

Simulating Avian Influenza Spread over Singapore Clinic Networks

Xiuju Fu, Wei Jian Ian Teo*, Harold Soh, Gaoxi Xiao*, Gary Lee,
Terence Hung, Limsoon wong⁺, Stefan Ma[◇]

Institute of High Performance Computing
Science Park 2, Singapore 117528

* School of Electrical and Electronic Engineering

* Nanyang Technological University

+ School of Computing

+ National University of Singapore

◇ Ministry of Health

Singapore

Email: fuxj@pmail.ntu.edu.sg

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Abstract

Avian influenza is evolving and becoming a pandemic threat to the world. This study covers the modeling of an Avian Influenza [2][3][4] outbreak over spatial and temporal domains in Singapore. We proposed a simulation model with the geographic clinic network and demographic data of Singapore using cellular automata [1]. The human transmissible avian influenza cases might initially start their infections without public awareness. The community clinics are vulnerable to the spread of avian influenza transmissions especially at the early stage. As a country with high population density, the infections occurred in clinics might lead to relatively large scale spread quickly. It is important to simulate and analyze the spread of avian influenza beforehand. In this work, simulation models were developed

to simulate the avian influenza spread and evaluations were made for control strategies accordingly. The quarantine measure was simulated as a way to control the spread of H5N1. As a result, the effectiveness of this measure was analyzed and a significant difference in the infection ratios was observed over the clinic network transmission. The study also shows the number of days of delay that can be afforded for nation-wide quarantine. Especially, our model is focusing on the impact of the clinic network as key transmission nodes for Avian Influenza spread in an urban city. It concludes that the simulation is very useful and forms the necessary framework for future analysis in Singapore and other countries in order to analyze the impact of various key nodes in infectious disease spread.

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References

- [1] SHIH CHING FU , Modelling Epidemic Spread using Cellular Automata, University of Western Australia, 2002
- [2] CODD, E. F. Cellular Automata. Academic Press, 1967
- [3] KOU Z, LEI FM, YU J, FAN ZJ, YIN ZH, JIA CX, XIONG KJ,SUN YH, ZHANG XW, WU XM, GAO XB, LI TX (2005) New genotype of avian influenza H5N1 viruses isolated from tree sparrows in China. J Virol. 79 (24) 15460-15466
- [4] ANDREWES, C. H. The Natural History of Viruses. W. W. Norton Company, 1967