

Modeling the Dynamics of Avian Influenza Epidemics and Possible Pandemics

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Abstract

Avian influenza, or “bird flu”, is a contagious disease of animals caused by viruses that normally infect only birds; however there exist a dramatic number of infected human cases. This research aims to understand the dynamics of avian influenza epidemics in a closed, finite area by using system dynamics methodology. The model is a network that links wild bird, duck, poultry and human population sectors which are formed by several classical SIR-model building blocks. The dynamics of recent outbreak is analyzed with a base model; additionally some scenario and policy analyses are done with modified models. The simulation experiments show that a highly pathogenic avian influenza outbreak is highly dependant on the density of poultry population in the region. Growing duck and poultry populations pose a great risk. A policy involving the recognition and quarantining of low pathogenic virus infected birds is suggested at the end as a tentative one.

1. Introduction

Contagious diseases have been among the biggest threats for human race for centuries. The developments in medicine and technology have decreased the risks of contagious diseases dramatically but the recent outbreak of “Avian Influenza” has showed us that any pandemic of a disease may still be a big danger for the human race.

Avian influenza or “bird flu” is a contagious disease of animals caused by viruses that normally infect only birds. There are several types of avian influenza viruses which have been very dangerous for animals, especially for birds for centuries. However, through mutations, the virus crossed the species barrier and evolved to be able to infect other species and humans, too. Since the disease is fatal, any possible pandemic is a serious threat for the human race. For example, during a pandemic of another type of avian influenza virus, more than 43 million people died in 1918. (Morens and Taubenberger, 2006). For this reason, understanding the epidemiological dynamics of avian influenza is extremely important.

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1.1. Avian Influenza

The avian influenza virus, current strain under consideration, H5N1, causes two distinctly different forms of disease. The first one is “low pathogenic avian influenza” (LPAI) which is common and mild and has only signs such as ruffled feathers, reduced egg production, or mild effects on respiratory system in birds. The outbreaks can be so mild that the virus may not be detected without any regular testing. In contrast, the second form, “high pathogenic avian influenza” (HPAI) is rare but highly lethal and it can be characterized by sudden onset of severe disease, rapid contagion and a mortality rate that can approach 100% within 48 hours (WHO,2006a).

Moreover, H5N1 virus can be easily transmitted by the movement of live birds, people (especially with shoes and other clothing) and contaminated vehicles, equipment, feed and cages. As a characteristic of HPAI virus, it can survive up to 35 days in the environment due to low temperature. (WHO, 2006a) When we look at the agents which carry the avian influenza virus, we can categorize them such as migratory/resident wild birds, domestic water birds, terrestrial poultry, and live bird markets (FAO 2005).

The virus carriers to different regions are “migratory wild birds” which are seen to be the natural reservoir of the low pathogenic avian influenza (LPAI) virus and they are not affected by the disease. In different regions wild birds get into contact with “domestic water birds”, such as ducks. As a result of these contacts “domestic water birds” contract the LPAI. Then the LPAI passes to the “terrestrial poultry” as a result of contacts with “domestic water birds”. A direct contact between “migratory wild birds” and “poultry” is also possible, but the contact rate is extremely low as compared to the contact rate between “poultry” and “domestic water birds”. The LPAI virus turns into the high pathogenic avian influenza (HPAI) virus in “poultry”, via mutation. HPAI spreads very rapidly among poultry flocks causing deaths. Then HPAI can pass back to “domestic wild birds” through contact with “poultry”.

The HPAI virus can pass to the “human” from “poultry” and “domestic water birds”. Also “pigs” and some other mammals are considered as auxiliary actors in epidemics of avian influenza. It is known that pigs contract the disease, but no cases of human’s contracting the disease from a pig or another mammal is known yet. *Figure 1.1* summarizes the epidemics of avian influenza. The solid lines are observed paths and the dotted lines are theoretical but not yet observed paths (Webster et. al, 2006).

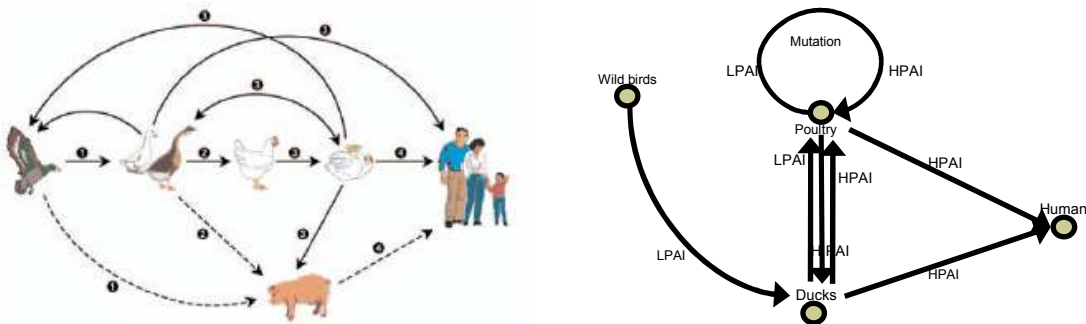


Figure 1.1 a) The path of virus between species b) Illustration of flow of virus

An interesting fact about the virus' behavior in different species is that it has been observed that the recovered ducks continue to excrete appreciable amounts of HPAI virus that is fatal for the poultry. Thus, they act as a silent reservoir for HPAI as they do not show any symptoms but still carry the disease.

Influenza viruses normally infect different species and stay specific to those species. H5N1 is different form other influenza viruses as it caused by far the greatest number of severe human cases and the greatest number of deaths. In the recent outbreak more than half of those infected with the virus have died. Furthermore, the risk of a possible mutation of H5N1, which can enable it to spread efficiently and sustainably among humans, is more serious. This may cause a pandemic like the one during 1918-1919, which resulted in one third of the world's population (~500 million) being infected and more than 43 million being killed (Morens and Taubenberger, 2006). The mutation might happen suddenly which would not give any time for an action, or there may occur an adaptive mutation, which would provide the world some time to take defensive action (WHO 2005b).

2. Problem Identification

Currently, HPAI is considered to be epidemic among the poultry in different regions of the world. The recent outbreaks of highly pathogenic avian influenza are the largest and most severe on record. Never before in the history of this disease have so many countries been simultaneously affected, resulting in the loss of so many birds. The causative agent, the H5N1 virus, has proved to be especially persistent. Despite the death or destruction of an estimated 150 million birds, the virus is now considered endemic in many parts of the world (WHO, 2005a).

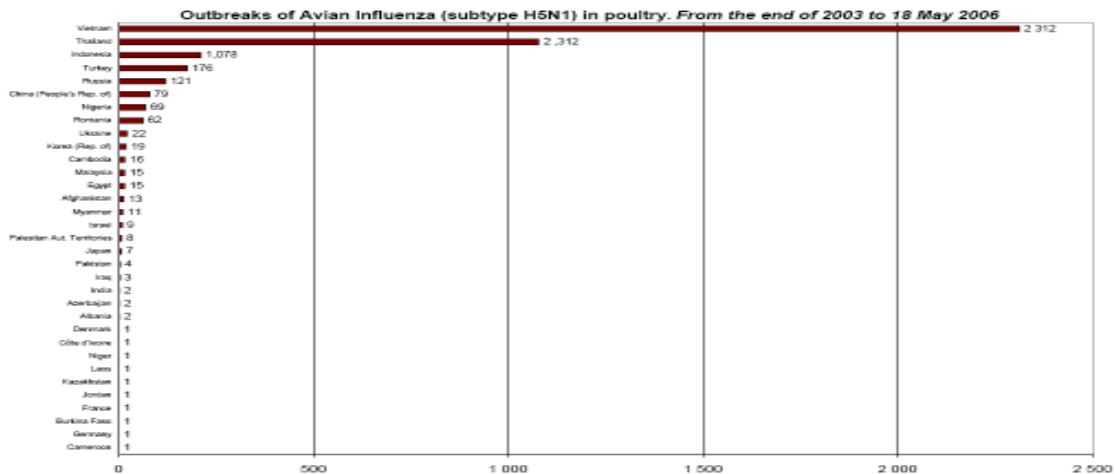


Figure 2.1 Outbreak of avian influenza in poultry

The regions where the avian influenza outbreaks occurred can be considered as closed areas without many ducks or poultry incoming or outgoing. This abstraction enables us to analyze the degree to which conditions the internal structure of the system is capable of producing dynamics representing an epidemic.

Figure 3.2, shows the relationship between the sectors. First the LPAI virus comes to the region by the wild birds. Then ducks contract the low pathogenic disease from wild birds via physical interactions. The virus in ducks passes to the poultry through physical interaction. The most crucial step in the process happens in the poultry sector. This is the mutation of the LPAI virus to a high pathogenic form (HPAI). These high pathogenic and low pathogenic viruses in the region begin to travel between ducks and poultry. At the same time if any human contracts HPAI virus from poultry or ducks, the virus passes to the human sector.

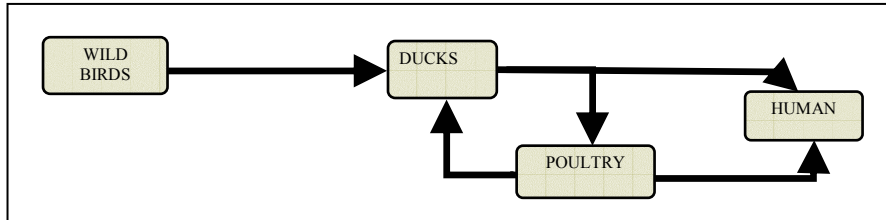


Figure 3.2 Interactions between the sectors

3.1.1. Wild Bird Sector

The wild birds are modeled as an exogenous factor. Since the modeling effort aims to analyze the dynamics of the disease in a region and the migratory wild birds do not stay in the region the whole time; their internal dynamics are out of the boundaries of the model. The most important aspect of the wild birds for the model is their carrying the disease to the region. Therefore, the wild birds sector is modeled such that wild birds come with respect to a graph function seasonally and bring LPAI virus to the region.

3.1.2. Duck Sector

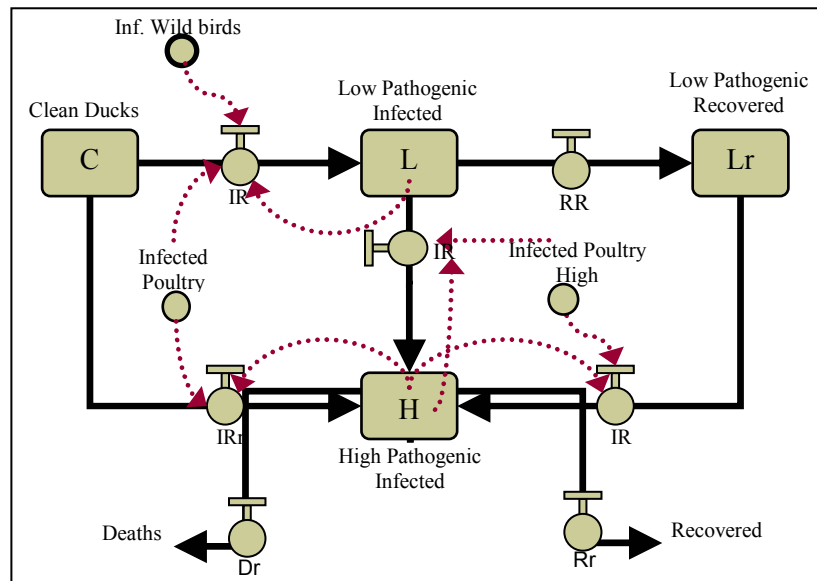


Figure 3.3 Illustration of the duck sector

There are four main stocks in the ducks sector. These are clean ducks (C) which do not carry any type of virus (low or high pathogenic) and are susceptible to any type of the virus; low pathogenic infected ducks (L) which have LPAI virus and susceptible for HPAI virus; low pathogenic recovered (Lr) which are recovered ducks from LPAI virus and immune to LPAI but susceptible to HPAI virus and HPAI ducks (H) which contracted the fatal disease. As seen in *Figure 3.3* clean ducks may contract the LPAI from wild birds or infected poultry or infected ducks. On the other hand, clean ducks may contract the HPAI from just poultry or infected ducks, because it is widely accepted that wild birds do not bring the HPAI virus. The low pathogenic infected ducks may recover the disease or may contract HPAI virus from poultry animals, or previously infected ducks. At the same time, low pathogenic recovered ducks contract the HPAI from poultry animals or previously infected ducks. Lastly, high pathogenic infected ducks recover or die.

3.1.3. Poultry Sector:

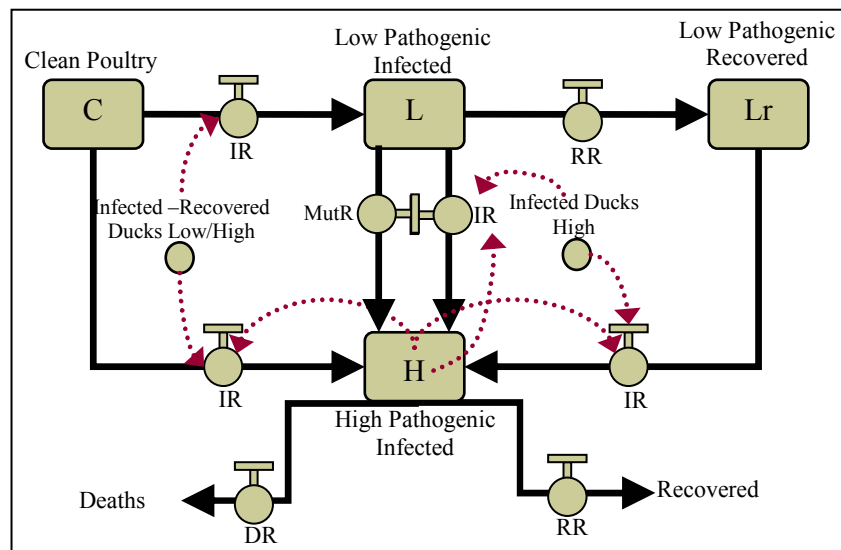


Figure 3.4 Illustration of the poultry sector

The main difference from the duck sector is the existence of the mutation structure and the mutation flow (MutR) between L and H stocks. This triggers the flows into H stock. The modeling of this flow is discussed in the formulation section. Another difference is that poultry can also contract HPAI from the HPAI recovered ducks as indicated in *Section 1.1*.

3.1.4. Human Sector

Since LPAI cannot settle in the human body to the extent that it can cause a disease, only HPAI dynamics have been modeled. Clean human may contract the disease from

poultry animals or ducks via physical contact. Infected human may recover with a certain rate or die.

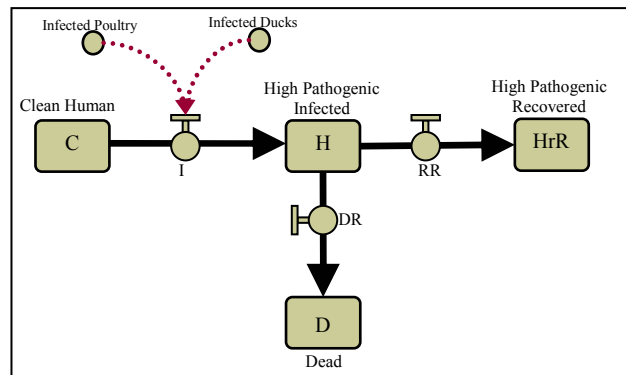


Figure 3.5 Illustration of the human sector

3.1.2. Formulations

3.1.2.1. Infection Rate (IR) Formulations

There are two kinds of infection rate formulations used in the model:

- Intra-species: The rate of infection among the same species. (e.g. duck to duck infection rate)

$$IR = Susceptible * c * (Infected / N_{total}) * infectivity \quad (3.1)$$

$$c = c_{ref} * effect(N_{total}) \quad (3.2)$$

Variable “c” in the Equation (3.1) is the number of contacts per susceptible per unit time. It changes as a function of the total number of the relevant species. There is an effect of total population on the contact rate and this effect is formulated with a multiplicative effect formulation. The graph of the effect vs “ N_{total} / N_{ref} ” can be seen in Figure 3.6.

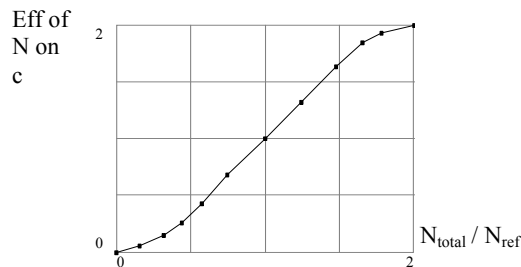


Figure 3.6 The Graph of “effect of N on c” vs “ N_{total} / N_{ref} ”

- Inter-species: The rate of infection between different species. (e.g. duck to poultry infection rate)

$$IR_{x2y} = Susceptible_x * Infected_y * a * infectivity \quad (3.3)$$

$a = constant$

In the Equation (3.3), multiplication of the number of susceptible and the total number of infected gives the total number of possible contacts which can result in infection. However, all of these possible contacts can not be realized. The total number of possible contacts is reduced to realized contacts by multiplication with a constant which is smaller than 1. Also, all of these contacts do not result in infection and the infectivity of the disease determines the fraction that causes infection.

3.1.2.2. Recover and Death Rate Formulations

Recover and death rates are formulated as first order material delays:

$$RR = \frac{Infected}{InfectionDuration} \quad (3.4)$$

3.1.2.3. Mutation Formulation

There is a mutation flow only in the poultry sector in the current version of the model. Mutation formulation is done considering the following principles:

- Mutation probability increases linearly with every new LPAI infection and every day that a chicken stays LPAI infected.
- Mutation happens instantaneously.

The structure is shown in Figure 3.7.

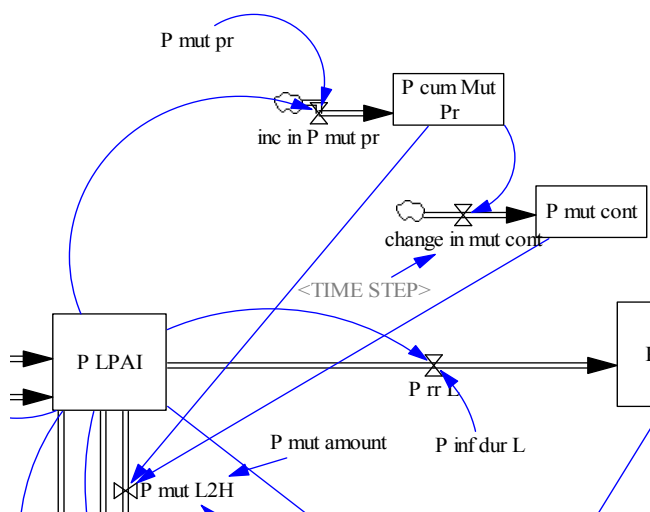


Figure 3.7 The mutation structure of the model

- $increase\ in\ P\ mut\ prob. = P_{lpa1} * P_{mutationPR}$ (3.5)

- $Change\ in\ Mutation\ Control = IF\ THEN\ ELSE\ (P\ cum\ mut\ pr \geq 1, 1/timestep, 0)$ (3.6)

- $P_{mut\ I2H} = IF\ THEN\ ELSE\ (P\ cum\ mut\ pr \geq 1 : AND\ P_{mut\ control} \approx 0, P_{mut\ amount}/timestep, 0)$ (3.7)

$P_{mutationPR}$ is a constant and the probability of a mutation.

The formulation does the following. Every poultry in the P LPAI stock increases the chance of mutation cumulatively as the low pathogenic virus circulating among the poultry becomes more open to mutation. When the cumulative probability hits 1, 1 poultry goes to the P HPAI stock. After that HPAI infection flows start operating. However, a control mechanism does not let the mutation happen more than once as the cumulative probability stock exceeds 0.

4. Validation

The validation is not done in a procedural manner. The validation of every element of the model is done as soon as they are added to the model and the model has been updated when an inconsistency with the common knowledge has been encountered.

However, the validation process can be examined in a manner proposed by Barlas (1996).

4.1. Direct Structure Tests

4.1.1. Theoretical Tests

- Structure-confirmation test: The determination of the overall structure has been done according to the reports of prestigious organizations such as World Health Organization (WHO), Food and Agriculture Organization of UN (FAO), World Organization of Animal Health (OIE), and according to the scientific publications (All papers, reports, or books in the reference section are considered).

- Parameter-confirmation test: The estimation of some parameters are based on some published papers. For example, the mortality of poultry or humans are based on World Health Organization's reports.

- Direct extreme-condition Tests: The equations are tested with respect to their extreme conditions. For example, when there are no contacts between ducks and the poultry, disease does not flow between the two sectors. Another example is that when any stock is equal to zero, flows out of it is also equal to zero, or when the mutation probability is zero, no HPAI infection occurs.

- Dimensional Consistency: As soon as any variable is added to the model, the equations regarding it are checked for dimensional consistency. Moreover, there are no arbitrary constants to ensure this; every variable has a meaning attached to it.

4.1.2. Empirical Tests

- Structure-confirmation test: Some common sense and qualitatively observed behaviors have been applied while determining the structure of the model. For example, in the policy analysis, the case about the culling decision is based on judgments about how soon farmers may perceive that something is wrong with their flock.

- Parameter-confirmation test: Two rules are used while validating the reference contact rates and interspecies contact constants. It is an empirical knowledge that species tend to contact with their own kind rather than with other species and it is known that poultry are more inclined to contact each other than ducks do within themselves.

4.2. Structure-Oriented Behavior Tests

The first runs obtained are used to see if they conform to the suggested behaviors by the theories. When the runs were not conforming to them, a strong reason has been looked for. When such a reason cannot be found, more sensitivity analysis with the parameters are run to see if they are able to explain such behavior. It should be reminded to the reader that these analyses are all done along with direct structural tests, not in some arbitrary range.

- Behavior-sensitivity test: This has been done extensively. As a result the system is not that much sensitive to the reference contact rates. However, it is highly sensitive to the infectivity constant. This sensitivity is normal when the way that the infection spreads among a bird population is considered. As the value of the constant is very low, 0.01, small absolute changes affects the system very much and as the infectivity is multiplied in the infection rates, the effect of increased infectivity cumulates over time.

- Boundary adequacy test: Births and deaths of ducks and poultry in their natural rates have been included but nothing has changed, so it is omitted from the original model. However, it is included as a scenario analysis as it may trouble some readers. Also, the wild bird and poultry relationship has been proved to be ineffective in any case, so this link has been discarded.

5. Output Analysis

5.1. Base Run

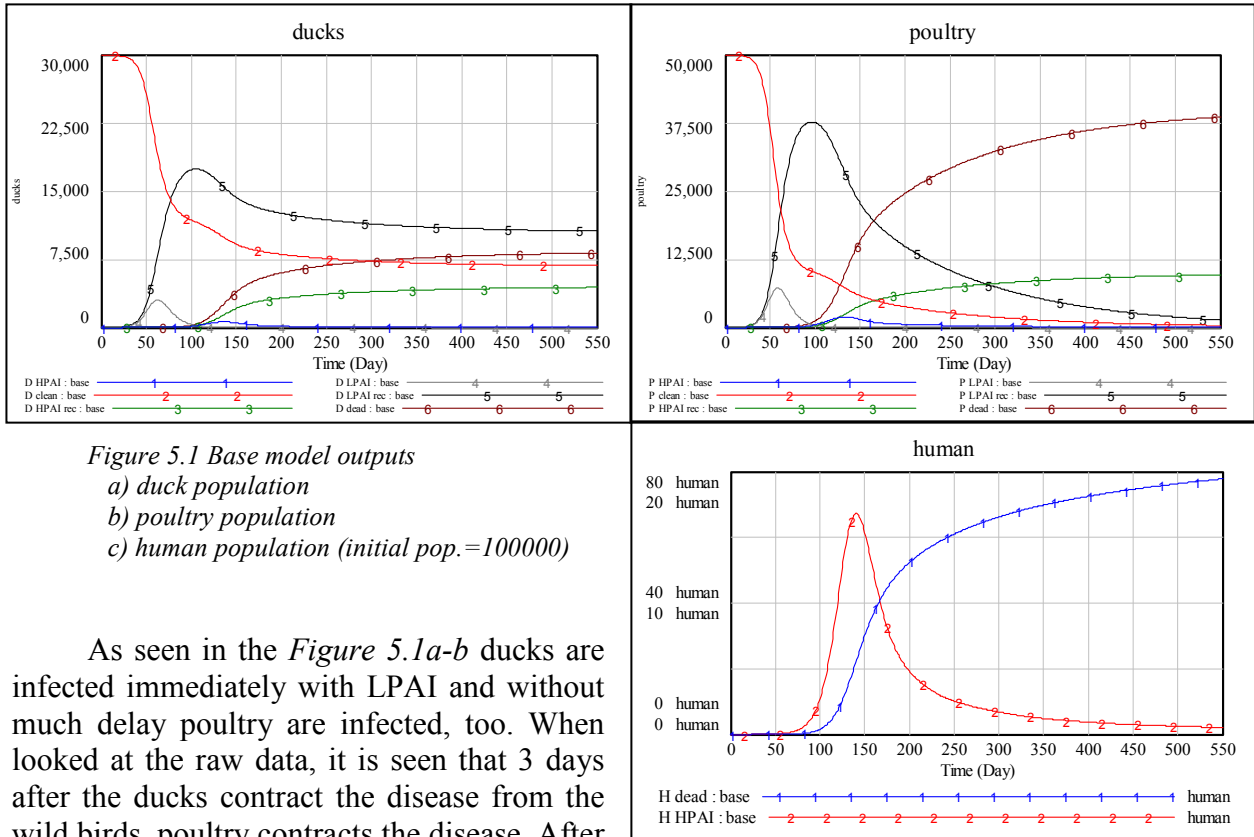


Figure 5.1 Base model outputs
a) duck population
b) poultry population
c) human population (initial pop.=100000)

As seen in the Figure 5.1a-b ducks are infected immediately with LPAI and without much delay poultry are infected, too. When looked at the raw data, it is seen that 3 days after the ducks contract the disease from the wild birds, poultry contracts the disease. After that, an LPAI outbreak occurs among both ducks and the poultry. Since the poultry produce more contacts among themselves than ducks, the outbreak among the poultry is more severe than the outbreak among the ducks, meaning a larger percentage of the poultry are infected with LPAI. At 24th day LPAI mutates into HPAI form among the poultry. After that HPAI epidemic breaks out. The epidemic ceases among ducks after around 450 days with a positive number of uninfected ducks. Around 25% of all the ducks are never infected and around 33% is only LPAI infected and then recovered. The disease kills around 25 % of ducks.

Among the poultry, a different pattern is observed at the later stages of the epidemic. This is caused by the ducks, which continue to excrete viruses that are infectious to poultry even after they are recovered. Due to this fact, poultry continue to get infected at the later stages. So, at the end of 550 days, almost all of the poultry are infected with HPAI. The disease kills around 80% of the poultry at the end. The poultry deaths approach the mortality rate that the system assumes.

Figure 5.1c. shows the behavior of two important variables of the human sector: Dead humans and HPAI infected humans. It can be observed that around 80 people dies and as the model assumes 50% mortality rate for humans, we can infer that around 160 people contract the disease. It can be observed that HPAI infected people peaks at around

140th day, which coincides with the peak of number of infected birds in the system as expected.

5.2. Scenario Analysis

5.2.1. Increased / Decreased Number of Initial Clean Poultry

5.2.1.1 Number of Poultry Increased to 100000

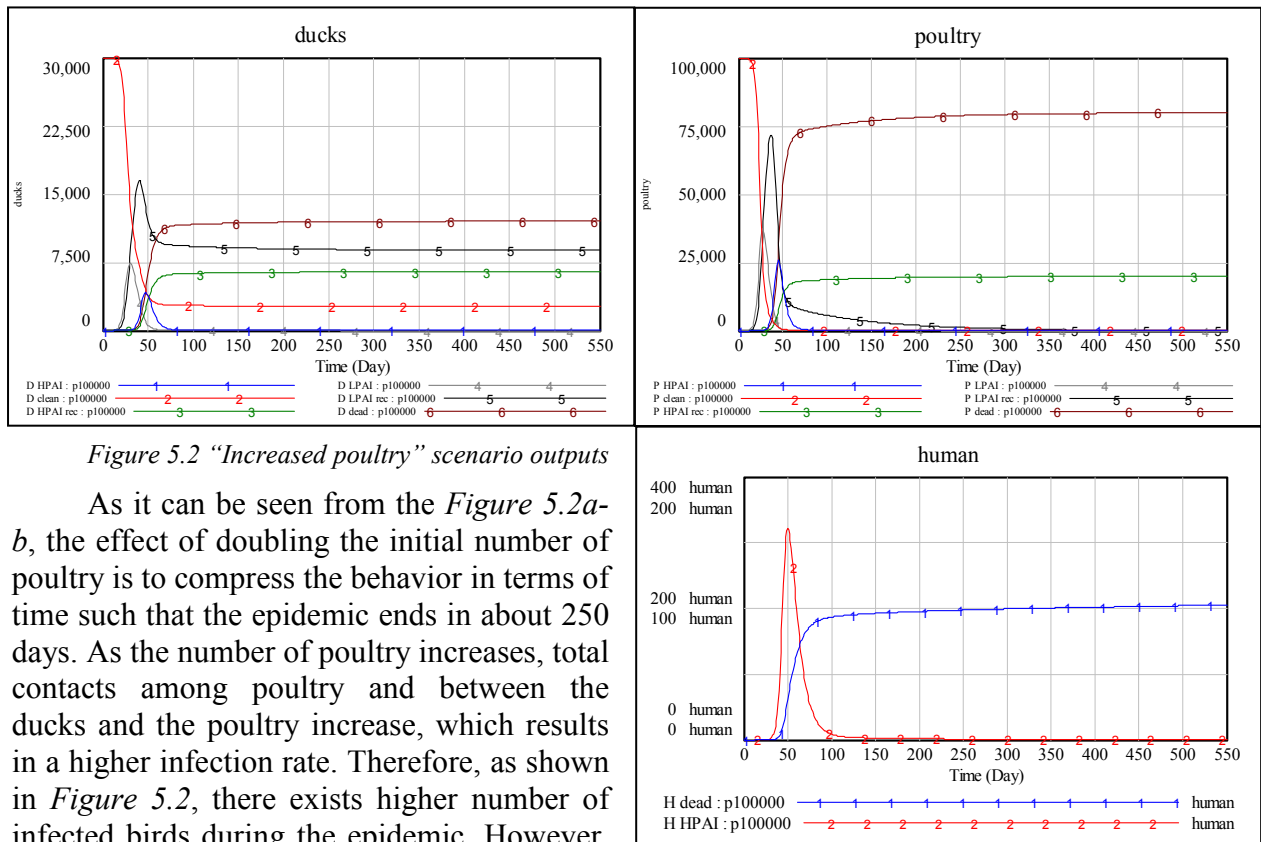


Figure 5.2 “Increased poultry” scenario outputs

As it can be seen from the *Figure 5.2a-b*, the effect of doubling the initial number of poultry is to compress the behavior in terms of time such that the epidemic ends in about 250 days. As the number of poultry increases, total contacts among poultry and between the ducks and the poultry increase, which results in a higher infection rate. Therefore, as shown in *Figure 5.2*, there exists higher number of infected birds during the epidemic. However, the equilibrium values attained for the poultry does not differ much from the base run. However, for the duck sector, more ducks die and become infected as there are more poultry to infect them. For the humans, around 200 are dead due to more poultry to get into contact (*Figure 5.2c*). Also a higher peak is achieved in terms of HPAI infected humans curve.

5.2.1.2. Number of Poultry Decreased to 25000

Figure 5.3 shows the behavior when the initial number of poultry is decreased to 25000. In this case, the LPAI infection does not persist in ducks and does not cause a serious epidemic. As a result, the virus cannot mutate into the HPAI form. Thus, none of the humans die.

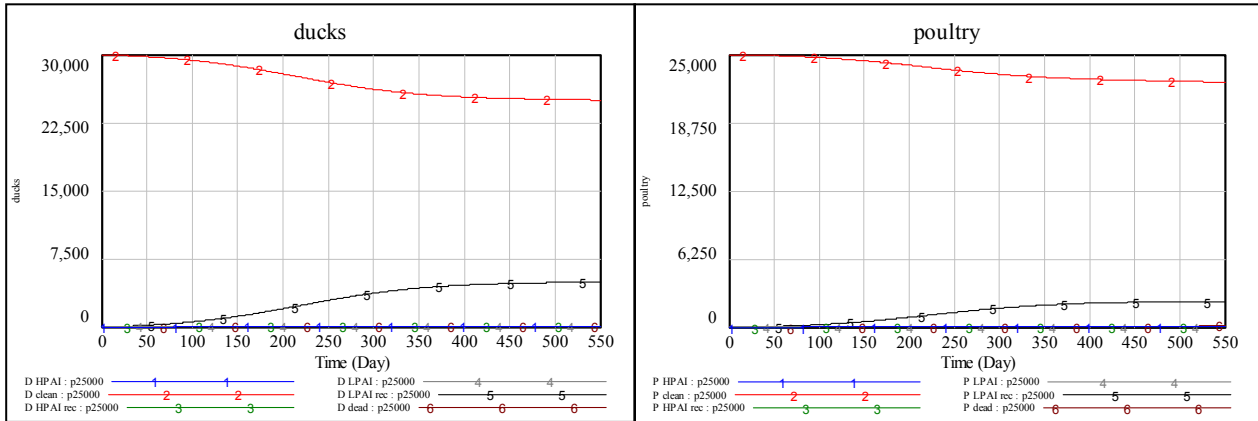


Figure 5.3 “Decreased poultry” scenario outputs

The results on the change in initial number of poultry implies that the initial number matter as the mutation will happen earlier or later to kill more or less humans, and it may never happen.

5.2.2. Wild Birds Stay

Figure 5.4 shows the behavior of the system when the wild birds stay in the region, instead of leaving the region after 10 days. Nothing changes with respect to the base model behavior.

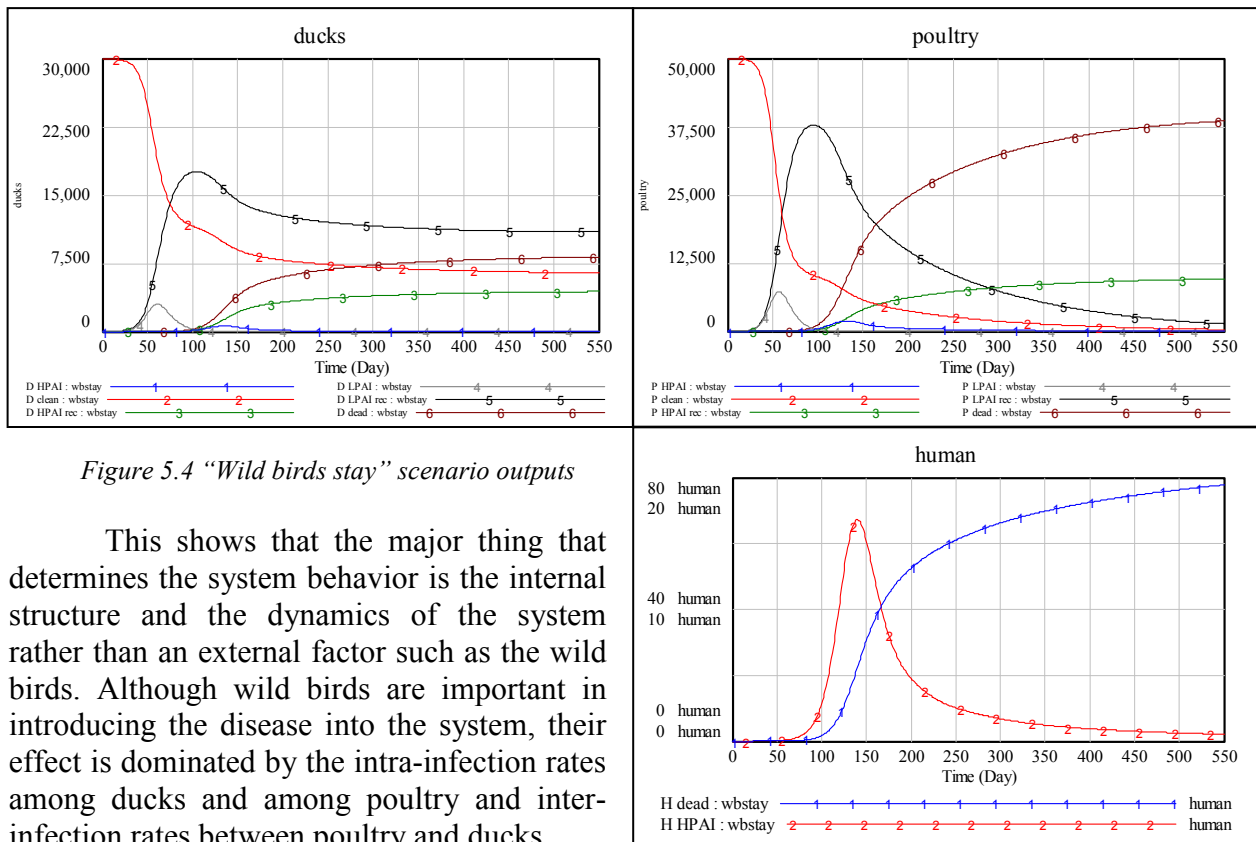


Figure 5.4 “Wild birds stay” scenario outputs

This shows that the major thing that determines the system behavior is the internal structure and the dynamics of the system rather than an external factor such as the wild birds. Although wild birds are important in introducing the disease into the system, their effect is dominated by the intra-infection rates among ducks and among poultry and inter-infection rates between poultry and ducks.

5.2.3. Wild Birds Bring HPAI

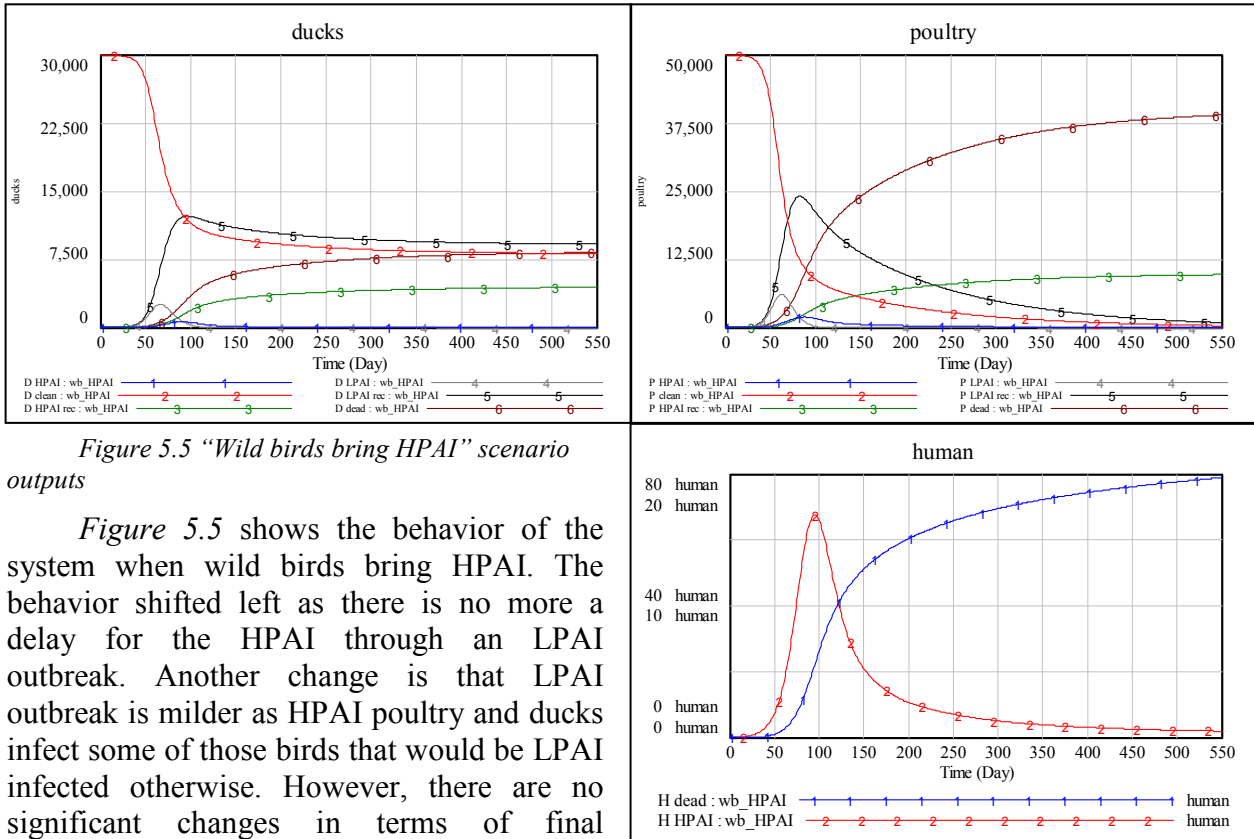
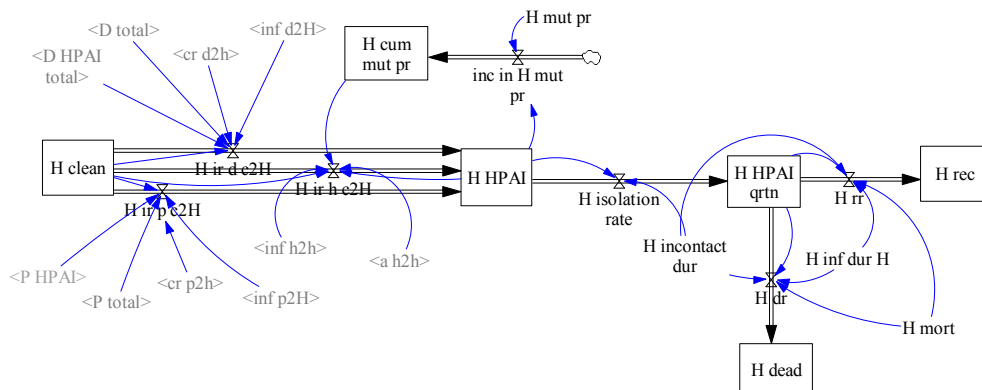


Figure 5.5 “Wild birds bring HPAI” scenario outputs

Figure 5.5 shows the behavior of the system when wild birds bring HPAI. The behavior shifted left as there is no more a delay for the HPAI through an LPAI outbreak. Another change is that LPAI outbreak is milder as HPAI poultry and ducks infect some of those birds that would be LPAI infected otherwise. However, there are no significant changes in terms of final equilibrium levels. Percentage of dead poultry and of ducks do not change. Also, there are no changes in human cases and deaths although the behavior unfolds earlier. Thus, unless LPAI is detected beforehand, direct introduction of HPAI is not more dangerous.

5.2.4. Pandemic Outbreak

This scenario analyzes what happens if the virus mutates to be able to pass from human to human. For that reason, it is assumed that after some number of infected cases, the virus mutates and then the virus enables intra-species infection. An assumption of the scenario is that after 5 days of infection, humans tend to quarantine themselves, either by applying to the hospitals, or confining to their houses. The modified human sector with respect to pandemic outbreak scenario is shown below in Figure 5.6.



The behavior of the model under pandemic outbreak scenario is shown in *Figure 5.7*. The behavior shows that about 25% of the people die, i.e. 50% of humans contract the disease at the end of 550th day and equilibrium is reached

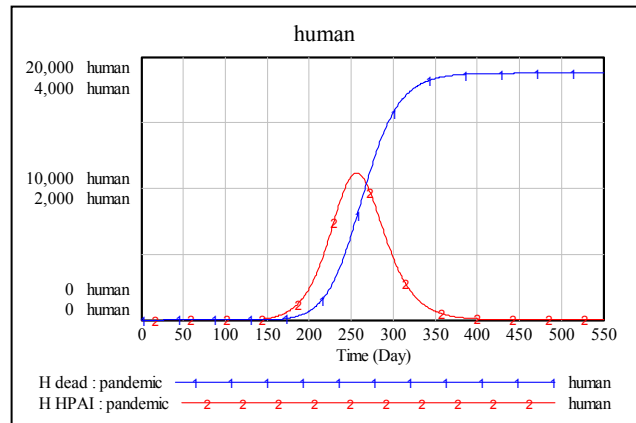


Figure 5.7 “Pandemic outbreak” scenario outputs

5.2.5. With Natural Deaths and Births (bf=df=1/3650)

Natural births and deaths of the birds are introduced. The life-time of ducks or poultry is assumed to be 10 years. The main assumption of this set of scenarios is that new born chicks are clean independent of the parent bird’s disease or immunity. For example, a duck which is LPAI recovered (immune) or LPAI (sick) has chicks that are clean.

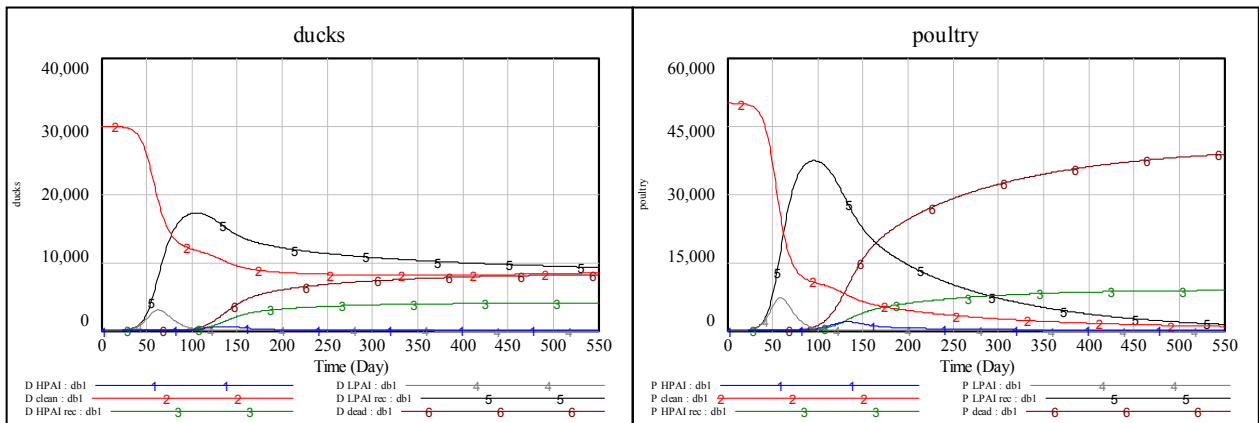


Figure 5.8 With natural birth and death outputs

As seen in the *Figure 5.8* the behavior does not change. So in fact, the natural births and deaths of ducks and poultry are not important in determining the dynamics.

5.2.5.1. Birth and Death Fractions Increased (bf=df=1/100)

As seen in the *Figure 5.9*, the behavior seems changed. Clean ducks are replenished while the other stocks are depleted towards the equilibrium. Due to this fact, the number of dead ducks, poultry and humans are reduced a bit. However, the change does not seem to be that significant. Also, the increase in clean poultry is induced by the mutation of HPAI at first, as an HPAI bird infects the birds in all of the clean, LPAI, and LPAI recovered stocks. The total number of birds continue going down with the deaths due to sickness. (*Figure 5.10*)

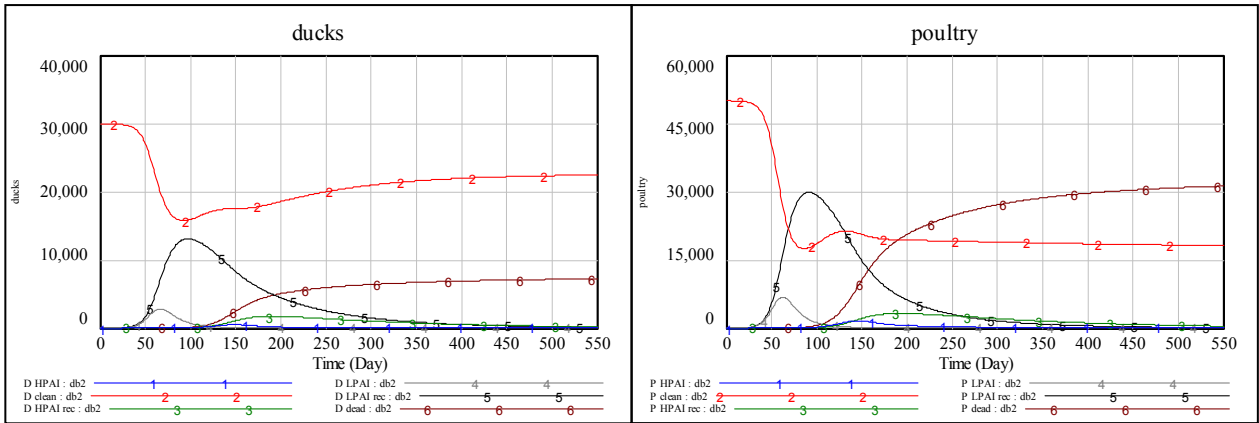


Figure 5.9 Increased birth and death fractions outputs

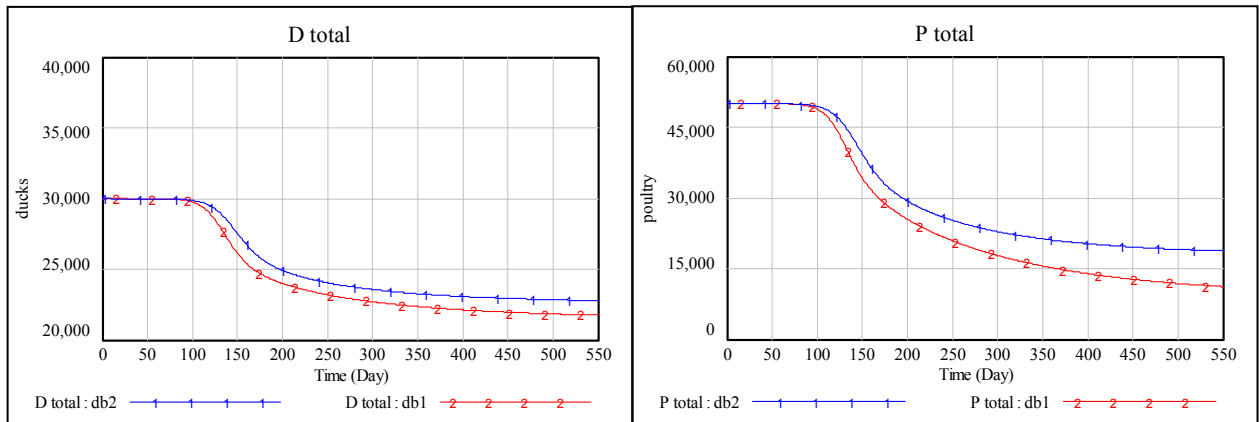
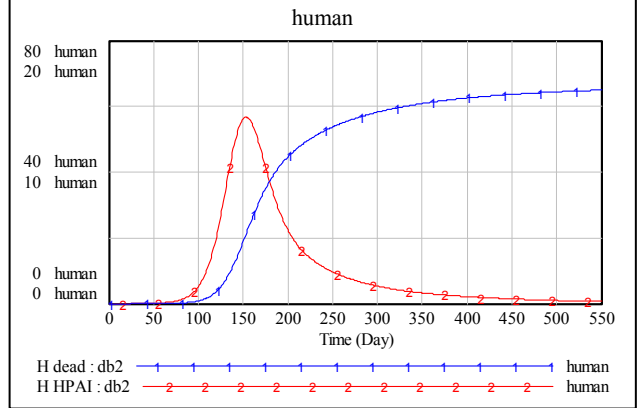


Figure 5.10 "Increased birth and death fractions" total duck and poultry outputs

5.2.5.2. Birth Fraction More than Death Fraction (bf=1/75, df=1/100)

This scenario assumes that birth fraction of birds is more than the death fraction, so that birds continue increase in number exponentially if there are no viruses in the flocks.

Figure 5.11 shows the behavior in this case.

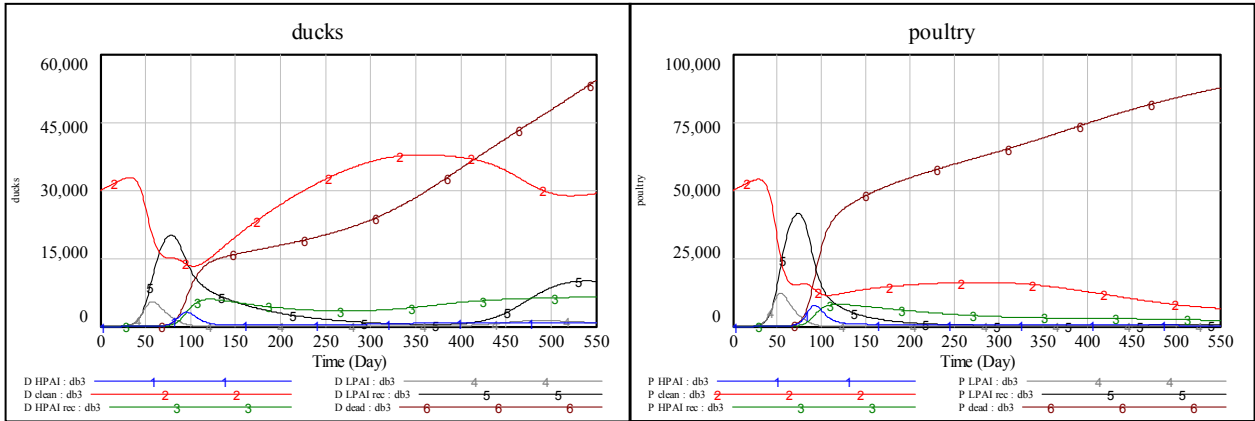
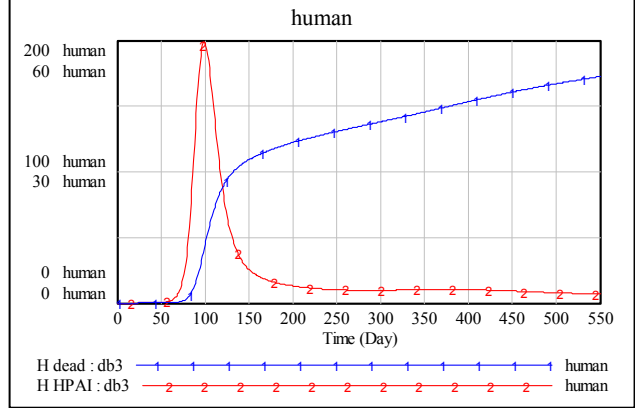


Figure 5.11 “Birth fraction > death fraction” outputs

The behavior significantly changes in this case. After a short increase in number, ducks are decreased with the introduction of HPAI into the sector. After the first wave of epidemic dies out among the ducks, clean poultry starts to increase, but at some point as the susceptible ducks increase in number so that the tipping point is reached and ducks start get infected at a faster rate again. An interesting fact is that as the number of ducks increases (see Figure 5.11 and 5.12). dead ducks also increase at a faster rate seen in the previous figure.



Poultry stocks show a similar behavior to the case where the birth and death fractions are both equal to 1/100 until the 150th day. However, after the major 1st wave of HPAI epidemic slows down, clean poultry start to increase in number. However, this cannot avoid the killing of all poultry as the virus is still sustained in ducks as HPAI or recovered HPAI. (see Figure 5.11 and 5.12)

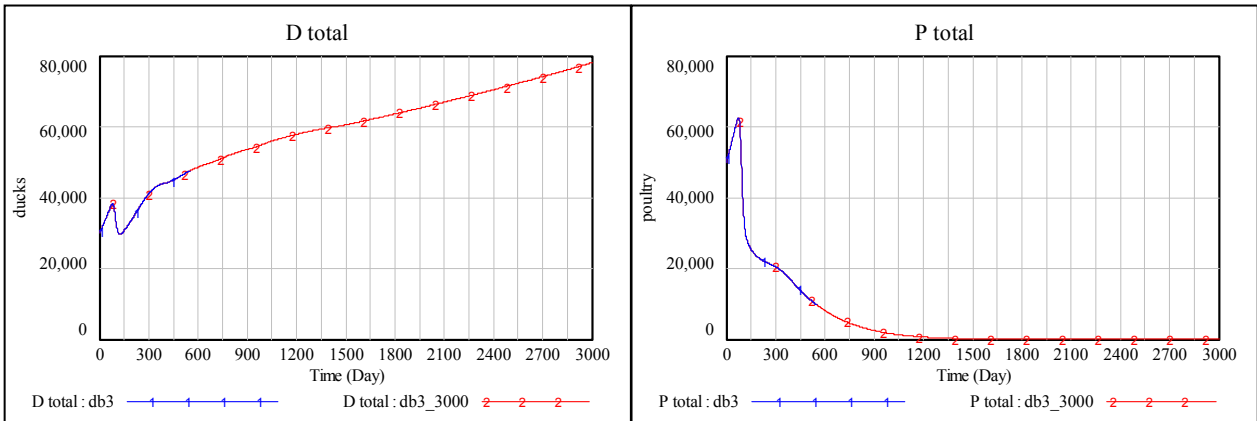


Figure 5.12 “Birth fraction > death fraction” total ducks and poultry graphs

5.3. Policy Analysis

5.3.1. Culling Poultry After Detection of HPAI ($days\ to\ cull = 2$)

The culling policy states that after detecting HPAI in the poultry, all of them are exterminated. However, there are two important delays before making the decision. First is the perception delay. The breeder would perceive that there is a sickness inside his flock after repeatedly observing sick poultry. However, if the deaths in the poultry are at a low rate, then he will not consider these deaths as deaths from sickness and attribute them to normal conditions. After breeder perceives that there is some sickness inside his flock, he informs the authority about the matter. Then the viruses are isolated from animals, taken to the laboratory and then tested to make sure that the disease is HPAI. All the diagnosis process takes about 2 days after the authorities are informed (Tiensin et al.,2005).The breeders take the dead poultry as a sign of sickness out of their consideration after 1 week (7 days).

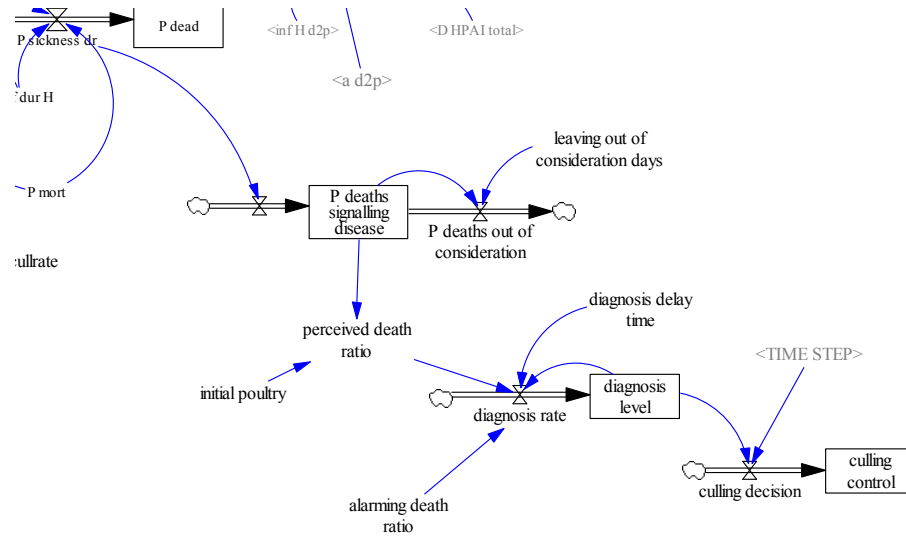


Figure 5.13 The model structure of culling policy

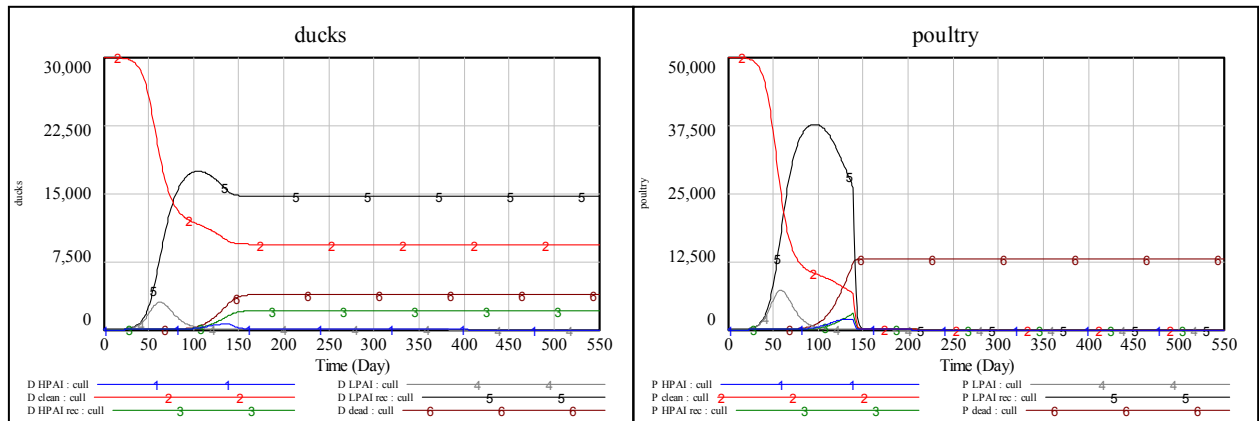
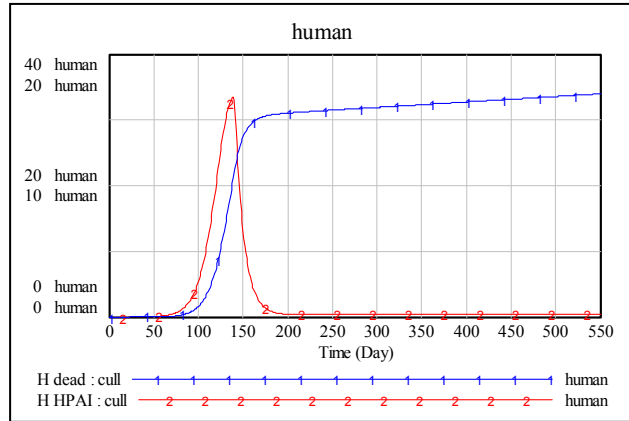


Figure 5.14 Culling policy outputs

Figure 5.14 Culling policy outputs (cont'd)

The culling decision kills all poultry in about 2 days. As a result about 30 humans, just short of half of the dead humans in the base model, die. Although the policy prevents the killing of another 50 people, it is not as effective as it is thought to be due to delays in the process.



Another consideration is the economic side of this issue. If all the poultry are culled, then the breeders have no means of making money. Also, as the domestic ducks are not culled, there stays a silent reservoir for the poultry that might be brought into the region. The ducks can be culled, too but the adverse effects of culling resident wild birds might also pose an ecological problem.

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5.3.2. Quarantining the LPAI Poultry and Ducks (time for ducks=5, time for poultry=3)

Quarantining LPAI policy is based on the action that when LPAI poultry or ducks are seen to be bearing any symptoms of LPAI disease, they are to be quarantined. However, as there is some incubation time and identification delay before being able to identify the LPAI infected birds. The assumption is that it takes 3 days to identify sick poultry and it takes 5 days to identify a sick duck. The resulting behavior is in Figure 5.15.

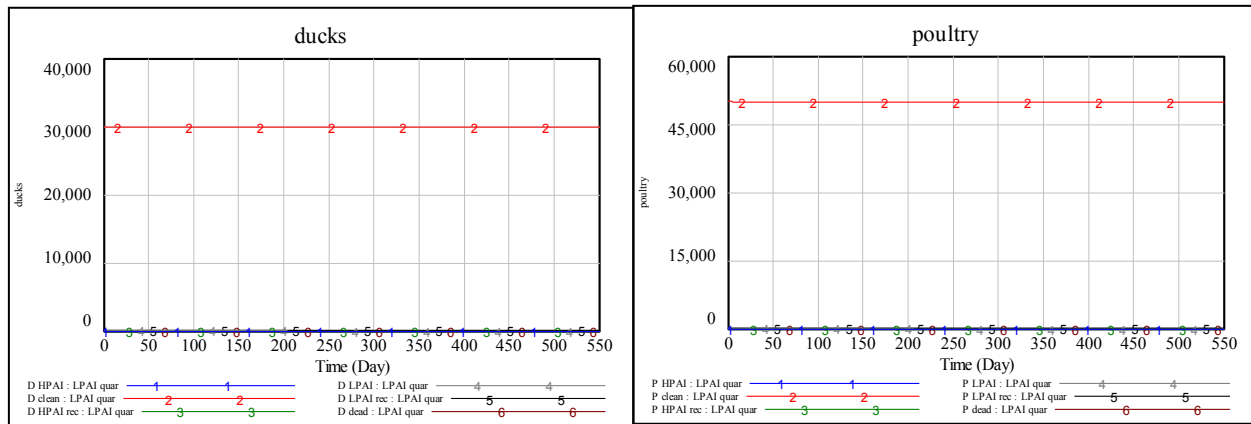


Figure 5.15 Quarantining policy outputs

Applying quarantine to ducks is hard to implement, so the policymakers might only implement quarantine to poultry. The same time for quarantine is valid for the poultry, 2 days.

5.3.2.1. Applying Quarantine Only To Poultry

Applying quarantine to ducks is hard to implement, so the policymakers might only implement quarantine to poultry. The same time for quarantine is valid for the poultry, 3 days.

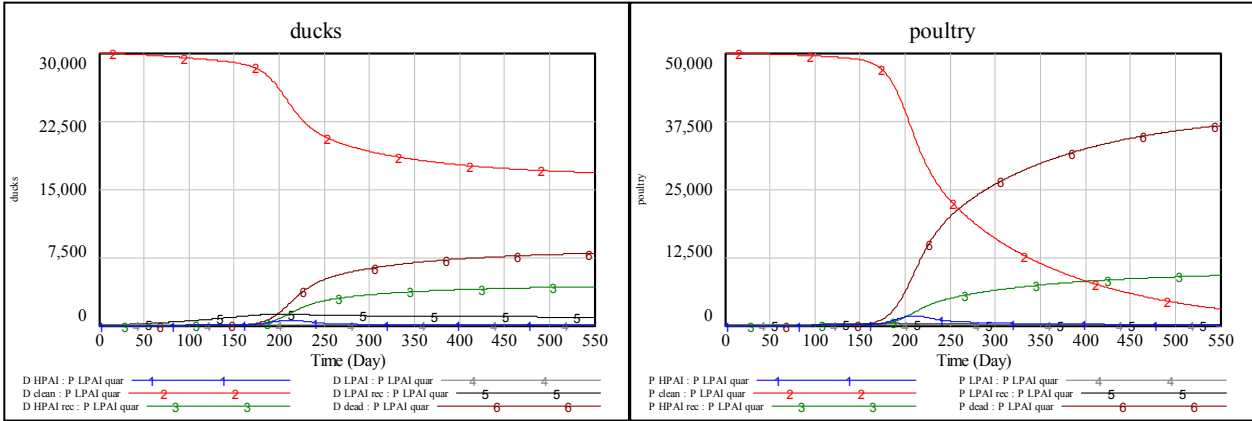


Figure 5.16 Quarantining only poultry policy outputs

Figure 5.16 indicates that a quarantining policy applied only to the poultry is not effective in the long term. It just delays the HPAI outbreak as the ducks start to spread the infection to the poultry.

6. Discussion and Conclusion

The aim of the project is achieved as a model that represents the dynamics of avian influenza has been developed and several scenario and policy analyses have been applied to it. The base model is a generic model which can be applied to different situations with different set of parameters or with a little change in the model structure.

The base model by itself gives little insight about the problem. It just represents the general situation that might be happening right now in a broad manner. However, the scenario and policy analyses provide some basis for discussions and maybe suggestions.

As discussed in the scenario analysis section, the appearance of the epidemics is dependant on the density of poultry in the region. This implies that the current high density poultry farms might be providing advantageous conditions for the avian influenza outbreaks.

Another important implication of the model is that the epidemiological dynamics are independent of the wild birds' decision to stay in some region not migrating again. This shows that the internal dynamics are responsible for the outbreak rather than an external output, which only triggers the system.

One of the most feared scenarios is that wild birds are themselves carrying the HPAI virus, but it again does not change any indicator except that the epidemic starts sooner. Therefore, as the authorities do not react to avian influenza before high pathogenic form appears, this does not imply any worse scenario than today's setting.

The pandemic outbreak is important, as discussed by the academicians and authorities there is high risk of mutation and the virus can achieve a form that can sustainably pass from human to human in the near future. The model predicts that the death rate will be high in such a scenario, so we should avoid any human cases to start with not to allow any chance of adaptive mutations on humans.

The increased turnover of the population induces somehow a smaller epidemic as the new born chicks are clean even if an infected has it. However, another problem is that in a growing population this proves to be detrimental as the increased number of susceptibles in the system increases the infection rate and the disease might become endemic in such a population.

The current culling policy is effective in saving lives. However, there seems to be no future for the region such that HPAI epidemic can start again if some poultry are brought into the area again, and if no poultry is brought into the area there would be a huge economic loss for the farmers.

The LPAI quarantining policy seems to be effective when we can recognize and can quarantine poultry in 2 days and quarantine ducks in 4 days. If we just focus on the sick poultry for quarantine as the ducks are still serving as a reservoir of avian influenza virus. The hard part of this policy is that every breeder should be aware of the sickness and actively be monitoring it.

As more data about the issue comes up, by using more direct data and extra knowledge generated, the parameters and the structure of the model can be updated in the future. This will enable the model to easily explain the actual behavior with updated data. As data about more specific cases come up, the model can be applied to those cases as a test for behavioral validation and better explanations for behavior. As policy alternatives; vaccination and anti-viral drug application can be incorporated into the system as they are developed.

References

Barlas, Y., (1996), Formal aspects of model validity and validation in system dynamics, *System Dynamics Review*, 12(3), 183-210.

FAO - Food and Agriculture Organization of UN (2005), Epidemiology of H5N1 Avian Influenza in Asia and Implications for Regional Control.

FAO - Food and Agriculture Organization, OIE - World Organisation for Animal Health in collaboration with WHO - World Health Organization, (2005) A Global Strategy for the Progressive Control of Highly Pathogenic Avian Influenza (HPAI), <http://www.fao.org/ag/againfo/subjects/documents/ai/HPAIGlobalStrategy31Oct05.pdf>

WHO - World Health Organization (2005a), Avian influenza frequently asked questions, http://www.who.int/csr/disease/avian_influenza/avian_faqs/en/index.html

Morens, D. M., and Taubenberger, J. K., (2006), 1918 Influenza: the Mother of All Pandemics, *Emerging Infectious Diseases* Vol. 12, No. 1, January.

Sterman, J.D., (2000) Business Dynamics, Systems Thinking and Modeling for a Complex World, Irwin McGraw-Hill.

Tan, B., (2005), A Dynamic Analysis of Long Term Impacts of Genetically Modified Crops on Agriculture, MS Thesis, Bogazici University, Istanbul.

Tienson, T., Chaitaweesub, P., Songserm, T., Chaisingh, A., Hoonsuwan, W., Buranathai, C, Parakamawongsa, T., Premashthira, S., Amonsin, A., Gilbert, M., Nielen, M., Stegeman, A., (2005), Highly Pathogenic Avian Influenza H5N1, Thailand, 2004, *Emerging Infectious Diseases*, Vol. 11, No. 11, November.

Webster, R.G., Peiris, M., Chen, H., Guan, Y., (2006), H5N1 Outbreaks and Enzootic Influenza, *Emerging Infectious Diseases*, Vol.12, No.1, January.

WHO - World Health Organization (2005a), Ten things you need to know about pandemic influenza, <http://www.who.int/csr/disease/influenza/pandemic10things/en/index.html>

WHO - World Health Organization (2005b), Avian influenza: assessing the pandemic threat, <http://www.who.int/csr/disease/influenza/H5N1-9reduit.pdf>

WHO - The Writing Committee of the World Health Organization Consultation on Human Influenza A/H5 (2005c), Avian Influenza A (H5N1) Infection in Humans, *The New England Journal of Medicine* Volume 353:1374-1385, September 29, Number 13 <http://content.nejm.org/cgi/content/full/353/13/1374>

WHO - World Health Organization (2006a), Avian influenza (" bird flu") - Fact sheet, http://www.who.int/mediacentre/factsheets/avian_influenza/en/index.html

WHO - World Health Organization (2006b), Avian influenza: significance of mutations in the H5N1 virus, http://www.who.int/csr/2006_02_20/en/index.html

WHO - World Health Organization (2006c), Cumulative Number of Confirmed Human Cases of Avian Influenza A/(H5N1) Reported to WHO.