in silico Surveillance: Using Detailed Computer Simulations to Develop and Evaluate Outbreak Detection

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OBJECTIVE

Developing and evaluating detection algorithms in noisy surveillance data is complicated by a lack of realistic noise, meaning the surveillance data stream when nothing of public health interest is happening. These jobs are even more complex when data on the precise location of cases is available. This paper describes a methodology for plausible generation of such noise using agent-based models of infectious disease transmission based on highly resolved dynamic social networks.

BACKGROUND

Developing and evaluating outbreak detection is challenging for many reasons. A central difficulty is that the data the detection algorithms are "trained" on are often relatively short historical samples and thus do not represent the full range of possible background scenarios. Once developed, the same dearth of historical data complicates evaluation. In systems where only a count of cases is provided, plausible synthetic data are relatively easy to generate. When precise location data is available, simple approaches to generating hypothetical cases is more difficult.

Advances in epidemiological modeling have allowed for increasingly realistic simulations of infectious disease spread in highly detailed synthetic populations. These agent-based simulations are capable of better representing real-world stochastic disease transmission process and thus show highly variable results even under identical initial conditions. Due to their ability to mimic a wide range outcomes and more fully represent the unknowns in a system, models of this class have become increasingly used to help inform decisions about public policies about hypothetical situations (eg pandemic influenza [1]). This characteristic also makes them a powerful tool to represent the processes that create surveillance information.

METHODS

A dynamic social network for the Boston metropolitan area (4.1 million individuals) was constructed using previously described methods [2]. In brief these methods are based on "agents," or individual digital representations, of every person. These agents visit specific locations throughout the area of study and interact with other agents. The individuals, locations, and activity patterns are all based on data collected from the real world and are combined in large scale simulations run on a high-performance computing platform. The natural history of generic influenza-like (ILI) illnesses were modeled and their spread was simulated across this realistic dynamic social network. In addition true-influenza outbreaks were also modeled and simulated in this same population. Combining these simulations can be done in a variety of ways which allows the creation of a highly customizable outbreak embedded in a realistic background of clinically similar disease.

The resulting *in silico* surveillance data was analyzed to determine the ability of SaTScan software to detect the true-influenza outbreaks among the ILI noise.

RESULTS

This methodology was capable of producing data that had many of the characteristics of existing surveillance data. SaTScan was able to detect true-influenza.
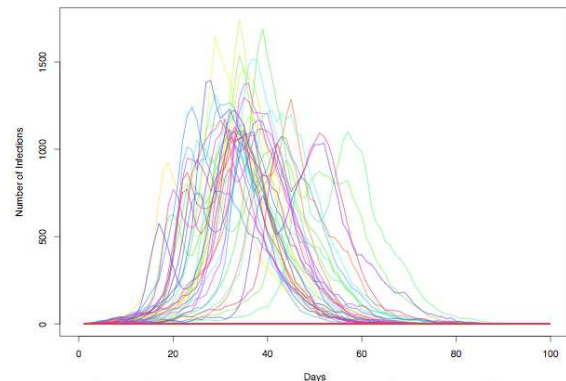

Figure 1. Family of epidemics possible from same initial conditions, demonstrating the variability of these simulations

CONCLUSIONS

Simulations based on highly detailed and dynamic social networks provide a good platform for creating realistic spatial surveillance data. The ability to manipulate and finely control the structure of this data makes it a valuable tool for further refining and evaluating outbreak detection algorithms.

REFERENCES

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