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Modeling the emergence and control of infectious diseases

Mathematical models are increasingly being used to understand and predict the spread of infectious diseases. Often deterministic models suffice for tracking the dynamics of well-established diseases, but the initial stages in the emergence of new infectious diseases are often marked by considerable stochasticity. This stochasticity enters in at least two important ways. First, many new diseases arise from cross-species transmission, and some degree of evolutionary adaptation is often required before the pathogen can spread. Stochasticity in the evolutionary process in terms of which mutations arise and reach fixation plays a key role is whether or not such diseases take hold. Second, once a pathogen has adapted and is beginning to spread, medical interventions (e.g., quarantine) will typically be imposed. The relatively small initial number of cases during this phase also means, however, that stochasticity will play an important role in the extent to which such interventions are effective. I will present some recent modeling results treating both of these phenomena, with reference to the emergence of pandemic influenza as well as the 2003 outbreak of SARS.