

# Multi-Agent Model Analysis of the Containment Strategy for Avian Influenza (AI) in South Korea

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**Abstract**—This research presents a multi agent model to estimate and predict the spread of Avian Influenza (AI) in various attributes and environments in a given population. AI can be transmitted by air and is a critical hazard to birds, especially chickens and ducks. The virus occurs naturally in birds and is capable of being transmitted from an infected bird to another. It is conceivable that AI could be a major threat to human health if the virus becomes capable of transmission to human beings. The next outbreak of AI could lead to millions of deaths unless a feasible strategy for AI containment can be developed.

This paper focuses the flexibility that a multi agent system offers. Agent-based models can closely mimic the situations that exist in real system where several autonomous components may be interacting with each other. The modeling approach offers the advantage of examining the interactions between the agents. This research studies the interactions of three critical factors that characterize AI outbreaks. These properties are quarantine range, incubation period and infection probability. The multi agent model investigates the nature of spreading of AI by incorporating these three properties. We illustrate the potential benefits of multi agent modeling in containing the spreading of AI by presenting how efficiently the virus can be contained. Our work exploits data on the 2008 outbreak of AI in South Korea.

## I. INTRODUCTION

Until almost a decade ago, AI was just a threat for various birds, such as chickens, ducks and so on, but not a threat to human beings. However, over the past decade, the global threat from AI has greatly increased for humans despite widespread implementation of control measures.

Typically, “AI virus” refers to influenza A (H5N1) viruses found mainly in birds, but infections with these viruses can occur in humans [10]. The risk from AI was generally low to most people, because the viruses do not usually infect humans. However, confirmed cases of human infection from several subtypes of AI infection have been reported since 1997 [2]. Because all influenza viruses have the ability to change, scientists are concerned that H5N1 virus some day could be able to infect humans and spread easily from one person to another. Since these viruses do not commonly infect humans, there is little or no immune protection against them in the human population. If H5N1 virus were to gain the capacity to spread easily from person to person, an influenza pandemic (worldwide outbreak of disease) could begin [13], [6].

This paper focuses on the results of numerical experimentation on our multi-agent model with data from an AI outbreak in South Korea in April, 2008. This research studies the characteristics and behavior of a model by answering “what-if” types of questions. Performing such types of experimentation using actual data with a model is one of the advantages of a simulation-based study over other types of model based analysis, most of which are built using mathematical or statistical equations. The outcome of the experimentation also reflects the capabilities of the model we have used [12]. Therefore, it is important to design a model that captures the true and representative properties of the problem at hand.

This work is organized as follows. In Section I, we start with introduction followed by a brief description of related work in Section II. In Section III, we focus on describing the multi agent model considered here and discuss the details of our numerical experiments. In Section IV, we present the results of this study in three sub sections based on three critical properties associated with the spreading of the AI outbreak. We close with a discussion of the results in Section V.

## II. RELATED WORK

The first known attempts to analyze patterns of epidemic outbreaks date back to Hippocrates [1]. Over the centuries the understanding of the biological and chemical processes leading to diseases improved. As the mathematical sophistication improved, the models for outbreaks became more complex. At the beginning of the 20th century Kermack and McKendrick [9] published the famous and often cited Ordinary Differential Equation (ODE) system for the simulation of a simple SIR (Susceptible, Infected, Recovered) type epidemic [3].

Since then the differential equation methods have been refined and improved in various ways. In the second half of the last century, with the rise of computers and increased computing power, cellular automata (CA) became a mature field. An advantage of CA is that it allows the simulation of systems with heterogeneous populations. The computers of the 1990s already made it possible to handle even more complex systems, which are referred to as multi-agent-systems (MAS) [7], [11]. These systems offer significant flexibility

in modeling realistic processes where the agents may hold (many) different characteristics, such as age, sex, etc. [5].

### III. MULTI-AGENT MODEL

#### A. Multi-agent System

A multi-agent system consists of components (entities) that represent the features of the system. The entities communicate with each other and with the environment they live in, and are modeled and implemented using agents [4], [12], [14], [11]. The agents have behaviors and characteristics and they represent the various components that make up the model.

We constructed a spatially explicit simulation of about 102 million chickens and ducks in 2,990 poultry farms in South Korea. The model explicitly incorporates interactions among chickens and ducks, as these are known to be the primary contexts of influenza transmission and because control measures can readily target these locations. Random contacts among bird groups are associated with day-to-day relocation by trading in public markets.

#### B. Modeling

We have identified agents for different bird types, chickens and ducks, where each species are associated with characteristic parameters. In addition, there are parameters that can be used for all the species in the model. Table I shows the significant parameters of the AI multi-agent model while Figure 1 gives a schematic of the simplified model used in our studies.

Among the various attributes of the agents and the environments, the infection probability,  $\tau$ , is a key factor that has been used to model the spreading of the disease. Higher value of probability mean faster and easier transmission of influenza among poultry farms. We have simulated four different infection rates - 0.1, 0.4, 0.7 and 1.0. The parameters  $\mu$  and  $\nu$  are the incubation periods for chicken and duck, respectively. During the incubation period no control method could be applied to the agent and the environment because the symptoms associated with the infection cannot be easily discerned.

The next attribute for the agent is the infection spreading distance,  $\gamma$ . Agents at distances that are less than the infection spreading distance will be infected by the avian flu with an infection probability  $\tau$ . Quarantine radius,  $\lambda$ , is to be used for calculating the range of the culling area in order to control the spreading of the disease when there is an outbreak of AI. Various other attributes and parameters could be applied to further enrich this model. However, for the sake of simplicity, only the necessary parameters have been chosen in this study.

### IV. RESULTS

The parameters shown in Table I were used on a of 1 x 1 unit (1 unit  $\approx$  100Km) square for the numerical experiments shown in Figure 1. In this space, we introduced 500 agents, each representing 250 groups of chicken farms and 250 groups of duck farms. We measured the transition of the status on the agent population by analyzing the interaction among the agents

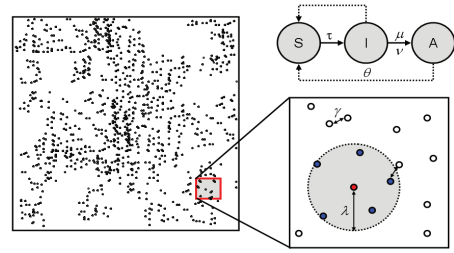


Fig. 1. The schematic represents how the multi-agent model used in our simulations works. An individual agent (a group of chickens or ducks) is the susceptible state (S); if infected, it moves into incubation status (I) for 2-17 days (varies for chickens and ducks). In this status, an agent could transfer a virus without knowing the self infection. After the period of incubation, it moves into activation status (A) where it could die by death probability on infected birds. Parameters used in this model are shown in Table I.

parameter	description	value
$\tau$	infection probability	0.1, 0.4, 0.7 1.0
$\mu$	chicken incubation period	3 days (1-5 days)
$\nu$	duck incubation period	8 days (1-17 days)
$\lambda$	quarantine radius	0.02-0.30 unit (1 unit $\approx$ 100 Km)
$\omega$	agent relocation probability	0.05 (per day)
$\gamma$	infection spreading distance	0.05 unit
$\theta$	death probability on infected birds	0.5 (per day)

TABLE I  
PARAMETERS TO DESCRIBE THE CHARACTERISTICS OF AI

for 50 time steps (1 time step  $\approx$  1 day). Parameters are set up based on the data on AI outbreak of South Korea 2008.

Before we evaluate AI spreading and containment strategies, we first provide an statistical overview of AI outbreaks in South Korea. We will focus on simulation results based on different values of three critical parameters on AI spreading: (1) the effect of control zone or quarantine area, (2) the effect of different incubation period of different kinds of birds, and (3) the effect of different AI transmission rates.

#### A. Effect of Increased Quarantine Range

Authorities in South Korea have officially reported that there were forty three H5N1 AI outbreaks after the first outbreak on April 1, 2008 [8]. Figure 2 shows the locations of the outbreaks during 44 days. Figure 3A and 3B show the number of outbreaks as a function of period and the number of outbreaks as a function of province.

Strategies with an optimal quarantine area are necessary to efficiently minimize the risk of AI spreading. Strategies involving a larger than optimum radius of quarantine area are inefficient and strategies with a smaller than optimum radius of quarantine area are ineffective. Targeted strategies are therefore needed to minimize damages by AI infection. One way to achieve this may be by slaughtering the infected while maximizing the number of healthy chickens and ducks.

Figures 4A and 4B shows the effects of increasing the quarantine area. Each of the four different lines of each

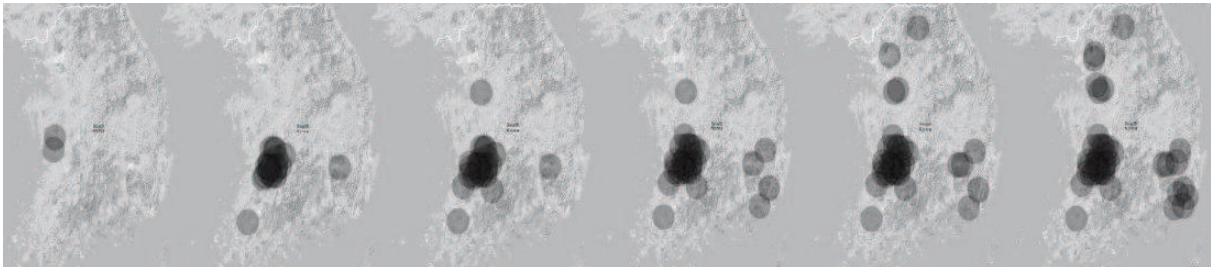


Fig. 2. Time sequence (in days) of an AI outbreaks, showing spreading based on the source at the Ministry of Food, Agriculture, Forestry and Fisheries in South Korea. From the left figure to the right figure, it is time frame for 4 days, 12 days, 20 days, 28 days, 36 days and 44 days after the first outbreak respectively [8].

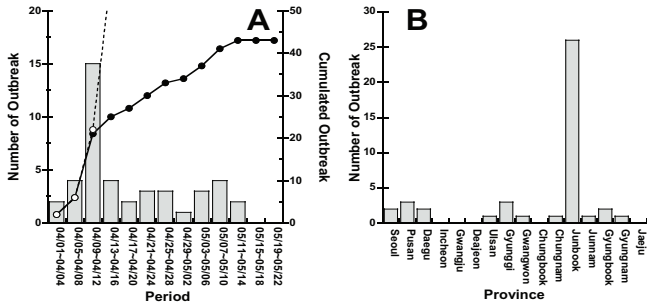


Fig. 3. A, The number of AI outbreaks in poultry farms is shown after the first outbreak. Gray bars represent the number of outbreaks during the specified period. The line with black solid circles represents the cumulative number of AI outbreaks in poultry farms based on the outbreak reports by Ministry for Food, Agriculture, Forestry and Fisheries in South Korea 2008 in which the authorities instituted a quarantine in the area. The dashed line with open circles is the estimated cumulative number of AI outbreaks without a containment strategy based on the statistical data from South Korea. B, The number of outbreaks on poultry farms is shown by the province in South Korea 2008.

figure is based on different AI infection transmission probabilities, 0.1, 0.4, 0.8 and 1.0. Figure 4A demonstrates the intuitively obvious idea that the number of healthy poultry farms increases with as transmission probability decreases. The optimal quarantine radius corresponding to each of these transmission probabilities are: 0.04, 0.10, 0.18 and 0.20, respectively. This finding suggests that the efficient control of AI spreading could be possible if AI transmission rates can be well identified. In practice, estimating infection transmission probability during an epidemic is difficult. However, efficient containment strategy could be initiated based on prior data and progressively refined once estimates are available.

Figure 4B shows the number of culled poultry farms as a function of the circular region of quarantine. For small quarantine radii (0.0-0.04), the number of culled poultry farms increases rapidly whereas for the optimal range of quarantine radii (0.06-0.20), the number of culled birds decreases. Our analysis indicates that the additional increases in quarantine radius (0.22 and more) beyond the optimal range of quarantine radius causes decreases the total number of healthy poultry farms. With this knowledge, the optimum quarantine area

could be identified.

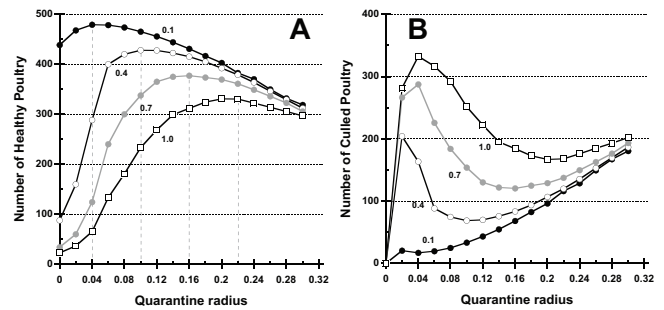


Fig. 4. A, The number of healthy poultry farms are plotted as a function of the quarantine radius. Each line represents different infection probabilities, 0.1, 0.4, 0.7 and 1.0 and optimal quarantine radii, which are 0.04, 0.10, 0.16 and 0.22 units, are found respectively. B, The number of culled poultry farms as a function quarantine radius is shown. Each line represents the same parameter values as in figure A.

### B. Effects of Increased Incubation Period

Highly Pathogenic AI (HPAI) viruses can survive for longer periods at lower temperatures. The incubation period for AI ranges from 3-7 days (17 days maximum) depending on the state of isolation, dose, species, and age. Viruses with longer periods of incubation could potentially have greater adverse effects because of difficulties in detecting the initiation of infections. Thus, understanding the effects of varying incubation periods remains an important factor in designing an effective containment model.

Figure 5A shows the number of healthy poultry farms as a function of the incubation period. The four lines represent no control, minimum control, mid control, and maximum control and correspond to quarantine radii of 0, 0.04, 0.11, and 0.18 distance units. For the case of no control, the incubation period does not exhibit a significant effect on the number of healthy poultry farms. However, the incubation period has more critical impacts on the number of healthy poultry farms with the presence of control strategies. For mid level control, almost 89% of poultry farms are healthy when incubation period is 1 day whereas only 11% of poultry farms are healthy when incubation period is 17 days.

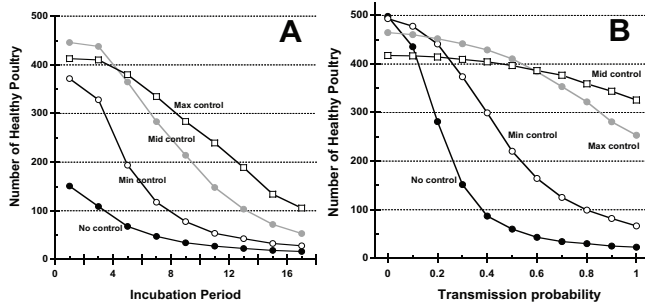


Fig. 5. A, The number of healthy poultry farms as a function of the incubation period (days). B, The number of healthy poultry farms as a function of AI transmission probability. Each line stands for the different size of quarantine area. (min=0.04, mid=0.11, max=0.18 unit)

### C. Effects of Increasing the Virus Transmission Probability

Many uncertainties remain with regard to pathogenesis and ecology of the AI virus and potential pathways for its transmission. Because the poultry farms in South Korea house chickens and ducks at high densities in small areas, the likelihood of virus transmission can be high. In our numerical experiments, we assume that higher probability of transmission (0.8-1.0) was applicable for the AI outbreaks in South Korea. However, we also investigated a range of transmission levels between 0.0-0.8.

Figure 5B shows the number of healthy poultry farms as a function of the AI transmission probability. The four lines represent no control, minimum control, medium control, and maximum control and correspond to quarantine radii of 0, 0.04, 0.11, and 0.18 distance units, respectively. For all four different levels of control, over 82% of poultry farms are healthy at the lowest values of transmission probability (0.0-0.1). We find that when the transmission probability is at its lowest, medium level of control results in the lowest numbers of healthy poultry farms. This happens because of the large numbers of poultry farms eliminated by the aggressive culling procedure. However, at the higher transmission probabilities (0.5-1.0), the medium and maximum levels of control lead to much higher numbers of healthy farms compared to cases where minimal or no control are exercised.

Our analyses indicate that transmission probability and the level of control should be tuned for efficient management of AI spreading. Aggressive control with low transmission probability causes unnecessary culling of healthy farms whereas inadequate control at higher transmission probabilities causes rapid spread of the virus.

## V. DISCUSSION

We have shown that containment and elimination of the AI spread at the point of origin is conceivable using a combination of quarantine area, virus incubation period and virus transmission probability. A key conclusion is the needs for striking a balance among these three important factors. Setting a simple aggressive quarantine area is unlikely to be

efficient if the virus has lower transmission probability than presumed in that area.

Effective quarantine strategies should also be set up based on reliable information about the incubation period and the transmission probability in order to achieve high levels of containment. However, the level of transmission is unlikely to be well known when quarantine policies are implemented. Thus, a balanced analysis among existing references to the known environmental factors would be the best strategy.

The obstacles to practical implementation of such a strategy are undoubtedly formidable. However, performing such types of experimentation with a model provides advantages on planning efficient strategies for future AI outbreaks and epidemics. Thus, it is important to design a model that captures the true and representative properties of the problem. We believe that this type of simulation will become a standard tool for preparedness planning and for modeling of new disease outbreaks. A feasible strategy for containment of the AI spread offers the potential to save millions of poultry farm industries as well as prevent possible threats on the human health.

## VI. ACKNOWLEDGMENTS

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