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Constructing Representative Social Networks for Disease Simulation

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ABSTRACT

Diseases spread mechanisms have been questioned and studied for many years. The ability to make predictions about an epidemic could enable scientists to evaluate inoculation/ isolation plans, control the mortality rate, and prevent the future course of an outbreak. Accurate predictions, however, are extremely hard to make and requires interdisciplinary solutions from epidemiology, sociology, statistics, graph theory, and Computer Science. For making the prediction, currently few network analysis platforms written in C++ are designed and optimized. The research is aimed to address this gap by exploring methods of constructing social contact network, simulating disease spreading, and proposing mitigation strategies for use by public health officials. We present a network construction and simulation library which allows studying the progress of an epidemic in a large scale social contact network. The library easily manipulates large graphs, generates regular and random graphs, and supports various compartmental models in epidemiology. The library allows network construction of the population given publicly available census information in the geographical area under consideration. Given the characteristics of the disease, the library is able to simulate a single or multiple outbreaks over the network. Standard outputs are the evolution of the prevalence of the disease and different possible mitigation strategies given a variety of constraints. The network analysis platform serves as a handy tool designed to help us to understand the paths followed by outbreaks in a given community and to generate strategies for preventing and controlling them.

KEYWORDS

C++, graph theory, epidemiology, social contact network, simulation, mitigation

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