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Be-FAST: A spatial model for studying Classical Swine Fever Virus spread between and within farms. Description and validation.

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Abstract

Classical swine fever is a viral disease of pigs that causes severe commercial restrictions to the affected areas. The knowledge of its spread patterns and risk factors would help to implement specific measures for controlling future outbreaks. In this article, we describe in detail a spatial hybrid model, called Be-FAST, based on the combination of a stochastic Individual Based model for between-farm spread with a Susceptible-Infected model for within-farm spread, to simulate the spread of this disease in a given region. First, we focus on the mathematical formulation of each component of the model. Then, in order to validate this model, we perform various numerical numerical experiments considering the Spanish province of Segovia. Obtained results are compared with the ones given by other models and real outbreaks data.

keywords: *Epidemiological modeling; Individual based model; Susceptible-Infected model; Risk mapping; Model validation; Classical swine fever.*

1 Introduction

Modeling and simulation are important tools to fight diseases [2, 3]. Each disease has its own characteristics and, therefore, most of them need a well-adapted mathematical model in order to be able to tackle real-life situations [4].

In this article, we consider the Classical Swine Fever (CSF). CSF is a highly contagious viral disease of domestic and wild pigs caused by the Classical Swine

Fever Virus (CSFV) [28]. It generates important economical losses (as infected pigs cannot be commercialized [41]) in the affected regions [17, 30, 35]. Despite the efforts to control and eradicate CSF, this disease remains endemic in many countries of America, Africa and Asia and sporadic outbreaks have been affecting half of the European countries from 1996 to 2007 [9, 10, 32, 33]. Due to the different ways of CSFV spread (airborne, contact with infected animals, etc.) [5, 10, 21, 34], it is difficult to extrapolate the routes of infection and consequences of a CSF epidemic from one region to another. Furthermore, the magnitude and duration of a CSF epidemic change depending on the epidemiological and demographic characteristics of the infected region and the timing and effectiveness of the applied control measures [15, 19, 38].

The study of the potential spread patterns of CSFV into a region may help to identify risk areas to improve the prevention and management of future outbreaks. In CSF-free areas, a good way to quantify the magnitude of potential CSF epidemics and evaluate the efficiency of different control measures is to use mathematical models. Recently, some models have been developed to simulate CSFV spread into CSF-free regions such as Belgium, Germany, Australia and Netherlands [11, 15, 18, 37, 39]. Martinez et al., [27] also have described a spatial stochastic model for Spain by using a commercial available software: InterSpread Plus [36, 40]. However, most of those models only focus on the between-farm spread of the CSFV, with poor assumptions regarding the within-farm spread and do not explicitly consider the specific farm to farm contact patterns (such as commercial network, shared vehicles, etc.) into the studied region.

In this work, we consider a spatial hybrid model, called Be-FAST (Between-Farm-Animal Spatial Transmission), used to simulate both within-farm and bet-ween-farm CSFV spreads and to provide CSFV risk maps of the considered region. This model is based on the combination of a stochastic Individual Based model [7, 15], simulating the between-farm spread, with a Susceptible-Infected model [4, 18], simulating the within-farm spread. It has been previously described from the veterinarian point of view (i.e., choice of the CSFV transmission routes to be modeled or neglected, interpretation of the results, etc.) in [25].

Here, after recalling in Section 2 the main characteristics of the CSF, we give an extended description of the Be-FAST model from the mathematical perspective (i.e., detailed equations, numerical schemes, etc.) in Section 3. Finally, during Section 4, we focus on the model validation. More precisely, we consider numerical experiments, based on real databases (i.e., farms description, commercial network, etc.) of the Spanish region of Segovia provided by the Regional Government of Castilla and Leon [12] and the Spanish Ministry of the Environment and Rural and Marine Affairs [23]. We compare the results given by our model with those obtained with another model, namely InterSpread Plus, considering the same simulations. Moreover, we also take into account the outputs generated by the model described in [16] on a different region and real data observed during various CSF outbreaks in Spain [1] and Netherlands [11].

2 Classical Swine Fever characteristics

In order to help in the understanding of the Be-FAST model, described in Section 3, we briefly explain the CSF evolution process, the routes of transmission and present some control measures used to fight CSFV. A complete justification of the assumptions and simplifications described in this Section, and considered in our model, can be found in [25].

2.1 CSF evolution

CSF results from infection by CSFV, a member of the genus Pestivirus and family Flaviviridae [28]. CSFV affects both domestic and wild pigs. When a pig is not infected by CSFV, it is categorized in the Susceptible state (denoted by S_p). Once it is infected, it passes successively through the following states [30, 31]:

- Infected (denoted by I_p): The pig is infected by CSFV but cannot infect other pigs and have no visible clinical signs (fever, lesion, etc.). The mean duration of a pig in this state is 7 days and it is called latent period. Then, it passes to be infectious.
- Infectious: The pig can infect other pigs but does not have clinical signs yet. The mean duration from infectious to the development of clinical sign is 21 days and it is called incubation period. Then, the pig has clinical signs.
- Clinical Signs: The pig develops visible clinical signs and still infect other pigs. After a period between two weeks and three months the pig can be recovered or died due to the disease. The CSF death and recuperation of pigs are assumed to be neglected, because the time period considered in our simulation is short ($\leq$ one year) and the slaughter of infected animals is considered.

Those four states can be also applied at the farm level by considering that a farm is [15]:

- Susceptible (denoted by S_f): If all pigs in the farm are susceptible.
- Infected (denoted by I_f): If at least one pig is infected.
- Infectious (denoted by T_f): If at least one pig is infectious.
- Clinical Signs (denoted by C_f): If at least one pig has clinical signs.

A farm either in the state I_f, T_f or C_f is assumed to be a contaminated farm. Moreover, a farm in the state T_f or C_f is considered as a spreading farm.

2.2 Routes of transmission

The main ways of CSFV spread (i.e., that a susceptible pig becomes infected) are the following [5, 10, 21, 34]:

- By contact with an infected animal. This way of spreading is called direct contact. By opposition, all the other routes of spreading are referred to as indirect contacts.
- By contact with contaminated fomites such as vehicles, materials or peoples (in particular, veterinarians, visitors or neighborhood farmers).
- By airborne spread.

Historically, those ways of spreading have been reported as the main routes of CSFV spread [6], although other routes (such as movement of wild animals) have also been described as potential ways of CSFV transmission but with a minor impact on the CSF epidemics [10]. Thus, those alternative routes have been neglected here.

2.3 Control measures

Once an animal becomes infected, another important concept in epidemiology is its detection and application of control measures by the authorities [30].

When an infected pig is detected in a farm, this farm is classified as Detected. Generally, in a zone free of CSFV (i.e., before the detection of the first contaminated farm, called index case), the detection occurs when pigs present clinical signs and is due to the awareness of the own farmers or private veterinarians [19]. When the first farm is detected, the awareness of the farmers and authorities is widely increased and the detection delay decrease [15, 37]. Moreover, the detection can be also due to the control measures presented below.

Finally, in order to control a potential CSF epidemic, some measures defined by the European and Spanish legislation, described in [11, 12, 20, 24] and in Section 3.6, are considered here:

- Movement restrictions: Outgoing or incoming movements in farms inside the considered region are limited during a specified time interval (in our case, between one and three months).
- Zoning: Zones, called control and surveillance zones, are defined around a detected farm (considering a radius of 3km and 10km, respectively). Surveillance activities are applied within those zones during a fixed time period (30 and 40 days, respectively).
- Depopulation: All the animals of a detected farm are slaughtered.
- Tracing: Tracing activities involve the process of determining contacts that have left or entered a detected farm during a time interval preceding the detection (here, two months). The objective of tracing is to identify

potentially infectious contacts which may have introduced CSFV into the farm or spread CSFV to other farms.

3 Mathematical description of the model

In this Section, we describe in detail the Be-FAST model. First, we present the general structure of our model. Then, one by one, we introduce the mathematical formulation of all the Be-FAST processes related to the input parameters, the within-farm and the between-farm CSFV spread and the control measures.

3.1 General description

The Be-FAST model is used to evaluate the daily spread of CSFV within and between farms into a specific region.

At the beginning of the simulation, the model parameters are set by the user. Those referring to farms and transport of pigs are described in detail in Section 3.2. The other ones are described in Sections 3.3-3.6 and are summarized in Table 1. Furthermore, control measures, presented in Section 2.3, are also implemented and can be activated/deactivated, when starting the model, in order to quantify their effectiveness to reduce the magnitude and duration of the CSF epidemic.

Remark 1 *We note that the values of the parameters used by the model Be-FAST should be set in function of the studied region (due to, for example, the specific legislation, production characteristics, control measures efficiency, etc.). For instance, the parameter values presented in this work are adapted for their application to the province of Segovia, the region considered during the numerical experiments presented in Section 4. In particular some parameters, referenced by 'J.C.L' and 'M.A.P.A., 06' in Table 1, have been obtained by expert opinions of the Spanish Regional Government of Castilla and Leon [12] and the Spanish Ministry of the Environment and Rural and Marine Affairs [23].*

The Be-FAST model is based on a Monte Carlo approach that generates $N_S \in \mathbb{N}$ possible epidemic scenarios (i.e., evolution of the CSFV). More precisely, at the beginning (i.e., at time $t = 0$) of each scenario, denoted by (SCE_m) with $m = 1, 2, ..., N_S$, all the farms are in the susceptible state except one randomly selected farm, which is assumed to have one infectious pig and is classified as infectious. Then, during a time interval $[0, T_{\max}]$, with $T_{\max} \in \mathbb{N}$ a maximum simulation day number, the within-farm and between-farm daily spread routines, described in Sections 3.3 and 3.4, respectively, are applied. Moreover, a daily process simulating the detection of contaminated farms by authorities and a daily process modeling the activated control measures, presented in Sections 3.5 and 3.6, respectively, are also run. If, at the end of a simulation day, the CSF epidemic disappears, the scenario (SCE_m) is stopped and we start the next scenario (SCE_{m+1}).

When the simulation is over (i.e., the scenario (SCE_{N_S}) is finished), many kind of outputs can be generated: for instance, in Section 4.1.3, we present the most typical ones used to analyze the performance of an epidemiological model.

A diagram summarizing all those steps is presented in Figure 1.

3.2 Farm and transport of pigs inputs

We consider a study region containing $N_{fr} \in \mathbb{N}$ farms. For each farm, identified as farm number i (also called, in order to simplify the notations, farm i), with $i = 1, ..., N_{fr}$, the following data are given:

- $(X_i, Y_i) \in \mathbb{R}^2$: the geographical location (i.e., latitude and longitude) of the farm centroid.
- $N_i(0) \in \mathbb{N}$: the number of pigs at the first day of the simulation ($t = 0$).
- $T_i \in \mathbb{N}$: the type of production of the farm. The model allows to distinguish three types of production: Farrowing (young pigs), Fattening (adult pigs) or Farrow-to-Finish (mixed pigs) [18].
- $INT_i \in \mathbb{N}$: the integrator group (i.e., groups of farms who share material and vehicles) identifier.
- $SDA_i \in \mathbb{N}$: the Sanitary Defense Association (SDA) group (i.e., groups of farms who share veterinarians) identifier.

Furthermore, the following information of all farm to farm pig shipments, occurring during a specific time interval (here, in Section 4.1.1, the year 2008), are also provided:

- The number of pigs shipped.
- The date of the shipment.
- The farms of origin and destination of the shipment.

3.3 Within-farm CSFV spread

The daily CSFV spread within a particular contaminated farm i is modeled by using a discrete time stochastic Susceptible-Infected (SI) model [4, 18]. The pigs in this farm are characterized to be in one of those two states: Susceptible or Infected, described in Section 2.1. In order to reduce the computational complexity of our model (see Remark 2), the Infectious and Clinical Signs states are simulated only at the farm level (more details are given in Section 3.4). Because the time period considered is shorter than one year, the natural pig mortality is also neglected.

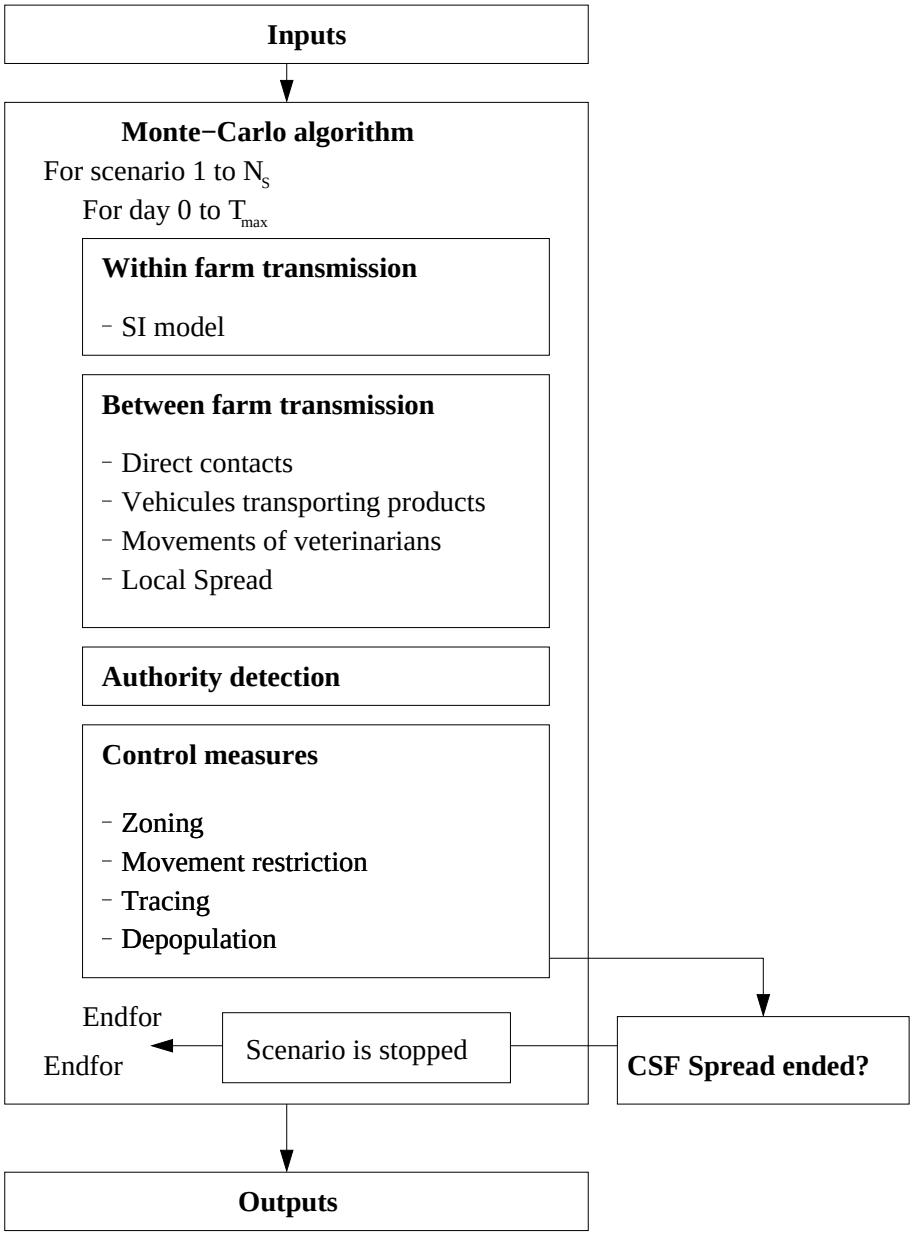

Figure 1: Diagram summarizing the Be-FAST model steps presented in Section 3.1.

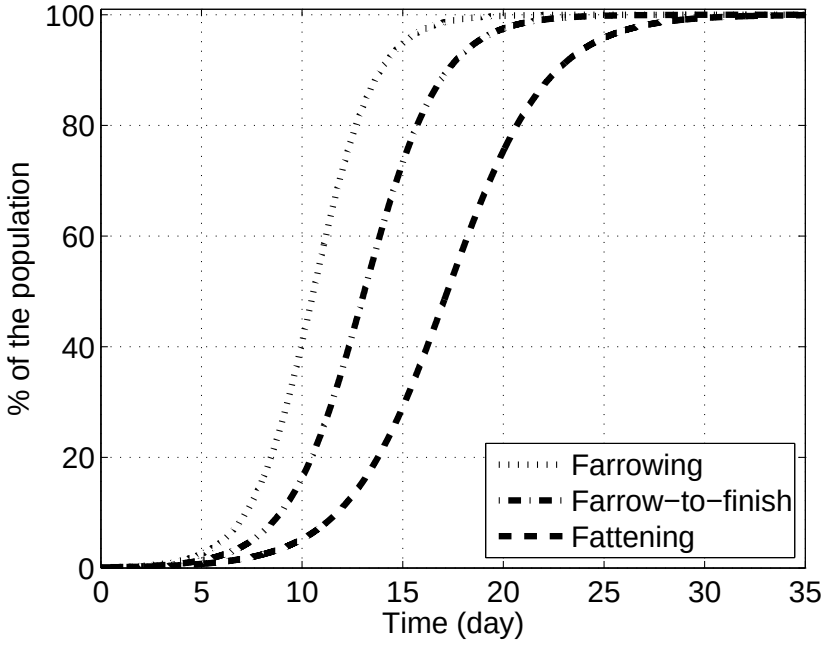

Figure 2: Evolution of the percentage of infected pigs obtained by considering the model given by System (1) and a farm containing 1000 pigs and starting with one infected pig, in function of the farm type: Farrowing, Fattening and Farrow-to-Finish.

Under those assumptions, the evolution of $S_{p,i}(t)$ and $I_{p,i}(t)$, denoting the number of susceptible and infected pigs in farm i at time t, respectively, is given (in a continuous version) by

$$\begin{cases} \dfrac{\mathrm{dS_{p,i}(t)}}{\mathrm{dt}} = -\beta_i \dfrac{S_{p,i}(t) I_{p,i}(t)}{S_{p,i}(t) + I_{p,i}(t)}, \\ \dfrac{\mathrm{dI_{p,i}(t)}}{\mathrm{dt}} = \beta_i \dfrac{S_{p,i}(t) I_{p,i}(t)}{S_{p,i}(t) + I_{p,i}(t)}, \end{cases} \tag{1}$$

where $\beta_i \in \mathbb{R}$ is the daily transmission parameter set to β_{far} =0.66, β_{fat} =0.40 or β_{ftf} =0.53 depending of the farm type T_i: Farrowing, Fattening or Farrow-to-Finish pig farms, respectively [18]. The evolution of the proportion of infected pigs governed by System (1) and obtained by considering a farm containing 1000 pigs and starting with one infected pig, in function of the farm type, is presented in Figure 2.

In order to obtain integer values of infected and susceptible pigs inside a farm and to introduce some randomness in System (1) (the within-farm CSFV spread may be slightly different for each farm), but respecting its general behavior, we

have considered the following daily discrete version of System (1) [18]

$$\begin{cases} S_{p,i}(t+1) = S_{p,i}(t) - \min(P(t), S_{p,i}(t)), \\ I_{p,i}(t+1) = I_{p,i}(t) + \min(P(t), S_{p,i}(t)), \end{cases} \tag{2}$$

where t corresponds to the day in the simulation and $P(t) \in \mathbb{N}$ follows a Poisson distribution with mean $\beta_i \dfrac{S_{p,i}(t) I_{p,i}(t)}{S_{p,i}(t) + I_{p,i}(t)}$.

Remark 2 *Although the SI model, presented here, seems to be too simple (with only two pig states) to model the within CSFV spread, in practice, it gives a good ratio between spread modeling accuracy and computational time. Indeed, we have to consider that this model is applied to each farm infected during a Monte-Carlo scenario, which can dramatically increase the computational time needed by the Be-FAST model. For example, we have tried to consider the infectious and clinical sign sates at the pig level. In that case, we obtained results similar to ones given by the model presented here (± 2% of variation) with a significant loss of speed performances (the computational time increases by 30%). For the same reasons, considering a model more complex than a SI (such as one that simulates the spatial diffusion of the CSFV inside a farm) does not appears to be a reasonable choice in terms of model efficiency (for instance, if an epidemiological model is used to take decisions in case of real outbreak, its outputs should be given within a day [12]).*

3.4 Between-farm CSFV spread

The CSFV spread between farms is modeled by using a spatial stochastic Individual Based model [7, 15]. In this model, farms are classified in one of those four states: Susceptible (S_f), Infected (I_f), Infectious (T_f) and Clinical signs (C_f). Those states are described in Section 2.1.

The daily transition from a particular farm state to other state is modeled by considering direct contacts, indirect contacts and the natural evolution of the CSF presented in Sections 2.1 and 2.2. Those transition processes are described in detail in Sections 3.4.1-3.4.3.

3.4.1 State transition due to direct contacts

The CSFV spread by direct contacts is assumed to occur due to the movements of infected pigs between farms. Those movements are estimated by using the data of the shipment of pigs introduced in Section 3.2. Since the transports of pigs are similar from one year to another [12, 23], we generate random movements, respecting the database behavior (with data from previous years), instead of using the exact ones.

More precisely, at each simulation day t, we simulate those shipments by performing this process:

- We compute $ENM(t)$, the estimated number of movements occurring during the simulation day t, by considering a Poisson distribution with

mean $NM(t)$, where $NM(t) \in \mathbb{N}$ is the number of movements occurring at day t in our database.

- Then, for each simulated movement:

  - We select randomly the farm of origin of the movement $i \in [1, ..., N_{fr}]$ and the farm of destination of the movement $j \in [1, ..., N_{fr}]$, with $j \neq i$, by considering the discrete probability $\mathbb{P}_M$, computed once before the simulations and only each time we get a new database (we note that other parameters related to the database may be calculated once before running the model), defined by:

$$\mathbb{P}_M((i,j) = (k,l)) = \frac{M_{\text{mov}}(k,l)}{\sum_{m=1}^{N_{fr}} \sum_{n=1, n\neq m}^{N_{fr}} M_{\text{mov}}(m,n)}, \tag{3}$$

    where $k \in [1, ..., N_{fr}]$, $l \in [1, ..., N_{fr}]$, $k \neq l$ and $M_{\text{mov}}(k,l) \in \mathbb{R}$ is the number of movements from farm k to l in the database plus 10^{-6} (to take into account, with a low probability, possible movements not occurring in our database).

  - We compute $np_{(i,j)}(t) \in \mathbb{N}$, the number of pigs moved during this movement from farm i to farm j, by considering:

$$np_{(i,j)}(t) = \min\left\{ \text{Ceil}\left(\overline{np_{(i,j)}} \frac{S_{p,i}(t) + I_{p,i}(t)}{N_i(0)} \right), S_{p,i}(t) + I_{p,i}(t) \right\}, \tag{4}$$

    where $\overline{np_{(i,j)}} \in \mathbb{R}$ is the mean number of pigs moved between those farms in our database and $\text{Ceil}(x)$ returns the nearest integer greater or equal to $x \in \mathbb{R}$. In the case of no movement from farm i to farm j in the database, $\overline{np_{(i,j)}}$ is set to the mean number of moved pigs, considering all the database movements.

  - Finally, we move $np_{(i,j)}(t)$ pigs from the origin farm i to the destination farm j. Those pigs are selected randomly in $S_{p,i}(t)$ and $I_{p,i}(t)$, considering that each pig has the same probability to be selected than the other ones. We denote by $np_{(i,j),S}(t) \in \mathbb{N}$ and $np_{(i,j),I}(t) \in \mathbb{N}$ the number of susceptible and infected pigs that are moved during the simulated shipment, respectively. Thus, the evolution of pigs in farm i and j are governed by

$$\begin{cases} S_{p,i}(t+1) = S_{p,i}(t) - np_{(i,j),S}(t), \\ I_{p,i}(t+1) = I_{p,i}(t) - np_{(i,j),I}(t), \\ S_{p,j}(t+1) = S_{p,j}(t) + np_{(i,j),S}(t), \\ I_{p,j}(t+1) = I_{p,j}(t) + np_{(i,j),I}(t). \end{cases} \tag{5}$$

    In addition, if $np_{(i,j),I}(t) > 0$, the state of farm j is set to the state of farm i in the following cases:

    · The state of farm j is S_f or

· The state of farm j is I_f and the state of farm i is T_f or C_f or
· The state of farm j is T_f and the state of farm i is C_f.

In all other cases, the state of farm j remains unchanged.

3.4.2 State transition due to indirect contacts

As specified in Section 2.2, the CSFV spread due to indirect contacts is assumed to occur by either movements of vehicles transporting pigs, movements of vehicles transporting products, movements of SDA persons or the so called 'local' spread (i.e., spread due to contacts with the neighborhood which include: airborne spread and contacts with contaminated persons and fomites in the vicinity).

In Paragraphs *A-D*, we describe in detail those four kinds of indirect contacts and the way they contribute to the CSFV spread from farm to farm. Then, in Paragraph *E*, we show how this spread affects farms at the level of pig number and state.

A- Movements of vehicles transporting pigs:
We consider the same movements as the ones generated in Section 3.4.1. If the farm of origin of the transport is either in the state T_f or C_f, the truck transporting pigs is considered as contaminated and, thus, can infect the farm of destination. In that case, we assume that the probability of CSFV infection in the farm of destination due to contact with the contaminated vehicle is modeled by using a Bernoulli distribution with mean 0.011 [38].

B- Movements of vehicles transporting products:
Contacts with vehicles transporting products from farm to farm (also called integrator vehicles) are assumed to occur only among the farms belonging to the same integrator group and with the following assumptions:

- The daily number of contacts with integrator vehicles per farm is assumed to be Poisson distributed with a mean of 0.4 [15].
- An integrator vehicle can visit a maximum of 4 farms per day [12].
- An integrator vehicle is contaminated if, previously, it has visited a spreading farm (i.e., a farm either in the state T_f or C_f, see Section 2.1) [15, 38].
- The probability of CSFV infection in a farm per contact with a contaminated integrator vehicle is modeled by using a Bernoulli distribution with mean 0.0068 [38].

Thus, for each simulation day, we build the routes of those integrator vehicles and simulate the way they spread CSFV by considering the following process:

For each integrator groups INT, we perform those steps:

– For each farm in INT, we compute the number of integrator vehicles visiting it by using a Poisson distribution with mean 0.4.
– Then, we list the farms that are visited by integrator vehicles and we rearrange this list, denoted by L_{INT}, randomly (taking into account that a same farm cannot be visited two times consecutively).
– Next, a first vehicle is sent to visit the first four farms in L_{INT}, following the list order. Each fourth farm, until the end of L_{INT}, we consider a new integrator vehicle (non contaminated) starting from the next farm in L_{INT}.
– During each simulated trip, a vehicle becomes contaminated at the moment it visits a spreading farm and can infect other farm by considering a Bernoulli distribution with mean 0.0068.

C- Movements of SDA persons:

The CSFV spread by contact with SDA persons visiting farms is assumed to occur only between farms belonging to the same Sanitary Defense Association (SDA) group.

The same process used in Paragraph B, to model the movements of integrator vehicles, is applied to simulate those contacts with the following parameters:

- The daily number of SDA people contacts per farm is assumed to be Poisson distributed with a mean of 0.3 [15].
- A SDA person can visit a maximum of 3 farms per day [12].
- A SDA person can only be contaminated if, previously, he has visited a spreading farm [15, 38].
- The probability of CSFV infection in a farm per contact with a contaminated SDA person is modeled by using a Bernoulli distribution with mean 0.0065 [38].

D- Local spread:

The CSFV local spread is assumed to occur to farms in the proximity of a farm either in the state T_f or C_f. It is mainly due to the airborne spread and contacts with contaminated neighborhood persons and fomites.

In our case, the daily probability of CSFV infection in a farm j due to the local spread from a spreading farm i at simulation day t is modeled by considering a Bernoulli distribution with mean

$$\frac{I_{p,i}(t)}{\overline{N(0)}} LSM(d(i,j)), \tag{6}$$

where $\overline{N(0)} = \dfrac{\sum_i N_i(0)}{N_{fr}}$ is the mean number of pigs per farm at day 0, $d(i,j)$ is the distance between farms i and j and $LSM(x) \in [0,1]$ is the mean daily

probability of CSFV infection due to local spread between two farms at a distance of $x > 0$ (in meter). Moreover, $LSM(x)$ is build by interpolating the data presented in Table 2 [15].

E- New infection and state transition:

For each new CSFV infection occurring in farm j during the processes described in Paragraphs A to D, if $S_{p,j}(t) \geq 1$, we infect one new pig in farm j by considering:

$$\begin{cases} S_{p,j}(t+1) = S_{p,j}(t) - 1, \\ I_{p,j}(t+1) = I_{p,j}(t) + 1. \end{cases} \tag{7}$$

Furthermore, if the state of farm j is S_f, we change it to I_f.

3.4.3 State transition due to CSF natural evolution

According to the characteristics of the CSF evolution described in Section 2.1, we consider the following changes in the farm state:

- Transition from I_f to T_f: when a farm reach the state I_f, it will pass at state T_f after a latent period that follows a Poisson distribution with mean 7 days [15].
- Transition from T_f to C_f: when a farm reach the state T_f, it will pass at state C_f after an incubation period that follows a Poisson distribution with mean 21 days [15].

3.5 Contaminated farm detection

As specified in Section 2.3, a contaminated farm is generally detected by the observation of the clinical signs of its pigs (i.e., the farm is in state C_f) [19]. This detection is simulated differently before and after detecting of the first contaminated farm (i.e., the index case):

- Before detecting the index case: For each farm in the state C_f, the probability of detection per day is modeled by using a Bernoulli distribution with mean 0.03 [15].
- After detecting of the index case: As the awareness of the farmers and private veterinarians increase, the daily probability of detection of a farm in the state C_f is increased and is simulated by considering a Bernoulli distribution with mean 0.06 [15].

Furthermore, a contaminated farm can be also detected due to the control measures presented in Section 3.6.

3.6 Control measures

We now describe the control measures, introduced in Section 2.3, implemented in our model.

3.6.1 Movement restrictions

A drastic restriction on movements (outgoing or incoming on farms) is applied to detected farms. Restrictions on transports of animals, integrator vehicle movements and SDA people movements in the detected farms are assumed to be Bernoulli distributed with a mean of 0.99, 0.95 and 0.8, respectively (i.e., movements are reduced by 99%, 95% and 80%, respectively). Furthermore, after each detection, a general movement restriction, considering the three kinds of movements, is applied to all farms during a period of 90 days and following a Bernoulli distribution with mean 0.4 [12, 23].

Remark 3 *This control measure is adapted to the Spanish province of Segovia considered during the numerical experiments presented in Section 4. For larger areas (such as, e.g., a country), the movement restrictions should be limited to a part of the studied region.*

3.6.2 Zoning

The farms at a distance of less than 3 km of a detected farm are set in a control zone, whereas the farms at a distance between 3 km and 10 km of a detected farm are set in a surveillance zone [23].

A movement restriction is applied during 30 days to farms in control zones and 40 days to farms in surveillance zones [23]. In both cases, pig transports, movements of SDA persons and movements of integrator vehicles are randomly reduced by considering a Bernoulli distribution with mean 0.95, 0.9 and 0.7, respectively [12]. Overlapping of the movement restrictions of control and surveillance zones is allowed (i.e, if a farm has an active movement restriction, we add the days of the new restriction to those of the old restriction).

Furthermore, we apply another surveillance process to the farms within those zones, in addition to the one described in Section 3.5. The daily probability detection of a farm j in the state C_f due to this surveillance is assumed to be dependent of the proportion of infected animals and modeled by considering [12]:

- a Bernoulli distribution with mean $0.98 \times \dfrac{I_{p,j}(t)}{S_{p,j}(t) + I_{p,j}(t)}$ if the farm j is within a control zone,
- a Bernoulli distribution with mean $0.95 \times \dfrac{I_{p,j}(t)}{S_{p,j}(t) + I_{p,j}(t)}$ if the farm j is within a surveillance zone and is not within a control zone.

3.6.3 Depopulation

The depopulation (i.e., the slaughter of all animals) of a detected farm i occurs after a random time period, generated by using the data provided by Table 3 [10], starting from the day of its detection. However, the maximum number of farms to be depopulated per day is assumed to follow a Poisson distribution

with mean 20 [12]. Thus, if this limit is reached, the farm is depopulated the following days. When the farm i is depopulated, its number of pigs is set to 0 and it is not considered anymore by the model. Then, after a time period following a Poisson distribution with mean 90 days [23], the farm is repopulated (i.e., new pigs are introduced): the number of susceptible pigs is $N_i(0)$, the farm state is set to S_f and the farm is again taken into account by the model.

3.6.4 Tracing

The objective of tracing is to identify infectious contacts which may have introduced CSFV into a detected farm or spread CSFV to other farms. We include the tracing of all contacts (i.e., farms sending or receiving animals, sharing SDA persons or sharing integrator vehicles)of a detected farm occurring 60 days before the detection [23]. However, due to failures in the administrative system (error in databases, lack of personnel, etc.) tracing all the contacts is not always possible.

More precisely, when a farm i is detected, we list all the farms who have shared, 60 days before the detection, at least one integrator vehicle, one SDA person or one transport animal vehicle with farm i . Then, for each farm in this list, we decide if it is traced or not according to following probabilities: the probability of tracing a farm due to animal transport, integrator vehicle movement or SDA people movement is assumed to be Bernoulli distributed with a mean of 0.99, 0.7 and 0.4, respectively [12]. Next, for each farm to be traced, we select the day of tracing, taking into account, as in Section 3.6.3, that the maximum number of farms to be traced per day is assumed to follow a Poisson distribution with mean 60. Finally, we perform a detection process to the traced farms, the day of their tracing, by considering that the probability of detecting a contaminated traced farm follows a Bernoulli distribution with mean 0.95 [23].

4 Model Validation

In order to validate the Be-FAST model, we perform various numerical experiments, described in Section 4.1. Those experiments are also run by considering a commercial epidemiological model, called InterSpread Plus, briefly introduced in Section 4.2. The results obtained by both models are compared with the outputs generated by the Individual Based model presented in [16] considering similar experiments; and with data observed during real CSF outbreaks occurring in Spain [1] and Netherlands [11] and reported in Section 4.3. Finally, in Section 4.4, we analyze and discuss all those results.

4.1 Numerical experiments

Now, we present the numerical experiments used for the model validation. In particular, we detail the inputs related to farms and pig shipments, the scenarios parameters and the considered outputs.

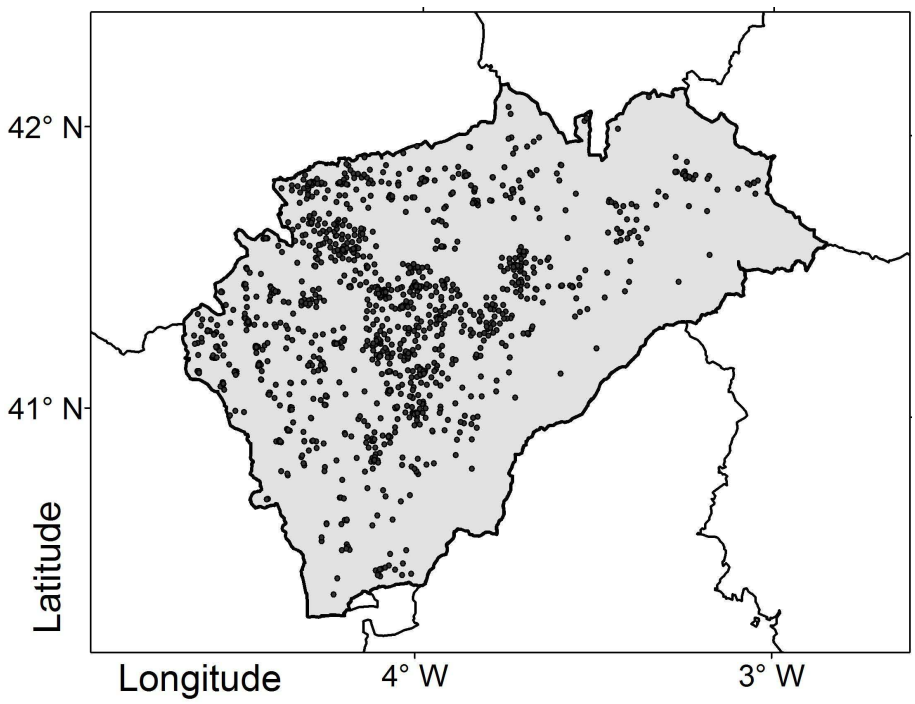

Figure 3: Coordinates and boundaries of the province of Segovia (in gray). The location of the considered pig farms is represented by black spots (•).

4.1.1 Farms and pig transports inputs

We consider the province of Segovia, one of the most important areas of pig production in Spain, which have a surface of 6796 km^2. A real database, provided by the Spanish Regional Government of Castilla and Leon [12] and the Spanish Ministry of the Environment and Rural and Marine Affairs [23], corresponding to the inputs, described in Section 3.2, of the year 2008 is used.

In 2008, N_{fr} =1400 pig farms, containing a total of 1403800 pigs, were located in Segovia. Those farms were divided in 11 integrator groups and 34 SDA groups. Furthermore, 208 farms were of the type Farrowing, 510 of the type Fattening and 682 of the type Farrowing-to-Finish. Finally, during this year, there were 10046 pig shipments. A graphical representation of the locations of those pig farms and the province of Segovia is shown in Figure 3.

4.1.2 Scenarios parameters

We have considered two kind of simulations:

- In the first one, we do not consider any control measure, and we run

the model during $T_{\max} = 200$ days. This case is denoted by **NM** (No Measure). The interest of this experiment is to evaluate the principal routes of CSFV spread.

- In the second one, all the control measures described in Section 3.6 are activated and the model is running during a maximum period of three years ($T_{\max} = 1095$), which is large enough to ensure the end of the CSF epidemic [25]. This case is denoted by **WM** (With Measures). In this experiment, which is more realistic and classical (i.e., this experiment is considered in other works, such as [16] and [22]) than **NM**, we are interested in evaluating the magnitude of the epidemic and the efficiency of the control measures.

In both cases, we set $N_S = 1000$ scenarios. This value gives a good compromise, in the particular cases considered here for the Be-FAST model, between the outputs stability (with variations less than 3%) and the computational complexity [26]. Furthermore, we want to point out that, in the literature, some models are run with a much lower value. For instance, in [15, 14, 16], the number of scenarios of the considered Individual Based model is 100. This reinforce the idea of precision of the results obtained during this work.

4.1.3 Considered outputs

After each experiment (i.e., the scenario (SCE_{N_S}) is over), many kinds of outputs can be obtained. Here, we consider the most typical ones used to evaluate the performances of an epidemiological model [11, 16, 27].

More precisely, for each scenario (SCE_i), with $i = 1, ..., N_S$, we compute:

- The number of infected farms.
- The duration of the epidemic: the number of days between the beginning of the scenario and the day that all farms are in the susceptible state. If this case never occurs in the considered scenario, the duration is $T_{\max}$.

For those both quantities, we calculate, regarding all the scenarios, their mean, minimum and maximum values, their 95% prediction interval, their quartiles and their discrete distribution functions.

In addition, taking into account the N_S scenarios, we evaluate:

- The percentage of infections due to local spread, integrator vehicles, SDA persons and transport of pigs (i.e., direct contacts and contaminated pig transport trucks).
- The percentage of detection of contaminated farms, after detecting the index case, due to observation of the clinical signs, zoning and tracing.

Furthermore, for each farm i, we compute its risk of CSFV introduction, denoted by $RI(i)$. It is defined as the number of times that farm i becomes

contaminated during the whole Monte-Carlo simulation. In particular, in order to identify the risk zones in the studied region, we are interested in obtaining the geographical distribution of RI. Typically [29], the risk zones are classified in three categories: high, medium and low risk. This is useful, for instance, to design preventive control measures to fight CSFV (see Section 5 for more details). To do so, and to compare the values of RI given by the models presented in Section 4.2, we first normalize $RI(i)$ by considering

$$\bar{RI}(i) = \frac{\hat{RI}(i)}{\max_i \hat{RI}(i)}$$

where $\hat{RI}(i) = RI(i)/\Big(\sum_i RI(i)\Big)$. Then, we obtain the spatial distribution of $\bar{RI}$, in Segovia, by interpolating the values of $\bar{RI}(i)$ considering an Inverse Distance Weighted method [42]. Finally, the identification of the three risk zones is done by considering the Jenks Natural Breaks (JNB) classification method [13]. Those both last steps are done by using ArcGIS Ver. 9.1 (`http://argis.com/`).

Remark 4 *We could also have considered $RE(i)$, the effective reproduction ratio of farm i, as the risk value, defined as the number of times that the farm i infects another farm in the susceptible state during the complete simulation [2, 3]. Using $RE(i)$ instead of $RI(i)$, the results and their interpretations obtained with this risk measure are similar to the ones obtained with RI, as showed in [25] and [26]. Thus, they are not included in this document.*

4.2 Considered models

In order to validate the BE-FAST model, we perform the experiments, presented in Section 4.1, by using the following models:

A) A MatLab Ver. 2009.a (`http://www.mathworks.com/`) script implementation of the Be-FAST model. This model is denoted by **BF**.

B) We also consider the InterSpread Plus software Ver. 1.0.49.5 (`http://www.interspreadplus.com/`). InterSpread Plus is a commercial C++ implementation of a state transition model [36, 40]. It is one of the most popular epidemiological model software used in the world. However, in our opinion, it has several drawbacks, as, for instance, the low transparency of the code (it is a black-box program) and the difficulty to incorporate complex databases with real movements or contacts from farm-to-farm.

We intend to reproduce the same processes as the one used by the Be-FAST model. As it is out of the scope in this paper, we are not describing the InterSpread Plus model in detail, we only present the main differences between both models:

- InterSpread Plus does not allow to model the within-farm transmission (it is a purely between-farm spread model), so it is not possible

to compute the number of infected or susceptible pigs per time period of a particular farm. For that reason, the model coefficients cannot be expressed in function of the number of infected or susceptible pigs. Thus, all the coefficients depending of number of animals are set to constant values: the daily probability of infection due to local spread is set to $LSM(x)$ without interpolation; the probability of infection due to a pig shipment coming from a contaminated farm is 1; the daily probability of detection of a contaminated farm in a control or surveillance zone follows a Bernoulli distribution with mean 0.98 and 0.95, respectively. However, for each contaminated farm i, InterSpread Plus allows to associate to this farm a weight coefficient, depending on the delay after the farm infection, that is multiplied to all probabilities of infection due to contact with farm i. This process intends to consider that the infectiousness of a farm increases with the time. The weight coefficients are reported in Table 4 and fit the SI evolution of a Farrow-To-Finish farm, depicted by Figure 2.

- The real commercial networks (i.e., pig shipments, SDA groups and integrator groups) cannot be integrated directly in InterSpread Plus. First, the animal transport process is simulated as follows. For each simulation day and farm i, we have to compute the number of pig transports sent by farm i. This is done by considering a Poisson distribution with mean $MRT(i)$, where $MRT(i)$ is the mean number of daily sent pig transports of farm i. Then, for each shipment, we select randomly a farm of destination according to the the farm distance and the probability distribution given in Table 5. The values of $MRT(i)$ and Table 5 are obtained from our database. Secondly, the SDA and integrator contacts are simulated as in our model but considering only one SDA and integrator group. The farms being visited are randomly selected in function of their distances according to Table 5. From all those simplifications, we see that InterSpread Plus does not allow to incorporate the real commercial contacts between farms.
- Some other minor differences are the following: A farm infected by a pig shipment is set to the I_f state; there are no limit on the daily number of farms to be traced or depopulated.

This model is denoted by **IS**.

Finally, we also compare some results obtained by **BF** and **IS** models to those given by the Individual Based model presented, in detail, in [15, 14]. This model only simulates the between-farm spread and is applied to a fictitious German region, but based on real statistics, in [16]. The considered region, which has an area of 2230 km^2, is composed by 2986 farms (1896 Fattening farms, 543 Farrowing farms, 546 Farrow-to-Finish farms). No data on the commercial network between farms are considered. The simulated processes for the CSFV spread and control measures are similar to the ones used by models **BF** and

IS (except the artificial insemination spread process which has been neglected in **BF** and **IS** due to its low proportion of infection). Furthermore, the model parameters are adapted to the German country and can be found in [15]. However, they are close to the ones used in this work. Here, we denote this model by **KM** and we only present the results available in literature [16].

4.3 Real epidemic data

In order to compare the results given by models **BF** and **IS**, we have considered data obtained during various real CSF outbreaks. More precisely, we have considered the information of the following three epidemics:

- Segovia (1997-98): A full description of this epidemic can be found in [24] and we use data provided by [12]. During this event, 22 farms were infected, all belonging to the same company and thus sharing the same SDA and integrator groups. The epidemic duration was estimated to be approximatively 60 days. As the affected region is Segovia, we consider the geographical position of the infected farms to validate the risk maps generated by **BF** and **IS** models.

- Netherlands (1997-98): This outbreak is detailed in [11]. Here, we are interested in the proportion of infection due to each CSFV route measured during this epidemic and reported in Table 6-(**Route** columns).

- Cataluña, Spain (2000-01): This case is presented in [1]. The interesting data of this report, is the proportion of detection of each control measure described in Table 6-(**Measure** columns).

4.4 Results

All the simulations, presented in this Section, are run on a computer with a CPU Core2 Duo P8600 of 2.4Ghz, 4Gb of DDR3 memory and Windows Vista 32bit Operating System.

The outputs, described in Section 4.1.3, obtained during those experiments are reported in Tables 6-7 and, some of them, depicted in Figures 4-5.

The computational times needed by **BF** and **IS** models to solve the **NM** and **WM** cases are presented in Table 6-(columns **C. Time**). We can see that the **IS** model is the faster one. In particular, for the **NM** scenarios (with highest numbers of infected farms), the difference between both model is quite high (**BF** is 7 times slower). In the **WM** case, which is a more realistic and classical case, the difference is reasonable. This can be explained, in part, by the fact that our model has a more complex and complete structure (for instance: the use of SI model for each contaminated farm, dynamic coefficients, etc.) than InterSpread Plus, and, therefore, requires more computations. Another explanation is the difference of performances between the program language used by **BF** and **IS**. Our model is implemented in Matlab script, an interpreted language known to be a very slow in comparison to the compiled languages, such

as C++ used to implement **IS** [8]. Matlab was chosen in order to obtain quickly a first implementation of our model and for the easiness to process the outputs. The computational time needed by **BF** model can be significantly decreased by programming it in FORTRAN or C.

The percentage of infection in function of the CSFV routes is given in Table 6-(**Route** columns). We can see that both models identify the local spread as the main source of infection. Moreover, the proportion due to SDA people is quite similar in the two cases. The main difference between models **BF** and **IS** is obtained when regarding the transport of animals and the integrator vehicles proportions. In that case, **IS** considers the animal shipments as the second most important cause of CSF infection instead of the integrator vehicles. This difference is due to the fact that **IS** does not take into account the number of infected pigs when performing the animal transport, whereas **BF** uses this information. Thus, when the number of infected animals in the farm of origin of the transport is low, many of the pig shipments, simulated by **BF**, do not infect the destination farms, decreasing the proportion of infection due to this route. When we compare those results with the proportion observed during the 1997-98 epidemic in Netherlands [11], we see that the **BF** outputs fit better those real data (in particular regarding the *INT* and *TA* columns) than the **IS** ones.

The percentage of contaminated farm detection in function of the control measures is reported in Table 6-(**Measure** columns). On one hand, **IS** considers that the zoning is the most efficient control measure, then the observation of the clinical signs and, finally, the tracing. On the other hand, **BF** returns the observation of clinical signs as the main detection technique, the zoning and tracing presenting similar efficiency. This can be explained by the fact that, as described in Section 3.6.2, **BF** uses the proportion of the number of infected animals in zoned farm to generate the probability of detection due to the zoning process (thus, the efficiency of this control measure may be reduced for farms with a low proportion of infected animals), whereas **IS** does not allow this possibility. As previously, the proportions generated with **BF** are closer to the real data reported during the 2001-02 epidemic in Spain [1] than those given by **IS**.

Both results, in the proportions of infection and detection, seem to indicate that our approach, that consists in simulating the number of infected animals in farms and use it in the formulas of the Individual Based model coefficients, provides better results and is suitable for generating epidemiological models presenting a realistic behavior.

The statistical values relative to the number of infected farms (NF) and the duration of the epidemic (DR), obtained by considering **BF** and **IS** models and the **NM** and **WM** experiments and some of those values available for the **KS** model, are reported in Table 7. The discrete distribution functions of NF and DR are presented in Figure 4. We can observe on the table, that the **IS** model generates slightly larger values of NF and DR, but of the same order, than **BF**. This is an expected result when regarding the differences on the model coefficients, in particular, the use (or not) of the proportion of infected animals

which increases or decreases the risk of infection and detection. In fact, the main difference can be observed on the amplitude of the extreme scenarios (i.e., scenarios with a high number of infected farms) which is higher for **IS** than **BF**. This can be observed in Figure 4, where the discrete densities are quite similar for both models except for the last proportions (NF >9 and DR >18). This is confirmed, in the **WM** cases, by the fact that the minimum, PI[2.5%], Q1, Q2 and Q3 values of both models are close and the PI[97.5%] and maximum values are twice higher for **IS** than **BF**. In the **NM** experiment, since the mean value of **NF** is higher (there are more extreme scenarios) the difference between the two models is more important: Q2 and Q3 are also more than twice higher for **IS** than for **BF**. When regarding the results produced by the **KS** model in the **WM** case, and taking into account that the considered region has a double number of farms and the area is smaller than Segovia, results can be consider similar to those produced by models **BF** and **IS**. Regarding the effect of applying or not the control measures, in both models, we observe a similar behavior: the epidemic is reduced by ten when comparing the **NM** and **WM** experiments.

Finally, when considering the amplitude of the 1997-98 epidemic in Segovia, which consisted in 22 infected farms and had a duration of 60 days, it is difficult to compare it with the **BF** and **IS** results obtained in the *WM* case: the *DR* values are close to the real outbreak length, but the *NF* ones are much lower. We have to take into account that 10 years separate the 2008 database used in experiments and the real 1997 situation in Segovia. During this period, more than half of the farms have disappeared, due to an economical crisis in 2006 [24], and the control measures have been highly reinforced after the tremendous CSF epidemic in Europe during 1997-98 (for instance, around 500 farms were infected in Netherlands [10]). Moreover, it is possible that this epidemic represents an extreme scenario of the model. A better way to compare those real data with the outputs of the models considered here, is to considerate the risk maps and see if the 1997-98 infected farms are in high risk zones.

The $\bar{RI}$ risk maps generated by models **BF** and **IS**, for the **NM** and **WM** experiments, are presented in Figure 5. The Jenks Natural Breaks (JNB) classification, containing (for a better understanding of the maps) 9 intervals corresponding to 9 gray colors, is also reported in this Figure: the first three intervals [0-0.03],[0.03-0.05] and[0.05-0.07] correspond to the low risk areas; the intervals [0.07-0.10], [0.10-0.12] and [0.12-0.15] correspond to the medium risk areas; and the last three intervals [0.15-0.17],[0.17-0.20] and [0.20-1] correspond to the high risk areas. This classification is obtained by considering the **NM** case (i.e., the worst case) with **BF** model and is extended to other maps. We point out that the JNB classifications obtained by **IS** are similar to the **BF** ones.

As we can observe on those maps, the risk distributions obtained by both models decreases drastically from the **NM** cases to the **WM** ones. We can also see that, although both models identify similar high risk zones in the south west of the studied region, **IS** concentrates the risk in some specific regions in the north and east parts, whereas **BF** identifies the center of the region as presenting a high risk of CSFV spread. This is particularly visible on the **WM**

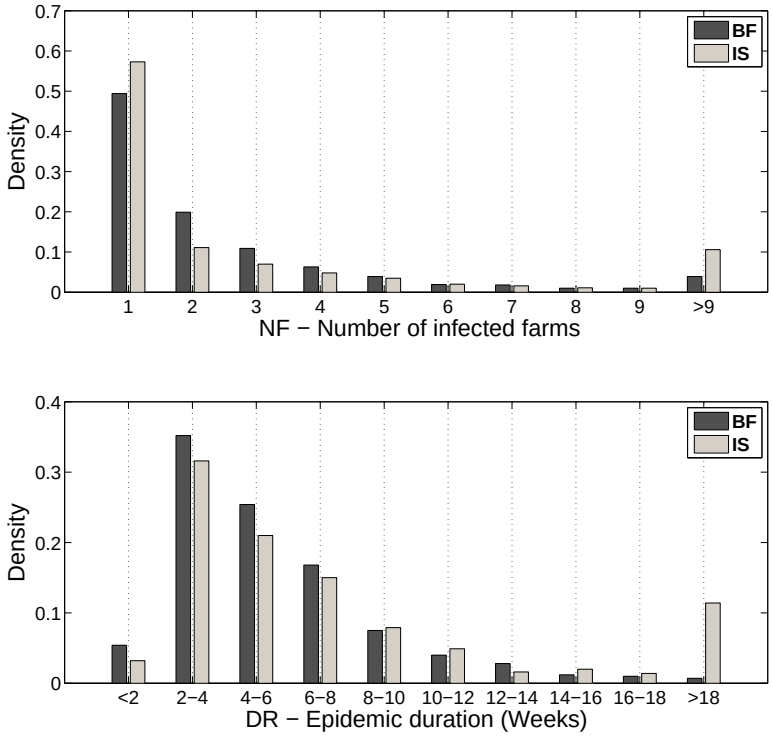

Figure 4: Discrete distribution of (**TOP**) the number of infected farms *NF* and (**BOTTOM**) the epidemic duration *DR* (in weeks) obtained with models **BF** (dark gray) and **IS** (light gray) in the **WM** case.

maps. Focusing on this case, we consider the farms infected during the 1997-98 epidemic in Segovia and see the risk zones where they are included. In Figure 6, we incorporate those farms to the **BF** and **IS** risk maps and we detail the zone where most of the farms are included. We can see that, in the **BF** case, most of the infected farms are situated in a dark (high risk) zone and other farms in medium or low risk zones. In the **IS** case, the high risk zone does not include those farms, and the farms are mainly located in low risk areas. The mean $\bar{RI}$ value of the 1998-97 infected farms given by **BF** model is 0.201, which corresponds to the highest risk in the considered JNB classification. In the **IS** model, the mean risk value of those farms is 0.032, which is included in the low risk area. This result tends to show that the maps generated by model **BF** are more consistent with real data than those generated with model **IS**. This can be explained by the fact that our model uses the real commercial network (i.e., transport of animals, SDA and integrator groups) between farms, whereas this information is not suitably processed by **IS**. This shows the importance of the use of this database to obtain a fine representation of the risk areas, and one should use this input in an epidemiological model as soon as it is available. As previously, we insist on the fact that 10 years separate the used databases and the 1997-98 outbreak in Segovia, explaining why some farms could be included in low risk zones, even in the **BF** map. However, this also shows the robustness of the **BF** risk maps, which seem to be valid for years different from those generating the database.

5 Conclusions

During this work, we have given an extended mathematical description of the spatial model called Be-FAST, used for the study of CSFV spread into a region. The principal originality of this model is that it combines a Susceptible-Infected model, for the within-farm spread process, with an Individual Based model, for the between-farm spread process. The proportion of infected animals given by the Susceptible-Infected model is used to calibrate some coefficients of the Individual Based model. Another important feature of the model, is the possibility of using of a real database of the commercial network between farms. We have seen, when comparing the results given by the model Be-FAST with those obtained by other models (in particular, InterSpread Plus) and real outbreaks data, that these new characteristics are very important for the quantification of the epidemic magnitudes and the identification of the risk zones.

One of the next steps will be the implementation of the model using a faster programming language. In addition, we will also include the economical aspects (for instance, the prices of pigs, control measures, etc.) and will use the risk map distribution to design CSF preventive campaigns, in order to reduce the economical impact and the risk of possible future outbreaks. Those two last ideas are currently in progress.

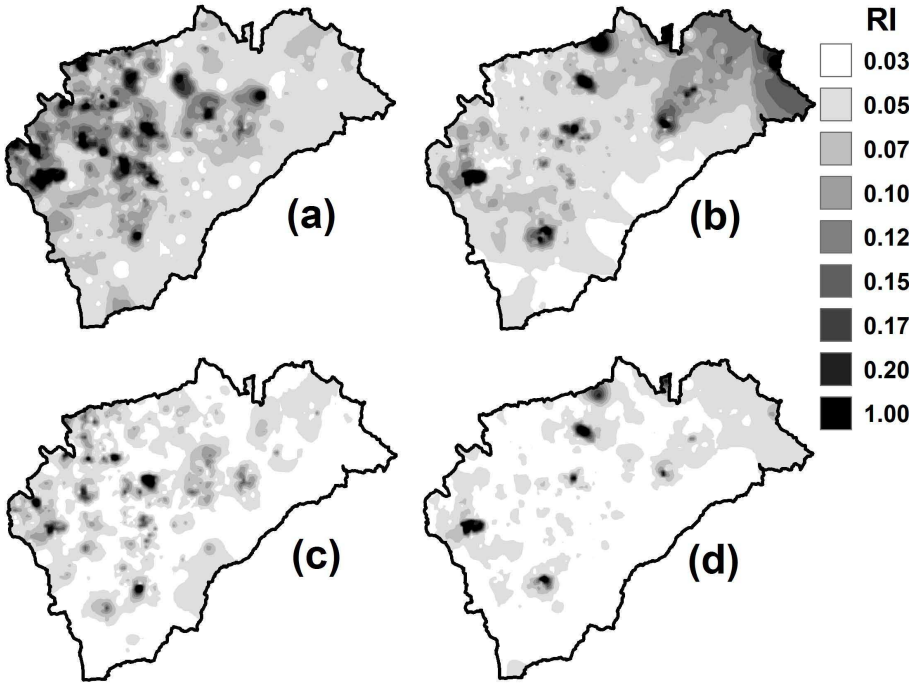

Figure 5: Interpolated $\bar{RI}$ maps obtained by models (**LEFT**) **BF** and (**RIGHT**) **IS** for the (**TOP**) **NM** and (**BOTTOM**) **WM** cases. The considered JNB classification is also reported.

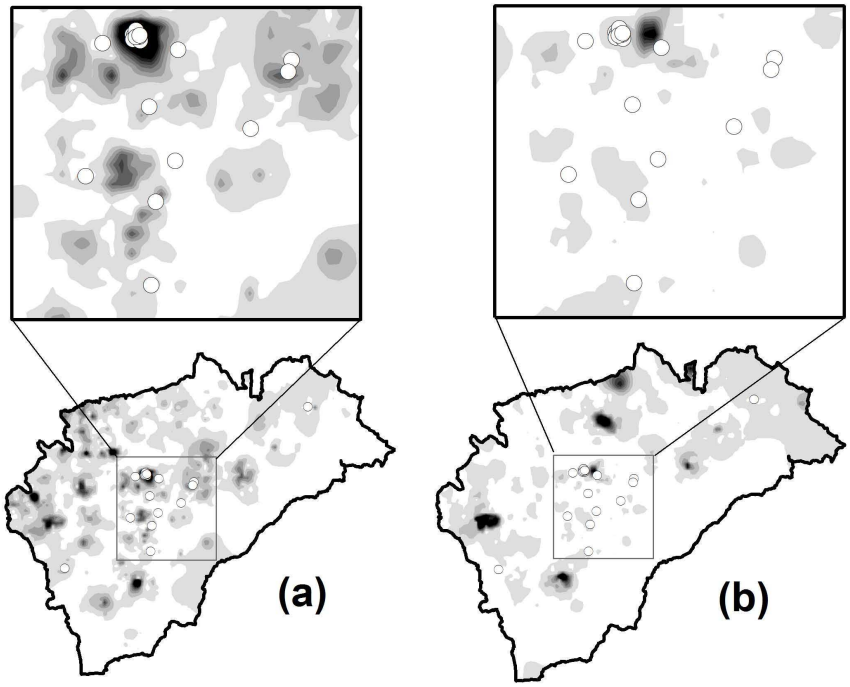

Figure 6: Interpolated $\bar{RI}$ maps obtained by models (**LEFT**) **BF** and (**RIGHT**) **IS** for the **WM** case. We also report, with white spots (∘), the location of the farms infected during the 1997-98 CSF epidemic in Segovia. Furthermore, we present, in the square region, a zoom of the zone where most of those farms are situated (except two of them).

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Parameter description	**Dist./Val.**	**Ref.**
Daily transmission parameter $\beta_{\text{far}}/\beta_{\text{fat}}/\beta_{\text{ftf}}$	0.7/0.4/0.5	[18]
Daily PI due to local spread	Table 2	[14]
PI due to vehicles transporting infected pigs	BN(0.011)	[39]
PI due to vehicles transporting products	BN(0.0068)	[39]
PI due to infectious SDA persons	BN(0.0065)	[39]
Daily PD of the index case	BN(0.03)	[14]
Daily PD due to clinical signs	BN(0.06)	[14]
PD due to tracing	BN(0.95)	[23]
Maximum Daily PD in control zone	BN(0.98)	[12]
Maximum Daily PD in surveillance zone	BN(0.95)	[12]
PR of animal movements on detected farms	BN(0.99)	[12]
PR of vehicle movements on detected farms	BN(0.95)	[12]
PR of SDA movements on detected farms	BN(0.80)	[12]
PR of animal movements in zoned farms	BN(0.95)	[12]
PR of vehicle movements in zoned farms	BN(0.90)	[12]
PR of SDA movements in zoned farms	BN(0.70)	[12]
PR of movements of non zoned farms	BN(0.40)	[12]
PT of animal movements	BN(0.99)	[12]
PT of vehicle movements	BN(0.70)	[12]
PT of SDA movements	BN(0.40)	[12]
Duration of general movement restriction	30	[23]
Duration of control and surveillance zones	30 and 40	[23]
Radius (km) of control and surveillance zones	3 and 10	[23]
Maximum number of daily traced farms	PO(60)	[12]
Maximum number of daily depopulated farms	PO(20)	[12]
Delay to repopulate a depopulated farm	PO(90)	[12]
Delay to depopulate farms	Table 3	[10]
Tracing period	60	[23]
Latent period	PO(7)	[14]
Incubation period	PO(21)	[14]
DNC with integrator vehicles	PO(0.4)	[14]
Number of farms visited by an INT vehicle	PO(4)	[12]
DNC with SDA persons	PO(0.3)	[14]
Number of farms visited by SDA persons	PO(3)	[12]

Table 1: Summary of the parameters used by the Be-FAST model (except those referring to farms and transport of pigs, presented in Section 3.2). From Left to Right: short parameter description; distribution and value (**Dist./Val.**) considered for the experiments reported in Section 4; and literature reference (**Ref.**). We have used the following abbreviations: PI=Probability of Infection; PD=Probability of Detection; PR=Probability of Restriction; PT=Probability of Tracing; DNC=Daily Number of Contacts; PO(X)=Poisson distribution with mean X; BN(X)=Bernoulli distribution with mean X.

Table 2: Interpolation points used to compute $LSM(x)$, the Daily probability of CSFV infection (DPCI), in function of the farms distance x (in meter) [15].

Distance in meter	0	150	250	500	1000	2000
DPCI	0.02	0.014	0.009	0.0038	0.0019	0

ND	0	1	2	3	4	5	6	7	8
Prob.	0.11	0.58	0.2	0.06	0.04	0.004	0.003	0.0015	0.0015

Table 3: Probability distribution (Prob.) of the number of days (ND) to wait before depopulating a detected farm [10].

Number of days	1	5	10	13	15	20	22
Weight	0.001	0.03	0.17	0.55	0.7	0.95	1

Table 4: Weight coefficient of the contaminated farms, in function of the delay after the farm infection (in days), used in our simulations with the InterSpread Plus model.

Distance (km)	15	30	45	60	80	120
Probability of movement	0.4	0.29	0.18	0.07	0.04	0.02

Table 5: Probability distribution of selecting a destination movement farm, in function of the distance in km, used in our simulations with the Inter Spread model.

	C. Time		Route				Measure		
Model	**NM**	**WM**	*LS*	*INT*	*SDA*	*TA*	*CS*	*ZO*	*TR*
BF	28000	4000	54	26	14	6	47	30	23
IS	14500	11000	51	13	10	26	38	50	12
REAL	-	-	52	25	16	7	44	28	28

Table 6: Results obtained when solving the **NM** and **WM** cases considering models **BF** and **IS**. In **C. Time** columns, we report the computational times, in seconds, needed to solve each case. In **Route** columns , we show the proportion (in %) of infection due to each CSFV route obtained by considering the **NM** case. The routes are: Local spread (*LS*), integrator vehicles (*INT*), SDA people (*SDA*) and transport of animals (*TA*). In **Measure** columns, we present the proportion (in %) of detection of contaminated farms due to each control measure obtained by considering the **WM** case. Control measures are: observation of clinical signs (*CS*), zoning (*ZO*) and tracing (*TR*). We also report, in line **REAL**, the proportions observed during real epidemics occurring in 1997-98 in Netherlands [11], in the **Route** columns, and in 2001-02 in Cataluña, Spain [1], in the **Measure** columns.

MD	**OP**	Mean	Min.	PI[2.5%]	Q1	Q2	Q3	PI[97.5%]	Max.
				NM					
BF	*NF*	32	1	1	4	16	40	122	339
IS	*NF*	58	1	1	7	33	84	255	523
				WM					
BF	*NF*	3.3	1	1	1	2	3	14	53
BF	*DR*	63	14	25	38	51	80	178	428
IS	*NF*	4.6	1	1	1	1	3	34	68
IS	*DR*	79	14	28	38	54	81	326	729
KS	*NF*	7.5	1	-	-	-	-	-	56
KS	*DR*	84	20	-	-	-	-	-	230

Table 7: Number of infected farms (NF) and epidemic duration (DR) obtained by considering the **NM** and **WM** cases and models (**MD**)**BF** and **IS**. For each output (**OP**), we present its mean, minimum (Min.) and maximum (Max.) values, its 95% Prediction Interval lower (PI[2.5%]) and upper (PI[97.5%]) bound, and its quartiles (Q1, Q2 and Q3).

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