# Supplement B – Model Documentation [1]

## CSFMM – Classical Swine Fever Management Model

The following documentation details the structure of the model as implemented in C++ programming language. The description orients to the ODD protocol (Overview, Design, Details) for documentation of complex models (Grimm et al., 2006. A standard protocol for describing individual-based and agent-based models. Ecol.Modell. 198, 115-126) and extends the OD parts already provided in the manuscript. Description focuses on the model version as applied to the presented simulations – a full featured description of the CSFMM may be found at (EcoEpi, 2011).

### *Purpose*

The CSFMM was developed to evaluate different aspects of CSF-outbreak management by simulating the geographical spread of the infection on a "landscape" of pig herds.
The formulation of model rules on how the disease spreads through an area as well as on how different management measures interfere with this spread is determined by the existing expert concepts. The simulation tool collates the relevant expert rules on the very grainy basis thus the outbreak dynamics seen in the model are emerging bottom-up from the conceptual model input. The main purpose of the modelling initiative is to test suggested management concepts or control schemes given the state-of-the-art knowledge on the disease.

### *Overview*

The CSFMM is a spatially explicit, stochastic, state-transition model comparable to several similar models (Bates et al., 2003;Garner and Beckett, 2005;Harvey et al., 2007).
The model construction orients to the approach of the more generic NAADSM (Harvey et al., 2007). The description was prepared to parallel the model documentation of these authors to enhance comparability although the CSFMM was not a reimplementation of the former and its focus is exclusively on CSF management problems.
The model is organised in an object-oriented manner to enhance efficient alterations according to simulation protocols on the level of control activities and their interaction.
In CSFMM, disease spread occurs between pig herds at specified locations, and is dependent on relative locations and distances between herds. After introduction of the virus into the herd, the infection follows a predictable cycle over time, moving the herd from one disease state to the next. This cycle may be interrupted by intervention of disease control mechanisms. Stochastic decisions drive all processes within the model for which empirical probability distributions are reported (i.e. detection, spread, testing).
The model reflects an administrative border between two halves of the simulation area that allow for alternative cooperation scenarios with regards to the adjustment of control and mitigation measures in both subareas.
*The components and input parameters of the model are described in the following sections: Section organisation, Section disease, Section spread, Section disease detection, Section tracing out, Section control measures, Section priorities of actions and Section costs.*

[1] Version with different densities and different management practice on to sides of an assumed border (Documentation derived from template: Version 8.0 October 2010, see EcoEpi 2011)

## *Organisation*

### Entities, state variables, scales

The CSFMM was formulated with two hierarchical entities: herd and landscape.

The low-level entities are individual herds and the transmission of the infection is followed on the herd level (cf. units in (Harvey et al., 2007). Animals inside a herd are reflected by numbers and within herd spread follows deterministic epidemic dynamics (e.g. (Klinkenberg et al., 2003).
The state variables of the herd entities that are stochastically pre-assigned during initialisation are its geographical position (x,y coordinates; random distribution), and its size (stocking number; see eq.1). Additionally, each herd is assigned an initial age (time since last restocking).
Disease state variables reflect the herd's CSF status (susceptible, infected, infectious), and whether it is involved in the outbreak (detected or not detected, number of infected or sero-converted animals) or any control activity (standstill zone, surveillance zone, pre-emptive culling, vaccination, tracing or testing).
The herd size is assumed to be static: herd size is not altered by the movement of animals. Only when a herd is destroyed or not restocked the number of animals will be affected (i.e. herd gets empty). Finished herds [**Par**: DaysNeededTillSell] are instantaneously restocked assuming slaughter of all pigs and disinfection i.e. the age and infection features are reset.

The second level entity is the landscape (simulation area) that maintains information on the whole population, the density and the actual stage of control measures (i.e. outbreak detected, or final success). The landscape comprises two subareas arranged horizontally above and below a line that represents an administrative border. Both subareas of the landscape are independently initialised at the beginning of each simulation by distributing a number of herds per sq km [**Par**: HerdDensity] and the realisation of an average herd size [**Par**: PigsPerHerd] following the distribution:

eq.1 Herd size = PigsPerHerd/4 + random number between 0 and 1.5 * PigsPerHerd
(e.g.: if PigsPerHerd=1000; then herd size is between 250 and 1750)

### Scheduling

The model steps forward in time by one day. On each simulation day, a regular sequence of processes is scheduled by the landscape:

*Init*: Generate farm landscape (herds with age, position, size)

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*Update Status*: Increment of the disease and vaccination status of each single herd.

*Pass Infection*: Evaluate potential transmission to next herds (regional and local)

*Detect Infection*: Test every infected herd whether detected today

*Sell:* Handle finished finisher herds (welfare or pre-tested slaughter);

*Make Priorities:* Organise scheduling of control measurements (culling & testing);

*Start Measure*: Perform control measures along the schedule up to daily capacity;

*Check Stop Condition*: Eradication; or maximum number of control days

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*Stop*: Output and Statistics

Process operations are performed synchronously for all related herds (i.e. resulting changes in status of a herd does not affect the process itself during one day).
At the end of the simulation run the overall statistics are prepared.

## Design Concepts

Emergence: The model is designed and parameterised to allow emergence of dynamics on the level of epizooty from simple and expert approved epidemiological details – rule-based modelling approach.

Stochasticity: Most dynamic processes are modelled stochastic. The reason is high uncertainty about very particular realisations for e.g. herd assemblages, daily disease transmission pathway and temporal order, detection distribution, traceability of the infection network, human compliance with regulations.

Table 1: Overview of stochastic components of the CSFMM

| **Process/Mechanism** | **Distribution** | **Parameter(s)** |
|---|---|---|
| Locations of herds | 2D uniform(0;p) | p: AreaSize (per subarea) |
| Stocking size (eq.1) | Uniform(1/4*p; 7/4*p) | p: PigsPerHerd (per subarea) |
| Detection by clinics | Uniform($p_u$;$p_o$) | $p_u$: MinFarmerDetectTime<br>$p_o$: MaxFarmerDetectTime |
| Regional transmission<br>- Distance (eq.2b) | Negative Exponential($p_1$)<br>Censored at $p_2$ | $p_1$: RegionalMeanInfectDist<br>$p_2$: RegionalMaxInfectDist |
| - Infection given contact | Bernoulli(p) | p: RegionalInfectProb |
| Movement ban | | |

| | | |
|---|---|---|
| - Standstill effect | Bernoulli(p) | p: StandstillEfficency |
| Local infection<br>- up to 500m<br>- up to 1000m | <br>Bernoulli($p_1$)<br>Bernoulli($p_2$) | <br>$p_1$: D500<br>$p_2$: D1000 |
| Traceability of infection network | Bernoulli(p) | p: TracingEfficiency |

# Submodels (ordered by schedule)

## *Disease*

### Disease dynamics within the basic entity (herd)

When a susceptible herd is infected, it transits instantaneously to incubating, and further to infectious according to the parameter describing herd incubation [**Par**: HerdIncubDays]; e.g. when an infected herd is assumed to be able to cause infections itself. When infected herd switches to infectious the infectious animal population of the herd is seeded randomly with 2-4 infectious pigs. Further growth of the infectious respective recovered cohort follows standard exponential growth with random increments [**Par**: EpidemicGrowthRate], i.e. for each virus positive pig one comes up with daily rate of 0.0822 (parameterised according to (Klinkenberg et al., 2003)).
The course of the disease in an infected herd is not altered by re-infection (i.e. no super-infections are modelled). Technically, a herd that receives an infection (e.g. by animal transport) could be regarded as immediately infectious. Treating newly infected herds as incubating, however, reflects the fact that most of the animals in the herd still need to progress through the early state of the infection.

### Transmission

According to the literature the model differentiates two modes of CSF transmission (Staubach et al., 1997;Stegeman et al., 2002;Ribbens et al., 2004): Distance dependent or local transmission refers to all processes that cause decreasing risk by distance in the vicinity of an outbreak herd (e.g. insects, children, farmer's movement etc.) and is usually attributed to surroundings up to 500-1000m (Staubach et al., 1997;Stegeman et al., 2002). Distance independent or regional transmission refers to routes by which the risk of transmission does not depend on this distance (Lorry or service personal moving around (Ribbens et al., 2004)). Any infected herd that is no longer incubating is assumed infectious i.e. is capable of spreading disease.

<u>Local transmission:</u>

Local transmission summarizes distance dependent transmission events. These are associated to any neighbourhood transportation of the virus making the infection risk continuously decreasing by distance from the source.
According to the analysis by Stegeman et al. (2002) two parameters for local transmission are used (Table 1): An infectious herd passes the infection either of its neighbours according to a Bernoulli probability up to 500m [**Par**: D500] and further up to 1000 meters [**Par**: D1000]. Local transmissions are recorded as such but cannot be identified during tracing investigations.

Regional transmission:

Regional transmission simulates distance independent virus transport (Staubach et al., 1997) or "direct contact" spread (Harvey et al., 2007). The scale of the transmission events is "regional" i.e. they may cover large parts of the pig area without decreasing final risk of infection.

The regional transmission occurs from an infectious source herd according to a twofold random procedure: First, on each simulation day, a distance is randomly drawn from the regional distance distribution, i.e. negative exponential with specified mean [**Par**: RegionalMeanInfectDist], and up to a specified maximum distance [**Par**: RegionalMaxInfectDist] but beyond 1000m. Distances are calculated according to the Euclidean metric.

eq.2b Distance = negexp(P->RegionalMeanInfectDist); on 1≤ Dist.≤ RegionalMaxInfectDist

With the resulting distance a geographic position of a recipient herd is searched that is closest by the randomly drawn distance. If necessary, the recipient is randomly selected out of multiple, evenly matching candidates.

If the recipient herd is not susceptible, or was already destroyed, the contact does not occur. If the recipient herd is susceptible the model randomly determines whether an infectious contact happens based on the regional transmission probability [**Par**: RegionalInfectProb]. Then the recipient status becomes infected.

Successful transmission events are recorded and can be identified later during tracing investigations. The number of animals in a movement is not considered (Harvey et al., 2007).

## *Detection*

Infected herds are detected by routine check for clinical suspicion, routine testing according to surveillance schemes, or targeted testing after successful establishment of a contact by tracing investigations or diagnostic protocols.

There are no false-positive detections in model.

The order of potential detection in the model is:

D1) Tracing related tests (diagnostic test; census or sample)
D2) Visit according to surveillance scheme (vet)
D3) Otherwise routine daily check (farmer)

Only infectious herds are detected by D2 and D3. D1 can detect even earlier according to the rtRTPCR test characteristics. After detection the herd is designated as detected and measures that are dependent on detection are initiated subsequently, e.g. tracing of backward and forward contacts will be schedule for the next day. Dependent on border scenario first detection is handled independent for both subareas of the landscape.

### Basic detection

If a herd gets infected a regular day post infection is fixed for detection. The value is randomly drawn of the interval [**Par**: MinFarmerDetectTime; **Par**: MaxFarmerDetectTime].

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DayOfFarmerDetection = today + MinFarmerDetectTime
        + integer[uniform[0,1] * (MaxFarmerDetectTime - MinFarmerDetectTime)];
```

The standard interval is parameterized according to Dutch outbreak data (Klinkenberg et al., 2005) and covers MinFarmerDetectTime = 21 and MaxFarmerDetectTime = 55 days post infection. The resulting distribution reread from the model generally mimics the data while particularities might change with outbreak realisation.

Any process that is supposed to alter detection modulates the regular detection date per herd. For example, as long as the first notification is missing the respective detection date per herd

is shifted later by 14 days [**Par**: FirstDetectDelay] (Stegeman et al., 1999b). Thus, during the high risk period the detection happens between day 35 and 69 (i.e. 5$^{th}$ to 10$^{th}$ week post infection; see (Fritzemeier et al., 2000))

### Farmer

Every day the model tests if a herd has reached the detection date. These notifications relate to the successful confirmation of the disease after farmers suspicion.

### Veterinary Service

After outbreak notification inside of designated surveillance zones once a week a targeted visit by an expert is assumed that shortens time till detection by a number of days [**Par**: SurveillanceDetectReduction].

### Tracing

If an infected herd was detected, next day tracing happens along the recorded transmission history. Tracing might establish the source contact (one step back; tracing backward) or any herd infected by the detected one (multiple one step forward; tracing forward). The actual identification of these links during tracing investigations is reflected by a probability value i.e. the tracing efficiency [**Par**: Forward/BackwardTracingEfficiency]. For example, assuming 100% tracing efficiency will guarantee the stepwise but full reconstruction of all regional transmission events. Traced herds are marked for diagnostic testing. Herds could be involved in multiple tracing investigations. Tracing only works if animals are present. If the herd traced next is already culled the tracing is terminated on that branch. Dependent on border scenario tracing of cross-border infection events may be possible or excluded.

### Diagnostic Testing

Diagnostic testing is simulated whenever the strategy requires diagnostic tests as basis for decisions on a herd status. Possible examples are: infected herds designated for testing from a traced link, herds designated for pre-emptive destruction, or final screening before the lift-up of restrictions. The diagnostic failures in confirmatory tests, e.g. after farmer suspicion, are not modelled explicitly but covered by the basic detection period. The model test system comprises of the following features:
Test target: virus positive test units [**Par**: TestSystem],
Test sensitivity: the usual probability to detect a truly positive test unit [**Par**: TestSensitivity]
Test operability: the time period necessary after infection until the test will notice CSF infections [**Par**: TestDaysTillDetect]
Test sample: The sampling in a tested herd covers all animals (census) [**Par**: TestSample]

## *Selling/Restocking*

For all herds that are not yet detected as infected and are not emptied, the time since simulated last restocking is checked against the maximum fattening age [**Par**: DaysNeededTillSell]. If maximum fattening age was reached the slaughter and immediate restocking is simulated by resetting of disease state and age. If the CSF outbreak in the simulation area was already detected, slaughter was completely excluded due to movement restrictions and the aging herd finally will be destroyed for welfare reasons.

## *Intervention measures*

Intervention measures refer to the establishment of surveillance and standstill zones. Before first notification none of these measures is activated in the model. Dependent on border scenario simulated zones overlap or are cut along the borderline.

### Surveillance zone

The circular area [**Par**: SurveillanceRadius] established around infected herds yet detected. Following detection of the centre herd the zone remains activated at least as long as strategy concept foresees [**Par**: SurveillanceDuration]. Subsequent detections during simulation might cause prolonged effective duration.
The intervention measure causes increased awareness e.g. by regular veterinary inspection. Thus likely more timely detection of an infected herd is based on an additional stochastic test once per week against a reduced basic detection time [**Par**: SurveillanceDetectReduction] (see chapter Detection).

### Standstill zone

The circular area [**Par**: StandstillRadius] established around infected herds yet detected. The zone is activated after time necessary for legislative process [**Par**: StandstillDelay]. Following detection of the centre herd the zone remains activated at least as long as strategy concept foresees [**Par**: StandstillDuration]. Subsequent detections during simulation might cause prolonged effective duration. This happens if any herd already in standstill zone A, became contained in a further newly established standstill zone B. In consequence, the standstill time [**Par**: StandstillDuration] is restarted also for the complete previous standstill zone A.
The intervention measure aims at halting of all animal movements. Thus, regional (or distances independent) transmission events initiated by the transmission process are suppressed with certain efficiency [**Par**: StandstillEfficiency] for contacts originating from or connect into active standstill zones. Any herd that becomes emptied by control measures will not be restocked if it is assigned to a standstill zone. Standstill is assumed not to influence the local neighbourhood of the centre herd which is intended to result in less favourable outcome for any strategy that does not apply control measures to the core neighbourhood of an outbreak herd. The basic motivation was inconsistent knowledge. Certain contact in the close vicinity of an outbreak, however, should also be excluded by movement ban in practice.
After lift-up of standstill restriction in an area all empty herds are assumed to be restocked immediately (Mangen et al., 2002).

## *Control measures*

Control measures simulated by CSFMM are stamping-out and pre-emptive culling. Before first notification none of these measures is activated in the model.

### Destruction

Immediately with the infected herd that is detected first, the destruction program starts. There are three cases where herds are destroyed in the model: stamping out of infected herds after detection, pre-emptive culling in a circular neighbourhood of detections (i.e. ring destruction), and welfare slaughter inside of standstill zones.
There is a limit to the number of animals that can be destroyed per day. This is referred to as the culling capacity [**Par**: CullCapacityPerDay]. Herds designated for destruction queue by priority (see list below). Every day queuing herds are culled upon saturation of the daily capacity. Queuing herds are not quarantined.

Stamping-out:

In the model all detections of infected herds are destroyed after a number of days reserved for preparation [**Par**: CullDelay]. Herds designated for stamping-out are assigned with the highest priority for destruction. Hence, they instantaneously will be destroyed. Therefore, if on one day the capacity limit is already reached by necessary stamping-out, it is assumed that ad hoc destruction capacity will become available to allow instantaneous destruction of all detected infected herds.

Pre-emptive culling:

Subsequent to stamping-out all herds in a circular area around the detected herd may be designated for pre-emptive culling in accordance with the simulated strategic concept. The size of the control area is defined by a radius [**Par**: CullRadius]. The culling zone is cleared by concentric distances from the centre either from inner to outer herds or vice versa. Herds designated for pre-emptive culling measures have second highest priority in the waiting list.

Welfare slaughter:

Finisher herds in standstill zone that reach fattening age remain in the model for an additional of number of days [**Par**: SelldayExtension]. If then the standstill has still not been lifted these herds are destroyed and not restocked. Welfare slaughter designation results in the lowest priority for culling.

## *Initialisation*

On the squared simulation area [**Par**: AreaSize] two horizontal subareas are determined (i.e. AreaSize * 0.5 AreaSize). Independently for both subareas herds are distributed randomly according to herd density parameterization [**Par**: HerdDensity]. Herds are populated according to mean herd size parameter [**Par**: PigsDensity] randomly drawn between 26%-175% the parameter value. Each herd is randomly assigned with a fattening age up to a maximum [**Par**: DaysNeededTillSell]. The herd in the lower subarea that is closest to the geometric point horizontally centred and 10km apart of the borderline is seeded as infected.

## *References*


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