

Modelling the Spread of African Swine Fever using Grid SIR Models

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1 Executive Summary

We applied a variant of the Susceptible-Infected-Recovered (SIR) model to the spread of African Swine Fever (ASF) through Europe. The SIR model has been researched extensively, and is accurate for describing epidemics of human disease in populous cities. Our result suggests that the simplest model one might consider for ASF in the wild, an SIR model on a grid, does not accurately describe the observed scale and speed of the spread of disease when the output of the simulation is compared with an extensive data set gathered from Europe. Notably, the real-world outbreak spread wider and lasted much longer than outbreak predicted by the best fitting model we could produce. Given this result, it is likely that any conclusion made based on the same type of model will underestimate the severity of a real epidemic. In order to correctly estimate the impact that African Swine Fever (ASF) would have if it spread to Canada, it will be necessary to design a more advanced model.

It is possible that the reason the model failed to fit is that the sylvatic disease cycle, which is the disease cycle whereby infected wild boar spread ASF to domestic pigs by via ticks, is not the dominant cause of the spread of ASF. If this is indeed the case, countries with relatively low boar populations, like Canada, may be in more danger from ASF than they would be if spread via boar was the main cause of epidemics. It is possible that infected ticks can carry disease between pig farms over significant distances even in the absence of infected wild boar, and if this is a major cause of ASF spread then any region with many pig farms in close proximity is highly vulnerable, even if, like Canada, it is too cold to have a large boar population.

Our best-fitting model predicted that no outbreak would occur within 10 years in several locations including Italy and Estonia where outbreaks did occur in the real world. This strongly suggests to us that another mechanism of transmission frequently causes long-distance spread of infection. The most likely candidate for this mechanism is human action, in particular the shipping of infected meat. Given the difficulty of predicting the severity of a epidemic, and the economic damage ASF could cause, we recommend that any pigs or pork products imported to Canada be tested very carefully, or not imported at all if possible.

The next step is to design models of these alternate mechanisms by which ASF might spread and test them to see if they produce better results. In particular, the possibility of transmission directly from farm to farm by ticks alone should be investigated closely, since most areas of Canada have few wild boar but many ticks. It is important that we find a way to estimate the rate of spread of a possible ASF outbreak in Canada so that government agencies can respond proportionately to any report of suspected infection.

Abstract

Millions of pigs have recently been killed in Asia and Europe due to a recent resurgence of the African Swine Fever (ASF). In this paper, we attempt to further observe the spatial spread of ASF by creating a grid Susceptible-Infectious-Recovered (SIR) model. The model is based off outbreak data released by the World Organization for Animal Health and attempts to fit the SIR model to the observed outbreaks. Using the model, we describe the diseases behavior and the next steps required to build a more accurate model and predict the spread of the disease.

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2 Background

The African Swine Fever (ASF), a highly contagious disease that affects the domestic pig and wild boar population, was largely eradicated in Europe in the late 1990s [1]. Recently, there has been a resurgence of the virus primarily in Eastern Europe and South-East Asia. This disease is naturally endemic in wild boar (family of *Sus Scrofa*) but is also able to cause disease in domesticated pigs. Since there is no vaccine available, and large numbers of domestic pigs are kept in close confinement, once a farm is exposed to ASF there is a high likelihood that all pigs will be infected.

Since the mortality rate after infection is extremely high, farmers typically respond to ASF infection by culling their entire herd. According to a recent report by Reuters, in China alone a projected 200 million pigs will be culled or killed by the disease [2]. This practice of culling the entire susceptible population is vital as no treatment or vaccines exists and from a study done on outbreaks in the Russian Federation, the expected number of secondary cases produced by a single infection of the virus (\mathcal{R}_0) was estimated within a farm or herd to be between 8 and 11 and around 2.5 between different farms or herds in Russia [3]. If farmers do not cull their animals at the presence of an infected swine, the number of deaths due to the virus can be detrimental on their herd and on neighbouring herds.

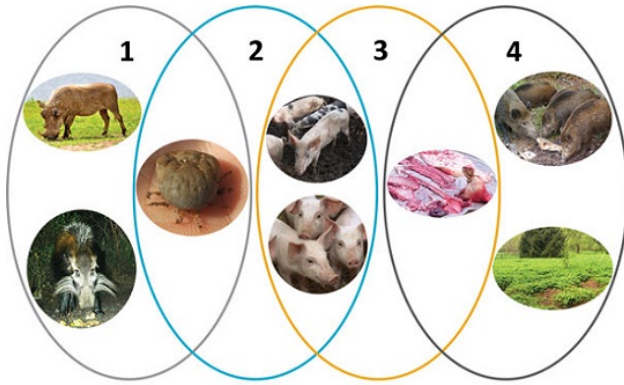


Figure 1: The four transmission cycles of ASF with the main transmission agents depicted. The role of the bushpig in the sylvatic cycle remains unclear. Illustration: Magdalena Hellström, photographs by Erika Chenais, Klaus Depner and Karl Ståhl. The figure was originally published in Emerg Infect Dis 24, 810 [4]

Transmission cycles of the virus vary depending on the region. The disease originated and continues to be perpetuated in its natural reservoir of warthogs and soft ticks in Africa without causing disease in the vertebrate host[5]. Wild boar populations are particularly important for the persistence of the disease as they can continually be exposed to the virus with the tick population and their wide distribution and ecology aids in the virus' ability to move to new regions and infect domestic pigs [6]. The virus is transmitted from the sylvatic cycle to the domestic population from the ticks from the wild pig population. The presence of ticks in a region aids in its persistence. The domestic cycle allows for the virus to transmit

from one domestic herd to another through contaminated carcasses being consumed by the domestic and wild pig populations. Examine figure 2 to see the transmission hosts. [4].

3 Introduction

There exists a considerable body of research on the spatial spread of infectious disease, and model of spatial spread can be divided into two basic types, those which are continuous and those which are discrete. Since we are dealing with a dispersed population of animals, with no concentrated population centres like cities, we believe that a continuous disease model, based on a combination of an SIR model and a diffusion equation, is appropriate. In order to integrate numerically, we use a fine grid of discrete points as an approximation to a continuous population.

To justify this discrete approximation, we examined the literature on the structure of solutions to continuous spatial SIR models. The paper [7] predicts the existence of traveling waves of infection for certain continuous SIR models, and experimental simulations of an SIR model on a fine grid shows qualitative similarities to these traveling wave solutions. Following this, our hypothesis is that the spread of ASF is described well by a model of this type, and that by fitting the model parameters based on gathered data we can predict how the "wave of infection" will travel.

In order to obtain a tractable problem, we make the following assumptions:

1. The spread of this virus in boars is locally described by an SIR model
2. Grid SIR model with nearest-neighbour coupling is good approximation of the nature of the spread

3. Opportunities for infection scale linearly with the population density
4. The frequency of ASF reports scale linearly with the local infected population of boar

Although the population of boars at each point of the grid would normally be considered too small to apply an SIR model to, we believe that very simplified approach is valid for the "local" model since primarily what we are interested in is the global rate of spread, not the local growth on infection. For this reason, we feel the first assumption is justified. The choice of the grid SIR model is based on the qualitative similarities between the numerical solutions we constructed and the solutions of the continuous diffusion equation SIR model discussed earlier in this section.

The third assumption is justified by the fact that the population at each point of our grid is relatively small. If the population was too large, there might be obstructions to boar interacting with a linearly increasing number of other boar. If the population is small linear scaling is reasonable, as discussed in [8]. The final assumption is just an approximation, since we lack data directly relating the infected boar population to the number of reported outbreaks. We can consider whether or not the model fits as evidence for or against this relationship between infected boars and infected farms.


These assumptions are made for simplicity. There are more complex models than the SIR model, and there are non-linear scaling relationships that could be tried instead of assumptions 3 and 4. It is not helpful to introduce such complications until the simpler models have been tried.

[6].

4 Methods

4.1 Data Collection

In order to construct the model, and correlate boar population density with the spread of the disease, first we need sources on boar populations and on the incidents of infections. Since this disease has such a high mortality rate, incidents of the disease infecting populations of domestic pigs are being recorded in daily and weekly outbreak reports by the World Organization for Animal Health (OIE). This is kept in their World Animal Health Information Database (WAHIS) [9] which is available online. The reports are held each in their own web pages, in a consistent table format. By processing the HTML of these pages, the date and location of each reported incident of African Swine Fever can be saved. Using Google's Python API (Application Programming Interface), the longitude and latitude of the outbreaks can be easily found. Using this method, a list of over 1300 outbreaks across the world can be generated with their exact locations, country, and date.

These outbreaks can be compared to a model of the wild boar population density, which has been modelled in Europe with a correlation coefficient of 0.83 relating observed boar populations and model predicted boar populations [10]. Using , we recreated the population density map by analysing the pixel brightness of their population density map. This was used as the initial conditions of the susceptible population of wild boars and converted the pixels into longitude and latitude. The code was derived from the work of Stack Exchange

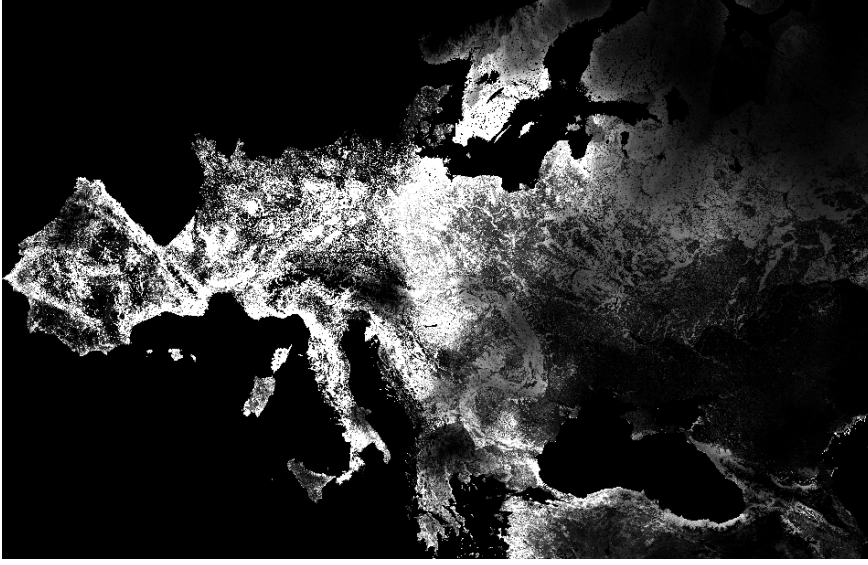


Figure 2: Mosaic model of wild boar populations in Europe[11]

user Jeffrey Adams on April 10th, 2015 [4.1](#) [11].

With these two resources, we can begin the development and parameter estimations for our model.

4.2 Grid SIR Model with Neighbour Coupling

As an approximation of the spatial spread of disease in wild boars, we will use a system of SIR models indexed by a two-dimensional array, with nearest-neighbour coupling. This is a rough approximation of the more precise analytical models discussed in the background, which can be described by partial differential equations or continuous convolution equations.

In reasonable parameter ranges the solutions to these analytical models take the form of a sort of "traveling wave" of infection. Although the SIR model on a grid with neighbour coupling is not nearly as elegant as partial differential models, numerical simulations indicate that solutions still take the form of slowly expanding waves of infection. For this reason, we believe it is justified to use the grid SIR model as an approximation, and that the solutions will have sufficient qualitative similarities for our purposes.

Our model can be written

$$\frac{dI(x, y)}{dt} = \beta S(x, y)[I(x, y) + \lambda(I(x + 1, y) + I(x - 1, y) + I(x, y + 1) + I(x, y - 1))] \quad (1)$$

$$- \gamma I(x, y) \quad (2)$$

$$\frac{dS(x, y)}{dt} = -\beta S(x, y)[I(x, y) + \lambda(I(x + 1, y) + I(x - 1, y) + I(x, y + 1) + I(x, y - 1))] \quad (3)$$

with initial data satisfying $I(0) + S(0) = D(x, y)$ where D is a function representing the local boar population. As we discussed in the biological assumptions section, implicit in this model is that the number of opportunities for infection per unit time scales linearly with the

local boar population. Thus β is the number of opportunities for infection per capita per time. λ is a coupling constant representing the ratio of opportunities for infection by a boar in a neighbouring population over the opportunities for infection by a boar from the same population.

Using the data we have collected, we will find a set R of reports, and let t_i be the report times and l_i the report locations. We make the assumption that the first ASF reports in a region occur shortly after the local infected population hits some small positive quantity k . We want to minimize the mean squared error

$$E(\beta, \lambda) = \sum_R (\chi\phi(l_i, t_i) - 1)^2 \quad (4)$$

to optimize the parameters. The sum is taken over our set of reports R . Since we are also uncertain of initial locations and quantities of infected animals, we introduce four possible locations of initial infection, and introduce the initial quantities of infected boar at those locations as parameters to be optimized for.

5 Results

We minimized the error by applying an optimization algorithm based on finite differences. At each step, the error was evaluated at several parameter values very close to the previous parameters. These nearby values were used to approximate the gradient of the error as a function of parameters. The parameters were then updated by adding a small change in the direction of fastest descent.

Even after running for several hours, the model was only able to reduce the error by about 3%. We hoped that allowing the algorithm to optimize the initial conditions would improve the results, but this had little effect. At this point, we had to give up on improving our error results, due to time constraints. It is likely that any significant improvement would require an entirely different model.

The lines plotted above represent the quantities of infected boar at the (x, y) coordinates listed in the legend. Each coordinate is listed in the legend next to the country which contains it, as a guideline to visualize where these points lie. Even though the model did not explain the data very well, the graphs produced by integrating the equations at the optimal parameter values did have some similarities to the order in which real-world epidemics occurred. Hungary, Belgium, and the Czech Republic all experienced outbreaks early this decade, as the graph suggests. However, these epidemics are still ongoing, unlike the epidemics predicted by the model, which all burn out within a year or two. Furthermore, we can see on the graph above that no disease is predicted to reach as far south as Italy or as far north as Estonia within 8 years, but in reality both of these countries experienced major outbreaks.

6 Discussion

There are a few factors that could have contributed to the failure of the optimization process. The first is the possibility that the sylvatic cycle, whereby domestic pigs are infected by ticks

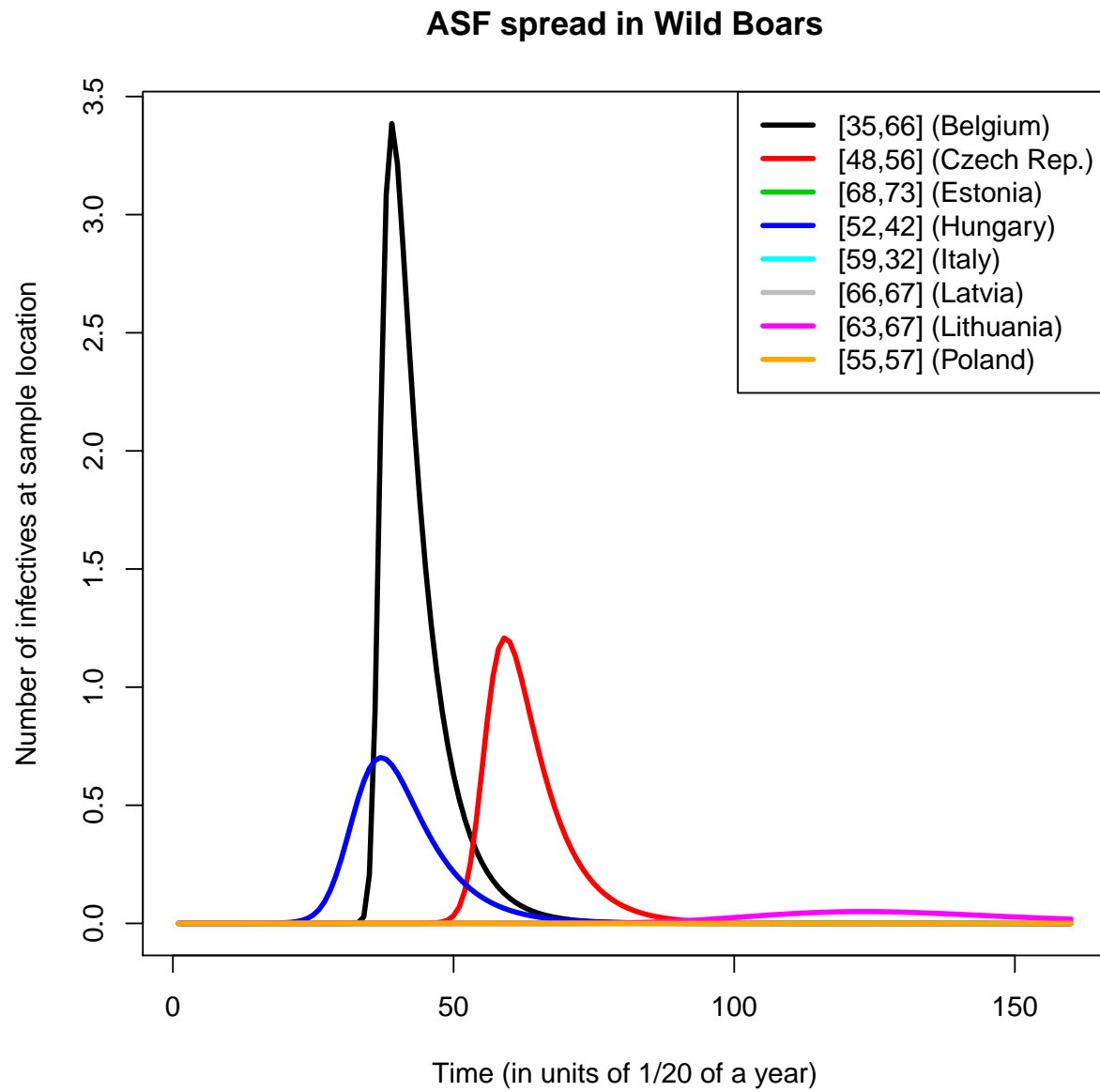


Figure 3: Using the data collected and the simulation algorithms, this is the output

carried by infected wild boar, is less significant than we expected. This is possible, as there are multiple known mechanisms which spread ASF, and the primary cause of the spread is a matter of ongoing research and debate. If human factors like the shipping of infected meat dominate the spread of infection, our model will not capture those effects. If this is the case, then the dynamics of the SIR model may not be appropriate for this disease. More research is required for the population dynamics of boars to predict its spread accurately.

The second possibility is that our model needed demographic stochasticity to succeed. We assumed that the infected populations at each point on our grid could be described by an SIR model. However, the density data we obtained indicates that most of the points have a population of less than 100 boar. At this population scale, it is certain that introducing stochasticity would have some effect on the outcome, though we do not know if it will improve the ability to fit the data. Given more time, this is an approach that could be tried.

The third possibility is the data we gathered is too noisy and sparse for a good fit to be found. Although we used over 5,000 reports, it is almost certain that the reports are not directly representative of the underlying quantities of infected boar. In particular, more populated areas are probably much more likely to produce reports. The fact the reports will cluster around populated areas, even if the proportion of infected boar is not actually higher in these areas, may lead to difficulty finding a realistic fit. Given much more time to experiment, a sounder statistical model could have been devised and analyzed, possibly based on an assumed relationship between human populations, infected boar populations, and ASF reports.

The fact that the model predicted no outbreak within 10 years in several countries where outbreaks did occur indicates that some mechanism other than migration of infected boar is likely responsible for some of the long-range spread of ASF. It is possible that introducing demographic stochasticity would have allowed parameters to be found which predicted outbreaks in these locations purely based on the sylvatic cycle. However, it seems more likely that what we are missing is the effect of human action, since it is already known that the shipping of infected meat can act as a cause of long-distance spread. In any case, there is much more investigation to be done.

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