

# **What Could Bird Flu do to a Human Population?**

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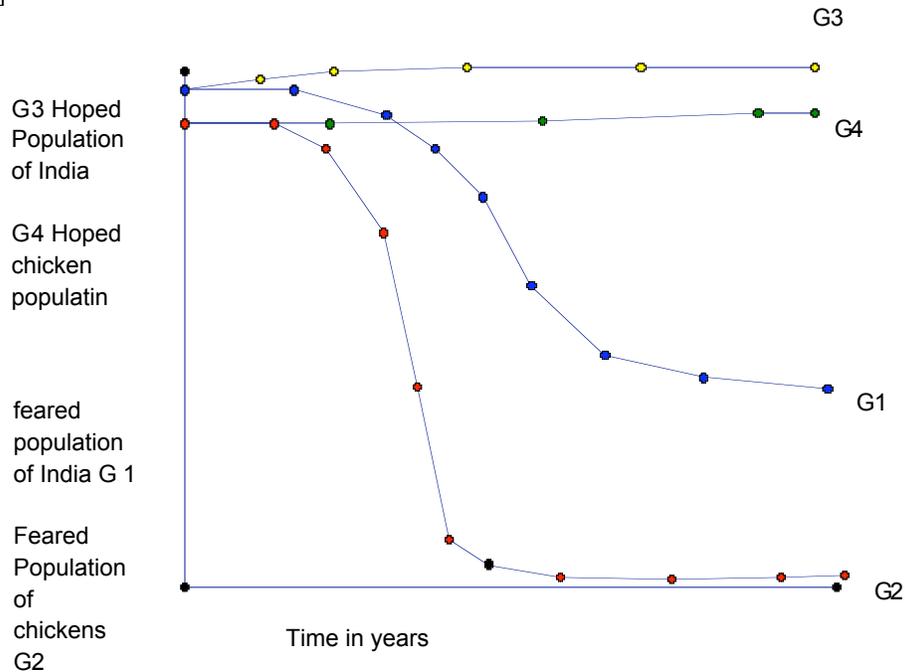
## **Introduction:**

Throughout human history, we have been plagued by many diseases. We have experienced countless sicknesses over time, and are, without a doubt, going to experience many more. Diseases range from the common cold to much more deadly diseases like Ebola. Sometimes they are wide spread like the well remembered black plague which devastated much of Europe and Asia during the middle ages. Diseases such as the black plague are called epidemics because they affect a wide range of people, or even pandemics in which case, they affect the whole world like the Spanish flu of the early 1900's. We are always on the watch for new potential epidemics/pandemics because they are obviously very worrisome to many people.

Diseases usually develop in stages. First they are dormant, and then they mutate and affect a species of animals. Eventually they can cross the species barrier, often by exchanging DNA with other diseases, and some work their way into us. Small pox was obtained from domesticated animals. One of the many diseases on the horizon is the potentially deadly H5N1 (avian flu) virus. This virus has affected many birds in the world, and has so far killed millions of them. The reason we are concerned about this particular virus is it appears to be right on the edge of transferring from human to human, and so far it has killed roughly 65% of the people it has infected. There have only been about 300 confirmed infections, but the fact that it can occasionally spread from animals to humans makes it something to watch out for. New viruses spread very easily, especially air born flu viruses, and if bird flu were able to transfer from human to human, we would most likely have a pandemic on our hands that could potentially kill 20-60% of the people it infected. There is no way of telling how many people it could kill because diseases mutate over time and it could in fact become less harmful over time.

This model deals with the hypothetical situation of the chicken population of India being affected by the avian flu, and then the human population being infected with a strain that spreads from person to person. The purpose of this is to simply observe what bird flu would do to an evenly distributed population with a 65% kill rate. Though it is most likely not accurate, it gives an idea of what bird flu could potentially do, and why it's something to watch out for. The reason the model is useful is because it has a unique way of looking at the problem. It plugs in values I have obtained through research, and generates a situation displayed, in graphs, that could probably not be easily expressed through other methods such as mathematical equations. This model observes the population of India, affected by bird flu, over the span of one year in this particular graph.

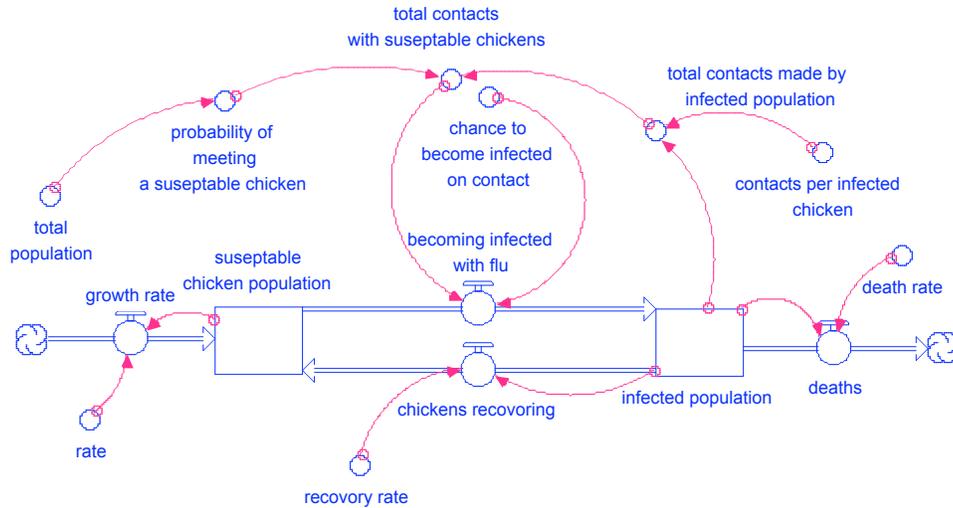
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**Figure 1:** A reference graph of what I initially believed a bird flu outbreak would do to the population. There are 2 graphs for the human and chicken populations, one being a hoped outcome and one a feared outcome.

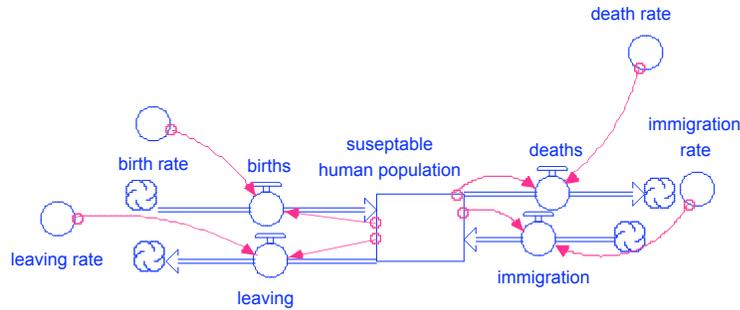
### **Process of Model Building:**

When introduced to this project, I experimented with a variety of ideas for a Stella model. I tried “how would global warming affect Portland’s water supply in the next 100 years?” but I couldn’t find the necessary data to do this model. I then proceeded to try modeling the relationship between pollution and asthma rates, but I couldn’t find the necessary data for this either. Finally, I remembered the avian flu, something I couldn’t recall hearing anything about for several years, and decided this would be something worth looking into. I first created my first basic structure for the model, which was an epidemic model for a chicken population. I didn’t fill in any values or do much research yet, because I wanted to see if I could build a reasonable structure first. This is what the very first structure looked like.



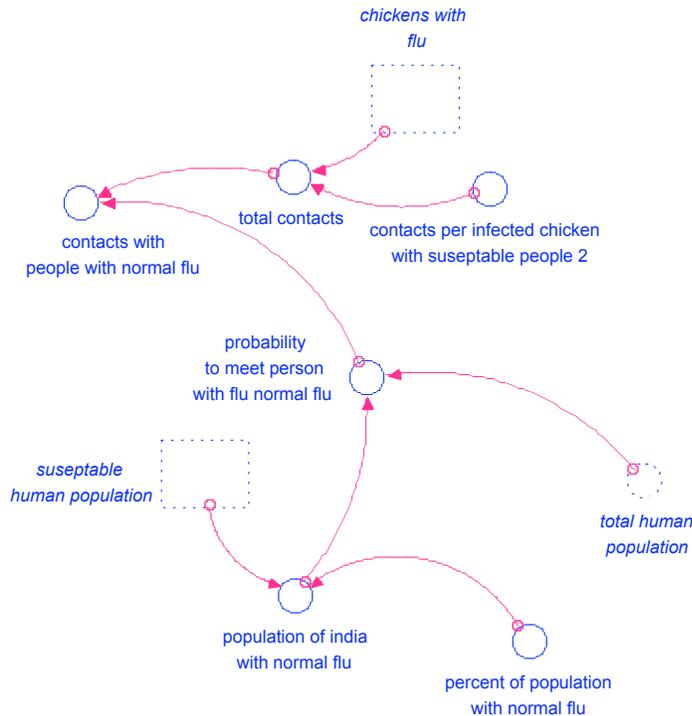
**Figure 2:** Simple epidemic model for a chicken population effected by a disease. No values have been put in

I had the foundation for the model down, but I needed to add values, and I didn't know if I would find any for a disease I hadn't heard anything about for almost 4 years. I also had to add many more parts to the model if it was to become what I wanted it to be. I had to go from a simple chicken epidemic model, and add on to it, a human epidemic model, and something that would somehow make the disease able to infect humans. First, values needed to be found so the system would work at all. It was only going to be as accurate as the values that would be found, and I was in luck. I found a list of the total cases next to the total deaths in humans, a description of how bird flu affected birds, including its approximate death rate. In epidemic models, you do not just need facts about the disease, but you also need to know how it will spread and to know this, you need to find the size of the population, and its distribution. Epidemic models work by calculating the chance for infected people to meet up with susceptible people and then it uses the chance for an infection on a contact to calculate the total people infected. I found much of this information on the CIA world fact book. It gave me the chicken population of India, sitting at approximately 850 million, and the human population sitting around 1.16 billion. I then found the total land area in India, and divided both populations by this land to find the approximate amount of chickens/humans per square mile. There were about 300 chickens per square mile and 350 people, if they were evenly distributed, which unfortunately had to be the case in this model, unless I was to make it very, very complicated. I experimented with values to try to find out a reasonable amount of contacts per day person/chicken would have with a person/chicken. The ones that seemed reasonable for the population density made the simulation happen way too fast, so I used 10 for chickens contacting chickens. I had not yet finished the model, but I would eventually need values for people contacting people, and chickens contacting people. These contacts would be inconsistent because people have different contacts each day, and not everyone handles chickens, but there is no other way to put it for the model to understand it other than a constant value in this case. Eventually I created the beginning of a population model for India.



**Figure 3:** Simple population model for susceptible population of India with values plugged in.

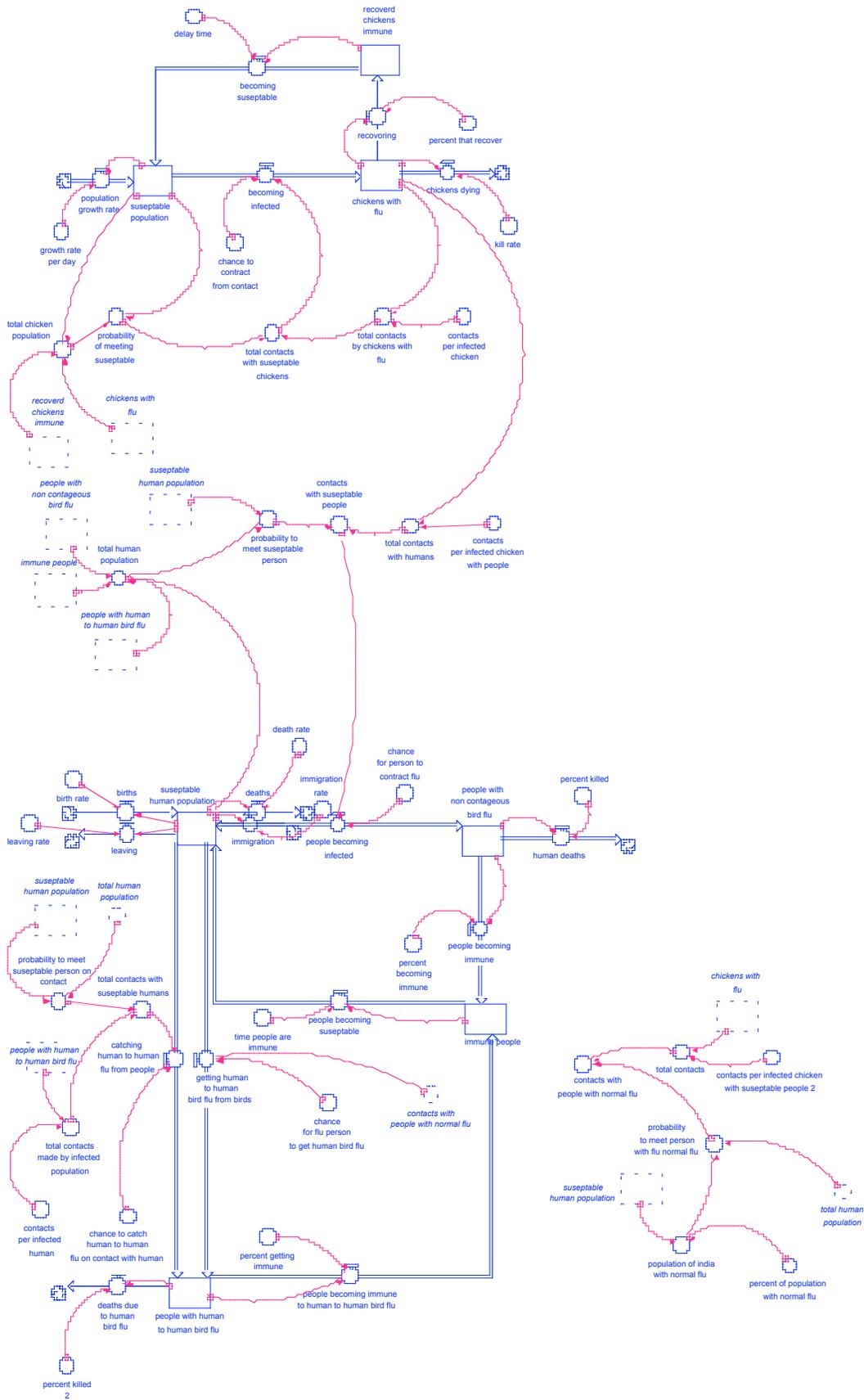
I then turned this into an epidemic model similar to the chicken population, and proceeded to combine the two models. This part was especially difficult, because I wasn't exactly sure where to connect them. It made sense that the infection would start in the chicken population, then spread to humans from the chickens, and then somehow mutate into a human to human strain. I managed to connect the two models with some problematic unit inconsistencies which I didn't manage to solve for about 3 weeks, but it worked ok. I then created a new structure after learning how diseases mutate and cross the species barrier. It turns out that bird flu could turn into a human-human strain by infecting a person who already has a type of flu, and while inside the person, the two viruses could exchange DNA. This unlikely exchange could allow bird flu to spread from human to human. The structure that would model this I created looked like this.



**Figure 4:** Part of model allowing a human-human strain of bird flu to be created, similar to previous epidemic models.

Adding this portion into the model complicated things a bit and added similar unit inconsistencies, which took me a while to solve, but I managed to connect everything correctly, and the model worked well. The first simulation killed 2/3 of the population of India following the 65% death rate among people, which in real life is highly unrealistic. The flu, in the model was allowed to infect everyone, and was allowed to infect people more than once. In the world, a pandemic would not infect everyone and it would most likely infect each person only once with a few exceptions. By making it a bit harder for the model to spread, and reducing death rates, a more reasonable graph was obtained. The final model, after handing it into my instructor and fixing unit/model errors looked like this.

**The Final Model (see next page):**



**Figure 5:** *Final model displaying the spread of a bird flu epidemic into a human population. The situation starts in the top segment of the model which is the bird flu epidemic in chickens. It begins to spread, and eventually people begin to catch the disease in the second epidemic model in the middle. This then spreads through a third epidemic model which is the human one for chicken-human cases. To the right, there is a 4th epidemic like structure that “mutates” the virus into a human-human form by calculating the chance for this to happen. The human-human disease then spreads into a 5<sup>th</sup> and final epidemic structure located on the far left connecting to the bottom part which allows the human-human strain to spread throughout the human population.*

This model works by starting with an initial infected chicken population of 5, uninfected of 850 million, and a human population of about 1.16 billion with no infections. The 5 infected chickens infect a vast amount of the susceptible population which starts an epidemic among the chickens. The chicken problem is connected to a human population/epidemic model structure. A few rare human-chicken cases of bird flu are developed throughout the simulation, just as they are happening today. They do not make a significant impact on the model, but it makes it more accurate. The third part of the model takes into account the percent of the human population infected with the normal flu on average, year round, which is about 5%. This is then connected to the human-chicken flu contraction part of the model, and has a very, very low chance on contact (.0001%) with a chicken to mutate bird flu into a human-human form. This is a representation of the bird flu virus and a different flu virus exchanging DNA inside a person and forming a new form of bird flu that can transfer between people. Once one unlikely case happens, which happens fairly early considering the amount of people, the human-human strain strikes the population. Over the span of 1 year it manages to kill roughly 10% of the human population in the final model. This is much more reasonable than the first test in which the disease killed 60% of the people and 90% of the chickens because in reality not all the population would even get the disease. Here’s basically the stages in which the model works.

Infected chickens infect chicken population  
Some chickens infect people  
A person with the flu comes into contact with an infected chicken  
Person become infected with new strain  
Human-Human strain infects human population

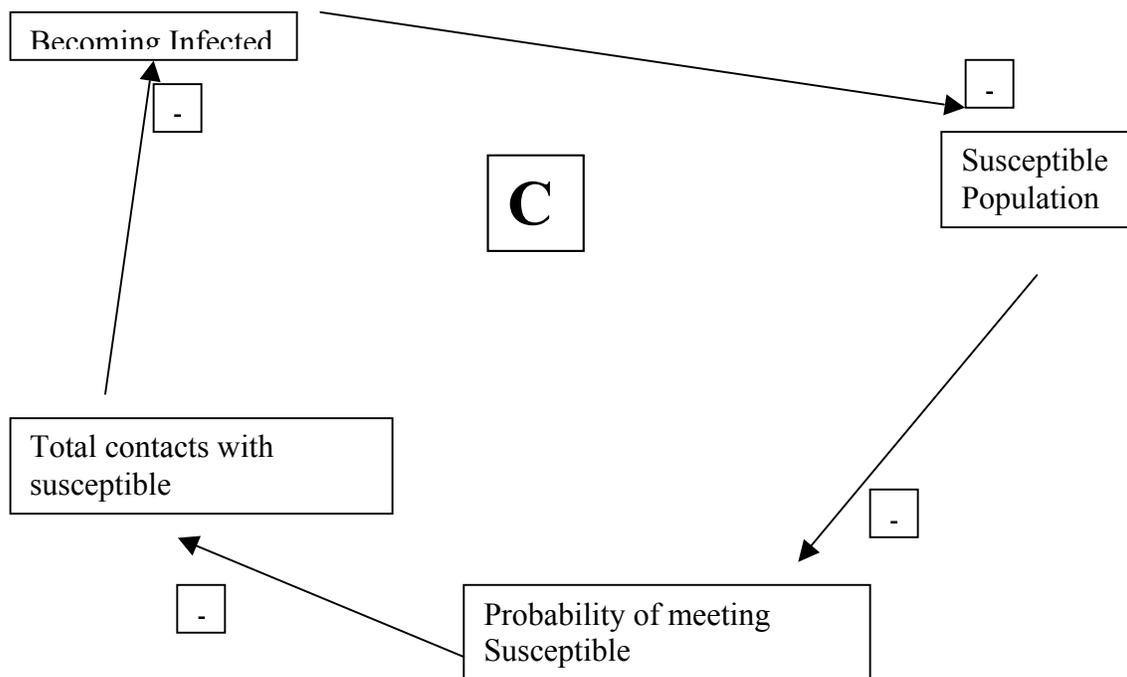
This follows how diseases work in the real world pretty well. First an animal with somewhat similar DNA to humans catches the disease. It starts crossing the species barrier, and then later a new form of the disease is created which can spread among us.

The most important converters in this model are the ones that change the outcome in the end the most. These converters are death rates, birth rates, immunity times, contacts per day, and chance to catch disease on contact. The death converters like the ones labeled “kill rate 1, 2” “death rate” etc, affect the percent of people or chickens that are killed by the flu. It is pretty obvious how this affects the final product. By doubling the kill rates, significantly more infected people/chickens will die. The birth rates “growth rate” effects how fast the population increases each day. By changing these, the final product will be changed in a way similar to that of the death rate. The immunity times are a bit different in the way they change the model. If a person is immune for 20 days, they cannot be

infected again for another 20 days, so the population is 1 higher no matter what for those 20 days. By reducing the delay time to 1, people are pretty much immediately infected again, and this dramatically reduces the population depending on the death rate. The contacts per day affect the model by changing the amount of infected people that meet other people each day. By increasing this, you most likely increase the number of infections every day. The “chance to infect on contact converters” Are pretty straight forward. Increasing the chance causes more infections where decreasing it causes fewer infections.

### **Feedback Loop Story:**

The way STELLA models behave is often expressed in feedback loops, and this model has quite a few of them. There are 2 major feedback loops in this situation that connect the human structure to the chicken structure. There is one for the infected chicken population. The susceptible chicken population increases the probability of an infected meeting a susceptible chicken and infecting it which and takes away from susceptible population. This is a counteracting feedback because it continuously reduces the susceptible population.

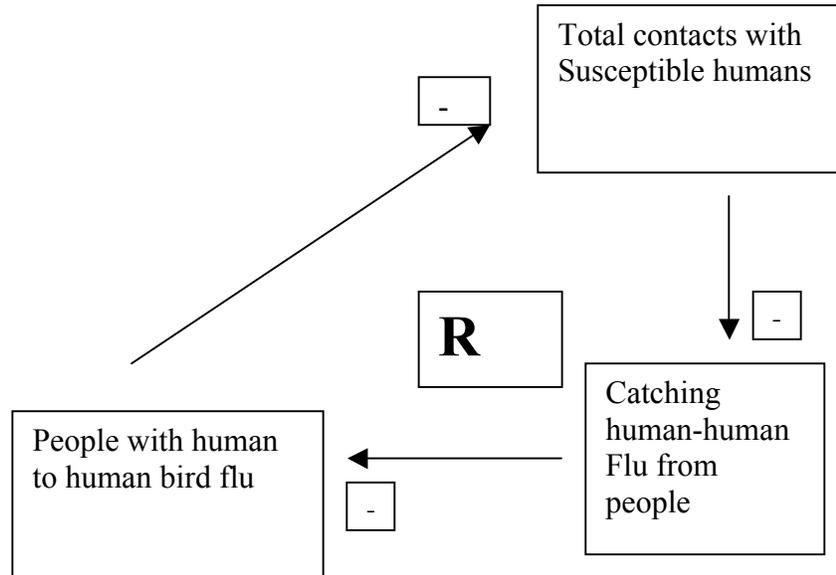


**Figure 6:** A counteracting feedback loop displaying the relationship between the susceptible chickens and the infected chickens.

This feedback affects the entire model by increasing the number of infected chickens rapidly. This dramatically reduces the chicken population and also increases the odds of a

person meeting an infected chicken and either becoming infected, or generating a human-human strain. This eventually leads to an infection in the human part of the model which then reduces the human population by about 10% by the end of the simulation.

The second major feedback loop is the one displaying the relationship between the immune people, the sick people with the human-human strain, and the susceptible people.



**Figure 7:** Feedback loop diagram displaying the relationship between the human populations, the sick population with the human-human strain.

This feedback Affects the model by reducing the human population dramatically. The human to human strain created by the chicken part of the model spreads as easily through the human population as the chicken strain spread through the chicken one. This loop doesn't do anything to the chicken segment of the model, but it does do a lot to the human segment.

It would make sense that there would be a third feedback connecting the chicken population to the human population but unfortunately, there is not. This is because, although the populations are linked in the model quite obviously, the human population, in no way, affects the chicken population. In reality, we eat chickens, but that doesn't take place in this model. The chickens make us sick in this situation, and we do absolutely nothing to them, so there is no feedback. Feedbacks need to be able to loop around and affect their starting point in some way. If the chickens make the people sick, that's only half a loop if it doesn't work its way back, which unfortunately makes it a bit hard to show the way this model works through feedback. The feedback in this case makes it look like two separate epidemic models. There are however, several smaller

feedback loops that represent the individual epidemic structures such as the human-human strain of bird flu spreading through the human population.

### **Model Boundaries:**

Like many models, there are many factors that are left out in order to allow the model to work. For example, if you were to model the population of a country, you may choose to leave out something like an issue in another country causing an immigration increase. Although they would make the model possibly more accurate, they also make things needlessly complicated, or cause the system to not work. In my model, probably the largest thing I left out was a population carrying capacity. The disease is the one thing that prevents this particular population from reaching infinity. I didn't take land area, food availability, pollution, or distribution of wealth into account for the sake of simplifying the model. To illustrate these other factors in a much simpler way, I just used India's annual population growth rate as the thing that would increase the population. It is obviously much less accurate, but at the same time much less complicated and actually allows the model to work. There are also several smaller things I had to change that are not necessarily accurate. For example, there were several values that created unreasonable situations in the model, and I had to change them so things worked more reasonably. One of these was determining how many contacts chickens would have with chickens, humans with humans, and humans with chickens. There is no good way to determine this, so I just divided the land area by the population and assumed each population was distributed evenly. I then tried what seemed like reasonable contact values if the population was distributed evenly, and changed them many times until they balanced the model. Another one of these changes was determining the chance for a normal flu infected person to create a human-human strain of bird flu when contacting an infected chicken. There is also no reasonable way to determine this, so I just picked a value that caused a case within about 5 or 6 days of the simulation's start time.

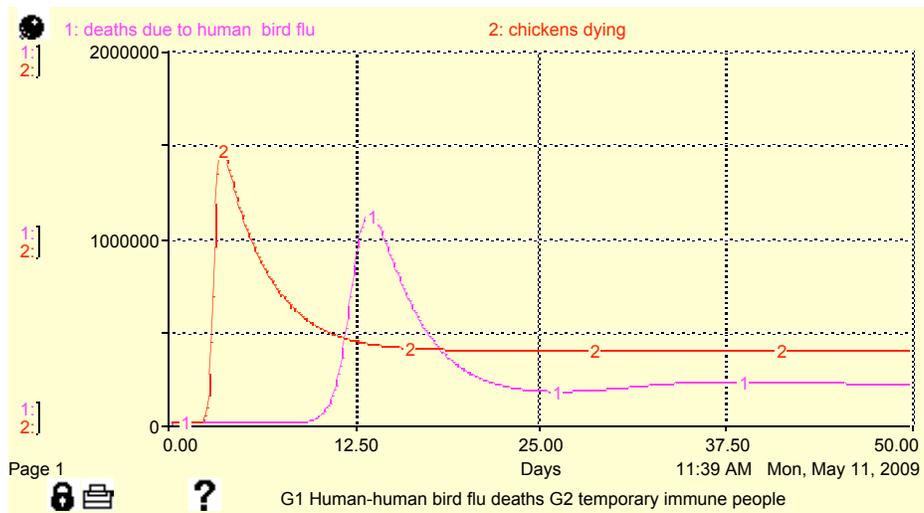
For time on the model, I first tried years, but it seemed unreasonable for a chicken to have bird flu for a whole year, so it got changed to days. For some of the less important graphs, such as immune people, or dying people, I picked a run time of 50 days just to show the general trend in the graph. Then for the over all chicken and human population graph, I picked a run time of 365 days to get a better idea of the long term effect of the sickness on the population. Considering the disease would eventually just wipe out the population, unlike what would happen in the real world, I didn't make the run time too long.

### **Model Testing:**

Throughout the model building, I had to do many tests to make sure it was working right. Looking at past epidemic/pandemics, they appear to wipe out between 1% and 20% of the population over time. I figured that the final graph for the populations should not look too dramatic, but at the same time decrease a bit. In order to get a graph that looked like this, I had to change many different values several times. The contacts/day converters, % killed/% survived and chance to contract the disease on contact had the most dramatic

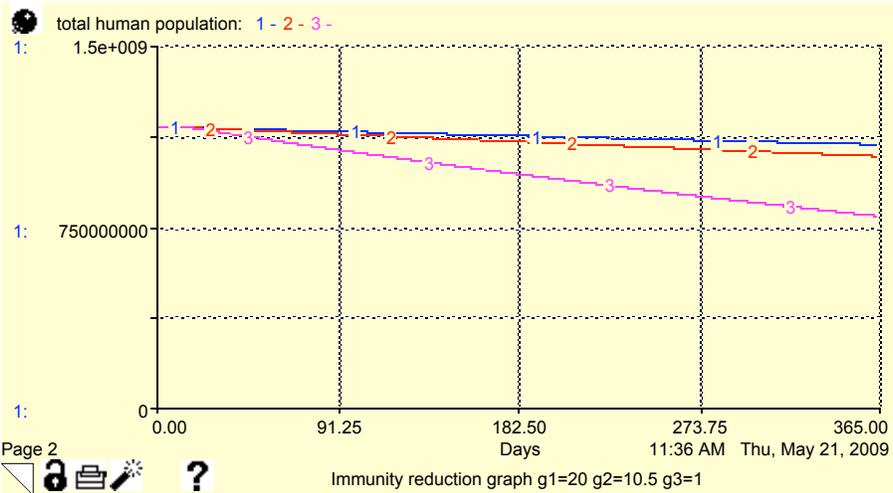
effect on the final results. During the first tests, my time choice of years caused the model to kill off about 70% of the population very quickly. Once changed to days, and once all of the converter values previously mentioned were divided by 365, the model behaved much better only killing around 10% of the population after a year.

The model seems to agree with the BOTG. The values in the model that determine the rate at which people and chickens are killed seems to be reflected well in the graphs. The graphs also do not reflect any irrational behavior that the model shouldn't allow. For example, the BOTG that displays the human deaths per day and the chicken deaths per day agrees with the way the model works. It shows the deaths spiking in the chicken population and then shortly after, the human population gets the human-human strain and the deaths then spike there. This is the order things are supposed to happen according to the model. The deaths may be in the millions, but in comparison to the over all population, it is a low percentage around 5%.



**Figure 8:** BOTG displaying the chicken deaths and human deaths happening each day in this STELLA model.

The effects of the models that most dramatically affected the model can be seen in sensi spec graphs in which the values are changed. Inputs like contacts per day, the death rate, the infection rate, and immunity time were the values that I had to change the most times until the model worked again. When viewed in the human population graph, with different values, the changes are very obvious.



**Figure 9:** A graph displaying how the time people are immune effects the population.

The graph above displays a very important converter that determines how long people are immune to the flu after they catch it. The original value I used was 20 days because it made the model behave reasonably. To show how dramatic of an effect this value has on the model I made this graph which shows different immunity values, one is 20 days, the next is 10.5, and the 3<sup>rd</sup> is 1 day. You can see how dramatically this one converter affects the model. All the other effective ones are unchanged in this situation, but there are over 10 more that could produce scenarios similar to this one if changed. Because these values can change the results so much, I'm confident the model is working because it seems reasonably balanced. It could very easily be unbalanced, but eventually I found a set of values for these important converters that didn't kill the population in 10 days.

The tables are also important in this model because they can show exact values unlike the graphs where one has to estimate. The most important table shows the majority of the human stocks, containing one for susceptible population, and 2 for the people who are infected. It shows a more accurate version of the susceptible population going down, and the infections going up. It is important because the human population is the focus of this model.

Days	Susceptible human pop	People with human-human strain	People with chicken strain
0	1163012000	0	0
30	214584778	104196833	276
60	192739507	119470081	266
90	191474118	118655942	262
120	190464442	118020665	259
150	189452851	117393863	255
180	188446567	116770327	252
210	187445630	116150102	248
240	186450010	115533171	245
270	185459678	114919516	242
300	184474606	114309121	238
330	183494766	113701969	235
Final	182520131	113098041	232

## **Results:**

Looking at the progression of bird flu so far, it appears it has taken about 10 years to make just 300 world wide cases that spread from chickens to people. In this time, there has not been 1 human to human case as far as we know. My model managed to make 276 chicken-human cases in 30 days and over 100 million human to human cases in this same amount of time. In reality, if a human to human strain were to break out, millions or possibly hundreds of millions of people could catch the flu within a few months, but this model is obviously accelerating things quite a bit.

## **Key Learning:**

Making this model has taught me a variety of things about modeling, and the situation it is modeling.

-Learned that STELLA models can never be entirely accurate, but just make hypothetical situations based on the data. They are only as accurate as what you plug in.

-Learned that it is difficult to model a disease accurately, especially when it comes to how many people it kills, and how easily it spreads.

-Modeling a disease crossing the species barrier cannot be accurate in terms of How long it would take.

-The over all results of what effect an epidemic has on a population can be somewhat accurate. Epidemics seem to kill between 1 and 20% of the population. In my model about 10% of the population was killed.

-The problem I modeled probably can't be modeled accurately in terms of how long it would take for the disease to spread and cross the species barrier, but it can be accurate when it comes to the over all impact on the population.

What could bird flu do to the population of India?

India is a very overpopulated area, and if an epidemic were to strike there, the result would most likely be disaster due to often unsanitary conditions making it incredibly easy for a disease to spread. If a disease such as bird flu were to strike there in a form that could spread from human to human, it would probably kill off a large portion (large being over 10%) of the population. Flues, especially new flues, spread very easily, and are often fatal if we have little immunity. Bird flu has shown that we have little immunity to it and it has so far killed 65% of its victims. This is most likely an inaccurate statistic because many of the deaths were in third world countries where people may have already been in bad health, but even if it is really a 10% death rate, it is still a potential disaster. As diseases mutate, they can also become more, or less deadly. For all we know, bird flu could mutate and become harmless, but this is unlikely. If bird flu were to spread from human to human and hit India it would probably wipe out between 5, and 25% of the people it infected. The disease would not infect everyone, but new diseases affect large

portions of a population once they manage to mutate into an easily spreading form. An example of this would be the recent swine flu which so far hasn't done much harm, but if it were to mutate into a more contagious form, it is estimated it would infect 30% of the population. Although this doesn't sound like much, the regular flu effects between about 1 and 15% of the population depending on the time of the year, and this is considered to be fairly contagious.

To test other models, such as different diseases, or various things that spread, say religion, all that would need to change would be the names of the converters, the subject of the model, the data plugged in, and possibly a few structures like the one that allows bird flu to change to a human-human form. If you were to model the spread of a different disease, you would just change the information according to what it was infecting, how quickly it spread, and what the death rate would be.

### **Bibliography:**

Regional Office for Asia and the Pacific. Table 98. Chicken: population. Online. Internet. April 3, 2009. <http://www.fao.org/docrep/004/ad452e/ad452e30.htm>.

MediLexicon International Ltd. Total Cumulative Human Bird Flu Cases Reaches 228 With 130 Deaths. Online. Internet. April 3, 2009. <http://www.medicalnewstoday.com/articles/45643.php>.

MedicineNet, Inc. Bird Flu (Avian Flu, Avian Influenza). Online. Internet. April 4, 2009. [http://www.medicinenet.com/bird\\_flu/article.htm](http://www.medicinenet.com/bird_flu/article.htm).

Central Intelligence Agency. CIA World Fact Book: India. Online. Internet. April 4, 2009, April 6 2009, April 9, 2009. <https://www.cia.gov/library/publications/the-world-factbook/geos/in.html>

**Appendix:** Documentation, Units, Equations, Graphs, Tables, and Model diagram

Omitted