Modeling classical swine fever spread using a spatial hybrid model

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Resumen

Classical swine fever (CSF) is a highly contagious viral disease of pigs and wild boars that causes severe commercial restrictions to the affected countries. The knowledge of spread patterns and risk factors that are involved in the transmission of CSF would help to implement specific measures and to reduce the disease spread in future outbreaks. In this article, we introduce a new spatial hybrid model developed for the spread of CSF. It is based on the combination of a stochastic individual Based model with a Susceptible-Infected model. The coefficients and parameters of the models are estimated using real data.

1. Introduction

Classical swine fever (CSF) is a highly contagious viral disease of domestic and wild pigs which generates important economical losses in the affected regions. Despite the efforts to control and eradicate CSF, this disease remains endemic in many countries of South and Central America, Africa and South-east of Asia and sporadic outbreaks has been affecting 49 % of the European countries from 1996 to 2007 [11, 12].

During a CSF epidemic, the spread of CSF from an infected animal to other susceptible ones may occur either by direct or indirect contacts [3]. Direct transmission implies animal-to-animal effective contact from an infectious animal to a susceptible one. Indirect transmission requires an effective contact between a contaminated fomite (i.e. vehicle, insect, material or people) and a susceptible animal.

Historically, the movement of infected animals and contaminated trucks has been reported as one of the main routes of CSF spread, although other routes such as airborne spread, movement of people, use of infected semen or feed has also been described as potential ways of transmission [1]. Nevertheless, the spread patterns and magnitude and duration of an CSF epidemic change depending on the epidemiological and demographic characteristics of the infected region and the timing and effectiveness of the control measures applied. For this reason, it is difficult to extrapolate the routes of infection and consequences of an CSF epidemic from one region to another.

Study of the potential spread patterns of CSF into a region may help to identify risk factors for disease spread and to improve the prevention and management of future outbreaks. In CSF-free areas, a suitable way to quantify the magnitude of potential epidemics and evaluate the effectiveness of different control measures to be applied is to use epidemiologic and mathematic models. Those models intended to simulate the potential spread of CSF into a region in order to identify risk factors, evaluate effective measures to control disease and have a decision support system to better manage real outbreaks. Recently, some models have been developed to simulate the potential spread of CSF into free regions such as Belgium, Germany, Australia and Netherlands [5, 7]. Martinez et al., [9] also described an spatial and stochastic model for Spain by using a commercial available software (InterSpread Plus). However, most of those models focus only on the between-herd transmission of the CSF, with poor assumptions regarding within-herd transmission and, do not explicitly consider the specific herd-to-herd contact patterns into the study region.

The study, presented here, intends to provide quantitative estimates of the magnitude and duration of potential CSF-epidemics by using a stochastic and spatial model to simulate both within and between herd transmission.

Section 2 describe the model developed during this work. In Section 3, this model is applied to two numerical test cases using a real data base provided by the "Regional Government of Castilla and Leon" and the Spanish "Ministry of the Environment and Rural and Marine Affairs" [10].

2. model description

2.1. general description

A spatial stochastic model, referred to as CSF-Spread Model, was developed to evaluate the daily spread of CSF within and between herd into a specific region. It is based on a Monte Carlo approach in order to generate $M \in \mathbb{N}$ possible epidemics scenarios.

More precisely, at the beginning of each scenario all herds are in the susceptible state (i.e. non infected) except one randomly selected herd, called index case, which was assumed to have one infected pig and was classified as infected. Then during a time interval $[0, T]$, with $T \in \mathbb{N}$ a maximum day number, the within and between herd daily transmission process, described in Sections 2.2-2.4, is applied . Furthermore, control measures presented in Section 2.5 were also implemented into the model and can be activated/deactivated in order to quantify their effectiveness to reduce the magnitude and duration of the epidemic. At the end of the simulation, various output are analyzed especially those referring to risk management.

2.2. Model input data

For each herd, identified as herd i, the following data are given: $(X_i, Y_i) \in \mathbb{R}^2$, the geographical location; $N_i(0) \in \mathbb{N}$, the number of pigs at the first day of the simulation; $T_i \in \mathbb{N}$, the type of production of the herd (i.e. fattening or breeding herds, etc ...); $INT_i \in \mathbb{N}$, its integration group (i.e. group of herds who share material and trucks); $ADS_i \in \mathbb{N}$, its Sanitary Defense Association (ADS) group (i.e. group of herds who share veterinaries); and the kind of breeding pigs: weaner, slaughter or mixed pigs.

Furthermore for each pig shipment occurring from January 1st to December 31 of 2008 the number of pigs shipped from herd-to-herd, date of shipment and, herd of origin and destination of the shipment was also available.

2.3. Within-herd CSF transmission

The CSF spread within a particular pig herd i was modeled using a stochastic Susceptible-Infected (SI) model [7], in which a pig was characterized, for the sake of simplicity [1], to be in one of two states: susceptible (free of CSF) and infected (infected by CSF).

The daily evolution $S_i(t) \in \mathbb{N}$ (respectively, $I_i(t) \in \mathbb{N}$) of the number of susceptible (respectively, infected) pigs at herd i at day t, was generated using a random variable $P(t) \in \mathbb{N}$ following a Poisson distribution with mean of $\beta_i \frac{S_i(t)I_i(t)}{S_i(t)+I_i(t)}$ where β_i is the transmission parameter set to 8.52, 1.85 or 5.18 depending if we consider weaner, slaughter or mixed pig herds, respectively [7]. More precisely:

$$S_i(t + 1) = S_i(t) - P(t), I_i(t + 1) = I_i(t) + P(t). \tag{1}$$

2.4. Between-herd CSF transmission

CSF transmission between herds was modeled by using a spatial and stochastic state transition model with four states: susceptible (S_H), infected (I_H), infectious (F_H) and Clinical signs (C_H). More precisely, a herd was assumed to be in the "susceptible" state when no pig within the herd is infected. The "infected" state was assumed for a herd with at less one infected pig (but it is still not infectious for other pigs). The "infectious" state was assumed for those herds with at least one pig reaching the latent period [1] (it is infectious for other pigs). Finally the "clinical signs" state was assumed for herds with at least one pig reaching the incubation period (it present physical symptoms, such as fever). Herds in either "infectious" and "clinical signs" state were assumed to be a potential source of infection to other pig herds.

The order of transition from a state to the other is: $S_H \rightarrow I_H \rightarrow F_H \rightarrow C_H$. The assumptions and parameters regulating transition from a particular sate to the next one are described in Sections 2.4.1-2.4.3.

2.4.1. Transition from "susceptible" to "infected"

The transmission of CSF from herd to herd was modeled by considering both direct and indirect contacts.

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[1]Here, in order to reduce computational complexity, the infectious and clinical sign states are simulated only at the herd level (see Section 2.4) and the natural and disease mortality are neglected.

Direct contacts   corresponds to the movement of animals from herd-to-herd. The move-
ment from herd-to-herd was simulated by using the animal movement contact network
between herds in 2008 and considering a random function to take into account eventual
movements not occurring during this particular year [8]. The probability of transmission
per day due to the introduction of an infected pig depends on the number of infected pigs
$I_i(t)$ at day t at the herd i where the shipment was originated, described in Section 2.3.

Indirect contacts   include the movement of vehicles transporting animals, vehicles
transporting products (food, slurry, ...), movement of people and local spread. More pre-
cisely:
     The contacts from herd-to-herd of vehicles transporting pigs are the same as those used
for simulating the "direct contacts". The probability of transmission due to the contact
of a vehicle transporting pigs from and "infected" herd i to another herd j was modeled
using a Bernoulli distribution with mean 0.011 [3].
     The contacts by vehicles transporting products from herd to herd was assumed to occur
only among herds belonging to the same integration group INT. The number of contacts
by vehicles transporting products per herd per day was assumed to be Poisson distributed
with a rate of 0.3 [5]. The trip of each vehicles was simulated assuming that each vehicle
visits 4 herds per day [10]. The probability of CSF introduction into a herd due to the
contact with a vehicle, that has previously visited an "infected" herd, was modeled using
a Bernoulli distribution with mean 0.021 [6].
     The contacts of people visiting herds was assumed to occur only randomly among those
herds belonging to the same ADS group. The number of contacts of people per herd per
day was assumed to be Poisson distributed with a rate of 0.4 [5]. The trip of each person
was simulated assuming that each person visits 3 herds per day [10]. The probability of
CSF introduction into a herd due to the contact with a persons, that has previously visited
an "infected" herd, was modeled using a Bernoulli distribution with mean 0.017 [6].
     The transmission of CSF by local spread was assumed to occur between herds in the
proximity of an infected herd by indirect contacts such as airborne spread or fomites. The
probability of CSF-infection per day by local spread from one "infected" herd i to another
herd j at day t is denoted by $LS(i,j,t) = \frac{I_i(t)}{N_m}LSM(i,j)$, where N_m is the mean number
of animals in all considered herds and $LSM(i,j)$ is the mean probability of infection due
to local spread computed as a function of the distance between herds i and j and built by
interpolating data presented in Table 1 [6].

Distance (m)	150	250	500	1000	2000
Probability of infection per day	0.014	0.009	0.0038	0.0019	0

Tabla 1: Mean probability of infection per day due to local spread in function of the
distance (m).

2.4.2.   Transition from "infected" to "infectious"

     The transition of a herd from "infected" to "infectious" state depends on a "latent"
period that follows a Poisson distribution with mean of 7 days after the first infection in

the considered herd [5].

2.4.3. Transition from "infectious" to "clinical signs"

The transition of a herd from "infectious" to "clinical signs" state depends on an "incubation" period that follows a Poisson distribution with mean of 21 days after the beginning of the infectious state in the considered herd [5].

2.5. Control measures

Measures used in the model and applied to "detected" herds were those defined by the European and Spanish legislation to control CSF [10] based on: zoning; restriction of movements of animals, vehicles and people; depopulation of herds detected as infected; increase of surveillance; and tracing of the historical contacts of the "detected" herd.

2.5.1. Detection of herds with "clinical signs"

Detection of disease was simulated differently before and after detection of the first infected herd. The probability of detection per day based due to "clinical signs" before detection of first infected herd was modeled using a Bernoulli distribution with mean 0.03. After the first detection, this probability was modeled using a Bernoulli distribution with mean 0.06 [6].

2.5.2. Zoning

A control (<3 km radius) and surveillance (<10 km radius) zone was defined around the "detected" herds, and movement restrictions were applied to herds within those radius during a time period of 51 and 40 days, respectively. Overlapping of control and surveillance zones after detection of new outbreaks in the area was allowed.

The probability of detection per day at day t of 'Zoned' farms was modeled using a Bernoulli distribution with mean $0.98\frac{I_i(t)}{S_i(t)+I_i(t)}$ for a herd i within the control zone, $0.95\frac{I_i(t)}{S_i(t)+I_i(t)}$ for a herd i within the surveillance zone [8].

2.5.3. Movement restrictions

Restriction of animal, vehicle and people movements in the "detected" herds, were assumed to be Bernoulli distributed with a mean of 0.99, 0.95 and 0.80, respectively. Those values were 0.95, 0.90 and 0.70, for the herds within the control and surveillance zones [10]. Furthermore, after each detection, a general movement restriction is applied to all considered herds for a period of 90 days following a Bernoulli distribution with a mean of 0.4.

2.5.4. Tracing

The objective of tracing is to identify potentially infectious contacts which may have introduced CSF into a "detected" herd or spread CSF to other herds. We trace all contacts of a "detected" herd occurring 60 days before detection. The probability of tracing an animal, vehicle or people movement was assumed to be Bernoulli distributed with mean

0.99, 0.70 and 0.40, respectively [10]. The probability of detecting an "infected" traced herd follows a Bernoulli distribution with mean 0.95 [10].

2.5.5. Depopulation

The depopulation of "detected" herds was assumed to occur after a random time period generated using data presented in the Table 2 [3]. The maximum number of herds to be depopulated per day was assumed to follow a Poisson distribution of 20 [10]. If this limit is reached, the herd will be depopulated the day after. A "depopulated" herd would be not "susceptible" nor "infectious" until its repopulation. The repopulation of the herd occurs after a period following a Poisson distribution of 90 days [10]. The number of susceptible animals used to repopulate the herd i is $N_i(0)$.

Days	0	1	2	3	4	5	6	7	8
Probability	0,11	0,58	0,2	0,06	0,04	0,004	0,003	0,0015	0,0015

Tabla 2: Probability distribution of the number of days to wait before depopulating a herd.

3. Numerical Experiments

3.1. Considered experiments

In order to illustrate the model performance we have considered the region of Segovia, one of the most important areas of pig production in Spain which was affected by the 1997-1998 CSF-epidemic. During 2008, Segovia had approximately 2,235 pig herds and 1,403,800 pigs, and there were 10,046 pig movements. The input variables of the model were estimated using real data provided by the "Regional Government of Castilla and Leon" and the Spanish "Ministry of the Environment and Rural and Marine Affairs".

We have considered two experiments. One without control measure, denoted by **NM**, and with $T = 100$ days. In the second one, all control measures described previously were activated and the model was running until the end of the CSF epidemic, this case is denoted by **WM**. In both cases, we have considered $M = 1000$ scenarios. The results are presented in Section 3.2.

The model was implemented using MatLab 2007b interface and ran on a Pentium 4 of 3.4Ghz with 2Gb and needed 15000 seconds for the **NM** case and 20000 seconds for the **WM** case.

3.2. Results and discussion

The results are showed in Table 3. For both scenarios, we have also depicted in Figure 1, the risk and reproduction ratio (denoted by $R0$) maps of the considered region. The risk of a particular herd i refers to the number of times that herd i was infected considering all scenarios. The reproduction ratio of a particular herd i refers to the number of times that a particular herd i infects other herds considering all scenarios.

Those preliminary results show that local spread is an important component in CSF transmission. Furthermore, considering control measures helps efficiently to reduce and

	NM			WM		
	Me	Min	Max	Me	Min	Max
Number of Infected herds	16	1	90	7	1	68
Duration of the epidemic in days	100	100	100	100	19	734
Number of infections due to local spread	6	0	77	4	0	40
Number of infections due to person contact	4	0	33	1	0	9
Number of infections due to vehicle contact	3	0	24	1	0	9
Number of infections due to pig transport	3	0	20	1	0	9
Number of detections due to clinical sign	-	-	-	6	1	74
Number of detections due to control zone	-	-	-	2	0	10
Number of detections due to vigilance zone	-	-	-	1	0	8
Number of detections due to tracing	-	-	-	1	0	6

Tabla 3: Results obtained considering **NM** and **WM** cases. For each quantity, we present its mean (Me), minimum (Min) and maximum (Max) value obtained during the Monte-Carlo simulation.

control the epidemic. This is consistent with other studies involving other kind of CSF spread model [2, 3, 4]. However, as we can observe on Figure 1, the application of control measures is not able to reduce the risk and $R0$ in some particular zones. In a forthcoming paper, we will use this model to test the efficiency of possible alternative preventive measures on the risk and $R0$ distribution.

3.3. Conclusions

During this works, we have introduced and described a new model for the study of CSF spread. This model has given preliminary results consistent with other works and presents interesting and novel characteristics respecting to other models, as the use of realistic database (for instance, transport data). Next steps, will be the study of the model sensitivity, its validation on historical outbreaks and its applications to risk and $R0$ management.

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Referencias

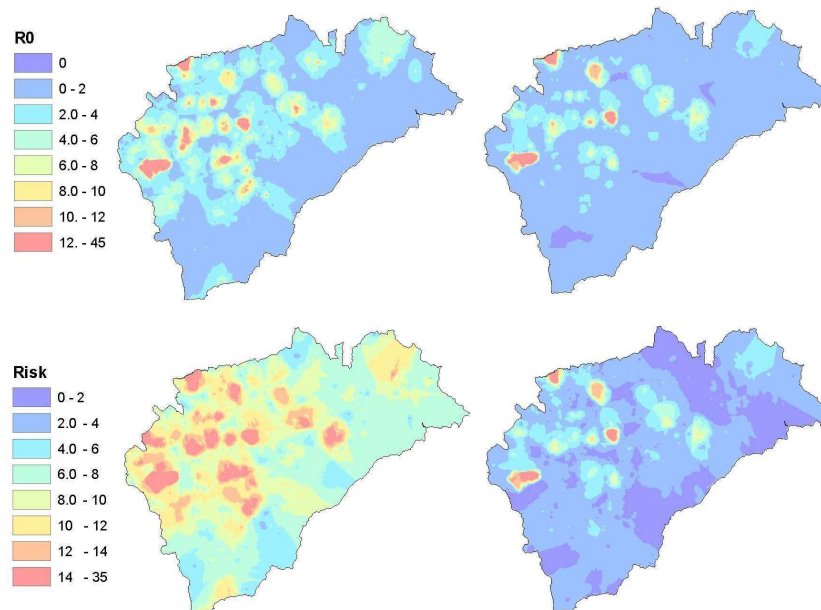[1] Anderson, R.M., May, R.M. (1979) Population biology of infectious diseases: Part I. Nature. 280: 361-367.

Figura 1: (**TOP**) $R0$ and (**BOTTOM**) Risk map for (**LEFT**) **NM** and (**RIGHT**) **WM** test cases.

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