other words, each school child becomes a member of their school’s mixing group for their age. For high-school children (age 16–18 years), the model assumes that students select a program based on their interests rather than the location of the school. Furthermore, the model assumes that high-school children are in contact with a somewhat larger group of students. Therefore, the model uses a unique mixing group for each school, program, and year (i.e., students in the same school and program mix with individuals of the same age). Operationally, the simulator assigns students randomly to high schools and programs based on actual schools and the number of students in each of the programs (i.e., the actual capacity of the actual high schools).

## Biological model details

The person-to-person transmission probabilities for the mixing group types [adjusted from 1, 3] that were kept constant in the experiments are presented in Tables S3 and S4, and the corresponding worker-to-worker transmission probabilities in Table S5. The latent period begins when the individual is infected and ends when viral shredding begins and the person is infectious. The incubation period begins when the individual is infected and ends when he or she develops symptoms. The duration of the latent and incubation periods follow empirical probability distributions [2]. The disease model used parameters from H1N1/2009. For adults, the minimal latent and incubation periods are 1 and 2 days, respectively. For children younger than 12 years, onset of viral shredding for a subset (25%) is estimated to take place within the first day after virus transmission and symptoms to appear 1 day later. The normal infectious period is set to 5–7 days among adults, while it is prolonged up to 14 days in a small subset (2%) consisting of immunocompromised individuals. Among young children, the infectious period is set to be prolonged up to 11 days in a subset of individuals (5%) also including healthy children. Table S6 summarizes the simulator settings for these disease stages used in the experiments. In Table S6, the infection is assumed to occur at the beginning of day number 0. During the infectious period, the infected person may or may not develop influenza symptoms. The probability that a person will be symptomatic given that person has been infected is 0.67. An asymptomatic infection is assumed to be 50% as infectious as a symptomatic infection. In the model, the probabilities that a person with symptoms withdraws to the household are 0.80, 0.75, and 0.50 for the age groups 0–5, 6–18, and 19– years, respectively, exposing only the other members of their household. People who do not withdraw continue circulating in their mixing groups.

References

**1. Germann TC, *et al*.** Mitigation strategies for pandemic influenza in the United States. *Proc Natl Acad Sci U S A* 2006; **103**: 5935-5940.

**2. Carrat F, *et al.*** Time lines of infection and disease in human influenza: a review of volunteer challenge studies. *American Journal of Epidemiology* 2008; **167**: 775–785.

**3. Halloran ME, *et al*.** Modeling targeted layered containment of an influenza pandemic in the United States. Proceedings of the National Academy of Sciences USA 2008; **105**: 4639–4644.