



1. Motivation

Influenza A has **many strains** and inhabits **many hosts**. Between-species transmission of influenza is possible. Occasionally, a strain enters the human population capable of causing **global pandemics**, most recently in 2009. There is a worrying gap in the modelling of spillover transmission from animals to humans. We aim to build a model incorporating this aspect.

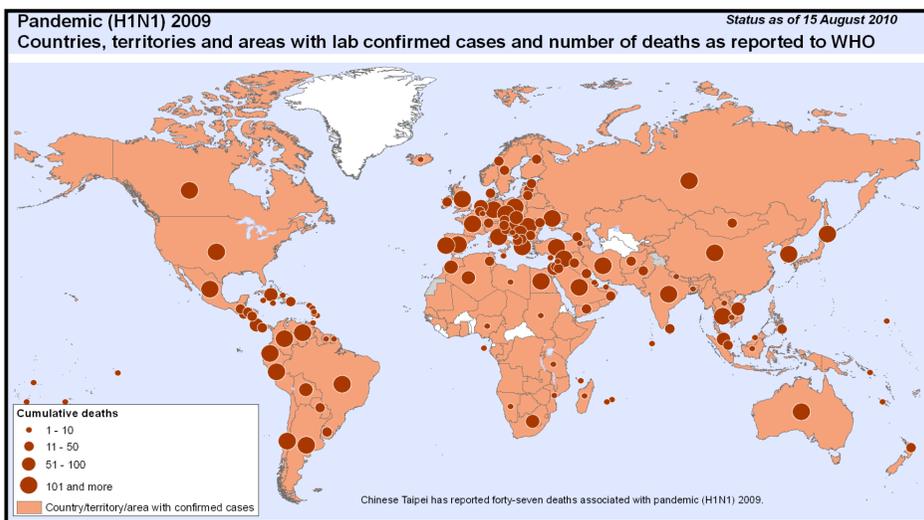


Fig. 1: Countries with lab confirmed cases and cumulative number of deaths at the end of the H1N1 pandemic, August 2010. Reproduced from the World Health Organisation, *Pandemic (H1N1) 2009 – update 115 (2010)*.

2. Objectives

It is critically important to understand how likely it is that more **lethal strains** will cause a **pandemic** in the human population.

Our model will be utilised as follows:

- Test the impact livestock and human spatial configurations have on the risk of spillover transmission from animals to humans.
- Fitted to influenza case data in regions with both livestock and human cases (e.g. H5N1 in Bangladesh)

3. Model Formulation

A multi-strain, multi-host **stochastic susceptible-infected-recovered (SIR) model** was used, focused on a local scale. Main features include:

- Once one animal is infected with a given strain, the entire population of that species on that farm is infected immediately with the same strain.
- Flock-level susceptibility and transmissibility are assumed to be the sum of the animal-level susceptibility and transmissibility.
- Epidemiological unit for humans are individuals.
- Individual humans and groups of animals can be infected by at most one strain at any one time; **“super infection” is not possible**.

Model simulations used the **Tau leap** method.

4. Results: Synthetic Data

Consider two host species, host 1 very clustered, host 2 randomly placed.

Strain 1 is more transmissible, but infectious period is half the length of strain 2.

For each strain, five host 1 sites are initially infected. Host 2 sites can **only** become infected via spillover transmission.

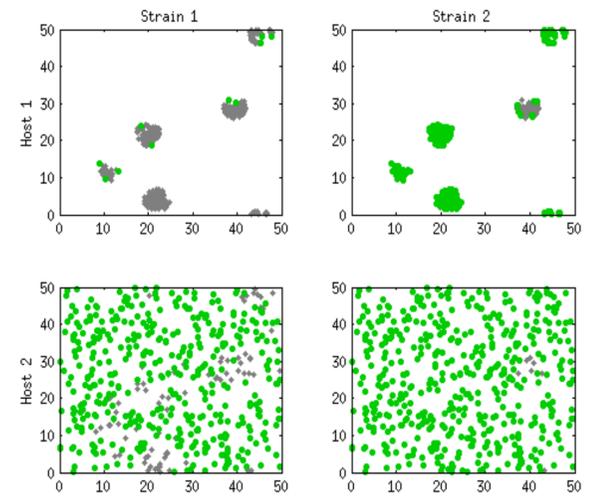


Fig. 2: Example output from one simulation run. Grey sites were infected. Green sites remained susceptible.

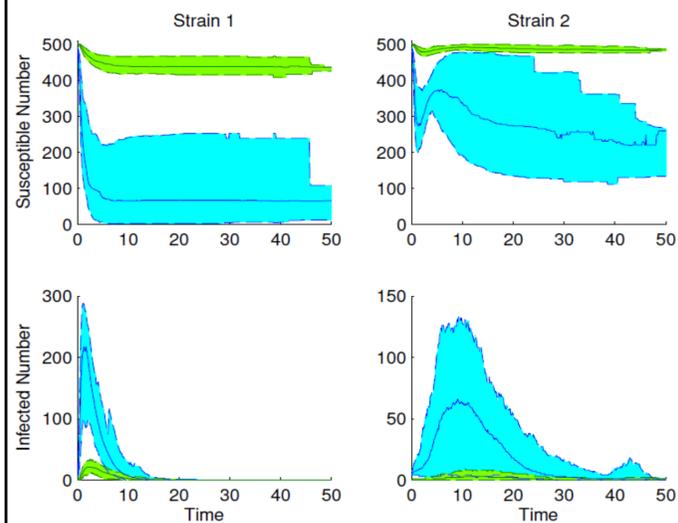


Figure 3: Traces of susceptible and infected numbers from 100 simulations. Host 1 in blue, host 2 in green. Median value given by solid line. Shaded regions correspond to 95% credible intervals.

Summary of findings:

- Amount of spillover transmission **higher for strain 1** (Figs. 2,3).
- When reversing the host configurations (host 1 – random, host 2 - clustered) **no spillover transmission observed**.

5. Future Work: H5N1 in Bangladesh

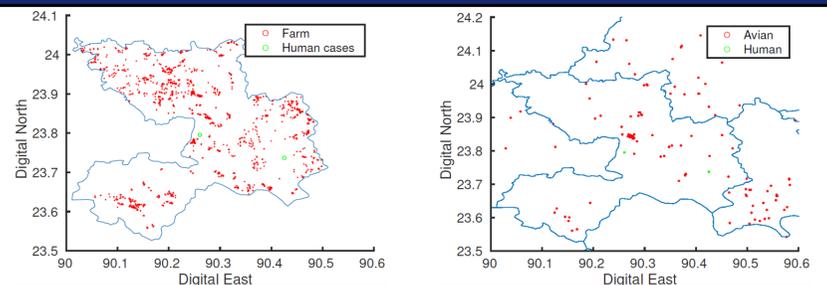


Fig. 4: Left -Human case locations and farm locations within the Dhaka district. Right – Human and avian case locations for the Dhaka district and surrounding area.

In Bangladesh, H5N1 avian influenza has infected over 500 poultry farms in Bangladesh, with 7 confirmed human cases. Our work will focus on the Dhaka district (Fig. 4) and includes:

- **Parameter inference** carried out using statistical techniques, such as Approximate Bayesian Computing (ABC).
- Potential to investigate the joint impact of **control strategies** applied to both humans (quarantine, anti-viral medication, vaccination) and animals (culling, vaccination, movement bans).

Acknowledgements

We would like to thank Xiangming Xiao, Marius Gilbert, Leo Loth and the Bangladesh office of the Food and Agriculture Organisation for the Bangladesh poultry data, and the Worldpop project for the human population data.