ODD PROTOCOL

ODD protocol of the FarmECS-IBR model

A model to support decision-making in the context of a national IBR eradication program

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List of Acronyms

BoHV-1	Bovine Herpes Virus Type 1
IBR	Infectious Bovine Rhinotracheitis
EU	European Union
ODD	Overview, Design Concepts, and Details
AIM	Animal Identification and Movement
DAFM	Department of Agriculture, Food and the Marine
SOM	Self Organizing Maps
POM	Pattern Oriented Modelling

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1.1 Overview

A stochastic large scale individual-based model of Bovine Herpes Virus Type 1 (BoHV-1) was developed in the framework of this contribution. The model, called FarmECS-Infectious Bovine Rhinotracheitis (IBR) is build up on the system understanding of the Irish cattle sector. This protocol provides a complete technical documentation of the developed model. The documentation of the model follows the Overview, Design Concepts, and Details (ODD) protocol a standardized scheme designed to produce a transparent and comprehensive model description following a generic structure (Grimm et al., 2006, 2010, 2020).

The FarmECS-IBR model is a compilation of a spatially explicit, stochastic, individual-based cattle herd-management and animal-trade model for the entire cattle sector of a geographic area. Superimposed to the herd-management and animal-trade model is a transmission and disease course model of BoHV-1 that represents the spread of IBR within and between herds.

1.1.1 Purpose

Purpose of the FarmECS-IBR model is the evaluation of different BoHV-1 control strategies to provide policy support and to assist with decision-making in the context of an Irish BoHV-1 eradication program.

1.1.2 Entities, state variables and scales

Spatial scale of the model is the Irish county Kerry located in the south-east of Ireland, with an area of approx. 5’000 km^2, 5’000 cattle herds and 360’000 individual cattle. The model runs in weekly timesteps and is individual-based, meaning that each animal is simulated explicitly.

The model consists of two entities, namely the animal and the herd entity (see Figure 1.1). Each entity is described by one or a set of state variables. Due to the application of an Entity-Component-System (ECS), state variables are grouped into Components that are attached to the entities. Components, and thus state variables, can be added to an entity or removed, depending on whether they are currently used or not.

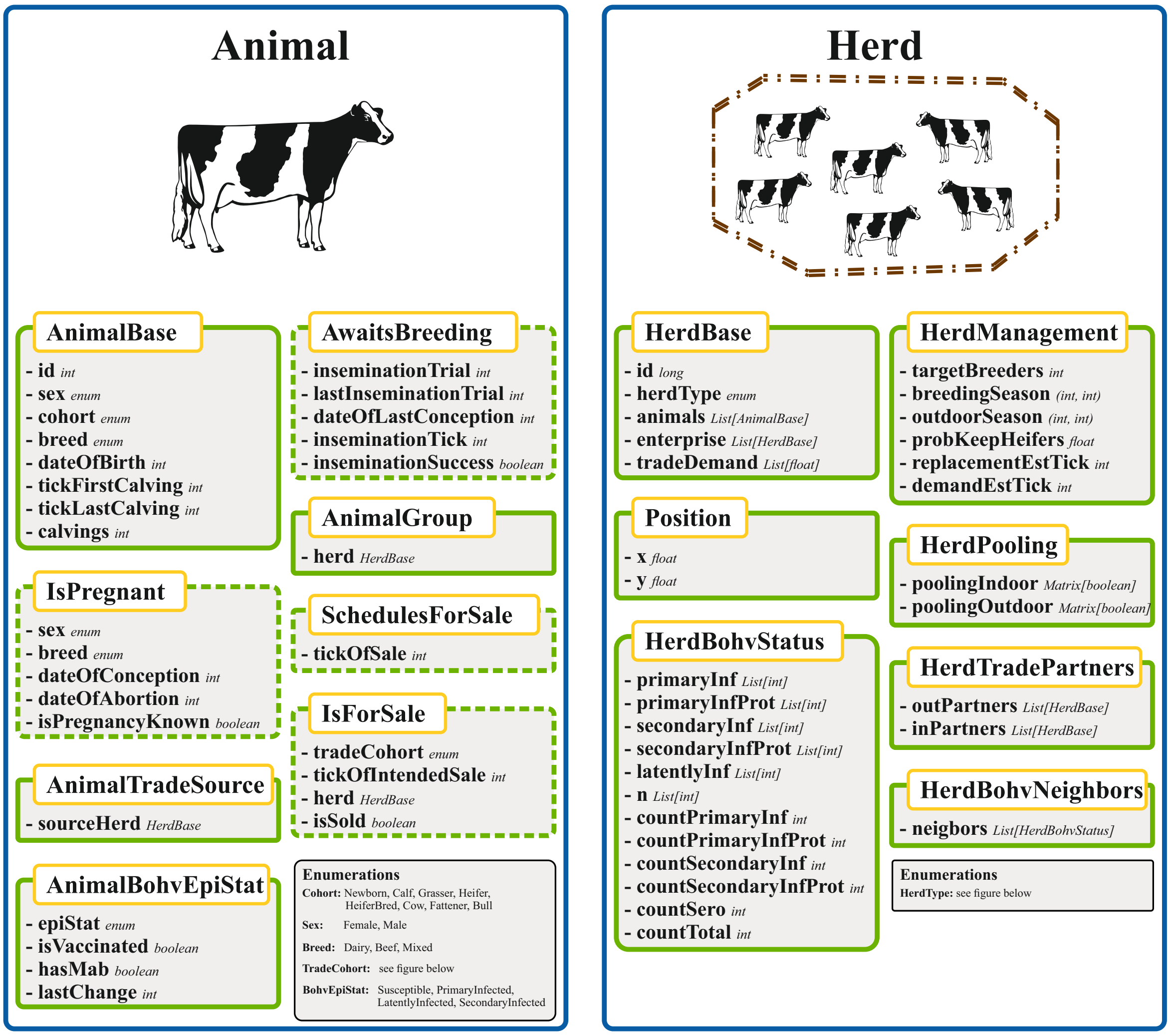

Figure 1.1: Entities, components and state variables of the FarmECS-IBR model. Solid green boxed indicate permanent components, while dashed boxed show optional components that are added to the entity when needed.

In the model, individual animals are the most complex entities. Each individual animal comprises at least an *AnimalBase* component that provides information on typical demographic variables such as an animal's age, sex, breed, date of death or membership in a management cohort. In addition each animals holds an *AnimalGroup* component specifying an animal's herd. The other components are optional and are attached to certain animals only temporarily. For example, female animals that have reached a specific age or are intended for breeding get the *AwaitsBreeding* component attached. This component stores all state variables necessary for breeding, such as the number of insemination trials, the last insemination trial, whether an insemination was successful (inseminatinoSuccess) and, if so, the date of conception (dateConception). If breeding was successful, the *AwaitsBreeding* component is detached and the *IsPregant* component is attached. Among other things, this component provides information about the sex or race of the fetus. The components *ScheduledForSale*, *IsForSale* and *AnimalTradeSource* are used to handle animal transports between the simulated herds. The *AnimalBohvEpiStat* component keeps information on the animal's BoHV-1 infection status and when it last changed.

The herd components listed in Figure 1.1 are permanent for all cattle herds in the model. The *HerdBase* component provides information on the ID of the herd, the herd type and lists all present animals. The *Position* component gives information on the spatial location of each herd and is used to determine neighbouring herds which is important for the epidemiological part of the model. Important herd management variables and parameters are stored in the *HerdManagement* component. This component describes how the farmer manages his herd (e.g. when he is breeding his animals or how many heifers he keeps annually to replace older cows). The *HerdBohvStatus* component stores herd BoHV-1 information, such as the number of animals in respective BoHV-1 health states or the total number of seropositive animals.

1.1.3 Process overview and scheduling

The FarmECS-IBR model runs in discrete timesteps of one week. At each timestep the main processes of the model are executed in the following order and animal- and herd-level state variables are updated wherever necessary:

1) Herd management: grouping of animals to cohorts, marking animals for sale
2) Breeding
3) Abortion
4) Calving
5) Trade/transports
6) BoHV-1 infection, recovery, reactivation
7) Background mortality/culling
8) Virus release

1.2 Design

According to Brock et al. (2020) the structure of the characteristics of cattle disease models can be described using three main features: [1] biological processes, [2] farming-related processes and [3] pathogen-related processes. In the FarmECS-IBR model, biological processes such as ageing, pregnancy, lactation, fertility and mortality are simulated at each time step for all individual animals. At herd level, management processes such as grouping, breeding, buying and selling of animals are simulated for each herd type. Independent of the biological- and management-related processes, pathogen-related processes are represented in the model. Thereby, each animal is assigned an epidemiological status, which can change according to individual infection or recovery.

1.2.1 Herd management processes

A detailed understanding of herd types and herd management is needed for animal disease control and surveillance activities, to inform epidemiological study design and interpretation, and to guide effective policy decision-making. Therefore, sixteen different herd types are defined in the FarmECS-IBR model, representing the typical management schemes of the cattle sector in Kerry/Ireland. The herd types were identified from a previous analysis where expert knowledge was coupled with a machine-learning algorithm called Self Organizing Maps (SOM) to explore multi-dimensional herd data extracted from the Irish Animal Identification and Movement (AIM) database.

For the sake of model development, we have assigned each of the 5000 herds in Kerry to one of our identified herd types based on a classification scheme we developed for the Irish cattle population. Overall, the cattle population in Kerry was classified into 5 main herd types, some of which can be further divided into subgroups (see Figure 1.2). The main herd types present in Kerry are dairy, beef, store, mixed and fattening herds, with beef herds accounting for the largest proportion (45%) of all of the approx. 5000 registered herds.

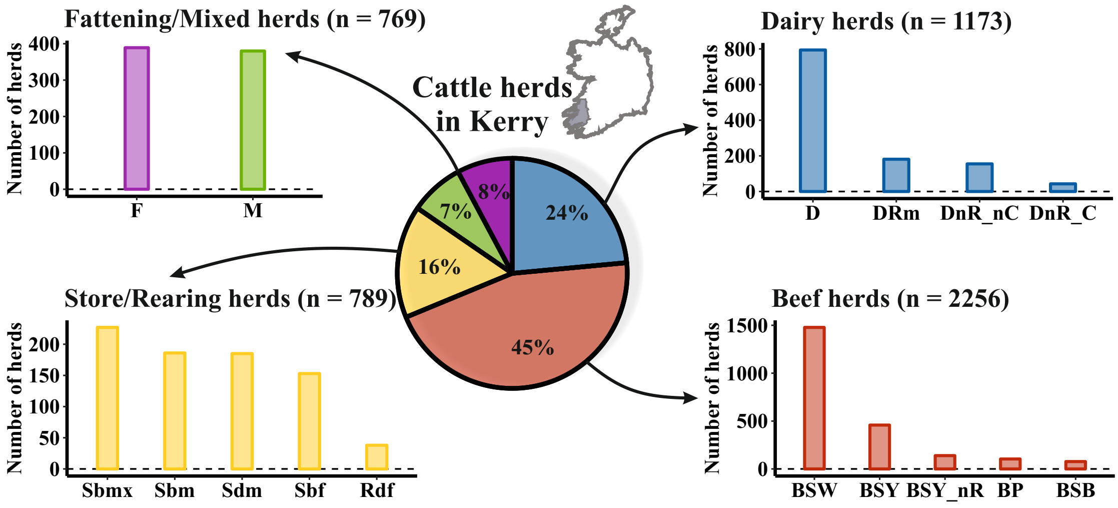

Figure 1.2: Herd types and their distribution in Kerry. Data extracted from AIM database maintained by DAFM.

In the model we have implemented a rule-based management system for each of the identified herd types, which is followed by all herds of the respective type. This management scheme determines, for example, how long herds of a certain type keep youngstock, at what age they sell them and whether herds maintain themselves through breeding. For each herd, its population structure emerges from a combination of biological parameters of individual animals and different management practices of herds. To ensure validity of the model, each herd types population structure is systematically compared to data extracted from the AIM livestock register.

In the following, a brief description of the identified/implemented herd types is given. Among the dairy herds, we identified four sub-groups that differ in terms of their management practices.

Typical dairy herds (**D**) that sell their male calves (to **Sdm** herds) at the age of a few weeks are the most prominent dairy herd type in Kerry. In these herds, female calves are kept and reared as replacements. Non-rearing dairy herds (**DnR-C**) sell most of their calves, but female calves are moved to external contract rearing herds (**Rdf**). Most of them return to the **DnR-C** herd as pregnant heifers before calving. A similar herd type is the **DnR-nC** herd type. There are similarities to the previous herd type, with the sale of all new-born calves within a few weeks after birth and the introduction of replacement heifers. In contrast to the **DnR-C** herds, however, replacement heifers are not purchased from contract rearing herds, but from other herds with a surplus of such animals. There are also dairy herds (**DRm**) that keep all their calves, including their males calves until they are sold as youngstock for fattening to fattening (**F**) herds.

Five different beef production systems were identified from the data and implemented in the model. The first type we extracted is the beef pedigree herd (**BP**) whose main production objective is breeding of purebred beef cattle. Purebred beef herds are important for providing breeding stock (e.g. Beef bulls) to other commercial cattle producers in both the dairy and beef sectors. The suckling to beef (**BSB**) system includes the full beef production cycle, from birth through to the age of slaughter. Typically, calves stay with their dams until weaning at 6-8 months. Then, the weaned calves are retained for rearing and fattening in the same enterprise. The beef suckling to youngstock (**BSY**) system is very similar to the **BSB** system, however these herds do not fatten their cattle intended for slaughter. Instead these animals are mainly sold to fattening herds as yearlings (youngstock for fattening). Non-rearing suckling to youngstock (**BSY-nR**) herds are a variation of the BSY herd type, with the difference being that all female calves are sold after weaning. These herds mainly purchase pregnant heifers for replacement from other suckling herds or **Sbf** herds. Beef suckler to weaning (**BSW**) herds are the most common beef system in Ireland. These herds sell most of their calves after weaning between six and eight months of age to store or fattening herds. A proportion of females are kept for replacement.

The store/rearing group mainly comprises herds that are non-calving. Overall, five sub-types (**Sdm**, **Rdf**, **Sbf**, **Sbm**, **Sbmx**) were identified and implemented, which differ in terms of their management practices. Store dairy bull (**Sdm**) herds typically purchase male calves between 10 and 30 days at age from dairy herds. These animals are reared and then sold to fattening herds. Three different types of beef store herds were identified, which differ in terms of their sex composition, rather than by management practices: store beef males (**Sbm**), store beef females (**Sbf**) and store beef mixed (**Sbmx**) systems. These herds purchase beef animals as weanlings and rear them until they are sent to fattening herds. In rearing dairy female (**Rdf**) herds, young female dairy calves are introduced, reared and inseminated, before being returned to their birth herd as pregnant heifers.

Herd which on average consist half pure-bred dairy animals and half animals cross-bred between dairy and beef were also identified and implemented. These herds produce milk on the one hand, but on the other hand they have another cattle enterprise, solely focused on beef production. We classified these dual purpose herds as mixed herds (**M**). Fattening herds (**F**) buy calves, weanlings and youngstock from a wide range of herd systems and fatten them until slaughter.

1.2.2 Animal transports

In the model animal movements emerge from supply and demand. Supply of and demand for animals by individual herds emerge from herd type specific management and stochastic processes, e.g. mortality or infertility.

Animals in supply and demand are classified into 7 trading cohorts, like e.g. youngstock for fattening or pregnant heifer dairy (see Figure 1.3). As an example, store dairy male herds (**Sdm**) herds have demand for male dairy calves (CDM) according to the free space in their premises. Dairy (D) herds supply male dairy calves (CDM) for rearing by trying to sell their male calves at an age of 2 weeks.

Animals intended to leave a herd are preferrably distributed to enterprise sites and trade partners. If this is not possible, supplied animals enter an open market, where demanders select supplies based on distance as well as demand and supply batch size. If demand can't be satisfied on the market for a certain time, it is satisfied by imports from outside the modelled region.

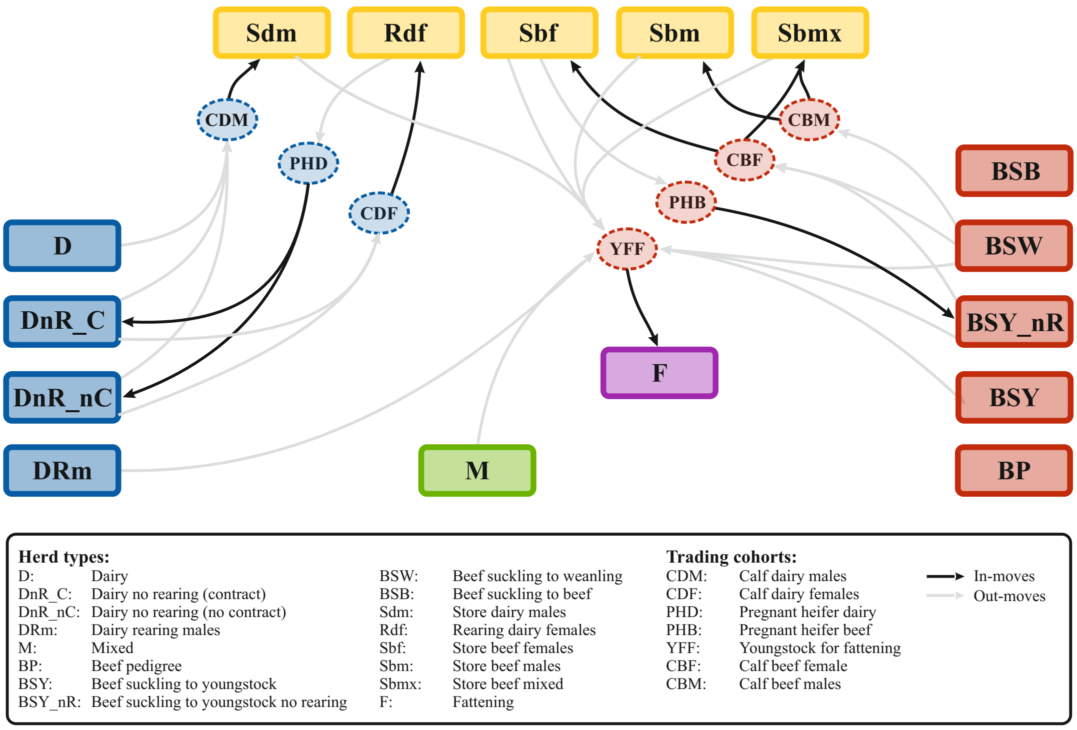

Figure 1.3: Typical animal transports under the Irish cattle management system. For a better overview only primary movement cohorts are shown.

1.2.3 Epidemiological processes

Epidemiological processes of BoHV-1 infection are driven by direct transmission between animals in the same herd, by indirect transmission between nearby herds, as well as animal transports. On farm, transmission of the infection is independently modelled within management groups compared to transmission between groups.

Individual probability to contract infection follows standard epidemiological formalisms as described by Brock et al. (2020), comprising all pathways of the animal's current exposure.

Reactivation of latently infected animals is explicitly modelled by means of a weekly probability. Infectiousness of primary infected animals is greater than of secondary infected animals.

1.3 Details

1.3.1 Globals

This section provides an overview on globally accessible data structures that are utilized by submodels to access global parameters. In the FarmECS-IBR model, globally available parameters are structured into two main groups: [1] biological parameters and [2] management-related parameters. Table 1.1 provides an overview of these parameters.

Table 1.1: Globally accessible parameters. Age-related parameters are given in weeks and were selected by using expert knowledge from a wide variety of Irish stakeholders (veterinarians from Technical Working Groups convened by Animal Health Ireland, analysts from ICBF, staff from Teagasc (the Agriculture and Food Development Authority) and researchers from UCD Centre for Veterinary Epidemiology & Risk Analysis. Parameters related to biological data were extracted from Thulke et al. (2018).

	Parameter	**Symbol**	**Type**	**Description**	**Value**
Biological data	gestationLength	τ_{gest}	int	Length of gestation (weeks)	40
	lactationLength	τ_{lact}	int	Length of lactation after calving (weeks)	44
Management data	maxAgeNewborn	a_{newb}	int	Age to move from cohort newborn to calf	2
	maxAgeCalf	a_{calf}	int	Age to move from cohort calf to heifer or grasser	26
	maxAgeGrasser	a_{gras}	int	Age to move from cohort grasser to fattener	104
	maxAgeFattener	a_{fatt}	int	Maximum age for animals in cohort fattener	160
	minAgeBreeding	a_{breed}	int	Minimum age of heifers for first breeding	57

1.3.2 Input data

The model does not require input data but in advance several datasets were analysed to provide an understanding of the Irish cattle system. Table 1.2 lists data used to describe and model the Irish cattle system. This table reflects the minimum information that would be needed to apply the model to other cattle populations.

Table 1.2: Data used to describe the Irish cattle system

Dataset	**Description**	**Source**
Herd population in 2017	List of all cattle registered in Ireland on 3 different dates (1st Jan, 1st May and 1st Sep) in 2017	AIM database
All births from 2016 to 2018	List of all births from 2016 to 2018	AIM database
All animal transports in 2017	List of all animal movements that took place in 2017	AIM database

Data listed in Table 1.2 was obtained from the AIM database maintained by the Department of Agriculture, Food and the Marine (DAFM). In accordance with European Union (EU) requirements, the AIM database comprises records on all births, movements and disposals (i.e. origin, destination and date), tracking each individual bovine in Ireland from birth or import to death or export (DAFM, 2017).

The herd population dataset, as well as the animal transport dataset were used to classify cattle herd types and to gain a detailed understanding of their management regimes. These datasets were also used to validate the model. The birth dataset was important to extract parameters relevant for breeding and calving.

1.3.3 Initialisation

The model is initialised by the following steps. First, all herds to be modelled are read from a table (herdTableFile, see Table 1.3) listing for each of the 5000 cattle herds in Kerry their position, herd type, target size, breeding and outdoor season. Then, for each herd in the table, animals are created and added to the engine. Important animal state variables, such an animals age, sex etc. are drawn from predetermined distributions. Afterwards, a 20-year pre-simulation is conducted to ensure a proper initial population structure and valid animal components and state variable values.

After the 20-year pre-simulation, an individual herd's population is written to the herdXmlFile (see Table 1.3). This file lists all animals from all herds, along with its initialised state variables. At model start up, individual herd populations are initialized from the herdXmlFile by randomly drawing animals until the desired number of animals per herd (target size listed in herdTableFile) is reached.

Table 1.3: Parameters relevant for model initialisation

Parameter	**Symbol**	**Type**	**Description**
herdXmlFile	-	String	Path to xml file with serialized herd populations
herdTableFile	-	String	Path to herd table
columns...	-	String	Column names of the herd table file (e.g. ID, Type, Size)
poolsIndoor	$P_i(ij)$	List[Matrix[boolean]]	Per herd type pooling/contact matrix indoor
poolsOutdoor	$P_o(ij)$	List[Matrix[boolean]]	Per herd type pooling/contact matrix outdoor
maxRadius	r_{neigh}	float	Neighborhood radius

During initialization, a contact structure between the animals is defined for each herd in the model, i.e. which groups of animals are to get in contact with each other. For each herd type, a contact structure is defined once for the indoor ($P_i(ij)$) and once for the outdoor ($P_o(ij)$) period.

In addition to the contact structure, herd neighbourhood connections are determined during initialisation. For each herd i, all other herds j are assigned to be neighbouring herds for which distance $d_{ij} \leq r_{neigh}$. These herds are then added to the state variable neighbours in the *HerdBohvNeighbors* component.

1.3.4 Submodels

1.3.4.1 Replacement

Replacement estimation In the model, each farmer of a breeding herd estimates how many of its pregnant heifers he is going to keep for replacement of older cows. At the beginning of the simulation, each herd is assigned a random time offset for the estimation, taking into account the time interval (τ_{est}) between the replacement estimates:

$$o_{est} = \lfloor U([0, \tau_{est})) \rfloor \tag{1.1}$$

At every model step (t), replacement estimation is performed for all herds where

$$t \bmod \tau_{est} == o_{est} \tag{1.2}$$

Then, for each herd to estimate in a step, the probability to keep pregnant heifers p_{keep} is estimated based on herd type, target breeders n_{targ} and number of cows n_{cow} and bred heifers n_{hb}. The number of required reproducing animals is

$$n_{req} = n_{targ} - n_{cow} \tag{1.3}$$

This number is used then to calculate a farm's probability to keep pregnant heifers as

$$p_{keep} = \frac{n_{req}}{n_{hb}} \tag{1.4}$$

The result is written to the *HerdManagement* component.

Replacement decision Based on the replacement estimate, a replacement decision operator decides for individual bred heifers to keep or sell them. For an individual animal the decision is made when

$$t == t_{conc} + \tau_{gest} - \tau_{est} \tag{1.5}$$

where t is the current model step, t_{conc} is the date of conception, τ_{gest} is the gestation length and τ_{est} a parameter determining how many weeks before calving to make the decision.

Each animal to decide for is stochastically kept with the herd's probability p_{keep}. If an animal is to be sold, a *ScheduledForSale* component is attached to the animal and the intended date of sale is calculated as

$$t_{sell} = t_{conc} + \tau_{gest} - \tau_{sell} \tag{1.6}$$

Table 1.4: Model parameters related to replacement. Parameters were estimated from expert input and refined during the calibration process described in section 2.5 and 3.1.1. in the paper.

Parameter	Symbol	Type	Description	Value
estimationInterval	τ_{est}	int	Time interval between replacement estimates (weeks)	4
ticksBeforeCalving	$\tau_{beforeCalving}$	int	How many weeks before calving to make replacement decision	15
sellTicksBeforeCalving	τ_{sell}	int	How many weeks before calving to sell	13

while τ_{sell} is a model parameter determining how many weeks before calving the animal is to be sold.

1.3.4.2 Grouping

In the model, a grouping behaviour operates on all herds at any given time step over the entire simulation period. The grouping operator is a rule-based management scheme which is followed by all herds of the respective type. In the model, it simulates the different management characteristics of the herds present in Kerry. It determines, for example, how long herds of a certain type keep youngstock, at what age they sell them, and whether herds maintain themselves through breeding of their own replacement females or by purchase. Table 1.5 provides an overview of the management rules for all 16 herd types represented in the model.

Whenever an animal is born into a self-maintaining herd (see Table 1.5 for breeding herds), a decision is made on the basis of the sex and a defined probability (*proportion of female calves sold*) if the animal will be kept as a breeding animal. If the newborn is female and based on the *proportion of female calves sold* intended as a breeding animal, it remains in the herd, is reared and inseminated if age is at least *minAgeBreeding*. All male animals and females not needed for replacement get the *IsForSale* component attached and the age (in weeks) at which the animal is intended to leave the herd is drawn from a uniform distribution (*age to sell female calves* & *age to sell male calves*), provided for each self-calving herd type (see Table 1.5 for calving herds). As an example, dairy herds (D) sell all their male calves at between two and 13 weeks of age. In contrast, female calves not needed for replacement are sold at an age between four and eight weeks of age.

Male animals and females not needed for replacement are predominantly moved to store or fattening herds. In the model, these herds are non-breeding and non-calving, and therefore completely dependent on the purchase of animals. Store herds rear their purchased animals until they reach a certain age (*age to sell from store*) at which point they are sold as youngstock to fattening herds. The current number of animals in each individual herd and the actual number of traded animals emerges from the herd-management rules given in Table 1.5.

Table 1.5: Management rules characterizing differences in herd management among the 16 represented herd types. U(x,y) stands for a uniform distribution between the specified x and y values, here given in weeks. Abbreviations for herd type and trade cohort (supply/demand for) as in Figure 1.3. Parameters for the grouping submodel were chosen using expert knowledge and qualitatively refined in an iterative process using a technique called Pattern Oriented Modelling (POM) (described in section 2.5. in the paper).

Herd type	Breeding/ calving	Prop. of female calves sold	Age to sell female calves (weeks)	Age to sell male calves (weeks)	Age to sell from store	Supply for	Demand for
D	Yes/Yes	5%	U(4,8)	U(2,13)	-	CDM, CDF	-
DRm	Yes/Yes	15%	U(4,8)	U(13,104)	-	YFF, CDF	-
DnR_C	No/Yes	85%	U(4,8)	U(2,6)	-	CDM, CDF	PHD
DnR_nC	No/Yes	85%	U(4,8)	U(2,6)	-	CDM, CDF	PHD
BSW	Yes/Yes	60%	U(26,39)	U(26,39)	-	CBM, CBF, YFF	-
BSY	Yes/Yes	60%	U(60,104)	U(60,104)	-	CBF, YFF	-
BSY_nC	No/Yes	90%	U(52,78)	U(52,78)	-	CBF, YFF	PHB
BSB	Yes/Yes	-	-	-	-	-	-
BP	Yes/Yes	50%	U(78,104)	U(78,104)	-	CBF, PHB	-
Sbm	No/No	-	-	-	U(78,104)	YFF	CBM
Sbf	No/No	-	-	-	U(78,104)	YFF	CBF
Sbmx	No/No	-	-	-	U(78,104)	YFF	CBM, CBF
Sdm	No/No	-	-	-	U(78,104)	YFF	CDM
Rdf	Yes/No	-	-	-	-	PHD	CDF
M	Yes/Yes	-	-	-	-	YFF, PHD	-
F	No/No	-	-	-	-	-	YFF

1.3.4.3 Breeding

All animals eligible for breeding are subject to a breeding process that determines the future time point of conception. Cows and Heifers eligible for breeding are inseminated when the herd is in its breeding season (see *HerdManagement* component). Cows are bred if breeding success has not yet been determined and they have exceeded the waiting time after their last calving:

$$t \geq t_{conc} + \tau_{gest} + \tau_{wait}^{(?)} \tag{1.7}$$

where t is the model step, t_{conc} is the date of last conception, τ_{gest} is gestation length and $\tau_{wait}^{(?)}$ is the herd type dependent waiting time (either w_D or w_B). Heifers are eligible for breeding if their age is at least *minAgeBreeding*.

All eligible animals are inseminated and it is decided stochastically by drawing from a predetermined herd dependent probability (f_D or f_B) if breeding will be successful.

If breeding is successful, the state variable inseminationSuccess in the *AwaitsBreeding* component is set to *true* and the future time point of conception/successful insemination is drawn from the herd type dependent distribution cd_D or cd_B:

$$t_{conc} = t + bin \cdot \tau_{bins} + \lfloor U([0, \tau_{bin}))\rfloor \tag{1.8}$$

where bin is an index of the distribution $cd_?$, drawn with probabilities proportional to the values in the distribution list.

Animals with breeding success are converted to pregnant when the model step equals their insemination tick: $t == t_{conc}$. The *AwaitsBreeding* component is detached and the *IsPregnant* component is attached. The state variables dateOfConception fromt he AwaitsBreeding component is transferred to the IsPregnant component. Sex of the fetus is determined stochastically according p_{female}. Breed of the fetus is taken from the dam's breed, except for dairy herds.

For Irish dairy herds, artificial insemination has become the breeding norm on the majority of dairy farms in the Republic of Ireland. But also the breeding bull (a beef bull used for breeding purposes) remains an integral part of the breeding process in many farms. It is used after the breeding season to inseminate cows that have not become pregnant through artificial insemination. To cover this in the model, we have extended the breeding season of all dairy farms by the parameter *dairyBullBreedingDuration*. The fetus of all dairy animals that conceive during this extended period will be mixed, otherwise the dairy breed is assigned.

If the inseminated animal is in Cohort Heifer, it's Cohort is changed to HeiferBred. Animals without breeding success are converted to Cohort Fattener. Further, component *AwaitsBreeding* is detached.

Table 1.6: Model parameters related to breeding. All parameters were extracted from the analysis of Irish cattle birth data.

Parameter	**Symbol**	**Type**	**Description**	**Value**
probFertilityDairy	f_D	float	Fertility of animals in dairy herds	0.95
waitingTimeBreedingDairy	$\tau^{(D)}_{wait}$	int	Waiting time between calving and first breeding trial in dairy herds	4
distributionDairy	cd_D	List[float]	Distribution of conception time after waiting time in dairy herds	[0.1, 0.2, 0.3, 0.2, 0.1, 0.05, 0.03, 0.02]
probFertilityBeef	f_B	float	Fertility of animals in beef herds (B, BnF)	0.95
waitingTimeBreedingBeef	$\tau^{(B)}_{wait}$	int	Waiting time between calving and first breeding trial in beef herds	4
distributionBeef	cd_D	List[float]	Distribution of conception time after waiting time in beef herds	[0.1, 0.2, 0.3, 0.2, 0.1, 0.05, 0.03, 0.02]
probFemale	p_{female}	float	Sex ration: share of female calves	0.5
distributionBinSize	bin	int	Bin size of distributions (weeks)	3
dairyBullBreedingDuration	$dairyBullBreedingDuration$	int	Duration during which dairy herds use bull breeding (weeks)	4

1.3.4.4 Abortion

In the model, pregnant animals can abort their fetus. After successful breeding, abortion occurs with probability p_{abort}. In case of abortion, the time point is drawn uniformly distributed over the gestation length:

$$t_{abort} = t_{conc} + U([0, \tau_{gest}]) \tag{1.9}$$

where t_{conc} is the date of conception and τ_{gest} is the gestation length. When the date of abortion t_{abort} equals the current model tick, the *IsPregnant* component is removed from the entity and the *AwaitsBreeding* component is attached. Pre-calculation of abortion date is done for performance. The alternative way of stochastic evaluation of abortion per model step would require the generation of large amount of random numbers, which is computationally expensive.

Table 1.7: Model parameters related to abortion. Abortion probability extracted from Damman et al. (2015).

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Parameter	Symbol	Type	Description	Value
abortionProb	p_{abort}	float	Probability that a pregnant animal will abort during pregnancy	3%

1.3.4.5 Calving

In the model, each pregnant animal gives birth to a calf when model step

$$t = t_{conc} + \tau_{gest} \tag{1.10}$$

where t_{conc} is the date of conception of the pregnant animal and τ_{gest} is the gestation length.

Sex and breed of the calf are taken from *IsPregnant*.sex and *IsPregnant*.breed (set at successful breeding by the breeding submodel). The *AnimalBase* state variable dateOfBirth is set to the current model tick. *AnimalGroup*.herd is set to the dam's herd, and the calf is added to the herds list of animals (*HerdBase*.animals).

The BoHV-1 status of the calf depends on the BoHV-1 status of the dam. Generally, each newborn animal is born susceptible, but it can have maternally derived antibodies (*AnimalBohvEpiStat*.hasMab == *true*) if the dam is either primary or secondary infected during birth. Latently infected animals can also transmit maternally derived antibodies if their last epidemiological status change is smaller than $\tau_{durationMAB}$. All animals with maternally derived antibodies are seropositive.

Table 1.8: Model parameters related to calving. The duration during which an animal transmits MAB following primary or secondary infection was extracted from Lemaire et al. (2000) in accordance with expert advice.

Parameter	Symbol	Type	Description	Value
durationMAB	$\tau_{durationMAB}$	int	Duration (weeks) during which an animal transmits MAB following an epi. status change	13

1.3.4.6 Transports

Animal transports emerge from supply and demand, which emerges from the herd type specific management practices. At the animal level, the process of trade consists of multiple stages.

Whenever an animal is intended to leave a herd through the herd type specific management processes, a *ScheduledForSale* component is added to the animal giving information on the intended date of sale. When the date is approached the animal gets the *IsForSale* component making the animal enter a virtual open market. If the animal is not sold for a certain time, the animal is removed. The decision to which herd an animal is moved is managed by two submodels (demand & supply) that are explained in the following.

Demand At the beginning of the simulation, each herd is assigned a random week of the year (1-52) at which the herd is to estimate its demand. Based on this initial time, the herd will continuously calculate its demand with the frequency of the estimation interval.

For each herd to estimate in a step, the absolute demand for trade cohorts is estimated based on herd type, target size/breeders and the total number of animals or cows and bred heifers. For breeding herds the demand ($D_{breeding}$) is estimated as

$$D_{breeding} = n_{target} - (n_{cows} + n_{bredHeifers}) \tag{1.11}$$

while n_{target} is the desired number of target breeders (given in the initialization table) and n_{cows} and $n_{bredHeifers}$ the current number of cows and bred heifers, respectively.

Demand of non-breeding herds is calculated as

$$D_{nonBreeding} = n_{target} - n_{totalAnimals} \tag{1.12}$$

while *totalAnimals* refers to the total number of animals present in the herd while demand estimation.

A tolerance parameter is accounted for, targeting to produce fewer movements, but larger batches of animals, resulting in fewer trade partners per herd.

Supply In the model, supply of animals is generated by the herd type specific management rules (see Table 1.5). Animals are marked there as scheduled for sale and get the component *ScheduledForSale* attached. In this component the future tick of sale is given. When the date is approached the *ScheduledForSale* component is detached and the animal gets the *IsForSale* component. Then, the trading cohort is assigned based on the herd type of the source herd and an animal's sex and pregnancy status.

Trade The trade submodel simulates the open market to balances supply and demand between the modelled herds. For each herd in the model that supplies animals, supply batches are simulated in which all animals intended for sale (all animals that have the *IsForSale* component) are listed. A supply batch is the set of all animals that come from the same herd, and that are of the same trade cohort. A demand batch is the total demand of a herd for a trade cohort. Each batch (list) has a time stamp denoting the model tick of its first registration to, serving to calculate waiting time. For demand batches, a new time stamp is only assigned if demand was completely satisfied and the herd re- enters trade. For supply batches, the time stamp is updated every step to reflect the market entrance time of the longest-waiting animal.

At each simulation step, supply and demand batches are filtered for waiting time. Only batches waiting at least τ_{supply} or τ_{demand} weeks, respectively, are eligible for trade. Then, all eligible demand batches are processes in random order. For each demand batch, the following selection procedure is executed:

First, supply candidates are collected. This is done by randomly drawing from all supply batches (without returning). Each drawn batch is checked to be included based on demand and supply batch size. A particular supply batch is included with probability

$$P_{include=\left(1-\frac{|S-D|}{max(S,D)}\right)^{ex_{cand}}} \tag{1.13}$$

where S is supply and D is demand. Random drawing and checking of supply batches is continued until either n_{cand} candidates were collected, until $n_{cand}^{(max)}$ batches were checked, or until no supply batches to draw are available anymore.

Then, if any supply candidates were collected, one of them is selected for trade. Eligible candidates are ranked by decreasing batch size fit R_{batch} and increasing distance R_{dist}. A weighted rank sum is formed according

$$R_{sum} = (w_{batch} \cdot R_{batch}) + (w_{dist} \cdot R_{dist}) \tag{1.14}$$

and the best-ranked supply candidate (lowest R_{sum}) is selected for trade. The number of animals transported from supplier to demander is

$$n_{trade} = min\,(S, D + s_d \cdot \delta_{hs}) \tag{1.15}$$

where s_d is the target size of the demanding herd. n_{trade} animals are removed from the supply batch as well as from the supplying herd, and are subsequently added to the demanding herd. For each animal, the herd is changed to the demanding herd and component *IsForSale* is detached. For all supply batches, all animals are removed from the batch as well as the simulation if their waiting time exceeds a_{supply}.

For each demand batch with a waiting time of at least τ_{import}, or with a relative demand $d(c_{trade})$ of at least h_{import}, animals are cloned from randomly selected template animals to satify the absolute demand. This should reflect imports from outside the modelled region.

For the cloning of animals, a list is filled with references to animals from supply batches until at least $maxNumClones$ animals are in the list, or no more supply animals are available. These animals serve as templates for cloning, in order to generate imports. If less than $minNumClones$ animals are available, no import is possible for the trade cohort in this step. Otherwise, imports are performed.

Table 1.9: Model parameters related to transports. Parameters for the transport submodel were initially set using expert knowledge and then qualitatively refined using POM to adequately replicate the Irish cattle transport network (described in section 2.5. & 3.1.2. in the paper).

Parameter	**Symbol**	**Type**	**Description**	**Value**
waitingTimeSupply	τ_{supply}	int	Waiting time of supply batches before eligible for trade, in weeks	4
waitingTimeDemand	τ_{demand}	int	Waiting time of demand batches before eligible for trade, in weeks	4
maxAgeSupply	a_{supply}	int	Maximum individual waiting time on market (weeks)	10
numCandidates	n_{cand}	int	Maximum number of supply batch candidates to rate per demand batch	20
maxCandidates	$n_{cand}^{(max)}$	int	Maximum number of supply batches to consider as candidates	20
candidateFitExponent	ex_{cand}	float	Exponent to apply to batch size fit during candidate collection	2.0
distanceWeight	w_{dist}	float	Weight of distance in candidate rating	0.5
batchSizeWeight	w_{batch}	float	Weight of batch size fit in candidate rating	0.5
herdSizeTolerance	δ_{hs}	float	Maximum herd size overload when moving large supply batches	0.05
importTimeThreshold	τ_{import}	int	Maximum time demand batches wait before serving by imports (weeks)	26
importDemandThreshold	h_{import}	float	Maximum relative demand of batches before serving by imports	0.25
minNumClones	$minNumClones$	int	Minimum number of animals required for cloning for imports	10
maxNumClones	$maxNumClones$	int	Maximum number of animals required for cloning for imports	500

1.3.4.7 Infection

In the model, each individual animal is assigned to one of four BoHV-1 epidemiological states (see Figure 1.4). Healthy animals that have never been exposed to BoHV-1 are susceptible animals. If a susceptible animal becomes infected it enters the primary infection state and will be a lifelong carrier of the virus. The infectious period of a primary infected animal is two weeks. During this period the animal sheds high levels of virus and is highly contagious. After primary infection hosts recover and enter the latent infection health-state. Latently infected animals are still BoHV-1 positive but do not shed the virus. Latently infected animals can reactivate the virus, which causes a secondary infection. In the model the secondary infection period lasts for one week and affected individuals again pose a risk of infection to susceptible animals. After recovery from secondary infection, animals enter the latent infection health-state.

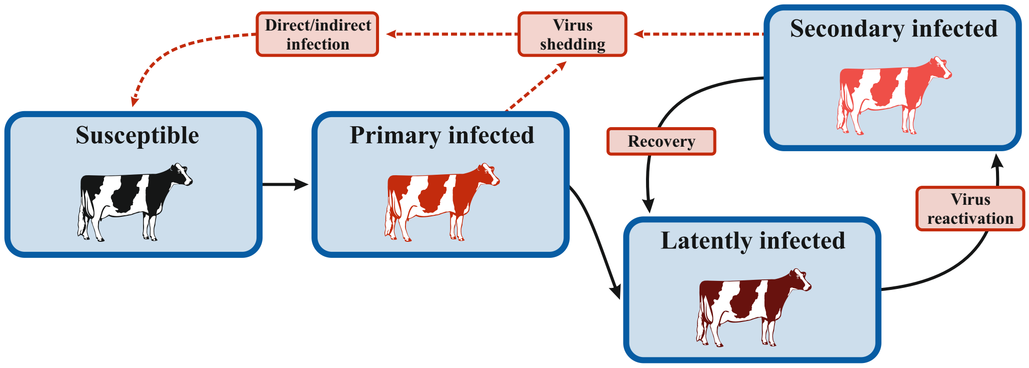

Figure 1.4: BoHV-1 epidemiological states in the model.

In addition to the epidemiological states, animals can have a certain level of protection due to maternal antibodies or vaccination. Even if animals have these level of protection, they can still become infected with the virus. In the model, these animals do also excrete virus, but to a lesser extent. Also the probability to which seropositive animals reactivate the virus depends on the level of protection.

Virus transmission The event of getting infected with BoHV-1 is modelled stochastically by means of a frequency-dependent transmission rate that is converted into an individual probability of getting infected. The frequency-dependent transmission rate accounts for the event of contracting the infection via direct contact and via the neighbourhood.

In the model animals of a herd are split into separate pastures. We assume that infection occurs within and between these pastures by primary and secondary infected animals. First, each herd counts its numbers of primary infected and secondary infected animals (including the vaccinated and those with maternal antibodies), total animals and seropositives, per pasture and in total, and writes them to the state variables of its HerdBohvStatus component. These are in the next stage used to calculate infection probabilities.

Then, each herd stochastically determines individuals to be infected according the following scheme: The herd sums up the number of PIs and total animal number in it's neighboring herds k for neighborhood infection.

Next, the herd iterates over all possible Pasture-to-Pasture combinations ij and calculates the individual probability of infection for each pasture i from animals in pasture j as a combination of three frequency-dependent transmission rates:

$$P_{inf,i} = 1 - \exp^{-(withinPool+betweenPool+betweenHerds))} \tag{1.16}$$

The $withinPool$ transmission rate describes the rate at which an individual receives the infection from its own pasture as follows, while pi_j, si_j, $piProtect_j$, $siProtect_j$ and n_j are the number of primary (protect) infected, secondary (protect) infected and total animals in pasture j.

$$\begin{aligned} withinPool = {} & \beta_{pi}^{(i)} \frac{\sum_j^{j=i\wedge p_{ij}} pi_j}{\sum_j^{j=i\wedge p_{ij}} n_j} + \beta_{si}^{(i)} \frac{\sum_j^{j=i\wedge p_{ij}} si_j}{\sum_j^{j=i\wedge p_{ij}} n_j} + \\ & \beta_{piProtect}^{(i)} \frac{\sum_j^{j=i\wedge p_{ij}} piProtect_j}{\sum_j^{j=i\wedge p_{ij}} n_j} + \\ & \beta_{siProtect}^{(i)} \frac{\sum_j^{j=i\wedge p_{ij}} siProtect_j}{\sum_j^{j=i\wedge p_{ij}} n_j} \end{aligned} \tag{1.17}$$

Transmission between different management groups (between cohort transmission) is only triggered by unprotected primary and secondary infected animals, calculated as follows:

$$betweenPool = \beta_{pi}^{(p)} \cdot \frac{\sum_j^{j\neq i\wedge\neg p_{ij}} pi_j}{\sum_j^{j\neq i\wedge\neg p_{ij}} n_j} + \beta_{si}^{(p)} \cdot \frac{\sum_j^{j\neq i\wedge\neg p_{ij}} si_j}{\sum_j^{j\neq i\wedge\neg p_{ij}} n_j} \tag{1.18}$$

In addition, between herd infection is modelled as:

$$betweenHerds = \beta_{pi}^{(h)} \frac{pi_{neigh}}{n_{neigh}} \tag{1.19}$$

Here, pi_{neigh} describes all primary infected animals in the neighbouring herds and n_{neigh} all total animals in the neighbouring herds.

In a last step, the herd iterates over all susceptible animals in all pastures i where $P_{inf,i} > 0$, and infects each individual with probability $P_{inf,i}$. Infected individuals are converted to primary infected animals.

Virus reactivation Latently infected animals have the potential to reactivate the virus which causes a secondary infection. Virus reactivation is simulated as a binomial random process, with a constant weekly reactivation probability calculated as

$$P_{reactivate} = 1 - (1 - r_{reactivattion})^{1/52} \tag{1.20}$$

with $r_{reactivattion}$ being the annual reactivation rate for animals in the latent infection state. The reactivation rate differs, depending on the protection level of the animals. Vaccinated animals or those with maternal antibodies have a lower risk of reactivating the virus, compared to those with no level of protection. Animals transports increases the reactivation probability by orders of magnitude.

Recovery Primary infected animals convert to latently infected animals $\tau_{primaryInfected}$ steps after infection. Secondary infected animals remain $\tau_{secondaryInfected}$ steps infectious before they become latently infected again. Animals with maternal antibodies loose their level of protection, if not vaccinated, when their age equals $\tau_{maternalAntibodies} + 1$ (in weeks).

Table 1.10: Model parameters related to infection. Reactivation rates were extracted from Noordegraaf et al. (1998, 2002); ? (?) and refined through calibration tests aiming to replicate pre-control prevalence by sectors. The beta values were determined by systematically replicating the reproduction ratios of primary and secondary infected animals in simulation experiments. The duration of the infectious period of primary and secondary infected animals was extracted from data retrieved from Bosch et al. (1997); Kaashoek, Van Engelenburg, et al. (1996); Kaashoek, Straver, et al. (1996).

Parameter	**Symbol**	**Type**	**Description**	**Value**
betaPrimaryInfectedWithin	$\beta_{pi}^{(i)}$	float	Trans. rate primary infected within pools	1.1
betaPrimaryInfectedBetweenPools	$\beta_{pi}^{(p)}$	float	Trans. rate primary infected between pools	0.6
betaPrimaryInfectedBetweenHerds	$\beta_{pi}^{(h)}$	float	Trans. rate primary infected between herds	0.02
betaPrimaryProtectInfectedWithin	$\beta_{piProtect}^{(i)}$	float	Trans. rate primary infected within pools (vaccinated)	0
betaSecondaryInfectedWithin	$\beta_{si}^{(i)}$	float	Trans. rate secondary infected within pools	0.6
betaSecondaryInfectedBetweenPools	$\beta_{si}^{(p)}$	float	Trans. rate secondary infected between pools	0.3
betaSecondaryProtectInfectedWithin	$\beta_{siProtect}^{(i)}$	float	Trans. rate secondary infected within pools (vaccinated)	0
probReactivation	$r_{reactivation}$	float	Yearly virus reactivation probability	4%
probReactivationProtected	$r_{reactivationProtected}$	float	Yearly virus reactivation probability (vaccinated)	0%
probReactivationAfterTransports	$r_{reactivationTransports}$	float	Reactivation probability after transport	20%
stepsInfectedPrimaryInfected	$\tau_{primaryInfected}$	int	Duration primary infection (weeks)	2
stepsInfectedSecondaryInfected	$\tau_{secondaryInfected}$	int	Duration secondary infection (weeks)	1
maxAgeMaternalAntibodies	$\tau_{maternalAntibodies}$	int	Maximal age of maternal antibody protection (weeks)	36

1.3.4.8 Mortality

The model accounts for a background mortality, representing all possible reasons for dead (natural death, culling etc.). Instead of evaluating mortality at each simulation step, life expectancy is calculated for each animal (whenever an animal is added to the system/model) based on the annual background mortality parameter $r_{mortality}$ as

$$LifeExpectancy = -\left(\frac{\log(x)}{r_{mortality}}\right) \tag{1.21}$$

with x being a random number between 0 and 1. If the calculated $LifeExpectancy$ exceeds a predefined threshold (see Table 1.1) a new life expectancy is calculated by a means of a new $r_{mortality}$. The $r_{mortality}$ parameter is chosen depending on the belonging of an animal to a certain age class and can be read from Table 1.11. The date of death is calculated accordingly and set in the *AnimalBase* component. If the current model step equals an animals date of death, the animal is removed from the engine.

Table 1.11: Model parameters related to mortality. Parameters were initially set using expert knowledge and systematically refined by fitting simulated herd type specific age structures to observed data. See also section 2.5 and 3.1.1. in the paper

Parameter	**Symbol**	**Type**	**Description**	**Value**
backgroundMortalityNewborn	$r_{newborn}$	float	Annual mortality rate of newborn animals	0.87
backgroundMortalityCalf	r_{calf}	float	Annual mortality rate of calfs	0.05
backgroundMortalityYoungstock	$r_{youngstock}$	float	Annual mortality rate of youngstock	0.05
backgroundMortalityAdults	r_{adults}	float	Annual mortality rate of adults	0.01
backgroundMortalityOldAdultsDairy	$r_{oldAdultsDairy}$	float	Annual mortality rate of old dairy adults	0.3
backgroundMortalityOldAdultsBeef	$r_{oldAdultsBeef}$	float	Annual mortality rate of old beef adults	0.05
backgroundMortalityFattener	$r_{fattener}$	float	Annual mortality rate of fatteners	3

1.3.4.9 Virus release

In the model, we released the virus by setting animals over 3 years old to latently infected in 60% of all herds (randomly selected). This was done to ensure a valid age-dependent prevalence in the herds and to reduce the burn-in period after virus release.

Bibliography

Bosch, J., Kaashoek, M., & van Oirschot, J. (1997). Inactivated bovine herpesvirus 1 marker vaccines are more efficacious in reducing virus excretion after reactivation than a live marker vaccine. *Vaccine*, *15*(14), 1512–7.

Brock, J., Lange, M., More, S., Graham, D., & Thulke, H. (2020). Reviewing age-structured epidemiological models of cattle diseases tailored to support management decisions: Guidance for the future. *Preventive Veterinary Medicine*, *174*(October 2019), 104814.

DAFM. (2017). *AIM Statistics Report 2017 (2018)* (Tech. Rep.). Retrieved from `https://www.agriculture.gov.ie/media/migration/animalhealthwelfare/animalidentificationandmovement/AIMStatisticsReport2017260618.pdf`

Damman, A., Viet, A. F., Arnoux, S., Guerrier-Chatellet, M. C., Petit, E., & Ezanno, P. (2015). Modelling the spread of Bovine viral diarrhea virus (BVDV) in a beef cattle herd and its impact on herd productivity. *Veterinary Research*, *46*(1), 1–14.

Grimm, V., Berger, U., Bastiansen, F., Eliassen, S., Ginot, V., Giske, J., … DeAngelis, D. (2006). A standard protocol for describing individual-based and agent-based models. *Ecological Modelling*, *198*(1-2), 115–126.

Grimm, V., Berger, U., DeAngelis, D., Polhill, J., Giske, J., & Railsback, S. (2010). The ODD protocol: A review and first update. *Ecological Modelling*, *221*(23), 2760–2768.

Grimm, V., Railsback, S., Vincenot, C., Berger, U., Gallagher, C., DeAngelis, D., … Ayllón, D. (2020). The ODD Protocol for Describing Agent-Based and Other Simulation Models: A Second Update to Improve Clarity, Replication, and Structural Realism. *Journal of Artificial Societies and Social Simulation*, *23*(2), 7.

Kaashoek, M., Straver, P., Van Rooij, E., Quak, J., & Van Oirschot, J. (1996). Virulence, immunogenicity and reactivation of seven bovine herpesvirus 1.1 strains: Clinical and virological aspects. *Veterinary Record*, *139*(17), 416–421.

Kaashoek, M., Van Engelenburg, F., Moerman, A., Gielkens, A., Rijsewijk, F., & Van Oirschot, J. (1996). Virulence and immunogenicity in calves of thymidine kinase- and glycoprotein E-negative bovine herpesvirus 1 mutants. *Veterinary Microbiology*, *48*(1-2), 143–153.

Lemaire, M., Weynants, V., Godfroid, J., Schynts, F., Meyer, G., Letesson, J. J., & Thiry, E. (2000). Effects of bovine herpesvirus type 1 infection in calves with maternal antibodies on immune response and virus latency. *Journal of Clinical Microbiology*, *38*(5), 1885–1894.

Noordegraaf, A., Buijtels, J., Dijkhuizen, A., Franken, P., Stegeman, J., & Verhoeff, J. (1998). An epidemiological and economic simulation model to evaluate the spread and control of infectious bovine rhinotracheitis in the Netherlands. *Preventive Veterinary Medicine*, *36*(3), 219–238.

Noordegraaf, A., Nielen, M., Franken, P., & Dijkhuizen, A. (2002). Simulation modelling of BHV1-control programme at national level, with special attention to sensitivity analysis. *Livestock Production Science*, *76*(1-2), 153–170.

Thulke, H. H., Lange, M., Tratalos, J. A., Clegg, T. A., McGrath, G., O'Grady, L., … More, S. J. (2018). Eradicating BVD, reviewing Irish programme data and model predictions to support prospective decision making. *Preventive Veterinary Medicine*, *150*(November 2017), 151–161.