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1 Pig herd management and infection transmission dynamics: a
2 challenge for modellers.

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7 **Abstract**

8 The control of epidemics requires a thorough understanding of the complex interactions between pathogen trans-
9 mission, disease impact, and population dynamics and management. Mechanistic epidemiological modelling is
10 an effective way to address this issue, but handling highly structured and dynamic systems, remains challenging.
11 We therefore developed a novel approach that combines Multi-Level Agent-Based Systems (MLABS) with spatial
12 and temporal organization, allowing for a tuned representation of the transmission processes amongst the host
13 population. We applied this method to model the spread of a PRRSV-like virus in pig farms, integrating the
14 clinical consequences (conception and reproduction failures), in terms of animal husbandry practices. Results
15 highlighted the importance to account for spatial and temporal structuring and herd management policies in epi-
16 demiological models. Indeed, disease-related abortions, inducing reassignments of sows in different batches, was
17 shown to enhance the transmission process, favouring the persistence of the virus at the herd level. Supported by
18 a declarative Domain-Specific Language (DSL), our approach provides flexible and powerful solutions to address
19 the issues of on-farm epidemics and broader public health concerns. The present application, based on a simple
20 Susceptible-Exposed-Infected-Recovered (SEIR) model, opens the way to the representation of more complex
21 epidemiological systems, including more specific features such as maternally derived antibodies, vaccination, or
22 dual infections, along with their respective clinical consequences on the management practices.

23 **1 INTRODUCTION**

24 Understanding the mechanisms of pathogen spread in a highly structured population is a key
25 element for epidemic control. This requires capturing the spatial and social structures, defining

26 the contact rates between individuals and groups of hosts in the population. Livestock manage-
27 ment clearly illustrates that problematic, obeying predefined rules ensuring a balance between
28 animal welfare, good sanitary conditions, and productivity. The spread of pathogens in a pig
29 farm, managed with batch-rearing procedures, therefore represents an ideal application for the
30 integration of an innovative organizational pattern within a multi-level agent-based modelling
31 framework dedicated to epidemiological modelling (Sicard et al., 2021b).

32 To further understand the impact of batch management, housing, and possible deviations in herd
33 management practices on the spread of pathogens at different scales, and to identify realistic
34 levers, new modelling approaches had to be developed. In the era of open and reproducible
35 science, ensuring legibility, revisability, and flexibility of models is pivotal. The response provided
36 by the EMULSION framework, based on AI methods and complemented with an organizational
37 pattern, offers solutions to epidemiological modelling issues (Picault et al., 2019).

38 In a previous study, we first developed a model of swine influenza A in pig farms, highlighting
39 the impact of the spatio-temporal structure of the herd on the transmission dynamics and its
40 impact on virus spread and control based on EMULSION extended with an organizational
41 pattern (Sicard et al., 2021a). However, in this study, influenza infections were not considered
42 to have any consequence in terms of animal management. Therefore, the present study aims to
43 account for the interplay between infectious dynamics, clinical consequences, and management
44 practices. For this purpose, we developed an epidemiological model representing the spread of a
45 disease transmitted by direct contact between animals (e.g. porcine reproductive and respiratory
46 syndrome virus or porcine circovirus of type 2), and assuming clinical reproductive consequences
47 in sows leading to modifications of the management rules. This assumption would reflect the
48 situation early after introduction of Porcine Reproductive and Respiratory Syndrome (PRRSv)
49 virus in a farm.

50 To ensure realistic epidemiological modelling regarding field situations, including the contact
51 structure between animals and different observation levels (e.g. farm, herd, individual), agent-
52 based simulation (ABS) has proven its value (Roche et al., 2008). ABS provides methods for
53 handling behaviours, interactions, and tracking of individuals. For further explicit representation
54 of complex systems, multi-level agent-based simulation (MLABS) allows several scales (individ-
55 uals, groups, batches, populations, etc.) to be associated with agents endowed with their own

66 behaviours ([Mathieu et al., 2018](#)). Besides, MLABS makes it possible to separate procedural
67 knowledge (calculations and processes involved in stochastic epidemiological models, according
68 to the modelling paradigm and scale: e.g. compartmental models, individual-based, metapop-
69 ulations), from declarative knowledge (model structure, assumptions, description of groups and
70 processes, parameter values, initial conditions), as set out in symbolic AI ([Weyns, 2005](#); [Mathieu
71 et al., 2015, 2018](#)). This separation of concerns provides the ability to make models modular
72 and easy to use by defining independent processes (e.g. infection, population dynamics, trade
73 movements, detection) which can be coupled, rather than a representation with a single, huge
74 and tangled flow diagram.

75 We propose a prototype model architecture accounting for the complex interplay between
76 pathogen transmission dynamics and consequences of clinical cases on herd management, by
77 coupling a mechanistic multi-level agent-based modelling approach (EMULSION framework)
78 with specific organizational considerations, [including exceptions in management practices re-
79 lated with clinical consequences of infections in reproductive sows](#). The EMULSION modelling
80 framework enables the specification of different scenarios by varying the population dynamics in
81 the breeding sectors (e.g. batch management, exceptions). These scenarios were used to assess
82 the impact of clinical outcomes of infectious diseases on population and transmission dynamics
83 at the herd level. We illustrate this approach through a PRRSv-like disease spreading in a
84 fine-grained realistic pig farm model.

75 2 MATERIALS AND METHODS

76 2.1 Model overview

77 The management of the involved batches aligned with the procedures described in ([Sicard et al.,
78 2022](#)), such as sector allocation according to physiological state durations. To represent the
79 clinical reproductive consequences of infections in sows, a probability of insemination failure was
80 considered, [leading to potential batch downgrading for infected sows](#). Infection consequences
81 [were modulated upon different periods of gestation with specific impacts on the health status
82 of piglets at birth, including abortions, vertical transmission, and maternally derived antibodies
83 delivery](#). Furthermore, the model was able to represent batch management at a fine-grained
84 level, encompassing both litter and pen levels (Fig. 1), thus providing the ability to represent

85 zootechnical practices such as adoptions, pig gathering procedures, and sow renewal process.

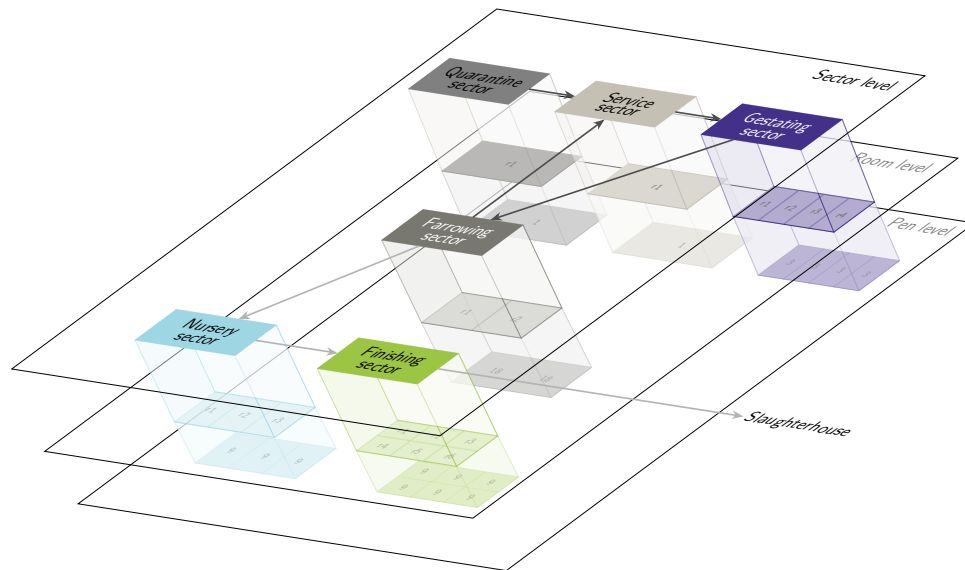


Figure 1: Representation of the three spatial levels: Sector, Room, and Pen levels. Each sector (Sector level) is further divided into rooms (r_n at the Room level), and each room is further subdivided into pens (Pen level, where the numbers correspond to the number of pens per room).

86 2.2 EMULSION Framework

87 The model was developed using the EMULSION framework (Picault et al., 2019), which is dedi-
88 cated to stochastic mechanistic epidemiological modelling. An essential concept of the framework
89 is the separation between knowledge representation (the model as a structured text), and the
90 simulation processes (provided by a generic engine which reads and executes the model descrip-
91 tion).

92 The EMULSION framework, extended with its organizational component (Sicard et al., 2021b),
93 was used to account for the complex herd structure in both space and time, including multi-
94 level aspects. An organization is an entity made up of groups to which individuals belong.
95 Organizations and groups encapsulate environments that correspond to spaces where agents are
96 located (either groups or individuals). The organizational pattern systematically describes three
97 levels: organization, group, and individual.

98 A particular feature of the pattern is its ability to be used recursively. In other words, a group
99 can itself be an organization (thus becoming a sub-organization) (Figure 2), thereby describing
100 multi-level dynamics and relationships between levels.

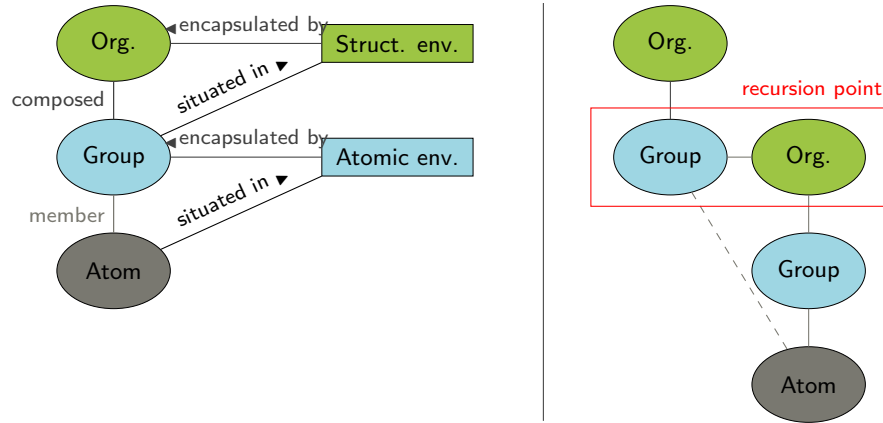


Figure 2: Structure of the organizational pattern. The agent *Organization* encapsulates an environment where agents *Group* are situated. Each agent *Group* encapsulates an environment where the atomic agents (atom) are situated. The pattern can be used recursively, i.e. an agent *Group* can itself be an organization. The environment in the pattern can be either spatial or social. (Sicard et al., 2021b)

101 2.3 Population dynamics

102 The pig production herd was raised according to a seven-batch-rearing system with a 21-day
103 between-batch interval, and all-in-all-out procedures, the main management practice held in
104 France, which was fully described in Sicard et al. (2022). Two subpopulations, breeding sows
105 and growing pigs, were represented, structured and managed according to husbandry constraints
106 (d'Agriculture de Bretagne, 2010). The batches remained consistent, i.e. all animals remain
107 within the same batch throughout their life cycle, being in the same physiological state at the
108 same time and obeying an all-in-all-out procedure.

109 Sows evolved through three physiological states over 147 days: insemination (34 days), gestating
110 (85 days) and farrowing/lactating (28 days). Growing pigs evolved through three stages over 182
111 days before being sent to the slaughterhouse: farrowing/suckling (28 days), post-weaning (40
112 days) and finishing (114 days) (Figure 3). Each physiological stage corresponded to a specific
113 physical sector of the farm. In the field, the duration spent in different states may vary, especially
114 due to variations in parturition timing. These variations can occur within a time window of two
115 days, either before or after the predicted date. However, the practice of all-in-all-out remains
116 observed on farms. This means that the timing of animal movement can be deterministically
117 scheduled in the model.

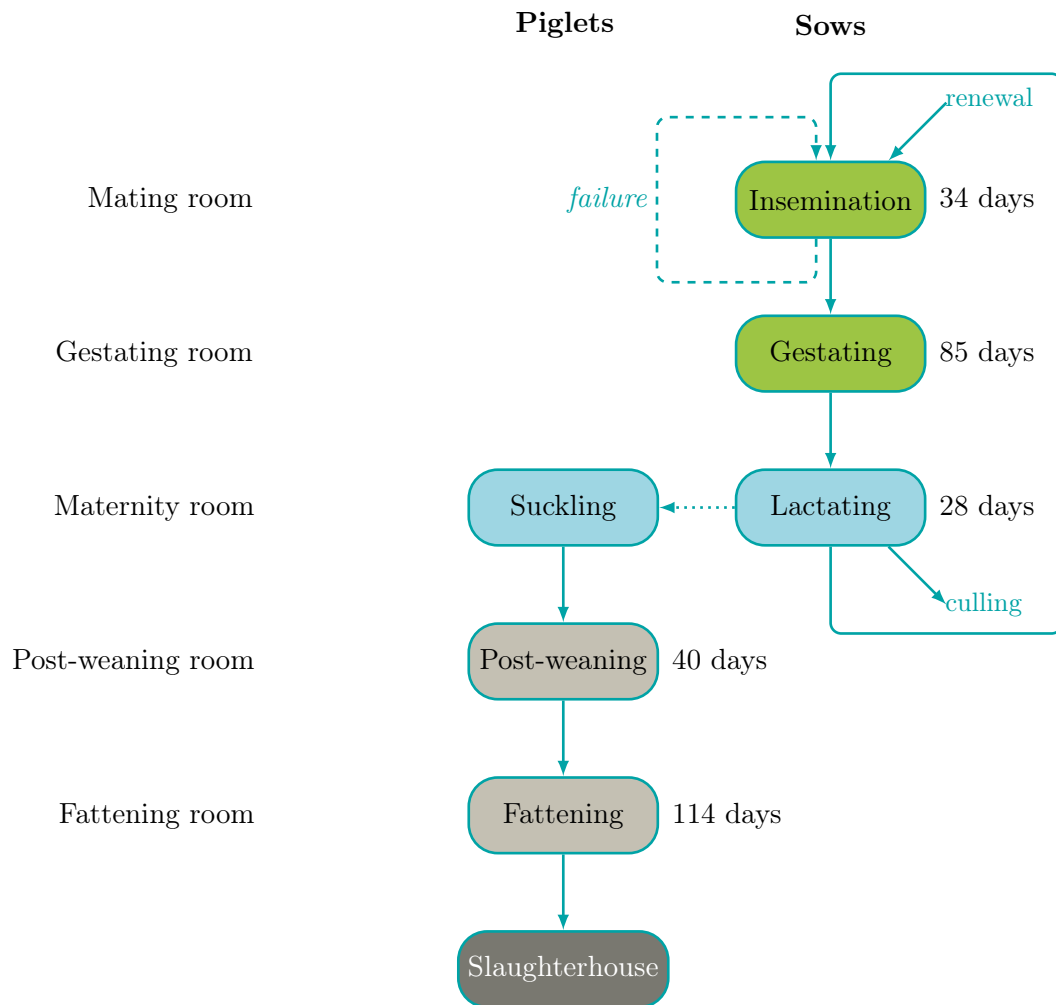


Figure 3: Illustration of the duration of physiological stages in relation to housing. The dotted arrow represents piglet production from sows and the dashed one represents sows that are retrograded to the previous batch in case of insemination failure.

118 The *housing* organization ensures that the spatial sectorial structure of the housing is adequate
 119 for the physiological needs of the individuals. The sectorial organizations are divided into down-
 120 stream levels corresponding to the rooms in the herd. Each level was considered an organization,
 121 which could be further subdivided into downstream sublevels. The rooms are subdivided into
 122 pens to represent the direct and indirect contact of animals within and between pens (Fig. 4).
 123 Batches were managed by several organizations: *Batches* for main herd management, *Litter* for
 124 making the link between breeding sows and their piglets, *Litter_group* for gathering purpose in
 125 nursery pens, and *Housing* specifying the exact location of each animal (or group of animals) in
 126 corresponding sectors, rooms, and pens.

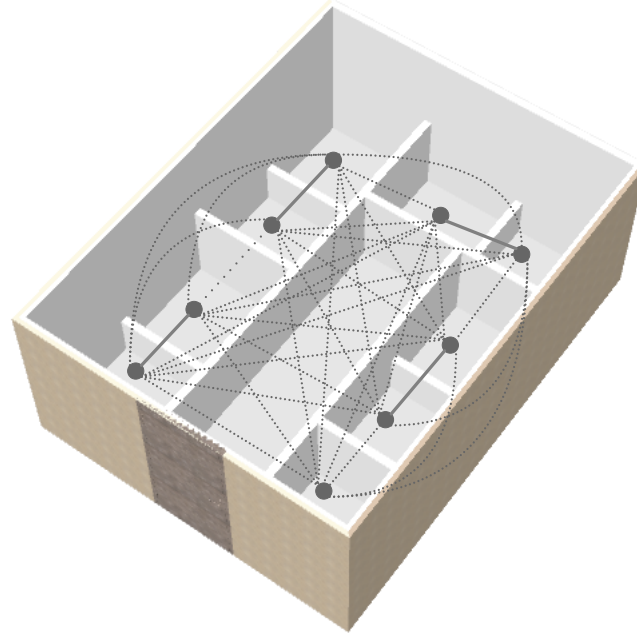


Figure 4: Representation of a room in the finishing sector: physical division into pens, including a network of contacts. It illustrates the model's ability to represent fine-grained contact networks, both direct contacts between adjacent pens, indicated by solid lines, and indirect contacts with other pens, shown as dotted lines.

127 At initialization, 98 (14 sow per batch) sows were homogeneously distributed among the 7-batch
128 organization. At farrowing, newborn piglets were assigned to the same batch and same pen
129 as their mother. The *litter* organization was designed as the dams and their relative piglets,
130 located in the same space (pens) in farrowing rooms. [The pen organization level included](#)
131 [determining the number of pens required to accommodate all sows in case of overcrowding due](#)
132 [to insemination failures or gestation-related abortions in other batches \(Figure 1\)](#). Sows were
133 alternatively placed in designated organizational spaces, while piglets were housed in the same
134 pen as their respective mothers during farrowing.

135 *litter_group* was designed to represent pig gathering policy in nursery rooms after weaning.
136 Indeed, pig litters are frequently gathered into larger groups within pens when entering the
137 nursery sector. In our model, it was assumed that each pen in the nursery rooms housed two
138 litters from the farrowing rooms. The location of the litters within the pens was managed by
139 one of the *housing* sub-organisations.

140 Herd renewal might be a factor influencing disease spread by introducing susceptible animals
141 into the system. In commercial pig production, sows are selected for replacement based on
142 productivity criteria. For example, old sows are known to have smaller litters, and farmers
143 cannot afford to keep sows that experience multiple gestation failures. In the present model, for
144 the sake of illustration, the decision to cull based on their condition (*condition_to_cull*) was
145 made :

- 146 • sows with parity higher than 5, or
- 147 • sows with more than 5 gestation failures.

148 The maximum number of sows that could be replaced at each batch-cycle was set to 2 and
149 adjusted to ensure a stable population in each batch, ranging between the initial number of
150 sows in the herd (14 sows per batch) and the total number of pens in farrowing room (18
151 pens). Sow replacement was managed as follows: a sow with parity rank higher than 5, or after
152 two unsuccessful inseminations, could be culled. The adjustment of the number of sows was
153 evaluated regardless of the reason for replacement, due to culling. The renewal was managed by
154 the *culling* state machine accounting for three states: *to_keep* corresponding to sows that will
155 be not renewed, *to_cull* corresponding to sows that will be renewed, and *culled* corresponding
156 to sows that leave the system. The decision on the status of the sows is made when entering in
157 farrowing room; after the lactation period, sows are culled and replaced by renewal susceptible
158 gilts for the next reproduction cycle.

159 Insemination failure was represented by the state machine *inseminationStatus*. On entering the
160 insemination sector (corresponding to the gestating state of the *physiologicalStep* state machine),
161 sows were inseminated (inseminate status of the statemachine *inseminationStatus*). 42 days (i.e.,
162 two batch intervals) after insemination, sows are checked for gestation, with a failure probability
163 defined as *proba_failure_ins*. Sows that were successfully inseminated were moved to *SuccessInf*
164 state. Sows that had failed insemination were retrograded from two previous batches. Owing
165 to the 7 batch-farrowing system, an insemination failure for a sow in batch N led to a transfer
166 into batch $N - 2$, for new insemination attempt. Such event will be next mentioned as a batch
167 reassignment event.

Parameter	Description	Value	Source
β	direct transmission rate	0.24 days ⁻¹	Rose et al. (2015)
β_{ind}	indirect transmission rate	$\beta/10$ days ⁻¹	Andraud et al. (2008)
γ	recovery rate	0.18 days ⁻¹	Nodelijk et al. (2000)
duration of state M	gamma law distribution	$\Gamma(\text{shape} = 3.6, \text{scale} = 1.35 \text{ days})$	Andraud et al. (2019)

Table 1: Table of epidemiological parameter values

168 2.4 Health states

169 Four health states were considered: animals protected by maternal immunity (M), susceptible
 170 (S), infectious (I), and recovered (R). These health states were managed by the state machine
 171 *health_state* (Figure 5). The state *M*, corresponding to a piglet protected by maternal immu-
 172 nity, was managed separately by the state machine *maternal_immunity*. The epidemiological
 173 parameters were based on a PRRSV-like disease, and are reported in the Table 1. Parameter β_{ind}
 174 represented the rate of transmission resulting from occasional contacts between individuals from
 175 adjacent pens. Parameter β represented the direct transmission between individuals. Parameter
 176 γ corresponded to the recovery rate, i.e., the rate at which individuals become recovered (R).
 177 The duration in state M was distributed according to a gamma distribution, after which pigs
 178 became fully susceptible.

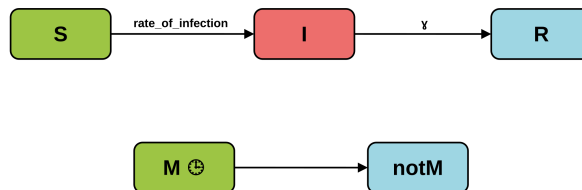


Figure 5: Representation of the two state machines: *health_state* (on the top) and *maternal_ - immunity* (on the bottom). A susceptible individual (S) becomes exposed (I) with a rate (rate_ - of_infection), and then recovers (R) with a rate γ . Piglets with maternal immunity (M) stay in the state M for a duration described in Table 1 and then lose their immunity. Maternal immunity provides protection against infection.

179 To account for the complex spatial structure of the animal housing, calculating the force of
 180 infection, including the direct pairwise contact in the pens, was a cumbersome task. To facilitate
 181 the representation of transmission routes and increase the flexibility of the contact structure,

182 a graphic-based approach was adopted. Specifically, the housing system was represented as
183 a graph, where the nodes corresponded to the physical environmental spaces such as pens,
184 corridors, and rooms, and the links represented the interactions between these spaces. The
185 links were weighted by the epidemiological information of each space. This approach provided
186 a comprehensive and flexible representation of the transmission dynamics within the housing
187 system (Fig. 4).

188 Specifically, each space in the housing system was associated with the number of infectious
189 animals it contained, and this information was propagated through the graph. The cumulative
190 information obtained from the graph was then used to compute the force of infection:

$$\text{force_of_infection} = \beta \times \text{info_total_I_my_pen} \quad (1)$$

191 where *info_total_I_my_pen* corresponded to a function that the EMULSION framework auto-
192 matically generates. This function retrieves the value of the total number of infectious individuals
193 (*total_I*) of the current space (*my_pen*).

194 Piglets' epidemiological status at birth was assumed dependent on the period of gestation the
195 sows were infected. Sow infected in the first third of their gestation produce susceptible piglets;
196 Sow infected in the second third of their gestation produce piglets infected through trans-
197 placental transmission; finally, piglets born to sows infected in the last phase of the gestation
198 period acquire maternally derived antibodies in the "M" state.

199 2.5 Scenarios

200 Four scenarios were established to represent several types of management, taking into account
201 the exchange of sows between batches in case of insemination failure or abortion, the type of
202 grouping in gestating, and the rate of occasional contact (Table 2). Each scenario was run
203 with 100 stochastic replicates over a period of 1500 days, including a burning period of two
204 reproductive cycles (2×147 days). The virus was introduced through an infected sow in batch
205 1, at the beginning of the third reproductive cycle of the batch, assuming the introduction of an
206 infected gilt into the system (294 days). In terms of the allocation process, the gilt was assigned
207 to litter 1, indicating its location in room 1, pen 1 within the gestating sector.

Scenario	Description
Scenario 1	Sows grouped by 6 without batch reassignment
Scenario 2	Sows grouped by 6 with batch reassignment
Scenario 3	All-in-One grouped sows without batch reassignment
Scenario 4	All-in-One grouped sows with batch reassignment

Table 2: Description of the four scenarios. Each scenario corresponds to a combination of grouping type in the gestation sector (grouped by 6 or All-in-One), and batch management policies (batch reassignment due to insemination failure or batch stability)

208 3 RESULTS

209 The results provided a measure of the impact of management changes (grouping) of breeding
210 sows on the infectious dynamics. Scenarios with no grouping in the gestation sector showed a
211 weak impact of batch changes due to insemination failure. For the scenarios with β_{ind} of 0 and
212 $\beta/10$, the dynamic profiles were similar (Figure 6).

213 In the scenarios with β_{ind} of 0 (scenarios 3 and 4), the first peak occurred approximately 34
214 days after the virus was introduced and corresponded to the entry into the gestation sector. As
215 sows in the same batch were mixed, the virus spread rapidly within the batch. The second peak,
216 about 85 days after the first, corresponded to farrowing sector. The following peak, about 28
217 days later, corresponded to piglets entering the post-weaning sector. In the farrowing sector,
218 each pen contained one litter consisting of sow and her piglets, and the pens were assumed
219 independent, with no possible contact with neighbouring pens. With a β_{ind} value of 0, only
220 within-pen transmission occurred. Conversely, in the post-weaning sector, where pens were not
221 independent, litters were grouped in pairs in pens, and transmission occurred between adjacent
222 pens with $\beta_{ind} = \beta/10$. This demonstrated batch changes for infected sows following failed
223 insemination in the $n - 2$ batch in the insemination sector broke the infectious dynamic within
224 the batch.

225 The duration of infection was 56 days, which is longer than the period between entry into the
226 insemination sector and the detection of insemination failure (42 days). Therefore, a retrograded
227 infected sow could potentially infect other individuals, at least in the insemination sector, and
228 potentially as far as the gestating sector (if a sow was infected a few days before being retro-
229 graded, it would arrive in the gestating sector of its new batch at 36 days, and could be infectious
230 for about 20 days). For the scenarios without grouping, changes to nominal batch-rearing man-

231 agement did not have a notable impact on the transmission dynamics. For the scenarios with
232 grouping (per 6) in the gestating sector, exceptions to batch rearing substantially impacted the
233 infection dynamics, with transmissions occurring between non-adjacent pens in fully susceptible
234 groups of sows.

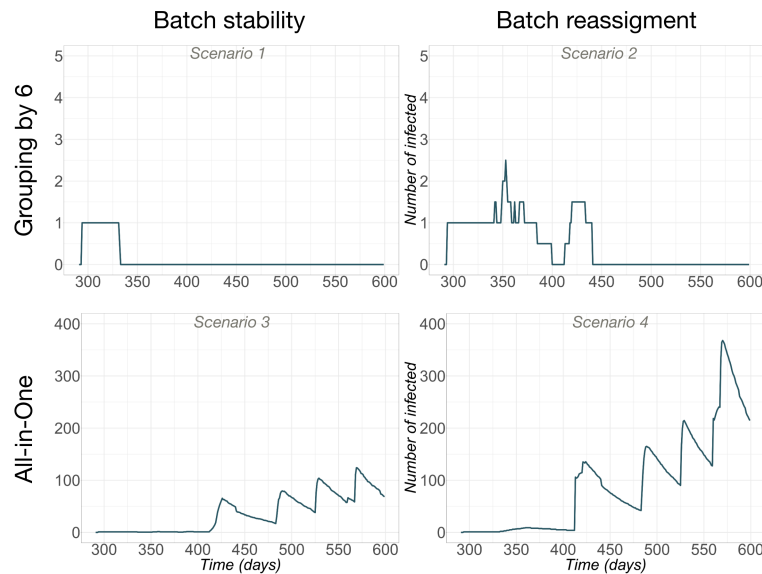


Figure 6: Infection dynamics for scenarios with grouping in gestating sector. This shows the median number of infected sows over time across the whole farm after the introduction of an infected sow in batch 1 at 294 days. The time scale started at 294 days, which corresponds to the date of introducing an infectious gilt into the system, following the burning period.

235 For the scenarios with a value of β_{ind} of 0.24 (scenarios 1 and 2) (Figure 6), the first peak
236 corresponded to the entry into the gestating sector. Due to the grouping by 6 of the sows in this
237 sector, the batch reassignment strongly impacted the transmission dynamics, with higher peaks
238 of incidence due to the potential introduction of infected sows in fully susceptible pens.

239 4 DISCUSSION

240 We developed a model to better understand the interplay between social and spatial organiza-
241 tion of a pig production herd and infection dynamics. Indeed, several pathogens (e.g. PRRSv,
242 PCV-2, influenza viruses, *Mycoplasma hypopneumoniae*) can yield to deviations in herd man-
243 agement due to clinical expressions in pigs, impairing the nominal management to be operated.
244 The complex interactions between disease management strategies and their impact on herd or-

245 ganization, together with the dynamics of disease spread, have not yet been fully accounted
246 for in the current model due to the complexity it introduces in the model design. To achieve
247 this, we applied an artificial intelligence-based approach (Ezanno et al., 2020). We introduced
248 an original multi-level agent-based design pattern to capture organizational features involved in
249 the complexity of highly structured populations in time and space. This approach was asso-
250 ciated with a dedicated modelling language to facilitate the specification of such organizations
251 without writing computer code, and it was integrated into the EMULSION framework. Our
252 approach facilitated the representation of the complex spatio-temporal herd structure, enabling
253 us to conduct a comprehensive study of the system.

254 The integration of AI methodologies into epidemiological modelling, including simulation ar-
255 chitecture and knowledge representation methods, extends the capabilities of epidemiological
256 models. This approach, through MLABS enhanced with organizational concerns (OMLABS),
257 allows for the representation of mechanisms previously unconsidered in the field. OMLABS
258 allows the study of various scales in a single simulation, facilitating a detailed analysis of the
259 impact of each level in the overall dynamic. This, in turn, allows for a focused identification of
260 effective measures and provides specific recommendations for action.

261 A literature review highlighted the role of mathematical models as tools for improving the
262 understanding of viral infection spread in pig production units (Andraud and Rose, 2020). Swine
263 influenza virus, PCV-2, or hepatitis E virus were indeed fields of application for models with
264 different paradigms, from individual-based approaches to population-based models, depending
265 on the transmission characteristics of the pathogens (Reynolds et al., 2014; White et al., 2017;
266 Andraud et al., 2008; Salines et al., 2020).

267 Multi-level Agent-based Systems provide solutions for unifying these modelling paradigms us-
268 ing a common framework, with high Readability, Reproducibility, and Flexibility (RRF). The
269 EMULSION framework provides real readability (R) through its specific language (DSL) in a
270 "no-code" approach and ensures, through its internal structure, reproducibility (R) (Picault
271 et al., 2019). The add-on of our organizational design-pattern offers the opportunity to tackle
272 population structures with fine-grained representations of their epidemiological consequences
273 with great flexibility (F), keeping the above-mentioned (RRF) advantages (Sicard et al., 2021b).
274 This was recently illustrated with a model representing the transmission of a swine influenza A

275 virus in a pig herds with different spatial configurations (Sicard et al., 2022).

276 Previous models represented the impact of management practices on the transmission dynam-
277 ics, to assess how husbandry practices could be modified to better handle health issues at the
278 herd level (Cador et al., 2016; Suksamran et al., 2017) Clinical aspects and their potential
279 consequences, in terms of management and infection dynamics, were nevertheless rarely consid-
280 ered. PRRS virus is recognized as a major economic burden for swine producers, inducing huge
281 loss due to growth retardation, abortions or reproduction failures, birth of stillborn fetuses or
282 weak-condition piglets (Le Coz, 2007; Renken et al., 2021; Charpin et al., 2012). Such clinical
283 outcomes necessarily induce exceptions in the management of the herds, affecting, in turn, the
284 transmission dynamics. We therefore developed a model, accounting for organizational features,
285 to study the impact of such disease-related exceptions on the transmission of an infectious agent
286 within a pig herd.

287 The model primarily focuses on representing the dynamics in the breeding sectors and their
288 impact on the whole farm. Our Results highlight the roles played by various transmission
289 routes, including batch change of sows after insemination failure, sow grouping in the gestating
290 sector, and indirect contact rate (β_{ind}), representing a potential airborne transmission route
291 (Cador et al., 2016). Introduction of infectious sows in susceptible batches clearly increased the
292 risk of persistence of the virus on farm.

293 Husbandry practices were highlighted as increasing the risk of transmission at group level and
294 persistence at herd level for different infectious agents, from both field observations and syn-
295 thetic data (Walachowski et al., 2014; Fablet et al., 2013; Cador et al., 2017). However the role
296 of deviations in nominal batch management due to clinical expressions, such as reproductive
297 issues in breeding sows or growth retardation in pigs, was not objectified. This could neverthe-
298 less favour the transmission between groups of pigs which could deserve further investigation to
299 develop farm-specific control solutions. Our model identified the primary transmission routes
300 and the impact of reinfection on the breeding population. These factors could lead to infec-
301 tion in maternity piglets and, ultimately, active immunity that could lead to virus extinction.
302 While establishing effective immunity in piglets with maternal immunity can be challenging, our
303 previous research highlighted its potential as a control measure for Influenza A (Sicard et al.,
304 2022).

305 This study considered only deviations of management due to insemination failures, which could
306 correspond to clinical consequences for sows infected by PRRSV during early gestation after in-
307 troduction of the virus on farm. **We did not consider the potential for adoption between litters,**
308 **whether within the same batch or from different batches. However, this aspect could be a topic**
309 **for future research.** However, the consequences of PRRSV infections are dramatic for animals
310 of all physiological stages. Late abortions would lead to mixing animals from different batches.
311 Culling rate might also be increased, inducing the introduction of renewal gilts, feeding the pool
312 of susceptible animals. In growing pigs, birth of piglets of weak condition, or growth retardation
313 due to infections could favour mingling of animals from different litters in nursery pens. These
314 impacts may have indirect consequences on herd management, leading to exceptions in nominal
315 management, such as mixing animals at different physiological stages. Our study showed that
316 exceptions due to batch reassignment for sows played an important role in infectious dynamics.
317 Our proposed methodological solution, which used artificial intelligence and organizational de-
318 sign patterns for multi-level agent-based simulation, provides a concrete way to represent these
319 phenomena. However, the model will need to be extended to account for the virus impact on
320 the management of exceptions at whole farm scale.

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