

Unfolding Infectious Disease Studies

Gabriela Gomes, Instituto Gulbenkian de Ciência, Portugal

Abstract:

The overarching goal of my current research is to empower infectious disease studies with the identification of dimensions where hidden phenomena may unfold. My research group develops and applies theory and methods to the design and analysis of specific host-pathogen studies, resulting in new protocols to assess intervention strategies. Our focus has two main components:

1) *Pathogen-dose dimension*. The impact of interventions against infectious diseases (such as vaccines, or other preventive or therapeutic tools) depends on the intensity of ongoing transmission (pathogen-dose dimension). Individual protection, on the other hand, varies between hosts, reflecting underlying biological variation and affecting population level protection. Owing to the nature of resistance mechanisms, distributions of protection entangle with pathogen dose in a way that can be decoupled by adequately representing the dose dimension. As a result, a global measure of protection that applies across epidemiological settings is extracted [1].

2) *Pathogen-evolution dimension*. Pathogens undergo genotypic and phenotypic evolution as they spread in a host population [2]. Moreover, biological and biomedical interventions are likely to modify pathogen evolution in ways that are difficult to predict. To the extent that epidemiological processes affect pathogen evolution, genetic sequencing is informative for the epidemiological model and starts to be used in inference studies.

Specific case studies in different host-pathogen systems are adopted to test and refine the representation of pathogen *dose* and *evolution* in mathematical models and study designs, while accurately monitoring host responses, over those axes, in intervention and non-intervention individuals. In the first instance, this provides freedom for quantitative and qualitative properties of the intervention mode of action to unfold. Further downstream in the modeling process, it allows for better anticipation of community strategies to face future outbreaks of infectious diseases and lead to more realistic impact assessment.

References:

1. Gomes MGM, Lipsitch M, Wargo AR, Kurath G, Rebelo C, Medley GF, Coutinho A (2014) A missing dimension in measures of vaccination impacts. *PLOS Pathogens* 10(3): e1003849.
2. Parisi A, Lopes JS, Nunes A, Gomes MGM (2013) Heterogeneity in antibody range and the antigenic drift of influenza viruses. *Ecological Complexity* 14: 157-165.