
Modelling influenza at the human-animal interface

Edward Hill*¹

¹Centre for Complexity Science [Warwick] – University of Warwick Gibbet Hill Road Coventry CV4
7AL, Royaume-Uni

Résumé

Influenza inhabits many hosts and has many strains. The biology and epidemiology of influenza is radically different depending on the host species: while ducks are essentially asymptomatic carriers of all influenza strains, in other birds and mammals influenza can be lethal. Very occasionally, humans become infected with a virus derived from non-human sources. These are essentially novel to humans. Due to the viruses meeting with little or no established resistance, they can, following mutation and adaptation to their new host, spread relatively easily in the human species. This can give rise to a localised outbreak that may develop into a worldwide influenza pandemic. Despite this, there is a worrying gap in the modelling of spillover transmission from animals to humans. While the within-species dynamics of influenza in poultry and humans has been well studied, we present a spatial model incorporating cross-species transmission. The model is focused at a local level, to incorporate locations of farms and markets where livestock and humans are in close contact. This framework will be applied to H5N1 case data in Bangladesh, with possible computational techniques to parameterise the model outlined. The methodology used allows for a broad range of future directions of study, in particular investigating how differing spatial configurations of human and animal populations impact the effectiveness of control strategies.

*Intervenant