

Bayesian analysis and prediction of infectious disease outbreaks based on temporal data

Professor Xavier Didelot and Professor Matt Keeling

Background

When an outbreak of an infectious disease takes place, field epidemiologists attempt to gather as much information as possible about each individual case of the disease. However, in the early stages of an outbreak, and sometimes even later on, the only data available is the number of reported cases per day. Such case reports are typically the result of infection that happened days before, may exclude some mild or even asymptomatic cases, and may also include unrelated cases that are not part of the outbreak.

Objectives

The aim of this project is to develop and apply a stochastic model of infectious disease outbreaks that accounts for the complexity of the real epidemiological process while remaining statistically tractable. After an initial prospective phase, the project will explore several questions of interest, for example how to detect when an outbreak starts, when can an outbreak be declared over, how to forecast the epidemic curve, and how to reconstruct changes in transmissibility, etc.

Proposed research plan

1. Develop a simple stochastic model of outbreaks, using either a compartmental approach or a branching process (or both, and investigate the similarities and differences)
2. Implement simple simulations under this model
3. Derive a mathematical formulation for the likelihood which may require the use of data augmentation techniques, numerical approximation and/or Monte-Carlo approximation (such as a particle filter)
4. Implement a Bayesian approach to infer the parameters of the model based on case report time series, for example using a Markov Chain Monte Carlo
5. Make predictions about the current status of the outbreak, or its future trajectory, or test competing hypothesis by calculating or approximating a Bayes Factor
6. Test the methodology using simulated datasets where answers are available and/or to real datasets on outbreaks of a complex disease such as tuberculosis

Starter References

1. Wallinga J, Teunis P. Different Epidemic Curves for Severe Acute Respiratory Syndrome Reveal Similar Impacts of Control Measures. *Am J Epidemiol.* 2004;160: 509–516.
2. Cori A, Ferguson NM, Fraser C, Cauchemez S. A new framework and software to estimate time-varying reproduction numbers during epidemics. *Am J Epidemiol.* 2013;178: 1505–12.
3. Didelot X, Fraser C, Gardy J, Colijn C. Genomic infectious disease epidemiology in partially sampled and ongoing outbreaks. *Mol Biol Evol.* 2017;34: 997–1007.