A Model of Population Movement, Disease Epidemic, and Communication for Health Security Investment

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Submitted to the Proceedings of the 32nd International Conference of the System Dynamics Society, Delft, Netherlands

1. Introduction

This paper outlines the formulation of a system dynamics model designed to compare investment alternatives intended to limit the onset and spread of human or animal disease. The model has been created to support the investment planning process for public health organizations worldwide, but also has relevance for public health systems research in general. It has been compiled from a sample of available generalized information as well as discussions with public health professionals. A scenario representing a common animal disease in a hypothetical developing country is used to demonstrate how the model can provide insight into investment impact. The details of the model structure are also discussed, which directly couples two well-known system dynamics constructs – the SEIR model and the population dynamics model – while adding a model of biosurveillance processes.

The goal of this model is to provide a collaborative canvas for assessing alternative options to improve disease prevention and health security. The model was partially inspired by the agent-based modeling work of Davey et al. (2008), which systematically analyzed strategies for influenza mitigation. That analysis was able to take the dynamics of individual interactions into account when planning for a broad range of influenza epidemic scenarios. A comparison between the system dynamics and agent-based approaches – specifically using contagious disease dynamics as an example – has been made by Rahmandad (2007). He found that when heterogeneity in agent attributes or network structures are important, an agent-based approach can lend additional insight over the system dynamics approach at the expense of increasing complexity and a decrease in model understandability. Inasmuch, the work presented herein is meant to complement the approach of Davey et al. (2008) in order to increase understandability and usability in an investment planning capacity.

This model is designed to help plan for both human and animal health systems, including zoonosis. For it to be useful to health security planners, two aspects beyond contagion dynamics are important. First, a description of the locations of carriers in relation to the locations of susceptible individuals is necessary for assessing techniques to spatially isolate a disease. Both passive options such as border quarantine procedures and responsive options such as border closings should be represented. This model concentrates specifically on investments to prevent or mitigate infectious, non-endemic agents entering a country through its borders. It does so by using a population dynamics model coupled to the model of contagion. In the future, additional dynamics related to population movement and location

within a country or region can be explored. The second area of specificity regards biosurveillance, or the process of detecting and communicating a disease outbreak so that it may be mitigated. There are several components to effective biosurveillance, highlighted in figure 1. In this version of the model, I partially test three components from this diagram in relation to animal health: clinical awareness, transport and testing, and reporting and decision making. This is accomplished with an additional information chain construct that proceeds from testing locations to a central office responsible for outbreak and mitigation decisions.

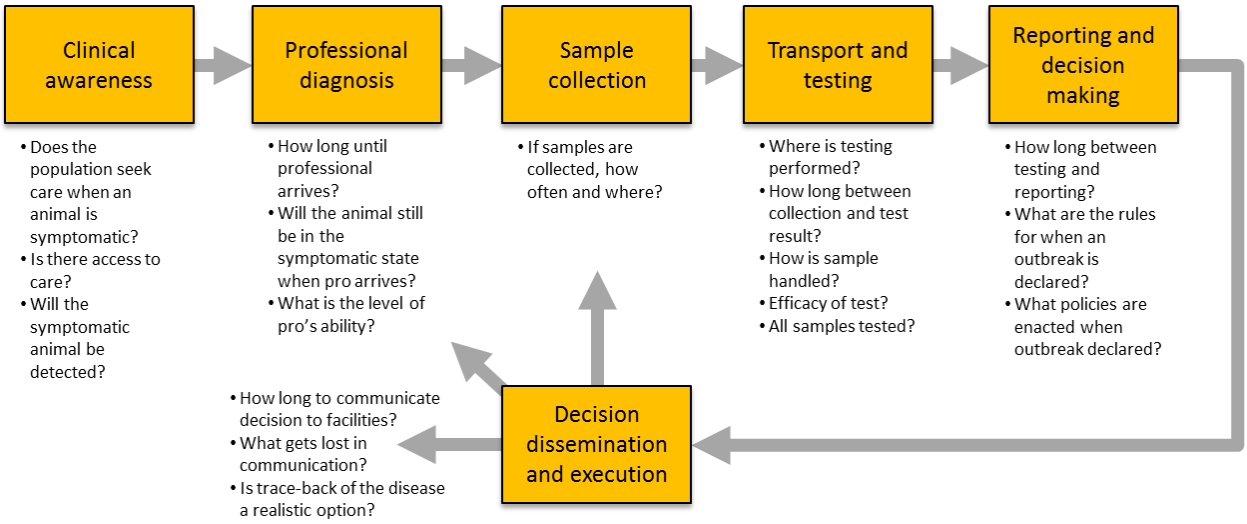

Figure 1. The stages of biosurveillance and questions raised at each stage.

To show how a system dynamics model of contagion, population movement, and biosurveillance can inform public health investment, I parameterize an initial model version using a hypothetical outbreak of Peste Des Petits Ruminants (PPR) in goat populations. PPR is one of the most economically important animal diseases in areas that depend on small ruminants. Many cultures use goats as currency, livelihood, and status symbols (Devendra, 1999). In this scenario, there is a hypothetical region that regularly trades goats across their borders. Within the region, all goats are initially susceptible to PPR and none are immune. The response of the model is tested by introducing infected animals to the population for a short amount of time via importation. Two performance metrics are tracked to judge the efficacy of investment options. The first – *deaths from disease* – estimates how well the investment performs in terms of health security. The second – *time until outbreak is conveyed* – estimates performance in terms of biosurveillance.

2. Model Description and Parameterization

The disease contagion component of the model is based on the popular system dynamics implementation of the SEIR model and is illustrated in Appendix A as figure A1 (Reed and Frost, 1920; Aron and Schwartz, 1984; Rahmandad, 2007; Thompson and Tebbens, 2008). SEIR stands for *susceptible*, *exposed*, *infectious*, and *recovered* respectively. It is disease agnostic and can be parameterized to match the characteristics of close contact spreading infectious diseases among humans or animals. Susceptible

animals are exposed to the disease of interest by coming into contact with other animals within their immediate population. When susceptible animals are exposed to disease, the chance the susceptible animal will be infected is described by the *infectivity* of the disease. After infected animals incubate and become infectious themselves, there is a distinct probability every day of death defined by the *mortality rate*. Animals that do not die recover after the *average infection duration*. Animals that survive the infection are recovered and can be considered immune, or the model can be parameterized such that they lose immunity at the *rate of immunity loss*.

To test disease epidemic behavior, infectious disease parameters were set to reflect theoretical behavior of PPR in goat populations (Kumar et al., 2003; Ahmad et al., 2005; Rashid et al., 2008; OIE, 2009). These parameters are included as table 1. PPR can exhibit mortality – defined as the fraction of the susceptible population that dies due to an outbreak – of greater than 50%, and morbidity – defined as the fraction of susceptible animals that become infected – of greater than 90%. It is transmitted mainly by aerosols and direct contact, potentially by fomites. Infected animals develop a discharge from eyes and nose between 4 and 6 days post-incubation as shown in figure 2. Infection commonly lasts 5-10 days post-incubation. Recovered animals likely have life-long immunity.

Table 1. SEIR component parameters

Parameter Name	Base Value	Units
Average infection duration	8	days
Contact rate [general population]	2.0	animals per day per animal
Contact rate [less secure checkpoints]	0.5	animals per day per animal
Contact rate [quarantine]	0.2	animals per day per animal
Contact rate [official quarantine stations]	0.5	animals per day per animal
Fraction of population susceptible after recovery	0	-
Incubation time	5	days
Infectivity	0.6	infections per animal
Mortality rate	0.2	per day
Rate of immunity loss	0	per day

To simulate the impact of population movements and specifically quarantine procedures on contagion, a population dynamics model was coupled with the SEIR model. The population movement component is illustrated in Appendix A as figure A2 (Ford, 2010). Coupling is achieved by subscripting the SEIR stocks by *Location*, and the population movement stocks by *SEIR Status*. Furthermore, each subscripted element of each integration equation is independently defined, and the flows that affect those elements from the coupled component are included in these equations. The reader can see in figures A1 and A2 multiple “ghost variables” affecting each stock. These ghost variables are the flows

from the coupled component. In this way, there is a full SEIR model within every population movement stock, and a full population movement model within every SEIR stock. Animals within the model have fully dynamic properties of *Location* and *SEIR Status* which are completely interdependent. If a susceptible animal moves from *quarantine* to the *general population*, it no longer becomes exposed to infectious animals in *quarantine*, but is exposed to infectious animals within the *general population* as expected. This coupling was influenced by the spatial system archetypes proposed by BenDor and Kaza (2012).

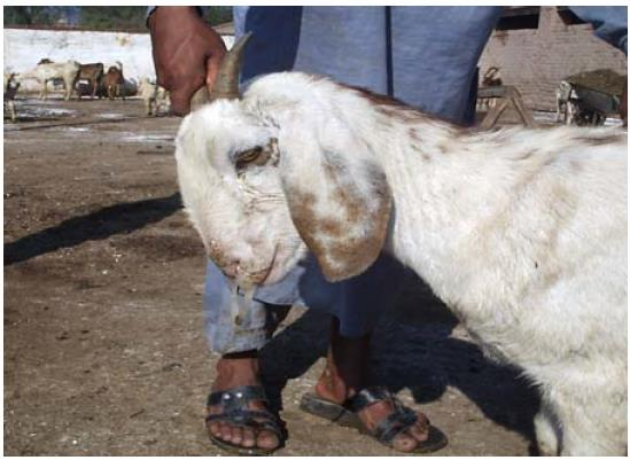

Figure 2. Common symptoms of PPR include eye and nose discharge (credit: Ahmad et al. 2005).

A base case was constructed to describe a situation with relatively poor health security. Base case settings for the parameters of the population movement component are included in table 2. The *general population* is assumed to start at 10,000 animals. Trade of animals across the border is balanced at 10 animals per day as long as the *total general population* is acceptable to the countrymen, but imports can increase to replenish population deficits. Insecure checkpoints and illegal trading may be a major issue in many countries, so the model splits animals entering the country via official quarantine stations versus less secure checkpoints. Animals entering via official quarantine stations are all tested for PPR, and these tests are acceptably sensitive and specific. Every animal that goes through official quarantine stations enters mandatory quarantine. In contrast, less secure checkpoints are characterized by fewer animals being tested, less accurate tests, and a fraction of animals that skip quarantine completely. The quarantine stock is modeled using the cohort control function for chronological aging in continuous time (Eberlein et al. 2012). The use of the cohort control functions ensures that animals remain in quarantine for the exact *quarantine time* and avoids unrealistic nonlinearities that can arise when using discrete flows. The option of varying fecundity rate is used to replace animals as they died over time – e.g. animals can be replaced through higher birth rates or via more importation.

To reflect the efficacy of biosurveillance practices, a testing and communication component was added to the coupled SEIR/population models. Its structure can be viewed in Appendix A figure A3. Base case parameters are shown in table 3. As animals are tested, the specificity and sensitivity of the tests determines the number of true positive and false positive results (Gordis, 2004; Aschengrau and Seage,

2008). In addition to the quarantine stations and checkpoints, animals are tested in the general population at a low rate. The sum of true and false positives is divided by the total animals tested to calculate the *test-based prevalence at all locations*. This information must move through a bureaucracy before decisions can be made. Using first-order smoothing, the test-based prevalence information passes to regional and then central offices after an average transportation time. At the central office, prevalence information is averaged over a time window, and this time-windowed average is compared to an outbreak threshold to determine whether the decision to declare outbreak should be made. The user also has the option of delaying the decision to end an outbreak declaration for a number of days after this windowed average passes below the threshold again. This logic is shown in figure 3, in which the *effective outbreak decision* is a logical -OR- between the base decision and a pulse with width of the chosen down-stroke delay starting at the time of the base decision's down-stroke. The effective decision is disseminated back to the field using the same transportation delay with which the information arrived at the central office. Only when the decision is disseminated to the field can further mitigation practices be employed.

Table 2. Population movement base case parameters

Parameter Name	Base Value	Units
Initial animals in general population	10,000	animals
Replenish if true	TRUE	-
Baseline animals entering the country per day	10	animals per day
Fraction entering via secure pathways	0.5	-
Time in official quarantine checkpoint	1	days
Time in less secure checkpoint	1	days
Fraction in less secure checkpoint skipping quarantine	0.5	-
Quarantine time	5	days
Average birth rate	0.2	per year
Average life span	5	years

After testing the fully coupled model, an unrealistic behavior was noticed in the coupling of quarantine and the SEIR component. Even when quarantine times were very long – on the order of 5 times the average infection duration – the continuous nature of the SEIR model caused there to be a non-zero probability that infectious animals would move into the general population. Even when a very small number of infectious animals – on the order of $1x10^{-6}$ – reached the general population, outbreak eventually occurred because the feedback between infectious animals and infections is strongly positive when the susceptible population is large. To dampen this, I inserted a new relationship between infectious population and contact rate in the loop, shown in figure 4. This relationship essentially decreases the probability that animals will come in contact with an infected animal when the number of

infected animals is much less than 1. There should be further discussion on whether this dampener is appropriate, since the argument can be made that a largely susceptible population such as that presented here will eventually be exposed to the disease no matter what health security mechanisms are in place.

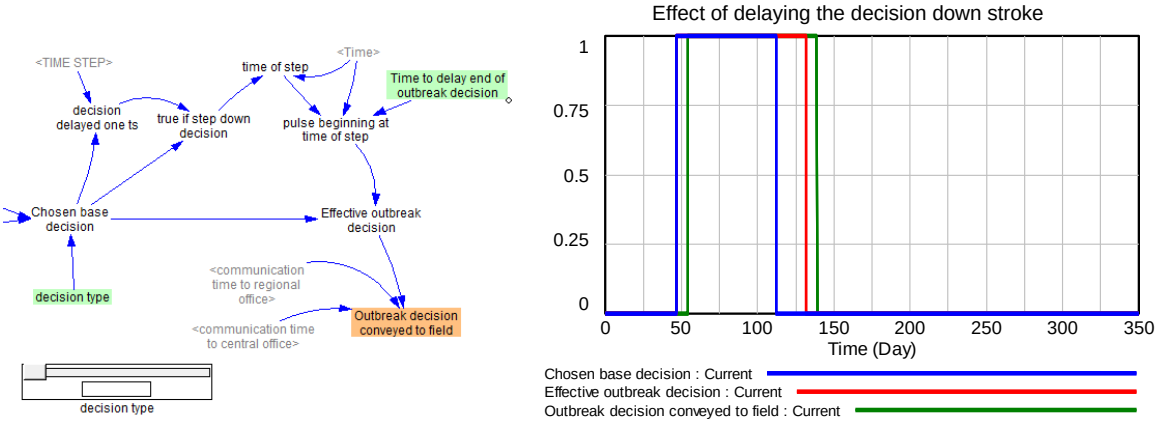

Figure 3. The logic at left causes only the down-stroke of the outbreak decision to be delayed. The entire decision is then delayed once more as it is disseminated to the field.

Table 3. Biosurveillance component parameters for the base case.

Parameter Name	Base Value	Units
Sensitivity [official quarantine station]	0.75	case per animal
Specificity [official quarantine station]	0.85	case per animal
Fraction animals tested [official quarantine station]	1	-
Sensitivity [less secure checkpoint]	0.6	case per animal
Specificity [less secure checkpoint]	0.7	case per animal
Fraction animals tested [less secure checkpoint]	0.8	-
Sensitivity [general population]	0.75	case per animal
Specificity [general population]	0.85	case per animal
Testing frequency [general population]	0.01	per day
Communication time to regional office	4	days
Fraction of cases skipping regional offices	0	-
Communication time to central office	3	days
Time window for decision at central office	10	days
Prevalence threshold for decision	0.18	-

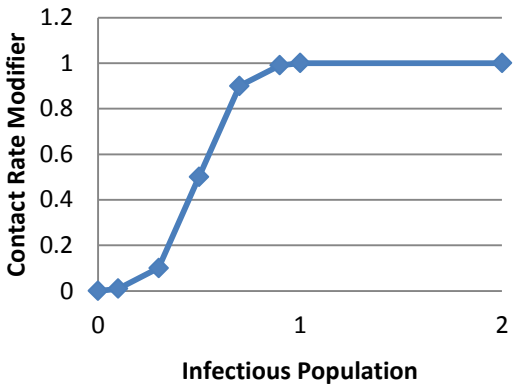

Figure 4. The contact rate exhibits cumulative probability behavior when the number of infectious animals is less than one.

3. Results of the Base Case

The base case, which is parameterized to represent a do-nothing scenario, was perturbed with an influx of one infected animal per day for 10 days as shown in figure 5. In this case, the country replenishes the deficit from dying animals by bringing more over the border, at a rate of 10% of the deficit per day. These replacements are assumed to have the same SEIR fractional status as animals within the country. The model is run for 350 days to allow the epidemic to run its course. With the parameters described in tables 1 through 3, the *deaths due to disease* and the *perceived prevalence by the central office* after receiving test results are shown in figure 6. A total of 7,816 goats die from PPR over the 350 day timespan, most of them dying while in the general population. At the beginning of the simulation, biosurveillance procedures detect roughly a 16% prevalence rate before the disease is introduced into the country due to false positives from overall test specificity. With a threshold for outbreak set at 18% prevalence, the central office does not detect the initial influx through the border. Outbreak is finally declared on the 54th day of the simulation using these biosurveillance measures.

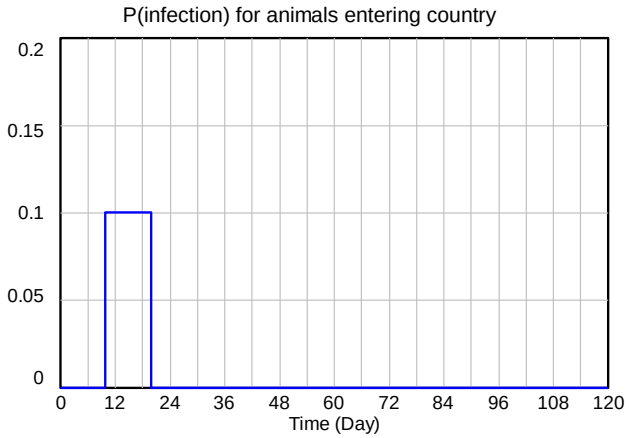

Figure 5. The probability of imported animals infected with PPR is 0.1 starting at day 10 and lasting 10 days.

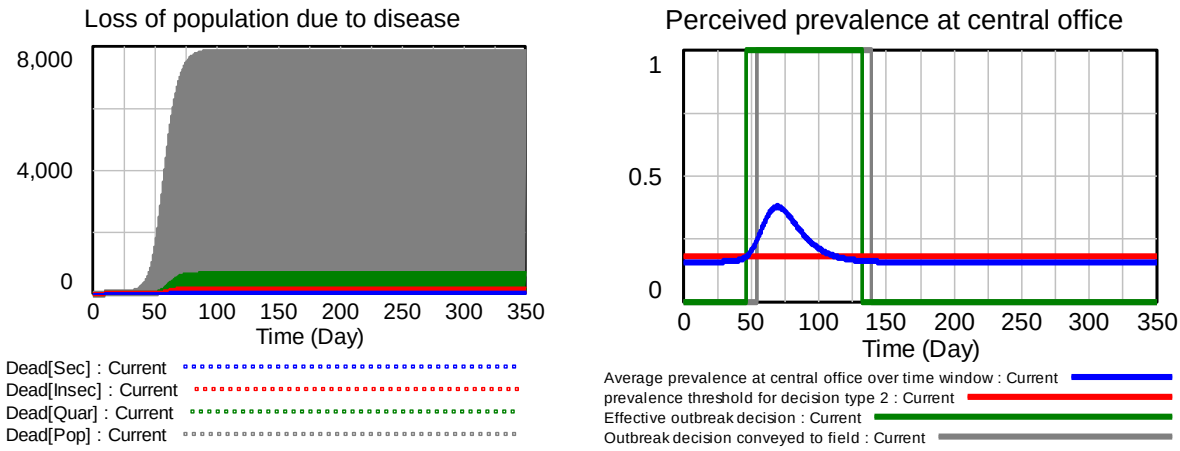

Figure 6. Behavior of the two primary performance metrics in the base case. The disease runs its course over 80 days and declaration of outbreak is delayed 44 days after the disease's onset.

Understanding where the animals are located during the course of the disease and the SEIR dynamics within the general population can help design improved health security measures. Figure 7 illustrates the dynamics of the total population in the different locations and the SEIR dynamics within the *general population* location. The graph of total population by location shows a large increase in the number of animals waiting in quarantine. The animals are coming into quarantine to replenish deaths from the disease. This information is useful to infrastructure planners who may have to design quarantine facilities for a large influx of animals or limit the number of imported animals per day. The graph of the disease status in the general population exhibits the classic SEIR dynamics, showing an extreme drop in the number of susceptible animals consistent with PPR's high morbidity. After the disease has run its course, the decay in the immune population is due to natural births and deaths.

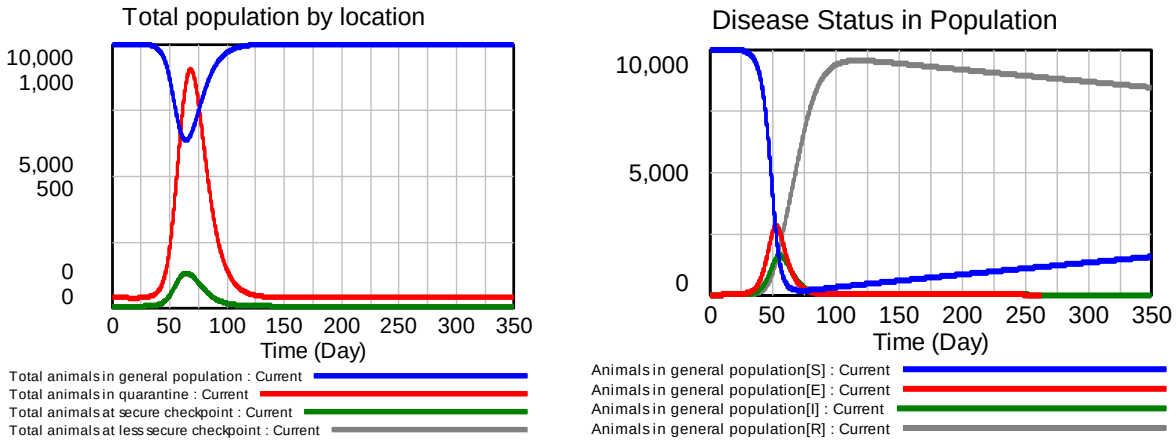

Figure 7. Population dynamics at left with animals in the general population (blue) having a separate axis from the other locations. SEIR dynamics at right shows the effect of decaying immunity due to natural births and deaths.

4. Designing and Testing Health Security Improvements

To test the effectiveness of a range of investment options, I developed a hypothetical alternative list and an estimate of the quantity of improvement given a constant capital investment. I translated these options into parameters within the model as illustrated in Table 4. It is our goal that during future uses of this model, a table such as this can be developed based on discussions with experts and combinations of options can be explored using the model in real time. With the hypothetical PPR case, I tested each option by itself and also explored a combination of options assuming a linear relationship between fractional investment and parameter change.

I quickly realized that no single option at this level of investment is sufficient to greatly reduce the onset and spread of PPR as I have parameterized it. Table 5 shows the results of the two performance metrics when choosing each option independently. Lengthening quarantine seems like a good option at first, but nearly 25% of animals entering the country evade quarantine in the base case. Doubling the quarantine time without changing other options decreases the total deaths from 7,816 to 7,780, and delays the peak in number of infected animals by approximately 2 days, but does not prevent the disease from entering the general population as expected. The most effective individual options to reduce deaths are to close the border and vaccinate. The closing of the border option, however, is dependent on the assumption that proportions of SEIR across the border are equal to proportions within the country. It also could have a negative impact on economy which was not considered in this study. The top independent options for improving biosurveillance are shortening communication times and improving the accuracy of tests. No alternative alone is able to catch the initial influx of infected population, likely due to the smoothing that occurs when averaging perceived prevalence over a time window at the central office. Also, there are no individual options that improve both mortality and biosurveillance.

Table 4. Alternative equal-capital investments and estimates as to their effect on model parameters.

Option	Parameter	Base Value	SME Estimate
Lengthen Quarantine Time (enlarge quarantine facilities)	Quarantine time	5 days	10 days
Improve quarantine facilities or procedures	Contact Rate [quarantine]	1 contact every 5 days	1 every 10
More animals to official quarantine stations	Fraction entering more secure	0.5	0.7
Improve security in other checkpoints	Fraction skipping quarantine	0.5	0.2
Vaccinate	Starting fraction immune	0	0.1
Improve communication of infectious cases	Total communication time	7 days	3 days
Improve testing facilities or procedures			
Improve sensitivity/specificity across the board	Sensi and spec (secure, less secure)	0.75/0.85, 0.6/0.7	0.8/0.9, 0.8/0.9
Increase testing frequency in general population	Testing frequency	1% per day	2% per day
Close borders	Days that border can be closed	0 days	90 days

During the process of testing the investment alternatives, two low-cost options for improving biosurveillance were suggested. The first option is to change the weighting of the *test-based prevalence* calculation such that positive results from checkpoints are weighted higher than those from the general

population. The second option is to average incoming cases over a smaller window at the central office. When increasing the weight of the checkpoint cases twofold and decreasing the averaging window from 10 to 2 days, the initial influx of infected animals is detected and disseminated 15 days after initial infection as shown in figure 8. These options show the benefit of a deep structural understanding that system dynamics modeling provides.

Table 5. Performance of the investment alternatives when chosen independently.

Option	Total dead	Day of decision
No change	**7816**	**54**
Lengthen Quarantine Time (enlarge quarantine facilities)	7779	56
Improve quarantine facilities or procedures	7815	54
More animals to official quarantine stations	7814	56
Improve security in other checkpoints	7720	57
Vaccinate	6836	57
Improve communication of infectious cases	7816	47
Improve testing facilities or procedures	-	-
Improve sensitivity/specificity across the board	7816	49
Increase testing frequency in general population	7816	55
Close borders	6666	54

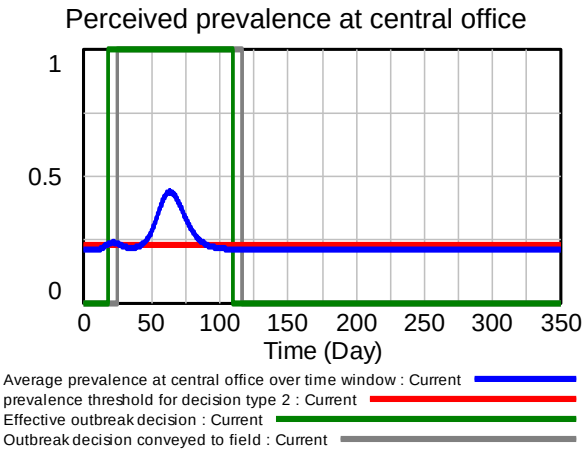

Figure 8. With the low-cost biosurveillance options in place, the initial influx of infected animals is detected.

I was interested in the investment necessary to have a properly functioning quarantine system given the PPR parameterization that is presented here. Through multi-parameter variation, the outbreak was contained using four full-cost options in addition to the low-cost biosurveillance options mentioned previously. By lengthening quarantine time, decreasing the contact rate within quarantine, sending more animals to official quarantine stations, and improving quarantine processes at the less secure checkpoints, the model suggests that a quarantine system can work effectively. Only 8 animals die from the disease given this investment package, and the disease is detected 15 days after the initial infection as suggested in figure 9. Notice that most animals die within quarantine as designed. This set of options could reflect a minimal suggested investment for acceptable health security to PPR.

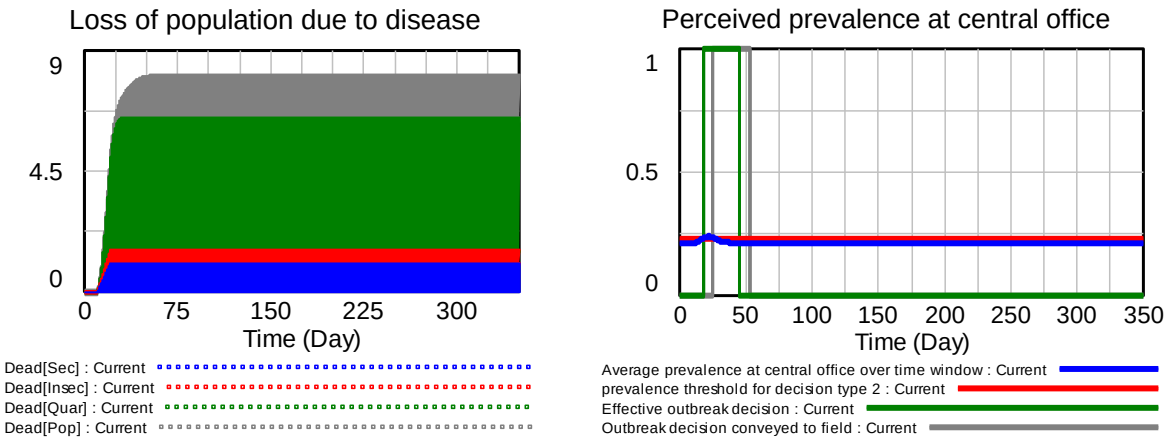

Figure 9. With a combination of alternatives, quarantine is effective at preventing outbreak in the general population. The initial flux of infected animals is also detected.

Given a scenario where funding is not available for the suggested investment, a lower-cost option that balances health security and biosurveillance was developed. This option employs the low-cost biosurveillance options in addition to closing borders, decreasing communication time from 7 to 3 days, and vaccinating as much of the population as funding allows. If funding were to allow a 5% vaccination of the general population in addition to these alternatives, the model suggests 6,076 deaths and notification of outbreak 7 days after initial infection, shown in figure 10. This constitutes an improvement of 22% in terms of animal deaths, and 84% in terms of biosurveillance speed. Figure 10 also highlights an unforseen problem with border closing: the perceived prevalence of the disease decreases once borders are closed because the central office relies heavily on tests performed at checkpoints. When the border is reopened on day 50, perceived prevalence increases because of the large influx of animals and the increase in false positives from the less secure checkpoints. This could cause confusion among those in the central office, and dissatisfaction when the population is notified of a second outbreak. More sophisticated methods of communication and determining prevalence may be able to eliminate this problem.

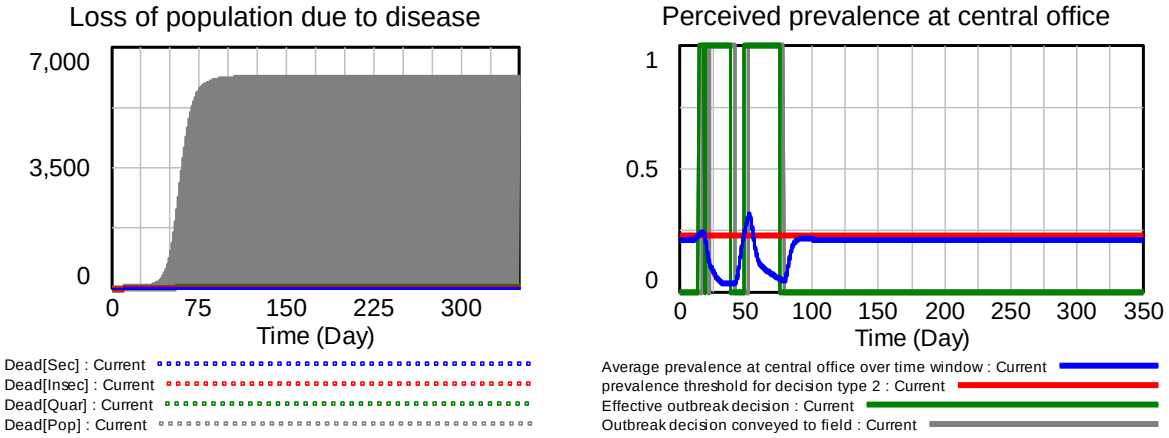

Figure 10. The biggest impact for limited investment scenario shows that outbreak still occurs and the central office has problems figuring out disease prevalence, but mortality and biosurveillance are improved.

5. Conclusions and Future Work

I have presented a system dynamics model of coupled animal importation and disease contagion with the inclusion of biosurveillance and communication dynamics. This model has been designed as a forum for discussion related to improving health security and biosurveillance systems. It is unique in that it fully couples a model of population movement and contagion in order to test checkpoint and quarantine procedures, in addition to testing biosurveillance procedures using the communication chain component.

To test the ability of the model to gauge the impact of alternative investment portfolios, I simulated a hypothetical introduction of PPR in to a country with a fully susceptible population. By design, this system performed poorly in two performance metrics that summarize health security and biosurveillance. The model helped me create and parameterize a list of alternatives assuming a constant amount of funding for each alternative. No single alternative was found to improve both health security and biosurveillance. However, two low-to-zero cost alternatives for improving biosurveillance were developed as a result of this exercise. These alternatives are related to the algorithms and techniques health organizations use to calculate and communicate disease prevalence.

Two additional scenarios were presented that represent a suggested minimal improvement and a best impact for the dollar. The suggested investment scenario concentrated on creating an effective quarantine system for health security, but also improved biosurveillance substantially. The impact for the dollar scenario was not able to prevent outbreak using the quarantine system, but combined effective biosurveillance with border closings to improve health security. I suggest that further thought be leant to improving biosurveillance algorithms within this model in order to eliminate the “double outbreak” notification that is presented here.

This model has potential to open new decision practices for health system planners because it offers a fast yet insightful description of health systems in terms of both health security and biosurveillance. Future work may concentrate on other forms of population movement dynamics that impact the spread of disease such as herd migration. Intentional culling of infected animals and population segregation were two options that were mentioned for investment but not included in this model version. An expanded population dynamics model could be compared to an agent-based modeling approach for academic insight into the differences in these methods, building on previous similar work by Rahmandad (2007). Additionally, increased fidelity in the biosurveillance portion of the model would help answer the questions posed in figure 1 and determine how these components relate to the overall system.

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Appendix A

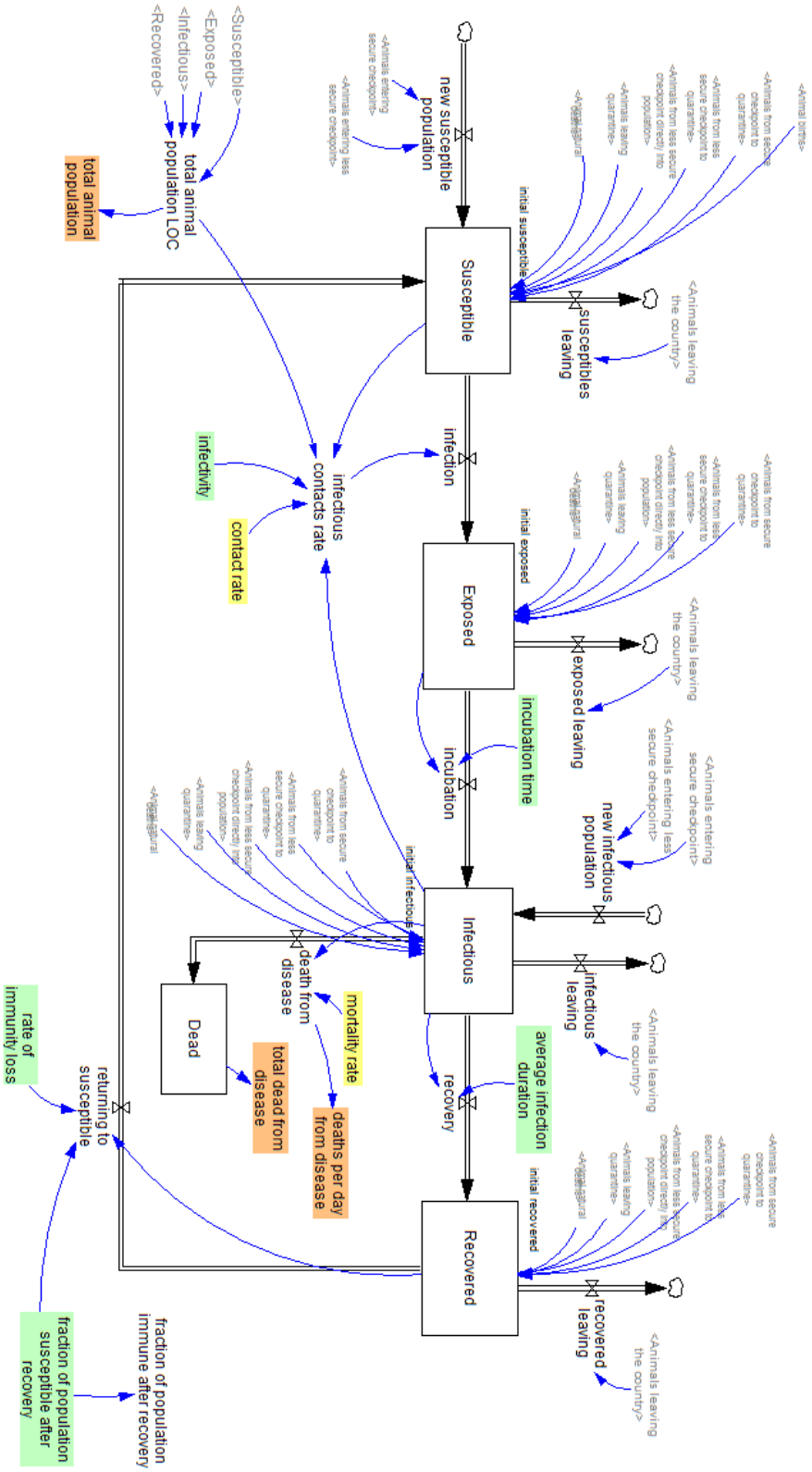

Figure A1. SEIR model component.

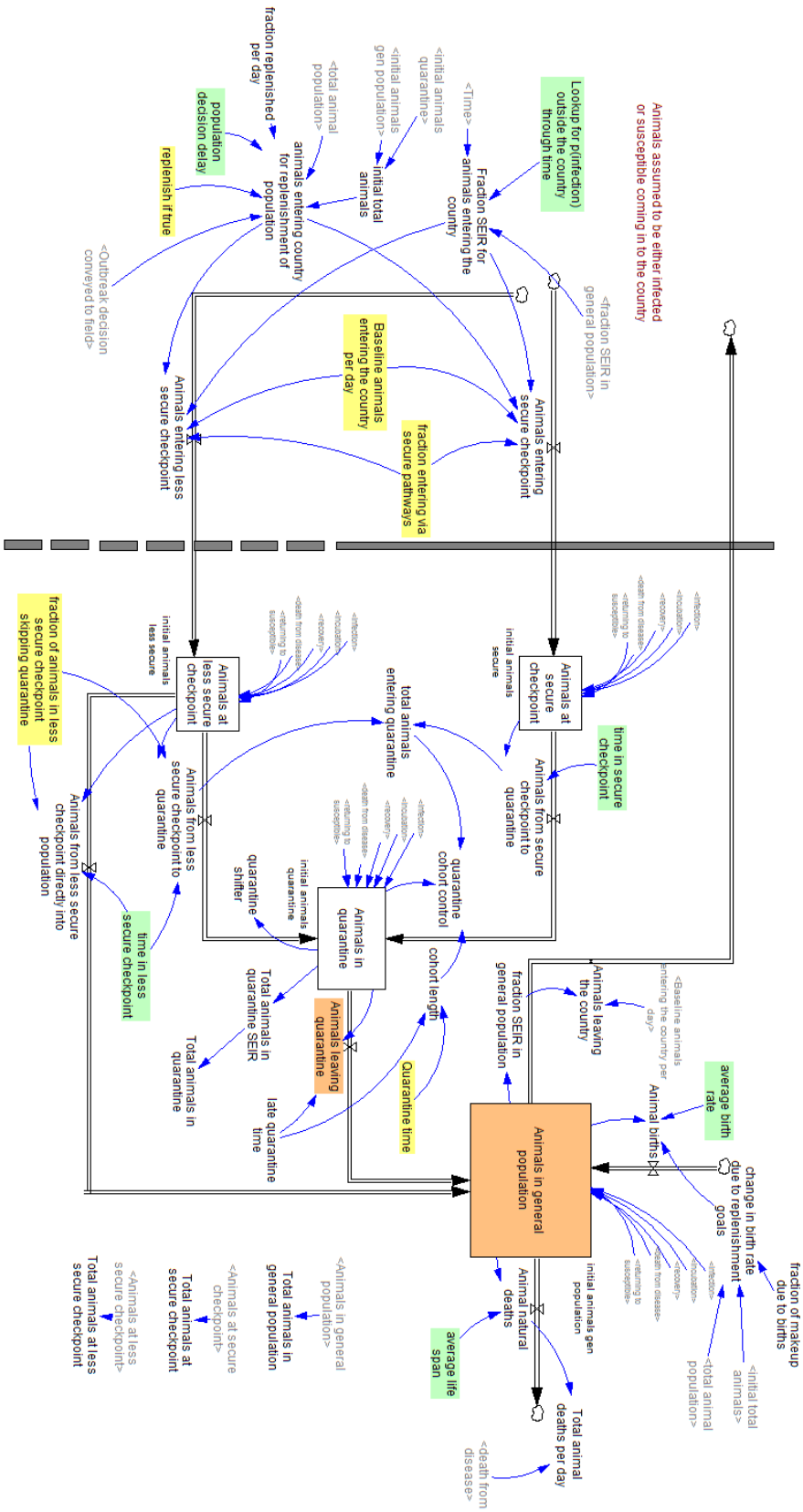

Figure A2. Population dynamics model component.

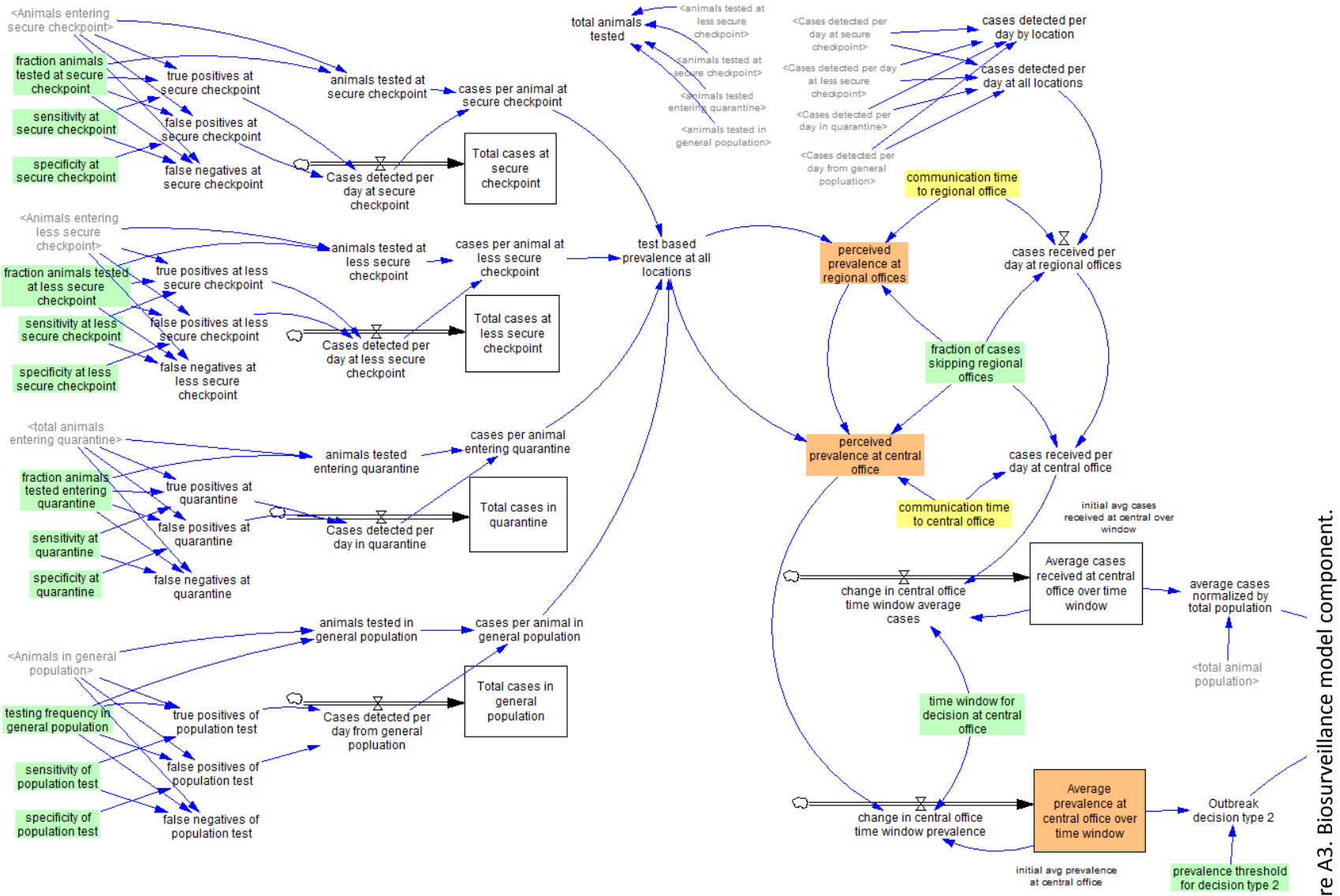

Figure A3. Biosurveillance model component.