Modeling disease spread using multi-dimensional Susceptible-Infected-Recovered (SIR) models

by

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Date	:	**26 June 2019 (Wednesday)**
Time	:	**11:00 a.m. – 12:00 noon**
Venue	:	**Seminar Room 3, G/F, Jockey Club Building for Interdisciplinary Research, 5 Sassoon Road**

Abstract:

Understanding the dynamics of infectious disease spread in a heterogeneous population is an important factor in designing control strategies for these diseases. In my talk I will present a novel tensor-driven multi-dimensional version of the classic Susceptible-Infected-Recovered (SIR) model. I will then show two studies where we fit the model to observed data and the insights gained about disease from this fit.

In our first study we fit the model to state-level Google search data from the United States pertaining to two viruses, Respiratory Syncytial Virus (RSV) and West Nile Virus (WNV). Although no prior assumptions on spatial structure were made, human movement patterns in the US explain 27-30% of variability in inter-state transmission rates, as calculated from the estimated model parameters. The inferred transmission rates within states are correlated with known demographic indicators, such as population density and average age. Moreover, using the model, spatial and temporal patterns of disease load for subsequent seasons can be predicted from model parameters estimated in previous seasons and as few as 7 weeks of data from the current season.

In our second study we developed a data-quality-sensitive optimization framework for fitting the model to observed data and applied it to the temporal profile of the number of people infected by one of six influenza strains in Europe, over 7 influenza seasons. We show that disease parameters remain relatively stable over seasons. Clustering of influenza strains by inferred disease parameters is consistent with genome sub-types. Surprisingly, our analysis suggests that inter-country human mobility plays a negligible role in the spread of influenza in Europe.

Our model, and the methods developed to fit it to observational data, can reveal information on the spreading mechanism of infectious diseases. These can be used to assist in disease surveillance and in control of influenza as well as of other infectious pathogens in a heterogenic environment.

Bio-sketch:

Elad Yom-Tov is a Principal Researcher at Microsoft Research. Before joining Microsoft he was with Yahoo Research, IBM Research, and Rafael. His primary research interests are in applying large-scale Machine Learning and Information Retrieval methods to medicine. Dr. Yom-Tov studied at Tel-Aviv University and the Technion, Israel. He has published four books, over 100 papers (of which 3 were awarded prizes), and was awarded more than 20 patents. His latest book is "Crowdsourced Health: How What You Do on the Internet Will Improve Medicine" (MIT Press, 2016).