

IE 69000: Computational Epidemiology

Overview. Computational epidemiology is a multidisciplinary field focusing on the study and development of computational techniques and tools for modeling, simulating, predicting, and mitigating the spread of infectious diseases. This course will include compartmental, agent-based and network-science based approaches, and how to utilize domain knowledge and data analytics methods within these contexts. The course will be composed of three primary sections, (1) disease spread models and dynamics, (2) inference and prediction, (3) mitigation, followed by a (4) section on advanced topics. A significant goal of the course will be for students to devise and solve optimization problems pertaining broadly to mitigation.

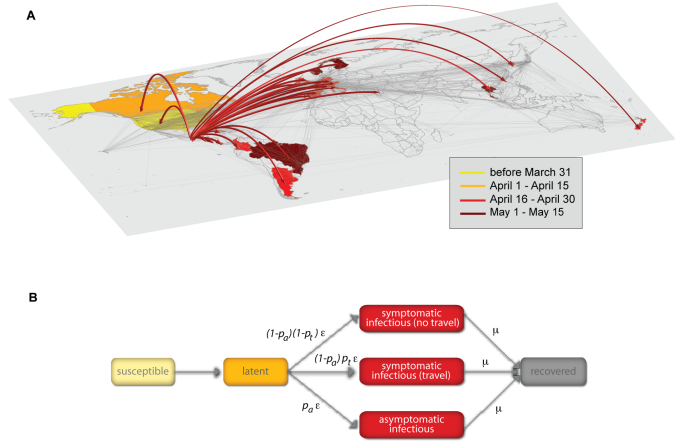


Figure 1: From [1]. (A) network representation of seeding of 2009 H1N1 pandemic, (B) disease progression model

Background. A background in epidemiology, immunology or biology is not expected, but may be useful. However, students should have a solid background (i.e., graduate level courses) in probability and statistics, discrete optimization or algorithm design, and be very strong programmers in at least one of C, Java, Python, R or Matlab. A mature background in network science and agent-based simulation would also be very beneficial, or will require students to conduct sufficient pre-course or aside readings (network science and agent-based simulation as concepts will not be heavily discussed in lecture, only their application to the course).

Evaluation. (tentative) A major component of student evaluation will be a project that consists of nontrivial programming, proper analysis/visualization of results, writing a strong technical paper and presentation. Hence, being proficient in these skills will be an asset. Students should also be prepared to perform, discuss or present multiple critical paper reviews/reports, including algorithmic and mathematical concepts.

References

- [1] Paolo Bajardi, Chiara Poletto, Jose J Ramasco, Michele Tizzoni, Vittoria Colizza, and Alessandro Vespignani. Human mobility networks, travel restrictions, and the global spread of 2009 h1n1 pandemic. *PloS one*, 6(1), 2011.