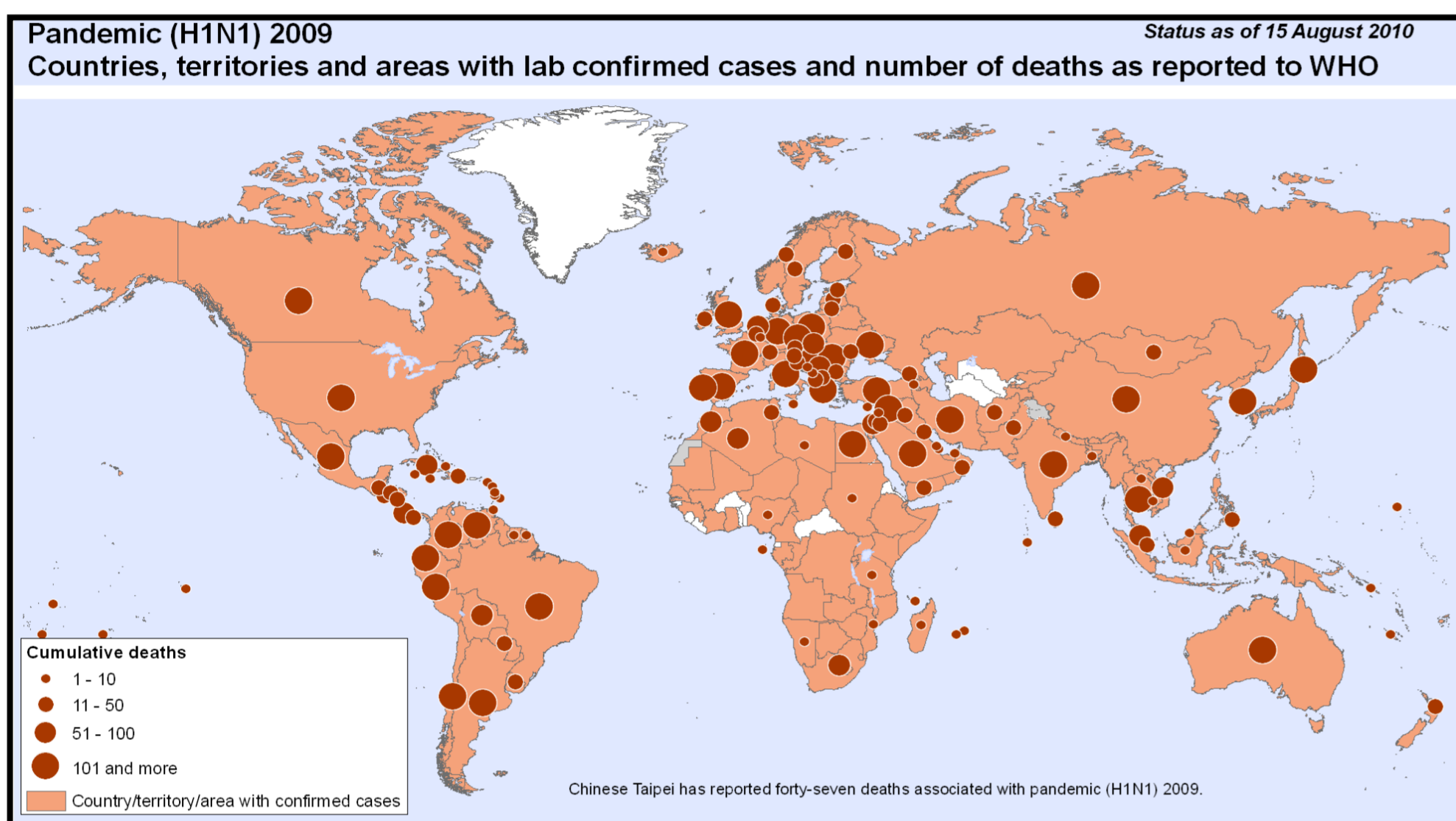




## 1. Motivation

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**.

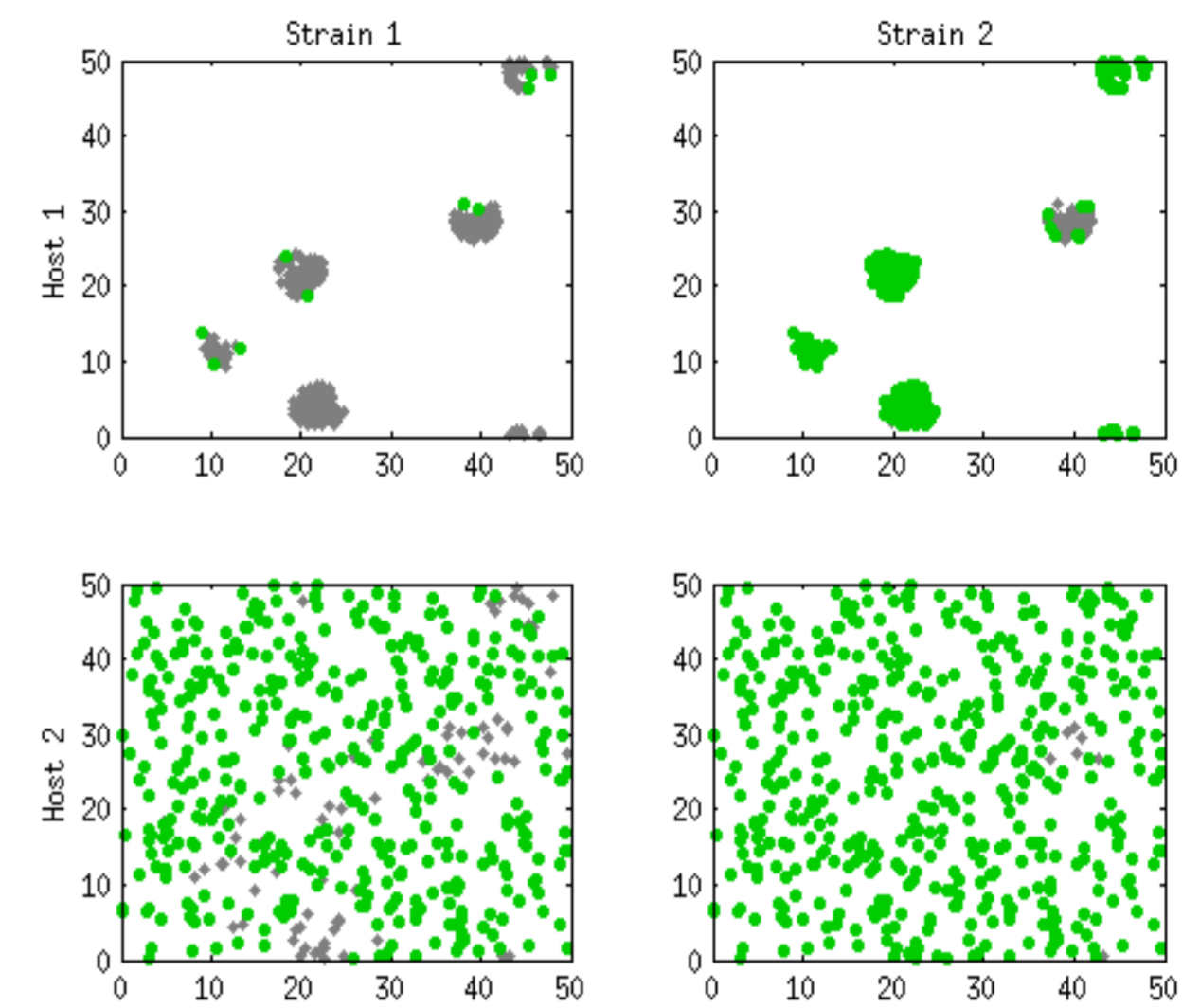
Model simulations used the **Tau leap** method.

## 4. Results: Synthetic Data

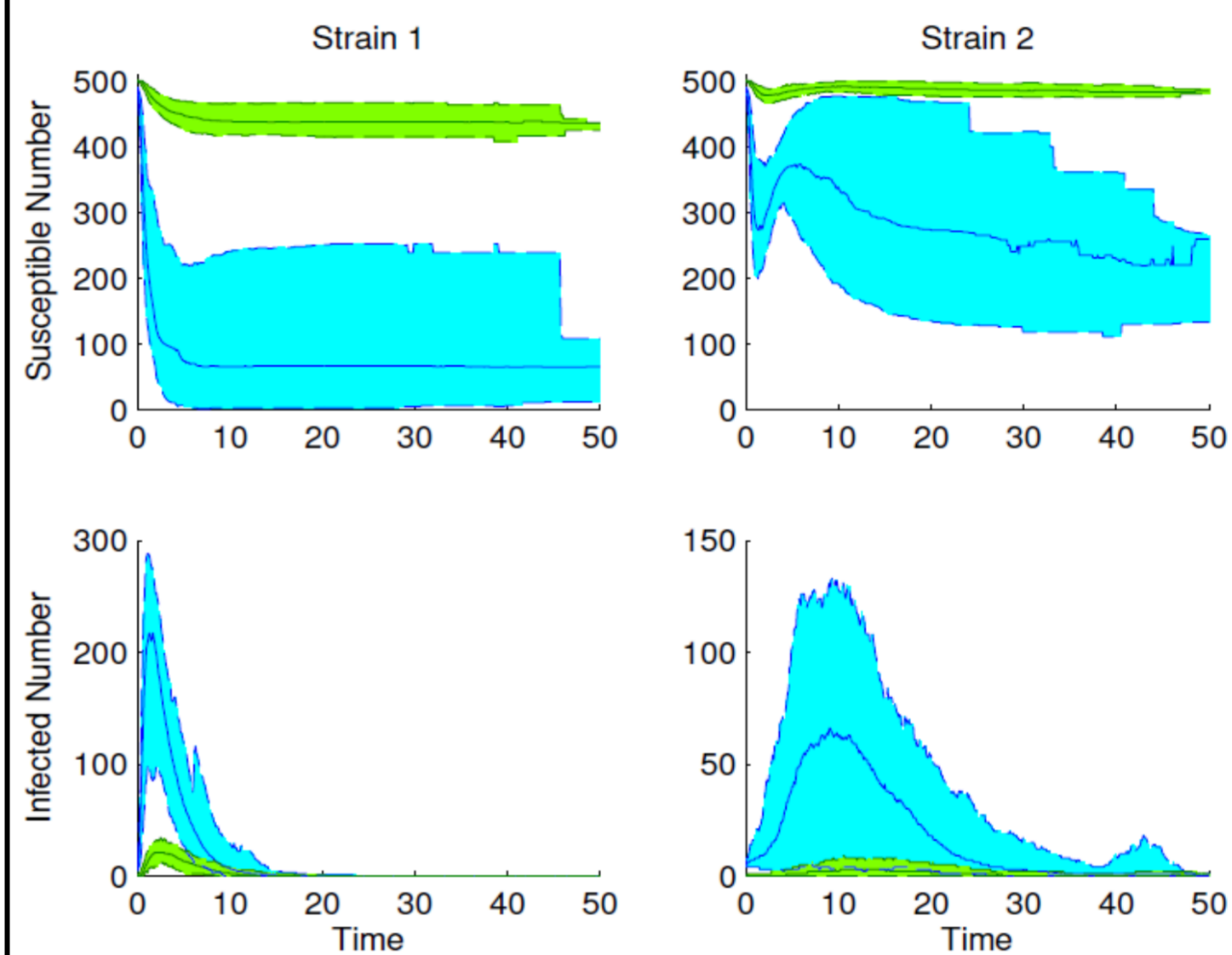
Consider two host species, host 1 very clustered, host 2 randomly placed.

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.

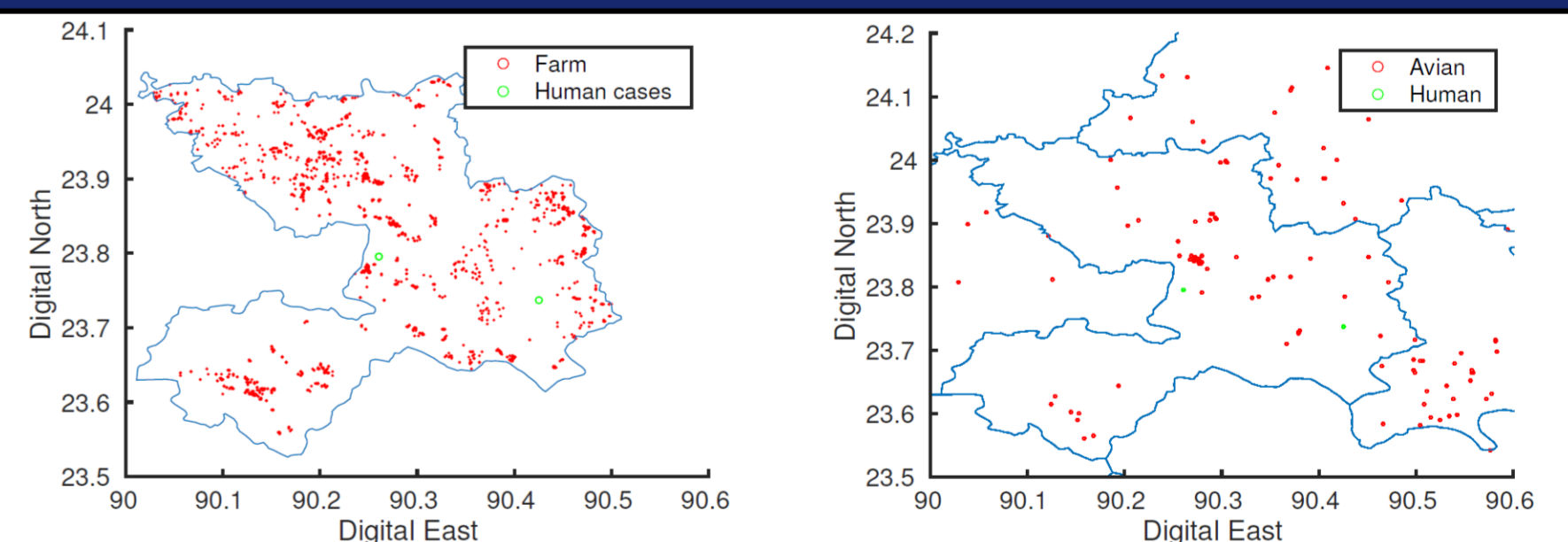


**Figure 3:** Traces of susceptible and infected numbers from 100 simulations. Host 1 in blue, host 2 in green. Median value given by solid line. Shaded regions correspond to 95% credible intervals.

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).

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