

Deconstructing SIR: urban space and strain structure in infectious disease dynamics

MERCEDES PASCUAL

University of Chicago and The Santa Fe Institute, USA, pascualmm@uchicago.edu

Keywords: urban environments, climate forcing, antigenic diversity, diarrheal diseases, spatial structure

An alternative title for my talk could have been about ‘scales that matter’ in the response of infectious diseases to climate forcing and intervention, in relation to the resolution in either space or pathogen population structure that needs to be incorporated in mathematical models of transmission. My presentation will rely on examples from our work on cholera, rotavirus and malaria to illustrate some aspects of this theme in the context of the application of SIR (Susceptible-Infected-Recovered)-type models that ignore such axes of heterogeneity.

The first part of my talk addresses the population dynamics of diarrheal diseases under climate forcing in a large urban environment of the developing world. Studies on responses of infectious diseases to climate variability have typically considered temporal records and models aggregated over whole cities, in part because drivers such as ENSO are thought to operate at large, regional scales. With extensive spatio-temporal records for cholera and rotavirus in the megacity of Dhaka, Bangladesh, the need to consider a higher spatial resolution is demonstrated. A general approach based on a probabilistic (Markov Chain) model is presented that identifies significant spatial heterogeneity in the ‘metapopulation’ dynamics of cholera (Reiner *et al.*, 2012). This analysis leads to the distinction of two parts of the city, and to a spatial resolution at which to ‘zoom out’ and aggregate the data to parameterize mechanistic models that incorporate epidemiological processes. Results reveal unexpected differences in seasonality and in the force of infection in the different parts of the city, which are discussed in the context of socio-economic and demographic heterogeneity.

The second part of my talk transitions via SIR-type models for rotavirus and malaria that attempt to implicitly represent antigenic variation within pathogen populations, to ask about the emergence of such strain structure in a dynamical context. Computational (individual-based) models are used to extend strain theory and consider strain structure in rotavirus under the evolutionary pressures of reassortment and (zoonotic) immigration of new types. Open questions related to the mathematical representation of pathogen diversity are discussed, on how such representation would matter to non-autonomous dynamics, whether as the result of environmental forcing or intervention.

Bibliography

- [1] R.C. REINER, A. KING, M. EMCH, MD. YUNUS, A.S.G. FARUQUE AND M. PASCUAL *PNAS*, Highly localized sensitivity to climate forcing drives endemic cholera in a megacity. 109, 6, 2033-2036, 2012