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Transmission of acute respiratory infections in a city: agent-based approach

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Motivation and Aim: Acute respiratory infections (ARI) are the major public health concern, being the principal cause of morbidity and mortality in many countries. They are caused by various pathogens with viruses accounting for the majority of cases. The purpose of this model is to combine heterogeneous data into a dynamic system that can reproduce a seasonal increase in the incidence of ARI, taking into account their etiology, in a city with a temperate climate and that can be used to explore additional scenarios, such as the effectiveness of interventions or the possible impact of global warming.
Methods and Algorithms: We developed an agent-based model to simulate the co-circulation of different respiratory viruses in a city (Fig. 1). We included seven predominant circulating viruses in Russian cities: influenza A and B, rhinovirus, respiratory syncytial virus, adenovirus, parainfluenza and coronavirus [1], with their properties, such as mean viral load [2], duration of incubation period [3], duration of symptoms [4] and probability of being asymptomatic [5], being estimated from the available literature. The model consists of multiple entities called agents, which are characterized by a set of properties. Such properties as age, sex, and economic status are set using city-specific demographic and socio-economic information from the Russian Census of 2010. Agents are assigned to households and can also be assigned to one main activity (school or work). The model simulates one year and has discrete time steps equal to a single day. Transmission of the viruses occurs when there is a contact between two agents in the same setting, which is modeled using contact networks represented as complete graphs for households and school classes, and Barabasi-Albert graphs for workplaces. Each agent can be as either susceptible, exposed, infectious, or recovered according to the stage of the infection. The probability of transmission is defined by the product of four main factors: infectivity of infectious agent, susceptibility to the virus of susceptible agent, duration of their contact and air temperature on the current step. Model calibration uses the simulation optimization that minimizes the normalized mean absolute error between the simulated and observed epidemic curves.
Results: We simulated the spread of respiratory infections observed in Moscow, Russia, in 1996–2002. The proposed model provided a good fit for the average epidemic curve, curves for 7–14 and 15+ age groups and curves for influenza A and B, respiratory syncytial virus, parainfluenza and adenovirus. We were able to capture the dynamics corresponding to the school holidays. Our estimates for 3–6 age group and rhinovirus were slightly underestimated. An incidence in 0–2 age group was greatly underestimated. Our model also greatly overestimated an incidence of coronavirus in February. We also examined two additional scenarios. In the first scenario, we simulated one-week school and class closures when student absences due to ARI were at or above 20 %, and found that it led to the reduction in the total number of diagnosed cases by

12 % and its maximum peak by 23 %. In the second scenario, representing a global warming, we increased the average air temperature by 2 °C and found that while the total number of diagnosed cases decreased by 7 %, the maximum peak size decreased by 12 %.
Conclusion: We created a model that can be used as a tool to simulate future outbreaks of emerging viruses in order to improve our understanding of the ongoing epidemic and to devise appropriate interventions.
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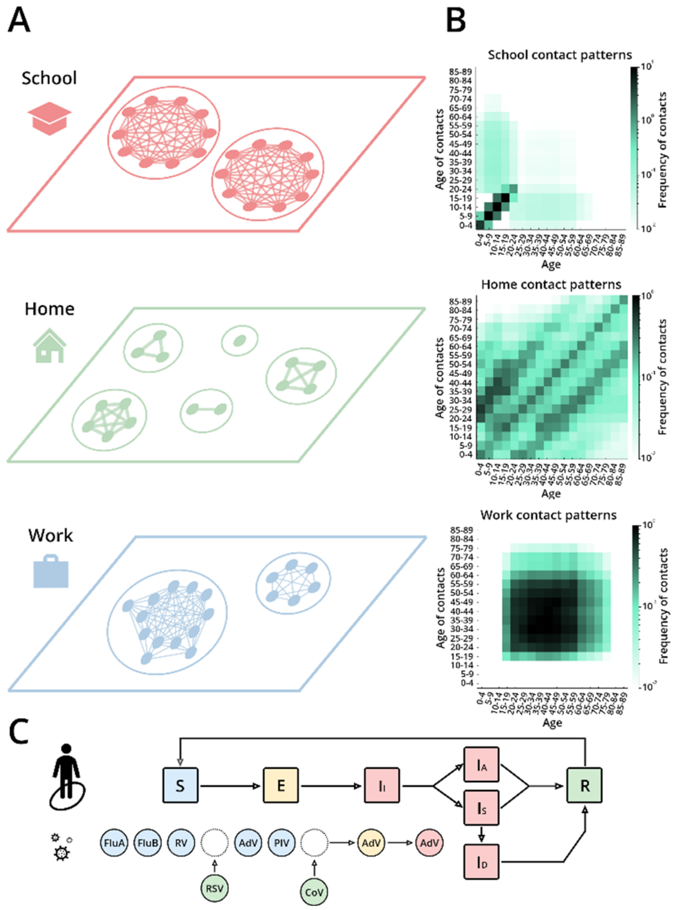

Fig. 1. Model structure. (A) Contact networks for different activities. (B) Age-specific contact patterns for different activities. (C) Within-host disease progression

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