

CSFMM – Classical Swine Fever Management Model

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42 **Documentation – Classical Swine Fever Management Model**

43 The following documentation details the structure of the model as implemented in C++
44 programming language. The description orients to the ODD protocol (Overview, Design,
45 Details) for documentation of complex models (Grimm et al., 2006. A standard protocol for
46 describing individual-based and agent-based models. *Ecol.Modell.* 198, 115-126) and extends
47 the OD parts already provided in the manuscript.

48 **Purpose**

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

57 **Overview**

58 The CSFMM is a spatially explicit, stochastic, state-transition model comparable to several
59 similar models (Bates et al., 2003; Garner and Beckett, 2005; Harvey et al., 2007).
60 The model construction orients to the approach of the more generic NAADSM (Harvey et al.,
61 2007). The description was prepared to parallel the model documentation of these authors to
62 enhance comparability although the CSFMM was not a reimplementations of the former and
63 its focus is exclusively on CSF management problems.
64 The model is organised in an object-oriented manner to enhance efficient alterations
65 according to simulation protocols on the level of control activities and their interaction.
66 In CSFMM, disease spread occurs between pig herds at specified locations, and is dependent
67 on relative locations and distances between herds. After introduction of the virus into the
68 herd, the infection follows a predictable cycle over time, moving the herd from one disease
69 state to the next. This cycle may be interrupted by intervention of disease control
70 mechanisms. Stochastic decisions drive all processes within the model for which empirical
71 probability distributions are reported (i.e. detection, spread, testing).
72 *The components and input parameters of the model are described in the following sections:*
73 *Section organisation, Section disease, Section spread, Section disease detection, Section*
74 *tracing out, Section control measures, Section priorities of actions and Section costs.*

75 **Organisation**

76 **Entities, state variables, scales**

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

78
79 The low-level entities are individual herds and the transmission of the infection is followed on
80 the herd level (cf. units in (Harvey et al., 2007). Animals inside a herd are reflected by
81 numbers and within herd spread follows deterministic epidemic dynamics (e.g. (Klinkenberg
82 et al., 2003).

83 The state variables of the herd entities that are stochastically pre-assigned during initialisation
84 are its geographical position (x,y coordinates; random distribution), its production type (sows,
85 others), and its size (stocking number; see eq.1). Additionally, each herd is assigned an initial
86 age (time since last restocking).

87 Disease state variables reflect the herd's CSF status (susceptible, infected, infectious), and
88 whether it is involved in the outbreak (detected or not detected, number of infected or sero-
89 converted animals) or any control activity (standstill zone, surveillance zone, pre-emptive
90 culling, vaccination, tracing or testing).

91 The production type accounts for pure finishing herds and potential mixed type with regard to
92 meat production chain (e.g., sows and others). The herd size is assumed to be static: herd size
93 is not altered by the movement of animals. Only when a herd is destroyed or not restocked the
94 number of animals will be affected (i.e. herd gets empty). Finished herds [**Par**:
95 DaysNeededTillSell] are instantaneously restocked assuming slaughter of all pigs and
96 disinfection i.e. the age and infection features are reset.

97
98 The second level entity is the landscape (simulation area) that maintains information on the
99 whole population, the density and the actual stage of control measures (i.e. outbreak detected,
100 or final success). The landscape is initialised at the beginning of each simulation by
101 distributing a number of herds per sq km [**Par**: HerdDensity] and the realisation of an average
102 herd size [**Par**: PigsPerHerd] following the distribution:

103
104 eq.1 Herd size = PigsPerHerd/4 + random number between 0 and 1.5 * PigsPerHerd
105 (e.g.: if PigsPerHerd=1000; then herd size is between 250 and 1750)
106

107 **Scheduling**

108 The model steps forward in time by one day. On each simulation day, a regular sequence of
109 processes is scheduled by the landscape:
110

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

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,
vaccination & testing);

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

Check Stop Condition: Eradication; or lift-up etc. (depends on experiment)

Stop: Output and Statistics

111

112

113 Within process operations are performed synchronously for all related herds (i.e. resulting
114 changes in status of a herd does not affect the process itself during one day).

115 At the end of the simulation run the overall statistics are prepared.
116

117 **Design Concepts**

118 **Emergence**

119 The model is designed and parameterised to allow emergence of dynamics on the level of
 120 epizooty from simple and expert approved epidemiological details – rule-based modelling
 121 approach.
 122

123 **Stochasticity**

124 Most dynamic processes are modelled stochastic. The reason is high uncertainty about very
 125 particular realisations for e.g. herd assemblages, daily disease transmission pathway and
 126 temporal order, detection distribution, traceability of the infection network, human
 127 compliance with regulations.
 128

129 Table 1: Overview of stochasticity components of the CSFMM

Process/Mechanism	Distribution	Parameter(s)
Locations of herds	2D uniform(0;p)	p: AreaSize
Stocking size (eq.1)	Uniform(1/4*p; 7/4*p)	p: PigsPerHerd
Detection by clinics	Uniform(p _u ;p _o)	p _u : MinFarmerDetectTime p _o : MaxFarmerDetectTime
Regional transmission - Distance (eq.2b)	Negative Exponential(p ₁) Censored at p ₂	p ₁ : RegionalMeanInfectDist p ₂ : RegionalMaxInfectDist
- Infection given contact	Bernoulli(p)	p: RegionalInfectProb
Regional transmission - Standstill effect	Bernoulli(p)	p: StandstillEfficiency
Local infection - up to 500m	Bernoulli(p ₁)	p ₁ : D500
- up to 1000m	Bernoulli(p ₂)	p ₂ : D1000
Traceability of infection network	Bernoulli(p)	p: TracingEfficiency

130
 131
 132

133 **Submodels (ordered by schedule)**

134 ***Disease***

135 **Disease dynamics within the basic entity (herd)**

136 When a susceptible herd is infected, it transits instantaneously to incubating, and further to
137 infectious according to the parameter describing herd incubation [**Par**: HerdIncubDays]; e.g.
138 when an infected herd is assumed to be able to cause infections itself. When infected herd
139 switches to infectious the infectious animal population of the herd is seeded randomly with 2-
140 4 infectious pigs. Further growth of the infectious respective recovered cohort follows
141 standard exponential growth with random increments [**Par**: EpidemicGrowthRate], i.e. for
142 each virus positive pig one comes up with daily rate of 0.0822 (parameterised according to
143 (Klinkenberg et al., 2003)).

144 The course of the disease in an infected herd is not altered by re-infection (i.e. no super-
145 infections are modelled). Technically, a herd that receives an infection (e.g. by animal
146 transport) could be regarded as immediately infectious. Treating newly infected herds as
147 incubating, however, reflects the fact that most of the animals in the herd still need to progress
148 through the early state of the infection.

149 **Transmission**

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

159 Local transmission

160 Local transmission summarizes distance dependent transmission events. These are associated
161 to any neighbourhood transportation of the virus making the infection risk continuously
162 decreasing by distance from the source.

163 According to the analysis by Stegeman et al. (2002) two parameters for local transmission are
164 used (Table 1): Occurrence of local transmissions are Bernoulli distributed and specified up to
165 500m [**Par**: D500] and further up to 1000 meters [**Par**: D1000]. Local transmissions are
166 recorded as such but cannot be identified during tracing investigations.

167 Regional transmission

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

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

178
 179 uniform:
 180 eq.2a $Distance = 1 + uniform[0;1] * (P \rightarrow RegionalMaxInfectDist - 1)$
 181 negative exponential:
 182 eq.2b $Distance = negexp(P \rightarrow RegionalMeanInfectDist)$; on $1 \leq Dist. \leq RegionalMaxInfectDist$
 183
 184 With the resulting distance a geographic position of a recipient herd is searched that is closest
 185 by the randomly drawn distance. If necessary, the recipient is randomly selected out of
 186 multiple, evenly matching candidates.
 187 If the recipient herd is not susceptible, or was already destroyed or protected by vaccination,
 188 the contact does not occur. If the recipient herd is susceptible the model randomly determines
 189 whether an infectious contact happens based on the regional transmission probability [**Par**:
 190 *RegionalInfectProb*]. Then the recipient status becomes infected.
 191 Successful transmission events are recorded and can be identified later during tracing
 192 investigations. The number of animals in a movement is not considered (Harvey et al., 2007).

193 **Detection**

194 Infected herds are detected by routine check for clinical suspicion, routine testing according to
 195 surveillance schemes, or targeted testing after successful establishment of a contact by tracing
 196 investigations or diagnostic protocols.
 197 There are no false-positive detections in model.
 198 The order of potential detection in the model is:
 199 D1) Tracing related tests (diagnostic test; census or sample)
 200 D2) Visit according to surveillance scheme (vet)
 201 D3) Otherwise routine daily check (farmer)
 202 Only infectious herds are detected by D2 and D3. D1 can detect even earlier according to the
 203 assumed diagnostic test characteristics. After detection the herd is designated as detected and
 204 measures that are dependent on detection are initiated subsequently, e.g. tracing of backward
 205 and forward contacts will be schedule for the next day.

206 **Basic detection**

207 If a herd gets infected a regular day of its detection is fixed. The value is randomly drawn of
 208 the interval [**Par**: *MinFarmerDetectTime*; **Par**: *MaxFarmerDetectTime*].
 209 $DayOfFarmerDetection = today + MinFarmerDetectTime$
 210 $+ integer[uniform[0,1] * (MaxFarmerDetectTime - MinFarmerDetectTime)]$;
 211 The standard interval is parameterized according to Dutch outbreak data (Klinkenberg et al.,
 212 2005) and covers *MinFarmerDetectTime* = 21 and *MaxFarmerDetectTime* = 55 days post
 213 infection. The resulting distribution reread from the model generally mimics the data while
 214 particularities might change with outbreak realisation.
 215 Any process that is supposed to alter detection modulates the regular detection date per herd.
 216 For example, as long as the first notification is missing the respective detection date per herd
 217 is shifted later by 14 days [**Par**: *FirstDetectDelay*] (Stegeman et al., 1999b). Thus, during the
 218 high risk period the detection happens between day 35 and 69 (i.e. 5th to 10th week post
 219 infection; see (Fritzemeier et al., 2000))

220 **Farmer**

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

223 **Veterinary Service**

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

227 **Tracing**

228 If an infected herd was detected, next day tracing happens along the recorded transmission
229 history. Tracing might establish the source contact (one step back; tracing backward) or any
230 herd infected by the detected one (multiple one step forward; tracing forward). The actual
231 identification of these links during tracing investigations is reflected by a probability value i.e.
232 the tracing efficiency [**Par:** Forward/BackwardTracingEfficiency]. For example, assuming
233 100% tracing efficiency will guarantee the stepwise but full reconstruction of all regional
234 transmission events. Traced herds are marked for diagnostic testing. Herds could be involved
235 in multiple tracing investigations. Tracing only works if animals are present. If the herd traced
236 next is already culled the tracing is terminated on that branch.

237 **Diagnostic Testing**

238 Diagnostic testing is simulated whenever the strategy requires diagnostic tests as basis for
239 decisions on a herd status. Possible examples are: infected herds designated for testing from a
240 traced link, herds designated for slaughter or pre-emptive destruction, companion test during
241 vaccine administration, or final screening before the lift-up of restrictions. The diagnostic
242 failures in confirmatory tests, e.g. after farmer suspicion, are not modelled explicitly but
243 covered by the basic detection period. The model supposes different diagnostic test systems to
244 consider basically different strategy concepts simultaneously.

245 The test system comprises of the following features:

246 Test target: virus or antibody positive test units [**Par:** TestSystem],

247 Test sensitivity: the usual probability to detect a truly positive test unit [**Par:** TestSensitivity]

248 Test operability: the time period necessary after infection until the test will notice CSF
249 infections [**Par:** TestDaysTillDetect]

250 Test sample: The sampling in a tested herd either covers all animals (census) or a randomly
251 selected part according to a specified sampling scheme e.g. accounting for herd size [**Par:**
252 TestSample]

253 **Selling/Restocking**

254 For all herds that are not yet detected as infected and are not emptied, the time since simulated
255 last restocking is checked against the maximum fattening age [**Par:** DaysNeededTillSell]. If
256 maximum fattening age was reached the slaughter and immediate restocking is simulated by
257 resetting of disease state and age. If the CSF outbreak in the simulation area was already
258 detected, then in accordance with the simulated strategy concept selling might be preceded by
259 a mandatory diagnostic test with false negative tests being recorded, or selling might be
260 completely excluded due to movement restrictions. In the latter the aging herd finally will be
261 destroyed for welfare reasons. Sold herds produce zero loss record.

262 **Intervention measures**

263 Intervention measures refer to the establishment of surveillance and standstill zones. Before
264 first notification none of these measures is activated in the model.

265 **Surveillance zone**

266 The circular area [**Par**: SurveillanceRadius] established around infected herds yet detected.
267 Following detection of the centre herd the zone remains activated at least as long as strategy
268 concept foresees [**Par**: SurveillanceDuration]. Subsequent detections during simulation might
269 cause prolonged effective duration.

270 The intervention measure causes increased awareness e.g. by regular veterinary inspection.
271 Thus likely more timely detection of an infected herd is based on an additional stochastic test
272 once per week against a reduced basic detection time [**Par**: SurveillanceDetectReduction] (see
273 chapter Detection).

274 **Standstill zone**

275 The circular area [**Par**: StandstillRadius] established around infected herds yet detected. The
276 zone is activated after time necessary for legislative process [**Par**: StandstillDelay]. Following
277 detection of the centre herd the zone remains activated at least as long as strategy concept
278 foresees [**Par**: StandstillDuration]. Subsequent detections during simulation might cause
279 prolonged effective duration. This happens if any herd already in standstill zone A, became
280 contained in a further newly established standstill zone B. In consequence, the standstill time
281 [**Par**: StandstillDuration] is restarted also for the complete previous standstill zone A.

282 The intervention measure aims at halting of all animal movements. Thus, regional (or
283 distances independent) transmission events initiated by the transmission process are
284 suppressed with certain efficiency [**Par**: StandstillEfficiency] for contacts originating from or
285 connect into active standstill zones. Any herd that becomes emptied by control measures will
286 not be restocked as long it is assigned to a standstill zone. Standstill is assumed not to
287 influence the local neighbourhood of the centre herd which is intended to result in less
288 favourable outcome for any strategy that does not apply control measures to the core
289 neighbourhood of an outbreak herd. The basic motivation was inconsistent knowledge.
290 Certain contact in the close vicinity of an outbreak, however, should also be excluded by
291 movement ban in practice.

292 After lift-up of standstill restriction in an area all empty herds are assumed to be restocked
293 immediately (Mangen et al., 2002).

294 **Control measures**

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

298 **Destruction**

299 Immediately with the infected herd that is detected first, the destruction program starts. There
300 are three cases where herds are destroyed in the model: stamping out of infected herds after
301 detection, pre-emptive culling in a circular neighbourhood of detections (i.e. ring destruction),
302 and welfare slaughter inside of standstill zones.

303 There is a limit to the number of animals that can be destroyed per day. This is referred to as
304 the culling capacity [**Par**: CullCapacityPerDay]. Herds designated for destruction queue by
305 priority (see list below). Every day queuing herds are culled upon saturation of the daily
306 capacity. Queuing herds are not quarantined.

307 Stamping-out:

308 In the model all detections of infected herds are destroyed after a number of days reserved for
309 preparation [**Par**: CullDelay]. Herds designated for stamping-out are assigned with the

310 highest priority for destruction. Hence, they instantaneously will be destroyed. Therefore, if
311 on one day the capacity limit is already reached by necessary stamping-out, it is assumed that
312 ad hoc destruction capacity will become available to allow instantaneous destruction of all
313 detected infected herds.

314 Pre-emptive culling:

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

320 Welfare slaughter:

321 Finisher herds in standstill zone that reach fattening age remain in the model for an additional
322 of number of days [**Par**: SellDayExtension]. If then the standstill has still not been lifted these
323 herds are destroyed and not restocked. Welfare slaughter designation results in the lowest
324 priority for culling or might be performed instantaneously.

325 **Vaccination**

326 Immediately with the infected herd that is detected first, the vaccination program starts with a
327 number of days reserved for preparation [**Par**: VacDelay]. Subsequently all herds in a circular
328 area around the detected herd (which is culled for emergency) are designated for vaccination.
329 The size of the control area is defined by radius [**Par**: VacRadius]. The vaccination is
330 operated by concentric distances from the centre either from inner to outer herds or vice versa.
331 There is a limit to the number of animals that can be vaccinated per day. This is referred to as
332 the vaccination capacity [**Par**: VacCapacityPerDay]. Herds designated for vaccination are
333 queued according to strategy design. Every day herds from the queue are vaccinated upon
334 saturation of the daily capacity. Queuing herds are not quarantined.
335 When a susceptible herd is vaccinated, it remains susceptible for a specified time until
336 immunity develops [**Par**: VacTimeTillImmune] which depends on the vaccine properties.
337 Then the herd becomes protected. Vaccine protection is assumed to be 100% effective
338 (“blocking immunity”): once a herd is protected, it cannot become infected.

339 Vaccination and infection:

340 By chance herds designated for vaccination may contract the infection either before vaccine
341 administration or later but before protection. The resulting state of these herds is defined
342 according to the first of the corresponding temporal state transitions:
343 If the infected (vaccinated) herd turns protected before becoming infectious, the infection is
344 neglected, i.e. if

$$345 \quad \text{DayOfVaccination} + [\mathbf{Par}: \text{VacTimeTillImmune}] < \text{DayOfInfection} + [\mathbf{Par}: \text{HerdIncubationDays}]$$

346
347
348 If the infected (vaccinated) herd turns infectious before becoming protected it proceeds as
349 infectious herd. If the herd reaches the protected state the model refers to it as partly protected
350 to cover simultaneously animals that already contracted the infection by within herd spread
351 and those that became protected by vaccination. As the infection cannot be spread further in a
352 herd that is partly protected, the herd turns to completely protected after a number of days
353 [**Par**: InfectiousDays]. As standard this model parameter refers to the mean infectious period
354 reported for naïve infected animals.

355 Vaccination and animal level:

356 If simulation experiments require detailed simulation of the within herd dynamics of the
357 infection in relation to vaccination effect then individual numbers of virus and antibody
358 positive pigs are equated according to standard epidemic model with exponential growth. If
359 an infected vaccinated herd turns (partly) protected, growth of virus positive is halted. After a
360 number of days [**Par**: InfectiousDays] the number of virus positives is set to zero.
361 If chronics have to be explicitly considered then after the time span of partly protection days
362 [**Par**: InfectiousDays] a random part is drawn of the virus positive animals at this day [**Par**:
363 PropChronics] and kept for ever, resulting in a herd with continued infectiousness but with
364 minimal number of animals.

365 **Initialisation**

366 On the squared simulation area [**Par**: AreaSize] herds are distributed randomly (or by given
367 geographic attribute) according to herd density parameterization [**Par**: HerdDensity]. Herds
368 are populated according to mean herd size parameter [**Par**: PigsDensity] randomly drawn
369 between 26%-175% the parameter value. Each herd is randomly assigned with a fattening age
370 up to a maximum [**Par**: DaysNeededTillSell]. The herd closest to the geometric centre is
371 seeded as infected.

372 **Costs**

373 Estimates of costs and losses are accumulated in the model to compare the economic
374 consequence of different strategic options. All monetary parameters (see Table
375 CostParameters) are given in Euro and relate to the individual animal unit. For destruction
376 measures bio-safety is assumed to increase the cost per animal unit (stamping-out and pre-
377 emptive culling) compared to the welfare slaughter of over-fattened animals. All cost
378 estimates for control application cover human resources and technical stuff (e.g. vaccine,
379 killing facilities)
380 Costs for diagnostic testing are based on pooled samples of 40 units.
381 For herds that are not restocked due to restriction, opportunity costs are considered as losses
382 per day and animal unit, targeting the market value of a finisher pig.
383

384 **Table Cost parameters**

385

If one animal is...	Unit cost in Euro	Unit
Destroyed (stamping-out + pre-emptive culling)	200	Per animal
Welfare slaughtered	150	Per animal
Vaccinated	6	Per animal
Not restocked (Opportunity cost)	0.5	Per day
Tested by RTPCR (pooled at 40)	3	Per animal

386

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