

Mathematical modelling of influenza A (H5N1) epidemics in Bangladesh



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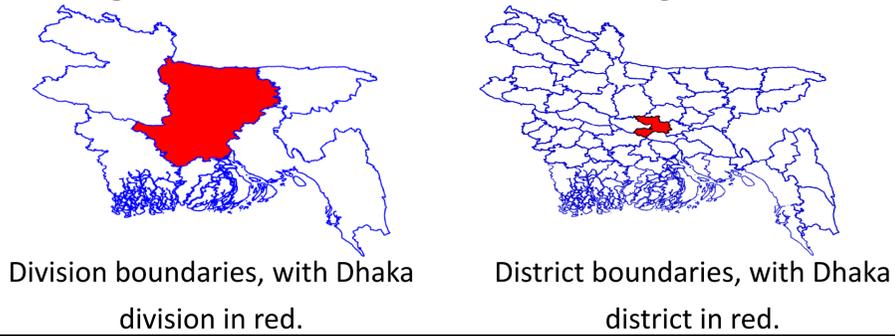
1. The Problem

Influenza A has **many strains** and inhabits **many hosts**. It is critically important to understand how likely it is that more **lethal strains** will cause a **pandemic** in the human population. One such example is **H5N1 avian influenza**, which has had a devastating impact in South-east Asia. In particular, since 2007, **Bangladesh** has had at least 550 commercial poultry premises infected and **8 human cases**.

2. Objectives

- Develop a model framework incorporating **zoonotic transmission**.
- Fit a set of models to **three H5N1 avian influenza epidemic waves** in Bangladesh, focussing on the **Dhaka region** (Fig. 1), to determine the key factors that best capture the observed cases. We used **waves 2,5 & 6** (from 2008, 2011 and 2012 respectively).

Fig. 1: Division and district boundaries of Bangladesh

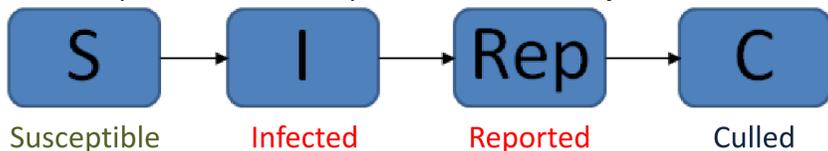


3. Model Formulation

Our modelling framework consists of two components:

i. Poultry component

Individual compartment based spatial model at the **premises level**.



- Compared a set of nested models, of varying complexity, for the force of infection (see Model boxes below).
- Various fixed values for delay in reporting infection: 2,4,7 days.
- Reporting to culling times known from data.

ii. Zoonotic transmission component

Currently assume human case occurrence is a Poisson process:

Daily Infection Rate: $\lambda(t) = \beta I_b(t) + \epsilon_h$

Daily Event Probability: $1 - \exp(-\lambda(t))$

where I_b - number of infected poultry, ϵ_h - human case spark term.

Parameter inference was performed using MCMC methods and plotting likelihood surfaces. **Stochastic simulations** were used to verify our model fitting procedure.

Model A – Parametric kernel

Farms only, fit the following:

- Individual transmissibility
- Transmission kernel
- Spark term

Model B – Nonlinear farm size

- Add population size exponents

Models C/D – Ecological

Two ecological models, incorporating different complex spark terms.

- Live bird markets (C & D)
- Presence of water bodies (C & D)
- Presence of ducks (C only)
- Presence of rice (C only)

4. Results: Poultry Model

Competing models were compared using **deviance information criterion (DIC)**. Preferred models are summarised below:

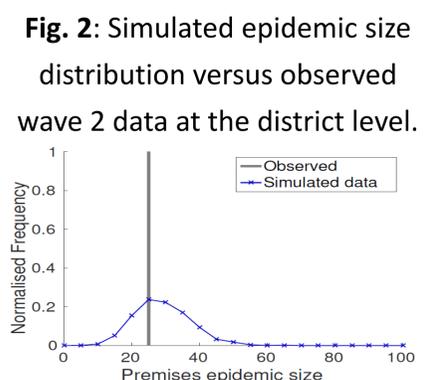
District

- Infected to Reported time: **7 days** preferred.
- (Wave 2) **Model D**; (Wave 5) **Model A**.

Division

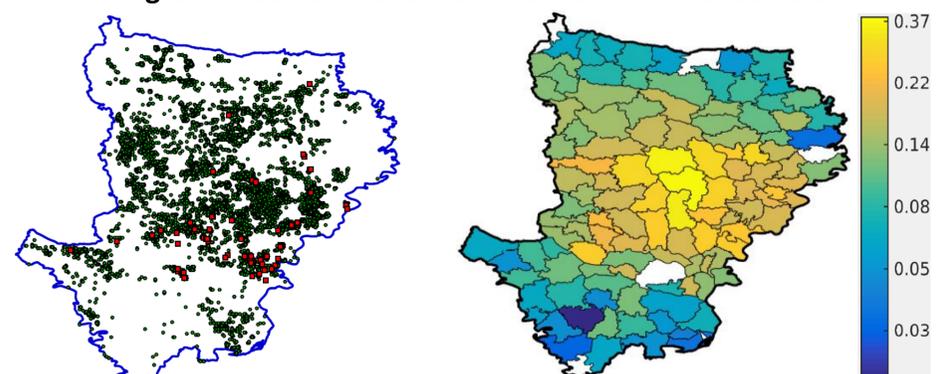
- Infected to Reported time: **7 days** preferred.
- Model B**, including exponents on premises populations.

District level simulations obtained **good correspondence** with **case size data** (Fig. 2).



Division level simulations found the areas infected most often lay north of the main band of observed infected premises (Fig. 3).

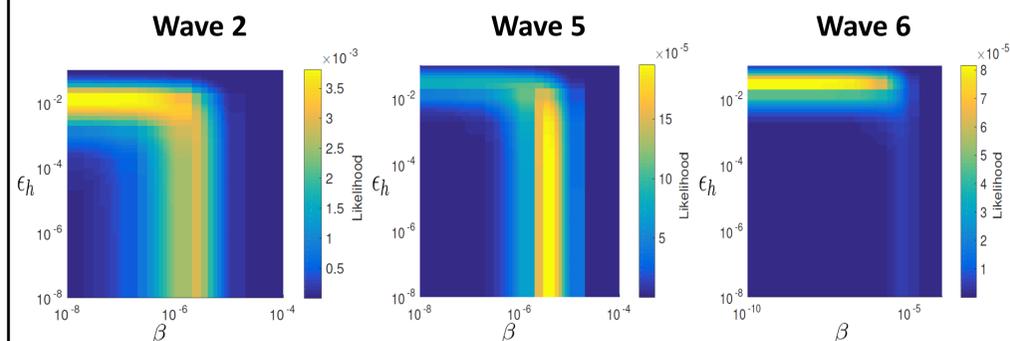
Fig. 3: Model verification for Dhaka division wave 5 data.



(left) Observed spatial infection profile; red squares for infected premises, green circles for uninfected premises. (right) Simulated risk of infection, aggregated at a subdistrict level.

5. Results: Zoonotic Transmission

Fig. 4: Likelihood surfaces for the zoonotic transmission model.



Suggestion of **differing causal mechanisms** for human cases (Fig. 4).

- Wave 5 suggests strong dependence on infected poultry.
- In contrast, waves 2 and 6 gave little support to that factor.

6. Future work

Investigate the impact of **control strategies** applied across both humans (quarantine, anti-viral medication, vaccination) and animals (culling, vaccination, movement bans).

Acknowledgements

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