

## Analytical Solutions for an Avian Influenza Epidemic Model incorporating Spatial Spread as a Diffusive Process

Phontita Thiuthad<sup>1,2</sup>, Valipuram S. Manoranjan<sup>3</sup> and Yongwimon Lenbury<sup>1,2,\*</sup>

<sup>1</sup> Department of Mathematics, Faculty of Science, Mahidol University, 272 Rama 6 Road, Bangkok 10400, Thailand.

<sup>2</sup> Centre of Excellence in Mathematics, CHE, 328 Si Ayutthaya Road, Bangkok 10400, Thailand.

<sup>3</sup> Department of Mathematics, Washington State University, Pullman WA 99164, USA.

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**Abstract.** We consider a theoretical model for the spread of avian influenza in a poultry population. An avian influenza epidemic model incorporating spatial spread as a diffusive process is discussed, where the infected individuals are restricted from moving to prevent spatial transmission but infection occurs when susceptible individuals come into contact with infected individuals or the virus is contracted from the contaminated environment (e.g. through water or food). The infection is assumed to spread radially and isotropically. After a stability and phase plane analysis of the equivalent system of ordinary differential equations, it is shown that an analytical solution can be obtained in the form of a travelling wave. We outline the methodology for finding such analytical solutions using a travelling wave coordinate when the wave is assumed to move at constant speed. Numerical simulations also produce the travelling wave solution, and a comparison is made with some predictions based on empirical data reported in the literature.

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### 1. Introduction

In the twentieth century, the world confronted three major influenza pandemics. One began in 1918, when about 50-100 million people were killed around the world, and then influenza pandemics again in 1957 and 1968 [9]. Pandemics test the ability of any nation to protect its population. According to the World Health Organization, there may be serious epidemics where each year millions of people die and several millions are infected [16].

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\*Corresponding author. *Email addresses:* thiuthadp@hotmail.com (P. Thiuthad), mano@wsu.edu (V.S. Manoranjan), scylb@yahoo.com (Y. Lenbury)

Avian influenza, also known as bird flu, is an infectious disease of birds and domestic poultry caused by the H5N1 virus. Avian influenza is one of the worst fatal diseases for poultry farming, because mortality rates are high (approaching 100% within 48 hours) and infected poultry must be killed (technically termed "culled") to avoid the spread of the disease. According to a report by the United Nations Food and Agriculture Organization (FAO) [3], avian influenza was known in Italy over 100 years ago. Low pathogenic avian influenza (LPAI) has been found in wild birds for some time. However, when low pathogenic strains of the subtypes H5 and H7 began to infect farmed poultry (such as fowls, ducks and geese) [14], these strains mutated into highly pathogenic AI (HPAI). Around 1996, highly pathogenic H5N1 was extracted from farmed geese in the Guangdong Province, China [26]. This strain spread to many Asian countries [11], and outbreaks have also occurred in Africa and Europe [15]. In South-east Asia, H5N1 has been reported in ten countries — viz. Cambodia, China, Indonesia, Japan, the Lao People's Democratic Republic, the Republic of Korea, Malaysia, Pakistan, Vietnam and Thailand. In 1997-8, an outbreak occurred in Hong Kong and again in 2003, and in the Republic of Korea in 2003. In Thailand avian flu infection was last found in 2003, with the outbreak officially confirmed in early 2004 [15]. Field studies in Cambodia [5, 24], Vietnam [4, 5] and China [13, 21] have indicated that the commercial poultry network has a crucial role in the spread of HPAI H5N1, with the poultry markets the "critical hub" [24]. There is a marked increase in sales during certain periods of the year, such as during the Chinese New Year, resulting in an increased risk of HPAI H5N1 infection [21]. However, insufficient detailed temporal and spatial information has been obtained to date. On the other hand, laboratory experiments have shown that the survival of the avian flu virus is conditional on environmental factors such as temperature, salinity and pH levels [22, 25].

Mathematical descriptions of the outbreak of avian influenza almost always involve differential equations. Since Kermack & McKendrick [8] constructed a system of ordinary differential equations in epidemiology in 1927, deterministic mathematical models have helped to understand the spread of many diseases. Iwami *et al.* [7] proposed an avian-human influenza epidemic model to explain the spread of avian influenza from birds to humans, involving autonomous ordinary differential equations. Two types of avian influenza outbreak were considered. Their SI-SIR (Susceptible Infected Susceptible Infected Recovered) mathematical model includes avian influenza mutation in both the bird and human populations, where the spread of the mutant influenza cannot be prevented even if the infected birds are exterminated. However, the model could be modified in various ways — e.g. to account for the influenza virus of a subsequent seasonal epidemic differing significantly from the current strain if it mutates rapidly.

Moreover, wild birds can carry the virus without showing any symptoms at all. Thus Samanta [20] modified the mathematical model proposed by Iwami *et al.* [7] to incorporate the spread of wild avian influenza from the bird population to humans, following the emergence of mutant avian influenza. He introduced time-dependent parameters and distributed time delay due to the intracellular delay between initial infection of a cell and the release of new virus particles, and established some sufficient conditions on the permanence and extinction of the disease by using inequality analytical techniques. He