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DECIDE

Data-driven control and prioritisation of non-EU-regulated contagious animal diseases

Deliverable 2.3

Open-source mechanistic disease-specific simulation models

WP2 – Methods for data analysis and modelling

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Glossary

EMULSION: an open-source framework for mechanistic epidemiological modelling, developed at INRAE [1]. This software provides a domain-specific language based on YAML to describe the models as structured texts and a simulation engine to execute them.

Mechanistic model: a mathematical or rule-based model that represents entities, interactions and processes which are expected to produce a given phenomenon.

PASTE: an open-source software for generating decision-support tools as web applications from a mechanistic epidemiological model, especially from EMULSION models, developed at INRAE [2]. This software provides a domain-specific language based on YAML to describe the input forms, specific parameters, scenarios, summary statistics and graphs of interest to make a mechanistic model usable autonomously by stakeholders.

YAML: human-readable formatting language for data structures, mainly based on lists and key-value associations (see https://yaml.org/).

Abbreviations

Abbreviation	Description
AMU	Antimicrobial use
BRD	Bovine Respiratory Disease
BRSV	Bovine Respiratory Syncytial Virus
CC-BY-NC-SA	Creative Commons license with Attribution, Non-commercial use, Share-alike obligation
DGLM	Dynamic Generalized Linear Model
DST	Decision-Support Tool
EU	European Union
IB	Infectious bronchitis
WP	Work Package

Partner short names

Short name	Organisation
UU	Universiteit Utrecht
UCPH	Københavns Universitet
UGent	Universiteit Gent
UoL	The University of Liverpool
INRAE	Institut National de Recherche pour l'Agriculture, l'Alimentation et l'Environnement
IRTA	Institut de Recerca i Tecnologia Agroalimentàries
IDELE	Institut de l'Elevage
accelCH	accelopment Schweiz AG

Executive Summary

Epidemic mechanistic models are crucial for understanding and predicting pathogen spread in host populations. To ensure that the mechanistic models developed in DECIDE could be readable, revisable, and reliable, they relied upon the EMULSION software [1], which is an open-source framework providing a generic simulation engine and a declarative language dedicated to epidemiological modelling.

This deliverable provides an overview on all open-source mechanistic models developed for the three terrestrial species within DECIDE. Each model comes with a short description, associated publications when already available, the link to the public Git repository and to the code archived in Software Heritage as a direct access to a stable version.

Objectives of the Deliverable

The objective of this deliverable is to provide access to the mechanistic models developed for respiratory diseases in cattle, pigs and poulty, either to re-use those models in new studies, or to serve as a basis for developing models for other diseases, other species, other production systems or other countries.

Activities

The BRD models presented here mainly result from Baptiste Sorin's PhD. To ensure the relevance and robustness of model structure and assumptions, INRAE collaborated with UGent (Bart Pardon) on the first published model. Another one required a collaboration with UCPH (Carolina Merca, Anders Ringgaard Kristensen) to couple EMULSION with a DGLM. INRAE organized three workshops during the project's in-person General Assembly Meetings (Zurich, 2022; Copenhagen, 2023; Nantes, 2024) to train potential modellers to the EMULSION software and provide concrete guidance and support for model development on specific case studies. This resulted in the development of a model for *M. hyopneumoniae* infection in pigs in collaboration with IRTA (Beatriz Garcia-Morante) and UU (Marloes Boeters). Specific meetings were also organized to adapt the BRD model from young beef cattle to veal calves (with UGent, Stan Jourquin & Bart Pardon). Similarly, a model for IBv control in poultry was developed with UU (Yara Slegers).

Outcome

With the provided models, which come with usage examples and (for most of them) publications illustrating how they were used for comparing intervention scenarios or better understanding the pathosystem, readers should be able to adapt the model description documents (YAML files) to address their own case studies.

Next steps

The next steps to develop, re-use or adapts those models are:

- Parameter estimation: whenever available, field data can be used with parameter estimation algorithms (D2.4) to better calibrate the models and make them specific to a given farm or farming system.
- Adaptation to other pathosystems (as was done for BRD in veal calves or *M. hyopneumoniae* in pigs).
- Integration of welfare concerns in the models (ongoing, in collaboration with Wilma Steeneveld, UU & William Gilbert, UoL).
- Dissemination through open-access publications and scientific and professional communications.

The last workshop in Nantes also introduced the PASTE software [2] which enables to create decision support tools (DST) as web applications from the mechanistic models (e.g., Eval'BRD [3]). This paves the way to further developments of DST on top of the species-specific models, to make those more usable in the field to address specific issues and support decisions of farmers and their veterinarians.

1 Introduction

Background

Mechanistic models are very useful to better understand and explain the processes and mechanisms involved in population dynamics, especially in the context of complex pathogen-host-environment interactions. They also help anticipate the spread of pathogens in host populations and make it possible to compare scenarios encompassing a broad diversity of assumptions (such as individual variability, batch composition, initial prevalence and nature of pathogens…) and of realistic interventions, in order to prioritize prevention or control strategies [4]. However, to be realistic enough, mechanistic models can require complex simulation code, which can be difficult to write, validate and modify.

To overcome this limitation, all mechanistic models in the DECIDE project were developed using EMULSION. EMULSION 23/02/2026 16:51:00 is an open-source framework developed by INRAE to facilitate and foster a co-construction of mechanistic epidemiological models between modellers and other scientists (e.g. veterinarians, biologists, economists…), by providing an explicit description of model structure, components, parameters, and outputs as a structured text (which is both machine- and human-readable) rather than pure code. EMULSION models are thus kept readable, revisable, and can be easily re-used or adapted from one specific pathosystem to another.

INRAE organized three workshops during the project's in-person General Assembly Meetings (Zurich, 2022; Copenhagen, 2023; Nantes, 2024) to train potential modellers to the EMULSION software and provide concrete guidance and support for model development on specific case studies. The four species targeted in the DECIDE project (cattle, pigs, poultry and salmon) were represented among workshop participants.

Deliverable objective & content

This deliverable provides a comprehensive list of the mechanistic models developed for specific diseases and usage in DECIDE. Each model comes with a short summary, associated publications when already available, and a link to the public repository where the model is available.

Unless specified, the models are distributed under the CC-BY-NC-SA 4.0 license.

Species, diseases and production systems

With the efforts to help colleagues from all species groups to develop a mechanistic model for their own case study, it was not always possible to achieve this goal within the timeframe of this deliverable. Not all case studies had the same level of "maturity" combining expert knowledge or literature with field data to calibrate model parameters. Also, the objective of some case studies was first oriented towards designing statistical models to provide early detection from routinely collected data, rather than starting with comparing intervention scenarios.

Mechanistic models are currently well developed for two species, targeting respiratory diseases: Bovine Respiratory Disease (BRD), and infections by *Mycoplasma hyopneumoniae* in pigs. BRD models were developed for fattening farms in France (INRAE) and are currently being adapted to veal calves in Belgium (UGent), and later on for veal calves in France (IDELE). The pig model was developed for an all-in/all-out Dutch fattening farm (UU) and will also be adapted for a Spanish fattening farm (IRTA). In addition, a model for swine influenza infections is developed by UU in collaboration with IRTA.

For poultry, a mechanistic model is being developed during the last year of the project to rank disease interventions in broilers.

For salmon, no mechanistic model will be developed given the focus on early warning and the very different structure of aquatic farming. An already existing mechanistic transmission model was deemed sufficient for ranking of disease control options [5].

2 Model list and description

The models described below share a set of assumptions corresponding to the specific features of the production systems and diseases under consideration. These systems are of the all-in, all-out type, with no vertical transmission. Transmission via an environmental reservoir is not considered either.

2.1 Pathogen-specific, multi-batch BRD model in cattle fattening farms (completed)

The model developed by Sorin-Dupont et al. [6] is a mechanistic, stochastic, individual-based model, designed to simulate the spread of BRD pathogens in multi-batch cattle fattening farms. It focuses on three major pathogens involved in bovine respiratory disease with contrasted characteristics: the Bovine Respiratory Syncytial Virus (BRSV), *Mycoplasma (M.) bovis*, and *Mannheimia (M.) haemolytica*, their specific dynamics being represented by variations in model structure and in parameter values. Those three agents can be found in the upper respiratory tract of the calves without causing any clinical sign, until they become pathogenic following a stress suffered by the animal (e.g. weaning, transport or grouping with unknown congeners). They can also be transmitted from an infectious calf to its neighbours. The model accounts for both pathogen transmission and asymptomatic carriage. The model also captures individual animal risk factors, pathogen-specific infection dynamics, the onset of clinical signs of varying severity, their detection, and antimicrobial usage (AMU), with particular attention to the effects of batch allocation (calves can be either allocated to a single large batch, allocated to several small batches randomly, or allocated to small batches with other calves having the same risk of developing BRD) and between-batch contact rates. The study compares 18 scenarios based on two contrasting proportions of high-risk cattle at arrival, three batch allocation methods, and the three pathogens. The time step of the simulation is 12 hours, corresponding to typical herd monitoring frequency by farmers. The simulated duration is 40 days, which covers the period during which BRD typically occurs after arrival in the fattening unit. Each scenario is simulated with 200 stochastic replicates.

Key findings from the simulations indicate that sorting cattle into separate batches by risk level reduces the use of antimicrobials by 15% on average (up to 20% for *M. bovis*) and the occurrence of BRDs by 10-30%, depending on the pathogen. The model also shows that lower between-batch contact rates enhance this effect, while high-risk individuals increase pathogen spread and treatment rates. Sensitivity analyses highlight the strong influence of infection duration, spontaneous shedding, and clinical detection sensitivity on outbreak dynamics. These insights support risk-based animal grouping as an effective BRD management strategy and establish a foundation for further modelling that includes coinfections or collective treatments.

Participants: INRAE, UGent

Publications: [6, 7]

Public git repository:

https://forge.inrae.fr/dynamo/brd-models/brd-public/-/tree/pathogen-specific-multibatch

Permanent link in Software Heritage:

https://archive.softwareheritage.org/browse/origin/directory/?branch=refs/heads/pathogen-specific-multibatch&origin_url=https://forgemia.inra.fr/dynamo/brd-models/brd-public.git&snapshot=3290910bcf28e861e1e885af6d554eed52110f6f

2.2 Criteria for triggering collective treatments in BRD (completed)

This work extends the previous study to better understand which criteria could prove relevant to trigger collective treatments at batch scale to mitigate a possibly large BRD outbreak, rather than treating only detected cases. This mechanistic, stochastic individual-based model simulating the spread of *Mannheimia haemolytica* in a multi-batch fattening cattle farm incorporates individual characteristics (i.e.: the health status, moderate or severe clinical signs, hyperthermia caused either by infection or by other factors, a risk of developing BRD discretized in low, moderate and high levels, and the treatment status). It introduces collective treatment strategies based on three criteria: a conventional incidence threshold, a severity-based function emphasizing clinical sign intensity, and a novel criterion based on the speed of disease spread ("slope").

The model simulates 16 scenarios that vary in population risk profiles, pen assignment strategies, and possible interventions (individual treatments only vs. collective treatments triggered by different methods). The time step of the simulation is 12 hours, corresponding to typical herd monitoring frequency by farmers. The simulated duration is 40 days, which covers the period during which BRD typically occurs after arrival in the fattening unit. Each scenario is simulated with 200 stochastic replicates. Outputs measured include disease incidence, antibiotic use (AMU), treatment misuse, treatment delays, and severity duration. Results suggest that collective treatments based on the slope criterion can reduce both BRD incidence and AMU more effectively than conventional strategies, particularly by targeting high-risk pens early while sparing low-risk ones. This highlights the operational value of dynamic, data-driven criteria for antimicrobial stewardship in livestock systems.

This model is used as the basis for the development of a BRD tool for early detection and intervention ranking based on on-farm real-time sensor data (Connect'BRD).

Participants: INRAE

Publications: [8]

Public git repository:

https://forge.inrae.fr/dynamo/brd-models/brd-public/-/tree/PCI_animal_science2024

Permanent link in Software Heritage:

https://archive.softwareheritage.org/browse/origin/directory/?branch=refs/heads/PCI_animal_science2024&origin_url=https://forgemia.inra.fr/dynamo/brd-models/brd-public.git&snaphot=3290910bcf28e861e1e885af6d554eed52110f6f

2.3 Coupling between the BRD model and a DGLM for Decision Support (completed)

The study presents the proof of concept for a novel decision support tool for managing BRD in fattening cattle by integrating two complementary modelling approaches: mechanistic epidemiological modelling and dynamic generalized linear models (DGLMs). The mechanistic model, implemented using the EMULSION framework, simulates the spread of *Mannheimia haemolytica* over the initial 40-day period post-farm entry. It accounts for animal-specific risk levels and processes like infection, clinical signs, detection and treatment. On top of this, a hierarchical multivariate binomial DGLM estimates the risk of infection in each batch over time based on observable signs (e.g., hyperthermia, mild/severe symptoms, detection), providing early warnings to trigger timely collective treatments. This statistical model extends the classical Dynamic Generalized Linear Model (DGLM) allowing dynamic (possibly time-varying) relationships between predictors and outcomes by handling multiple related outcomes simultaneously and accounting for the hierarchical structure of the data (calves within pens with a farm) and was developed in D2.1 and D2.2.

This coupled model was tested on 48 synthetic scenarios combining batch sizes, risk levels, allocation strategies, and treatment interventions (individual, conventional collective, and DGLM-triggered collective). The time step of the simulation is 12 hours, corresponding to typical herd monitoring frequency by farmers. The simulated duration is 40 days, which covers the period during which BRD typically occurs after arrival in the fattening unit. Each scenario is simulated with 200 stochastic replicates. Results showed that early-warning-based treatments often led to lower BRD incidence (-30% in large batches) and severity (-10 to -25%) compared to conventional strategies, especially in medium to high-risk scenarios. These interventions also optimized AMU (-20% in high-risk scenarios), though low-risk settings occasionally suffered from over-treatment due to overestimated infection risks. Overall, the tool enables more targeted BRD management and has the potential for real-time on-farm deployment, pending validation with empirical data.

Participants: INRAE, UCPH

Publications: [9]

Public git repository:

https://forge.inrae.fr/dynamo/brd-models/brd-public/-/tree/sorin-merca-2024

Permanent link in Software Heritage:

https://archive.softwareheritage.org/browse/origin/directory/?branch=refs/heads/sorin-merca-2024&origin_url=https://forgemia.inra.fr/dynamo/brd-models/brd-public.git&snapshot=3290910bcf28e861e1e885af6d554eed52110f6f

2.4 Mitigating co-circulation of BRD pathogens through vaccination (completed)

This model extends the BRD model described in 2.1 to investigate the impact of co-circulation of two pathogens (a virus, the BRSV, and a bacterium, *M. haemolytica*). In this extension, two infectious processes are modelled in parallel, so that both pathogens can circulate in animals introduced in the farm and can infect cattle in sequence or simultaneously. The model accounts for the interactions between pathogens and their impact on disease severity. Three vaccines are also considered (monovalent against each pathogen vs. divalent), with their mitigation effect on transmission and disease severity. The model was used to study 1) the impact of co-circulation of pathogens, and 2) prevention based on vaccination strategies (vaccination at purchase at the breeder vs. vaccination upon arrival in the fattening facility, with either monovalent or divalent vaccines).

The first results [10] highlight the crucial role of early vaccination strategies to mitigate both morbidity and mortality. This model was used by Théo Salles in his veterinary thesis [3] to design a web DST (Eval'BRD) in which the possible strategies are assessed in terms of health impact (disease occurrence, duration and severity), antimicrobial usage, and costs (net gain, but also treatment cost and labour cost).

Participants: INRAE

Publications: [10]

Public git repository:

https://forge.inrae.fr/dynamo/brd-models/brd-public/-/tree/coinfection-metaphylaxis

Permanent link in Software Heritage:

https://archive.softwareheritage.org/browse/origin/directory/?branch=refs/heads/coinfection-metaphylaxis&origin_url=https://forgemia.inra.fr/dynamo/brd-models/brd-public.git&snapshot=3290910bcf28e861e1e885af6d554eed52110f6f

2.5 BRD model for veal calves (ongoing)

This model is intended to adapt the previous BRD model to a different production system (veal calves instead of young beef cattle) in a different country (Belgium). It was mainly developed by Stan Jourquin (UGent), Baptiste Sorin and Sébastien Picault (INRAE). The model represents the co-circulation of BRSV and M. haemolytica, with a particular focus on vaccination-based prevention of lung lesion development, assessed using lung ultrasound, a promising method for early detection of pneumonia in calves.

To simulate early detection of diseased calves through lung ultrasound, the model accounts for the development of pneumonia, with a probability based on field observations, for infected veal calves. Pneumonia and other clinical signs are increased in co-infected animals, as well as the mortality. The vaccine can be either monovalent (BRSV only) or bivalent (BRSV + *M. haemolytica*) and reduces the infectious duration, the severity of clinical signs, and the transmission of pathogens to susceptible animals. The model also accounts for the influence of vaccination on development of pneumonia and ultrasonographic cure, as there is some evidence that vaccination reduces the prevalence of ultrasound confirmed pneumonia in the later stages of production (week 10 after arrival), at which point it is associated with losses in average daily growth and cold carcass weight. The model was calibrated using empirical data from available datasets and parameters derived from peer-reviewed literature.

In further developments, the model could benefit from a fine-tuning of the contact structure to better account for building structure in actual fattening facilities. Also, periodic lung ultrasound detection could be simulated, with a probabilistic trial depending on the status of the calf (pneumonic or not) and the ultrasound sensitivity and specificity. This model will also be adapted in the coming months for the French veal calves' facilities by Laure Brun-Lafleur, Magdéléna Chanteperdrix and Carole Toczé (IDELE).

Participants: UGent, INRAE, IDELE

Publications: to be done in 2026

Public git repository:

https://github.com/decide-project-eu/BRD_model_veal_calves

Permanent link in Software Heritage:

https://archive.softwareheritage.org/browse/origin/directory/?branch=refs/heads/main&origin_url=https://github.com/decide-project-eu/BRD_model_veal_calves&snapshot=ce993e36925c184d2ac345ae043987942ce7510e

2.6 Model for *Mycoplasma hyopneumoniae* in pig farms (completed)

This model was mainly developed by Marloes Boeters (UU) as part of her Ph.D. thesis and Beatriz Garcia-Morante (IRTA), with the support of Sébastien Picault (INRAE). The aim of this work was to estimate multiple burdens of *Mycoplasma* (*M.*) *hyopneumoniae* infection on a Dutch commercial fattening farm. Additionally, the model was used to evaluate a range of intervention strategies and their effects on these burdens. Specifically, the model provides insights into development of clinical signs and lung lesions and quantifies the impact of infection and interventions on various outcomes, including pig health indicators, antibiotic use, production performance, economic results, labour requirements, and CO_2 emissions from feed use.

The model is mechanistic, stochastic, and individual-based, and accounts for multiple levels to represent a realistic spread of infection (within-pen, between-pen and airborne transmissions), accounting for the spatial organization of a fattening unit. The individual pigs are organised into 12 pens of 12 pigs each and remain in the same pen from arrival at an age of on average 10 weeks until slaughter. The model accounts for infection dynamics (including both acute and chronic phases), and the development of coughing or lung lesions in a subset of infected pigs. To aid the estimation of the labour and economic burden of the disease, the model includes production performance (i.e. weight gain and feed intake), which may be impacted by the disease. Additionally, the model estimates the effects of interventions, namely vaccination, compartment-level antimicrobial treatment and individual treatment, and identifies trade-offs across burdens. Model parameters were derived from scientific literature, representative industry reports and expert elicitation. Additional economic values (e.g. average costs and prices) were based on 2024 Dutch market data.

In the coming months, this model could be adapted to represent Spanish farms in which longitudinal epidemiological data are available. Together with deliverable D2.4, this would make it possible to estimate parameter values on real fattening farms, which is necessary to use the model as a basis for a future decision-support tool.

Participants: UU, IRTA, INRAE

Publications: [11–14]

Public git repository:

https://github.com/decide-project-eu/Mycoplasma_hyopneumoniae

Permanent link in Software Heritage:

https://archive.softwareheritage.org/browse/snapshot/a3da6f54347f9d32c602bde33344f8d641e90679/branches/?origin_url=https://github.com/decide-project-eu/Mycoplasma_hyopneumoniae&snapshot=a3da6f54347f9d32c602bde33344f8d641e90679

2.7 Model for Swine influenza in weaning and fattening pig herds (ongoing)

This model adapts the model described in section 2.6 to simulate an outbreak of swine influenza in a batch of pigs during the weaning and finishing stages. It is mainly being developed by Jingyi Liu, a master student of MSc Epidemiology (UU), under supervision of Marloes Boeters (UU), Gerdien van Schaik (UU) and Beatriz Garcia-Morante (IRTA), and with the support of Sébastien Picault (INRAE). This model aims to quantify the epidemiological, production and economic impacts of swine influenza outbreaks at batch level, and to explore differences in economic burden for two pathogen introduction scenarios (1: piglets are sourced from an endemic farm, and 2: virus introduction occurs during transportation to the simulated farm) and for two vaccination strategies (1: vaccination of sow population, 2: vaccination of piglets at weaning).

The model follows a similar structure to the model described in section 2.6 to include within-pen and between-pen transmission processes. The model also represents different production stages (from weaning age, at 4 weeks, to slaughter) and pig movements between stages. The model includes infection dynamics, while accounting for maternally derived antibodies (MDA) in piglets and their waning over time. Following infection, clinical signs associated with swine influenza are modelled, including the development of respiratory clinical signs (e.g. coughing, sneezing and running nose) and fever. To estimate the economic burden of disease, the model links infection to changes in production performance (e.g. average daily gain and feed intake). All parameters were derived from scientific literature and expert opinion.

Final steps before completion include further calibration, sensitivity analyses and validation with pig experts.

Participants: UU, IRTA

Publications: to be done

Public git repository: to be done

Permanent link in Software Heritage: to be done

2.8 Model for infectious bronchitis in broilers (ongoing)

During the last year of the project (June 2025-March 2026), Yara Slegers (UU) is developing an EMULSION model for broiler chickens, targeting infectious bronchitis (IB) caused by the infectious bronchitis virus (IBV). The batch scale was considered most relevant. Modelling poultry at individual scale would be necessary to study fine-grained outcomes such as the distributions of weights, at the expense of a high computational cost, whereas the batch scale provides less detailed but more performant simulations, enabling to compare more scenarios in the same amount of time.

The model targets conventional broiler chickens and aims at ranking possible interventions (e.g., comparing vaccination schemes, or different interventions such as stocking density). If possible, the model outputs will be used to account for the impact of the disease on growth rates, mortality and slaughterhouse condemnation. As IBV infection can lead to an increased susceptibility to *Escherichia coli* (*E. coli*), this effect is also accounted for in the model, as well as antibiotic treatments.

The model will primarily target researchers, as it is not yet planned to develop a decision-support tool. The results from the model and from scenario comparisons will be useful to broiler farmers.

The development is in progress, and the model will be shared on the DECIDE GitHub repository, starting with a model for IB without interventions (choosing parameters and building the model, 6 months), then adding at least two different interventions (4 months).

Participants: UU

Publications: to be done in 2026

Public git repository:

https://github.com/decide-project-eu/IB-model-broiler-chickens

Permanent link in Software Heritage:

https://archive.softwareheritage.org/browse/origin/directory/?origin_url=https://github.com/decide-project-eu/IB-model-broiler-chickens

3 Summary and Outlook

WP2 of the DECIDE project has pushed consortium members to deliver a coherent suite of open-source, mechanistic simulation models that span (or will span) several contagious animal diseases in the three terrestrial species targeted in the project (calves, pigs and poultry). Each model is implemented in EMULSION, ensuring that structure, assumptions and parameters remain transparent, version-controlled and immediately reusable by researchers and stakeholders. Public GitHub repositories and Software Heritage snapshots both guarantee long-term accessibility and citability.

Key achievements

- Rich, pathogen-specific BRD models for cattle. Successive developments now cover multi-batch fattening systems, formal rules for collective treatments, early-warning coupling with DGLMs, and vaccination against co-circulating agents.
- Cross-species transferability. Based on the BRD model developed for young beef cattle, other models could be developed for other pilot-specific implementations, such as veal calves and pigs, and provide a template for similar adaptations.
- Integrated burden assessment in pigs. The stochastic model for *M. hyopneumoniae* quantifies health, economic, labour and environmental impacts, and evaluates both conventional and innovative interventions.
- Open pipelines from model to decision support. The first web-based tools generated with PASTE demonstrate how research models can be turned into practical applications (e.g. Eval'BRD) with minimal additional code.

Connections with other work packages

- Collaborations within WP2 were carried out between INRAE and UCPH to combine statistic and mechanistic models (see section 2.3).
- The BRD models were used to design two cattle tools in WP3: Eval'BRD for intervention ranking (based on the model presented in 2.4) and Connect'BRD (2.1) for early detection and intervention ranking. The model for *M. hyopneumoniae* in pigs (2.6) is considered to develop a tool similar to Eval'BRD.
- The model used in Eval'BRD (2.4) and for *M.* hyopneumoniae (2.6) integrated costs and benefits in relation with WP4 and will be extended to account for other disease burdens such as animal welfare, labour constraints and emissions.
- The choice of scenarios and outputs of the mechanistic models, as well as the evaluation of the DST based on the models, were carried out in collaboration with WP3 and WP5.

Outlook for the remainder of the project

The next steps to be carried out during the project are the following:

- Parameter estimation with Deliverable 2.4: model calibration will be done against field data from France & Belgium (for BRD/veal calves), the Netherlands and Spain (for pigs), to validate the models and ensure that they are tailored to reflect realistic farm conditions and credible scenario ranking.
- Widening the scope: the models will be extended to other pathogens (e.g. swine influenza) and other burdens (e.g. welfare indicators) to provide an estimation of the impact of possible interventions on the multidimensional burden of the diseases and provide a better alignment with stakeholders or public policies expectations.
- New species/models: infectious bronchitis in broilers.

These next steps will provide a potential to transform these research models into actionable tools that help veterinarians and farmers make evidence-based choices while minimising antimicrobial use and safeguarding animal welfare.

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