

# Modelling of avian influenza A(H5N1) in Thailand

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## **Background**

Since 2003, highly pathogenic avian influenza viruses of the H5N1 subtype has killed or forced the culling of more than 400 million domestic poultry and caused an estimated \$20 billion in economic damage worldwide [1]. For the past twelve years, persistent outbreaks have occurred in South and Southeast Asia. Highly pathogenic avian influenza viruses can potentially recombine with human influenza strains, occasionally leading to infection in humans and posing a major public health concern [2].

The epidemiology of influenza is radically different depending on the host species. Ducks are essentially asymptomatic carriers of most influenza strains, while in other birds and mammals influenza can be lethal. The mortality rate of H5N1 is in excess of 90% in chickens. It remains of vital importance to understand how the interaction between ducks and chickens, the density of farms and the size of flock sizes have influenced previous epidemics, and how possible future outbreaks could be controlled or prevented [3].

## **Project Objectives**

In Thailand, the first confirmed cases of H5N1 were reported in 2004 [4]. An extensive dataset will be used, detailing the number of poultry farms in Thailand at the village level, along with H5N1 infection status, to try and understand transmission dynamics of H5N1 influenza. Two competing stochastic models for infection of poultry farms in Thailand by H5N1 influenza will be developed; one at a sub-district level, and the other at the village level. Parameter inference will then be carried out using statistical techniques, fitting model output to the outbreak data. These outputs will be used to simulate “future” epidemics and investigate the impact of a variety of control strategies, including vaccination and culling.

## **Outcomes**

The aim of the project is to compare how well the spread of H5N1 influenza in poultry within Thailand is captured by competing candidate models, which use the same modelling framework but at different scales of spatial aggregation. Progress will be possible on this within three months, providing the student with an excellent foundation in epidemiological modelling. Furthermore, the broad research question is a large one and lends itself to extension in many different directions.

Only the level of coding taught during the MathSys MSc is a prerequisite for this project. The model will be built in Matlab and depending on progress may be recoded in C or similar to allow for more intensive simulations to be carried out.

The student will be encouraged to interact with PhD students and staff at the weekly WIDER meetings. This project also complements work being carried out by an international collaborative team working on modelling of H5N1 in southeast Asia.

## References

[1] FAO H5N1 Highly Pathogenic Avian Influenza Global Overview Issue no.32 (2012).

Link: <http://www.fao.org/docrep/016/ap387e/ap387e.pdf>

[2] Jennings R and Read RC, *Influenza: Human and Avian*, Royal Society of Medicine Press 2<sup>nd</sup> ed. (2006).

[3] Gilbert M, Xiao X, Pfeiffer DU, Epprecht M, Boles S, Czarnecki C et al. (2008) Mapping H5N1 highly pathogenic avian influenza risk in Southeast Asia. *PNAS* **105**(12): 4796-4774.

[4] Tiensin T, Chaitaweesub P, Songserm T, Chaisingh A, Hoonsuwan W, Buranathai C, et al. (2005) Highly Pathogenic Avian Influenza H5N1, Thailand, 2004. *Emerging Infectious Diseases* **11**(11).